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Short Communication

Veterinarians and Wildlife Biologists Should Join Forces to End Inhumane Mammal Trapping Technology.

Proulx G.

World Vet. J. 11(3): 317-318, 2021; pii:S232245682100043-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj43

ABSTRACT: Current mammal trapping standards uphold the use of inhumane trapping technology. For example, killing neck snares for the capture of canids, and rotating-jaw traps, and steel-jawed leghold traps for procyonids and mustelids, are being used by trappers despite decades of research showing that they are inhumane, and cause serious injuries and distress in captured animals. Many wildlife biologists unsuccessfully raised concerns about inhumane mammal trappings. This short communication stresses the need for veterinarians and wildlife biologists to work together to improve the fate of mammals captured in



Proulx G (2021). Veterinarians and Wildlife Biologists Should Join Forces to End Inhumane Mammal Trapping Technology. World Vet. J., 11 (3): 317-318.

killing or restraining traps, and modify mammal trapping standards on the basis of animal welfare science. **Keywords:** Humaneness, Mammal trapping, Traps, Trapping standards

[Full text-PDF] [XML] [Google Scholar]

Review

Stray Animal Population Control: Methods, Public Health Concern, Ethics, and Animal Welfare Issues.

Abdulkarim A, Goriman Khan MAKhB, and Aklilu E.

World Vet. J. 11(3): 319-326, 2021; pii:S232245682100044-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj44

ABSTRACT: Stray animal overpopulation has become one of the most serious global problems with many negative impacts on the community, environment, and public health. Most of the stray animals do not depend on humans for food and shelter, and therefore, can reproduce uncontrollably. The uncontrolled reproduction of stray animals increases their population that leads to a higher chance of predation, road traffic accidents, transmission of zoonotic diseases, and therefore, becoming vectors for some diseases. There are several methods for stray animal population control depending on the situation and the nature of the stray animals. These methods include contraceptives, trap-neuter-return, poisoning, euthanasia, and gun shooting among others. Each of the outlined methods has its advantages and disadvantages as to their practicality, ease of conducting, cost, effectiveness, ethics, and animal welfare issues. In conclusion, to achieve successful control measures of the stray animal population and the problem they create, the concerned authorities need to design and enact animal rights laws, provide medical



care (treatment and vaccination), feeding, shelter for the animals, and control their reproduction. Public health and environmental agencies may improve the services by regulating personal and environmental hygiene, prevention, and control of zoonotic and transmissible diseases that can be transmitted from stray animals to the public and other livestock respectively.

Keywords: Animal welfare, Ethics, Population control methods, Public health, Stray animals

[Full text-<u>PDF</u>] [XML] [Google Scholar]

Research Paper

Comparison of Painful Response to Mechanical Stimulation of the Plantar and Dorsal Surface of Paw Following Chronic Constriction Injury-induced Neuropathic Pain.

Ghanbari A and Mohammadi M.

World Vet. J. 11(3): 327-332, 2021; pii:S232245682100045-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj45

ABSTRACT: Mechanical and thermal stimuli were used to evaluate neuropathic pain-like behavior in animal models usually. Mechanical stimulation of paw plantar surface is commonly used to determine mechanical allodynia. In the present study, paw withdrawal response to plantar surface stimulation was compared with paw withdrawal response to dorsal surface stimulation. To this end, a total of 30 female Wistar rats (180-220 g), were assigned randomly to three groups as intact (without any manipulation), sham (incision of skin and muscles without nerve injury), and neuropathy (sciatic nerve lesion) with 10 in each group. To induction of neuropathy (chronic constriction injury), four movable ligations were established around the sciatic nerve using catgut chromic suture with a distance of one millimeter apart and then wound incision was closed. In the sham group, the incision site was closed without nerve ligation. Mechanical allodynia was examined by Von Frey filaments



Ghanbari A and Mohammadi M (2021). Comparison of Painful Response to Mechanical Stimulation of the Plantar and Dorsal Surface of Paw Following Chronic Constriction Injury-induced Neuropathic Pain. World Ver. J. 1 (18):327-332.

for four weeks. The findings indicated that the paw withdrawal threshold following dorsal surface stimulation was significantly reduced compared to the sham group at day 21 post-surgery. Moreover, paw withdrawal threshold following plantar surface stimulation significantly decreased compared to the sham group at day 21 post-surgery. The present results regarding the sham group showed that the paw withdrawal threshold after mechanical stimulation of the plantar surface was not significantly different from that of the dorsal surface paw. In addition, and there was no significant difference between the paw withdrawal response to plantar surface and dorsal one. In conclusion, paw withdrawal threshold to plantar surface mechanical stimulation was not significantly different from one in dorsal surface following neuropathic pain induced by chronic constriction injury.

Keywords: Mechanical allodynia, Neuropathic pain, Paw dorsal surface, Paw plantar surface, Rat

[Full text-PDF] [XML] [Google Scholar]

Research Paper

Isolation and Molecular Characterization of Fowl Adenoviruses Associated with Inclusion Body Hepatitis-hydropericardium Syndrome in Broiler Chickens in Egypt.

Al Naguib MG, Morsy EA, Samir M, Khattab MS, Khelfa DG, and Abdel-Alim GA.

World Vet. J. 11(3): 333-342, 2021; pii:S232245682100046-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj46

ABSTRACT: Avian adenoviruses are an extremely diversified group of pathogens that recently triggering a variety of problems for poultry production. In particular, Inclusion Body Hepatitis-Hydropericardium Syndrome (IBH-HPS), which has been observed in broiler birds from 3 to 6 weeks of age and is associated with anemia, hemorrhagic disorders, hydropericardium, and high mortality. The disease has been reported worldwide, and recently it was reported in many

Egyptian farms, causing severe economic losses. Therefore, the current study aimed to isolate, and genetically type the most common Adenovirus serotypes associated with this syndrome in Egyptian farms. A total of 50 broiler chicken farms (3-6 weeks old) located in different Egyptian governorates were examined. Macroscopically, the diseased flock revealed hydropericardium, enlarged friable livers with ecchymotic hemorrhages, and varying mortality rates 7.5%). (1 to Histopathologically, severe diffuse necrotizing enteritis, hepatitis, pericarditis, and diffuse lymphoid depletion of the spleen were the most prominent lesions. Liver tissues and cloacal swabs were collected from all examined flocks for FAdVs detection by conventional polymerase chain reaction (PCR) targeting the L1 loop in the hexon gene. The PCR products were sequenced for typing of the detected viruses. It was found that 10 out of 50 flocks examined were PCR positive for FAdVs (20%). Phylogenetic analysis of the sequenced genes revealed that the



Al Nagub MG, Mony EA, Samir M, Khattab MS, Khelfa DG, and Abdel-Alim GA (2021). Isolation and Molecular Characterization of Fow Adenoviruses Associated with Indusion Body Hepathis-hydropericardium Syndrome in Broile Chickens in Egypt. World WL 1, 11 (3):333-342.

obtained viruses clustered with reference strains belonging to FAdV type D and E serotype 2, 11, and 8a respectively. The isolation of both FAdV type D and FAdV type E were carried out on a primary cell culture chicken embryo liver cell (CEL) and the presence of these viruses was confirmed by PCR after the appearance of cytopathic effect (CPE). From this study, it could be concluded that both FAdVs types D and E are the most common adenoviruses circulating in poultry farms suffering from hydropericardium and inclusion body hepatitis.

Keywords: Broiler chicken, Chicken embryo liver cell, Fowl adenovirus, Hexon gene, Histopathology, Inclusion body hepatitis-hydropericardium syndrome, PCR

[Full text-PDF] [XML] [Google Scholar]

Research Paper

Molecular Identification of Trypanosoma theileri and Biology of Trypanosomes.

Fentahun T and Paeshuyse J.

World Vet. J. 11(3): 343-367, 2021; pii:S232245682100047-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj47

ABSTRACT: *Trypanosoma theileri* (*T. theileri*) is a non-pathogenic, cosmopolitan, and commensal protozoa of cattle. The main objective of the current study was to investigate the biology and feasibility of *T. theileri* as a model candidate for the discovery of a novel drug. In the present study, the isolates of *T. theileri* obtained from the Institute of Tropical Medicine (ITM) in SDM 79 were cultivated at 26°C. Eight experiments with different inoculum and different times were grown. The growth curve was plotted to check the growth trends. The doubling time in the logarithmic phase was determined to be 17.43 hours. In addition, an experimental infection was done on a 3-month-old Holstein Friesian calf to isolate the blood-streaming shape; however, it was not successful after the blood buffy coat smear and PBMC culture in RPMI 1640 and HMI 9. Furthermore, the viability was determined by quantitative



Fentahun T and Paeshuyse J (2021). Molecular Identification of Trypanosoma theileri and Biology o Trypanosomes. World Vet. J., 11 (3): 343-367.

colorimetric Resazurin assay in 96-well fluorescence Microplates containing 0.4 to 2.4 mM of Resazurin. On the other hand, the response to Pentamidine (1-100 ng/mL) showed a strong negative correlation between the fluorescence signal and the highest Pentamidine concentration. IC_{50} was 9.25 ng/mL. Genomic DNA was extracted using the phenolchloroform method. The gradient PCR amplification using *T. theileri* specific PCR (Tth625-PCR) primers was detected at 465 base pair (bp). In addition, the full-length 18S rDNA sequence was detected at 730 bp. In the silico analysis using common anti-trypanosome drug targets, no significant similarity could be found on either the DNA or the protein level. Nevertheless, homologous sequences have been identified among the drug targets for Ornithine decarboxylase. Therefore, the analysis might show the possibility of using *T. theileri* as a model for the search of new drugs once they have entire genome sequences. Analysis of the whole genome and transcriptome indicated a phylogenetic relationship between *T. theileri* and other pathogenic trypanosomes which can be the basis for novel drug development. **Keywords:** Drug model, Novel drug, PCR, Resazurin, SDM 79, *Trypanosoma theileri*

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Research Paper

Immunolocalization of Steroidogenic Enzymes (3 β -hydroxysteroid dehydrogenase, 17 β -hydroxysteroid dehydrogenase, and P450scc) in Rats with Testicular Dysfunction Treated with Mesenchymal Stem Cells-conditioned Medium.

Khasanah LM, Budipitojo T, and Fibrianto YH.

World Vet. J. 11(3): 368-376, 2021; pii:S232245682100048-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj48

ABSTRACT: About 60-80 million couples in the world are suffering from infertility disease. Infertility is a major problem in patients coping with chemotherapy. The chemotherapy process can degenerate non-target organs, especially in testes. Infertility in male or testicular dysfunction is caused by the failure of proliferation and differentiation of the spermatogenic cells. Many studies reported that mesenchymal stem cells-conditioned medium promoted regenerative processes. The present study aimed to investigate the effect of mesenchymal stem cells-conditioned medium on the cisplatin-induced testicular dysfunction by examining the immunolocalization of steroidogenic enzymes, such as 3β -hydroxysteroid dehydrogenase, 17β -hydroxysteroid dehydrogenase, and P450scc which are considered as markers of steroid production. All experimental animals were divided into three groups, namely the control



Khasansh LM, Badipitojo T, and Fibrianto YH (2021). Immunolecalization of Steroidogenic Enzymes (10-hydroxysteroid dehydrogenase, 170-hydroxysteroid dehydroaenaa and MOney) in Part with Tarticular Diselfaction. Teacher with Masarchanad Stars Collisconditional Medium. Work101, 17 (1): 583-756.

group, mesenchymal stem cells-conditioned medium treated group with an injection dose of 0.2 ml/kg body weight (BW, P1), and mesenchymal stem cells-conditioned medium treated group with an injection dose of 0.5 ml/kg BW (P2). Cisplatin was injected into both treated groups to induce testicular dysfunction. The testicular tissues were processed by the paraffin method, then cut to a thickness of 5 µm, followed by immunohistochemical staining. The HSD3B1 immunoreactivities were found only in Leydig cells, and the intensity increased every week after the injection of mesenchymal stem cells-conditioned medium. The variety of weeks and groups was significantly different in the number of immunoreactive cells of HSD3B1. The results indicated a significant difference between one week after the first injection and the one week after the third and fourth injection. The findings showed a significant difference between the treated group with an injection dose of 0.2 ml/kg BW and the control group. The number of immunoreactive cells of HSD3B1 and HSD17B1 increased every week. The p450scc immunoreactive cells were only found in Leydig cells of p450scc in the treated group with an injection dose of 0.5 ml/kg BW was greater compared to the group with an injection dose of 0.5 ml/kg BW was more intense, compared to the treated group with an injection dose of 0.5 ml/kg BW was more intense, compared to the treated group with an injection dose of 0.5 ml/kg BW was more intense, compared to the treated group with an injection dose of 0.5 ml/kg BW was more intense, compared to the treated group with an injection dose of 0.5 ml/kg BW was more intense, compared to the treated group with an injection of spermatogenic cells, and recover spermatogenesis proved by positive cells of HSD3B1, HSD17B1, and p450scc as markers of steroid production.

Keywords: Cisplatin, HSD17B1, HSD3B1, Mesenchymal stem cells-conditioned medium, P450scc, Testicular dysfunction

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Research Paper

The Influence of Basil Seed Hydroethanolic Extract on the Skin Wound Healing in Diabetic Male Rats.

Hadi M, Moghtadaei-Khorasgani E, and Etesamnia MH.

World Vet. J. 11(3): 377-383, 2021; pii:S232245682100049-11; DOI: <u>https://dx.doi.org/10.54203/scil.2021.wvj49</u>

ABSTRACT: Diabetic wounds and *cutaneous* wounds are important issues in medical science. Basil is an herbaceous plant and has compounds such as terpenes, flavonoids, and antioxidant properties. A total of 50 male Wistar rats were allocated into 10 groups including the healthy group

without treatment, the healthy group treated with 1% phenytoin, eucerin, 5% basil seed extract, 10% basil seed, diabetic group without treatment, 1% phenytoin, eucerin. After anesthesia of rats, we made a 4 cm2 wound on the back of the animal, and different histopathological characteristics were examined, and also on days 3, 7, and 21, the area of wounds was analyzed. In the healthy group treated with 10% basil seed extract, it was revealed that the wound size was significantly healed in the research days. In the diabetic rat groups, the decrease in the wound area was not significant and there was no significant difference between groups. Histopathological findings on day 21 in the healthy group treated with 10% basil seed extract revealed proper epidermis formation and relatively dense dermis containing collagen filaments. While in the diabetic groups, healing was slower. The results indicated that basil extract with anti-inflammatory antioxidant characteristics quicken and can the repair of cutaneous wounds. Keywords: Basil, Diabetes, Histopathology, Wound

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Research Paper

Concurrent Respiratory Disease in Broiler Chickens in Egypt during 2020.

Yehia N, Amer F, Samir A, Samy M, Sedeek A, Rebie N, Mohammed W, and Hagag N.

World Vet. J. 11(3): 384-394, 2021; pii:S232245682100050-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj50

ABSTRACT: Poultry production has been affected by multiple respiratory diseases triggering serious economic losses in Egypt. The current study aimed to investigate the situation and genetic evolution of respiratory diseases in Egypt during 2020. A total of 53 samples were collected from infected flocks suffering from respiratory signs and variable mortality rates from nine governorates in Egypt during 2020. The collected samples were examined for the detection of respiratory disease viruses (Avian influenza virus (AIV (H5N8, H9N2), Infectious bronchitis virus (IBV), and Newcastle disease virus (NDV)) by rRT-PCR. The single infection was confirmed in 90.6% (37.7% I.B, 30.2% AIV (H5N8), 9.4% I.B and 5.7% NDV) and co-infection of HPAIV (H5N8) + I.BV and LPAIV (H9N2) +IBV were detected in 3.8% of nine governorates. The HA gene of HPAIV (H5N8) was cluster to clad 2.3.4.4.1b in a new branch with characteristic specific mutations especially in T140A in antigenic site A



Yehia N, Amer F, Samir A, Samy M, Sedeek A, Rebie N, Mohammed W, and Hagag N (2021). Concurrent Respiratory Disease in Broiler Chickens in Egypt during 2020. World Vet. J., 11 (3): 384-394.

and R72S in the receptor-binding site, compared to A/duck/Egypt/F446/2017 with low A.A identity percent with vaccinal strains of H5N1 and H5N2 reaching to 91.9-94% and 84.6%, respectively. The HA gene of AIV (H9N2) belonged to A/quail/Hong Kong/G1/97-like virus clustered with group B with a specific mutation (212I) that may affect the human transmission of the virus. The HVRs of S1 gene of IBV cluster to GI23 (Egy Var I) clad with multiple mutations in HVR1 and HVR2, compared to IBV/CU/4/2014 and low identity percent (68.3-78.8%) with vaccine strains (H120, M41, 4/91). In conclusion, respiratory disease continues to circulate and rapidly evolve in Egypt during 2020. **Keywords:** HPAIV (H5N8), IBV, Genetic characterization, LPAIV(H9N2), Respiratory disease

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Research Paper

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Molecular Detection and Antibiotic Sensitivity of *Salmonella* Species Isolated from Goat Feces in Sylhet District of Bangladesh.

Sabur MA, Das MR, Uddin MB, Rahman MM, Islam MR, Chowdhury MSR and Hossain MM.

World Vet. J. 11(3): 395-401, 2021; pii:S232245682100051-11; DOI: <u>https://dx.doi.org/10.54203/scil.2021.wvj51</u>





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rst, second and third dishes are 5 minutes each: The steps were first absolute alcohol, 95, 100, 70 and distilled water, respectively, then staining hematoxis in the next age after washing with running water. Then impregnate with alcohol acid, rinns with nunning water and stain with osini dye to stain the cytoplasm. Then it goes rough the stages of alcohol 70, 80, 95% and absolute alcohol and its clarified agains with system its instructer.

ABSTRACT: The present study aimed at the molecular detection of *Salmonella* species from feces of goats and the characterization of the isolated *Salmonella* by biochemical and antimicrobial sensitivity techniques. A total of 220 goat feces samples were collected, of which 27 (12.27%) were positive for *Salmonella* by conventional culture methods and 20 (9.09%) by biochemical and PCR techniques. The prevalence was higher in goats under one year of age (20%), compared to older animals aged one to two years (7.8%) and more than two years of age (4.7%), respectively. Moreover, the prevalence of diarrheic goats was significantly higher (38.46%) than healthy animals (2.76%). DNA was extracted from *Salmonella* strains and amplified by PCR using the specific primers of *Salmonella* invasion gene (*invA gene*). The antibiotic sensitivity test indicated that Ciprofloxacin (100 percent sensitivity), Gentamycin (100 percent sensitivity), and Neomycin (100 percent sensitivity) were the most effective antibiotics for the majority of *Salmonella* isolates. On the other hand, *Salmonella* isolates were found to have substantially high resistance to Erythromycin (100%), Amoxicillin (100%), Trimethoprim-Sulfamethoxazole (81.48%), Streptomycin (62.96%), and Tetracycline (55.56 percent). Since the rate of *Salmonella* carriers was relatively high, eating goat meat could increase the risk of foodborne salmonellosis. **Keywords**: Antibiotic sensitivity, Goat isolation, PCR detection, *Salmonella*

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Research Paper

Antibiotic Resistance Profile of Escherichia coli Isolated from Bovine Subclinical Mastitis of Dairy Farms in Algeria from 2017 to 2019.

Ghallache L, Mohamed-Cherif A, China B, Mebkhout F, Boilattabi N, Bouchemal A, Rebia A, Ayachi A, Khelef D, Miroud K, and Ait-Oudhia Kh.

World Vet. J. 11(3): 402-415, 2021; pii:S232245682100052-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj52

ABSTRACT: Mastitis in cows is a major problem in dairy farms leading to a decrease in the quantity and quality of milk. The aim of the present study was to examine the association between the presence of *Escherichia coli (E. coli)* in milk and the subclinical mastitis, and to characterize the antibiotic resistance profiles of the isolated *E. coli.* In the current study, a total of 360 cow raw milk samples from three dairy farms of the region of Algiers were analyzed. The analysis period lasted from Spring 2017 to Winter 2019. The California Mastitis Test (CMT) was applied to detect subclinical mastitis. The *E. coli* strains were isolated from milk using conventional bacteriological methods. The antibiotic resistance profile of the isolated *E. coli* strains to 12 different antibiotics was tested using the disk diffusion method. On β -lactamase-producing strains, a double diffusion test was applied to identify the Extended-spectrum β -lactamase (ESBL) phenotype. Finally, the *ctXx-M* genes were



Ghallache L, Mohamed-Cherf A, China B, Mebkhout F, Bollattabi N, Bouchemal A, Rebia A, Ayachi A, Khelef D, Miroud K, and Air-Oudhia Kh (2021). Antibiotic Resistance Profile of Escherchic coll Isolated from Bovine Subclinical Mastitis of Dairy Farmis Antigeria from 2017 or 2019. World Vet. J. 1013;e0:2415-

amplified by PCR. Two-thirds (66.4%) of the milk samples were positive for the CMT test. A total of 97 *E. coli* strains were isolated from the milk samples, their resistance to antibiotics was tested, and 3.1% of the strains were resistant to trimethoprim-sulfamethoxazole, 6.2% to chloramphenicol, 12.3% to gentamicin, 13.4% to colistin, 23.3% to amoxicillin/clavulanate, 31.9% to kanamycin, 39.2% to enrofloxacin, 51.5% to cefotaxime, 52% to tetracycline, 57.7% to ampicillin, 74.3% to nalidixic acid, and 75.3% to amoxicillin. Furthermore, most of the *E. coli* strains (92.8%) were resistant to more than one antibiotic with a Multiple Antibiotic Resistance index ranging from 0 to 0.8. The 50 strains resistant to cefotaxime were analyzed for an ESBL phenotype. 39 of them (78%) were positive to the double-disk synergy test. Among the 39 ESBL positive strains, 27 (69.2%) were confirmed for the presence of a CTX-M gene by PCR. The present study showed that multiple drug-resistant *E. coli*, including ESBL-carriers, were frequently isolated from the milk of dairy cows in Algeria. The results underlined that the use of antibiotics on farms must be reasoned to avoid the spread of resistant strains in animals and human populations.

Keywords: Antibiotic Resistance, Cows, CTX-M gene, Escherichia coli, Milk, Subclinical Mastitis

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Research Paper

Effect of Larvicidal Extract N-Hexane Lime Leaves (*Citrus hystrix*) on Larva Instar III Mosquito (*Culex quinquefasciatus*)

Hanif M, Lastuti NDR, and Kurnijasanti R.

World Vet. J. 11(3): 416-421, 2021; pii:S232245682100053-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj53

ABSTRACT: *Culex quinquefasciatus* mosquitoes are a vector of transmission of several types of diseases, such as filariasis, Japanese encephalitis, and dirofilariasis. Larval control is the key strategy of disease control programs caused by vectors around the world because it can prevent larvae to enter the adult stage. Control of mosquito larvae that are often used is chemically controlled. Citrus hystrix is a natural plant and contains chemical compounds that have biological activity, such as flavonoids, carotenoids, and limonoids. The present study aimed to determine the effect of citrus leaf extract (*Citrus hystrix*) on the



Hanif M, Lastuti NDR, and Kurnijasanti R (2021). Effect of Larvicidal Extract N-Hexane Lime Leaves (Citrus hystrix) on Larva Instar III Mosquito (Culex quinquefasciatus). World Vet. J., 11 (3): 416-421. mortality of the larva *Culex quinquefasciatus*. The method used in the current study was a laboratory experimental study method with the experimental design using a completely randomized design. The research plot carried out was the rearing larvae of *Culex quinquefasciatus*, the manufacture of citrus leaf extract, the manufacture of larvicidal material, and the observation phase after treatment. Extract N-hexane *omplet name hystrix* leaf has high toxicity because it contains essential oils, flavonoids, alkaloids, terpenoids, saponins, and Limonoids. The Optimal concentration of N-hexane extracts of citrus leaves that lead to larval mortality of *Culex quinquefasciatus* in vitro amounted to 93.33% on 4 hours of observation with a concentration of 4000 ppm. Extract N-hexane lime leaf has a larvicidal effect on the larva *Culex quinquefasciatus* in vitro.

Keywords: Citrus hystrix, Culex quiquefasciatus, Extract, Mosquitoes, Larvicide

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Research Paper

Effect of Processed Lemon Pulp with Saccharomyces cerevisiae in Zaribi Goats Diet on Milk Production, Nutrients Digestibility, Blood Parameters, and Reproductive Performance

Sayed HAE, El-Maghraby MM, and Elbadawy MM.

World Vet. J. 11(3): 422-430, 2021; pii:S232245682100054-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj54

ABSTRACT: The aim of the present study was to evaluate the effect of replacing concentrate feed (CFM) mixture with different levels of treated lemon pulp (TLP) on milk production and composition, nutrients digestibility, and blood parameters of Zaribi goats. A total of 24 Zaribi female goats at the end of the pregnant period were divided into three groups of eight according to live weight. Concentrate feed mixture and clover hay at a rate of 50:50 were offered twice a day. Treatedlemon pulp replaced CFM at rates 0%, 25%, and 50 % in diets of R1, R2, and R3 treatment groups, respectively. The feeding trial lasted 90 days. Dry matter digestibility and Nitrogen free extract digestibility were significantly raised by the increased level of TLP in groups R2 (72.37% and 70.36%) and R3 (72.28% and 70.30%), compared to (70.99% and 68.51%) in R1, respectively. The same trend was observed for organic matter digestibility (OMD), crude protein digestibility (CPD), crude fiber digestibility (CFD), and ether extract digestibility (EED) with R3, compared with either R1 or R2. However, there were insignificant

Sayed HAE, El-Maghraby MM, and Elbadawy MM (2021). Effect of Processed Lemon Pulp with Saccharomyces cerevisiae in Zaribi Goats Diet on Milk Production, Nutrients Digestibility, Blood Parameters, and Reproductive Performance. *World Vet. J.*, 11 (3): 422-430.



differences between R1 and R2 in terms of OMD, CPD, and EED but CFD was significantly higher in R2, compared to R1. There was a significant increase in the milk yield by the increased level of TLP in the diet and for R2 (1448.4g/h/d) and R3(1558.7g/h/d), while it was reported as 1377.6 g/h/d in the control group. Feeding dams on the R3 diet had a significant effect on improving total antioxidant capacity by 63.5%, compared with control. The results of the present study indicated that the replacement of CFM by TLP decreased the costs of feed and increase milk production for the replacement level by 50% (R3). Moreover, no adverse effects were noticed on nutrients digestibility and blood parameters of the investigated samples.

Keywords: Blood parameters, Lemon pulp, Milk production, Saccharomyces cerevisiae

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Short Communication

The Effects of Different Concentrations of Bay Leaf Extract on Shelf Life of Preserved Scad Fish

Fuaidah P, Triastuti J, and Pramono H.

World Vet. J. 11(3): 431-438, 2021; pii:S232245682100055-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj55

ABSTRACT: Scad fish (*Decapterus kurroides*) is the most productive fish species. To provide the added value, fishermen can process scad fish into various forms of processed products, such as preserved fish, which extend the shelf life. In order to extend the shelf life of canned fish, natural preservatives could be used that contain antimicrobial agents, such as bay leaves. The present study aimed to determine the effects of bay leaf extract in different concentrations on the shelf life of preserved scad fish. In the present study, the completely randomized design was used as an experimental research method. The treatments given differed in terms of the concentration of the bay leaf extract. The groups were treated as the scad fish without bay leaf extract (A), scad fish soaked in 6% of bay leaf extract (B), scad fish soaked in 7% of bay leaf extract (C), scad fish soaked in 8% of bay leaf extract (D), and scad fish soaked



Fuaidah P, Triastuti J, and Pramono H (2021). The Effects of Different Concentrations of Bay Leaf Extract on Shelf Life of Preserved Scad Fish. World Vet. J., 11 (3): 431-438.

in 9% of bay leaf extract (E). The analyzed parameters included the total plate count, pH, and water level test using Analysis of Variance (ANOVA). The supportive parameters observed included an organoleptic test. The results indicated that the lowest total bacterial count from the beginning to the end of the experiment (18 hours) occurred on treatment C

(7% of bay leaf extract addition), which was 1.54×103 to 5.85×106 . Regarding the water level test from the beginning to the end of the experiment, treatment A (control) was not significantly different from other treatments. The difference in the concentration of bay leaf extract on scad fish effectively inhibited the growth of bacterial colonies. In conclusion, adding bay leaf extract to scad fish could inhibit bacteria for up to 12 hours. Treatment C (7% of bay leaf extract) gave the best results since this concentration level could inhibit the bacteria on scad fish. **Keywords:** Bay leaf, Preservation, Scad fish, Shelf life

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Research Paper

Effects of Laying Cycle Periods on Egg Quality, Egg Chemical Composition, and Reproductive Performance of Japanese Quail Breeders Reared in Northern Algeria

Berrama Z, SouamesS, Merati R, Korteby HM, Chirane MS, Negab N, Hettab K, Idris H, Morzouglal N, and Temim S.

World Vet. J. 11(3): 439-447, 2021; pii:S232245682100056-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj56

ABSTRACT: Egg quality traits in quail breeders depend on various factors which may influence embryo survival during incubation, affecting the chicks' production and quality. The current study aimed to determine the effect of the laying period on the external and internal quality of the egg, the chemical composition of albumen, yolk, and eggshell as well as the reproductive parameters of quail breeders. A total of 450 quails (*Coturnix japonica*) obtained from the same hatchery, were reared in a battery cage with a sex ratio of 1 male to 3 females. All the quails were subjected to standard breeding conditions and fed a balanced laying diet. A total of 960 eggs were collected at two different periods of the laying cycle, the beginning period of the laying (BP indicating 10 weeks of quail age) and the peak period of laying (PP showing 20 weeks of quail age).



Quail Breeders Reared in Northern Algeria World Vet. J. 11 (3): 439-447. <u>https://www.wvi.science-line.com/</u>

At each laying period, 30 eggs were used to analyze the various parameters of egg quality, and 450 eggs were randomly selected to assess the reproductive performances. Overall, no differences in the external quality of eggs, such as egg length, egg width, and the egg shape index, were recorded between the two laying periods. Apart from albumen weight that tended to be higher at the peak laying period, the shell and the yolk weights were not affected by the period of laying. Additionally, Japanese quail tend to deposit similar proportions of shell, albumen, and yolk at the two periods of laying. Likewise, the rate of dry matter of the three egg components, shell mineral concentrations, and yolk fat concentrations did not show any noticeable variation with the laying period. The most significant effect of the laying period was related to the potential reduction in the total protein content of the albumen and the yolk of eggs laid at the peak period of laying. Finally, the laying period did not significantly affect the fertility and hatchability rate of the incubated quail eggs but slightly improved the embryonic mortality rate during the peak laying phase. **Keywords:** Albumen, *Coturnix japonica*, Eggshell, Fertility, Quail

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Research Paper

The Role of Salinity in Histopathology Description of Jatim Bulan Tilapia Juvenile (*Oreochromis niloticus*) Exposed by Lead (PB)

Batista FR, Triastuti J, and Pursetyo KT.

World Vet. J. 11(3): 448-455, 2021; pii:S232245682100057-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj57

ABSTRACT: The decrease in the number of lands for aquaculture will cause the freshwater fish aquaculture, especially tilapia is reared. As one of the efforts to survive, the breeders use the coastal area to anticipate, so the freshwater fish can adapt to the sea waters. Heavy metal pollution near the coasts (or in the coastal waters) has great potential impacts on the environment. The present study aimed to find out the effect of Lead (Pb, heavy-metal) exposure on the Jatimbulan Juvenile tilapia with the different salinity towards histopathology description of the gill, intestine, and the skin tissues. The method used was an experimental method with a completely randomized design using six treatments and three times repetition. The observed parameters included the changes in histopathology description of gill, intestine, and skin organs of Jatimbulan juvenile tilapia. Kruskal-Wallis scoring method was used for data analysis



Histopathology Description of Jatim Bulan Tilapia Juvenile

and was continued by Mann-Whitney. The result of the current study showed the effect of salinity towards histopathology description of gill, intestine, and skin of Jatimbulan juvenile tilapia. The effect of changes was proven with the histopathology description in the form of the damage of edema, hyperplasia, and necrosis on the gill tissue; the damage of edema, atrophy, and necrosis on the gill tissue as well as the damage of edema, atrophy, hemorrhagic and necrosis on the gill tissue. From the result of the current study which has been conducted, it can be concluded that the heavy-metal exposure by lead was 0.03 ppm on the salinity of 10 ppt and 20 ppt. given the significant effect on the histopathology description of gill, intestine, and skin of Jatimbulan juvenile tilapia. **Keywords:** Histopathology, Lead, Metal, Oreochromis niloticus, Salinity

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Research Paper

In Vitro Antibiotic Activity of red Shallot (Allium ascalonicum), Mulberry (Morus indica), and Marigold (Tagetes erecta) Extracts against Streptococcus pyogenes

Mekvimol T, Chaipunna Ch, Poonthong G, and Pumipuntu N.

World Vet. J. 11(3): 456-461, 2021; pii:S232245682100058-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj58

ABSTRACT: Bacterial infection is a major global health concern. One of the critical problems is the widespread of antimicrobial-resistant bacteria from inappropriate and prolonged use of antimicrobial agents in both humans and animals. Plant extracts might afford the chance to replace antibiotic drugs and reduce the emerging of antimicrobial-resistant bacteria. This study aimed to examine the antibiotic activity of ethanolic crude extracts of some Thai medicinal plants grouping in their parts as whole onions of red shallot (*Allium ascalonicum*), petals of marigold (*Tagetes erecta*), mulberry leaves, and root barks (*Morus indica*) to inhibit the growth of *Streptococcus pyogenes*. The antibiotic activities of the crude extract of three Thai medicinal plants using absolute ethanol were trialed against *Streptococcus pyogenes* using the disk diffusion method. Erythromycin and Ceftriaxone discs were chosen to be positive control standards as the representative of antibiotic drugs. Each dried plant extracts was prepared to test the inhibition with a concentration at



Mekvimol T, Chaipunna Ch, Poonthong G, and Pumipuntu N (2021). In Vitro Antibiotic Activity of Red Shallot (Allium ascolonicum), Mulberry (Morus Indico), and Marigold (Tagetes erecta) Extracts against Streptococcus progenes. World Vet. J. 113:456-461.

25, 50, and 75 mg/mL stock solution. The results showed that three groups from all testing groups of Thai medicinal plant extracts had the potential of antibiotic activity against *S. pyogenes*. The highest antibiotic activity against *S. pyogenes* was detected from whole onion extract red shallot followed by the extract of the mulberry leaves and root barks of mulberry strain Nakhon Ratchasima 60 (Nak 60) while the extract of marigold petal did not present antibiotic activity. The results revealed that crude extract of those two Thai medicinal plants, including red shallot and mulberry, had antibiotic activity against bacterial growth of *S. pyogenes* in the experiment and these medical Thai plants had potential benefits for developing as alternative treatment agents for *S. pyogenes* infections in both humans and animals in the future. **Keywords:** Antibiotic activity, Ethanolic crude extract, Thai medicinal plants, *Streptococcus pyogenes*

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Research Paper

Controlling Food Poisoning Bacteria in Fermented Chicken Sausage Using Lactobacillus plantarum

Elsabagh R, Nada ShM, and Abd-Elaaty EM.

World Vet. J. 11(3): 462-468, 2021; pii:S232245682100059-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj59

ABSTRACT: Lactobacillus plantarum (L. plantarum) bacteria is generally recognized as safe and widely used in the food industry. The current study aimed to study the antimicrobial effects of L. plantarum against some food poisoning microorganisms, such as Staphylococcus aureus (S. aureus), Bacillus cereus (B. cereus), and Escherichia coli (E. coli) in oriental fermented chicken sausage for 18 days of storage at 4°C. The L. plantarum has broad-spectrum antimicrobial effects that enhance the quality and safety of food products. L. plantarum reduced the count of S. aureus, B. cerus, and E. coli to 1.54, 4.26, and 3.03 Log₁₀, respectively, after 18 days of refrigerated storage. Moreover, there were significant effects of L. plantarum on pH, thiobarbituric acid, total volatile basic nitrogen, and sensory attributes of fermented sausage samples during storage time. It was revealed that L. plantarum enhanced the physicchemical, sensory attributes, and shelf life of fermented chicken sausage. Moreover, L. plantarum inhibited the inoculated food poisoning bacteria



in fermented chicken sausage. In conclusion, it is recommended to use *L. plantarum* in fermented meat products as a starter and a bio-preservative to enhance the quality of the fermented chicken sausage. **Keywords**: Chicken sausage, Food safety, *Lactobacillus plantarum*, Probiotic

[Full text-<u>PDF</u>] [XML] [Google Scholar]

Short Communication

The Effect of the Different Artificial Insemination Time Periods on the Pregnancy Rate of Sapudi Ewes

Putri CD, Ismudiono, and Poetranto ED.

World Vet. J. 11(3): 469-473, 2021; pii:S232245682100060-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj60

ABSTRACT: Brucellosis Artificial insemination is required to increase the reproduction rate in ruminant breeding. The artificial insemination success rate in sheep only reaches 47.6%, whereas the proposed ideal rate is 70%. One of the factors influencing the artificial insemination success rates in sheep is improper estrus detection, resulting in no fertilization. The present study aimed to determine the effect of different artificial insemination time periods on the pregnancy rates of Sapudi ewes. The research design was based on a completely randomized design. A total of 20 female Sapudi sheep were divided into four treatment groups with five repetitions (for each group). In addition, the observed variables were artificial insemination time in Sapudi ewes.



Estrus synchronization in ewes was conducted by injecting PGF2a. The results of the research indicated that ewes subjected to artificial insemination 6, 12, 18, and 24 hours after estrus had a pregnancy rate of 20%, 100%, 60%, and, 60%, respectively. It can be concluded that the time differences in artificial insemination significantly influence the pregnancy rate in Sapudi ewes'.

Keywords: Artificial insemination, Estrus, Pregnancy rate, Sapudi ewes

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Research Paper

Milk Production and Reproductive Performance of Retained and Culled Cows in a Large Holstein Herd in Egypt

Fahim NH, Ibrahim MA-AM, Amin AH, and Sadek RR.

World Vet. J. 11(3): 474-483, 2021; pii:S232245682100061-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj61

ABSTRACT: The study aimed to identify the culling reasons of Holstein cows raised in a large commercial herd in Egypt with emphasis on the performance of retained and culled cows. A total of 31534 complete lactation records for 10994 cows calved from 2008 to 2019 were used. The overall rate of culling per lactation was 61.1%. Involuntary culling represented 92% of all culling cases. The reasons for culling included mastitis and udder problems (24.2%), reproductive disorders (18.7%), metabolic and digestive disorders (13.6%), lameness (13%), endemic diseases (10.8%), low milk yield (8.1%), respiratory diseases (4.3%) and unknown causes (7.3%). Means of 305-day milk yield and daily milk yield were significantly lower in culled cows than the retained ones. On the other hand, no significant differences were observed between culled and retained cows for days open and the number of services/conception.



The high involuntary culling rate of Holstein under the Egyptian conditions revealed that management practices regarding mastitis prevention and reproductive efficiency should be improved.

Keywords: Culling reasons, Egypt, Holstein, Milk production, Reproductive performance

[Full text-PDF] [XML] [Google Scholar]

Short Communication

The Effects of Borax $(NA_2B_4O_710H_2O)$ on Histopathology of Wistar Rats' Cerebrum (*Rattus norvegicus*)

Elfan F, Kuncorojakti S, and Triakoso N.

World Vet. J. 11(3): 484-488, 2021; pii:S232245682100062-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj62

ABSTRACT: The present study aimed to determine the effects of borax (Na2B407.10H2O) addition on the changes of histological cerebrum imaging in the brains of white mice (Rattus norvegicus). The current research was an experimental study with randomization of 24 white mice that were divided into four treatment groups with five replications. Borax was dissolved for each treatment with a dose of 19 mg/mouse/day, 26 mg/mouse/day, and 37 mg/mouse/day, and it was administered orally for 14 days. Then, it was analyzed statistically using the Kruskal-Wallis test. The statistical analysis results suggested that there were significantly different results in each treatment group. The control treatment with an administration dose of 26 mg/rat/day had a significantly different result in the worst cloudy swelling degeneration of





cerebrum in histopathology imaging on Wistar rats (Rattus norvegicus). Using the Mann-Whitney test, it was found that the dose of borax at 37 mg/rat/day led to significant difference, compared to the other treatment groups, which means that 37 mg/rat/day of borax caused the worst pyramidal cell necrosis in histopathology imaging of the cerebrum on white

mice. Borax exposure on Wistar rats (Rattus norvegicus) can cause cloudy swelling at a dose of 26mg/head/day, and pyramidal cell necrosis at a dose of 37 mg/head/day. **Keywords:** Borax, Cerebrum, Cloudy swelling, Necrosis

[Full text-PDF] [XML] [Google Scholar]

Research Paper

Evaluation of Milk Yield and Reproductive Performance of Pure Holstein and Its F1 Crossbreds with Montbeliarde in Egypt

Sadek RR, Abou-Bakr S, Nigm AA, Ibrahim MAM, Badr MM and Awad MAA.

World Vet. J. 11(3): 489-497, 2021; pii:S232245682100063-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj63

ABSTRACT: The present study was carried out to compare the milk yield and reproductive performance of pure Holstein (HO) cows with those of their first generation (F1) crossbreds with Montbeliarde cows (MO) in four commercial dairy herds under Egyptian conditions. Data used in the current study comprised 2268 records for the first four lactations of 531 HO and 536 MO × HO F1 crossbred cows during the period between 2012 and 2020. Data were analyzed using the least squares method by XLSTAT software. The MO × HO crossbred cows were significantly superior compared with pure HO cows for 305-day milk yield, scoring 9210 \pm 96 kg versus 7987 \pm 149 kg. Moreover, MO × HO F1 crossbred cows had a significantly higher daily milk yield (30.0 \pm 0.45 kg) than pure HO cows (25.9 \pm 0.52 kg). However, pure HO cows had significantly greater days in milk (399 \pm 6 days) than MO × HO crossbred cows (341 \pm 5.2 days). With regard to reproductive performance, MO × HO F1 crossbred cows had significantly less number of services per conception



and days open than pure HO cows $(2.6 \pm 0.16 \text{ vs. } 3.7 \pm 0.18)$ and $(132 \pm 5.2 \text{ days vs. } 190 \pm 6 \text{ days})$, respectively. However, the statistical difference between MO × HO F1 crossbred cows and pure HO cows for age at first calving was not significant $(22.9 \pm 0.11 \text{ vs. } 23.1 \pm 0.15 \text{ months}$, respectively). It can be concluded that under Egyptian subtropical conditions, the first generation of MO × HO crossbred cows exhibit better performance, compared to pure HO cows in milk yield and reproductive traits. These findings could provide an effective strategic option for the genetic improvement of dairy cattle in hot subtropical regions.

Keywords: Crossbreeding, Egypt, Holstein, Milk Yield, Montbeliarde, Reproduction

[Full text-<u>PDF</u>] [XML] [Google Scholar]

Short Communication

Intensity and Predilection of Helminth Parasites of the Red Snapper (*Lutjanus argentimaculatus*)

Prasetya AW, Kismiyati, and Subekti S.

World Vet. J. 11(3): 498-503, 2021; pii:S232245682100064-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj64

ABSTRACT: Marine fish, particularly the red snappers, are often exposed to helminth parasitic infestation. As a result of the parasitic infestation, the fish population, the fish weight, and the morphological changes in the fish are shrinking. The present research aimed to find out the intensity and predilection of the helminth ectoparasites over the infection of the red snapper (Lutjanus argentimaculatus) and employed the survey method for this purpose. The sampling was carried out by the purposive sampling technique. The sample obtained consisted of 30 fish, 20% of the total red snapper population of 150 fish reared in the floating net cages of Balai Besar Perikanan Budidaya Laut Lampung. The intensity of the fish infestation by a mixture of Haliotrema epinepheli and Benedenia epinepheli was 132.5 individuals/fish. Neobenedenia girellae and



Prasetya AW, Kismiyati, and Subekti S (2021). Intensity and Predilection of Helminth Parasites of the Red Snapper (Lutjanus argentimaculatus). World Vet. J., 11 (3): 499-503.

Haliotrema epinepheli infected fish with an intensity of 149.41 individuals/fish. The 66.7% of Benedenia epinepheli had a predilection for the dorsal fin, and 33.3% for the anal fin. In Neobenedenia girellae, 57.1% had a predilection for the body surface, 37.2% for the head surface, and 5.7% for the dorsal fin. In conclusion, all sampled fish were positively infected with helminth ectoparasites, including Neobenedenia girellae, Haliotrema epinepheli, and Benedenia epinepheli. **Keywords:** Ectoparasite, Helminths, Infestation, Red snapper

[Full text-PDF] [XML] [Google Scholar]

Research Paper

Cross Reaction of *Haemonchus contortus* Protein with *Toxocara vitulorum* Anti-L2 Serum Using Western Blot Technique

Asmorowati RW, Kusnoto, and Eliyani H.

World Vet. J. 11(2): 504-509, 2021; pii:S232245682100065-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj65

ABSTRACT: In the adult stage, *Haemonchus contortus* worms infect the abomasum host causing anemia and even death in animals. However, identifying the *H. contortus* protein can be used as a reference for the diagnosis of diseases. The diagnosis is performed by serological cross-reaction between *H. contortus* protein and anti-L2 *Toxocara vitulorum* (*T. vitulorum*) serum using the western blot technique. The main purpose of the current research was to identify the cross-reaction between *H. contortus* proteins and anti-L2 *T. vitulorum* serum using the western blot technique. The main purpose of the current research was to identify the cross-reaction between *H. contortus* proteins and anti-L2 *T. vitulorum* serum using the western blot technique. *T. vitulorum* worms were collected from the intestine of cattle and *H. contortus* worms were collected from the abomasum of goats. The first step was making antibodies by oral infection of rats with infective eggs (L2) of *T. vitulorum*. The blood was taken 21 days after infection. Then, the blood was centrifuged at 1500 rpm for 10 minutes to get the serum. The second step was making homogenates from the whole worm extract of *H. contortus*. After crushing the worms, it was centrifuged at



Asmorowati RW, Kusnoto, and Eliyani H (2021). Cross Reaction of Haemonchus contortus Protein with Toxocara vitulorum Anti-L2 Serum Using Western Blot Technique. World Vet. J., 11 (3): 504-

5000 rpm for 15 minutes and the supernatant was taken. The supernatant was then analyzed using Sodium Dodecyl Sulphate Polyacrylamide Gel Electrophoresis (SDS-PAGE) with coomassie brilliant blue staining. The third step was the analysis of *H. contortus* protein with serum anti-L2 *T. vitulorum* using the western blot technique. From the *H. contortus* homogenates analysis using SDS-PAGE, 16 protein bands were obtained. The cross-reactions were 141.3, 81.3, 64. 6, 51.3, 46.8, and 38 kDa. The data from cross-reactions suggested that the *H. contortus* protein cannot be used as a diagnostic material. It is serologically Haemonchosis because it caused false positives with diagnostic Toxocariasis. **Keywords:** Cross reaction, *Haemonchus contortus*, SDS-PAGE, *Toxocara vitulorum*, Western blot

[Full text-<u>PDF</u>] [XML] [Google Scholar]

Review

Archive

A Highlight on Avian Toxoplasmosis: One Health Disease with a Special Reference to the Current Egyptian Situation

Abd El-Ghany WA.

World Vet. J. 11(2): 510-520, 2021; pii:S232245682100066-11; DOI: https://dx.doi.org/10.54203/scil.2021.wvj66

ABSTRACT: This review article was developed to the infection of avian species with *Toxoplasma gondii* (*T. gondii*), diagnosis, pet bird and human infection, and control methods with a special reference to the current status of infection among the Egyptian poultry farms and population. Toxoplasmosis is a zoonotic disease caused by a unicellular, protozoan parasite *T. gondii*. Different domesticated and wild animals, as well as birds can harbor *T. gondii* and may be a potential source of infection to humans. Avian species could be infected with *T. gondii* through the ingestion of contaminated food, soil, and water with oocysts shed in the excreta of infected animals, especially cats. Poor sanitation and hygienic conditions increase the risk of infection. Consumption of food or water, as well as undercooked poultry meat or meat products containing the oocysts of the parasite, are the main sources of human infection with *T. gondi*. Diagnosis of *T. gondii* in the infected host depends on the serological detection of specific antibodies and molecular



detection of the parasite. Microscopic demonstration of the oocysts and other developmental stages of the parasite in the intestine, liver, brain, and skeletal muscles tissues is another means for rapid diagnosis. Generally, a high prevalence of the disease is also reported in pet birds. Toxoplasmosis in humans is associated with abortion, congenital disorders, stillbirth, and other complications, especially in immunocompromised patients. Application of hygienic measures, as well as public awareness, are essential for the prevention and control of toxoplasmosis. In different Egyptian governorates, a high prevalence of *T. gondii* has been detected in animals, birds, and humans. High incidence of infection was recorded due to the contact with *Toxoplasma* oocysts shed mainly from infected cats or other carriers. Egyptian chicken and turkey flocks and backyard birds revealed the presence of different developmental stages of the parasite and even its antibodies. In addition, human populations showed signs of toxoplasmosis with severe complications. **Keywords:** Bird, Egypt, Human, *Toxoplasma gondii*, Zoonosis

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Veterinarians and Wildlife Biologists Should Join Forces to End Inhumane Mammal Trapping Technology

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ABSTRACT

Current mammal trapping standards uphold the use of inhumane trapping technology. For example, killing neck snares for the capture of canids, and rotating-jaw traps, and steel-jawed leghold traps for procyonids and mustelids, are being used by trappers despite decades of research showing that they are inhumane, and cause serious injuries and distress in captured animals. Many wildlife biologists unsuccessfully raised concerns about inhumane mammal trappings. This short communication stresses the need for veterinarians and wildlife biologists to work together to improve the fate of mammals captured in killing or restraining traps, and modify mammal trapping standards on the basis of animal welfare science.

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INTRODUCTION

Trapping standards developed by the International Organization for Standardization (ISO) in the 1990s, the Agreement on International Humane trapping Standards (AIHTS) in 1997, and the USA Best Management Practices (White et al., 2021) are industrial standards to save the fur industry from trade bans (Proulx et al., 2020). These are sub-standard which do not meet, and have never met, state-of-the-art trapping technology and protocols associated with animal welfare (Proulx et al., 2020).

Red foxes (*Vulpes vulpes*), coyotes (*Canis latrans*), and grey wolves (*Canis lupus*) are snared annually in the fur trade or predator control programs in Canada and the United States (Iossa et al., 2007). However, nearly 40 years ago, Canadian researchers assessed the "humaneness" of manual killing neck snares, where the animal provides the energy necessary to tighten the noose and strangle itself, to quickly render red foxes irreversibly unconscious. They found that they could not cut off the airflow when the snare was held tight around the trachea (FPCHT, 1981). Less than a decade later, Proulx and Barrett (1990) showed that red foxes captured in power killing neck snares, where springs provide the energy to tighten the noose on an animal's neck, did not quickly lose consciousness. Finally, Proulx (2018) monitored a working trapline with remote video cameras and showed that a coyote and a wolf lost consciousness 14 hours 16 minutes, and 3 hours 39 minutes, respectively, after being captured in a manual killing neck snare. In both cases, animals struggled intensively and frequently, cut their tongue and gums, damaged their teeth, bled, and suffered from extreme swelling of the neck and head.

Killing neck snares are only examples of traps that are allowed in North America. Despite extensive research showing that rotating jaw-traps do not have the ability to quickly kill northern raccoons (*Procyon lotor*) (Proulx and Drescher, 1994), these traps have been certified (e.g., the Fur Institute of Canada, 2020) or accepted as Best Management Practices (AFWA, 2014). Likewise, steel-jawed leghold traps that seriously injure animals and cause them to self-mutilate (Proulx et al., 1993; White et al., 2021) are still being used in the United States.

Inadequate Mammal Trapping Standards

It is puzzling to see that traps that have been repeatedly found unacceptable for decades are still being used to capture mammals. Also, in most countries, animal anti-cruelty legislation is blatantly inadequate for wildlife. In the past, a handful of scientists have expressed opinions against inadequate mammal trapping standards and the use of trapping devices causing unacceptable pain and suffering (Iossa et al., 2007; Proulx and Rodtka, 2017; Proulx et al., 2020). Some environmental organizations have raised concerns but most of them are readily dismissed by government agencies (White et al., 2021).

In an effort to reform mammal trapping technology, and minimize harm to animals, veterinarians should join forces with wildlife biologists (Cattet, 2013). Wildlife biologists are responsible for the professional conservation and management of wildlife species and populations, and the wellbeing of individuals (Paquet and Darimont, 2010). The list

of injuries associated with trapping devices that are technologically outdated suffices to illustrate that animal welfare groups' concerns are neither exaggerated nor overemotional. When wildlife biologists and veterinarians remain passive and do not stand against cruelty in mammal trapping, they fail to act as professionals dedicated to the sound management of wildlife populations and the wellbeing of animals.

CONCLUSION

Inadequate mammal trapping standards uphold the use of inhumane trapping technology. Both veterinarians and wildlife biologists should take the lead in examining and modifying mammal trapping standards on the basis of animal welfare science.

DECLARATION

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I declare no conflict of interest.

Consent to publish

I agree with the publication of this paper.

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Stray Animal Population Control: Methods, Public Health Concern, Ethics, and Animal Welfare Issues

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ABSTRACT

Stray animal overpopulation has become one of the most serious global problems with many negative impacts on the community, environment, and public health. Most of the stray animals do not depend on humans for food and shelter, and therefore, can reproduce uncontrollably. The uncontrolled reproduction of stray animals increases their population that leads to a higher chance of predation, road traffic accidents, transmission of zoonotic diseases, and therefore, becoming vectors for some diseases. There are several methods for stray animal population control depending on the situation and the nature of the stray animals. These methods include contraceptives, trap-neuter-return, poisoning, euthanasia, and gun shooting among others. Each of the outlined methods has its advantages and disadvantages as to their practicality, ease of conducting, cost, effectiveness, ethics, and animal welfare issues. In conclusion, to achieve successful control measures of the stray animal population and the problem they create, the concerned authorities need to design and enact animal rights laws, provide medical care (treatment and vaccination), feeding, shelter for the animals, and control their reproduction. Public health and environmental agencies may improve the services by regulating personal and environmental hygiene, prevention, and control of zoonotic and transmissible diseases that can be transmitted from stray animals to the public and other livestock respectively.

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INTRODUCTION

Stray animals are un-owned domestic animals, particularly pets, such as cats and dogs (Sandøe et al., 2019). They mostly live independently, reproduce uncontrollably, overpopulate the environment, and often become a source of nuisance and global challenge to public health and environmental safety (Voslářová and Passantino, 2012). There have been many debates on the nature of stray animals especially animals' welfare and their problems in the community, such as hunting behavior, nuisance, and predating other livestock and poultry farms (Crowley et al., 2019).

It has been estimated that approximately 7.6 million pet animals enter into stray every year, of which about 3.4 million are cats (Statistics - National Kitten Coalition, 2020). According to the World Health Organization (WHO), the estimated number of stray dogs was approximately 200 million or more worldwide between 2009 and 2010 (Patti, 2011). With this number of strayed animals, four to five million are euthanized every year (Fournier and Geller, 2004). The abandoned pet animals neither affect their welfare nor pose a significant risk to public health and the environment. This condition makes them vulnerable to starvation, road transport accidents, diseases, and even death. Under some conditions, they may also harm the environment and native species through competition, predation, and spreading infectious diseases (Jessup, 2004). It has been observed that the stray animals in some communities are catered to by the residents who take care of and provide food and shelter for them (Centonze and Levy, 2002).

Animal professionals, such as veterinary doctors, animal scientists, and animal welfare officers have considered pet animal overpopulation as a people problem rather than an animal problem (Gerhold and Jessup, 2013). For the achievement of effective management of stray animals in an environment, there is a need to understand the relationship between the population of the strayed aminal and their impacts on a different dimension of the environments, and to know the way their relationship will be affected by other menace and environmental factors (such as climates) (Legge et al., 2017). It is difficult to estimate the number of stray animals in a community due to their high reproductive capacity. Under normal conditions, animals like dogs and cats with their puppies and kitten can make a population of more than a hundred in a year, this means that despite high mortality rates, their population can still be sustained (Stoskopf and Nutter, 2004). Highly adaptable, these animals thrive in environments ranging from villages up to metropolitan urban cities.

Different methods have been used to control stray animal populations for several years. These methods include poisoning, conducting Trap-Neuter-Return (TNR) programs, performing euthanasia using a high dose of anesthetic agents, such as a barbiturate, and administering some hormone-based contraceptive agents, such as progesterone (progestin) and testosterone propionate. Each of the outlined methods has its own advantages and disadvantages in terms

of their practicality, ease of conducting, cost, effectiveness, ethics, and animal welfare issues. Therefore, this literature review summarizes the impact of stray animals on the environment, the effect on the community and public health concern, and methods of stray animal population control with the ethics and animal welfare issues related to the different methods of stray animal population control.

Stray animals

Stray animals are free-roaming pet animals, especially dogs and cats that survive without human care and with an uncontrollable population increase. This condition leads to significant health and welfare problems for the animals concerning their public health and safety with environmental concerns (Fournier and Geller, 2004). Stray animals, such as dogs and cats, due to their predation nature may attract other wild predators, such as fox and coyotes, into society or community (Seimenis, 2004; Turner et al., 2012).

Stray animals are considered as one of the major public health problems worldwide in terms of their welfare and society. This concern mainly arises from the possible interactions of these strayed animals in many countries due to their interaction with people, especially children (Slater, 2001). Some may cause injuries to children through bites and scratches and may transmit zoonotic diseases. Interaction between humans and animals has been a common incidence over the past several centuries. Dogs play different roles in society, they act as pets, guards against thieves, crime detectors, runners, and hunters in champions, similarly, cats are also kept as pets and used for hunting rodents and reptiles that destroy properties at home (Bernstein, 2007).

It is essential to establish a long-term and sustainable approach to deal effectively with stray animal populations. The idea is to protect the people against those animals and safeguard the welfare and health of the animals. Experiences from the efforts in stray animal control show that effective control measures involve the adoption of more than one strategy. Among the strategies, western societies' concept of "ownership" is the most popular. This strategy focuses on a comprehensive, coordinated, and progressive program of owner education, mandatory registration and identification, environmental management, reproduction control of pets, and management of the animal population through regulated breeding and marketing (OIE, 2019). All these rules should be regulated by effective and enforced legislation. Implementing these rules successfully requires the cooperation and collaboration of more than one agency which in turn depends upon the willingness of government departments, municipalities, veterinary agencies, and non-government organizations (NGO's) to work together (Tasker, 2007).

Source of stray animals

In developing countries, many pet animals especially, cats and dogs, are abandoned on the streets and become part of a stray population. While in developed countries, stray cats and dogs are taken to animal shelters (Voslářová and Passantino, 2012).

Abandoned pet animals are increasing in number and have become a problem in many countries. Even though the proportion of the stray dog and cat population is not frequently measured, evidence shows that their numbers are increasing daily (OIE, 2019). The population density of the strayed animals may differ from the culture, habitat, and socio-economic conditions of the nation.

Stray dogs

Stray dogs are free-roaming dogs in communities that have become one of the major problems in society. They harm the environment and human health. Many studies have shown the important roles that pet animals are playing in the life of human being and dog is considered as one of the animals that kept as a pet in the past centuries (Ghasemzadeh and Namazi, 2015), but most of the pet dogs are going to stray due to owners cannot afford to take care of them. Many stray dogs roaming on the streets at night cause nuisance, defecate everywhere, scavenging on garbage, cause or get involved in road accidents, transmit diseases, and may die on the streets (Lyu, 2015). Stray dogs can cause an accident when running into the road, which might either result in injury to other people or themselves. Besides, stray dogs have become a threat to human lives and health by spreading deadly diseases, such as rabies. It had estimated by WHO that there are more than 200 million stray dogs worldwide, and every year 55000 people die from rabies transmitted by rabid dogs' bites (Chandran and Azeez, 2016).

Most of the dogs were considered as stray due to abandonment by their owners for some reason such as family immigration, diseases, and unbearable physiological behaviors of pets, no fund for treatment or feeding. Strayed dogs are facing many problems concerning their management. Sheltering alone cannot be an option for stray dog management because many conditions, such as feeding, disease treatment, annual vaccination and deworming, and appropriate quarantine require a lot of money to settle the conditions. In this regard, money and resources will never be sufficient to meet the sufficient demands for stray dog management (Lyu, 2015).

Dog population management (DPM) is an adaptable concept that aims to promote the health and well-being of stray dogs by minimizing the problems caused by the dogs while targeting to reduce their population size. Dog

population management can be achieved for many animal welfares, economic purposes, public health, and safety. These may be regulated through eradicating the transmission of infectious diseases and zoonotic diseases (especially rabies) by controlling dog bites or injuries to human beings and other animals, minimizing the occurrence of road or transport accidents, and reducing nuisance and fecal contamination of the environment caused by stray dogs during breeding (Taylor et al., 2017). In this regard, DPM programs have some goals depending on the conditions which may or may not be permanently limiting the size of the stray dog population. The means to achieve DPM objectives are planned to make a long-term positive impact on stray dog populations, in comparison to dog culling (Jackman and Rowan, 2007).

Stray cats

Stray cats, also known as feral cats, are free-roaming unowned cats mainly independent (Turner et al., 2012). The Feral domestic cat is one of the most challenging invasive species worldwide. The stray cat population has contributed to the extinction of some species of birds, such as Socorro dove (*Zenaida graysoni*) and Manx shearwater (*Puffinus puffinus*) among others, mammals, and reptiles in the environment which represent about 14% of modern extinctions in these vertebrate groups (Razgūnaitė et al., 2019). Many stray cats are roaming along the street, sometimes seen in restaurants, institutions, places of worship, and refuse dump looking for food. The same problem has also been observed in other developing countries (Legge et al., 2017).

It is difficult to estimate the number of stray cats in a community due to their high reproductive capacity. Cats are sexually mature by 5 to 6 months of age. Therefore, even with high mortality rates cat population can be sustained (Stoskopf and Nutter, 2004). The reproductive approaches, such as early sexual maturity, seasonally polyestrous cycling, and multiparous pregnancies, contribute to the prolific nature of the cat population (Kutzler, 2007). Highly adaptable, cats have thrived in environments ranging from villages, towns, and metropolitan urban cities (Legge et al., 2017).

Currently, the rate of cat eradication from society does not indicate significant changes in many societies where invasive cats are likely to challenge native wildlife (Medina et al., 2011). Therefore, to expand their biodiversity benefits, a new approach to cat eradication needs to be designed and implemented effectively. Furthermore, conservation biologists have a good understanding of and play an important role in the way stray cats impact native species of the environment (Medina et al., 2011).

Effect of stray animals on the community

The life activities of domestic animals mainly depend on their owners, which can be in form of personal ownership or a group of people in a community. Owners play an important role in the community or environments by regulating the management of pets (Taylor et al., 2017). In many cases, some of the owners may not afford to take care of the animals. These may pose any risk to the communities since they cannot maintain the well-being of the animals.

Due to the above conditions, pet animals are abandoned while roaming freely and join the stray population in the community and become a common source of spread of diseases to humans (zoonotic) and other pet animals across the community (Robertson, 2008). The main challenges and effects associated with stray animals on the community include predation, road traffic accident, defecation, urine spraying, nuisance, running and fighting during breeding, scavenging on open garbage and scattering all sealed refused, attacking people as in case of a rabid dog, soiling and threatening pet animals by attacking and biting (Trotman and Brown, 2007).

Stray animals and public health

Public health as a field of medicine is important because it comprises training in many fields and experience of working in teams with familiarity with interdisciplinary research. Stray animals are the major cause of public health problems and animal welfare concerns in any part of the world. Abandoned animals living in mass can reproduce and increase the number of the new stray animal population (Seimenis and Tabbaa, 2014). Public health plays an important role in minimizing stray animal overpopulation by controlling their reproduction, improving their health and well-being by vaccinating and treatment of sick ones among the animals, and increasing the responsibility by providing ownership to the animals.

The impact of public health on the occurrence of stray animals in both rural and urban areas includes the emergence and endemicity of many zoonotic diseases. Disease transmission from stray animals to humans and livestock depends on the nature of the countries, the climatic regions, and the health status and density of the human population (Robertson, 2008). Public health and epidemiology as disciplines are essential in understanding the impact of the stray animal population. The field of public health and epidemiology is critical in understanding the demographics, potential interventions, types of the problems, and required assessment of stray animal population control (Slater, 2001).

The Public health program will design control measures on stray animal populations and the spread of zoonotic diseases among the human population. These can be through public awareness of the harmful existence of stray animals in a society, public and environmental hygiene, controlling vectors that transmit the causative agents of the diseases, educating the public on zoonotic diseases, and performing measures to prevent and control the disease. The zoonotic

diseases of public health importance that can transmit to humans via stray animals include brucellosis, toxoplasmosis, rabies, campylobacteriosis, leishmaniasis, bartonellosis, salmonellosis, Pasteurellosis, and leptospirosis with others (Ghasemzadeh and Namazi, 2015).

The stray animal population control can be achieved by applying the aims of public health to determine why the animals are on strayed? Where are their sources? What are their populations? What are the problems they cause to people and livestock? Which way to evaluate and intervene in the situation and what are the costs to confront the situations (Slater, 2001)?.

Impact of stray animals on the environment

The impact of stray animals, especially dogs and cats, is more visible than other pet animals concerning the problems they create in the environment (Trotman and Brown 2007). Some species become tamed without showing fear of contact with humans and other domestic animals, which gives the chance of becoming the source of causing an effect on the environment and spread of infectious diseases (Seimenis and Tabbaa, 2014).

Stray animals also play an important role in transmitting diseases to humans and domestic animals through environmental pollution. These issues happen due to poor environmental hygiene and either directly from contact with feces (Traversa et al., 2014), urine, and other excretions from stray animals, or indirectly via infected or contaminated foods and food products obtained from diseased animals such as milk, and poorly prepared meat and meat products (Seimenis, 2004). Some Stray dogs and cats are scavenging around slaughterhouses for feeding, which may serve as an important source of disease transmission. In this regard, besides the control of scavenging stray animals, strict measures are to be taken by providing incinerators or disposal sites to prevent their access to the sources of infections, particularly the abattoirs and butcheries (Seimenis and Tabbaa, 2014).

Stray animals can become opportunistic predators (Medina et al., 2011) by attacking small animals, such as lizards, rats, and birds, and also by attracting other wild predators, such as fox, jackals, and coyotes into the environment (Turner et al., 2012) which can spread the impacts of predation across the environment (Dickman and Newsome, 2015). In an initial way, that was not the natural habitat of the ecological equations.

Ethics and animal welfare issues related to stray animal population control

To address the ethical issues and welfare of stray animals, there is a need to consider some factors, such as feeding, shelter, health care, and in some instant, their interaction with people (Briggs, 2013). The caretakers are expected to show sympathy and ethical concerns by providing the necessary care for the animals (Centonze and Levy, 2002). Neutering of stray animals improves their health and body score, minimizes roaming, and becomes friendly. It also observed that some offsprings of strayed animals die or disappear within some months of birth with trauma from children or other stray animals, starvation, disease, and mobile accident (Stoskopf and Nutter, 2004). Such conditions depend on geographical locations and other factors including weather and human population density. It is observed that the mortality rate of some stray animals was high, and the causes of death ranged from mobile accidents, poisoning, disease conditions, and attack from other stray animals that correspond with a poor standard of life (Aguilar et al., 2015).

The welfare of stray animals can vary noticeably. Some communities consider the elimination of stray animals as humane than allowing them to live a miserable life. Humanely considering stray animal population control, one method does not fit all the conditions due to their differences (Stoskopf and Nutter, 2004). Campaigning to educate and enlighten the public on domestic animal ownership responsibilities and their effects and implications of abandoning should be highlighted routinely (Param, 2016). Animal welfare agencies are the agencies that care and concern about the health and well-being of animals (domestic, wild, and stray). Some of these agencies include the American Society for the Prevention of Cruelty to Animals (ASPCA), Humane Society of the United States (HSUS) (Rowan and Kartal, 2018), International Fund for Animal Welfare (IFAW), Animal Welfare Institute, Animal Welfare Organization, Ipoh Society for the Prevention of Cruelty to Animals (ISPCA) (Param, 2016), World Animal Protection (WAP), International Animal Rescue, Global Alliance for Rabies Control, National Animal Welfare Trust among others. These agencies aim to control stray animal populations through enacting and enforcing appropriate policies that regulate humane animal population control and provide animal-control facilities. These include sterilization of all adopted animals. And the procedures require proper training, surveillance, and dedication from the staff and volunteers (Fournier and Geller, 2004).

The ethical approach for stray animal population control from both human and animal welfare points of view. The human welfare view usually focuses on the spread of zoonotic diseases and other effects caused by stray animals. The animal welfare view rests on the expectation that disease and death in uncontrolled populations of strayed animals cause suffering that prevails over the associated control programs (Kathy, 2006). These opinions are influenced by different views about the fundamental values related to suffering, freedom, and the existence of stray animals. The most used ethical way of resolving this issue is either by the humane killing of strayed animals (mostly euthanasia) or by controlling their reproduction (sterilization or neutering, OIE, 2019).

Methods of controlling the population of stray animal *Contraception*

Contraception is the method used to prevent the occurrence of pregnancy in female animals and can be achieved through the use of a medication, device, or procedure. Choices of contraceptive methods should address factors, such as efficacy, safety, availability, acceptance, and affordability (Bansode et al., 2019). Contraceptive agents can be used in different forms depending on the types (pills or injectable forms) and the method of use. Some contraceptive agents induce contraception by altering the hormonal activities, especially the hormone-based contraceptive like diethylstilbestrol, progestin, medroxyprogesterone acetate (MPA), proligestone (PROL), and mibolerone (Asa, 2018). While the use of implants is impaired through the use of an intrauterine device (IUD), such as the Depo-proveras and melengestrol acetate (MGA) implants (Boutelle and Bertschinger, 2010).

The use of the non-surgical contraceptive method is more accurate when owners request to breed their animals in the future (Massei and Miller, 2013) unless in the case of some diseases, such as rabies, where permanent sterilization is preferable. Most of the contraception techniques should be implemented by trained veterinarians, except for oral contraceptives. Most of the new devices are not licensed and require expert and trained personals to use them, and their cost is very high (Taylor et al., 2017).

Female animals treated with hormone-based contraceptives may experience some side effects, such as hormonal in-balance, uterine infection, pyometra, mammary tumor, diabetes mellitus, and other potentially life-threatening side effects that may arise from the drugs. Therefore, animals treated with hormone-based contraception require daily monitoring by veterinarians for the prevention of the mentioned complications (Asa, 2018).

The advantages of contraception include a longer duration before reverse, fewer side effects, suppression of sexual behavior, easy administration, a low cost, and also applicable for humans (Cathey and Memon, 2010). On the other hand, the disadvantages of this method are the need for repetition, quick reverse when discontinued using the repeated dose, possible slow onset of activity in some drugs, possible chance of a reaction at the injection site (Cathey and Memon, 2010).

Trap-neuter-return

Stray animal control population must require safety considerations for non-target animals and humans, be supported by municipal agencies or charitable organizations, including plans to reduce continuous stray dog and cat migration and reproduction, and be aesthetically acceptable to the public (Levy et al., 2003).

The considerable argument concerning the methods of controlling stray animals, particularly identifying the alternatives that are practicable, effective, and humane, TNR programs are designed to pause reproduction without causing harm to the animals (Scott et al., 2002).

In this method, animals are trapped, neutered, and returned to their previous habitat. The procedure is performed by veterinary surgeons through spaying the female animal or castration in a male animal. The concept of TNR as a humane method for stray animal population control is recommended by welfare organizations (Centonze and Levy, 2002). However, this method requires a regular surveillance and maintenance program that can be costly. The expenses of the TNR method depend on the level of resources that the stakeholders execute for the management of the problems.

Mostly, the ongoing costs of stray animal control through the TNR method will be high. The technique is expensive, inappropriate for large-scale implementation, and time-consuming, as well as requiring many expert veterinary surgeons (DEWHA, 2008). Other disadvantages of this method that may be encountered, in case of poor management after the surgery, there's a chance of some complications such as urinary incontinence and there will be an increase in the incidence of cystic, hematologic, and osteo-tumors (Scott et al., 2002). However, it has many advantages, such as producing complete sterilization, minimizing the incidence of sexual behaviors, and reducing the incidence of mammary, ovarian, and uterine tumors (Levy et al., 2003).

Euthanasia

The word euthanasia derived from a Greek called "safe killing" or "good death" is a humane method of killing animals through medical measures. It can achieve by administering a large volume of anesthetic agents such as barbiturates (Materstvedt et al., 2003), ketamine, a compound containing potassium (Harris, 2001) beyond accurate dosage. It is painless and induces rapid unconsciousness followed by respiratory and cardiac arrest, and finally causes death. In other words, it is the painless inducement of a quick death. The World Society for the Protection of Animals (WSPA) advocates that the killing of pet animals through euthanasia is a humane method and should be carried out only by trained professionals. The organization also accepts that euthanasia is humane and acceptable if the animal facing the hardship of life due to illness, injury, or behavioral problems, but WSPA avoided the use of euthanasia in healthy animals and considered it as cruelty (Veikune, 2014).

This method costs very high in many respects, concerning financing the officials that handle the activities, professionals that perform the euthanasia, the ideal way of disposing of the carcasses, and the workers that disposing of the carcasses. For many years, euthanasia has been desired as an alternative to deal with the overpopulation of pet

animals (Purswell and Kolster, 2006). Regardless of the technique used, it is good to reduce distress, anxiety, and pain by ensuring that the person who performs the euthanasia is well trained. Some of the euthanasia must use in combination with sedation before euthanizing the animal. The chemical agents used for euthanasia include Chloral hydrate, Formalin, Chloroform, Nitrous oxide, Ether, pentobarbital, and some neuromuscular blocking agents such as nicotine, potassium chloride, and magnesium sulfate (OIE, 2019). Based on the above conditions, euthanasia is a challenging method and is not suitable for controlling the stray animal population. It may help in reducing their populations, but should not be considered as an active measure for the control of the stray animal population. Besides, euthanasia is necessary for old age, seriously injured, and dying pets suffering from severe pain, but not suitable for healthy animals (Bartlett et al., 2005).

The advantages of euthanasia (OIE, 2019) as a method of control for stray animal populations include, it induces painless death without cruelness, not like poisoning, it is accepted ethically worldwide, the chemical agents are of low cost, and minimal materials are required.

Regarding the disadvantages, this method must be performed by an expert (OIE, 2019), is difficult for a large population, requires some chemical agents which are not always available, demands agents like barbiturate that have long withdrawal action may cause sedation or other complications to any predator that fed on the euthanized carcass, needs a large volume of the chemical agents for inducing euthanasia which may be expensive to perform (Purswell and Kolster, 2006).

Poisoning

Poisons are chemical substances that cause damages or harm to the organs, the system, or the body. It happens due to chemical reactions occurring when an animal absorbs or is exposed to the chemicals by a sufficient quantity. Poisoning has been one of the methods for the control of the stray animal population. The most commonly used chemicals are anticoagulants and Sodium monofluoroacetate (Sherley, 2004). The major problem associated with poisoning is that it is cruel, and animals suffer a painful and slow death (Robertson, 2008). The clinical signs associated with poisoning include excessive salivation, vocalization, vomiting, snapping and biting, diarrhea, nystagmus, twitching of facial muscles, pulmonary congestion, tremor, tonic convulsions with paddling of the limbs, and finally death due to cardiac and respiratory arrest (Sherley, 2004). Regarding risks of poisoning, it may affect other non-targeted species that may directly or indirectly be exposed to the poison in the targeted environment. Likewise, there will be a risk of human exposure to the poison, especially children who are close to animals on playgrounds (Lyu, 2015), for whom there will be a chance of being exposed to the poison, for this reason, it is not an ideal way of practice and must be abandoned. However, poisoning as a method of stray animal population control can be advantageous since it is easy and efficient, cheaper, and can be used in a large population, it has less labor-intensive than other techniques (Mitchell, 2011). However, it causes painful death, it is cruel compared to other methods, there is a risk to other non-target animals and human beings, mainly children, it has animal welfare implications (Mitchell, 2011).

Shooting

Shooting is another method of stray animal population control (McLaughlina and Aitken, 2011) that is quick, painless, and efficient. It can be achieved if the bullets hit the targeted animals. There is a challenge of handling a gun by everyone without government permission. Shooting stray animals on the street is dangerous and has many risks if the target missed and mistakenly hits people (Mitrofanova et al., 2018). In other cases, some stray animals may not die on shooting and stay alive with pain and injury for long. These cases are mostly considered inhumane and brutal acts. (Lyu, 2015).

The use of shooting as a method of stray animal control is beneficial since it is considered humane if used on target animals, is target-specific, can be used as clean-up techniques, is the fastest method of controlling rabid dogs, and it can be applied to other animals with the same conditions (Lyu, 2015). However, it requires a skilled and trained person to shoot, is dangerous to people and non-targeted animals, needs proper equipment, and may damage the brain if the animal was shot by the head, especially as in case of a rabid dog where the brain is required for the rabid test, can cause severe wounds and pain if the animal does not die by shot instantly, and it needs government approval before carrying out the operation.

CONCLUSION

Stray animal overpopulation has become a global challenge that requires immediate solutions to manage their population. The most common methods that are used for stray animal population control include surgical neutering (sterilization) and non-surgical contraception techniques. The non-surgical contraception methods entail immunocontraceptives agents and hormone-based contraceptives, while the surgical methods of controlling stray animals are through spying and castration of female and male animals, respectively. Other available control methods are trap neuter return, euthanasia, poisoning, trap and relocate, and gun shooting among others. To achieve successful control measures of stray animal populations and the problems they cause in a community or environment, the

concerned authorities have to design and enact animal rights laws. The law needs to address the feeding, shelter, medical care (treatment and vaccination), management, welfare, and legal rights of stray animals. To establish a prominent system of monitoring and management of the stray animal population, the community has to be educated about the problems that the animals are causing if they were on free-roaming and to provide a possible solution to the problem that may cause by the stray animals. Public health and environmental agencies may improve the services by regulating personal and environmental hygiene, prevention, control of zoonotic and transmissible diseases that can be transmitted from stray animals to the public and other livestock respectively.

DECLARATION

Authors' contributions

All authors contributed equally to this work.

Competing interests

The authors declare that they have no conflict of interest.

Ethical consideration

Ethical issues (including plagiarism, consent to publish, misconduct, double publication and/or submission, and redundancy) have been checked by the authors.

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ORIGINAL ARTICLE

Comparison of Painful Response to Mechanical Stimulation of the Plantar and Dorsal Surface of Paw Following Chronic Constriction Injury-induced Neuropathic Pain

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ABSTRACT

Mechanical and thermal stimuli were used to evaluate neuropathic pain-like behavior in animal models usually. Mechanical stimulation of paw plantar surface is commonly used to determine mechanical allodynia. In the present study, paw withdrawal response to plantar surface stimulation was compared with paw withdrawal response to dorsal surface stimulation. To this end, a total of 30 female Wistar rats (180-220 g), were assigned randomly to three groups as intact (without any manipulation), sham (incision of skin and muscles without nerve injury), and neuropathy (sciatic nerve lesion) with 10 in each group. To induction of neuropathy (chronic constriction injury), four movable ligations were established around the sciatic nerve using catgut chromic suture with a distance of one millimeter apart and then wound incision was closed. In the sham group, the incision site was closed without nerve ligation. Mechanical allodynia was examined by Von Frey filaments for four weeks. The findings indicated that the paw withdrawal threshold following dorsal surface stimulation was significantly reduced compared to the sham group at day 21 post-surgery. Moreover, paw withdrawal threshold following plantar surface stimulation significantly decreased compared to the sham group at day 21 post-surgery. The present results regarding the sham group showed that the paw withdrawal threshold after mechanical stimulation of the plantar surface was not significantly different from that of the dorsal surface paw. In addition, and there was no significant difference between the paw withdrawal response to plantar surface and dorsal one. In conclusion, paw withdrawal threshold to plantar surface mechanical stimulation was not significantly different from one in dorsal surface following neuropathic pain induced by chronic constriction injury.

Keywords: Mechanical allodynia, Neuropathic pain, Paw dorsal surface, Paw plantar surface, Rat

INTRODUCTION

Neuropathic pain is chronic pain, caused as a result of a lesion or disease of the central or peripheral nervous system. Spontaneous pain, allodynia (pain sensation following non-noxious stimuli), and hyperalgesia (exaggerated pain following noxious stimuli) are some of its signs (Ji and Suter, 2007; Popiolek-Barczyk and Mika, 2016; Carrasco et al., 2018). Despite several studies toward neuropathic pain treatment, no successful treatment has been presented so far (Kingery, 1997; Chanchal et al., 2016). Due to the ethical issues and the impossibility of creating a human model of pain, most of the available information is the result of research on animal models (Mogil, 2009; Deng et al., 2021), and a few available human studies have addressed people who have suffered from the pain caused by traumatic events. Since pain is a subjective matter and animals are unable to express it, the animal's response to the stimulus with behaviors, such as withdrawing the limb from the stimulus, does not necessarily mean pain-like behavior (Deuis et al., 2017), therefore, various methods have been introduced to evaluate pain-like behavior in animals, each of which has some advantages and disadvantages. However, there is a need to consider the benefits and drawbacks of each method to improve our understanding of pain.

There are different methods to determine pain-like responses in animals, including putting foot or tail in hot water, infrared radiation to paw plantar surface or tail, putting the animal on a hot plate device, clamping the skin with a certain amount of force, stimulating the plantar or dorsal surface of the paw or cheeks of the animal with polyethylene filaments, and applying pressure or pushing a sharp point object on the skin (Jensen and Finnerup, 2014; Deuis et al., 2017). Among the mentioned methods, mechanical stimulation of the paw plantar surface with polyethylene filaments is one of the most common methods used to evaluate mechanical pain in animals (Yam et al., 2020). In this method, the animal is placed in a cage with meshed metal floor and the researcher triggers the pain response by applying the Von Frey filament to the plantar surface of the paw (Jensen and Finnerup, 2014) which the animal responds by lifting and moving its foot away from the stimulus.

Recently, researchers have also used the dorsal surface of the foot to examine the response to mechanical stimulation. In each case, the animal is placed on a table and the researcher holds the animal with one hand and places

the filament on the animal's foot (the skin between the toes 2 and 3) to trigger a pain-like response by considering raising the leg as the criterion for pain (Ren, 1999; Safakhah et al., 2017; Pop et al., 2021). According to common methods, the plantar surface but not the dorsal surface, is used to determine thermal pain that may be different from the dorsal surface in point of withdrawal response to mechanical stimulus. Therefore, it is necessary to clarify whether the plantar surface of the foot is used to evaluate mechanical allodynia, and in others, the dorsal surface of the foot is used, so in the present study, the pain-like response of paw plantar surface was compared with that of dorsal surface in the chronic constriction injury-induced neuropathic pain in rats.

MATERIALS AND METHODS

Ethical approval

The present study was approved by the Ethics Committee of the Faculty of Medicine, Semnan University of Medical Sciences, Iran (Certificate Number: IR.SEMUMS. REC.1398.162). All experiments were performed in accordance with National Institutes of Health guidelines for working with laboratory animals. To minimize diurnal variations, all experiments were carried out between 2 and 5 PM.

Animals

In the present study, female Wistar rats, weighing 200 ± 20 g were housed in a place with controlled temperature $(22 \pm 2^{\circ}C)$, and 12 hours light-dark cycles were used. The rat fed and watered ad libitum. A total of 30 rats were divided into three groups of intact, sham, and neuropathy with 10 in each group. It should be mentioned that animals in the intact group did not receive the intervention (for comparison with the sham group to show the effect of incision on pain-like behavior). In the sham group (as the control group for neuropathy) only skin and muscles were incised while in the neuropathy [chronic constriction injury (CCI)] group, skin and muscles at the sciatic nerve were incised and sciatic nerve was sutured.

Neuropathic pain induction

Chronic constriction injury of the sciatic nerve was made using the method described by Bennett and Xie (1988). Animals were anesthetized using intraperitoneal injection of a mixture of ketamine hydrochloride and xylazine (80 and 10 mg/kg, respectively, Vafaei et al., 2020) and the upper right thigh was shaved and then a 2 cm incision was made in the place of the sciatic nerve. The sciatic nerve was exposed and separated from surrounding tissues. The nerve was ligated using four catgut chromic sutures 4/0, with a 1 mm distance between each and then the incision site was closed using silk suture 4/0. Animals in the sham group received surgery without nerve ligation. The rats were housed in individual cages until full consciousness was regained.

Evaluation of mechanical pain-like behavior

Mechanical allodynia was evaluated using Von-Frey filaments in the plantar and dorsal surface of the foot using methods described by Ren (1999), and Bennett and Xie (1988), respectively. Von-Frey filament is a polyethylene hair, which is calibrated according to its diameter. Each filament applies a certain amount of force to the surface on which it is pressed. The filaments are used increasingly from low strength toward stronger ones. Each filament was used 5 times with 10 seconds interval between each stimulation. If the animal responded to three consecutive stimulations, this force would be considered as the response threshold; and otherwise, the stimulation would be continued with the stronger filament. The experiments were performed first with the plantar surface as described by Bennett and Xie (1998) and then continued one hour later with the dorsal surface following the method proposed by Ren (1999). Pain-like behavior assessments were performed at the end of the first, second, third, and fourth weeks post-surgery. A force of 60 g was considered as the cutoff point.

Statistical Analysis

All data were analyzed using GraphPad Prism version 8.0 software (GraphPad, San Diego, CA, USA). Regarding the normal distribution of data (using the Kolmogorov–Smirnov test), two-way analysis of variance (ANOVA) and then Sidak's multiple comparisons test were used. All data were expressed as mean \pm SEM of the examined variable. P < 0.05 was considered statistically significant.

RESULTS

The obtained result showed that there was no significant difference between the intact and sham groups regarding the pain-like response to mechanical stimulation of the plantar and dorsal surfaces of the paw (p > 0.05). Moreover, the

withdrawal threshold following plantar surface stimulation was similar to the response of dorsal surface in both intact and sham groups (data not shown).

The current findings indicated that chronic constriction injury (CCI) significantly reduced paw withdrawal threshold following dorsal surface stimulation, compared to the sham group. The findings indicated that the paw withdrawal threshold significantly decreased during 21 days post-surgery (p < 0.05) and increased on day 28 in the CCI group, compared to the sham group (p < 0.05, Figure 1). Regarding plantar surface, the present results showed that paw withdrawal threshold following plantar surface stimulation significantly reduced in the CCI group during day 21 post-surgery, compared to the sham group, and continued to decrease until day 28 post-surgery (p < 0.05, Figure 2). Paw withdrawal threshold following mechanical stimulation of the plantar surface was not significantly different from that of the dorsal surface in the sham group (Figure 3).

In addition, in the sciatic nerve lesion group (CCI), there was no significant difference between the withdrawal responses induced by the mechanical stimulation of the plantar surface, compared to the dorsal surface response (Figure 4). Withdrawal response diagram following mechanical stimulation of the paw plantar and dorsal surface showed a downward trend from the seventh day following the injury and continued until the end of the experiment.



Figure 1. Withdrawal threshold following mechanical stimulation of the dorsal surface of the paw. Withdrawal response following mechanical stimulation of dorsal paw significantly reduced at third weeks in the neuropathy group, compared to the sham group, and continued to the end of the experiment (fourth week). Data are expressed as mean \pm SEM with 10 rats in each group. ** p < 0.01, *** p < 0.001



Figure 2. Withdrawal threshold following mechanical stimulation of the plantar surface of the paw. Withdrawal response following mechanical stimulation of paw plantar surface significantly reduced at third weeks in the neuropathy group, compared to the sham group and continued to the end of the experiment (fourth week). Data are expressed as mean \pm S.E.M. with 10 rats in each group. ** p < 0.01



Figure 3. Comparison of withdrawal response threshold following mechanical stimulation of the plantar surface and dorsal surface of the foot in the sham group. Paw withdrawal threshold following mechanical stimulation of the plantar surface did not show a significant difference, compared to the dorsal surface in the sham group. Data are expressed as mean \pm SEM with 10 rats in each group.



Figure 4. Comparison of withdrawal response threshold following mechanical stimulation of the plantar surface and dorsal surface of foot in the chronic constriction injury-induced neuropathy group. Paw withdrawal threshold following mechanical stimulation of the plantar surface did not show a significant difference compared to the dorsal surface in the neuropathy group. Withdrawal response diagram following mechanical stimulation of plantar and dorsal surface showed a downward trend from the seventh day following the injury and continued until the end of the experiment. Data are expressed as mean \pm SEM with 10 rats in each group.

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In the present study, the responses to mechanical stimulation of the plantar surface and dorsal surface of the foot following chronic constriction injury of the sciatic nerve were evaluated.

Comparison of animals' painful responses following mechanical stimulation of the paw plantar surface and dorsal surface in intact group and sham group showed that incision of skin and tissue around the nerve had no significant effect on the response to mechanical stimulation.

According to the present results, there was no significant difference between the withdrawal response of the plantar surface and dorsal surface due to mechanical stimulation of the plantar and dorsal surfaces following sciatic nerve injury. Several studies have been performed on different methods of determining pain in laboratory animals (Taiwo et al., 1989; Santos-Nogueira et al., 2012; Jensen and Finnerup, 2014; Deuis et al., 2017), however, there is no report about possible difference between the pain-like response due to plantar surface stimulation and dorsal surface stimulation in CCI-induced neuropathic pain rats.

The results of the current experiments showed that the withdrawal threshold following plantar surface stimulation was significantly different from the control group on day 21 after CCI, which was similar to the dorsal surface response. This result was in agreement with previous results indicating that two to three weeks after CCI surgery, the response threshold to mechanical stimulation significantly reduced, compared to the control group (Safakhah et al., 2016; Safakhah et al., 2017). The present results were also consistent with studies that showed two to three weeks after spinal cord injury; the paw withdrawal threshold significantly decreased, compared to the control group (Masri et al., 2009). Withdrawal response during plantar surface mechanical stimulation was not significantly different compared to dorsal surface stimulation in both the sham group and CCI group. This result was inconsistent with the results of Soignier et al (2011) indicating complete Freund's adjuvant (CFA)-induced pain which showed withdrawal threshold following dorsal surface stimulation was higher than the plantar surface threshold (Soignier et al., 2011). However, there were differences between the findings of the current study and those reported by Soignier et al (2011). Unlike neuropathic pain that was evaluated in the current study. Soignier et al (2011) assessed nociceptive pain. Furthermore, the current study examined pain-like behavior over a long period of time after the injury (at least 1 week), while Soignier et al (2011) evaluated pain behavior for a few hours following CFA administration. Finally, the method of pain induction in the current study was different from the method used by Soignier et al (2011).

Although there was no difference between the pain-like response following stimulation of the plantar surface and the dorsal surface of the foot, the determination of the pain-like behavior with the plantar surface method was associated with problems suggesting that the dorsal surface method was preferable. Pitcher et al. (1999) reported that the surface on which the animal stand can affect the animals' response by affecting sensory processing. They showed that if the animals' foot is on a wire mesh surface, determining the pain-like response from the plantar surface is associated with a lot of variation, whereas if a Plexiglas surface is used, this variation will be reduced. Given that in most cases, to assess the mechanical pain-like response, the animal is placed in cages with a wire mesh floor leading to a variety of responses, and then ambiguous and incorrect interpretations. Moreover, it has been reported that wire mesh floor possibly leads to tactile hyperstasis (Mizisin et al., 1998) which in turn affects the data.

It has also been reported that weight-bearing, which can be considered as pressure on the plantar surface of the foot, can be a confounding factor in assessing the pain-like response through the plantar surface (Kauppila et al., 1998).

According to the above reports, withdrawal response may be due to plantar surface stimulation could not be a result of von-Frey filament stimulation entirely, so part of which possibly is a result of tactile hyperstasia due to wire mesh floor contact. Possibly, discomfort due to the weight-bearing of the hind paws that are placed on the wire mesh can cause a change in sensory processing and create a non-pain response and thus mislead evaluating the pain-like response (Kauppila et al., 1998). Therefore, the observed reaction following the stimulation of the plantar surface of the foot is somewhat suspicious in comparison with dorsal surface stimulation. The following reasons, which are disadvantages of the plantar stimulation method for determining pain-like behavior, can further clarify the issue.

First, detection of withdrawal response through plantar surface stimulation takes a long time to stabilize the animal (in mice, it may take up to an hour, Minett et al., 2011), and therefore prolonged contact of the plantar surface of the foot with the wire mesh causes the animal to move. Second, the desired area for detecting withdrawal response may be covered by the wire mesh and thus the determination of pain from the same area may not be recorded in all animals (Pitcher et al., 1999). Third, moving the foot after one stimulation may cause the different area to be accessible and so the stimulation of the next time at the previous area is impossible and therefore creates a different response. In this regard, it has been reported that the thickness of the epidermis and CGRP-releasing fibers in the medial and lateral regions of the plantar surface are different from each other, and especially that surgical intervention increases the effect of filaments from the medial to the lateral (Duraku et al., 2012) which can lead to a different response. Moreover, there was a need to contact the filament perpendicular to the surface of the plantar surface of the animals' foot, so insufficient visual control of the desired position makes it impossible to stimulate the same area in all cases. In addition, the filament

may come in contact with the plantar surface of the foot suddenly or diagonally, which in both cases can cause scratches, and therefore the animal moves its foot away from the stimulus and this movement may consider as a pain-like response. Moreover, it is possible that repetitive stimuli may cause the animal to learn to move its foot away to prevent further stimulation and the inexperienced researcher may mistakenly consider this answer as a pain-like behavior. The fifth reason is that, in this method, a strong filament can move (raise) the foot and the researcher considers the observed response to be a pain-like behavior in the animal (Tal and Bennett, 1994; Xiao and Bennett, 1994; Ren et al., 1995). On the other hand, in the dorsal surface stimulation method, the withdrawal response following the stimulation is quite obvious and creates more confidence in the observed response as a pain-like reaction. This idea is consistent with Soignier et al (2011), who stated that the stimulation on the dorsal surface shows a much more accurate correct painful response (Soignier et al., 2011). According to the above-mentioned points, determining the pain-like behavior following stimulation of the dorsal surface can give a more obvious and acceptable criterion than stimulation of the plantar surface of the foot and increase the validity of the obtained data.

CONCLUSION

The pain-like response due to mechanical stimulation of the plantar surface of the foot is not significantly different from the response due to the stimulation of the dorsal surface, but assessing the pain-like response from the dorsal surface of the foot is easier and more reliable than the method of determining the response from the plantar surface.

DECLARATIONS

Authors' contribution

Ali Ghanbari designed the overall study and wrote the paper. Ali Ghanbari and Mohadeseh Mohammadi performed the experiment, collected, and processed the data. All authors discussed the results and commented on the manuscript. The final draft of the manuscript and statistical analysis were confirmed by the authors.

Conflict of interests

The authors declare no conflicts of interest in the present study.

Ethical consideration

Plagiarism, consent to publish, misconduct, data fabrication and or falsification, double publication and or submission, and redundancy have been checked by all the authors.

Consent to publish

Hereby, the authors agreed to publish the article.

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ORIGINAL ARTICLE

Isolation and Molecular Characterization of Fowl Adenoviruses Associated with Inclusion Body Hepatitis-hydropericardium Syndrome in Broiler Chickens in Egypt

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ABSTRACT

Avian adenoviruses are an extremely diversified group of pathogens that recently triggering a variety of problems for poultry production. In particular, Inclusion Body Hepatitis-Hydropericardium Syndrome (IBH-HPS), which has been observed in broiler birds from 3 to 6 weeks of age and is associated with anemia, hemorrhagic disorders, hydropericardium, and high mortality. The disease has been reported worldwide, and recently it was reported in many Egyptian farms, causing severe economic losses. Therefore, the current study aimed to isolate, and genetically type the most common Adenovirus serotypes associated with this syndrome in Egyptian farms. A total of 50 broiler chicken farms (3-6 weeks old) located in different Egyptian governorates were examined. Macroscopically, the diseased flock revealed hydropericardium, enlarged friable livers with ecchymotic hemorrhages, and varying mortality rates (1 to 7.5%). Histopathologically, severe diffuse necrotizing enteritis, hepatitis, pericarditis, and diffuse lymphoid depletion of the spleen were the most prominent lesions. Liver tissues and cloacal swabs were collected from all examined flocks for FAdVs detection by conventional polymerase chain reaction (PCR) targeting the L1 loop in the hexon gene. The PCR products were sequenced for typing of the detected viruses. It was found that 10 out of 50 flocks examined were PCR positive for FAdVs (20%). Phylogenetic analysis of the sequenced genes revealed that the obtained viruses clustered with reference strains belonging to FAdV type D and E serotype 2, 11, and 8a respectively. The isolation of both FAdV type D and FAdV type E were carried out on a primary cell culture chicken embryo liver cell (CEL) and the presence of these viruses was confirmed by PCR after the appearance of cytopathic effect (CPE). From this study, it could be concluded that both FAdVs types D and E are the most common adenoviruses circulating in poultry farms suffering from hydropericardium and inclusion body hepatitis.

Keywords: Broiler chicken, Chicken embryo liver cell, Fowl adenovirus, Hexon gene, Histopathology, Inclusion body hepatitis–hydropericardium syndrome, PCR

INTRODUCTION

Adenoviruses (AdVs) belong to the family Adenoviridae which are non-enveloped double-stranded DNA viruses. This family is distributed worldwide and has been recently classified into five genera, including Aviadenovirus, Mastadenovirus, Atadenovirus, Siadenovirus, and Ichtadenovirus (Hess, 2000). Virological analyses have enabled the division of the aviadenoviruses into five species of 12 serotypes (FADV-1 to FADV-8a and FADV-8b to FADV-11) based on genomic restriction digest patterns (FAdV-A to FAdV-E) (Hess, 2000). It has been shown that hepatitis inclusion body (IBH), hydropericardium syndrome (HPS), and gizzard erosion (GE) are the most common diseases associated with FadV infection in chickens (Mittal et al., 2014) The FAdVs' 12 serotypes have been associated with IBH outbreaks (Li et al., 2018, Chen et al., 2018). However, FAdVs type D and E including serotypes; FAV-2, -3, -11 and FAV-6, -7, -8a, -8b respectively, are the most common relevant isolates (Schachner et al., 2018a).

Recently, outbreaks of IBH-HPS have hit several countries over the globe such as Japan (Nakamura et al., 2011), Malaysia (Mohamed Sohaimi et al., 2019), China (Li et al., 2018), India (Raj et al., 2018; Suohu et al., 2021) Spain (Oliver-Ferrando et al., 2017), Iran (Morshed et al., 2017), South Africa (Maartens et al., 2014) and Saudi Arabia (Hemida and Alhammadi 2017). The disease mortalities reach 5-10% and may surge to 30% if it is co-infected with other immunosuppressive agents, such as Chicken infectious anemia virus CIAV and Infectious bursal disease virus (IBDV) (McFerran and Smyth, 2000). Moreover, virulent HPS caused by FAdV serotype 4 (FAdV-4) leads to high mortality varying from 30-70% (Mansoor et al., 2011; Schachner et al., 2018; Khan et al., 2019).

Grossly, the infected broilers revealed lesions in the liver and heart in the form of the enlarged, pale, friable liver with ecchymotic hemorrhages in addition to the accumulation of straw yellow-colored fluids in the pericardium (Schachner et al., 2018). Histologically, the most common findings were hepatitis, pancreatitis, nephrosis, thymic and bursal atrophy, and lymphoid depletion in the bursa and spleen. Basophilic and eosinophilic inclusion bodies of variable

appearance were recorded in liver infected with IBH and rarely in the kidney. Moreover, HHS syndrome results in inflammatory and degenerative lesions mainly in the heart, kidneys, lungs, and intestine (Schachner et al., 2018).

Polymerase chain reaction (PCR) using primers specific to L1 loop as the most conserved region in hexon gene is used for characterization of FAdVs. Hexon is the main adenovirus protein and is typically used to detect FAdVs molecularly. Further FAdV typing was carried out using restriction enzyme length polymorphism (RFLP) and/or DNA sequencing (Hess, 2000) In Egypt, FAdVs outbreaks have been reported and confirmed by the sequence analysis of the viruses in collected samples (El-Tholoth and Abou El-Azm, 2019; Radwan et al., 2019; Elbestawy et al., 2020). Therefore, the current study was conducted for isolation, molecular characterization, typing, and histopathological picture of the most recent FAdVs circulating in broiler farms suffering from IBH/HPS in different Egyptian governorates.

MATERIALS AND METHODS

Ethical approval

The procedures for chicken handling were carried out in compliance with the applicable legislation of the Institutional Animal Care and Use Committee of the Faculty of Veterinary Medicine, University of Cairo, Egypt (VetCU24112020261).

Sample collection

The examined farms were in Egypt at Menofya, Menia, Giza, Beheira, and Fayum Governorates during 2019-2020. Liver tissues and cloacal swabs were collected from 50 broiler chicken farms (5 birds from each farm with a total number of 250 birds as 200 freshly dead and 50 birds with severe clinical signs that were euthanized) with the age range of 3-6 weeks for the detection of FAdVs. In addition, the bursa of Fabricius was collected for the detection of IBDV. The pooled cloacal swabs from each farm were dissolved in 1 mL normal saline with a pH of 7.4 containing (1 mg/mL) streptomycin (50 μ g/mL) gentamycin and (100,000 IE/mL) penicillin. The liver and bursa tissue samples were collected in phosphate-buffered saline (PBS) then transported to the laboratory in an icebox. All samples were stored at -20 °C for further processing and virus detection. In addition to the tissue specimens that were collected for histopathological examination.

Preparation of collected samples

The collected cloacal swabs samples were centrifuged at $700 \times g$ for 10 minutes to clarify them. The collected supernatant was filtered by 0.2-µm pore size syringe filters. The pooled liver samples (5 from each farm) were ground by sterile mortar and pistol. A 20% (w/v) suspension was prepared using sterile saline solution. Centrifugation of the suspensions was carried out for 20 minutes at 2000 rounds per minute (r.p.m.) Collected supernatants were preserved at - 20°C till use. (Radwan et al., 2019)

Histopathology

Tissue specimens from the intestine, liver, heart, and spleen of chickens in suspected farms were fixed in 10% neutral buffered formalin. The tissues were dehydrated, cleared, embedded in paraffin, and sectioned by microtome into 4 μ m thick (Suvarna et al., 2018). Tissue sections were stained by hematoxylin and eosin stain, examined by a light microscope, and photographed by a digital camera (Olympus XC30, Tokyo, Japan).

Virus detection and Identification by PCR

Extraction of nucleic acid

The Genomic DNA isolation kit (Genedirex, Cat no. SN026-0100, Taiwan) was used to extract the total viral nucleic acid from $300 \ \mu$ L of the supernatant following the manufacturer's instructions.

Oligonucleotide primers

In this study, the forward (HexL1-s) and reverse (HexL1-as) primers corresponding to a conserved area in the hexon gene L1 region were used (Raue et al., 2005) and are listed in Table 1.

Target gene/Amplicon size	Primer name	Nucleotide position	Sequence	Reference
Hexon/589 bp	Hex L1-s	301-323	5-ATGGGAGSACCTAYTTCGACAT-3	(Raue et al. 2005)
	Hex L1-as	890-868	5-AAATTGTCCCKRAANCCGATGTA-3	(1440 01 41, 2005)

Table 1. Hexon gene L1 region primers sequence

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Polymerase chain reaction

Amplification of the target gene was achieved in a reaction volume of 25 μ L containing 5 μ L DNA template (congruent to 20% of the total reaction volume), 1 μ L of 10 μ M forward (HexL1-s) and the same of reverse (HexL1-as) primers, 12.5 μ L 2X One PCRTM polymerase chain reaction (PCR) master mix (One PCRTM, Genedirex; Cat. No. MB203-0100), and 5.5 μ L nuclease-free water. One initial denaturation cycle of 4 minutes at 94°C was required for the PCR cycling profile, followed by 35 amplification cycles of 45 seconds for denaturation at 94°C, 45 seconds for annealing at 51°C, and 1 minute for the extension at 72°C, and a final extension stage at 72°C for 10 minutes. In 1.5% agarose gel stained with ethidium bromide, the resulted amplified PCR products were electrophoresed and visualized under ultraviolet transillumination.

Sequence and phylogenetic tree analysis

The nucleotide sequence alignment was assembled and analyzed with representative reference to FAdVs strains' hexon gene sequences obtained from the GenBank database (http://www.ncbi.nlm.nih.gov/) using the NCBI BLAST server to confirm the identity with FAdVs strains. In BioEdit version 7.0.1.4 (Tom Hall, Ibis Biosciences, Carlsbad, CA, USA), sequences of FAdV hexon genes were downloaded from the NCBI GenBank and aligned using the Clustal W program. The subsequent phylogenetic analysis was carried out using Molecular Evolutionary Genetics Analysis version 6.0 constructed by the maximum likelihood approach based on the approximately 590-bp region corresponding to nucleotides 301-890 of the hexon gene and was used to demonstrate the clustering of the discrete species based on their hexon gene sequences. A similarity matrix has been created using the DNASTAR program (Lasergene, version 8.0).

Detection of concurrent infection with infectious bursal disease virus and chicken infectious anemia virus by conventional PCR

Detection of accompanied infections with infectious bursal disease virus (IBDV) and chicken infectious anemia virus (CIAV) was performed using the extracted viral DNA/RNA from the liver for CIAV and bursa of Fabricius tissues for IBDV from Adenovirus positive cases by conventional PCR assay as previously reported by Metwally et al. (2009) and Elbestawy et al. (2020).

Virus isolation on primary chicken embryo liver cells

Virus preparation

The supernatant of the collected FAdVs positive by PCR samples was passed through syringe filters with 0.2-µm pore size. Primary chicken embryo liver (CEL) cell was obtained from the liver of 15-day-old SPF embryonated chicken eggs (ECE) (Kumar et al., 2003).

Virus propagation

Flasks containing complete monolayer were washed two successive times with serum-free medium and inoculated with 0.1mL of the forementioned supernatant. For virus adsorption onto cells the inoculated flasks were incubated at 37°C for one hour then a maintenance medium containing 2% fetal bovine serum (FBS) was added. Daily observation of the inoculated cells for CPE was done using an inverted microscope during the first three successive days post-inoculation (pi). After obvious CPEs development, the flasks were harvested three times by repeated freezing and thawing before centrifugation at 216 x g for 10 minutes. Viral fluid was collected and stored at -20°C for further process. Complete monolayers were prepared for subsequent passage and inoculated with 0.1 mL of viral fluid. However, one monolayer was left uninoculated and was used as control cells (Mansoor et al., 2011)

Confirmation of fowl adenoviruses in cell culture by PCR

After the appearance of CPE in cell culture, the presence of FAdVs was confirmed by conventional PCR.

RESULTS

Clinical cases and gross lesions

During 2019-2020, 50 broiler flocks suffering from hydropericardium IBH syndrome in different governorates in Egypt were examined. The distribution and mortalities are summarized in Table 2 and Figure 1. Clear postmortem lesions in the form of a clear straw yellow serous fluid accumulation in the pericardium, swollen livers with necrotic foci, and petechial hemorrhages were observed (Figure 2).

Histopathological findings

Microscopy of the intestine showed severe diffuse necrotizing enteritis which was either acute or chronic according to the stage of infection. Intranuclear basophilic inclusion bodies were seen in infiltrating cells (Figure 3a, b, c). The hepatic lesions varied from vacuolation and necrobiotic changes to massive necrosis and dissociation of hepatocytes at the periphery of hepatic lobules with the presence of intranuclear eosinophilic inclusion bodies (Figure 3d, e, f). The heart had endothelial cell hypertrophy of blood vessels, pericarditis, degeneration of muscle bundles, necrotic foci with

mononuclear cells infiltration, edema, heterophils infiltration in between muscle bundles, and perivascular mononuclear cells infiltration in addition to the presence of intranuclear inclusion bodies in infiltrating leukocytes (Figure 3g, h, i). The spleen showed lymphocytolysis, lymphoid depletion, and reticular hyperplasia. Prominent intranuclear eosinophilic inclusion bodies were observed in lymphocytes and reticular cells (Figure 3j, k, l).

Virus detection by PCR

Ten out of 50 examined flocks were positive for FAdVs (20%). Positive samples with a DNA length fragment of 590 bp were detected from cloacal swabs and liver tissues (Figure 4). The percentage of positive flocks from different governorates is listed in Table 2. In addition, all FAdVs positive samples were negative for IBDV and CIAV by -PCR.

Table 2. Distribution of fowl adenovirus infections and mortality percentage in broiler flocks at different governorates in Egypt

Governorate	Number of	Number of Positive flocks	Type of sample		Mortality	Percentage of
	investigated farms		Pooled livers	Pooled cloacal swabs	(During the disease course, %)	positive flocks/ Governorate
Menofya	7	2 -	Positive	Negative	7.5	
	7		Positive	Negative	6.6	28.5
			Negative	Positive	3	
Fayoum	10	3	Positive	Negative	5	- 30
			Negative	Positive	2	
Menia	11	2 -	Negative	Positive	4	
	11		Negative	Positive	1	18.1
Giza	10	1	Negative	Positive	3.5	10
Dakhlya	6	1	Negative	Positive	4	16.6
Behera	6	1	Negative	Positive	2	16.6
Total	50	10	3	7	38.6	



Figure 1. Fowl adenoviruses distribution in broiler chickens at different Egyptian governorates (Blue points)

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Figure 2. Gross pathology of naturally infected chickens with Inclusion Body Hepatitis-Hydropericardium Syndrome. **a** and **b**: Hydropericardium with necrosis and enlargement of the liver. **c**: hydropericardium and nephrosis.



Figure 3. Histopathology of naturally infected chickens with Inclusion body hepatitis-hydropericardium syndrome. **a-c:** Chicken intestine, **a:** Chronic diffuse necrotizing enteritis (X100), **b:** Basophilic Intranuclear inclusion body (IN IB) (arrows) in the glandular epithelium, **c:** karyorrhexis in the glandular epithelium (X400). **d-f:** Chicken liver, **d:** Severe diffuse vacuolar degeneration of hepatocytes (X200), **e:** Necrobiotic changes and karyorrhexis of hepatocytes (arrow) (X400), **f:** Dissociation of hepatocytes with eosinophilic IN IB (arrow) (X400), **g:** Severe diffuse pericarditis (X100), **h:** Heterophils infiltration between muscle bundles (X200), **i:** Perivascular edema and perivascular mononuclear cells infiltration with eosinophilia in ib (arrow) (x400), **j-l:** Chicken spleen, **j:** Moderate diffuse depletion of white pulp (X200), **k:** Lymphocytolysis with small basophilic IN IB (arrow) (X400), **l:** Large eosinophilic IN IB in lymphocytes (arrow, X400, H & E stain).

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Figure 4. Visualization of 590-bp PCR product of hexon gene of FAdVs by agarose gel electrophoresis (1.5%) after staining with ethidium bromide. Lane M: 100bp DNA ladder, Lanes 1, 2: positive samples, Lane 3: Control negative, Lane 4: Control positive.

Phylogenetic analysis

A phylogenetic tree was created based on our sequences, and the reference strain's hexon gene sequences from different countries (Egypt, France, Brazil, Malaysia, China, Japan, and India) that were available on the GenBank (Table 3) to confirm the clustering of the various species. Phylogenetic analysis showed that the isolated FAdVs were classified as Fowl adenovirus type D serotype FAdV-2 and FAdV-11 in addition to Fowl adenovirus serotype FAdV-8a type E (Figure 5). Inter and intra-species analyses of genetic distance among the obtained sequences and other 14 aligned sequences available in the NCBI GenBank database of FAdV were performed (Figure 6). The genetic identity of FAdVs-type D had a high sequence homology (93.98% similarity) with the Indian FAdV type D, serotype 2 strains (MK816406.1 and MF770580.1) which previously has been isolated from liver tissues of broilers. On the other hand, the isolated FAdVs-type E viruses had a high sequence homology (99% similarity) with the Egyptian FAdV type E, serotype 8a (KT781516.1 and KT781517.1) that were isolated from cloacal swab samples of broiler chickens as illustrated in Figure 6. The partial hexon gene sequences of the two strains of FAdV-D and the FADV-E strain were submitted to the NCBI GenBank under accession numbers (MT386509.1, MT356630.1, MT893206.1, and MW847902), respectively (Table 3).

Virus isolation on cell culture

Three positive samples, including FAdV-D serotype 2, FAdV-D serotype 11, and FAdV-E (serotype-8a), were passaged on CEL. Different degrees of CPE on cell culture were observed in the inoculated cells as early as 24hr post inoculation after first passage with type E virus and after second passage from type D virus (Figure 7).

Accession No.	Country	Host	Sample type	Strain	Collection date
MT708028.1	France	Numida meleagri guinea fowl	Pancreas	Fowl aviadenovirus A (fowl adenovirus type 1)	2018
KT781516.1	Egypt	Chicken	Cloacal swabs	Fowl adenovirus 8a	2015
KT781517.1	Egypt	Chicken	Cloacal swabs	Fowl adenovirus 8a	2015
MN453821.1	Brazil	Gallus gallus with RSS	Intestinal content	Fowl adenovirus 8a	2010
MT127100.1	Malaysia	SPF Embryonated Chicken Eggs	-	Fowl adenovirus 8b	2017
MT127101.1	Malaysia	SPF Embryonated Chicken Eggs	-	Fowl adenovirus 8b	2017
MT561444.1	Malaysia	SPF Embryonated Chicken Eggs	Chicken embryo liver cell	Fowl aviadenovirus E	2019
MT233532.2	Malaysia	Broiler	Chicken embryo liver cell	Fowl aviadenovirus E	2017
MK816406.1	India	Gallus gallus	-	Fowl aviadenovirus D	2017
MF770580.1	India	Poultry	Liver	Fowl aviadenovirus D	2016
MH492324.1	Japan	layer chickens	Oviducts	Fowl aviadenovirus 4	2014
MH159176.1	China	Chicken	-	Fowl aviadenovirus 4	2008
MH159177.1	China	Chicken	-	Fowl aviadenovirus 4	2017
MT386509.1	Egypt	Broiler chickens	Liver tissue	Fowl aviadenovirus D	2019
	671			Serotype	Current study
MT893206.1	Egypt	Broiler chickens	Liver tissue	Fowl aviadenovirus D	2019
	871			Serotype	Current study
MT356630.1	Egypt	Broiler chickens	Liver tissue	Fowl aviadenovirus D	2019
	-8714			Serotype	Current study
MW847902	Egypt	Broiler chickens	Cloacal swabs	Fowl aviadenovirus E 8a	2019 Current study

Table 3. Reference isolates of Fowl aviadenovirus serotypes on GenBank and isolates of the current study

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Figure 5. Phylogenetic tree of the partial hexon gene fragment nucleotide sequences of our isolates and reference strains from the GenBank (accession number of the reference strain's hexon gene sequences were mentioned beside each nucleotide sequence)

									F	ercent	Identi	ty									
[1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18		
	1		57.8	57.8	58.0	57.2	57.2	57.2	57.2	57.2	56.8	60.2	57.0	60.2	60.2	56.4	56.4	56.0	57.6	1	MT708028.1_Fowl_aviadenovirus_A_strain_
	2	62.0		100.0	99.2	79.0	79.0	79.0	79.0	79.0	68.2	55.2	68.4	54.6	55.2	68.0	68.0	68.2	99.8	2	KT781516.1_Fowl_adenovirus_8a_isolate_M
	3	62.0	0.0		99.2	79.0	79.0	79.0	79.0	79.0	68.2	55.2	68.4	54.6	55.2	68.0	68.0	68.2	99.8	3	KT781517.1_Fowl_adenovirus_8a_isolate_M
	4	61.5	0.8	0.8		79.6	79.6	79.6	79.6	79.6	68.0	55.0	68.2	54.6	55.0	67.8	67.8	68.0	99.0	4	MN453821.1_Fowl_adenovirus_8a_isolate_U
	5	63.1	25.0	25.0	24.1		100.0	100.0	100.0	100.0	65.8	51.4	66.0	51.8	51.4	66.2	66.2	66.4	78.8	5	MT127099.1_Fowl_adenovirus_8b_isolate_U
	6	63.1	25.0	25.0	24.1	0.0		100.0	100.0	100.0	65.8	51.4	66.0	51.8	51.4	66.2	66.2	66.4	78.8	6	MT127100.1_Fowl_adenovirus_8b_isolate_U
	7	63.1	25.0	25.0	24.1	0.0	0.0		100.0	100.0	65.8	51.4	66.0	51.8	51.4	66.2	66.2	66.4	78.8	7	MT127101.1_Fowl_adenovirus_8b_isolate_U
8	8	63.1	25.0	25.0	24.1	0.0	0.0	0.0		100.0	65.8	51.4	66.0	51.8	51.4	66.2	66.2	66.4	78.8	8	MT561444.1_Fowl_aviadenovirus_E_isolate
lend	9	63.1	25.0	25.0	24.1	0.0	0.0	0.0	0.0		65.8	51.4	66.0	51.8	51.4	66.2	66.2	66.4	78.8	9	MT233532.1_Fowl_aviadenovirus_E_isolate
/erg	10	62.7	41.5	41.5	41.9	45.9	45.9	45.9	45.9	45.9		52.8	99.8	52.2	52.8	93.8	93.8	93.4	68.0	10	17_nonfunctional_hexon_gene_partial_seq
ă	11	51.0	62.0	62.0	62.5	71.5	71.5	71.5	71.5	71.5	69.2		53.0	96.6	100.0	52.4	52.4	52.4	55.0	11	MH159177.1_Fowl_aviadenovirus_4_strain_
	12	62.2	41.2	41.2	41.5	45.5	45.5	45.5	45.5	45.5	0.2	68.6		52.4	53.0	94.0	94.0	93.6	68.2	12	MF770580.1_Fowl_aviadenovirus_D_isolate
	13	51.0	63.8	63.8	63.8	70.6	70.6	70.6	70.6	70.6	70.8	3.7	70.3		96.6	52.6	52.6	52.6	54.4	13	2016_hexon_gene_partial_cds
	14	51.0	62.0	62.0	62.5	71.5	71.5	71.5	71.5	71.5	69.2	0.0	68.6	3.7		52.4	52.4	52.4	55.0	14	MH159176.1_Fowl_aviadenovirus_4_strain_
	15	63.7	42.0	42.0	42.4	45.2	45.2	45.2	45.2	45.2	6.6	70.2	6.4	69.8	70.2		100.0	99.6	67.8	15	MT386509.1
	16	63.7	42.0	42.0	42.4	45.2	45.2	45.2	45.2	45.2	6.6	70.2	6.4	69.8	70.2	0.0		99.6	67.8	16	MT356630.1
	17	64.7	41.5	41.5	41.9	44.8	44.8	44.8	44.8	44.8	7.0	70.2	6.8	69.7	70.2	0.4	0.4		68.0	17	MT83206.1
	18	62.4	0.2	0.2	1.0	25.2	25.2	25.2	25.2	25.2	41.9	62.5	41.5	64.3	62.5	42.3	42.3	41.9		18	MW847902
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18		

Figure 6. Similarity (percent identity) of L1 loop of the hexon gene sequences and their amino acids translate of FAV from broiler chickens in Egypt (representing numbers 15, 16, 17, and 18) as compared with the most similar reference sequences (GenBank).



Figure 7. Different stages of growth of FAdV on chicken embryo liver. **a:** Spindle shape of the liver cells. **b:** Cytopathic effect after 24 hours appeared as (small areas of cell death). **c:** large areas of focal cell death with the beginning detachment of the cells (CPE after 2 dpi).

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Over the past decade, inclusion body hepatitis-hydropericardium syndrome (IBH-HPS) has gained importance as one of the pivotal vertically transmitted diseases in broiler chickens that tackle the growing poultry industry all over the globe (Hafez, 2011; Shah et al., 2017; Schachner et al., 2018). In many countries, especially in Egypt, FAdV is considered to be the main pathogen within the first five weeks of broilers causing significant economic losses (Radwan et al., 2019).

In the current study, the examined flocks grossly revealed hepatic enlargement with pale pinpointed foci, liver ecchymotic hemorrhage, and straw-yellow fluid in pericardium up to 15 mL. In addition, nephrosis and enlargement of the spleen were noticed. These lesions resemble IBH-HPS findings previously described by (McFerran and Smyth, 2000; Hafez, 2011).

These gross lesions and mortality were attributed to the replication of FAVS in liver cells and extensive hepatic damage which leads to a decrease in the colloid osmotic pressure and increase of blood vessel permeability with a massive accumulation of fluid around the heart and finally cardiac tamponade and death (Niu et al., 2019). Histologically, degenerative and inflammatory lesions were recorded in the intestine, liver, pericardium, and heart with the presence of eosinophilic intranuclear inclusion bodies similar to previous studies (Steer et al., 2015; Niu et al., 2019; Radwan et al., 2019c).

Although it was assumed before that the heart was not the target organ of FAdV-4, severe pericarditis and heterophils infiltration were the most prominent lesions observed in the heart in the present study in addition to interstitial edema and widening of the gap between myocardial fibers (Niu et al., 2019).

Mortalities in the positive FAdVs tested flocks had a wide range from 1 to 7.5%. Variation in broilers mortalities due to IBH was recorded in many countries including Canada (Ojkic et al., 2008), Japan, Iran (Rahimi and Minoosh Siavosh Haghighi, 2015), China (Changjing et al., 2016), and Egypt (Hafez, 2011; Radwan et al., 2019).

IBDV and CIAV have been reported as common co-infection of FAdVs positive flocks which exacerbate the death rates as described by (Elbestawy et al., 2020). Despite this, there have been reports that IBH can cause mortality even when no other infective agent is present (Mohamed et al., 2018). Neither CIAV nor IBDV was detected in all FAdVs positive flocks in the current study. Therefore, FAdVs could be the primary pathogen responsible for mortality in the examined flocks.

Nevertheless, the clinical signs, post mortem lesions, and histopathology were highly indicative for FAdV infection, molecular detection by PCR assay was used to confirm the disease as previously reported earlier by (Raue et al., 2005; Günes et al., 2012; Mittal et al., 2014). By using the conventional PCR technique, only 10 out of 50 examined flocks were positive (20%) and this low percentage of virus detection by PCR may be interpreted by the usage of a conventional PCR in viral recognition, which is less sensitive in comparing with a real-time PCR (Günes et al., 2012). Only three farms were positive for liver tissue samples, and seven farms were positive for cloacal swabs. Consequently, sampling by cloacal swabs is considered better than liver tissues for detection of FAdv in broiler chicken, and this finding agrees with that recorded by (Radwan et al., 2019). In addition, FAdV virus isolation was carried out using primary CEL and cytopathic effects were noticed after 24 hours of virus inoculation in the form of cell rounding and small focal cells' areas detachment from the surface. Similar CPE in CEL of FAdVs was previously described by(Soumyalekshmi et al., 2014; Mohamed Sohaimi et al., 2019).

Further typing of the isolated viruses indicated that they are belonged to FAdV-type D serotypes 2 and 11, in addition to FAV- type E serotype 8a. The obtained sequences were clustered with fowl Adenoviruses strains isolated from Europe, Brazil, Malaysia, China, Japan, and India. Many countries all over the world reported detection of FAdV-D including Canada (Ojkic et al., 2008), South Africa (Maartens et al., 2014), China (Changjing et al., 2016), Poland (Niczyporuk, 2016), Lebanon (Shaib et al., 2017), Saudi Arabia (Mohamed et al., 2018) and Egypt (El-Tholoth and Abou El-Azm, 2019; Elbestawy et al., 2020). In addition, Radwan et al., 2019 previously detected two strains of serotype FAdV-8a (FAdV-E) in Egyptian chicken farms during 2015. These viruses had a high sequence homology with the viruses isolated during the current study that throws light on the nature, and resistance of adenoviruses over time.

Detection and characterization of FAdVs serotypes play a major role in epidemiologic studies of the disease spread, the development of preventative measures, and the application of vaccination programs. The current study spots light on the distribution and molecular characterization of FAdVs from cases of IBH-HPS that have been recently increased in broiler chicken flocks in Egypt and resulted in significant economic losses to the poultry industry.

CONCLUSION

In conclusion, the necessity to update the recent situation of Adenoviruses associated with hydropericardium syndrome in different broiler farms in many governorates in Egypt prompts us to conduct this study. Virus detection by PCR and sequence analysis indicated that both type D and type E adenovirus are the most common adenovirus associated with this syndrome in broiler farms in different governorates in Egypt. Further study will be conducted to study the pathogenicity of these isolated viruses in broiler chickens.

Ethical considerations

Ethical issues including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy have been checked by the authors.

Competing interests

The author has no conflict of interest.

Authors' contributions

DGK, MGA, EAM, and GAA contributed to the design of the study, sample collection, isolation, identification of the virus, sequencing, and sequence analysis. MS carried out virus isolation, identification, and titration on cell culture. MSK carried out the histopathological examination. All authors drafted the manuscript and participated in the subsequent discussions and revisions of the entire text. All authors read and approved the results and final manuscript.

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Molecular Identification of *Trypanosoma theileri* and **Biology of Trypanosomes**

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ABSTRACT

Trypanosoma theileri (T. theileri) is a non-pathogenic, cosmopolitan, and commensal protozoa of cattle. The main objective of the current study was to investigate the biology and feasibility of T. theileri as a model candidate for the discovery of a novel drug. In the present study, the isolates of T. theileri obtained from the Institute of Tropical Medicine (ITM) in SDM 79 were cultivated at 26°C. Eight experiments with different inoculum and different times were grown. The growth curve was plotted to check the growth trends. The doubling time in the logarithmic phase was determined to be 17.43 hours. In addition, an experimental infection was done on a 3-month-old Holstein Friesian calf to isolate the blood-streaming shape; however, it was not successful after the blood buffy coat smear and PBMC culture in RPMI 1640 and HMI 9. Furthermore, the viability was determined by quantitative colorimetric Resazurin assay in 96-well fluorescence Microplates containing 0.4 to 2.4 mM of Resazurin. On the other hand, the response to Pentamidine (1-100 ng/mL) showed a strong negative correlation between the fluorescence signal and the highest Pentamidine concentration. IC₅₀ was 9.25 ng/mL. Genomic DNA was extracted using the phenolchloroform method. The gradient PCR amplification using T. theileri specific PCR (Tth625-PCR) primers was detected at 465 base pair (bp). In addition, the full-length 18S rDNA sequence was detected at 730 bp. In the silico analysis using common anti-trypanosome drug targets, no significant similarity could be found on either the DNA or the protein level. Nevertheless, homologous sequences have been identified among the drug targets for Ornithine decarboxylase. Therefore, the analysis might show the possibility of using T. theileri as a model for the search of new drugs once they have entire genome sequences. Analysis of the whole genome and transcriptome indicated a phylogenetic relationship between T. theileri and other pathogenic trypanosomes which can be the basis for novel drug development.

Keywords: Drug model, Novel drug, PCR, Resazurin, SDM 79, Trypanosoma theileri

INTRODUCTION

The trypanosomatid parasites cause one of the most notorious human and animal trypanosomiasis in all parts of Africa and South America. Even if trypanosomes are the main cause of diseases in humans (sleeping sickness) and animals (Nagana), many other species are not pathogenic (Mott et al., 2011). Such pathogenic trypanosomatids occur globally and infect a large number of hosts. Among these, *Trypanosoma theileri* (*T. theileri*) is ubiquitous, 'truly cosmopolitan' cattle protozoan commensal found worldwide (Mott et al., 2011 and Lee et al., 2013).

Natural infections could be found in all age groups of cattle although they are rare in cattle younger than one year old. Neither its life cycle nor its host relationship is fully understood in the mammalian host. The main vector responsible for the transmission of the parasite is Tabanidae. However, ticks including *Hyalomma anatolicum* and *Boophilus microplus* were also later reported as vectors (Latif et al., 2004). Hence, *T. theileri* is typically characterized by a stercorarian type of transmission (Latif et al., 2004). After ingesting infected blood, trypanosomes develop in the vector's hindgut. The infection is then transmitted to new hosts through fecal contamination of the mucus membrane or abrasions of the skin (Lukes, 2009). In the newly infected host, the epimastigotes multiply in the bloodstream by binary fission. Besides epimastigotes and large trypomastigotes in the peripheral blood, flagellates have also been found in extravascular sites of lymph nodes, kidneys, spleen, and brain (Braun et al., 2002).

In order to isolate pathogenic African Trypanosomes, a kit called KIVI (Kit for In Vitro Isolation of trypanosome) was designed (Aerts et al., 1992). Similarly, Verloo et al. (2000) proved that this kit can be used as an excellent device for isolating *T. theileri* with much higher sensitivity than the Roswell Park Memorial Institute (RPMI) medium. On the other hand, there was evidence that the growth of *T. theileri* on the RPMI medium could be easily confirmed (Lee et al., 2013). Many trypanocidal drugs are available in the market. Among these drugs, pentamidine, diminazene aceturate (Berenil), isometamidium chloride (Samorin), and ethidium bromide are important anti-trypanosomal drugs (Shapiro and Englund, 1990).

High-Throughput Screening (HTS) and virtual screening are used as a standard means in drug discovery to identify novel lead compounds that target a biomolecule of interest. However, the latter is considered a cost-effective means

(Ekins et al., 2007; Fatumo et al., 2013). Editing of trypanosomatid RNA could be used to identify the drug target for protozoal parasites that cause diseases, such as trypanosomiasis. Amaro et al. (2008) reported that RNA-Editing Lgase-1 (REL-1) could be used as drug-like inhibitors of a key enzyme in the editing machine. The identification of inhibitors was done through a strategy employing molecular dynamics to account for protein flexibility (Amaro et al., 2008). New parasitic inhibitors had been identified due to the availability of an automated approach to high content microscopy (Alonso-Padilla and Rodriguez, 2014).

For better pharmacology hypotheses and tests, the development of computational (In Silico) methods plays a significant role. This methodology comprises pharmacophores, databases, quantitative structure-activity relationships, homology models, and other molecular modeling approaches, machine learning, network analysis tools, and data analysis tools using a computer.

Although *T. theileri* was not naturally pathogenic, it can cause disease in stressed cattle. Moreover, little is known about *T. theileri*. Recently, however, it has become an area of interest and is viewed as a tool and a vector for treating pathogenic microorganisms, particularly protozoan parasites (Mott et al., 2011). Furthermore, the mixed infection of *T. theileri* cause pathogenic trypanosome on the same host (cattle), and the presence of homologous sequences with specific sequences of anti-trypanosomal drug targets from pathogenic trypanosomes could lead to the use of this parasite (*T. theileri*) as a model candidate for the development of new drugs for the treatment of pathogenic trypanosomes. To this end, the basics of the parasite should be studied to manipulate the parasite as a tool to combat pathogenic trypanosomes. Furthermore, little is known about the biology, cell growth pattern, doubling time, and viability of the parasite. There is little convincing data to determine whether *T. theileri* could be used as a model for discovering new drugs for the treatment of pathogenic trypanosomiasis.

The general aim of the present research was to provide fundamental insights into the biology of *T. theileri* to verify its feasibility as a model organism for the discovery of the new drug. The specific objectives were cultivation of *T. theileri* both *in vitro* and *in vivo*, comparing and analyzing the growth pattern with others to check viability with Resazurin assay analysis and response to the drug, and determining the presence of homologous sequences between its genome and the specific target (conserved) sequence of anti-trypanosome drugs.

MATERIALS AND METHODS

Ethical approval

During the entire experimental period, the care and maintenance of the calf in its pen was performed based on the guidelines of the European Convention for the Protection of Vertebrate Animals used for Experimental and other Scientific Purposes. Furthermore, the experimental protocols were used after the approval by the Animal Research and Ethical Review Committee at the KU Leuven University (Permit No: P024/2017)

Parasites and in vitro culture

The sample used in the current study was *T. theileri*, kindly donated by the Diagnostic Parasitology Department of the Institute of Tropical Medicine, Belgium. These cryogenically preserved trypanosomes in culture were isolated from a small farm nearby Antwerp, Belgium by Verloo et al. (2000). Different growth media and conditions, under which other trypanosomes were grown in the institute, were assessed to determine the optimal conditions and favorable growth media for culturing the parasite. After identifying the appropriate medium (SDM 79) and the growth condition (at 26°C, without CO₂), the cryostablate was seeded (1: 10 ratio) and propagated three times with SDM 79 medium (BioConcept AMIMED company, Switzerland) in a cell culture flask ($25cm^2$, Thermo ScientificTM NuncTM Cell Culture Flasks). It was counted daily with a hemocytometer and recorded in the logarithmic table. A growth curve was then plotted to determine the growth pattern. In addition, the minimum and the maximum number of cells in the eight-cell culture flasks (eight experiments) that could serve as a potential indicator of the logarithmic phase and considered for both the experimental infection and Resazurin assay development were stored. Moreover, *T. theileri* was sub-passaged every three days. Epimastigotes were harvested in the exponential growth phase. Epimastigoteswas were centrifuged (1500 rpm for 10 minutes to sediment, washed, and re-suspended with phosphate buffer saline (PBS, pH = 7.2) before inoculation to the experimental calf while it was being used for DNA extraction.

Experimental animal and infection

A Holstein Friesian calf (aged three months) was randomly selected from the zootechnical Centre, KU Leuven, Belgium. It was confirmed to be trypanosome-negative by taking the blood sample and smear and culture in HMI-9 medium. After confirmation, it was inoculated with the sub-cultured epimastigotes of *T. theileri* (4.5×10^6 /mL to 7.3 $\times 10^6$ /mL), intravenously (IV) through the jugular vein in a volume of 5-9 mL. In addition to parenteral inoculation, the calf was orally drenched with the same amount of inoculation. The calf was monitored and examined for parasitemia for three consecutive weeks. Blood samples (10 mL) were collected using Ethylenediaminetetraacetic Acid (EDTA) coated

vacutainer tubes. The samples were collected two times after experimental infection (every week after experimental infection). After the blood samples were transported to the Host-Pathogen Interaction Laboratory of KU Leuven, Belgium, the samples were examined for the presence of trypanosomes using the standard parasitological methods of the wet and thin blood smear (stained with Giemsa), PBMC, and buffy coat technique within two to three hours of sampling per day (Murray et al., 1977).

The buffy coat/PBMCculture

After extracting the buffy coat (Murray et al., 1977) and PBMC (Ficoll-Paque method), the buffy coat samples were transferred to two cell culture flasks (25 cm^2 , Thermo ScientificTM NuncTM Cell Culture Flasks) containing HMI-9 medium and RPMI 1640 supplemented with 10% fetal calf serum (FCS, Sigma) and 200 IU/mL of penicillin and 100µg/Ml streptomycin (Invitrogen, Carlsbad, CA) according to Hirumi and Hirumi (1989). A ratio of 1:10 (1 ml of buffy coat sample to 10 ml of the HMI-9 medium) was used. The inoculated cell culture flasks containing HMI-9 medium were then incubated at 37° C and exposed to 5% CO₂. The tests were checked daily under an inverted microscope at $40 \times$ magnification to monitor the progress of growth in both cell culture flasks inoculated for a maximum of two weeks.

In vitro sensitivity assays (Resazurin assay)

A reagent, Resazurine obtained from Sigma-Aldrich, was used as a quantitative colorimetric assay based on the oxidation (blue) and reduction (pink) indicators to measure *T. theileri* viability and its response to pentamidine. Resazurin stock solution (0.4 to 2.4 mM) was prepared in PBS withpH 7and filter-sterilized (Miriam et al., 2006).

Optimization of Resazurin to Trypanosoma theileri viability

To reduce the background signal for a better sensitivity assay and also to avoid light piping between wells, the Black Microtiter® 96-Well Fluorescence microplates were used. Cells ranging from 5.2×10^5 /mL to 8.5×10^6 /mL with a logarithmic phase were obtained after incubation in cell culture flasks at 26°C for 48 hours. Then, 120 µL cells of *T. theileri* were removed from this cell culture flask into wells of Microtiter® 96-Well Fluorescence Microplates (Thermo Scientific) and incubated again at 26°C for 48 hours. After 48 hours of incubation, 20 µl of different concentrations of Resazurin solution (0.4 to 2.4 mM) was added to each inoculum while an equivalent amount of SDM 79 medium was added for blank wells. The plates were returned to the incubator for 24 hours for optimal oxidation and reduction. The Fluorescence signal was read 1, 3, 5, 7, 18, and 24 hours after the addition of Resazurin by dual-wavelength using a GFP protocol-VICTORTM X Series Multi-label Plate Reader (Perkin Elmer Instruments Inc.) at Λ_{exc} 485, and Λ_{em} 535 nm. A single micro-titer plate was used for three different concentrations of Resazurin per experiment. The background was subtracted from each reading. The experiments were performed three times and an average was taken.

Standard curves

Following incubating epimastigotes in the range of 1.3×10^6 to 5.3×10^6 epimastigotes/mL for 48 hours, 120 µL of epimastigotes /mL per well were seeded to a 96 well microtiter plate for further 48 hours of incubation at 26°C. Then, 20 µL of 2.4 mM Resazurin was added followed by fluorescence signal reading after 7 hours of incubation. This procedure was performed twice in all three times.

Drugs sensitivity assay

Pentamidine was dissolved in concentrations from 1.0 to 80 ng/ml. In each wellofCostarTM 96-well microtitre plates, 120μ l of epimastigotes of *T. theileri* in the logarithmic phase (1.4-5.3 ×10⁶/mL) was seeded with 20 µL of different concentrations of pentamidine (1.0 to 80 ng/ml). Three drug concentrations were tested per plate (column 1-3 with 1.0 ng/ml, column 4-6 with 40 ng/ml, column 7-9 with 80 ng/ml pentamidine, column 10 without the drug, and column 11SDM 79 medium used as control medium). The plates were then incubated with pentamidine for 48 hours. The trypanosome density was counted with a hemocytometer up to 48 hours of incubation before the addition of Resazurin. Afterwards, the plates were incubated by adding a 20 µL Resazurin to each well and incubated at 26°C for an additional seven hours. IC₅₀ values were also calculated at concentrations 1-100 ng/mL using this assay and microscopic counting. Columns 1-10 were tested for drugs, column 11 was without the drug, and column 12 included only SDM 79 as the control medium.

Data Evaluation and analysis

The plate was read at an excitation wavelength of 485 nm and an emission wavelength of 535 nm in a fluorescence/microplate reader (GFP protocol-VICTORTM X Series Multi-label Plate Reader (PerkinElmer Instruments Inc.). The data were transferred into a graphics program (Excel) and analyzed using the GraphPad Prism 7.0. Descriptive

statistics and Pearson $r^2(r)$ correlation coefficient were also calculated. To measure the anti-epimastigotes activity (%AE), the following formula according to Miriam et al. (2006) was used.

AE (%) = $\frac{(Gc-Gp)}{Gc} \times 100$ (Equation 1)

Where, Gc represents the mean number of parasites per milliliter in the control, and Gp shows the mean number of parasites per milliliter according to the different doses of drugs.

Furthermore, the doubling time was calculated based on the following equation used for *T.b.brucei* by Sykes and Avery (2009) and Melissa et al. (2009).

 $TD = (t2 - t1) \frac{\log(2)}{\log(q2/q1)} (Equation 2)$

Where, Td refers to doubling time (q1), t1 is the first quantity for the first time, and (q2) at the time (t2) denotes the second quantity at the second time.

Genomic DNA extraction and PCR amplification

A *T. theileri* culture in a high density of the logarithmic phase ranging from 3.6×10^6 cells/ml to 7.8×10^6 epimastigotes/mL was utilized to extract genomic DNA. Both the phenol-chloroform method and DNeasy®Blood and Tissue Kit (Qiagen, Hilden, Germany) were used. The concentration and purity of the DNA were determined with NanoDrop TMSpectrophotometer (Thermo Fisher Scientific) and agarose gel electrophoresis (1%).

DNeasy®Blood and tissue kit

The genomic DNA extraction was conducted according to the protocol recommended by the manufacture Purification of Total DNA from Animal Blood or Cells (DNeasy 96 Protocol), DNeasy®Blood and tissue kit (Qiagen, Hilden, Germany).

Phenol-chloroform method

Cultivated *T. theileri* cells $(3.6 \times 10^6 \text{ cells/ml} \text{ to } 7.8 \times 10^6 \text{ cells/ml})$ in 2ml Eppendorftubeswere lysed by centrifugation at 13000 rpm for a minute. The supernatants were removed and 500 µL of T10N150E10wereadded and mixed thoroughly by pipetting several times. The content was then centrifuged at 13000 rpm for 10 minutes and the supernatant was removed, followed by the addition of 500 µL of T₁₀N₁₅₀E₁₀. This step was repeated twice.

Eight hundred microliter of freshly prepared Glouton-Buffer (10mM Tris HCl, 10 mM EDTA, 100mM NaCl, 10% SDS, 3.9Mm DTT) were added and mixed well by pipetting up and down. It was then incubated at 65°C for one hour. Afterwards, 20µl of 10 µg/mL proteinase K was added and incubated at 56°C overnight.

An equal volume(1000 μ L) of phenol/chloroform/isoamyl alcohol in the ratio of 25:24:1 was added and mixed gently. After centrifuging at 13000 rpm for 10minutes, the supernatant was transferred to a new tube. The same amount of phenol/chloroform was added to a new tube, mixed, and centrifuged as above-mentioned. The supernatants were transferred to a new tube again and the same amount of chloroform was added, mixed, and centrifuged as indicated above. The aqueous layer (500 μ l) was transferred to a new tube and mixed gently with 1166 μ L 100 % Ethanol. The supernatants were removed after centrifugation at 13000 rpm for 1 minute. The tubes were left open to dry DNA for 3 hours, then it was resuspended with 30 μ L of Mili-Q water.

PCR amplification and gel electrophoresis

Species-specific PCR identification was performed using the following primers in Table 1 as described by Rodrigues et al. (2003) and Lee et al. (2013). Amplification was conducted using 25 μ L reaction mixture with 200 ng template DNA (genomic DNA), 2.5 IU (International Unit) TagDNA polymerase (Promega, U.S.A), 0.2 mM dNTP, PCR buffer, 1.5 mM MgCl₂, (Promega, U.S.A), and 0.3 μ M of primer, according to the manufacturer's instructions. For gradient PCR Amplification, the procedure involved 95°C for 5 minutes, followed by 20 cycles of 94°C for 10 seconds, 53°C for 15 seconds, and 67°C for 1 minute, with a final extension at 72°C for 3 minutes.

Finally, PCR products were run on 1% agarose gel (Sigma) electrophoresis using $1 \times$ TBE buffer and stained with 7μ L ethidium bromide in 50 mL agarose (0.5 ng/ mL) and made visible using UV transillumination (Vilmar Lourmat).

	Primer (Forward and Reverse)	Purpose
1	Tth625a (5'-CCG CTG GAG CTA AGA ATA GA-3') and	For species-specific PCR amplification
1	Tth625b (5'-AAT TGC ATA AAC ACA GCT CCC-3')	(Tth625-PCR)
	Forward primer 18STnF2 (5'-CAA CGA TGA CAC CCA TGA ATT GGG GA-3')	The full length 18S ribosomal DNA
2	and	soquence Analysis
	Reverse primer 18STnR3 (5'-TGC GCG ACC AAT AAT TGC AAT AC-3')	sequence Analysis
	Kin1 reverse (5' GCG TTC $\Lambda \Lambda \Lambda$ G Λ T TGG GC Λ Λ T 3') and	For single PCR amplification to anneal
3	Kin1 levelse (5 - CCC CCC AAA CAT TOO CCA A1-5) and V_{in2} forward (5' CCC CCC AAA CTT CAC C 2')	internal transcribed spacer of
	$\operatorname{Kin}_{2}\operatorname{101waru}\left(3\operatorname{-COC}\operatorname{CCO}\operatorname{AAA}\operatorname{OT}_{1}\operatorname{CAC}\operatorname{C-3}\right)$	ribosomal genes (ITS) sequence

Table 1. Primers used to detect Trypanosoma theileri

Source: Rodrigues et al. (2003) and Lee et al.(2013)

In silico analysis by multiple sequence alignments

Multiple Sequence Alignments (MSA) were conducted with commonly used anti-trypanosomal drug target sequences (Table 1) from pathogenic *Trypanosoma* species and *T. Theileri* genome/proteome using FFT in ExPASy tool, Switzerland (Rodrigues et al., 2003). In addition, phylogenetic trees were created to study the relationships between the different drug targets and the *T. theileri* genome/proteome, as well as between the drug target sequences.

Risk analysis

The *T. theileri* is a non-pathogenic parasite and does not cause disease in either livestock or humans. There is no biological hazard to the calf from parasite inoculation. Therefore, there are no biochemical hazards for the farm and environment when carrying out such an experiment.

RESULTS

Growth medium and conditions

Different types of cell culture media commonly used to culture other types of *Trypanosoma* in ITM were screened to assess the optimal and conducive conditions to culture *T. theileri* epimastigotes. Cryogenically preserved 2.5×10^6 epimastigotes/mL were seeded into a cell culture flask ($25cm^2$, Thermo ScientificTM NuncTM Cell Culture Flasks) in four different media and growth conditions (Figures 1 and 2). It was seeded at a 1:10 ratio and sub-passaged every three days for two consecutive weeks. Finally, the optimal conditions and favorable growth media for *T. theileri* epimastigotes were identified. As a result, significant growth of the *T. theileri* could be observed in SDM 79 at 26°C without CO₂, and RPM'3I 1640 at 37°C with 5 % CO₂ with 10 % Fetal Calf Serum (FCS), as shown in Figures 1 and 2, respectively. However, relatively slower growth was observed for the later third day. On the other hand, there was a prominent growth in RPMI 1640 with 10 % FCS than other serum types used (Figure 2).

Growth pattern and doubling time

After inoculation $(2.5 \times 10^6 \text{ epimastigotes/mL})$ of *T. theileri* in eight flasks containing SDM 79 with10 % FCS, the growth pattern was determined by counting 10 µL from each flask daily with a Haemocytometer. As indicated in Figure 3, maximum growth was observed on the sixth day in the entire eight-cell culture flask, except for the seventh experiment, which took place on the seventh day. The maximum number of epimastigotes that could be grown among the eight flasks was estimated to be 1.7×10^7 cells/mL (Experiment 2). The doubling time was calculated per day assuming they were in the logarithmic phase from the third to sixth day as indicated in Figure 3. Since there was a significant growth of the parasite in this period, from 3.2×10^4 cells/mL, which was the lowest on the third day from the second experiment to the highest 1.3×10^7 cells/mL from the same flask on the sixth day. The calculation was based on the manipulation of the doubling time equation used for *T.b.brucei* from Sykes and Avery(2009) and Melissa et al. (2009) as described in materials and methods. Therefore, the doubling time calculated in the logarithmic growth phase averaged 17.43 hours (0.73 day) for eight experiments.



Figure 1. Growth of *Trypanosoma theileri* with various media at 26° C without CO₂ in cell culture flasks. It was performed at the Institute of Tropical Medicine Antwerp, Belgium for two consecutive weeks



Figure 2. Growth of *Trypanosoma theileri* with RPMI 1640 in different serum types at 37°C with 5 %CO₂ in cell culture flask at ITMor two weeks



Figure 3. The growth pattern of *Trypanosoma theileri* in eight tissue culture flasks considered as experiments for nine days incubated in SDM 79at 26°C without CO₂. Exp: Experiment

To assess the morphology and the relative difference between other stages, Giemsa and DAPIstains (4',6diamidino-2-phenylindole) were performed on slides. Some of the slides were stained at ITM and some others in the Host Interaction lab, KU Leuven, Belgium (Figure 4).



Figure 4. Light microscopy of *Trypanosoma theileri* epimastigotes cultured at 26° C (Giemsa and DAPI stained, $400 \times$ magnifications). A kinetoplast is anterior to the nucleus, unlike a trypomastigote which has a kinetoplast posterior to the nucleus. N: Nucleus, K: Kinetoplast.

Resazurin assay

After optimization, *T. Theileri* was grown in microtiter plates and reached the level to produce a detectable fluorescence signal by incubation with 20 μ L of each Resazurin solution. The magnitude of fluorescence increased remarkably up to7 hours, after which the fluorescence saturation occurred, particularly at 3.5×10^6 epimastigotes /mL, which had the highest density and then gradually decreased (Figure 5).

A statistically significant difference in the fluorescence of Resazurin solution at three concentrations (0.4 mM to 2.4 mM) was observed (p < 0.05) with an increase in the number of parasites and the incubation time (7 hours) during the assay (Figures 5 and 6). There was a positive correlation (r=0.75 to 0.925) between the magnitude of fluorescence of various cell densities and the three Resazurin concentrations (Table 6). However, the growth declined from 3.5×10^6 to 7.9×10^6 epimastigotes/mL, which indicated that the epimastigote was reaching the stationary phase. Hence, the upper limit of the assay was a plating density of 3.5×10^6 epimastigotes/ml (Figure 5).

Trypanosoma theileri were seeded with 1.6×10^6 epimastigotes/ml, which resulted in a low level of fluorescence on the first reading (in the first hour after the addition of Resazurin) at the beginning of the assay process. Then, it gradually increased and a maximum signal was received seventh hours after adding Resazurin, and then significantly declined until the last reading (24 hours after adding Resazurin, Figure 6). Overall, the fluorescence signal of Resazurin solutions had a positive correlation (r = 0.75 to 0.925) with cell density and incubation time. There was a statistically significant difference between Resazurin fluorescence and the number of epimastigotes and also with reading time after incubation (p < 0.05, Table 6).

There was a positive, and linear correlation between the fluorescence and density of epimastigote at 1.6×10^6 cells/mL for a 2.4 mM Resazurin concentration at7hours of incubation (r = 0.8297), compared to the other two concentrations of Resazurin (Table 3). After incubation of 2.4 mM Resazurin at 26°C for 7 hours, a very high and linear association (r = 0.9876) in the range of 1.3×10^6 to 5.3×10^6 was observed in the fluorescence signal of the parasite (Table 3). For a comparative demonstration of the Resazurin based colorimetric assay, 1.8×10^6 epimastigotes/MI (300 µL/well) with 2.4 mM (25 µL) of Resazurin was seeded in a Corning® 24-well culture plate (Sigma Aldrich) containing to appreciate the color changes from blue to pink. The test showed a gradual colorimetric change in the three concentrations of Resazurin and one control (Figure 8).



Figure 5. The relationship between the different fluorescence concentrations of Resazurin and the growth of epimastigote cultures after 7 hours of incubation time

Table 2. Statistical	values of fluorescence	for	different	cell	concentrations	concerning	Resazurin	concentrations
i ubic 2. Statistical	values of fluorescence	101	uniterent	con	concentrations	concerning	Resuzurin	concentrations

			Cells/ml	and their re	espective flue	orescence			r-	P-
Resazurin	1.3X10 ⁵	7.6X10 ⁵	9.8X10 ⁵	1.2X10 ⁶	3.1X10 ⁶	3.5X10 ⁶	5.8X10 ⁶	7.9X10 ⁶	value	value
0.4 mM	156.63	217.6	230	243	280	292	268	290	0.752	0.0315
1.2 mM	145	187	201	216	255	310	298	341	0.925	0.0010
2.4 mM	184	240	275	341	380	489	450	490	0.865	0.0056



Figure 6. Fluorescence of Resazurin concerning incubation time and cell density of 1.6×10^6 epimastigotes/mL of *Trypanosoma theileri*. All experiments were performed two times each in three duplicates, and average values were taken.

Table 3. Correlation between fluorescence signal and an incubation time of Trypanosoma theileri epimastigote

			Time (Hours)			r voluo	D voluo
Resazurin	1	3	5	7	18	24	I -value	I -value
0.4 mM	169	197	210	233	219	214	0.5066	0.3051
1.2 mM	205	217	251	268	257	246	0.4851	0.3295
2.4 mM	244	260	295	351	350	363	0.8297	0.0410



Figure 7. Standard curves for Resazurin fluorescence and the number of epimastigotes in the logarithmic growth phase, r = 0.9876, p < 0.05



Figure 8. A plate to see the colorimetric changes of Resazurin (2.4 mM) in each reading time after incubation with pentamidine (80 ng/mL)

Drug sensitivity assays

Based on the optimized Resazurin assay for cell density, Resazurin concentration, and incubation period (Figure 5), Resazurin was deployed for the sensitivity of *T. theileri* epimastigote to pentamidine. Accordingly, Resazurin solution at a concentration of 2.4 mM was used to assess the response of *T. theileri* epimastigotes to different concentrations (1-80 ng/mL) of pentamidine (Figure 9). Therefore, there was a negative correlation (-0.8826) between the reduction in fluorescence signal and a significant increase in drug concentration (p < 0.05), as described in Figure 9and Table 4.



Figure 9. The reduction in fluorescence of epimastigotes of *Trypanosoma theileri* due to the pentamidine at different concentrations using 2.4 mM Resazurin solution

Table 4. Signals from Resazurin (2.4 mM) after addition of three different concentrations of pentamidine

			Cells/mI	with its re	spective flu	orescence			r value	P value
Pentamidine	1.3×10^{6}	2.3×10^{6}	2.6×10^{6}	3.7×10^{6}	4.5×10^{6}	4.9×10^{6}	5.1 ×10 ⁶	5.3×10^{6}		
1ng/ml	254	213	222	220	254	284	255	256	0.533	0.1740
40ng/ml	254	209	204	188	187	224	186	193	-0.649	0.0817
80ng/ml	249	190	202	156	158	140	165	160	-0.8826	0.0037



Figure 10. Viability of epimastigote after exposure to Pentamidine (1-100ng/mL) using Resazurin and microscopic counting

The role of Resazurin colorimetric assay was compared by calculating percentages of anti-epimastigotes (% AE) activity of pentamidine(1 to 100 ng/mL). For this purpose, a microscopic count was done and calculated based on Equation 1as described in materials and methods. As indicated in Figure 10, the Resazurin assay and microscopic count were compared. As a result, there was a significant reduction in the percentage of viability of the epimastigotes as the pentamidine concentration increased after 48 hours of contact time. IC₅₀ values of 9.25ng/mL and 16.29 ng/mL were determined using Resazurin (r = -0.957; p < 0.05) and manual counting (r = 0.90, p < 0.05), respectively.

Experimental infection of Trypanosoma theileri

Before inoculating a calf with *T. theileri*, blood samples were taken to check whether there was a natural infection. No *T. theileri* was confirmed either in Giemsa stained slides or by culturing PBMC and buffy coat in RPMI 1640 and HMI 9 medium. The calf was inoculated intravenously through a jugular vein with a density of 4.5×10^6 /mL to 7.3×10^6 /mL in 5-8ml. Moreover, the same amount and concentration were administered orally. Experimental infections were performed three times.

PCR confirmation of Trypanosoma theileri

WithDNeasy®Blood and Tissue Kit (Qiagen, Hilden, Germany) a very low concentration of DNA could be achieved. As a result, a higher DNA concentration (16.5-274 μ g/m) could be extracted using the phenol-chloroform method. Gradient PCR amplification using *T. theileri* specific PCR (Tth625-PCR) revealed the 465 bp amplification product (Figure 11). In addition, the full-length 18S ribosomal DNA sequence of *T. theileri* DNA was detected at 730 bp (Figure 12). They were stained with ethidium bromide in 1% agarose gel. A DNA ladder (100 bp) was used on the left side of the gel. The PCR amplification for the third primer (for annealing the Internal Transcribed Spacer (ITS) of the sequence of the ribosomal gene) was not included due to the poor image quality.



Figure 11. Detection of PCR of *Trypanosoma theileri* DNA from the cultured epimastigote using species-specific Tth625-PCR primers. The products were separated on a 1% agarose mini-gel



Figure 12. Detection of PCR of *T. theileri* of 18S ribosomal DNA from the cultured epimastigote using 18STnF2 and 18STnR3. The products were separated on a 1% agarose mini-gel

In silico analysis

Multiple Sequence Alignment of the sequences of commonly used trypanocidal drug targets (Figure 13) with *T. theileri* nucleotide found in the NCBI database was run. Multiple Sequence Alignment was performed at both the genomic (DNA) and protein levels. The Basic Local Alignment Search Tool (BLAST) and Clustal W program (from ExPASy bioinformatics resource portal) was run to demonstrate homology between *T. theileri* genome/ proteome and /or drug target sequences. Based on the determined protein/nucleotide sequence, phylogenetic trees were constructed to find out the possibility of evolutionary relationships. At the genomic (DNA) level, no significant similarity was found. However, to a lesser extent, a similarity of 294/392 (75%) was observed between *T. grayi* cathepsin L-like protein (CATL) gene (NCBI Gene bank accession No: XM_009318006.1) and HQ664735.1 of *T. theileri* isolate Tthb19 clone 3 cathepsin L-like protein (CATL) gene. The Cluster W alignment of these two similar genes from both species of *Trypanosome* was is described in Figure 14.

On the other hand, MSA among anti-trypanosome drug targets excluding *T. theileri* showed that there was above 99.85% identity among accession number of XM_824336.1(100%), J02771.1(99%), and AF042286 (99%). These listed accession numbers all indicated the Ornithine decarboxylase gene in *T.brucei*. In addition, the phylogenetic tree showed that these were similarities with accession Numbers: DQ887563.1 and XM_009318006.1, which both described the topoisomerase gene from *T.congolense* and the CATL gene from *T. grayi*, respectively (Figure 15).

CLUSTAL format alignment by MAFFT FFT-NS-i (v7.215)

XM_009318006.1 HQ664735.1	AACGGCGGCTTGATGGACGACGCCTTCACATGGATCATCCAGGACCACAACGGCACGGTG AATGGCGGCTTGATGGACGACGCCCTTCCAGTGGCTCGTGGATTCGAACAAGGGCAAGGTG
~	** • ****************** • *** * * * * *
XM_009318006.1 HQ664735.1	GACACAGAGGCCAGCTACCCCTACGTCTCGGGCGCGGGCTACTCCCCGAAGTGCAGGACA TACACGGAGAACAGCTATCCCTACGTCTCTGGCTCCGGTCAAACGCCGGCGTGCTCGACA ****.***. *****.**********************
XM_009318006.1 HQ664735.1	GCTAGCCACGAGTTCGGCGCAGCCATCAGCGGCTACAATGACCTGCCGAATGATGAGGAC AGTGAACATGAGGTTGGTGCGACAATCACCGGCTTTGTGGACTTGCCAAAAGATGAGGAC . * **.*** *.**.** **** ***** ***.******
XM_009318006.1 HQ664735.1	AAGATGGCCGCGTGGCTGGCTGTCCACGGCCCCATTGCCATCGCCGTCGACGCCACCAGC AAGATGGCGGCATGGCTTGCTACCAATGGCCCCATTGCTATCGCTGTCGACGCCAACAGC ******* **.**** **** *.*************
XM_009318006.1 HQ664735.1	TTCCAGTTCTACATGGGTGGCGTCCTGACGAACTGCATCTCTGAGCAGCTCGACCACGGG TTTCTGTCGTACGTAAGTGGTGTTTTTGACGAACTGTGAATCGGACCAGTTGAACCACGGT **.* **. ***.*****.***************
XM_009318006.1 HQ664735.1	GTGCTTCTTGTGGGCTACGACGACAGCAACAGCCCGCCGTACTGGATCATCAAGAACTCG GTGCTTCTTGTCGGCTACGACGACGACAGCAACCACCGTACTGGATCATCAAGAAC

Figure 13. Cluster W alignment of *Trypanosoma theileri* (HQ664735.1) and *T.grayi* (XM_009318006.1) for the cathepsin L-like protein gene



Figure 14. Multiple sequence alignments phylogenetic tree of the genome (DNA) of trypanosome showing relationships between common drug targets. ORC: Ornithine decarboxylase, TPI: Topoisomerase, CTP: Cathepsin L-like protein partial mRNA, NMT: N-myristoyl transferase

Table 5. Percentage of identity and divergence between common anti-trypanosomal drug targets identity

		1	2	3	4	5	6	7	8	
	1: XM_824336.1	100	99.93	99.85	44.01	41.48	40.87	44.4	42.34	1
د	2: J02771.1	99.93	100	99.93	42.89	41.22	41.2	43.46	42.2	2
enc	3: AF042286.1	99.85	99.93	100	43.07	41.22	41.25	43.42	42.08	3
verg	4: DQ887563.1	44.01	42.89	43.07	100	58.45	43.5	44.17	43.38	4
Di	5: XM_009318006.1	41.48	41.22	41.22	58.45	100	41.52	43.44	40	5
	6: XM_822811.1	40.87	41.2	41.25	43.5	41.52	100	63.21	65.15	6
	7: XM_009314999.1	44.4	43.46	43.42	44.17	43.44	63.21	100	68.7	7
	8: HQ587038.1	42.34	42.2	42.08	43.38	40	65.15	68.7	100	8

XM_824336.1 J02771.1 AF042286.1	TCTGTGAATTGTCTTGTAGCACAAACGGAGAAATCTATGGACATTGTCGTGAACGATGAC TCTGTGAATTGTCTTGTAGCACAAACGGAGAAATCTATGGACATTGTCGTGAACGATGAC TCTGTGAATTGTCTTGTAGCACAAACGGAGAAATCTATGGACATTGTCGTGAACGATGAC ************************************
XM_824336.1 J02771.1 AF042286.1	TTGAGTTGTCGCTTTCTTGAAGGGTTTAATACGAGGGATGCCCTCTGTAAAAAGATCAGT TTGAGTTGTCGCTTTCTTGAAGGGTTTAATACGAGGGATGCCCTCTGTAAAAAGATCAGT TTGAGTTGTCGCTTTCTTGAAGGGTTTAATACGAGGGATGCCCTCTGTAAAAAGATCAGT ************************************
XM_824336.1 J02771.1 AF042286.1	ATGAATACGTGTGACGAAGGTGATCCGTTTTTTGTTGCCGATCTCGGGGACATTGTAAGG ATGAATACGTGTGACGAAGGTGATCCGTTTTTTGTTGCCGATCTCGGGGACATTGTAAGG ATGAATACGTGTGACGAAGGTGATCCGTTTTTTGTTGCCGATCTCGGGGACATTGTAAGG ******************************
XM_824336.1 J02771.1 AF042286.1	AAGCACGAAACATGGAAAAAATGCCTTCCCCGCGTCACGCCGTTTTACGCGGTCAAATGC AAGCACGAAACATGGAAAAAATGCCTTCCCCGCGTCACGCCGTTTTACGCGGTCAAATGC AAGCACGAAACATGGAAAAAATGCCTTCCCCGCGTCACGCCGTTTTACGCGGTCAAATGC ************************************
XM_824336.1 J02771.1 AF042286.1	AACGATGACTGGCGCGTACTTGGAACGCTGGCGGCTCTCGGCACGGGATTTGATTGTGCT AACGATGACTGGCGCGCTACTTGGAACGCTGGCGGCTCTCGGCACGGGATTTGATTGTGCT AACGATGACTGGCGCGCTACTTGGAACGCTGGCGGCTCTCGGCACGGGATTTGATTGTGCT ********************************
XM_824336.1 J02771.1 AF042286.1	AGCAACACTGAGATACAACGTGTGAGAGGGCATTGGTGTGCCACCGGAAAAAATAATATAT AGCAACACTGAGATACAACGTGTGAGAGGGCATTGGTGTGCCACCGGAAAAAATAATATAT AGCAACACTGAGATACAACGTGTGAGAGGGCATTGGTGTGCCACCGGAAAAAATAATATAT ***********************
XM_824336.1 J02771.1 AF042286.1	GCGAACCCTTGTAAACAAAATTCACACATACGGTACGCGCGTGATAGCGGCGTTGATGTC GCGAACCCTTGTAAACAAATTTCACACATACGGTACGCGCGTGATAGCGGCGTTGATGTC GCGAACCCTTGTAAACAAATTTCACACATACGGTACGCGCGTGATAGCGGCGTTGATGTC ********************
XM_824336.1 J02771.1 AF042286.1	ATGACATTTGATTGCGTGGATGAACTGGAAAAGGTCGCTAAAACGCATCCAAAGGCAAAG ATGACATTTGATTGCGTGGATGAACTGGAAAAGGTCGCTAAAACGCATCCAAAGGCAAAG ATGACATTTGATTGCGTGGATGAACTGGAAAAGGTCGCTAAAACGCATCCAAAGGCAAAG ***************************
XM_824336.1 J02771.1 AF042286.1	ATGGTATTAAGAATTTCTACGGATGATTCGTTGGCTCGATGCCGTCTCAGTGTGAAGTTT ATGGTATTAAGAATTTCTACGGATGATTCGTTGGCTCGATGCCGTCTCAGTGTGAAGTTT ATGGTATTAAGAATTTCTACGGATGATTCGTTGGCTCGATGCCGTCTCAGTGT A AAGTTT *********************************

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XM_824336.1 J02771.1 AF042286.1	GGTGCAAAGGTGGAAGACTGTAGGTTTATCTTGGAGCAGGCAAAGAAACTGAATATCGAC GGTGCAAAGGTGGAAGACTGTAGGTTTATCTTGGAGCAGGCAAAGAAACTGAATATCGAC GGTGCAAAGGTGGAAGACTGTAGGTTTATCTTGGAGCAGGCAAAGAAACTGAATATCGAC ***********************************
XM_824336.1 J02771.1 AF042286.1	GTCACTGGTGTGAGTTTTCACGTGGGAAGCGGATCTACAGATGCCTCTACCTTCGCTCAA GTCACTGGTGTGAGTTTTCACGTGGGAAGCGGATCTACAGATGCCTCTACCTTCGCTCAA GTCACTGGTGTGAGTTTTCACGTGGGAAGCGGATCTACAGATGCCTCTACCTTCGCTCAA **********************************
XM_824336.1 J02771.1 AF042286.1	GCCATATCTGACTCCCGTTTCGTTTTCGACATGGGTACTGAGCTTGGGTTCAATATGCAC GCCATATCTGACTCCCGTTTCGTTT
XM_824336.1 J02771.1 AF042286.1	ATTCTTGATATCGGTGGTGGGTGTGCGTTTCCAGGGACGAGGGATGCACCACTTAAATTTGAAGAG ATTCTTGATATCGGTGGTGGGTTTCCAGGGACGAGGGATGCACCACTTAAATTTGAAGAG ATTCTTGATATCGGTGGTGGGTTTCCAGGGACGAGGGATGCACCACTTAAATTTGAAGAG *************************
XM_824336.1 J02771.1 AF042286.1	ATTGCTGGTGTCATCAACAATGCGCTGGAAAAACATTTTCCACCTGACCTCAAGCTTACC ATTGCTGGTGTCATCAACAATGCGCTGGAAAAACATTTTCCACCTGACCTCAAGCTTACC ATTGCTGGTGTCATCAACAATGCGCTGGAAAAACATTTTCCACCTGACCTCAAGCTTACC *********************************
XM_824336.1 J02771.1 AF042286.1	ATTGTTGCCGAGCCGGGAAGGTACTACGTTGCTTCAGCTTTCACACTTGCCGTAAATGTT ATTGTTGCCGAGCCGGGAAGGTACTACGTTGCTTCAGCTTTCACACTTGCCGTAAATGTT ATTGTTGCCGAGCCGGGAAGGTACTACGTTGCTTCAGCTTTCACACTTGCCGTAAATGTT ******
XM_824336.1 J02771.1 AF042286.1	ATTGCCAAGAAGGTGACACCAGGGGTTCAGACCGACGTCGGTGCCCATGCTGAATCAAAC ATTGCCAAGAAGGTGACACCAGGGGTTCAGACCGACGTCGGTGCCCATGCTGAATCAAAC ATTGCCAAGAAGGTGACACCAGGGGGTTCAGACCGACGTCGGTGCCCATGCTGAATCAAAC
XM_824336.1 J02771.1 AF042286.1	GCACAGAGTTTTATGTATTATGTGAATGATGGCGTGTATGGTTCATTTAATTGCATCCTG GCACAGAGTTTTATGTATTATGTGAATGATGGCGTGTATGGTTCATTTAATTGCATCCTG GCACAGAGTTTTATGTATTATGTGAATGATGGCGTGTATGGTTCATTTAATTGCATCCTG **********************************
XM_824336.1 J02771.1 AF042286.1	TATGACCACGCAGTCGTCAGGCCTTTGCCCCAGAGGGAGCCAATCCCCAATGAAAAGCTC TATGACCACGCAGTCGTCAGGCCTTTGCCCCAGAGGGAGCCAATCCCCAATGAAAAGCTC TATGACCACGCAGTCGTCAGGCCTTTGCCCCAGAGGGAGCCAATCCCCAATGAAAAGCTC ***********************************
XM_824336.1 J02771.1 AF042286.1	TATCCCTCAAGTGTATGGGGTCCCACATGTGATGGTCTTGATCAGATAGTTGAACGATAC TATCCCTCAAGTGTATGGGGTCCCACATGTGATGGTCTTGATCAGATAGTTGAACGATAC TATCCCTCAAGTGTATGGGGTCCCACATGTGATGGTCTTGATCAGATAGTTGAACGATAC
XM_824336.1 J02771.1 AF042286.1	TATCTTCCCGAGATGCAAGTGGGGGGAATGGCTGCTCTTTGAGGATATGGGTGCCTACACG TATCTTCCCGAGATGCAAGTGGGGGGAATGGCTGCTCTTTGAGGATATGGGTGCCTACACG TATCTTCCCGAGATGCAAGTGGGGGGAATGGCTGCTCTTTGAGGATATGGGTGCCTACACG
XM_824336.1 J02771.1 AF042286.1	GTCGTAGGAACTTCTTCCTTTAATGGATTCCAGAGTCCGACTATTTACTATGTAGTCTCC GTCGTAGGAACTTCTTCCTTTAATGGATTCCAGAGTCCGACTATTTACTATGTAGTCTCC GTCGTAGGAACTTCTTCCTTTAATGGATTCCAGAGTCCGACTATTTACTATGTAGTCTCC *********************************
XM_824336.1 J02771.1 AF042286.1	GGGCTACCAGACCATGTTGTCCGGGAGTTGAAAAGTCAAAAATCATAAGGGCTACCAGACCATGTTGTCCGGGAGTTGAAAAGTCAAAAATCATAAATGGAAGCGAAG GGGCTACCAGACCATGTTGTCCGGGAGTTGAAAAGTCAAAAATCATAAATGGAAGCGAAG *****************************



Furthermore, apart from the genomic level (DNA), MSA was conducted at the protein level. After the BLAST and Cluster W analysis of protein sequences of drug targets with *T. theileri* proteome, which was found in NCBI databases, these drug targets showed a 12/17 (71%) homology with hypothetical *T. theileri* proteins (TM35) and pyruvate kinase (Figures 17 and 18).

On the other hand, among the drug targets themselves, the highest identity was detected in accession number of XP_829429.1 (445/445(100%)), which indicates ornithine decarboxylase protein (Figure 19). Furthermore, there was homology with AAD02222.1 and AAA30219.1, which encode the same protein from *T.grayi* and *T.brucei*, respectively. The MSA and the phylogenetic trees witnessed the homology of these sequences.

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 XP_829429.1 0.00049	Ornithine decarboxylase	ТВ
AAD02222.1 -0.00118	Ornithine decarboxylase	TG
AAA30219.1 0.00118	Ornithine decarboxylase	TB
ORC93851.1 0.37181	Dihydroxy-3-ketomethyldioxygenase	TT
ORC93850.1 0.37127	Hypothetical protein TM35_000017270	TT
ORC93848.1 0.37177	Hypothetical protein TM35_000017250	TT
XP_827904.1 0.18659	N-myristoyl transferase	TB
XP_009313274.1 0.1557	N-myristoyl transferase	TG
AEP82716.1 0.14652	N-myristoyl transferase partial	TC
ORC93856.1 0.40966	Hypothetical Protein TM35_000017330	TT
ORC93859.1 0.41854	Hot spot (RHS) protein, partial	TT
ORC93840.1 0.42146	Hypothetical protein TM35_000017170	TT
ORC93853.1 0.41573	Hypothetical protein TM35_000017310	TT
ABI96917.1 0.39109	Topoisomerase	ТС
ORC93854.1 0.36738	Hypothetical protein TM35_000017310	TT
ORC93843.1 0.31262	Hypothetical protein TM35_000017200	TT
ORC93842.1 0.41766	Coatomer alpha subunit	TT
ORC93849.1 0.3919	Hypothetical protein TM35_000017260	TT
XP_009309990.1 0	Pyruvate kinase 2	TG
KEG11772.10	Pyruvate kinase 2	TG
ORC92589.1 0.05295	Pyruvate kinase 2	TT
ESL09806.1 0.05353	Pyruvate kinase 2	TR
3QV9_B 0.05068	Pyruvate Kinase(Tcpyk)	TC
CCC94421.1 0.05016	Pyruvate kinase 1	TC
CCC52316.1 0.03772	Pyruvate kinase 1, partial	TV
EAN78782.1 0	Pyruvate kinase 1	TB
XP_827894.1 0	Pyruvate kinase 1	TB
ORC93858.1 0.38152	Hot spot (RHS) protein, partial	TT
ORC93855.1 0.4241	Hypothetical protein TM35_000017320	TT
XP_009316281.1 0.3720	Cathepsin L-like protein	TG
ORC93844.1 0.37795	Proteasome beta 7 subunit	TT
ORC93841.1 0.40854	Alkylated DNA repair protein	TT
CAA44870.1 0.37945	Trypanothione reductase	TB
ORC93857.1 0.2975	Hypothetical Protein TM35_000017340	ТТ
ORC93847.1 0.31333	RNA-binding protein	TT
ORC93852.1 0.40894	Hypothetical protein TM35_000017300	TT
ORC93845.1 0.36971	Phosphatidylinositol 3-kinase tor	TT
ORC93846.1 0.38247	Cell differentiation protein	TT

Figure 16. Phylogenetic tree following MSA of the drug targets and *Trypanosoma theileri*. TB: *T. brucei*, TG: *T. grayi*, TT: *T. theileri*, TC: *T. cruzi*, TR: *T. rangeli*, TV: *T. vivax*, TC: *T. congolense*

XP_009309990.1	GPSTQSVEALKGLMKSG	MSVARMNFSHGSHE-Y	HQATINNVRT	AAAELGLHIG	GIALDTK
3720					
KEG117721	GPSTQSVEALKGLMKSG	MSVARMNFSHGSHE-Y	HQATINNVRT	AAAELGLHIC	GIALDTK
3720					
ORC925891	GPSTQSVEALKGLMKSG	MSVARMNFSHGSHE-Y	HQTTINNVRT	AAAELGMHIG	JALDTK
3720		MOMADMARCHOOVE A			אשת דגדי
3720	GL2102AFURGTWV2G	MSVARMINE SIGSTE-1	INQI I INN V KA	AAALLGLUIG	JALDIK
CCC523161	CDOTOOVENTKCIMKCC	MCVARMNFCHCCHF-V	ͶϤϤͲͲϫͶͶϽϷϤ	AARTCIHT	איייראד
3720					
ESL098061	GPSTOSIEALRSLIKSG	MSVARMNFSHGSHE-Y	HOTTINNVRA	ASAELGVHIC	GIALDTK
3720			<u>£</u>		
30V9 в	GPSTQSVEALKGLIRSG	MSVARMNFSHGSHE-Y	HQTTINNLRA	AATELGAHIO	GLALDTK
3720					
XP 0093099901	GPEIRTGLFVGGEAVL-	NPGDTVFVTTDPAFE-		KKGTKEKFY\	/DYPRLAT
3780					
KEG117721	GPEIRTGLFVGGEAVL-	NPGDTVFVTTDPAFE-		KKGTKEKFY\	/DYPRLAT
3780					
ORC925891	GPEIRTGLFVGGEAIL-	MTGDTVLVTTDPAFE-		KTGTKEKFYI	DYPRLAT
3780					
XP 0093099901	FHRLTDRKGCNLP	GCDVDLPAVSAKDREI	DLKFGVEOGVD	IIFASFIRTA	EOVOEVR
3850	1	002122111011121122			
KEG117721	FHRLTDRKGCNLP	GCDVDLPAVSAKDREI	DLKFGVEQGVD	IIFASFIRTA	AEQVQEVR
3850					
ORC925891 3850	GHRLTDRKGCNLP	GCEVDLPAVSAKDREI	LKFGVEQGVD	MIFASFIRTA	EQVREVR
CCC944211	HHRLTDRKGINLP	GCEVDLPAVSEKDRKI	DLQFGVEQGVD	MIFASFIRTA	ADQVREVR
3850					
CCC523161	HHRLTDRKGCNLP	GCDVELPAVSEKDRKI	DLIFGVEQGVD	MIFASFIRTA	AEQVREVR
3850					
ESL098061	AHYLTDRKGCNLP	GCEVDLPAVSEKDREI	DLKFGVEQGVD	MIFASFIRTA	AEQVREVR
3850					
3QV9_B	AHFLTDRKGCNLP	GCEVDLPAVSEKDREI	DLKFGVEQGID	MVFASFIRTA	AEQVQEVR
3850					
EAN / 8 / 8 Z I	HHRLTDRRGINLP	GCEVDLPAVSEKDRKL	JLEFGVAQGVD.	MIFASFIRTA	AEQVREVR
XP 8278941	HHRLTDRRGINLP	GCEVDI.PAVSEKDRKI		MIFASFIRTZ	EOVREVR
3850					
VEC117701	AOMMI TERCHIDACE	T			
3970	AQUINIT SUCH AGU		VICAIQMLES.	MIANE RE	-IKAEV5D
ORC925891	AOMTLISKCNVAGK	₽	VICATOMLES	MTTNPRP	TRAEVSD
3970	-		-		
CCC944211	AQMCIISKCNVAGK	B		MTTNPRP	-TRAEVTD
3970					
CCC523161	AQMCIISKCNVAGK	B	VICATQMLES	MTTNPRP	-TRAEVSD
3970					
ESL098061	AQMILISKCNVAGK	E	PVICATQMLES	MTTNPRP	-TRAEVSD
3970					
3QV9_B	AQMILISKCNVAGK	E	PVICATQMLES	MTTNPRP	-TRAEVSD
3970	A OMOTITIC CONTRACTOR	-			
LAN / 8 / 821	AQMCIISKCNVVGK	E	YICATQMLES.	MISNPRP	TRAEVSD
ур 82780/1		 t	$\nabla V T \cap \Delta \Psi \cap M T = O$	MTSNPPP	
3970		L	• • • • • • • • • • • • • • • • • • •	~	

XP_0093099901 4010	VANAVFNG	ADCVMLSGETAKGKYPNEVV	RYMARICVEAQSATNQ
KEG117721 4010	VANAVFNG	ADCVMLSGETAKGKYPNEVV	RYMARICVEAQSATNQ
ORC925891	VANAVFNG	ADCVMLSGETAKGHYPNEVV	YMARICVVAQSATNQ
4010			
CCC944211 4010	VANAVFNG	ADCVMLSGETAKGKYPNEVV(QYMVRICIEAQSATHD
ESL098061 4030	VANAVFNG	ADCVMLSGETAKGKYPSEVV(QYMARICVEAQSATNQ
ЗQV9_В 4030	VANAVFNG	ADCVMLSGETAKGKYPNEVV(QYMARICLEAQSATNQ
EAN787821 4030	VANAVLNG	ADCVMLSGETAKGKYPNEVV(QYMARICVEAQSATHD
XP_8278941 4030	VANAVLNG	ADCVMLSGETAKGKYPNEVV(QYMARICVEAQSATHD
XP_0093099901 4150	SNSGRSARLTSKYR	PDCPIICVTTRMRTCRQ	LNVTRSVE
KEG117721 4150	SNSGRSARLTSKYR	PDCPIICVTTRMRTCRQ	LNVTRSVE
ORC925891 4150	SNSGRSARLASKYR	PNCPIICATTRMRTCRQ	LNITQSVE
CCC944211 4150	SNTGRSARLISKYR	PNCPIICATTRLLTCRQ	LNVTRSVE
AAD022221 4210	GPTCDGLDQIVERY	YLPEMQVGEWLLFEDMGAYTVVGTS-	SFNGFQSPTIYYVVSGLP
AAA302191 4210	GPTCDGLDQIVERY	YLPEMQVGEWLLFEDMGAYTVVGTS-	SFNGFQSPTIYYVVSGLP
XP_8294291 4210	GPTCDGLDQIVERY	YLPEMQVGEWLLFEDMGAYTVVGTS-	SFNGFQSPTIYYVVSGLP
XP_0093099901 4210	SVFYDAERCGADED	KENRVQLGVESAKKKGYVVPG	DIVVAVHADHKVKGYP
KEG117721 4210	SVFYDAERCGADED	KENRVQLGVESAKKKGYVVPG	DIVVAVHADHKVKGYP
ORC925891 4210	SVFYDAERYGPDDD	KENRVQLGVEFAKKKGYVVPG	DVMVVVHADHKVKGYP
CCC944211 4210	SVYYDVDAHGEDND	REKRVQLGVDWAKTKGYVSAG	DVMVIVHADHSVKGYP

Figure 17. Alignment of drug targets with Trypanosoma theileri (XP_0093099901) protein found in the NCBI database

AAD022221	EIQRVRGIGVP-PEKIIYANPCKQISHIR		550
AAA302191	EIQRVRGIGVP-PEKIIYANPCKQISHIR		
XP 8294291	EIQRVRGIGVP-PEKIIYANPCKQNSHIR		
ESL098061	YLTDRKGCNLPGCEVDLPAVSEKDREDLK		
3QV9 B	FLTDRKGCNLPGCEVDLPAVSEKDREDLK		
XP 0093099901	RLTDRKGCNLPGCDVDLPAVSAKDREDLK		
ке <u></u> 117721	RLTDRKGCNLPGCDVDLPAVSAKDREDLK		
CCC523161	RLTDRKGCNLPGCDVELPAVSEKDRKDLI		
EAN787821	RLTDRRGINLPGCEVDLPAVSEKDRKDLE		
XP_8278941	RLTDRRGINLPGCEVDLPAVSEKDRKDLE		
110000001			610
AADUZZZZI AAA202101		SLARCRESVEFGARVEDCR	610
AAASUZI9I VD 9204201		SLARCRESVEFGARVEDCR	
NP_0294291		VIENUCCIONIDATEA CO	
ESTOROD		KIENHQGVQNIDAIIEASD	
3QV9_B		KIENHQGVQNIDGIIEASD	
XP_0093099901		KIENHQGVQNIDGIIAVSD	
KEGII//ZI		KIENHQGVQNIDGIIAVSD	
UUU523101		KIENHQGVQNIDAIIEASD	
EAN / 8 / 8 / 1		KIENHQGVQNIDSIIEASN	
XP_82/8941		KIENHQGVQNIDSIIEASN	
CCC944211		KIENHQGVQNIDAIIEASD	
XP_0093132741			
AEP827161	EXILEPRKICEINFLCVHKLLRAKKLAPILIKEVTRRVH	ILMNIWQAVYTAGRLLPTP-	
AAD022221	FILEQAKKLNIDVTGVSFHVGSGSTDASTFAQ	AISDSRFVFDMG	670
AAA302191	FILEQAKKLNIDVTGVSFHVGSGSTDASTFAQ	AISDSRFVFDMG	
XP 8294291	FILEQAKKLNIDVTGVSFHVGSGSTDASTFAQ	AISDSRFVFDMG	
ESL098061	GIMVARGDLGVEIAAEKVVVAQMILISKCNVAG	KPVICATQMLESMT	
3QV9 B	GIMVARGDLGVEIPAEKVVVAQMILISKCNVAG	KPVICATQMLESMT	
XP 0093099901	GIMVARGDLGVEIPAEKVVVAQMMLISKCNVAG	KPVICATQMLESMT	
KEG117721	GIMVARGDLGVEIPAEKVVVAQMMLISKCNVAG	KPVICATQMLESMT	
CCC523161	GIMVARGDLGVEIPAEKVVVAQMCIISKCNVAG	KPVICATQMLESMT	
EAN787821	GIMVARGDLGVEIPAEKVCVAQMCIISKCNVVG	KPVICATQMLESMT	
XP_8278941	GIMVARGDLGVEIPAEKVCVAQMCIISKCNVVG	KPVICATQMLESMT	
CCC944211	GIMVARGDLGVEIPAEKVVVAQMCIISKCNVAG	KPVICATQMLESMT	
XP_0093132741	FTSGRYFHRSLNPEKLVAIAFSRIPPQYQKF	QNPMSMLKRFYQVP	
AEP827161	FATADYYHRSLNPEKLVAVGFSXIPQQYQKF	QNPLSMIKRFYELP	
XP_8279041	FAKGHYFHRSLNSQKLVDVKFSGIPPHYKRF	QNPVAVMERLYRLP	
AAD022221	KKVTPGVQTDVGAHAESNAQSFMYYVNDGVYGSFNCILYDE		910
AAASUZI91			
XP_0294291			
ESTORODI			
SQV9_В VD 0002000001			
XP_0093099901			
KEGII//ZI	SPEEAVCCSAVNSVIEVRAKVLLVLSNSGRSARLISKIRPL		
EAN787821	CPEEAVCSSAVASAFEVQAKAMLVLSNTGRSARLISKYRPN	ICPIICVTT	910
XP_8278941	CPEEAVCSSAVASAFEVQAKAMLVLSNTGRSARLISKYRPN	ICPIICVTT	
AAD022221	REPIPNEKLYPSSVWGPTCDGLDOIVERYYLPEMOVGE	WLLFEDMGA	
AAA302191	REPIPNEKLYPSSVWGPTCDGLDQIVERYYLPEMOVGE	WLLFEDMGA	970
XP 8294291	REPIPNEKLYPSSVWGPTCDGLDQIVERYYLPEMOVGE	WLLFEDMGA	-
ESL098061	RMRTCRQLTITRSVEPVFYDAERYGDDESKEKRVOLG	VEWAKKRG	
3QV9 B	RMRTCRQLTITRSVDAVFYDAERYGEDENKEKRVQLG	VDCAKKKG	
XP 0093099901	RMRTCRQLNVTRSVESVFYDAERCGADEDKENRVQLG	VESAKKKG	
KEG117721	RMRTCRQLNVTRSVESVFYDAERCGADEDKENRVQLG	VESAKKKG	
	- ~ ~ ~ ~		

Figure 18. Multiple sequence alignments among the drug targets excluding *Trypanosoma theileri* protein

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	
1: XP_829429.1	100	99.78	99.76	18.72	17.82	17.82	17.52	15.81	17.22	16.92	17.03	17.03	14.58	14.5	13.33	10.98	18.22	1
2: AAD02222.1	99.78	100	100	18.72	17.82	17.82	17.52	15.81	17.22	16.92	17.03	17.03	14.88	14.5	13.33	10.98	18.22	2
3: AAA30219.1	99.76	100	100	19.23	16.5	16.5	16.18	13.47	16.18	15.53	16.79	16.79	15.19	14.41	13.53	10.98	18.6	3
4: ABI96917.1	18.72	18.72	19.23	100	24.4	24.4	25.81	23.55	24.8	24.19	23.36	23.36	20.66	15.37	14.78	10.68	18.86	4
5: XP_009309990.1	17.82	17.82	16.5	24.4	100	100	82.97	88.18	86.37	86.17	80.34	80.34	22.2	16.77	18.81	16.81	18.37	5
6: KEG11772.1	17.82	17.82	16.5	24.4	100	100	82.97	88.18	86.37	86.17	80.34	80.34	22.2	16.77	18.81	16.81	18.37	6
7: CCC94421.1	17.52	17.52	16.18	25.81	82.97	82.97	100	91.21	82.16	82.36	86.89	86.89	23.17	17.07	18.51	16.38	19.59	7
8: CCC52316.1	15.81	15.81	13.47	23.55	88.18	88.18	91.21	100	84.55	85.15	87.91	87.91	23.59	17.14	19.25	16.74	17.2	8
9: ESL09806.1	17.22	17.22	16.18	24.8	86.37	86.37	82.16	84.55	100	89.58	80.34	80.34	22.44	17.38	20	17.67	15.92	9
10: 3QV9_B	16.92	16.92	15.53	24.19	86.17	86.17	82.36	85.15	89.58	100	80.63	80.63	21.71	17.07	18.81	17.24	16.33	10
11: EAN78782.1	17.03	17.03	16.79	23.36	80.34	80.34	86.89	87.91	80.34	80.63	100	100	23.16	17.86	17.77	14.97	18.27	11
12: XP_827894.1	17.03	17.03	16.79	23.36	80.34	80.34	86.89	87.91	80.34	80.63	100	100	23.16	17.86	17.77	14.97	18.27	12
13: CAA44870.1	14.58	14.88	15.19	20.66	22.20	22.20	23.17	23.59	22.44	21.71	23.16	23.16	100	14.33	13.65	14.07	19.83	13
14: XP_827904.1	14.5	14.5	14.41	15.37	16.77	16.77	17.07	17.14	17.38	17.07	17.86	17.86	14.33	100	59.64	63.52	13.58	14
15: XP_009313274.1	13.33	13.33	13.53	14.78	18.81	18.81	18.51	19.25	20	18.81	17.77	17.77	13.65	59.64	100	69.45	11.93	15
16: AEP82716.1	10.98	10.98	10.98	10.68	16.81	16.81	16.38	16.74	17.67	17.24	14.97	14.97	14.07	63.52	69.45	100	12.28	`6
17: XP_009316281.1	18.22	18.22	18.6	18.86	18.37	18.37	19.59	17.2	15.92	16.33	18.27	18.27	19.83	13.58	11.93	12.28	100	17

 Table 6. Percent identity and divergence of Cluster W alignment of drug targets

Target protein	Species/strain	
XP_829429.1 0	Ornithine decarboxylase	ΤI
AAD02222.1 -0.00239	Ornithine decarboxylase	ТС
AAA30219.1 0.00239	Ornithine decarboxylase	TE
XP_009316281.1 0.40926	Cathepsin L-like protein	TC
XP_827904.1 0.19547	N-myristoyl transferase	TE
XP_009313274.1 0.14334	N-myristoyl transferase	TC
AEP82716.1 0.16212	N-myristoyl transferase partial	TC
ABI96917.1 0.38256	Topoisomerase	TC
CAA44870.1 0.39386	Trypanothione reductase	TI
XP_009309990.1 0	Pyruvate kinase 2	ТС
KEG11772.1 0	Pyruvate kinase 2	TC
ESL09806.1 0.05239	Pyruvate kinase 2	Tł
3QV9_B 0.05182	Pyruvate Kinase(Tcpyk)	TC
EAN78782.1 0	Pyruvate kinase 1	TE
XP_827894.1 0	Pyruvate kinase 1	TH
CCC94421.1 0.05135	Pyruvate kinase 1	тс
CCC52316.1 0.03653	Pyruvate kinase 1, partial	TV

TB: T.brucei, TG: T. grayi, TT: T. theileri, TC: T.cruzi, TR: T. rangeli, TV: T.vivax, TC: T.congolense

Figure 18. Phylogenetic tree following multiple sequence alignments showing relationships among common trypanocidal drug targets

Growth media and condition

Trypanosoma theileri is one of the least studied trypanosomes although it is prevalent worldwide. This distribution may be due to the pathogenic nature of the parasite, which, compared to pathogenic ones, cannot cause a remarkable loss of production and productivity in livestock. However, nowadays researchers are focusing on *T. theileri* since it has been used as a setup and new tool for trypanosomatid-based delivery (Mott et al., 2011) for the treatment of pathogenic trypanosome and other hemoparasites affecting livestock and humans. Nevertheless, due to its low parasitemic nature, it is rarely detected by direct smear microscopy. In view of this, Verloo et al. (2000) developed a kit called KIVI as an excellent tool for isolating *T. Theileri* which they found successful.

There are a number of media that must be cultured for both epimastigote and trypanosome's blood flow stages. For the blood flow stages of *T. theileri* (Trypomastigotes), RPMI medium 1640 with 10% FCS, supplemented with murine spleen cells as a feeder layer, was used (Verloo et al., 2000). In addition, it could be cultured in tissue culture fluid NCTC-109 (Splitter and Soulsby, 1967), 50% HMI-9 medium (Hirumi and Hirumi, 1989) supplemented with 20% FCS, 10% Serum, and 50% MDBK-conditioned media (Mott et al., 2011).

In the present study, it was possible to grow *T. theileri* epimastigotes in SDM 79 with 10 % FCS at 26°C without CO₂betweenfour media tested (Figure 2). Under similar growth conditions, Wink (1979) cultured *T. Theileri* epimastigotes at 25°C with 10 % FCS, but with different growth media, Glossina Cell culture Medium (GCM). Moreover, in the second growth condition (at 37°C with 5% CO₂) there was slight growth of *T. theileri* epimastigotes in RPMI 1640 (Figure 3), which was confirmed by Verloo et al. (2000), who could culture *T. theileri* with RPMI 1640. However, the growth of *T. theileri* epimastigote in RPMI 1640 at 26°C with CO₂ was less than the time cultivated at 26°C without CO₂ (Figure 2) in the present study. This could be due to the reluctance to use PMI conditioning since they used a feeder layer of murine spleen cells. In addition, Verloo et al. (2000) cultured the blood flow stage that was directly isolated from the blood.

Growth pattern and doubling time

The culture of *T. theileri* in eight different tissue culture flasks showed maximum growth on the sixth day during the eight experiments, except for the seventh experiment on the seventh day. On the other hand, as can be seen in Figure 3, the log phase starts clearly from the third day. This indicated that the logarithmic phase of growth was started from the third to the seventh day for the seventh experiment. The maximum number of cells that could be grown among the eight flasks was estimated to be 1.7×10^7 cells/mL (Experiment 2). Hence, the logarithmic phase extended from 3.2×10^4 cells/mL, which was on the third day of the experiment. Second, to the highest 1.3×10^7 cells/mL from the same flask on the sixth day except for Experiment seven. The doubling time in the logarithmic growth phase was estimated to range from 13.43 to 19.0 hours with an average estimate of 17.43 hours (0.73 day) in eight experiments. The doubling time of the present study is slightly higher than the doubling time of *T. theileri* reported by Wink (1979) with a doubling time of 10-14 hours. However, the growth pattern of *T. theileri* is2.5 times higher than the doubling time of *T.b.brucei* as described by Sykes and Avery (2009) and Melissa et al. (2009).

The doubling time could indicate that *T. theileri* grows more slowly than other similar reports. The slow growth rate could be due to different media types and growing conditions. It is in a sense that, if the parasite has got a favorable growth environment, they may have the opportunity to divide within a short period. Furthermore, the slower growth of *T. theileri* compared to the growth of other pathogenic Trypanosomesmay be linked to the factors that could make the parasite a pathogen. This means that the longer replication time and the lower parasitemic features can naturally cause the least amount of anemia. The serious losses from pathogenic trypanosomes are principally due to anemia. Furthermore, the lower detection level in the blood can limit the distribution of the parasite to different visceral organs and haemopoietic tissues, such as the spleen. Moreover, virulent trypanosomes have a shorter incubation period than pathogen ones (Magona et al., 2008). The longer the doubling time which was needed in the present study, can be related to this point. The same applies to the study by Böse et al. (1987), who reported that after identifying the stages of infection of *T. theileri* in the gut and feces of tabanids, it could be determined that the minimum prepatent period of around four days in infected cattle despite no apparent signs of disease were detected.

Resazurin assay

The epimastigote $(5.2 \times 10^5/\text{mL} \text{ to } 8.5 \times 10^6/\text{mL})$ was grown in a microtiter plate for three different concentrations of Resazurin. Initially, there was a lower fluorescence signal throughout the three Resazurin concentrations. However, it increased significantly from 1.2×10^6 cells/ml and reached the highest fluorescence signal detection at 3.5×10^6 cells/mL following the seventh hour of incubation with Resazurin. It indicated that there was a positively correlated (r = 0.7517-0.9252; p < 0.05) fluorescence signal with an increase in cell density and Resazurin concentrations.

On the other hand, there was a positive correlation (r = 0.8297; p < 0.05) among fluorescence signals as a result of 2.4 mM Resazurin than the other two concentrations with an increase in incubation time (Figure 8) until 7 hours using an optimal 1.2×10^6 cells/mL of cell density. The fluorescence decreased dramatically after the seventh hour of incubation with Resazurin (Figure 7). It is in agreement with a study by Tana et al. (2012) who reported that Resazurin was reduced linearly after three to four hours of incubation with 25 mg/mL (20 µL/well) Resazurin though it was done on T. brucei. They also reported that the maximum fluorescence was recorded in the range of $2-5 \times 10^6$ cell/mL which was almost similar to the optimal cell density found for higher fluorescence $(1.2-3.5 \times 10^6 \text{ cells/mL})$ with 2.4Mm Resazurin. There was a very high and linear correlation (r = 0.9876) observed in the fluorescence signal of the parasite in the range of $1.3 \times$ 10^6 to 5.3×10^6 cells/ml upon incubating with 2.4 mM Resazurin for 7 hours at 26°C. It is slightly higher than the incubation time used for fluorescence assay for T. cruzi which was 5 hours as reported by Miriam et al. (2006). Similarly, according to Tana et al. (2012), there was a linear reduction of Resazurin after a 3-4 hours period of contact time since there might be a saturation of the fluorescence at such high parasite densities. A report by Miriam et al. (2006) also showed the highest concentrations of Resazurin (3 mM) among the Resazurin concentrations they tested (0.5 to 3 mM), showed the highest Resazurin reduction. The same is true from our experiment since the highest Resazurin concentration (2.4 mM) showed a similar pattern. It may be due to the fact that whenever we use the lowest concentration of Resazurin, the Resazurin (blue) can be converted to a more fluorescent resorufin(pink) immediately within a short time. Then, if it was allowed for a long incubation time, the resorufin which is the fluorescent one will be converted to a non-fluorescent stage finally. It shows an imbalance between the highest numbers of cells with the lowest concentration of Resazurin used. Due to this, maybe the highest concentration showed a significant correlation in the magnitude of fluorescent signal with an increase in cell density and incubation time.

Drug sensitivity

The Resazurin assay enables the measurement of parasite viability as an indicator of the ability to recover from compound effects (Nare et al., 2010; Tana et al., 2012). By using the optimization conditions we established for cell density and Resazurin concentration, the Resazurin-lead assay was applied to assess the susceptibility of T. theileri epimastigotes to Pentamidine (Sigma, 1-100 ng/mL). As a consequence, a negatively correlated (r = -0.8826) and statistically significant (p < 0.05) difference were observed between the reduction in fluorescence signal and an increase in pentamidine concentration predominantly in the highest drug concentration. A study was done on *T.b.brucei* by Tana et al. (2012) also indicated a similar response of the parasite following 72 hours of incubation with Pentamidine which result in a dramatic reduction of Resazurin signal. The viability percentage was determined by comparing both microscopic counting which is anti-epimastigotes (%AE) and the resazurin assay with Pentamidine (1-100 ng/mL). IC₅₀ values of 9.25 ng/mL and 16.29 ng/mL were found by using Resazurin (r = -0.957, p < 0.05) and microscopic counting (r= 0.90, p < 0.05) respectively. These two tests showed roughly similar outcomes though Resazurin assay was more preferable since it has relatively lower IC₅₀ (Figure 11). Furthermore, it allowed screening a large sample size as far as microscopic counting is time-consuming. It was in agreement with the report by Miriam et al. (2006) and Sykes and Avery (2009) mentioning that Resazurin was preferable to test the viability of *T.b. brucei* for Pentamidine and Suramin. The IC₅₀ value was higher than the reports by Sykes and Avery (2009) and Tana et al. (2012), who reported 5ng/mL and 40 nM, respectively for T.brueci.

Experimental infection of calves

During the experimental infection of the present study, the identification of parasites both in Giemsa stained slides and through culturing the PBMC and the buffy coat in RPMI 1640 and HMI 9 medium was unsuccessful. However, a similar method of experimental infection was followed by Mott et al. (2011). The problems could be, first, the parasite could die in transit prior to inoculation since the farm was a few kilometers away from the laboratory where the parasite was cultured. Secondly, it might be due to the time it took for replication to happen. According to the doubling time calculated during the in vitro culture, they needed 13.43 to 19 hours. Third, based on the amount of the parasite, the calf was inoculated between five and nine ml. Finally, maybe another co-founding factor has not yet been realized. Nevertheless, a similar study was done by Mott et al. (2011) after experimental infection. However, they extracted DNA directly from whole blood samples than growing the parasite after identification from buffy coat and/or PBMC since it's rarely detected due to the low level of parasitemia. However, the focus of the present study was on the culturing of the blood-streaming form in mass after isolating from the blood for further proteomic studies; to compare the epimastigote and trypomastigotes proteomics.

PCR confirmation of Trypanosoma theileri

Trypanosoma theileri could be differentiated from other trypanosomes through a species-specific primer (Tth625) as described by Rodrigues et al. (2003), PCR-amplified spliced-leader transcript, 18S ribosomal DNA, and internal transcribed spacer of ribosomal genes (ITS gene, Geysen et al., 2003). In the present study, the results obtained by PCR

and agarose gel electrophoresis based on Species-specific primers confirmed a 465 bp amplification product which was comparable with 450 bp DNA fragment (Tth625 fragment) by Rodrigues et al. (2003)and 472 bp by Lee et al. (2013). For the second amplification for the 18S rDNA sequence of *T. theileri*, a band with a size of730 bp was detected, which was almost expected to be 722 bp, as reported by Geysen et al. (2003).

In silico analysis

The BLAST and Clustal W alignment were done both at nucleotide (DNA) and protein level with target sequences of common anti-trypanosome drugs. Following a BLAST and Cluster W alignment using these common drug targets, there was only one slight homogeneity (75%) gene (CATL gene) which was found in both *T.grayi* (XM_009318006.1) and HQ664735.1 of *T. theileri* isolate in common. On the other hand, among the drug targets only, excluding *T. theileri* genome; they had a very high identity especially among XM_824336.1 (100%), J02771.1 (99%), and AF042286 (99%) which entirely indicated Ornithine decarboxylase gene in*T.brucei*. The phylogenetic tree and ClusterW alignment also showed these relationships. Lee et al. (2013)have got the homology of their isolate (TWTth1) from Taiwan with isolates by Rodrigues et al. (2003), Gene Bank Accession No: AF537201 (99.5%) and AF537202 (98.8%) from Brazil. They did the comparison based on *T. theileri* DNA. In addition, based on the full-length 18S rDNA sequence amplicon of their isolate, they found 100% identity with AB007814.1. Based on ITS sequences, Lee et al.(2013)reported that there was a similarity amongAB007814 (100%), AY773707 (97.3%), and AY773708 (98.0%) which are Japanese and Brazilian isolates.

At the protein level, there was almost no similarity of these drug targets with the proteins found in the NCBI database except a slight similarity with hypothetical *T. theileri* proteins (TM35). However, among the drug targets, a prominent homology was detected among XP_829429.1(100%), AAD02222.1, and AAA30219.1 which indicated ornithine decarboxylase protein as was obtained after analyzing at DNA level in the current study. The MSA and the phylogenetic trees witnessed the homology of these sequences.

Accordingly, BLAST was used in the current study and aligned only with partial and hypothetical sequences of the *T. theileri*. However, there were homologies of sequences from anti-trypanosome drug targets specifically for Ornithine decarboxylase from *T.brucei*. Similarly, Rodrigues et al. (2003) reported that *T. theileri* and '*T. brucei* clade' trypanosomes shared artiodactyl host species with overlapping distributions and commonly bovids carrying mixed trypanosome infection in the field.

CONCLUSIONS

In the present study, *T. theileri* was successfully cultured *in vitro* in SDM 79 at 26°C. The growth pattern, viability, and response to pentamidine were assessed by Resazurin assay. *T. theileri* parasite took a longer time to double the population, compared to other trypanosomes. Moreover, the Resazurin assay using pentamidine was deployed as the reference drug to confirm the effectiveness of this assay technique. Consequently, it could be possible to use such a sensitive and inexpensive assay for high-throughput screening of anti-trypanosome compounds. On the other hand, after extraction of the DNA by the PhenolChloroform protocol from cultured *T. theileri*, the parasite was confirmed using PCR amplification by species-specific primers.

Furthermore, the BLAST and MSA were performed with common anti-trypanosome target sequences. Subsequently, in contrast to the anti-trypanosome targets of pathogenic trypanosomes, significant similarity at both the DNA and protein level with *T. theileri* was detected. However, some similarities to hypothetical. *theileri* proteins (TM35) were observed. Both at DNA and protein level, significant homologyamongXP_829429.1, AAD02222.1, and AAA30219.1 were detected which all referred to ornithine decarboxylase protein in *T.brucei*. The lack of homology in *T. theileri* might be due to the lack of a complete genome sequence. Finally, whole-genome and transcriptome analyses using *T. theileri* can reveal the phylogenetic relationship between *T. theileri* and other pathogenic trypanosomes, which can be used as a tool in the development of new therapeutic drugs for the treatment of the pathogenic trypanosome.

Based on the above conclusions, the following recommendations are put forward. The present study provides baseline data for the next research on the parasite. In the case of experimental infection, it is better to infect the test animal as soon as possible, while the parasite could soon die if transported with PBS. Long and continuous blood sampling should be performed after experimental infection. In the present study, only two consecutive weeks were checked after each infection. There is a chance that the parasite may not be immediately naturally isolated due to a low level of parasitemia. Hence, most of the isolation of *T. theileri* from natural infection was not purposively confirmed. Rather, it was found in an unexpected time. It can be isolated while researchers pursue other goals. For example, the total leukocyte and differential count, and PCV are examined during the macrophage culture while the Bovine Leukemia Virus(BLV) is examined from lymphocyte cultures of cows infected with it. It is better to use a reader with higher fluorescence to get a higher magnitude of the fluorescence signal. Better to use more than two drugs for treatment so that the drug sensitivity assay is representative and comparable.

DECLARATIONS

Authors' contribution

Tewodros Fentahun contributed to data collection, lab activities, and a write-up of the manuscript. Jan Paeshuyse was involved in data analysis. Both authors confirmed the final revised manuscript.

Competing interests

The authors have no conflicts of interest.

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Ethical considerations

Ethical issues (including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by the authors.

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ORIGINAL ARTICLE

Immunolocalization of Steroidogenic Enzymes (3β-hydroxysteroid dehydrogenase, 17β-hydroxysteroid dehydrogenase, and P450scc) in Rats with Testicular Dysfunction Treated with Mesenchymal Stem Cells-conditioned Medium

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ABSTRACT

About 60-80 million couples in the world are suffering from infertility disease. Infertility is a major problem in patients coping with chemotherapy. The chemotherapy process can degenerate non-target organs, especially in testes. Infertility in male or testicular dysfunction is caused by the failure of proliferation and differentiation of the spermatogenic cells. Many studies reported that mesenchymal stem cells-conditioned medium promoted regenerative processes. The present study aimed to investigate the effect of mesenchymal stem cells-conditioned medium on the cisplatin-induced testicular dysfunction by examining the immunolocalization of steroidogenic enzymes, such as 3β-hydroxysteroid dehydrogenase, 17β-hydroxysteroid dehydrogenase, and P450scc which are considered as markers of steroid production. All experimental animals were divided into three groups, namely the control group, mesenchymal stem cells-conditioned medium treated group with an injection dose of 0.2 ml/kg body weight (BW, P1), and mesenchymal stem cells-conditioned medium treated group with an injection dose of 0.5 ml/kg BW (P2). Cisplatin was injected into both treated groups to induce testicular dysfunction. The testicular tissues were processed by the paraffin method, then cut to a thickness of 5 µm, followed by immunohistochemical staining. The HSD3B1 immunoreactivities were found only in Leydig cells, and the intensity increased every week after the injection of mesenchymal stem cells-conditioned medium. The variety of weeks and groups was significantly different in the number of immunoreactive cells of HSD3B1. The results indicated a significant difference between one week after the first injection and the one week after the third and fourth injection. The findings showed a significant difference between the treated group with an injection dose of 0.2 ml/kg BW and the control group. The number of immunoreactive cells of HSD3B1 with an injection dose of 0.5 ml/kg BW was greater compared to the group that received an injection dose of 0.2 ml/kg BW. The intensity of HSD3B1 and HSD17B1 increased every week. The p450scc immunoreactive cells were only found in Leydig cells. The intensity of positive cells of p450scc in the treated group with an injection dose of 0.5 ml/kg BW was more intense, compared to the treated group with an injection dose of 0.2 ml/kg BW. The results of the current study showed that the injection of mesenchymal stem cells-conditioned medium can improve the regeneration of spermatogenic cells, and recover spermatogenesis proved by positive cells of HSD3B1, HSD17B1, and p450scc as markers of steroid production.

Keywords: Cisplatin, HSD17B1, HSD3B1, Mesenchymal stem cells-conditioned medium, P450scc, Testicular dysfunction

INTRODUCTION

About 60-80 million couples in the world are suffering from an infertility disease, and about 40-50% of the infertility is caused by male factors. Infertility is an extremely common physical disorder in adults, which occurs due to trauma, infections, tumor growth, and radiation therapy in patients coping with chemotherapy (Zhang et al., 2017). The chemotherapy process can degenerate non-target organs, especially in testes, that decrease the quality and quantity of sperm. Infertility in male or testicular dysfunction is caused by the failure of proliferation and differentiation of the spermatogenic cells. Testicular dysfunction in an animal model can be induced by anticancer drugs, such as busulfan, cyclophosphamide, doxorubicin, procarbazine, or cisplatin (Atessahin et al., 2006). Cisplatin is an anticancer drug potential; however, a high dose of cisplatin is extremely toxic for testicles. Some researchers reported that the administration of antioxidants, such as lycopene, royal jelly, curcumin, melatonin, Vitamin C, montelukast, resveratrol, selenium, and amifostine, can improve the degeneration of testis (Beytur et al., 2012; Reddy et al., 2016; Simsek et al., 2016).

Mesenchymal Stem Cells (MSCs) have been used widely in the treatment of organ dysfunctions, such as testicular dysfunction. Many studies have reported the improvement of androgen deficiency after stem cell therapy. Human Umbilical Mesenchymal Stem Cells (HUMSCs) can increase testosterone levels, and Leydig-like cells are functioning

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well in hypogonadism models (Zhang et al., 2017). Transplanted rat adipose-derived MCSs into D-galactose-treated aging rats can improve testicular function by being differentiated into $3-\beta$ -Hydroxysteroid Dehydrogenase (HSD3B1) positive Leydig-like cells (Yang et al., 2015). Tamadon et al. (2015) reported that transplanted Bone Marrow-Mesenchymal Stem Cells (BM-MSCs) could successfully induce spermatogenesis in seminiferous tubules of azoospermia hamsters. Mesenchymal stem cells-conditioned medium or secretome is a factor secreted by stem cells containing growth factors and cytokines. Many studies reported that mesenchymal stem cells-conditioned medium promotes regenerative processes, such as healing diabetes mellitus type 1 by improving the pancreatic beta cells (Nugroho et al., 2016), and regenerating the healing burns (Padeta et al., 2017). It also regenerates the incise wound healing (Kusindarta et al., 2016). The present study aimed to investigate the effect of mesenchymal stem cells-conditioned medium in cisplatin-induced testicular dysfunction by examining the immunolocalization of HSD3B1, 17 β -Hydroxysteroid Dehydrogenase (HSD17B1), and P450 Side-Chain Cleavage enzyme (P450scc).

MATERIALS AND METHODS

Ethical approval

The present study was approved by Ethical Clearance from Universitas Gadjah Mada, Yogyakarta, Indonesia with number 00035/04/LPPT/V/2017

Experimental animals

A total number of 36 healthy male Wistar rats (Rattus norvegicus) aged three-month-old, with an average weight of about 300 grams, were randomly divided into three groups. The groups included the control group, and the mesenchymal stem cells-conditioned medium treated groups with an injection dose of 0.2 ml/kg BW (P1), and the mesenchymal stem cells-conditioned medium treated groups with an injection dose of 0.5 ml/kg BW (P2). The control group was not injected with cisplatin, but injected with 0.9% physiological NaCl. The P1 and P2 groups were injected with cisplatin to induce testicular dysfunction, and continued with an injection dose of 0.2 ml/kg BW and 0.5 ml/kg BW of mesenchymal stem cells-conditioned medium. The rats in the treated groups were injected with Cisplatin (PT Dankos Farma, Kalbe Company, Indonesia) at a dose of three mg/kg BW three times at three-day intervals (Reddy et al., 2016; Prihatno et al., 2018). The mesenchymal stem cells-conditioned medium was injected one time a week for four times after all doses of cisplatin were injected.

Sample collection

Testicular tissues were collected one week after the first, second, third, and fourth injection of mesenchymal stem cells-conditioned medium. Testicular tissues were fixed in Bouin's solution for 24 hours, embedded in paraffin, sectioned to a thickness of 5 μ m, and stained with the immunological method (Prihatno et al., 2020) to visualize the immunoreactivity of HSD3B1, HSD17B1, and P450scc.

Immunohistochemical staining

The first step of immunohistochemical staining was deparaffinization with xylene. Then, the slides were rehydrated with ethanol, and rinsed in running water for 5 minutes. Distillate water was placed in the microwave for 20 minutes for pre-heating the antigen retrieval, and then the slides were immersed in pre-heating distillate water for 10 minutes for antigen retrieval. Endogenous peroxide activity was blocked by incubating the slides in H₂O₂ 3% in absolute methanol (1 mL H₂O₂ 30%, 9 mL absolute methanol) for 30 minutes at room temperature. The slides were washed in Phosphate Buffer Saline (PBS) for five minutes, then repeated three times. Immunoreactivity was visualized with rabbit Diaminobenzidine (DAB) Detection IHC Kit (Fine Test, Wuhan Fine Biotech Co., Ltd., China) (Prihatno et al., 2020). After that, the slides were incubated overnight at 4^oC with HSD3B1 polyclonal antibody (1: 200, MBS2530192, Mybiosource, USA), HSD17B1 polyclonal antibody (1:400, A10839, ABclonal, USA), and Cytochrome P450scc Enzyme polyclonal antibody (1:500, AB1244, MilliporeSigma, USA). After that, the slides were washed again in PBS for five minutes, then it was repeated three times, and they were incubated with poly-HRP Goat Anti-Rabbit IgG for 60 minutes, and then for the last time, the slides were washed again in PBS three times for five minutes. Sites of immunoreactivity were visualized with DAB Chromogen. Harris hematoxylin was used for counter-staining the slides, followed by rinsing the slides with running water for 10 minutes. Lastly, the slides were dehydrated, cleared, and mounted. A light microscope was used to examine the stained slides, and Optilab® camera was used to take a photomicrograph.

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Statistical analysis

The number of immunoreactive cells of HSD3B1 was analyzed statistically using the Analysis of Variance (ANOVA) test followed by Duncan's post hoc test with software IBM SPSS Statistic 22. In this study, p < 0.05 was considered significant.

RESULTS

The immunoreactivity of HSD3B1 was detected in Leydig cells, and the intensity increased every week (Figures 1 and 2). The intensity of both treated groups, P1 and P2, on one week after the first injection, the immunoreactivity showed weak intensity (Figures 1-A and 2-A). One week after the second injection, the immunoreactivity of treated groups, both P1 and P2, showed no difference compared to the control group. One week after the third and the fourth injections, the intensity of both treated groups was stronger compared to the control group.

The obtained results of different time periods (one week after the first, second, third, and fourth injections) indicated a significantly different number of immunoreactive cells of HSD3B1 (p < 0.05). The investigated groups (P1, P2, and the control group) were significantly different regarding the number of immunoreactive cells of HSD3B1 (p < 0.05, Table 1). The results revealed a significant difference between the obtained results of one week after the first injection and one week after the third and fourth injection. However, one week after the first injection was not significantly difference between the P1 and control groups (p < 0.05). However, the P1 group was not significantly different in the number of immunoreactive cells of HSD3B1 compared to the P2 group. The control group was not significantly different in the number of immunoreactive cells of HSD3B1 compared to the P2 group (Table 3). The number of immunoreactive cells of HSD3B1 in the P2 group was greater compared to the P1 group (Table 3).



Figure 1. Immunoreactive cells of HSD3B1 with injection dose of 0.2 ml/kg BW mesenchymal stem cells-conditioned medium. A: One week after the first injection, B: One week after the second injection, C: One week after the third injection, D: the control group; black arrow: Immunoreactive cells of HSD3B1

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Figure 2. Immunoreactive cells of HSD3B1 with injection dose of 0.5 ml/kg BW mesenchymal stem cells-conditioned medium. A: One week after the first injection, B: One week after the second injection, C: One week after the third injection, D: One week after the fourth injection, E: Control group, black arrow: Immunoreactive cells of HSD3B1

Table 1.	Analy	sis of	variance	at the	number	of immu	noreactive	cells	of HSD3B1
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Source	Type III Sum of Squares	df	Mean Square	\mathbf{F}	p value
Corrected model	7115.575 ^a	5	1423.115	9.591	0.000
Intercept	37238.450	1	37238.450	250.973	0.000
Weeks	6189.083	3	2063.028	13.904	0.000
Groups	2551.800	2	1275.900	8.599	0.001
Error	5044.800	34	148.376		
Total	55391.000	40			
Corrected Total	12160.375	39			

^{a.} R Squared = 0.585 (Adjusted R Squared = 0.524). R Squared (R^2) showed that the variety of weeks effects on a variety of groups was 58,5%. The significance level less than or equal to 0.05 was considered statistically significant (p < 0.05).

Table 2. The mean of immunoreactive cells of HSD3B1 one week after the first, second, third, and fourth injection of mesenchymal stem cells-conditioned medium, and in the control group in rats with testicular dysfunction

Week	Mean
One week after the first injection	21.80 ^a
One week after the second injection	30.90 ^a
One week after the third injection	41.70 ^{bc}
One week after the fourth injection	52.40 ^c
$\overline{a,b,c}$ Means within a column with different superscripts differ significantly (p < 0.05).	

Table 3. The mean of immunoreactive cells of HSD3B1 in the P1, P2, and control group in rats with testicular dysfunction

Group	Mean
The P1 group	26.93 ^a
The P2 group	35.55 ^{ab}
Control group	40.00 ^b

The P1 group: mesenchymal stem cells-conditioned medium treated group with an injection dose of 0.2 ml/kg BW; The P2 group: mesenchymal stem cells-conditioned medium treated group with an injection dose of 0.5 ml/kg BW; a,b Means within a column with different superscripts differ significantly (p < 0.05).

The immunoreactivity of HSD17B1 was detected in Sertoli cells, Leydig cells, and spermatids. The intensity was increased every week. At first, the intensity of immunoreactive cells detected in spermatids and Sertoli were weak at one week after the first injection in the P1 group. The spermatogenic cells in one week after the first and the second injections were still not complete compared to one week after the third injection (Figure 3). The intensity of HSD17B1 increased in the P2 group (Figure 4). One week after the second injection of the P2 group, the spermatogenic cells improved similar to the ones in the control group. One week after the first injection, the intensity was weak. One week after the second and the third injections, the intensity was strong, and one week after the fourth injection, it was very strong. The spermatogenic cells in the group with cisplatin-induced testicular dysfunction were destroyed and lost

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(Figure 5). The immunoreactivity of p450scc was detected in Leydig cells. The immunoreactivity in the P2 group was increased one week after the second injection of mesenchymal stem cells-conditioned medium. One week after the first injection, the intensity was weak. However, one week after the third and the fourth injections was strong. The number of positive cells increased every week (Figure 6). The immunoreactivity of p450scc was detected weak one week after the first injection of 0.2 ml/kg BW mesenchymal stem cells-conditioned medium. Although in one week after the second and the third injections, it was strong (Figure 7). The immunoreactivity of p450scc on the control group was detected in Leydig cells with strong intensity (Figure 8-B). The immunoreactivity of p450scc in the group with cisplatin-induced testicular dysfunction was not expressed. A lot of spermatogenic cells have been damaged (Figure 8-A).



Figure 3. Immunoreactive cells of HSD17B1 of the treated group with an injection dose of 0.2 ml/kg BW of mesenchymal stem cells-conditioned medium. Immunoreactive cells were detected in Sertoli cells and spermatids with a weak intensity one week after the first injection dose of 0.2 ml/kg BW mesenchymal stem cells-conditioned medium. A: One week after the first injection, B: One week after the second injection, C: One week after the third injection, black arrow: IMMUNOREACTIVE cells of HSD17B1



Figure 4. Immunoreactive cells of HSD17B1 in the treated group with an injection dose of 0.5 ml/kg BW of mesenchymal stem cells-conditioned medium treated group. A: One week after the first injection, B: One week after the second injection, C: One week after the third injection, D: One week after the fourth injection, black arrow: Immunoreactive cells of HSD17B1

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Figure 5. Immunoreactive cells of HSD17B1 in the cisplatin-induced group with the testicular dysfunction and the control group. A: Cisplatin-induced testicular dysfunction, B: Control group, black arrow: Immunoreactive cells of HSD17B1



Figure 6. Immunoreactive cells of p450scc in the treated group with an injection dose of 0.5 ml/kg BW of mesenchymal stem cells-conditioned medium. A: One week after the first injection, B: One week after the second injection, C: One week after the third injection, D: One week after the fourth injection, black arrow: Immunoreactive cells of p450scc.



Figure 7. Immunoreactive cells of p450scc in the treated group with an injection dose of 0.2 ml/kg BW of mesenchymal stem cells-conditioned medium. A: One week after the first injection, B: One week after the second injection, C: One week after the third injection, black arrow: Immunoreactive cells of p450scc.

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Figure 8. Immunoreactive cells of p450scc in the cisplatin-induced group with the testicular dysfunction and the control group. A: Cisplatin-induced testicular dysfunction group. B: Control group. Black arrow: Immunoreactive cells of p450scc, black star: Damage of seminiferous tubules.

DISCUSSION

Steroidogenesis involves multiple processes for the biosynthesis of steroid hormones (testosterone) from cholesterol in Leydig cells. Steroid hormones regulate sexual development and are essential for physiological functions. In males, the Leydig cells are considered important for producing the testosterone hormone that is critical for spermatogenesis and maintenance of secondary sexual functions (Wang et al., 2017). Steroidogenesis depends on the steroidogenic enzyme, including P450scc, HSD3B1, HSD17B1, 17a-hydroxylase/C17, 21 lyases (P450c17), and aromatase cytochrome P450 (P450arom) as markers of steroid production (Kobayashi et al., 1998).

The HSD3B1 is a key enzyme necessary for the synthesis of testosterone in Leydig cells in rats. This enzyme has a major catalytic activity in changing pregnenolone, 17-OH-pregnenolone, dehydroepiandrosterone (DHEA), and androstenediol. The deficiency of HSD3B1 affects the gonads (testes in males) and adrenal glands, which reduces the production of the testosterone hormone. The HSD17B1 enzyme is involved in the local regulation of sex steroids (Gunnarsson et al., 2005). The HSD17B1 is involved in the final step of the biosynthesis of testosterone, which catalyzes androstenedione to testosterone hormone (Baker et al., 1997). In immunohistochemistry methods, the immunoreactivity expresses in Leydig cells of interstitial cells of testes (Hanukoglu, 1992). The P450scc catalyzes three chemical reactions, 20a-hydroxylase, 22- hydroxylase, and cuts the side chain of cholesterol into pregnenolone. In the testis, P450scc is detected in Leydig cells (Hanukoglu, 1992; Ulloa-Aguirre and Conn, 2014).

The present study showed that the injection of a mesenchymal stem cells-conditioned medium in rats with cisplatin-induced testicular dysfunction promoted the recovery of testicular degeneration. The immunohistochemistry method detected the expression of HSD3B1, HSD17B1, and p450scc as markers of steroidogenesis. The immunoreactivity of HSD3B1, HSD17B1, and p450scc was shown in Leydig cells, and the intensity increased every week after the injections of mesenchymal stem cells-condition medium. In the immunohistochemical staining, localization of HSD3B1 and HSD17B1 was on steroidogenic cells, selectively expressed in Leydig cells in the interstitial cells of the testis, and it was not found in seminiferous tubules. The upregulation of cellular factors and the testicular microenvironment can occur along with the regeneration and differentiation of Leydig cells via secretion of cellular factors such as epidermal growth factors, insulin-like growth factors-1, and platelet-derived growth factors, that contain in HUMSCs (Lin et al., 1998; Odeh et al., 2014; Zhanget al., 2017). The current study reported the p450scc positive in Leydig cells in both treated groups. The steroidogenic process maybe was developed to make steroid hormones. Stem cell therapy may help to reduce the effect of cancer therapy on testicular dysfunction in the patients coping with cancer (Tamadon et al., 2015). Transplantation of mesenchymal stem cells induced spermatogenesis in azoospermic models (Moreno et al., 2015); differentiated into germ cells, Sertoli cells, and Leydig cells (Lue et al., 2007; Monsefi et al., 2013). Mesenchymal Stem Cells (MSCs) might be able to recover the regeneration of testicular dysfunction by three mechanisms, firstly, MSCs may transform into target cells via appropriate induction conditions. Secondly, growth factors are secreted by MSCs to repair the cell function, and finally, MSCs are incorporated with the endogenous cells repairing the injured tissue function (Mansour et al., 2012; Leatherman, 2013; Tamadon et al., 2015).

Mesenchymal stem cells-conditioned mediums or secretome are factors secreted by stem cells containing growth factors and cytokines, such as vascular endothelial and epidermal growth factors, insulin growth factor, interleukin, tumor necrosis factor, and interferons, that potentially modulates cellular processes, including cell proliferation, differentiation, immunomodulation, migration, angiogenesis, and survival. Mesenchymal stem cells have been used in

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tissue repair, and they can differentiate into Leydig-like cells in vitro (Yazawa et al., 2006). These cellular factors can then promote the regeneration of Leydig cells, and enhance their functions (Ricci et al, 2012; Odeh et al., 2014).

CONCLUSION

The results of the present study showed that the injection of a mesenchymal stem cells-conditioned medium can improve the regeneration of spermatogenic cells, and recover spermatogenesis proved by positive cells of HSD3B1, HSD17B1, and p450scc as markers of steroid production.

DECLARATIONS

Authors' contribution

Linda M. Khasanah contributed to data analysis and the write-up of the manuscript, Teguh Budipitojo created the concepts and designed the experiments, interpreted the data, read and approved the final manuscript. Yuda H. Fibrianto developed the concepts and designed the experiment, and produced secretome. All authors approved the final manuscript and checked the ethical issues.

Competing interests

The authors declared no conflictS of interest.

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Ethical considerations

Ethical issues (including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by the authors.

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The Influence of Basil Seed Hydroethanolic Extract on the Skin Wound Healing in Diabetic Male Rats

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ABSTRACT

Diabetic wounds and *cutaneous* wounds are important issues in medical science. Basil is an herbaceous plant and has compounds such as terpenes, flavonoids, and antioxidant properties. A total of 50 male Wistar rats were allocated into 10 groups including the healthy group without treatment, the healthy group treated with 1% phenytoin, eucerin, 5% basil seed extract, 10% basil seed, diabetic group without treatment, 1% phenytoin, eucerin. After anesthesia of rats, we made a 4 cm² wound on the back of the animal, and different histopathological characteristics were examined, and also on days 3, 7, and 21, the area of wounds was analyzed. In the healthy group treated with 10% basil seed extract, it was revealed that the wound size was significantly healed in the research days. In the diabetic rat groups, the decrease in the wound area was not significant and there was no significant difference between groups. Histopathological findings on day 21 in the healthy group treated with 10% basil seed extract revealed proper epidermis formation and relatively dense dermis containing collagen filaments. While in the diabetic groups, healing was slower. The results indicated that basil extract with anti-inflammatory and antioxidant characteristics can quicken the repair of *cutaneous* wounds.

Keywords: Basil, Diabetes, Histopathology, Wound

INTRODUCTION

Diabetes mellitus is the most prevalent endocrine disease that is related to carbohydrate, fat, and protein metabolism disorders. The disease results from the lack of cellular absorption of blood sugar because of diminished insulin or resistance of body cells to insulin (Siljander et al., 2019). Diabetes is a common reason for delayed or compromised wound healing. 15% of individuals with diabetes mellitus develop lower-extremity ulcers (Walko et al., 2015). Cutaneous wounds and a decrease in their healing time are considered important concerns in medical and surgical sciences. Wound healing is an active process in which a series of associations take place between diverse cells, cytokine mediators, and extracellular matrix (Foo et al., 2017). which this process includes several stages. However, in general, it is a constant process, so that each stage overlaps with the next stage. These stages include coagulation, inflammation, proliferation, and resuscitation (Reinke and Sorg, 2012). Diabetes is a metabolic illness and leads to complications, such as neurological (neuropathy), ocular (retinopathy), and renal problems (nephropathy, Shahrokh et al., 2021). One of the most significant chronic complications of diabetes is diabetic foot ulcers, which can finally cause amputation. It is now well-known that diabetes leads to a rise in free radicals at the cell cytoplasm (Khaksar et al., 2011) . Free radicals are very reactive because of their single electrons, and their excessive production causes damage in macromolecules such as DNA and proteins (Ibrahim et al., 2018). Research has revealed that antioxidants lessen DNA fragmentation caused by oxidative stress due to diabetes (Guo et al., 2020). It has been revealed that oral administration of vitamins E, C, and A improves plasma levels of antioxidant enzymes in diabetic patients. Various reports indicate that plants have many antioxidant compounds, such as different types of vitamins, carotenoids, and phenols (phenolic acids, flavonoids, and tannins) (Miri et al., 2020). Although diverse approaches are applied today to treat diabetic wounds, so far no efficient and without side effect treatment has been provided (Everett and Mathioudakis, 2018; Pourmahdi and Faedmaleki, 2021). In this regard, medicinal plants are of superior significance, because medicinal plants have rich sources of natural antioxidants that are utilized in traditional medicine to control and treat many skin diseases (Aziz et al., 2017). Currently, there is a serious trend to use medicinal plants because of the lack of side effects and the effective compounds in plants (Amalraj and Gopi, 2017).

Basil is a herbaceous, annual, fragrant plant from the family Lamiaceae, which is currently grown in most parts of Iran. Basil leaves can be utilized in many cases such as treating insomnia, healing of scratches, and as a painkiller (Veith et al., 2019). Basil contains numerous compounds such as terpenes, sesquiterpenoids, and flavonoids. Flavonoids have strong antioxidant characteristics (Denaro et al., 2020). The significance of basil is that besides flavor in food, its main active ingredient has antimicrobial effects and is efficient against different types of Gram-positive, Gram-negative

pathogenic bacteria, molds, and yeasts. The antimicrobial impacts of basil extract are associated with its phenolic compounds. The most key phenolic compounds in basil are linalool and methyl chavicol (Adeli-Sardou et al., 2019). Consequently, basil extract because of its plentiful antioxidants and anti-inflammatory agents can be efficient in the healing process by stimulating angiogenesis (Gutiérrez-Grijalva et al., 2018). Therefore, this research aimed to examine the repairing effects of basil seed extract concerning its advantageous effects (anti-inflammatory, anti-apoptotic, and anti-free radical) on *cutaneous* wound healing in diabetic rats.

MATERIALS AND METHODS

Ethical approval

This is experimental laboratory research that was conducted in the Animal Research Laboratory of Shahrekord Azad University in 2019.

Preparing extract

If the substances in plant cells are extracted from plants with solvents such as water or organic solvents, this product is called an extract. If the extract is extracted with water or ethanol, it can be applied in medicines without eliminating the solvent. To prepare the extract, 500 g of plant seeds were added to 1000 ml of 70% ethanol alcohol and incubated in a water bath at 45 ° C for 3 days in a container covered with aluminum foil. The extract was then separated by filter paper and a funnel and concentrated by vacuum distillation at 70 °C as much as possible (Mirjalili et al., 2017).

Laboratory Animals

For this research, 50 male rats with a specific weight range (200-250g) were obtained from the Laboratory Animal Breeding Center of Islamic Azad University, Shahrekord Branch, Iran. The rats were randomly allocated into ten groups of five rats. The rats were maintained in standard temperature conditions at 25-30°C and light conditions of 12 hours of light and 12 hours of darkness. Likewise, in terms of access to water and food and space away from pollution, the animals were in good condition, and to a high degree, all the principles in "Ethical Guide to Animal Research" were applied.

Experimental design and grouping

In this study, 50 male Wistar rats were allocated into 10 groups (healthy group without treatment, healthy group treated with 1% phenytoin, healthy group treated with eucerin, healthy group treated with 5% basil seed extract, healthy group treated with 10% basil seed extract, diabetic group without treatment, diabetic group treated with 1% phenytoin, diabetic group treated with eucerin). To induce type 1diabetes in 5 groups of mice, intraperitoneal injection of streptozotocin made by Sigma Company of Germany was used at a dose of 50 mg/kg (Sadoughi, 2013). After anesthetizing the mice with an intraperitoneal injection of ketamine (50mg/kg) and xylazine (10mg/kg) (Pourmahdi and Faedmaleki, 2021), a wound of 4 cm²-width was created on the back of all animals in the experimental groups. Different histopathological characteristics were surveyed on days 3, 7, and 21, moreover, wound area was statistically analyzed on the same days according to Firoozeh et al. (2019).

Data analysis method

All values are reported as mean \pm S.E.M. and the statistical significance of differences among groups was assessed using one-way ANOVA. Tukey test was used to measure specific differences between pairs of means. A value of p < 0.05 was considered significant.

Ethical consideration

Ethics committee approval was received for this study from the ethics committee of Shahrekord University, Iran, is IR.IAU.SHK.REC.10501972024).

RESULTS AND DISCUSSION

Morphological findings in the healthy group treated with 10% basil seed extract indicated a significant tendency to wound healing in the research days. This healing trend was followed in the phenytoin group with almost a similar rate. This wound healing in the 10% extract group on days 7 and 21 was significant (p < 0.05), and in the phenytoin-treated

group indicated a significant reduction on day 21 (p < 0.05). Then, in the group treated with 5% extract and eucerin, the wound area was decreased at a slower rate and did not display a significant decrease (p > 0.05). In the diabetic rat groups, the decrease in wound area was small and there was no significant difference between the groups. But in terms of a decrease in the wound area, the 10% basil extract and phenytoin groups had a better improvement (Graphs 1, 2, 3). Histopathological findings in this research indicated that on the third day, almost all groups had significant inflammation, edema, and bleeding. Tissue examination on day seven also revealed that in the healthy group treated with basil, the amount of inflammation was very small, little new blood vessels were formed, and collagen filaments have good density. While in the diabetic group, the number of collagen filaments was low and tissue had edema. On the 21, in the healthy group treated with 10% basil extract, epithelium formation was proper and all-around, and relatively dense collagen filaments were visible in the tissue. While in the diabetic rat group treated with 10% basil extract, the epithelium was not formed properly and the collagen filaments were not in the required order and edema was considerable in the tissue. In general, based on the obtained results, particularly histopathologically, an excellent tendency to collagen formation and the lack of secondary infection in the site was witnessed, which is perhaps because of antimicrobial and anti-inflammatory characteristics and strong phenolic antioxidants in basil (Figure 1, Table 1). Wounds are clefts and modifications in the anatomical structure and activity of the skin. cutaneous wounds are caused by different reasons such as burns, mechanical injuries, etc. When a wound forms on the skin, a cellular reaction arises instantly. After a *cutaneous* wound, leukocytes are the first cells to appear at the wound site. After some hours, granulocytes and macrophages accumulate at the margin of the wound, and after a few days, the proliferation of derm begins and fibroblasts enter the area. Macrophages release compounds that lead to the attraction and proliferation of fibroblasts. Fibroblasts steadily replace most of the leukocytes, and collagen proliferation also enhances. The production of new vessels in wound tissue is essential for wound healing, and this process is affected by the mediators released by macrophages. The contractile phenomenon happens when fibronectin provides an appropriate substrate for cell migration and growth during granulated tissue development and attaches to myofibroblasts. Connects. After healing with collagen filaments, the wound site looks like the skin tissue before the wound is produced, and the blood and oxygen flow in the vessels of the wound site is increased through dilation of the arteries. Many efforts have been made to heal diabetic wounds, including:

In 2017, studied the influence of aqueous extract of Morus nigra fruit on wound healing in type 1 diabetic mice and the findings revealed that its fruit extract can quicken wound healing in diabetic mice. It also increases tissue repair indicators such as epithelial layer development and collagen layer density (Mirjalili et al., 2017). Bagheri et al. (2016) studied the effect of sesame alcoholic extract on the healing of diabetic wounds in male Wistar rats, and the results revealed that sesame alcoholic extract quickens the healing of *cutaneous* wounds in healthy and diabetic individuals.

Although diverse approaches are applied today to treat diabetic wounds, so far no efficient and without side effect treatment has been provided. In this regard, medicinal plants are of superior significance, because medicinal plants have rich sources of natural antioxidants that are utilized in traditional medicine in order to control and treat many skin diseases (Shahrokh et al., 2021). Currently, there is a serious trend to use medicinal plants because of the lack of different side effects and the effective compounds in plants (Denaro et al., 2020). Basil is a herbaceous, annual, fragrant plant from the family Lamiaceae, which is currently grown in most parts of Iran. Basil leaves can be utilized in many cases such as treating insomnia, healing of scratches, and as a painkiller. Basil contains numerous compounds such as terpenes, sesquiterpenoids, and flavonoids. Flavonoids have strong antioxidant characteristics (Salem et al., 2019). The significance of basil is that besides flavor in food, its main active ingredient has antimicrobial effects and is efficient against different types of Gram-positive, Gram-negative pathogenic bacteria, molds, and yeasts (Mostafavi et al., 2019). The antimicrobial impacts of basil extract are associated with its phenolic compounds. The most key phenolic compounds in basil are linalool and methyl chavicol (Filip, 2017). Consequently, basil extract because of its plentiful antioxidants and anti-inflammatory agents can be efficient in the healing process by stimulating angiogenesis (Brereton et al., 2015). Therefore, in this research, the repairing effects of basil seed extract on *cutaneous* wound healing in diabetic and healthy rats were evaluated concerning its advantageous effects (anti-inflammatory, anti-apoptotic, and antifree radical).

Histopathological findings in this research indicated that on the 3rd day, almost all groups had significant inflammation, edema, and bleeding. Tissue examination on day seven also revealed that in the healthy group treated with basil, the amount of inflammation was very small, little new blood vessels were formed, and collagen filaments have good density whreas the number of collagen filaments was low and tissue had edema in the diabetic group. On day 21, epithelium formation was proper and all-around, and relatively dense collagen filaments were visible in the tissue in the healthy group treated with 10% basil extract. However, in the diabetic rat group treated with 10% basil extract, the

epithelium was not formed properly and the collagen filaments were not in the required order and edema was considerable in the tissue.

Morphological findings in the healthy group treated with 10% basil seed extract indicated a significant tendency to wound healing in the research days. This healing trend was followed in the phenytoin group with almost a similar rate. This wound healing in the 10% extract group on days 7 and 21 was significant (p < 0.05), and in the phenytoin-treated group indicated a significant reduction on day 21 (p < 0.05). Then, in the group treated with 5% extract and eucerin, the wound area was decreased at a slower rate and did not display a significant decrease (p > 0.05).

In the diabetic rat groups, the decrease in wound area was small and there was no significant difference between the groups. But in terms of a decrease in the wound area, the 10% basil extract and phenytoin groups had a better improvement.



Graph 1. Comparison of the mean decrease in wound area compared to the first day in non-diabetic groups during the study period



Graph 2. Comparison of the mean decrease in wound area compared to the first day in diabetic groups during the study period

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Figure 1. Histological section of wound healed on days 3,7, and 21 post-surgery

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Table 1.	Results	of histopat	hological	examinations of	of wound 3.	, 7, and 2	21 day	ys after	wound	healing	
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Groups	Day	Inflammation	Bleeding	Angiogenesis	Collagen fiber	Epithelium Fiber	Clot
	3	+++	+++	++	+	_	-
Healthy without treatment	7	++	+++	+	+	_	-
	21	+	+	+	++	+	-
	3	++	++	++	+	-	+
Diabetic without treatment	7	+++	+	+	+	_	++
	21	+	+	+	++	_	_
	3	+	+	++	+	_	++
Healthy phenytoin	7	+	-	++	++	_	-
	21	_	_	_	+++	++	-
	3	++	++	-	+	_	++
Diabetic phenytoin	7	+	+	++	++	_	_
	21	+	+	+	++	_	_
	3	++	+	+	+	_	++
Healthy eucerin	7	++	++	++	++	-	_
	21	+	_	_	++	+	-
	3	+	+	++	+	_	++
Healthy with 5 %basil	7	++	+	+	+	_	_
	21	+	_	_	++	++	-
	3	++	++	+++	+	-	-
Diabetic 5%basil	7	++	+	++	+	-	-
	21	+	_	_	++	+	_
	3	+	+	+	++	_	-
Healthy 10% basil	7	_	_	++	++	_	-
	21	_	_	_	++	++	_
	3	+	+	+	+	_	+++
Diabetic 10%basil	7	+	+	+	+	_	-
	21	+	+	-	+	+	-

+++: Severe ++: Moderate +: Light -: Absence

CONCLUSION

In general, based on the obtained results, particularly histopathologically, an excellent tendency to collagen formation and the lack of secondary infection in the site was witnessed, which is perhaps because of antimicrobial and antiinflammatory characteristics and strong phenolic antioxidants in basil. Therefore, these seeds can be used in the production of wound healing ointments.

DECLARATION

Authors' contribution

All authors have read and agreed to the published version of the manuscript. Mehran Hadi, Elham Moghtadaei-Khorasgani, and Mohammad Hossein Etesamnia contributed to the design and implementation of the research, the analysis of the results, and the writing of the manuscript.

Competing interests

The authors have no competing interests. In addition, we have no authorship or article publication conflict. Ethical issues (including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by the authors.

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Ethical considerations

Ethical issues (including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by the authors.

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Concurrent Respiratory Disease in Broiler Chickens in Egypt during 2020

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ABSTRACT

Poultry production has been affected by multiple respiratory diseases triggering serious economic losses in Egypt. The current study aimed to investigate the situation and genetic evolution of respiratory diseases in Egypt during 2020. A total of 53 samples were collected from infected flocks suffering from respiratory signs and variable mortality rates from nine governorates in Egypt during 2020. The collected samples were examined for the detection of respiratory disease viruses (Avian influenza virus (AIV (H5N8, H9N2), Infectious bronchitis virus (IBV), and Newcastle disease virus (NDV)) by rRT-PCR. The single infection was confirmed in 90.6% (37.7% I.B, 30.2% AIV (H5N8), 9.4% I.B and 5.7% NDV) and co-infection of HPAIV (H5N8) + I.BV and LPAIV (H9N2) +IBV were detected in 3.8% of nine governorates. The HA gene of HPAIV (H5N8) was cluster to clad 2.3.4.4.1b in a new branch with characteristic specific mutations especially in T140A in antigenic site A and R72S in the receptor-binding site, compared to A/duck/Egypt/F446/2017 with low A.A identity percent with vaccinal strains of H5N1 and H5N2 reaching to 91.9-94% and 84.6%, respectively. The HA gene of AIV (H9N2) belonged to A/quail/Hong Kong/G1/97-like virus clustered with group B with a specific mutation (212I) that may affect the human transmission of the virus. The HVRs of S1 gene of IBV cluster to GI23 (Egy Var I) clad with multiple mutations in HVR1 and HVR2, compared to IBV/CU/4/2014 and low identity percent (68.3-78.8%) with vaccine strains (H120, M41, 4/91). In conclusion, respiratory disease continues to circulate and rapidly evolve in Egypt during 2020.

Keywords: HPAIV (H5N8), IBV, Genetic characterization, LPAIV(H9N2), Respiratory disease

INTRODUCTION

The poultry industry is one of the most significant industries impacting the national economy in Egypt by promoting investment and jobs availability. Moreover, the primary sources of inexpensive animal protein for poor people in Egypt are poultry meat and eggs (Abdelwhab and Hafez, 2011).

Regrettably, the poultry industry in Egypt has been affected mainly by viral respiratory diseases for several years (Haghighat-Jahromi et al., 2008; Sediek, 2013; Awad et al, 2016). The inability to control this disease results in significant economic losses in the poultry sector. Avian influenza (highly pathogenic, low pathogenic), Newcastle Disease Virus (NDV) and Infectious Bronchitis Virus (IBV) alone or mixed infection (with each other or other bacterial infection) are the main cause of respiratory disease affect poultry farm with a high mortality rate (Radwan et al., 2013; Hassan et al., 2016; Samy and Naguib, 2018).

Avian Influenza (AI) was the most severe respiratory disease in Egypt. The Highly Pathogenic Avian Influenza (HPAI) H5N8 was first recorded in 2016 from a wild bird (common coot) (Selim et al., 2017), then observed in domestic birds, including chickens and ducks, as single or co-infected with other respiratory viruses causing severe losses in poultry production (Salaheldin et al., 2018; Yehia et al., 2018; Shehata et al., 2018; Hassan et al., 2019). The low pathogenic avian influenza (LPAI) H9N2 was first recorded in 2010-2011 belonging to G1 lineage (El-Zoghby et al., 2012). It has immunosuppressive effects that lead to increased opportunism of the infection by other viral diseases as mainly observed in co-infection with H9N2 and I.B viruses (Hassan et al., 2017). In addition, the co-infection with other bacterial infections as Escherichia coli and Haemophilus paragallinarum contribute to increasing the virulence of H9N2 because it has an endoproteases enzyme that cleavage precursor HA proteins (Haghighat-Jahromi et al., 2008; Pan et al., 2012; Hassan et al., 2017).

Infectious bronchitis virus is one of the major significant respiratory infections (Hofstad, 1984). It is primarily recorded was in Egypt during the 1950s (Sheble et al., 1986) that related to the Dutch variant D3128 then D274, Mass, 4/91, and D-08880. (Eid, 1998) Novel endemic genotypes associated with Israeli variant 2 and mass serotypes were

detected in 2006 (Abdel-Moneim et al., 2006a). In 2011, the Egyptian virus was mutated and classified into variant I and variant II (Abdel-Moneim et al., 2012). Both types of IBV virus circulated in Egypt causing outbreaks despite vaccination programs, which all in all lead to high economic losses (Abd El Rahman et al., 2015; Zanaty et al., 2016). The most severe respiratory disease is Newcastle Disease (ND) that causing high mortality in poultry flocks (OIE, 2012). In Egypt, the NDV was first recorded in 1948 (Daubney and Mansy, 1948) then spread rapidly in Egypt despite vaccination programs (Abdel-Moneim et al., 2006b; El-Bagoury et al., 2015).

Virus isolation is the fundamental diagnostic test for avian respiratory viruses, but it appears to be expensive, slow, and labor-intensive (Suarez et al., 2007). Recently, reverse transcriptase-polymerase chain reaction (RT-PCR) and real-time RT-PCR (rRT-PCR) were rapid diagnostic tests used to detect viral nucleic acid (Spackman et al., 2002).

In the recent year, the respiratory viruses (HPAI (H5N8), H9N2 (LPAI)), IB, NDV has continuous evolution that may be affected on the pathogenicity of the virus and vaccine efficacy as previously recorded (Yehia et al., 2018; Hassan et al., 2017; Zanaty et al., 2016; Abdel-Moneim et al., 2006b). The aim of the current research was to explore the updated status of respiratory disease outbreaks in broiler Egyptian farms during 2020 using rRT-PCR and to study the genetic variation of the selected circulating respiratory viruses.

MATERIALS AND METHODS

Collection and preparation of specimens

In the present study, AIV (H5N8 and H9N2), NDV, and IBV were examined on 53 infected poultry flocks exhibiting severe respiratory manifestation and high mortality during 2020. The oropharyngeal swabs were obtained from disease or freshly dead birds in nine provinces of Egypt, including Alexandria, Giza, Dakhalia, El-sharqia, Qualiobia, El-Monofia, El-Behira, Domiat, and Cairo (Table 1, Figure 1). A total of 45 chicken flocks (including 36 broilers, 5 commercial layers, and 4 breeder farms), 2 flocks of turkeys, and 6 duck farms were examined. The samples from each flock were collected by 10-15 swabs were pooled in 2 ml of phosphate buffer saline (OIE, 2014; Naguib et al., 2017).

RNA extraction, identification, and subtyping of viruses

The QIAamp Viral RNA Mini Kit (Qiagen) was used for the extraction of viral RNA from pooled oropharyngeal swabs following the manufacturer's guidelines, then eluted into 50 µl of nuclease-free water. All samples were tested for the detection of M gene of influenza type A viruses by rRT-PCR (Fereidouni et al., 2012) using the AgPath Real-time Kit (Ambion) and the real-time PCR step one plus System (Applied Biosystems, Foster City, CA, USA). In the next step, subtyping using rRT-PCR targeted HA and NA genes as described by Hoffmann et al. (2016). In addition, all samples were tested for the detection of NDV, IBV using rRT-PCR target matrix gene of avian paramyxovirus-1 (Wise et al., 2004) then the positive samples were tested for the detection of NDV of genotype VII (velogenic strain) (Moharam et al., 2019). Furthermore, rRT-PCR was used for the detection of IBV RNA as described by (Naguib et al., 2017).

Virus isolation

The positive samples were isolated into specific pathogen-free (SPF) embryonated chicken eggs (ECEs) aged 10 days old in allantoic fluid with daily observation. The mortalities were recorded and the allantoic sac was collected and tested by rapid slide haemagglutination (HA) test (OIE manual, 2008).

Sequencing of the viral genome

The HA gene of AI (H5, H9) and HVRs of S1 gene of IBV amplification were examined by PCR using specific primers as described by Hoper et al. (2009), Selim et al. (2013) and Naguib et al. (2015), and high fidelity Phusion® DNA polymerase (Thermo Fisher Scientific, MA, USA). Using QIAquick Gel Extraction Kit, the PCR products were separated and purified from the gel (Qiagen).

Cycle sequencing reactions have been performed on PCR products using BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems). Using centri-sep columns (Macherey-Nagel GmbH & Co.) the sequence products were purified then sequenced on an ABI PRISM3130 Genetic Analyzer (Life Technologies). For each sequence, the blast search was performed (http://www.ncbi.nlm.nih.gov/BLAST). Mutation and phylogenetic analysis were conducted using MEGA version 6 program using a bootstrap of 1000 trials of the Clustal W alignment algorithm (Tamura et al., 2013). The amino acid identity was analyzed using DNA star software (DNAStar, Madison, WI). Then, it was published by the national center for Biotechnology Information with the accession number provided in Table 2.

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Table 1. Epidemiological data results of PCR of collected samples of collected samples

Number	Governorates	Species	Breeds	Age (day)	Results
1	El-Dakhlia	Chicken	Broiler	20	HPAIV(H5N8)
2	El-Dakhlia	Chicken	Layer	275	HPAIV(H5N8)
3	El-Dakhlia	Chicken	Broiler	25	IBV
4	Giza	Chicken	Breeder	90	IBV
5	Alexandria	Chicken	Broiler	30	IBV
6	Alexandria	Chicken	Layer	365	HPAIV(H5N8)
7	Giza	Chicken	Broiler	33	HPAIV(H5N8)
8	Giza	Chicken	Broiler	36	Negative
9	Giza	Turkey		65	HPAIV(H5N8)
10	Giza	Chicken	Broiler	40	NDV
11	El-sharqia	Chicken	Broiler	22	IBV
12	El-Monofia	Chicken	Layer	390	NDV
13	El-sharqia	Chicken	Broiler	15	LPAIV(H9N2)
14	El-Dakhlia	Chicken	Breeder	392	IBV
15	Cairo	Chicken	Broiler	23	IBV
16	Cairo	Chicken	Broiler	34	IBV
17	Domiat	Chicken	Broiler	42	HPAIV(H5N8)
18	El-Dakhlia	Chicken	Broiler	36	IBV
19	El-Dakhlia	Chicken	Layer	120	IBV
20	El-Dakhlia	Chicken	Broiler	22	HPAIV(H5N8)
21	El-Behira	Chicken	Breedrer	196	Negative
22	Giza	Chicken	Broiler	20	IBV
23	Beni-suief	Turkey		60	IBV
24	Beni-suief	Chicken	Broiler	25	IBV
25	El-Dakhlia	Chicken	Broiler	15	IBV
26	El-sharqia	Chicken	Broiler	30	IBV
27	Domiat	Chicken	Broiler	15	IBV
28	Domiat	Chicken	Layer	120	HPAIV(H5N8)
29	Giza	Chicken	Broiler	33	IBV
30	Alexandria	Chicken	Broiler	33	HPAIV(H5N8)+IBV
31	Alexandria	Chicken	Broiler	34	IBV
32	Cairo	Chicken	Breeder	95	IBV
33	Cairo	Chicken	Broiler	22	HPAIV(H5N8)
34	El-Behira	Duck		12	HPAIV(H5N8)
35	Domiat	Chicken	Broiler	18	Negative
36	Giza	Duck		15	LPAIV(H9N2)
37	Giza	Chicken	Broiler	20	IBV
38	Beni-suief	Chicken	Broiler	15	HPAIV(H5N8)
39	El-Monofia	Duck		95	IBV
40	El-Dakhlia	Chicken	Broiler	20	HPAI (H5N8)
41	Cairo	Chicken	Broiler	28	LPAIV(H9N2)
42	El-sharqia	Duck		27	IBV+LPAIV(H9N2)
43	El-Monofia	Chicken	Broiler	18	NDV
44	Domiat	Chicken	Broiler	33	HPAIV(H5N8)
45	Domiat	Chicken	Broiler	23	IBV+LPAIV(H9N2)
46	El-sharqia	Duck		33	HPAI (H5N8)+IBV
47	El-Dakhlia	Chicken	Broiler	15	HPAIV(H5N8)
48	Beni-suief	Chicken	Broiler	35	Negative
49	Cairo	Chicken	Broiler	34	HPAIV(H5N8)
50	El-Behira	Chicken	Broiler	15	HPAIV(H5N8)
51	El-Dakhlia	Duck		17	LPAIV(H9N2)
52	El-Behira	Chicken	Broiler	28	LPAIV(H9N2)
53	El-sharqia	Chicken	Broiler	18	Negative

Table 2. Accession number of HA gene of HPAI (H5N8 and H9N2) and S1 gene of infectious bronchitis virus samples

Number	Code	GenBank Accession number						
Number	Code	HA(H5)	HA(H9)	S1				
45	IBV/EGY/CH/AY1/2020, A/chicken/FW1/2020	-	MW227513	MW240842				
30	IBV/EGY/CH/AY2/2020 A/chicken/Egypt/FN1/2020	MW227501	-	MW240843				
3	IBV/EGY/CH/AY3/2020	-	-	MW240844				
11	IBV/EGY/CH/AY4/2020	-	-	MW240845				
15	IBV/EGY/CH/AY5/2020	-	-	MW240846				
39	IBV/EGY/CH/AY6/2020	-	-	MW240847				
13	A/chicken/FW2/2020	-	MW227514	-				
36	A/chicken/FW3/2020	-	MW227515	-				
28	A/chicken/Egypt/FN2/2020	MW227502	-	-				
40	A/chicken/Egypt/FN3/2020	MW227503	-	-				

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0.005

Figure 1. Phylogenetic tree of HA gene of highly pathogenic avian influenza (H5N8)

RESULTS

Result of real time-PCR

The findings indicated that 48 samples out of 53 tested samples were positive for RT-PCR for different respiratory diseases (20 samples were positive for IBV, 16 samples for HPAI (H5N8), and 5 samples for LPAI (H9N2), 3 samples for NDV (velogenic strain), 2 samples for HPAI (H5N8) +IBV, and 2 samples for LPAI (H9N2)+I.BV) as mentioned in Table.1.

Genetic characterization of the HPAI (H5N8) Virus HA gene

Phylogenetic analysis of full HA sequence of four selected AI (H5N8) isolates was named A/ CHICKEN/EGYPT/FN1/2020, A/ CHICKEN/EGYPT/FN2/2020 from co-infected farms and A/ CHICKEN/EGYPT/FN3/202, CHICKEN/EGYPT/FN4/2020 from other infected flocks belonged to clade 2.3.4.4b. They cluster with Egyptian viruses isolated in 2019 making a new subgroup with bootstrapping 95 as shown in Figure 1. They have five nucleotide mutations, compared to A/duck/Egypt/F446/2017, which is different from Egyptian viruses isolated in 2017 and 2018.

By mutation analysis in antigenic site A, one mutation (T140A) was detected in the A/chicken/Egypt/FN1/2020 and A/chicken/Egypt/FN2/2020 similar to A/Chicken/Egypt/186FL/2018. In addition, the receptor-binding site in A/chicken/Egypt/FN3/2020 had R72S was similar to A/Chicken/Egypt/185/2018 and A/Chicken/Egypt/186FL/2018. The S94R was also found only in the A/chicken/Egypt/FN3/2020. The A.A. identity of the current strains and H5N1 vectormune vaccine (A/mute_swan/Hungary/4999/2006), B.E.S.T Vaccine (A/duck/China/E319-2/03) was within the range of 91.9-94% and H5N2 CEVac Flukem (A/chicken/Mexico/232/1994) was 84.6% (Figure 2).

Genetic characterization of the H9N2 Virus HA gene

The phylogenetic analysis of the full HA sequence of three selected AI H9 isolate was named A/ farms CHICKEN/EGYPT/FW1/2020 from co-infected and A/CHICKEN/EGYPT/FW2/2020 and A/ CHICKEN/EGYPT/FW3/2020 from single infected flocks belonged to the A/quail/Hong Kong/G1/97-like virus lineage clustered with group B (Figure 3). The viruses in the current study were closely related to other Egyptian strains with identities of 94.9- 98.2% (Figure 4). Considering mutation analysis, mutations in S16N, M58K, T121I/V, I134M, T145S, N179T as specific to all Egyptian viruses were recorded and N41G, I75V, V212I, T413N resemble Egyptian viruses in 2018-2019, compared to the A/quail/Hong Kong/G1/97. In addition, R180K/Q was specific for viruses in the present study. The amino acid sequences at the cleavage site of HA contained a low pathogenic RSSR/GLF motif.

Genetic characterization of S gene of infectious bronchitis virus

The phylogenetic analyses of HVRs of S1 genes of six selected viruses were named IBV/EGY/CH/AY1/2020, IBV/EGY/CH/AY2/2020, and IBV/EGY/CH/AY3/2020 from co-infected flocks and IBV/EGY/CH/AY4/2020, IBV/EGY/CH/AY5/2020, and IBV/EGY/CH/AY6/2020 from single infected flocks. The viruses in this study were clustered to clad GI23 (Egy Var I) (Figure 5).

By mutation analysis of HVRs, the recorded mutation was compared with the reference strain of IBV/CU/4/2014. The HVR1 of three Egyptian viruses (IBV-EGY-CH-AY1-2020, IBV-EGY-CH-AY2-2020, IBV-EGY-CH-AY3-2020) had three A.A. and the other two viruses (IBV-EGY-CH-AY4-2020, IBV-EGY-CH-AY6-2020) had four A.A. However, the IBV-EGY-CH-AY5-2020 had two A.A. The HVRII had 7A.A. mutation in all viruses except IBV-EGY-CH-AY2-2020, which had six amino acid mutations, and IBV-EGY-CH-AY1-2020, IBV-EGY-CH-AY5-2020 which had four A.A. (Figure 6). The S1 gene identity of amino acids revealed that viruses in the current study related to vaccine seeds used commonly in Egypt (M41, H120, 4/91) within the range of 68.3-78.8% (Figure 7).

								P	ercent	Identi	ty							
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	
	1		97.2	98.5	98.5	98.7	99.4	99.6	99.4	98.9	99.6	99.4	99.4	99.2	91.9	94.0	84.6	1
	2	2.9		97.6	97.6	96.8	97.4	97.6	97.6	97.4	97.6	97.7	97.7	97.4	91.7	93.8	84.9	2
	3	1.5	2.5		100.0	98.1	98.7	98.9	98.7	98.1	98.9	98.7	98.7	98.5	91.7	94.0	84.6	3
	4	1.5	2.5	0.0		98.1	98.7	98.9	98.7	98.1	98.9	98.7	98.7	98.5	91.7	94.0	84.6	4
	5	1.3	3.3	1.9	1.9		98.7	99.1	98.9	98.1	98.9	98.7	98.7	98.5	91.5	93.4	84.4	5
	6	0.6	2.7	1.3	1.3	1.3		99.4	99.2	99.1	99.8	99.6	99.6	99.4	91.7	93.8	84.4	6
ξ,	7	0.4	2.5	1.1	1.1	0.9	0.6		99.8	98.9	99.6	99.4	99.4	99.2	91.7	94.0	84.6	7
5	8	0.6	2.5	1.3	1.3	1.1	0.8	0.2		98.7	99.4	99.2	99.2	99.1	91.7	94.0	84.6	8
2	9	1.1	2.7	1.9	1.9	1.9	0.9	1.1	1.3		99.2	99.2	99.2	99.2	91.9	94.0	84.2	9
5	10	0.4	2.5	1.1	1.1	1.1	0.2	0.4	0.6	0.8		99.8	99.8	99.6	91.9	94.0	84.6	10
	11	0.6	2.3	1.3	1.3	1.3	0.4	0.6	0.8	0.8	0.2		100.0	99.4	91.9	94.0	84.6	11
	12	0.6	2.3	1.3	1.3	1.3	0.4	0.6	0.8	0.8	0.2	0.0		99.4	91.9	94.0	84.6	12
	13	0.8	2.7	1.5	1.5	1.5	0.6	0.8	0.9	0.8	0.4	0.6	0.6		91.9	94.0	84.6	13
	14	8.2	8.4	8.4	8.4	8.6	8.4	8.4	8.4	8.2	8.2	8.2	8.2	8.2		97.0	87.4	14
	15	6.1	6.3	6.1	6.1	6.7	6.3	6.1	6.1	6.1	6.1	6.1	6.1	6.1	2.9		87.6	15
	16	16.4	15.9	16.4	16.4	16.6	16.6	16.4	16.4	16.8	16.4	16.4	16.4	16.4	12.9	12.9		16
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	

A-duck-Egypt-F446-2017 A-broiler-duck-Korea-Buan2-2014 A-goose-Jiangsu-QD5-2014 A-goose-Shandong-WFSG1-2014 A-Chicken-Egypt-17167-2017 A-Common-coot-Egypt-CA285-2016 A-duck-Egypt-SS19-2017 A-Duck-Egypt-175Fao-SI-2017 A-Chicken-Egypt-185-2018 A-Turkey-Eavpt-Al20285-2019 A-chicken-Egypt-FN1-2020 A-chicken-Egypt-FN2-2020 A-chicken-Egypt-FN3-2020 A-mute-swan-Hungary-4999-H5N1-vectoremu A-duck-China-E319-2-03-H5N1-B.E.S.T-Vac A-chicken-Mexico-232-1994-H5N2

Figure 2. Amino acid identities and divergence of HA gene of H5N8 viruses compared to other selected strains and vaccinal strains



0.02

Figure 3. Phylogenetic tree of HA gene of H9N2

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		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19		
	1		85.3	88.7	92.5	92.1	92.7	93.3	91.3	90.5	87.9	88.1	87.1	89.3	88.9	88.3	87.9	87.5	87.5	88.5	1	A-Quail-HongKong-G1-97
	2	14.8		87.5	84.2	83.6	84.6	84.2	83.6	84.0	83.6	82.4	82.2	83.4	83.2	82.6	82.8	82.4	82.4	82.8	2	A-duck-HongKong-Y439-1997
	3	10.8	12.3		89.5	89.3	89.1	89.5	87.7	89.3	87.1	87.1	86.3	87.5	87.5	87.3	87.1	86.5	86.5	87.9	3	A-chicken-HongKong-G9-1997
	4	6.4	16.5	10.1		98.2	93.3	93.3	91.3	90.7	87.9	88.1	87.9	89.3	88.9	88.3	87.9	87.7	87.7	88.9	4	A-chicken-Israel-421201-2004
	5	6.9	17.2	10.3	0.8		92.9	93.1	91.1	90.5	87.7	88.1	87.7	89.1	88.7	88.1	87.7	87.5	87.5	88.7	5	A-chicken-Israel-178-2006
	6	6.0	15.5	10.4	5.5	6.0		93.1	90.9	91.3	88.3	87.9	87.1	89.3	88.7	88.1	87.9	87.3	87.3	88.7	6	A-Chicken-Iran-TH81-2002
	7	5.5	16.3	10.1	5.8	6.0	5.8		92.7	92.7	89.3	89.1	89.3	90.9	90.5	89.9	89.5	89.5	89.5	90.3	7	A-chicken-Dubai-338-2001
	8	7.8	17.2	12.2	8.0	8.2	8.3	6.4		95.8	92.5	92.3	91.7	94.3	93.7	92.5	92.5	91.7	91.7	92.7	8	A-chicken-Saudi
92	9	8.7	16.9	10.5	8.9	9.1	7.8	6.4	3.3		93.7	93.3	93.1	95.8	95.2	93.9	93.7	93.1	93.1	93.7	9	A-chicken-Israel-1067-2010
g	10	11.8	17.5	13.2	12.2	12.5	11.3	10.3	6.9	5.9		98.4	95.2	96.2	96.8	97.4	97.8	94.9	94.9	97.6	10	A-chicken-FW1-2020
ĕ.	11	11.5	19.0	13.2	12.0	12.0	11.8	10.6	7.1	6.4	1.4		95.4	96.0	96.8	97.4	98.2	94.9	94.9	97.6	11	A-chicken-FW2-2020
	12	12.8	19.3	14.2	12.2	12.5	12.8	10.3	7.8	6.6	4.6	4.4		95.2	95.8	95.6	95.6	97.6	97.6	95.8	12	A-chciken-FW3-2020
	13	10.1	17.7	12.5	10.5	10.8	10.1	8.5	4.9	3.6	3.1	3.3	4.2		97.8	96.2	96.0	94.9	94.9	96.2	13	A-chicken-Egypt-2-2014
	14	10.6	18.0	12.7	11.0	11.3	10.8	8.9	5.5	4.4	2.7	2.7	3.8	1.4		97.2	97.0	95.8	95.8	97.0	14	A-chicken-Egypt-7-2015
	15	11.3	18.8	12.9	11.7	12.0	11.5	9.6	6.9	5.7	2.3	2.3	4.2	3.1	2.3		97.8	95.6	95.6	97.8	15	A-chicken-Egypt-v621-2018
	16	11.8	18.5	13.2	12.2	12.5	11.8	10.1	6.9	5.9	2.1	1.6	4.2	3.3	2.5	1.9		95.6	95.6	97.2	16	A-chicken-Egypt-V4001-2018
	17	12.3	19.0	13.9	12.5	12.7	12.5	10.1	7.8	6.6	4.8	4.8	2.1	4.4	3.8	4.2	4.2		99.6	95.8	17	A-chicken-Egypt-V2630-2019
	18	12.3	19.0	13.9	12.5	12.7	12.5	10.1	7.8	6.6	4.8	4.8	2.1	4.4	3.8	4.2	4.2	0.0		95.8	18	A-chicken-Egypt-V2633-2019
	19	11.1	18.5	12.2	11.0	11.3	10.8	9.2	6.6	5.9	2.1	2.1	4.0	3.1	2.5	1.9	2.5	4.0	4.0		19	A-chicken-Egypt-V2692-2019
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19		

Percent Identity

Figure 4. Amino acid identities and divergence of HA gene of H9N2 viruses compared to other selected strains and vaccinal strains



Figure 5. Phylogenetic tree of partial S1 gene of infectious bronchitis virus

390

	HVR1 (60-88)	HVR2 (115-149)
cu-4	SG~QCTAGSIYWSKNFSASSVAMTAPDT(YKNGQGSCPLTGLIPQNHIRISAMKNSSL
F859	I	
Eg-CLEVB-2-IBV-012	T	R.
IBV-Eg-CLEVB-1-IBV-012	.VA	
IVB-Eg-CLEVB-2-012	T	R.
IBV-EG-1586CV-SP1-2015	.HQN	Н.
IBV-EG-13280F-SP1-2013	.QAQN	
IBV-EG-1212B-SP1-2012	.g	
IBV-EG-1442F-SP1-2014	D	R.
IBV-D2930-3-1-1-15	.g	
IBV-D2572-2-2-14 EG	.g	
IBV-D1903-21-12	.Q	
IBV-D1456-1-5-10	.Q	
IBV-D1795-2-7-11		
IBV-D1887-2-3-12		
IBV-D1344-2-4-10	I	
IBV-EGY-CH-AY1-2020	SV.	
IBV-EGY-CH-AY2-2020	SV.	
IBV-EGY-CH-AY3-2020	G	
IBV-EGY-CH-AY4-2020	S	
IBV-EGY-CH-AY5-2020		
IBV-EGY-CH-AY6-2020		

HVD1 (60 99)

Figure 6. Amino acid mutation in HVRS in S1 gene of infectious bronchitis virus

			-							F	ercent	Identi	ty										
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20		
	1		90.7	71.7	75.3	71.7	72.1	73.3	71.7	72.5	72.5	80.0	68.3	75.0	72.1	76.7	74.2	75.0	78.8	76.7	73.3	1	IBV-H120
	2	10.1		76.3	75.3	73.2	69.1	69.1	70.0	68.0	69.1	81.7	70.1	76.7	69.1	78.3	72.2	76.7	76.3	78.3	70.1	2	IBV-M41
	3	34.4	25.2		67.0	68.8	77.1	77.9	75.0	77.1	77.5	80.0	86.2	78.3	77.1	80.0	75.4	78.3	77.1	80.0	76.7	3	IBV-D207
	4	30.2	30.4	40.0		67.0	64.9	64.9	66.7	67.0	67.0	70.0	69.1	70.0	66.0	71.7	70.1	71.7	72.2	71.7	68.0	4	IBV-QXIF
	5	36.2	33.9	39.6	43.7		74.1	74.3	68.3	71.1	73.8	70.0	69.3	71.7	71.1	70.0	71.8	68.3	75.1	70.0	71.5	5	IBV-UK-4-91
	6	33.7	36.7	27.2	43.6	32.2		94.0	81.7	96.8	98.0	95.0	83.8	98.3	97.5	96.7	92.8	95.0	91.7	96.7	94.2	6	IBV-IS-1494-06
	7	31.1	35.2	26.6	42.2	32.4	5.8		80.0	90.6	93.2	88.3	81.6	91.7	91.3	90.0	88.1	88.3	87.7	90.0	89.2	7	IBV-VAR2
	8	35.7	39.2	30.5	44.1	41.1	21.2	23.6		80.0	81.7	83.3	83.3	81.7	81.7	83.3	85.0	85.0	83.3	83.3	85.0	8	IBV-IS-885
8	9	32.9	38.4	27.1	39.7	34.2	2.6	8.1	23.4		98.2	91.7	83.8	96.7	98.6	96.7	93.5	95.0	93.5	96.7	94.9	9	IBV-cu-4
gen	10	33.0	37.0	26.6	39.9	33.5	2.6	7.2	21.1	1.7		93.3	84.5	98.3	98.9	98.3	93.1	96.7	93.1	98.3	94.6	10	IBV-EG-CLEVB-1
Ver	11	23.3	21.1	23.3	38.4	38.4	5.2	12.8	19.1	8.9	7.0		95.0	93.3	93.3	95.0	93.3	93.3	95.0	95.0	93.3	11	IBV-EG-13280F
ā	12	40.3	36.2	14.5	36.4	38.0	19.3	22.9	18.9	18.7	18.1	5.2		98.3	84.1	100.0	82.3	98.3	83.8	100.0	83.8	12	IBV-EG-1212B
	13	30.8	28.7	25.9	38.3	35.7	1.7	8.9	21.2	3.4	1.7	7.1	1.7		98.3	98.3	96.7	96.7	98.3	98.3	96.7	13	IBV-EG-1442F
	14	33.6	36.6	27.1	41.6	34.9	2.1	7.7	21.1	1.3	1.3	7.0	18.7	1.7		98.3	93.5	96.7	93.1	98.3	94.9	14	IBV-D1344-2-4-10
	15	28.2	26.1	23.4	35.6	38.5	3.4	10.8	18.9	3.4	1.7	5.2	0.0	1.7	1.7		98.3	98.3	100.0	100.0	98.3	15	IBV-EGY-AY1-2020
	16	31.8	35.5	28.9	38.3	33.7	5.7	10.5	16.8	5.3	6.2	7.1	18.7	3.4	5.7	1.7		100.0	94.6	98.3	97.1	16	IBV-EGY-AY2-2020
	17	30.8	28.7	25.9	35.6	41.6	5.3	12.9	16.8	5.2	3.4	7.1	1.7	3.4	3.4	1.7	0.0		98.3	98.3	100.0	17	IBV-EGY-AY3-2020
	18	25.0	29.0	26.4	35.0	29.2	7.1	11.5	18.9	5.7	6.2	5.2	17.6	1.7	6.2	0.0	4.7	1.7		100.0	93.9	18	IBV-EGY-AY4-2020
	19	28.2	26.1	23.4	35.6	38.5	3.4	10.8	18.9	3.4	1.7	5.2	0.0	1.7	1.7	0.0	1.7	1.7	0.0		98.3	19	IBV-EGY-AY5-2020
	20	31.7	34.9	27.7	38.0	33.5	5.3	9.6	16.8	4.8	5.7	7.1	18.1	3.4	5.3	1.7	1.3	0.0	4.4	1.7		20	IBV-EGY-AY6-2020
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20		

Figure 7. Amino acid identities and divergence of partial S1 gene of infectious bronchitis virus sequenced viruses compared to other selected strains and vaccinal strains

DISCUSSION

In Egypt during the last years, the outbreaks due to respiratory disease with high mortality rates have increased and affected poultry production. Many avian viral pathogens were the main cause of this problem (Malik et al., 2004; Roussan et al., 2008). The avian influenza virus (HP, LP), IBV, and NDV were the main detected viruses alone or as coinfected in broiler chickens (Hassan et al., 2016). The current study aimed to identify the incidence of viral respiratory disease in broiler chickens, especially AIV (HP, LP), IBV, and NDV in Egypt during 2020, and study the molecular characterization and evolution of detected viruses.

In the present study, multiple respiratory viruses as single or mixed infections were detected. The AIV subtypes and IBV were recorded in 48 out of 53 farms. Single infection represented 90.6% (37.7% I.B, 30.2% H5N8, 9.4% I.B and 5.7% NDV). Furthermore, co-presence of HPAI (H5N8) and IBV, unique detection of these co-infected flocks, and LPAI (H9N2) and IBV, were detected in 3.8% as previously recorded by El-Shall et al. (2019). The occurrence of IBV and HPAI (H5N8) in Egyptian poultry with a high mortality rate in different vaccinated poultry flocks has previously been reported by a number of researchers (Abdel-Moneim et al., 2006a, Abd El Rahman et al., 2015; Yehia et al., 2020). It was indicated the high incidence of respiratory disease in broiler chicken during 2020 in single infection more than coinfected with other viruses.

In recent years, the avian influenza situation in Egypt has been more complicated due to the detection and circulation of many serotypes, including HPAI (H5N1), HPAI (H5N8), and LPAI (H9N2) (Shehata et al., 2019). The

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phylogenetic analysis of four selected samples of the HA gene of HPAI H5N8 revealed that the four samples were clustered to clad 2.3.4.4.1b as previously recorded by Shehata et al. (2018) and El-Shall et al. (2019) in a new subgroup with characteristic specific mutations due to multiple mutations that may affect the pathogenicity and vaccine efficacy.

Considering mutation analysis, a change was detected in the (T140A) antigenic site A in two samples of A/chicken/Egypt/FN1/2020 and A/chicken/Egypt/FN2/2020 as previously reported by Yehia et al. (2020) that may be due to excessive use of avian influenza vaccine H5N1 and H5N2. In addition, the R72S in A/chicken/Egypt/FN3/2020 in the receptor-binding site was detected as previously mentioned by Nabil et al. (2020).

The A.A. identity was very low in H5N1 and H5N2 vaccine reaching 91.9-94% and 84.6%, respectively, similar to previous studies (Kandeil et al., 2018; Yehia et al., 2020). It explained where the outbreaks occurred in the vaccinated flocks and caused high mortality.

The phylogenetic analysis of three LPAI (H9N2) selected strains revealed that all viruses in the current study belonged to A/quail/Hong Kong/G1/97-like virus lineage clustered with group B as previously recorded (Kareem et al., 2015; El-Shall et al., 2019). Regarding mutation analysis, the LPAI (H9N2) Egyptian viruses had six A.A. mutation-specific. In addition, I75V, N41G, and T413N mutation specific to 2018-2019 Egyptian viruses and 212I mutation that recorded previously had an important effect on the increased pathogenicity of the H9N2 in mice as previously recorded (Yang et al., 2014) that may affect the human transmission of the virus. So, there is a need to conduct further studies to detect the effect of these mutations on the pathogenicity of the virus and vaccine efficacy in poultry.

In the current study, a high number of infected vaccinated flocks with IBV viruses by RT-PCR was recorded. Therefore, partial S1 gene sequencing is important to identify the IBV strains. Furthermore, the partial IBV S1 gene was sequenced, and the analysis revealed that six selected viruses were related to clad GI23 (Egy Var I) as previously indicated (Hassan et al., 2016; Zanaty et al., 2016; Abozeid et al., 2017). The Egyptian strains in this study had low identity percent with vaccine strains H120, M41, 4/91 ranging 68.3-78.8% that lead to the appearance of infection in vaccinated farms as previously recorded (Abd El Rahman et al., 2015; Sultan et al., 2019). Accordingly, future studies should be conducted to evaluate vaccine efficacy and update the vaccine used to give high protection against newly mutated strains.

The S1 subunit, which comprises three major hypervariable regions (HVRs) in the first 395 amino acids. The HVRs contain major antigenic sites between 38 and 67 amino acids for HVR-1, 97 and 141 amino acids for HVR2, and 274 and 387 amino acids for HVR-3 (Moore et al., 1997). The present study indicated multiple A.A. mutations in the HVR as previously recorded (Hassan et al., 2016; Zanaty et al., 2016; Abozeid et al., 2017) that may be due to widespread use of heterologous vaccine leading to vaccination pressure, which increases the pathogenicity of the virus and changes in tissue tropism (Cavanagh et al., 1992).

CONCLUSION

Infectious bronchitis virus and highly pathogenic avian influenza (H5N8) are the main causes of respiratory disease in Egyptian flocks alone or co-infected with other viruses with a high mortality rate. Circulation of avian influenza (H5N8) was detected with a mutation in the antigenic site and receptor binding site, low pathogenic avian influenza (H9N2) with a specific mutation, and infectious bronchitis viruses were rapidly evolved in hypervariable regions. The infectious bronchitis virus and highly pathogenic avian influenza H5N8 viruses were distinct from vaccine strains so it is important to surveillance of respiratory disease viruses and study the genetic evolution and its effect on pathogenicity and vaccine efficacy.

DECLARATIONS

Authors' contribution

Nahed Yehia contributed to molecular characterization and data analysis and the write-up of the manuscript and Fatma Amer contributed to sample collection and diagnosis.

Competing interests

The authors have not declared any conflict of interest.

Consent to publish

All the authors approved and agreed to publish the manuscript.

Ethical consideration

All authors approved the final draft of the manuscript for publication. Ethical issues (including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by the authors.

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Molecular Detection and Antibiotic Sensitivity of *Salmonella* Species Isolated from Goat Feces in Sylhet District of Bangladesh

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ABSTRACT

The present study aimed at the molecular detection of *Salmonella* species from feces of goats and the characterization of the isolated *Salmonella* by biochemical and antimicrobial sensitivity techniques. A total of 220 goat feces samples were collected, of which 27 (12.27%) were positive for *Salmonella* by conventional culture methods and 20 (9.09%) by biochemical and PCR techniques. The prevalence was higher in goats under one year of age (20%), compared to older animals aged one to two years (7.8%) and more than two years of age (4.7%), respectively. Moreover, the prevalence of diarrheic goats was significantly higher (38.46%) than healthy animals (2.76%). DNA was extracted from *Salmonella* strains and amplified by PCR using the specific primers of *Salmonella* invasion gene (*invA gene*). The antibiotic sensitivity test indicated that Ciprofloxacin (100 percent sensitivity), Gentamycin (100 percent sensitivity), and Neomycin (100 percent sensitivity) were the most effective antibiotics for the majority of *Salmonella* isolates. On the other hand, *Salmonella* isolates were found to have substantially high resistance to Erythromycin (100%), Amoxicillin (100%), Trimethoprim-Sulfamethoxazole (81.48%), Streptomycin (62.96%), and Tetracycline (55.56 percent). Since the rate of *Salmonella* carriers was relatively high, eating goat meat could increase the risk of foodborne salmonellosis.

Keywords: Antibiotic sensitivity, Goat isolation, PCR detection, Salmonella

INTRODUCTION

Capra aegagrus hircus, popularly the black Bengal goat domesticated in Bangladesh, preliminary reared for chevon by millions of poor women and landless peoples to increase poverty (Rahmanet al., 2017). Salmonellosis is one of the most important foodborne zoonoses all over the world. The pathogen has been isolated from the feces, lungs, and liver of goats worldwide (Ziinoet al., 2009). *Salmonella* can infect a wide range of animals, including poultry and other birds, horses, cattle, pigs, sheep, goats, dogs, cats, and reptiles (Songer and Post, 2004). These Gram-negative bacteria are mainly transmitted through contaminated food and water and are clinically characterized by septicemia and enteritis. However, the possibility of the upper respiratory tract bacterial transmission in the animal has been reported (Garg and Sharma, 1979). Salmonellosis in goats could occur at all ages during the year in both males and females and is responsible for the considerable loss of kids and may even cause abortion in adults (Arrudaet al., 2004). Salmonellosis is the most frequent disease in goats among the most common bacterial zoonotic diseases characterized by diarrhea (Radostits et al., 2007; Kahn et al., 2010). Detection of these organisms could be a serious public health concern (Adesiji et al., 2011).

The conventional laboratory cultural methods take a long time to achieve a positive or negative result. Molecular techniques, such as genetic probes and Polymerase Chain Reaction (PCR) enable rapid, sensitive, and pathogen identification in the atmosphere with precision (Josephson et al., 1991). Without displaying any clinical symptoms of salmonellosis, the infected animals may shed the *Salmonella* organism in their feces. As a result, a rapid, specific, and responsive *Salmonella* detection method is critical for animal and human health and as well as the diagnostic industry. Polymerase chain reaction detection of Salmonella in clinical samples from animals is faster than traditional culture techniques, with a sensitivity and specificity of 100 percent as compared to culture techniques. The method could be applied for rapid routine diagnosis (Stone et al., 1994). The objective of the present study was to estimate the prevalence of *Salmonella* in both diarrheic and healthy goats and to confirm it by PCR detection.

MATERIALS AND METHODS

Ethical statement

This study was approved by the Ethical Committee of Sylhet Agricultural University, Sylhet-3100, Bangladesh, as well as by mutual (verbal) understanding of the respective farm owners.

Geo-location of the study area

The present study was conducted in the Sylhet district of Bangladesh, which is located in the northeastern part of Bangladesh. The average maximum and minimum temperatures were 38°C and 7°C, respectively. The present study was conducted over a 12-month period from January to December 2018 and the data regarding climatic conditions were retrieved from Regional Meteorological Centre, Sylhet, Bangladesh.

Animals and samples

A total of 180 black Bengal goats of different ages from the Government Goat Development Farm, Sylhet, and 40 goats from individual farmers in Sadar Upazilla, Sylhet, constituted the study population. Fecal samples were collected directly from the rectum of apparently healthy goats and stored refrigerated at 4° C until processed for nucleic acid purification within 24 hours of collection. A cross-sectional study was conducted to isolate and identify the *Salmonella* from the feces of goats.

Salmonella isolation and identification

The conventional bacteriological methods were used to isolate the *Salmonella* from the samples as described (Khan et al., 2021). The samples were inoculated into the nutrient broth and incubated at 37° C for 24 hours. Fecal samples were subjected to initial nutrient pre-enrichment and incubated, and 0.5 mL was transferred to 10 mL Tetrathionate Broth (Merck) and incubated at 37° C for 24 hours. Pre-incubated brilliant green and Xylose Lysine Deoxycholate (XLD) agar was streaked with a loop of each enrichment broth and incubated. The plates were then analyzed for the existence of *Salmonella* colonies. Suspected colonies were inoculated into TSI (Triple Sugar Iron agar), peptone water, Simmon's Citrate, Urea medium, and MR-VP.

DNA extraction and PCR amplification

The DNA extraction was performed according to the manufacturer's instruction using the Addprep genomic DNA extraction kit (Addbio Inc. Ltd., Korea). These eluted DNA samples were stored at -80°C until further analysis. The PCR analysis was performed to detect the *Salmonella* invasion gene (*invA* gene) according to the manufacturer's instruction (Addbio Inc. Ltd., Korea). PCR assay performed in the thermal cycler TC1000G PCR System[®] (DLAB Scientific Inc., USA) with a heated lid. The cycling conditions included 50°C for 3 minutes (UDG Reaction), 95°C for 10 minutes (Initial Denaturation), 35 cycles of 95°C for 30 seconds (denaturation), 68°C for 45 seconds (annealing), and 72°C for 5 minutes for final extension (Khan et al., 2021). For the detection of *Salmonella*, the primers of invS-F (5'-TAA TGCCAGACGAAAGAGCGT-3') and invS-R (5'-GATATTGGTGTTTATGGG GTCGTT-3') were used (Khan et al., 2021). All reaction mixtures, including the negative control and *Salmonella* positive DNA, were tested in duplicate in the same run of PCR assay. PCR products were analyzed on 1.8% agarose gels stained with RedSafeTM (iNtRON Biotechnology, Korea) Nucleic Acid Staining Solution (20,000×), photographed, and stored as a digital image.

Antimicrobial sensitivity testing

The qualitative agar diffusion method (Kirby-Bauer method) was used for antibiotic sensitivity testing employing Mueller Hinton agar. The *in vitro* antibiotic sensitivity test was determined by the standard disc diffusion procedure according to the Clinical and Laboratory Standard Institute (CLSI, 2012). The antibiotic discs used in the present study were Erythromycin (ERY), Gentamycin (GEN), Streptomycin (STR), Amoxicillin (AMX), Ciprofloxacin (CIP), Tetracycline (TET), Neomycin (NM), and Trimethoprim-Sulfamethoxazole (SXT). The MIC (MIC50 and MIC90) was determined for each of the antibiotics used and the sensitivity or resistance was determined according to the protocol described (CLSI, 2012).

Statistical analysis

Microsoft Excel was used for the descriptive statistics. Chi-square tests were used to assess the significance of differences in prevalence between age, sex, and health status of the animals. P values less than 0.05 were considered significant using Chi-square tests (SPSS Inc., Chicago, IL, USA).

Prevalence of Salmonella in goats

From January to December 2018, a total of 220 goat feces samples (180 from Government Goat Development Farm, Sylhet, Bangladesh, and 40 from different private goat farms in Sadar Upazilla in Sylhet) were collected for isolation and identification and molecular detection of *Salmonella* and antibiotic sensitivity testing. Among 220 samples, *Salmonella* isolates were detected in 27 (12.27%) samples using the conventional cultural method. The isolates were followed by biochemical identification and PCR assays in which 20 (9.09%) samples indicated *Salmonella* positive (Table 1). Furthermore, the prevalence of *Salmonella* in the personal private farm was lower (3.89%) than the Goat development farm, Sylhet, which was estimated at 7.20% (Table 2).

Cultural and morphological characterization

All *Salmonella* colonies in Mac Conkey agar plates appeared as non-lactose fermenters, colorless and transparent (Figure 1C), and *Salmonella* turbidity produced on nutrient broth (Figure1A). The isolates of *Salmonella* grown in *Salmonella* (SS) agar plates indicated characteristic black-centered colonies (Figure 1B), but isolates were absent in the black dot. In microscopic analysis, the thin smears prepared with the colony from SS agar for Gram's staining showed Gram-negative, pink-colored, tiny rod-shaped appearance arranged in single or paired or short-chain (Figure 1D).

Biochemical characterization

Due to the cultural and morphological properties, all suspected *Salmonella* colonies were subjected to selected biochemical tests, including indole formation (Figure 2E), methyl red (Figure 2B), and Voges Proskauer reaction (Figure 2C), citrate utilization, and triple sugar iron agar. Of the 27 suspected *Salmonella* colonies, 20 were confirmed by biochemical test results. On TSI slants, most of the *Salmonella* isolates indicated fermentation of glucose (Figure 2A), gas production from glucose, H₂S formation, but none of the isolates fermented either lactose or sucrose (Figure 2D).

Antimicrobial susceptibility

The antibiotic sensitivity test indicated that the highest number of *Salmonella* isolates were sensitive to Ciprofloxacin (100%), Gentamycin (100%), and Neomycin (100%). Alternatively, there was significantly high resistance in *Salmonella* isolates to Erythromycin (100%), Amoxicillin (100%), Trimethoprim-Sulfamethoxazole (81.48%), Streptomycin (62.96%) followed by Tetracycline (55.56%, Table 3).

Detection of Salmonella by the polymerase chain reaction

All *Salmonella* suspected cultures subjected to PCR amplification generated a product of approximate molecular size 100 base per (bp) (*invA* gene) according to the manufacturer's instruction (AddBio Inc., Korea). A 100 bp DNA marker was used as a molecular weight marker (AddBio Inc., Korea). The band size detected in isolated *Salmonella* was consistent as analyzed by agarose gel electrophoresis (Figure 3). The estimated prevalence of *Salmonella* by using PCR was 9.09% (20/220) in goat feces.

Bunghudebin					
Factors	Animal	Number of examined animals	Positive fecal samples	Prevalence	p value
-	Up to 1 year	45	9	20%	
Age	1 - 2 years	90	7	7.8%	< 0.01
	> 2 years	85	4	4.7%	
Total		220	20	9.09%	
	Male	150	9	6.0%	
Sex	Female	70	11	15.71%	0.321
Total		220	20	9.09%	
Health status	Apparentlyhealthy	181	5	2.76%	< 0.01
ricatul status	Diarrheic	39	15	38.46%	< 0.01
Total		220	20	9.09%	

Table 1. Overall prevalence of Salmonella isolates in goats according to biochemical identification at Sylhet district of Bangladesh

Level of significance p < 0.05

Table 2. Farm-level prevalence of *Salmonella* isolates in goats according to conventional cultural methods and biochemical identification in Goat development farm, Sylhet

	Total number	Number of positive by	Number of positive by	Prevalence				
Farm type	of animal	conventional culture methods	biochemical tests	Conventional methods	Biochemical /PCR tests			
SGDF*	180	16	13	8.89%	7.20%			
IPF	40	11	07	27.5%	3.89%			
Total	220	27	20	12.27%	9.09%			

*Goat development farm, Sylhet, IPF: Individual private farm

Table 3. Overall susceptibility and resistance patterns of Salmonella isolates to selected antibiotics according to clinical and laboratory standard institute

Antimicrobial drug	Antimicrobial class	Abbreviation	Susceptible	Resistant*
Amoxicillin	β-lactams	AMX	-	100%
Ciprofloxacin	Quinolones	CIP	100%	-
Trimethoprim-Sulfamethoxazole	Folate pathway inhibitors	SXT	18.52%	81.48%
Erythromycin	Macrolids	ERY	-	100%
Gentamicin	Aminoglycosides	GEN	100%	-
Neomycin	Aminoglycosides	NM	100%	-
Streptomycin	Aminoglycosides	STR	37.04%	62.96%
Tetracycline	Tetracyclines	TET	44.44%	55.56%

*Salmonella isolates that indicate moderate resistance to some antibiotics were considered resistant according to the CLSI recommendations.



Figure1. A: Nutrient broth *Salmonella* produced turbidity, B: Black centered colony on *Salmonella-Shigella* (SS) agar, C: Colorless colonies on MacConkey agar, D: Gram staining under the microscope revealed Gram-negative, small rods arranged in single, paired, or clustered characteristics

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Figure 2. A: Sugar fermentation (Glucose and Mannitol +ve with the production of acid and gas, Sucrose –ve), **B:** MR Test (positive, red color), **C:** VP Test (Negative, no color change), **D:** TSI test (positive, Slant: red, butt: black); **E:** Indole Test (Negative, no color change)



Figure 3. Results of PCR under UV illuminator (bands corresponding to the 100 bases per marker line indicated representative of *Salmonella* positive samples (1~10). M: Marker, NC: Negative control, PC: Positive control

DISCUSSION

The isolation and identification procedure included cultural examination, morphological examination, staining properties, biochemical tests, and molecular detection by PCR technique. In the present study, a total number of 220 feces samples from goats were collected by Sylhet Goat Development Farm (SGDF) and Individual Private Farm (IPF) in Sylhet. The bacteriological examination revealed the isolation of *Salmonella* organisms from goats with an estimated prevalence of 12.27% (27/220). Several studies reported a similar prevalence of *Salmonella* in goat feces (Teklu and Negussie, 2011; Saha et al., 2013; Bosilevac et al., 2015). The prevalence of *Salmonella* was higher in young (up to 1 year) and sick (diarrheic) animals, estimated to be 20% and 38.46%, respectively. The age-related result of the present study is consistent with the findings of other researchers (Saha et al., 2013; Mahmood et al., 2014). The findings also coincide with the results of Hunduma et al. (2010), who stated diarrhea as the major problem in goats with a higher prevalence of 42.2%.

A total of 20 (9.09%) fecal samples were PCR positive for *Salmonella*, which is higher than others who reported only 1.05% PCR positive cases (Esmaeili and Rahmani, 2016). Similar studies were conducted on cattle in Bangladesh and found 8.50% positive by biochemical and PCR (Khan et al., 2021). In contrast, Teklu and Negussie (2011)found a higher prevalence of *Salmonella* in sheep and goats in an export abattoir in Ethiopia. They reported that 7.7% and 11.7%

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of the sheep and goats were positive for *Salmonella*. Gallegos-Robles et al. (2009) isolated and detected the *Salmonella* from cattle feces using microbiological and PCR methods, estimated the prevalence at 55% and was much higher than in the present study. For the detection of *Salmonella* genus using the PCR technique, it was found that all PCR products of the isolated positive control resulted in 100 bases per amplified fragment. The *invA* gene has been reported to be present in all strains and clinical isolates of *Salmonella* (Dahshan et al., 2010). The detection of *Salmonella* in clinical samples by PCR results in a faster than conventional culture methods (Stone et al., 1994). The conventional method of isolating *Salmonella* is more laborious and requires more manpower (Van der Zee and Veld, 2000). There are a very small number of viable organisms in the feces that may fail to grow in artificial laboratory media. Molecular tests were most successful than conventional micro-biological techniques (Jungkind, 2001).

The antibiotic disk diffusion indicated that some isolates were resistant to Streptomycin (62.96%), Amoxicillin (100%), Erythromycin (100%), trimethoprim/sulfamethoxazole (81.48%), and Tetracycline (55.56%). On the other hand, the highest number of *Salmonella* isolates was sensitive to Ciprofloxacin (100%), Gentamycin (100%), and Neomycin (100%). Isolation of *Salmonella* from food and water to antibiotic resistance is of great importance in the case of public health. While these infections are caused by animal feces, it is also essential to identify the antibacterial agents that are used to treat or prevent infections, as well as the promoters that are created (Graham et al., 2007). It has been reported that a high percentage of *Salmonella* isolates from healthy and diseased animals were resistant to two or more antimicrobial agents (Esaki et al., 2004), which explains the high spread of these organisms through feces of apparently healthy animals and their wide dissemination in the environment. There have been reports of the release of *S. Typhimurium* in a pig plant (Tanaka et al., 2014). Although the animals were found to be healthy, the release was very high several days after inoculation; therefore even normal feces could be a source within the herd infection. It has been reported that multi-resistant S. *Enteritidis* (resistant to two or more antimicrobial agents) with different patterns could reach up to 51.6% (de Oliveira et al., 2005).

The most common patterns of resistance were sulfamethoxazole, streptomycin, and tetracycline while ciprofloxacin resistance was the least common. In Japan, *S. Typhimurium* isolated from various animal species indicated that 20% of the isolates were resistant to ampicillin and 24% to tetracyclines (Esaki et al., 2004). In 2008, 31 Salmonella strains were isolatedfrom 12 different serovars forms in cattle, and the transmission of microbial resistance from *S. Heidelberg* to *S. Typhimurium* and bacteriophages that are resistant to several beta-lactam antibiotics and tetracycline blaCMY-2, tet (A), and tet (B), was demonstrated (Zhang and LeJeune, 2008). Later, 58% resistance to trimethoprim/sulfamethoxazole and 56% to tetracycline, followed by ampicillin and amoxicillin were reported (Yang et al., 2010). In Chile, in a preliminary study, 20.5% of the *Salmonella* strains isolated mainly from pigs, indicated multidrug resistance (MDR),with oxytetracycline being the drug with the highest resistance (69.1%, Junodet al., 2013).

CONCLUSION

From the findings of the present study, it could be concluded that *Salmonella* is an important cause of diarrhea in goats with salmonellosis in Bangladesh. Therefore, a rapid and proper diagnosis could prevent harm inflicted on the livestock industry. In this regard, the most accurate and quick diagnostic methods are required. The molecular basis of *Salmonella* identification techniques, such as the use of the *invA* gene-specific PCR method, could be useful in diagnostic and research laboratories. Ciprofloxacin, Gentamycin, and Neomycin might be the best choice among the antibiotics available on the market. The variation in antibacterial susceptibility or resistance pattern was also observed in the present study. This study suggests the strategic use of antibiotics for the control of *Salmonella* infections in animals.

DECLARATIONS

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Competing interests

The authors have declared no conflict of interest regarding the publication of this research.

Authors' contribution

This manuscript is from the master's degree thesis of Md. Abdus Sabur. Md. Mukter Hossain designed the study. Md. Abdus Sabur and Mouri Rani Das conducted the experiments. All authors were involved in data interpretation, write up and final approval of the manuscript.

Ethical considerations

Ethical issues (including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by the authors.

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Antibiotic Resistance Profile of *Escherichia coli* Isolated from Bovine Subclinical Mastitis of Dairy Farms in Algeria from 2017 to 2019

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ABSTRACT

Mastitis in cows is a major problem in dairy farms leading to a decrease in the quantity and quality of milk. The aim of the present study was to examine the association between the presence of Escherichia coli (E. coli) in milk and the subclinical mastitis, and to characterize the antibiotic resistance profiles of the isolated E. coli. In the current study, a total of 360 cow raw milk samples from three dairy farms of the region of Algiers were analyzed. The analysis period lasted from Spring 2017 to Winter 2019. The California Mastitis Test (CMT) was applied to detect subclinical mastitis. The E. coli strains were isolated from milk using conventional bacteriological methods. The antibiotic resistance profile of the isolated E. coli strains to 12 different antibiotics was tested using the disk diffusion method. On β -lactamase-producing strains, a double diffusion test was applied to identify the Extendedspectrum β -lactamase (ESBL) phenotype. Finally, the *ctXx-M* genes were amplified by PCR. Two-thirds (66.4%) of the milk samples were positive for the CMT test. A total of 97 E. coli strains were isolated from the milk samples, their resistance to antibiotics was tested, and 3.1% of the strains were resistant to trimethoprim-sulfamethoxazole, 6.2% to chloramphenicol, 12.3% to gentamicin, 13.4% to colistin, 23.3% to amoxicillin/clavulanate, 31.9% to kanamycin, 39.2% to enrofloxacin, 51.5% to cefotaxime, 52% to tetracycline, 57.7% to ampicillin, 74.3% to nalidixic acid, and 75.3% to amoxicillin. Furthermore, most of the E. coli strains (92.8%) were resistant to more than one antibiotic with a Multiple Antibiotic Resistance index ranging from 0 to 0.8. The 50 strains resistant to cefotaxime were analyzed for an ESBL phenotype. 39 of them (78%) were positive to the double-disk synergy test. Among the 39 ESBL positive strains, 27 (69.2%) were confirmed for the presence of a CTX-M gene by PCR. The present study showed that multiple drug-resistant E. coli, including ESBL-carriers, were frequently isolated from the milk of dairy cows in Algeria. The results underlined that the use of antibiotics on farms must be reasoned to avoid the spread of resistant strains in animals and human populations.

Keywords: Antibiotic Resistance, Cows, CTX-M gene, Escherichia coli, Milk, Subclinical Mastitis

INTRODUCTION

Algerian people are great milk consumers (120 l/inhabitant/year) but the local production is insufficient to fulfill this demand. The imported milk is expensive (around 1 trillion USD per year) for Algeria (MADR, 2003), therefore, Algerian authorities encourage local milk production. It is, thus, necessary to increase the local milk production yield. According to the Ministry of Agriculture and Rural Development (MADR), Algeria has a herd of 900000 dairy cows, including 23000 high potential dairy cattle (MADR, 2003). To achieve the goal of increasing the quantity and quality of milk production in Algeria, it is important to study the physiology of milk production and identify the causes that may affect it.

However, mastitis is the most expensive and the most important disease in the dairy industry. It is defined as an inflammation of one or more quarters of the mammary gland, characterized by physical, chemical, and microbiological changes in milk secretion as well as pathological changes in breast tissue (Sharif and Muhammad, 2009). The economic losses are due to the low yield of infected udders, veterinary treatments, milk seizures as well as the premature culling of cows (Peton and Le Loir, 2014).

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Clinical mastitis infections are those with symptoms like udder swelling or redness that are clearly visible. On the other hand, subclinical mastitis infections do not cause any visible changes in milk or udder appearance, making it difficult to detect. Nevertheless, subclinical mastitis infections affect the dairy producer's bottom line by reducing milk production, decreasing milk quality, and suppressing reproductive performance.

Regarding the incidence of subclinical mastitis, an average annual cost of around 5000 euros has been estimated in a herd of 100 dairy cows in the Netherlands (Halasa et al., 2009). However, the presence of pathogens and/or toxins in milk as well as residues of antibiotics resulting from the treatment of mastitis can seriously compromise public health. These infections are mainly caused by coliform bacteria *Escherichia coli* (*E. coli*), staphylococci, and streptococci (Baazise, 2006). The *E. coli* is the signature of fecal contamination although *Staphylococci* and *Streptococci* are members of the skin microbiota. To fight mastitis, massive doses of antibiotics are used selecting resistant and multi-resistant bacteria in milk.

The present study was dedicated to the characterization of antibiotic-resistant *E. coli* in the milk of dairy cows in dairy farms of the Algiers region from Spring 2017 to Winter 2019.

MATERIALS AND METHODS

Ethical approval

Since the experiments were performed on naturally collected milk, no ethical question was raised by this study. The samples were taken under the supervision of a veterinarian.

Sampling

A total of 360 milk samples (50 mL) coming from 149 different cows in three different farms (Figure 1) located in the region of Algiers were analyzed. The dairy farms in Algeria were rather small (less than 100 head of cattle) and the production system is mostly semi-intensive (MADR, 2003). Except for farm 2, the cows had access to meadows. The characteristics of the sampled farms are listed in Table 1. In order to examine a possible evolution in time, certain cows were sampled several times at different time periods. Therefore, the number of milk samples was higher than the number of cows.



Figure 1. Localization of the sampled farms of the Algiers region

Farm	Name	Location (town and GPS coordinates)	Number of sampled cows	Number of milk samples	Period of sampling
Farm 1	DOUMA	Kolea, 36°36'05.3"N 2°47'00.5"E)	32	120*	March to May 2017
Farm 2	CNIAAG	Birtouta 36°39'21.8"N 3°01'27.3"E	76	180	April to July 2019
Farm 3	ITELV	Birtouta 36°39'13.9"N 3°03'05.4"E	41	60	April to December 2019
Total			149	360	March 2017 to December 2019

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*: In this farm a sample of the bulk milk tank was also analyzed.

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California mastitis test

The California Mastitis Test (CMT) was employed on farms to identify subclinical mastitis by an indirect estimation of the Somatic Cell Count (SCC) in milk (Leach et al., 2008). A four-well plastic paddle was used, one well per udder quarter of the cow to be tested. Foremilk was discarded, and then about 50-100 ml of the milk was collected into each well. An equal volume of test reagent was added (COVETO, Montaigu, France), and gently manually agitated. The reaction was scored on a scale of 0 (mixture remained unchanged) to 3 (almost-solid gel forms), with a score of 2 or 3 being considered as a positive result. A cow was considered positive if at least one quarter was positive.

Microbiological analysis

In this phase of the study, 1 ml of each milk sample was used to inoculate a sterile tube containing 9 ml of Brain Heart Infusion Broth (BHIB, Oxoid, Basingstoke, UK). The tubes were incubated for 24 hours at 37°C. For the isolation of *E. coli*, a droplet of the enrichment medium was used to inoculate a Tryptone Bile X-glucuronide (TBX) Agar (Oxoid CM0945, Basingstoke, UK) plate using a sterile loop. The plates were incubated 24 hours at 37°C. The characteristic colonies were picked and streaked on a selective medium Basing (Hektoen Agar, Oxoid PO0142, Basingstoke, UK) to obtain a pure culture. For bacterial identification, catalase, oxidase, and coagulase tests were performed (Pilet and Bourdon, 1979).

The antibiotic resistance of the isolated *E. coli* strains was analyzed using the disk diffusion method (Brown and Kothari, 1975). The diameters of inhibition were measured and compared according to the instructions by The European Committee on Antimicrobial Susceptibility Testing (EUCAST) guidelines (SFM, 2019) to determine the phenotype (sensitive, intermediate, or resistant). The used antibiotics are listed in Table 2. The antibiotics were chosen following the recommendations of the Algerian Ministry of Health (MSPRH, 2014).

Multiple Antibiotic Resistance (MAR) index was defined as diving the number of resistant antibiotics by the number of tested antibiotics (Krumperman, 1983). For ESBL producers, the double-disk synergy test was used as previously described (Drieux et al., 2008). Commercially available disks (Oxoid, Basingstoke, UK) of Cefotaxime (CTX, 30 µg) together with 30 µg Amoxicillin-clavulanate (AMC) were placed 25 mm apart from each other on the surface of inoculated Muller-Hinton Agar (MHA) plate and incubated at 37°C for 24 hours. The test was considered positive when the decreased susceptibility to CTX and/or ceftazidime was associated with a clear augmentation of inhibition zone in front of the AMC antibiotic disk forming a characteristic "champagne cork" shape (Okoko et al., 2020). As a confirmation test, CTX (30 µg) disk and AMC (30 µg) were placed 30 mm apart on the surface of inoculated MHA, and incubated for one hour. Then, the AMC disk was removed and replaced by a CTX disk (30µg), and the plate was incubated at 37°C for 24 hours following the recommendations of the Algerian Ministry of Health (MSPRH, 2014).

Molecular detection of resistance genes

The E. coli strains that were positive for the double-disk synergy test (ESBL+) were analyzed for the presence of blaCTX-M genes using PCR as previously reported by Tabar et al. (2016). The forward and reverse primers used for bla-CTX-M-R PCR were bla-CTX-M-F 5'-ACCGCCGATAATTCGCAGAT-3' and 5'-GATATCGTTGGTGGTGCCATA -3, respectively (Tabar et al., 2016). Briefly, 1 ml of an overnight E. coli culture in BHI (Bio-Rad, France) was used to prepare DNA by the boiling method (Djahnit et al., 2018). To amplify the CTX-M gene by PCR, 5 µl of the DNA was used. The master mix consisted of 4 µl of 5X PCR Mix (miniPCR, USA), 0.2 µl of each primer (40 µM, Eurogentec, Belgium), and 10.6 µl of DNAse-RNAse free sterile water (miniPCR, USA). The PCR temperature cycles were applied once (94°C for 5 minutes), followed by 40 times (94°C for 30 seconds, 58.0°C for 30 seconds, and 72°C for 30 seconds), and finally once (72°C for 5 minutes). The PCR products were analyzed by 2% gel agarose electrophoresis (Green and Sambrook, 2019). A 584 bp product was expected. Two controls were used, namely a CTX-M15+ E. coli strain (DSM22664, DSMZ, Germany) and a CTX-M-2+ E. coli strain (provided by the Belgian National reference center of antibiotic-resistant Gram-negative bacilli, Yvoir, Belgium).

Statistical analysis

The statistical analyses were performed using the following free online statistics software. MedCalc (version 20.009, Schoonjans, 2017) was used for the odds ratios. For the independence Chi-Square test, BiostatGV (version 2020) was used (Huet et al., 2021). The confidence interval for the proportions was calculated using Sample size.net (version 2021, Kohn and Senya, 2021). For the hierarchical clustering, Wessa (version 1.2.1.) was used (Wessa, 2021) with the option complete linkage. All the statistics used in this work were described in the textbook by Thrusfield and Christley (2018).

The association strength between the presence of *E. coli* in milk samples and the CMT test results was performed using the Odds Ratio (OR) calculation (Thrusfield and Christley, 2018). A case sample was defined as a sample contaminated by *E. coli* and a control sample as an *E. coli* free sample. The association among antibiotic resistance profiles was calculated using the independence Chi-square test (Thrusfield and Christley, 2018). In order to accept or

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reject the null hypothesis, the following rules were adopted; p value < 0.01 was considered as a highly significant difference, p value < 0.05 was considered as a significant difference, and a p value ≥ 0.05 was considered as non-significant.

Hierarchical clustering analysis of the *E. coli* strains was made using the complete linkage method (Guess and Wilson, 2002). Briefly, a table was made with one row for each strain and one column for each antibiotic. The result of the antibiotic resistance was scored as zero for sensitive, one for resistant, and two for intermediate. The table was then used to introduce the data (as a Comma-separated Value (CSV) file) in a statistic software in R language (Wessa, 2021). The dendrogram was generated, and the length of the bars (height) indicated the distance among the strains.

Table 2. The list of used antibiotics with the disk loads and the used c

Antibiotic	Diskload (µg)	Cut-off (mm)
Ampicillin (AMP)	10	13-17
Amoxicillin (AMX)	20	13-17
Amoxicillin/Clavulanate (AMC)	30 (20-10)	13-18
Nalidixic acid (NAL)	30	13-19
Cefotaxim (CTX)	30	22-26
Gentamicin (GEN)	10	12-15
Trimethoprim- Sulfamethoxazole (SXT)	25 (1.25-23.75)	10-16
Chloramphenicol (CHL)	30	12-18
Colistin (CST)	25	10-11
Tetracycline (TET)	30	14-19
Kanamycin (KAN)	10	13-18
Enrofloxacin (ENR)	5	16-21

RESULTS

California mastitis test

In farm 1 (Douma), 120 milk sampling were collected from 32 cows. Of 120 milk samples, 78 (65%, CI 95%; 55.8-73.5) were positive to the CMT test, moreover, 31 cows (96.9%) showed at least one positive sample. In order to evaluate an evolution in time, one cow was sampled six times, 25 cows were sampled four times, two cows were samples three times, three cows were sampled two times, one cow was sampled once, and the bulk tank milk was also analyzed. Considering the obtained results, 14 out of 32 cows (43.75%, CI 95%: 26.36-62.34) presented 100% of the positive samples, 3 cows presented 75% of the positive samples, 1 cow presented 66.67% of the positive samples, 4 cows presented 50% of positive samples, 1 cow presented 33.3% of positive samples, 7 cows presented 25% of positive samples, and only 2 cows presented no positive sample. Concerning the evolution of the positivity of the samples in time, no clear pattern appeared. In farm 2 (CNIAAG), 180 milk samples coming from 78 cows were analyzed, 90 samples (50%, CI 95%: 42.5-57.5) were positive to the CMT test. Moreover, 57 out of 78 cows (73.1%, CI 95%: 61.8-82.5) showed at least one positive sample. Three cows were sampled four times, 37 cows were sampled three times, 19 cows were sampled two times and 19 cows were sampled once. Twenty-five out of 78 cows (32.1%) presented 100% of the positive samples, one (1.3%) cow presented 75% of the positive samples, one (1.3%) cow presented 66.67% of the positive samples, 7 (9%) cows presented 50% of positive samples, 17 (21.8%) presented 33.3% of positive samples, and 31 (39.7%) presented no positive samples. In farm 3 (ITELV), 60 milk sampling were performed on 40 cows; 51 samples (85%, CI 95%: 73.4-92.9) were positive. Thirty-three of the cows (82.5%, CI 95%: 67.2-92.7) showed at least one positive sample. Two cows were sampled three times, 16 cows were sampled twice, and 22 cows were sampled once. Furthermore, 31 out of 41 cows (77.5%) showed 100% of positive samples, 2 presented 50% of positive samples and 7 cows generated no positive results.

Globally, 239 out of 360 (66.39%, CI 95% 61.25-71.25) samples were positive to the CMT test, and 121 cows out of 150 (80.67%. CI 95%: 73.43-86.65) showed at least one positive sample. These results indicated a severe problem of subclinical mastitis in these farms.

Escherichia coli isolation

The results of the research on *E. coli* in the 360 milk samples (Table 3) indicated an overall prevalence of 26.9% (97/360). Therefore, the next step was to investigate if there was a correlation between CMT results and *E. coli* isolation

results (Table 4). The Odds ratio was significantly upper than one indicating an association between the presence of *E*. *coli* in the milk sample and the presence of a positive CMT test (p < 0.05).

Antibiotic sensitivity testing

The main purpose of this study was to examine the antibiotic resistance of isolated *E. coli*. The obtained results of the first serial of 12 antibiotics are summarized in Figure 2. Of the 97 tested *E. coli* strains, 1 was resistant to 10 different antibiotics, containing Ampicillin (AMP), Amoxicillin (AMX), Amoxicillin/Clavulanate (AMC), Cefotaxim (CTX), Trimethoprim-sulphamethoxazole (SXT), Chloramphenicol (CHL), Colistin sulfate (CST), Tetracycline (TET), Kanamycin (KAN), Nalidixic acid (NAL), five strains (5.2%) were resistant to eight different antibiotics (AM, AMX, AMC, CTX, CHL, K, NAL, Enrofloxacin (ENR)), nine strains (9.3%) were resistant to seven antibiotics, 22 strains (22.7%) were resistant to six antibiotics, 19 (19.6%) were resistant to five antibiotics, 11 (11.3%) were resistant to four antibiotics, eight strains (8.2%) were resistant to three antibiotics, 12 (12.4%) were resistant to two antibiotics, four (4.1%) were resistant to one antibiotic and only three strains (3.2%) were sensitive to all the tested antibiotics. Among them, two strains were isolated from two different cows of farm 2 (CNIAAG) and one stain from farm 1 (DOUMA). In other words, the MAR index was in the range of 0-0.8.

Interestingly, out of 97 strains, 85 (97.6%) different resistant types (resist types) were observed. Some clusters per farm were found as expected, but since it does not always indicate that similar resist types can be observed in different farms (Figure 3). The antibiotic resistances of the *E. coli* isolated were compared per antibiotic and among the farms in Table 5. There was a significant difference among AMP, AMC, CTX, CHL, TET, KAN, and ENR (p < 0.01).

The association among the resistances was also investigated (Figure 4). The results indicated that the AMP resistance profile was statistically associated with the AMC resistance, the CTX resistance, the TET resistance, the KAN resistance, and the ENR resistance (p < 0.05). The AMX resistance was associated with the KAN resistance, the NAL resistance, and the ENR resistance (p < 0.01). The AMC resistance was associated with CTX and CST resistance (p < 0.05). The CTX resistance was associated with the CST and the KAN resistance (p < 0.05). The GEN resistance was associated with the SXT resistance (p < 0.01). The SXT resistance was associated with the CHL (p < 0.01). The KAN resistance was associated with the NAL and with the ENR resistance (p < 0.05). The NAL resistance was associated with the ENR resistance (p < 0.05). The NAL resistance was associated with the ENR resistance (p < 0.01).

Extended-spectrum beta-lactamases

Among the *E. coli* tested samples, some seemed to potentially have an Extended Spectrum \Box -lactamase phenotype (ESBL). The double-disk synergy test has been performed on the 50 *E. coli* strains resistant to CTX, among which 39 strains presented a characteristic phenotype (Figure 5). The gene CTX-M encoding CTX-M \Box -lactamase was amplified by PCR on the 39 potentially ESBL + *E. coli*. 27 out of the 39 (69.2%) tested *E. coli* strains were CTX-M positive (Figure 6).

Farm*	Number of milk samples	Number of <i>E.coli</i> contaminated milk (%)
Farm 1(DOUMA)	120	45 (37.5%)
Farm 2 (CNIAAG)	180	30 (16.7%)
Farm 3 (ITELV)	60	22 (36.7%)
Total	360	97 (26.9%)

Table 3. Escherichia coli isolated strains from milk samples found in the different farms of the Algiers region

*: The farms are described in material and methods

Table 4. A	ssociation	between the	presence of	Escherichia	<i>coli</i> in	milk sam	ples and	the resu	ılts of	California	Mastitis 1	test
for cows of	f the studied	d farms of th	e Algiers re	gion								

	Case (<i>E. coli</i> +)	Control (E. coli -)
Exposed (CMT +)	74	147
Not exposed (CMT-)	23	116
Exposure rate (%)	76.3	55.9
Odds	3.2	1.3
Odds ratio (CI 95%)	2.:	5 (1.5-4.3)
P-value		< 0.05

CMT: California Mastitis Test, CI: Confidence Interval, E. Coli: Escherichia coli

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Antibiotic*	Farm	S	Ι	R	p-value (Khi2 test)
	CNIAAG	3	1	27	<0.01
AMP	DOUMA	31	4	10	<0.01
	ITELV	0	1	20	22
	CNIAAG	4	2	25	0.1
AMX	DOUMA	12	3	30	0.1 NC
	ITELV	1	0	20	INS
	CNIAAG	9	10	12	<0.01
AMC	DOUMA	32	2	11	<0.01
	ITELV	7	14	0	22
	CNIAAG	11	0	20	<0.01
CTX	DOUMA	24	0	21	<0.01
	ITELV	1	11	9	22
	CNIAAG	28	1	2	0.2
GEN	DOUMA	37	0	8	0.2
	ITELV	19	0	2	NS
	CNIAAG	23	8	0	0.07
SXT	DOUMA	27	15	3	0.07
	ITELV	19	2	0	INS
	CNIAAG	21	9	1	-0.01
CHL	DOUMA	41	0	4	<0.01
	ITELV	20	0	1	22
	CNIAAG	23	0	8	0.04
CST	DOUMA	38	3	4	0.04
	ITELV	20	0	1	51
	CNIAAG	17	3	11	-0.01
TET	DOUMA	12	11	22	<0.01
	ITELV	2	0	19	22
	CNIAAG	17	1	13	.0.01
KAN	DOUMA	40	1	4	<0.01
	ITELV	4	2	15	22
	CNIAAG	4	2	25	0.2
NAL	DOUMA	12	3	30	0.2 NC
	ITELV	2	0	19	NS
	CNIAAG	4	14	13	-0.01
ENR	DOUMA	24	9	12	<0.01
	ITELV	1	6	14	55

Table 5.	Comparison	of the	antibiotic	resistance	of	Escherichia	coli	per	antibiotic	in	the	different	farms	of the	Algiers
region															

S: sensitive; R: resistant; I: intermediate; SI: significant; SS: very significant; NS: not significant. * AMP: Ampicillin, AMX: Amoxicillin, AMC: Amoxicillin/Clavulanate, NAL: Nalidixic acid, CTX: Cefotaxim, GEN: Gentamicin, SXT: Trimethoprim-Sulfamethoxazole, CHL: Chloramphenicol, CST: Colistin, TET: Tetracycline, KAN: Kanamycin, ENR: Enrofloxacin



Figure 2. Resistance profile for 12 different antibiotics of the 97 *Escherichia coli* isolates from the farms of the Algiers region. AMP: Ampicillin, AMX: Amoxicillin, AMC: Amoxicillin/Clavulanate, NAL: Nalidixic acid, CTX: Cefotaxim, GEN: Gentamicin, SXT: Trimethoprim-Sulfamethoxazole, CHL: Chloramphenicol, CST: Colistin, TET: Tetracycline, KAN: Kanamycin, ENR: Enrofloxacin, S: Sensitive, R: Resistant, I: Intermediate.

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Figure 3. Dendrogram comparing the antibiotic resistance profiles of the 97 *Escherichia coli* strains. The *Escherichia coli* isolates were numbered from 1 to 97. The colors indicated the farm where the *Escherichia coli* strain was isolated. The length of the lines is proportional to the distance among the strains (Defays, 1977)

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Figure 4. Associations among resistances. An independence chi 2 test has been applied. The p values of the Chi 2 test were indicated. In green ($p \ge 0.05$); there was no association, in orange (0.05), there was a significant association; and in red (<math>p < 0.01), there was a significant association. AMP: Ampicillin, AMX: Amoxicillin, AMC: Amoxicillin/Clavulanate, NAL: Nalidixic acid, CTX: Cefotaxim, GEN: Gentamicin, SXT: Trimethoprim-Sulfamethoxazole, CHL: Chloramphenicol, CST: Colistin, TET: Tetracycline, KAN: Kanamycin, ENR: Enrofloxacin.



Figure 5. ESBL phenotype identification using synergy and double disk profiles. **A:** Synergy profile between AMC (30 μ g) and CTX (30 μ g). Due to clavulanate inhibition of ESBL; **B:** Double disk profile. The CTX (30 μ g) disk on the left showed a classical inhibition phenotype. The CTX (30 μ g) disk on the right showed no inhibition due to the pre-incubation for one hour with an AMC (30 μ g) disk.



Figure 6. Agarose gel electrophoresis (2%). M: molecular weight ladder (bp). S1, S4, S7, S10: negative samples. S2, S3, S5, S6, S8, S9, S11, S12: positive samples. CP1: CTX-M-1 + strain; CP2: CTX-M-2 strain; CN: Negative PCR control.

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Mastitis is a common inflammation of the cow udder leading to defect in milk production quantitatively and qualitatively leading to economic losses. In the present study, 239 (66.4%) cows presented a positive CMT test which was in accordance with the previous study in Algeria where 79% of the tested cows were CMT + (Asnoune et al., 2012), and with the study on milk quality in West Algeria (Aggad et al., 2009). *Escherichia coli* can harbor and transmit resistance to antibiotics. The virulence and the antibiotic resistance of bacteria are often linked (Cepas and Soto, 2020). *Escherichia coli* is one of the bacteria causing mastitis along with Staphylococci and Streptococci (Burvenich et al., 2003). Given its origin, it is not normal to find this bacterium in milk indicating fecal contamination.

In the current study, the prevalence of *E. coli* in milk samples was 26.94%. When this prevalence was compared with the prevalence of other studies of the literature, the present prevalence is high. For instance, a prevalence of 6.5% was found in Jordan (Ismail and Abutarbush, 2020), 10% in Mexico (Olivares-Pérez et al., 2015), 11.1% in China (Yu et al., 2020), 15.5% in Belgium (Verbeke et al., 2014) and 7% in Egypt (Ameen et al., 2019). Interestingly, the present *E. coli* prevalence in the current study was approximately close to the prevalence (26%) found in another recent study in Algeria (Tahar et al., 2020) or a study in Ethiopia (27.3%) (Haftu et al., 2012), and lower than the prevalence found in Tunisia (31.7%) (Saidani et al., 2018).

A positive association (OR > 1) was observed between the presence of *E. coli* and a CMT+ test. Indeed, *E. coli* is a bacterium often found in mastitis (Burvenich et al., 2003). The hygiene of the farm is very often involved in the contamination of milk by *E. coli*. Heavily soiled litter is a major source of contamination (Magnusson et al., 2007). Decontamination of udders during milking is especially important to eliminate bacterial contaminations as much as possible. Therefore, the presence of *E. coli* in milk is an indicator of the lack of hygiene during milking (Saidani et al., 2018). The generalization of antibiotic therapy has produced spectacular results in the treatment of mastitis. But it has an unfortunate corollary, the selection of Multi-Drug Resistant (MDR) germs. In addition, previous studies have shown that the use of antibiotic s for many years has acted as a selection agent of an antibiotic-resistant bacterial population on the farm prior to antibiotic use for a new clinical purpose (Avrain et al., 2003; Boonyasiri et al., 2014).

Food-producing animals harbor bacteria in their intestinal tract include potentially pathogenic bacteria for humans. These bacteria could serve as reservoirs of resistance determinants that could spread throughout the food chain, reducing the effectiveness of antimicrobials used in human and veterinary medicine (Gouvêa et al., 2015; Manyi-Loh et al., 2018).

The obtained results of the current study revealed a wide variation in resistance to the tested antibiotics. The resistance phenotype ranged from 3.1% (SXT) to 75.3% (AMX). It is worth mentioning that most of the *E. coli* strains (90/97, 92.8%) were MDR with a MAR index ranging from 0 to 0.8 with one strain resisting to 10 out of the 12 tested antibiotics. The presence of MDR strains was due to the significant pressure exerted by the extensive use of antibiotics on the farms analyzed. The appearance of MDR strains was favored by different mechanisms, including a resistance mechanism leading to the resistance of more than one antibiotic (efflux pump), the horizontal transfer of resistance by mobile genetic elements such as plasmids or transposons, and the presence of strains with a high mutation rate (Chang et al., 2015).

Recently in Algeria, multidrug-resistant *E. coli* in cows with clinical mastitis in 42 different dairy farms have been investigated (Tahar et al., 2020). The antimicrobial susceptibility testing was performed by the disk diffusion method on 52 *E. coli* strains. The observed resistances were AMX (86.5%), TET (75%), AMC (59.6%), SXT (36.5%), doxycycline (13.5%), and ciprofloxacin (13.5%). Multidrug resistance was observed in 38.4% of isolates (Tahar et al., 2020). In a similar study in Egypt (Ameen et al., 2019), the *E. coli* strains isolated from cow milk were resistant to AM (33%), SXT (23%), and TET (16%) or AMC (6.6%). In Switzerland (Nüesch-Inderbinen et al., 2019), the *E. coli* strains isolated from cow milk were resistant to AM (22%), TET (16%), SXT (9.8%), gentamicin (3.7%), or to AMC (2.4%). The observed differences in the different studies were mostly dependent on the used antibiotics in the farms. Therefore, SXT was the best choice in the present study, although AMC was the most appropriate choice in the Egyptian and Swiss studies.

The study of resistor types of the different strains underlined the existence of clusters in the same farm. Nevertheless, some similar resistance profiles were present in different farms. It is related to the fact that the same antibiotics were used in different farms (Österberg et al., 2016). When the resistance per antibiotic was compared among the farms, significant differences (p < 0.05) were observed for the prevalence of the resistance to several antibiotics (AMP, AMC, TET, KAN, and ENR). Therefore, the circulating strains were not the same for the different farms. It is due to the used antibiotics in the farms, and to the fact that the sampling period was not the same for all the farms. When the resistance is considered by the antibiotic family, the results were observed as follows; quinolones, NAL, and ENR (a fluoroquinolone) were tested. In fact, 74.3% and 39.2% of the *E. coli* strains were resistant to nalidixic acid and ENR, respectively. The resistances were significantly associated (p < 0.01), which is logical since the mechanisms of resistance were similar (mutations chromosomal genes *gyrA* and *parE*). The high levels of resistance can be related to the large use of ENR by the veterinarians in the sampled farms (personal communication).

For fluoroquinolones, a recent study in Algeria indicated 13.5% of the resistance of *E. coli* strains isolated from cow milk against ciprofloxacin (Tahar et al., 2020). In that study, the sampled region was located 200 km southeast of the current sampling region. The differences can be related to the fact that different antibiotics were used by veterinarians in this region. For example, in this study (Tabar et al; 2020), the most prevalent resistance was resistance to AMX (86.5%), TET (75%), and AMC (59.6%). In Tunisia, in a similar study, 11% of the *E. coli* isolates were resistant to ENR (Saidani et al., 2018).

For sulfonamides, the resistance against SXT in the present study was low (3%) compared to the data of the literature for comparative studies. For example, the resistance rate was 23.3% in Egypt (Ameen et al., 2019) or 17.8% in Tunisia (Burvenich et al., 2003). But the results indicated 25% of intermediate resistance which is concerning.

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Nevertheless, a low rate of resistance was also found in Canada (5.8%) (Saini et al., 2012). For TET, the resistance rate was 52%. In the same country for a similar survey, the resistance rate was 75% (Tahar et al., 2020). The same high level of resistance rate was observed in Tunisia (46.6%) (Saidani et al., 2018) or Brazil (92%) (Rangel and Marin, 2009). Tetracycline represents one of the oldest molecules used, both in therapy and preventively, generating remarkably high resistance.

Nevertheless, in regions where this antibiotic was used less, lower resistance rates were recorded, for instance, the rates were reported as 2.6% in Canada (Saini et al., 2012), 12% in China (Yu et al., 2020), as well as 16.66% (Ameen et al., 2019) and 27.5% in Egypt (Ombarak et al., 2018). Tetracycline has been used inappropriately in animal feed in many countries, leading to the development of resistance. This has prompted some countries to prohibit their use in animal feed, such as in European countries (OJEU, 2003).

For aminoglycosides, KAN and gentamicin were tested. Following the classification (Saberfar et al., 2008), the results indicated that the resistance rate of the strains found in the current study for KAN goes to group II of middle resistance with a resistance level of 31.9%. The resistance to KAN was significantly different (p < 0.01) among the tested farms with a farm presenting 71.4% of resistant *E. coli*. Kanamycin resistance was significantly associated (p < 0.02) with the resistance to beta-lactam antibiotics (AMP, AMX, and CTX), and to resistance to quinolones (NAL and ENR). These associations need to be investigated because these antibiotics belong to different families and the resistance mechanisms are different. Moreover, such association was not found for gentamycin.

The high sensitivity of *E. coli* strains to gentamicin was due to the non-use of this antibiotic in veterinary treatments in Algeria, and therefore, no selection of resistant strains. The prevalence of KAN-resistant *E. coli* isolated from cow milk was within the range of 2.8% in China (Yu et al., 2020), 4.1 % in Egypt (Ombarak et al., 2018), and 6% in France (Botrel et al., 2010).

For gentamicin, a rate of 12% was recorded which was close to what has been recorded in Tunisia (19.5%, Saidani et al, 2018), in Egypt (13.3%, Ameen et al, 2019), and In China (12%, Yu et al, 2020). In addition, the present results were extremely low compared to those reported in Brazil (Rangel and Marin, 2009), Lebanon (Barbour et al., 2015), or Iran (Fazel et al., 2019), where the reported rates were 67.9%, 77%, and 49.2%, respectively. For polymixins, colistin (polymyxin E) has been tested. Colistin is a cationic polypeptide antibiotic that interacts with the outer membrane of gram-negative bacteria. Despite colistin once was avoided due to its nephro-and neurotoxicity, this drug has now become a last-resort antimicrobial agent for treating life-threatening infections caused by MDR gram-negative bacteria. However, in November 2015, the first plasmid-borne colistin resistance gene *mcr-1*, encoding a phosphoethanolamine transferase, was detected in livestock and raw meat samples as well as humans in China (Liu et al., 2020).

In the current study, 13.4% of the *E. coli* strains were resistant to colistin. Colistin resistance was associated (p < 0.05) with CTX resistance. Interestingly, colistin and ESBL resistance are plasmid-borne, and can be co-transferred as previously described in China (Liu et al., 2020). It will be, therefore, interesting to study the plasmid profiles of the isolated strains to identify the genetic support of the colistin resistance.

 β -lactamins are classical antibiotics interfering with cell wall synthesis. In the present study, several β -lactamins were tested; AMP, AMX, AMC, and CTX. 75.3% of the *E. coli* strains were resistant to AMX, 57.7% to AM, 51.5% to CTX, and 23.3% to AMC. Therefore, β -lactamin resistance is common in the analyzed farms. The resistance of *E. coli* strains to AMP ranged widely, 2.6% in Canada (Saini et al., 2012), 22% in Switzerland (Nüesch-Inderbinen et al., 2019), 31.7% in China (Yu et al., 2020), 33.3% in Egypt (Ameen et al., 2019), and 59% in Brazil (Rangel and Marin, 2009).

The resistance to AMX was 86.6% in a similar study in another region of Algeria (Tahar et al., 2020), confirming that the *E. coli* strains resistant to AMX are common in cow milk suffering from mastitis in Algeria. Nevertheless, the use of a combination of AMC dropped the resistance rate to 23.7% in the current study and to 59.6% in the other Algerian study (Tahar et al., 2020), which was was confirmed in other studies conducted in Brazil (Rangel and Marin, 2009) and Egypt (Ameen et al., 2019) decreasing from 58% to 14% and 33.3% to 6.7%, respectively.

For CTX, the resistance rate was 4.5% in Egypt (Ombarak et al., 2018) and 18.1% in China (Yu et al., 2020). Therefore, the observed resistance rate in the current study was quite high indicating that *E. coli* strains producing β -lactamases were common in Algeria. This increase is particularly worrying because third-generation cephalosporins have been classified as critically important antibiotics (Collignon et al., 2009). Among the different mechanisms involved in β -lactamins resistance, the production of a β -lactamase, an enzyme hydrolyzing the β -lactam ring of the β -lactamins, is common. The emergence of ESBL and the widespread of this type of resistance is a major concern in animal and human health. Extended Spectrum β -lactamases are the enzymes having the ability to hydrolyze the β -lactam ring of broad-spectrum β -lactams such as oxyimino-cephalosporins, including cefotaxime, ceftriaxone, and ceftazidime. These antibiotics are the so-called "third-generation cephalosporins". Because diverse types of ESBLs genes are usually plasmid-borne, and since the plasmids can be transferred among various species of Gram-negative bacteria, the genes for ESBLs can be acquired by this horizontal transfer mechanism (Kawamura et al., 2017).

In the present study, by using the double-disk synergy test, among 50 *E. coli* strains resistant to CTX, 39 (78%) presented a classical synergy pattern of ESBL strains. Widespread resistance to newer generations of cephalosporins is attributed largely to the spread of CTX-M type Extended-spectrum β -lactamases (ESBLs) in Gram-negative bacteria, especially in *Escherichia coli*. As a result, the rapid global dissemination of the ESBL-producing *E. coli* is an emerging public-health concern (Pitout and Laupland, 2008).

In the current study, by using classical PCR (Tabar et al., 2016), the CTX-M gene has been identified in 27 (69.2%) of the strains. Besides, CTX-M and ESBL can be TEM-derived or SHV-derived (Kawamura et al., 2017), so it is possible that the ESBL *E. coli* strains are of these types. Moreover, the used PCR amplified mainly the CTXM-2 family genes (Figure 7). However, CTX-M-type ESBLs have been roughly divided into four groups based on the sequence

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similarity in amino acid residues; CTX-M-1 group, CTX-M-2 group, CTX-M-9 group, and CTX-M-8/CTX-M-25 group (Naas et al., 2007; Kawamura et al., 2017). Therefore, it is also possible that the mentioned ESBL strains were from another CTX-M group. For example, CTX-M-15 which is common at this moment is a part of CTX-M-1 group and was the most isolated CTX-M gene in dairy cattle (Afema et al., 2018).

CTX-M-1 CTX-M-9 CTX-M-2 CTX-M-25	TCGGGAGGAAGACTGGGTGTGGCATTGATTAACACAGCAGATAATTCGCAAATACTTTAT AGCGGAGGGCGGCTGGGCGTCGCGCTCATCGATACCGCAGATAATACGCAGGTGCTTTAT TCGGGAGGTCGGCTTGGCGTTGCGCTGATTAACACCGCCGATAATTCGCAGAT AGCGGGGGGACGACTGGGTGTGGCGTTGATTAACACCGCCGATAACACGCAGACGCTCTAC ** ** * ** ** ** ** ** * ** * ** ** **	251 289 194 289
CTX-M-1 CTX-M-9 CTX-M-2 CTX-M-25	CGTGCTGATGAGCGCTTTGCGATGTGCAGCACCAGTAAAGTGATGGCCGTGGCCGCGGGG CGCGGTGATGAACGCTTTCCAATGTGCAGTACCAGTAAAGTTATGGCGGCCGCGGGGGGG CGTGCCGATGAACGTTTTGCGATGTGCAGTACCAGTAAGGTGATGGCGGCGGCGGGGGG CGCGCCGACGAGCGTTTTGCCATGTGCAGCACCAGTAAAGTGATGGCGGCGGTAGCGGCGGTG ** * ** ** ** ** ** ** ** ******	311 349 254 349
CTX-M-1 CTX-M-9 CTX-M-2 CTX-M-25	CTGAAGAAAAGTGAAAGCGAACCGAATCTGTTAAATCAGCGAGTTGAGATCAAAAAATCT CTTAAGCAGAGTGAAACGCAAAAGCAGCTGCTTAATCAGCCTGTCGAGATCAAGCCTGCC CTTAAACAGAGCGAGAGCGATAAGCACCTGCTAAATCAGCGCGTTGAAATCAAGAAGAGC CTTAAGCAAAGTGAAACGCAAAAGGGCTTGTTGAGTCAGCGGGTTGAAATTAAGCCCTCA ** ** * ** ** ** * * * * * * * * * * *	371 409 314 409
CTX-M-1 CTX-M-9 CTX-M-2 CTX-M-25	GACTTGGTTAACTATAATCCGATTGCGGAAAAGCACGTCGATGGGACGATGTCACTGGCT GATCTGGTTAACTACAATCCGATTGCCGAAAAACACGTCAACGGCACAATGACGCTGGCA GACCTGGTTAACTACAATCCCATTGCGGAGAAACACGTTAACGGCACGATGACGCTGGCT GACTTGATTAACTACAACCCCCATTGCGGAAAAACACGTCAATGGCACGATGACATTCGGG ** ** ****** ** ** ** *** ** ** ** ** *	431 469 374 469
CTX-M-1 CTX-M-9 CTX-M-2 CTX-M-25	GAGCTTAGCGCGGCCGCGCTACAGTACAGCGATAACGTGGCGATGAATAAGCTGATTTCT GAGCTGAGCGCGGCCGCGTTGCAGTACAGCGACAATACCGCCATGAACAAATTGATTG	491 529 434 529
CTX-M-1 CTX-M-9 CTX-M-2 CTX-M-25	CACGTTGGCGGCCCGGCTAGCGTCACCGCGTTCGCCCGACAGCTGGGAGACGAAACGTTC CAGCTCGGTGGCCCGGGAGGCGTGACGGCTTTTGCCCGCGCGATCGGCGATGAGACGTTT CATCTGGGTGGTCCCGATAAAGTGACGGCGTTTGCTCGCTC	551 589 494 589
CTX-M-1 CTX-M-9 CTX-M-2 CTX-M-25	CGTCTCGACCGTACCGAGCCGACGTTAAACACCGCCATTCCGGGCGATCCGCGTGATACC CGTCTGGATCGCACTGAACCTACGCTGAATACCGCCATTCCCGGCGACCCGAGAGACACC CGTCTGGACAGAACCGAGCCCACGCTCAATACCGCCATTCCAGGCGACCCGCGTGATACC CGGCTCGATCGTACCGAGCCGACGCTCAACACCGCGATCCCCGGCGACCCGCGCGATACC ** ** ** * * ** ** ** ** ** ** ** ***** ** ** ****	611 649 554 649
CTX-M-1 CTX-M-9 CTX-M-2 CTX-M-25	ACTTCACCTCGGGCAATGGCGCAAACTCTGCGTAATCTGACGCTGGGTAAAGCATTGGGT ACCACGCCGCGGGGCGATGGCACAGACGTTGCGTCAGCTTACGCTGGGTCATGCGCTGGGC ACCACGCCGCTCGCGATGGCGCAGACCCTGAAAAATCTGACGCTGGGGTAAAGCGCTGGCG ACCACGCCGTTAGCGATGGCGCAGGCTCTGCGCAATCTGACGTTGGGCAATGCCCTGGGT ** * ** ** ** ** ** ** * * * * * * * *	671 709 614 709
CTX-M-1 CTX-M-9 CTX-M-2 CTX-M-25	GACAGCCAACGGGCGCAGCTGGTGACATGGATGAAAGGCAATACCACCGGTGCAGCGAGC GAAACCCAGCGGGCGCAGTTGGTGACGTGGCTCAAAGGCAATACGACCGGCGCAGCCAGC	731 769 674 769
CTX-M-1 CTX-M-9 CTX-M-2 CTX-M-25	ATTCAGGCTGGACTGCCTGCTTCCTGGGTTGTGGGGGGATAAAACCGGCAGCGGTGACTAT ATTCGGGCCGGCTTACCGACGTCGTGGACTGCAGGTGATAAGACCGGCAGCGGCGACTAC ATTCGGGCGGGTCTGCCGAAATCATGGGTAGTGGGCGATAAAACCGGCAGCGGAGATTAT ATTCAGGCAGGGCTACCCACATCGTGGGTTGTCGGGGATAAAACCGGCAGCGGCGGTTAT **** *** ** * * * * * * * * * * * * *	791 829 734 829
CTX-M-1 CTX-M-9 CTX-M-2 CTX-M-25	GGCACCACCAACGATATCGCGGTGATCTGGCCAAAAGATCGTGCGCCGCTGATTCTGGTC GGCACCACCAATGATATTGCGGTGATCTGGCCGCAGGGTCGTGCGCCGCTGGTTCTGGTG GGCACCACCAACGATATC GCGGTTATCTGGCCGGAAAACCACGCACCGCTGGTTCTGGTG GGTACGACGAATGATATCGCGGTTATTTGGCCGGAAGGTCGCGCCGCCCGC	851 889 794 889

Figure 7. Alignment of the main CT-X-M sequences using ClustalOmega software. CT-X-M-1 (genbank NG_048897.1), CTX-M-2 (genbank NG_048968.1), CTX-M-9 (genbank NG_049043.1), and CTX-M-25 (genbank NG_048974.1). The sequences of the used primers were highlighted. The identities were indicated by a star. The numbers corresponded to the number of the genbank sequences.

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CONCLUSION

In conclusion, the finidngs of the current study have indicated that cows producing milk are commonly positive to CMT test, and subclinical mastitis is an underestimated problem in Algeria. *Escherichia coli* is frequently isolated in cow milk indicating an improper hygiene level in the farms and an inappropriate disinfection procedure at the milking.

Antibiotic resistance is a major concern in animal and human medicine. The increase of MDR strains in animals and humans leads more and more to therapeutic dead ends. Most of the *E. coli* isolates were found as MDR, and a particular focus was put on ESBL. Of the studied *E. coli*, 40% were ESBL-carriers. Although animals should be cared for, the sparing use of antibiotics is recommended. In any case, the use of antibiotics as a growth promoter should be prohibited.

DECLARATIONS

Author's contributions

Ghallache Loubna and Mohamed-Cherif Abdellah conceived the study design, carried out laboratory work, participated in data analysis and interpretation, drafted the manuscript. Ghallache Loubna and Mohamed-Cherif Abdellah contributed equally to this work. China Bernard conceived the study design, participated in data analysis and interpretation, revised the manuscript. Benfodil Karima conceived the study design, drafted and revised the manuscript. Miroud Kamel revised the manuscript. Ait-Oudhia Khatima conceived the study design, took part in the coordination and management as well as field studies, participated in data analysis and interpretation, and revised the manuscript.

Competing interests

The authors declare that they have no conflict of interest.

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Ethical considerations

Ethical issues (including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by the authors.

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Effect of Larvicidal Extract N-Hexane Lime Leaves (*Citrus hystrix*) on Larva Instar III Mosquito (*Culex quinquefasciatus*)

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ABSTRACT

Culex quinquefasciatus mosquitoes are a vector of transmission of several types of diseases, such as filariasis, Japanese encephalitis, and dirofilariasis. Larval control is the key strategy of disease control programs caused by vectors around the world because it can prevent larvae to enter the adult stage. Control of mosquito larvae that are often used is chemically controlled. *Citrus hystrix* is a natural plant and contains chemical compounds that have biological activity, such as flavonoids, carotenoids, and limonoids. The present study aimed to determine the effect of citrus leaf extract (*Citrus hystrix*) on the mortality of the larva *Culex quinquefasciatus*. The method used in the current study was a laboratory experimental study method with the experimental design using a completely randomized design. The research plot carried out was the rearing larvae of *Culex quinquefasciatus*, the manufacture of citrus leaf extract N-hexane *omplet name hystrix* leaf has high toxicity because it contains essential oils, flavonoids, alkaloids, terpenoids, saponins, and Limonoids. The Optimal concentration of N-hexane extracts of citrus leaves that lead to larval mortality of *Culex quinquefasciatus* in vitro amounted to 93.33% on 4 hours of observation with a concentration of 4000 ppm. Extract N-hexane lime leaf has a larvicidal effect on the larva *Culex quinquefasciatus* in vitro.

Keywords: Citrus hystrix, Culex quiquefasciatus, Extract, Mosquitoes, Larvicide

INTRODUCTION

Indonesia is a tropical country that has optimal humidity and temperature so as to support insect survival. Mosquitoes are the type of insects that coexist with humans but can harm humans because of their role as destructive organisms and disease vectors (vector-borne diseases; Sumantri and Satar, 2015).

Culex (Cx.) guinguefasciatus mosquitoes are the vector of transmission of several types of diseases such as filariasis, Japanese encephalitis, and dirofilariasis (Hadi and Koesharto, 2006). Filariasis is an infectious disease caused by microfilarial worms. This disease can cause disability, psychosocial, and decreased patients' productivity. The number of filariasis cases in Indonesia increases annually. Japanese Encephalitis (JE) is a viral disease that causes encephalitis and is a problem of public health in Asia including in Indonesia. Mosquito control can be done at the larvae stage, but in the adult stage that mosquitoes can fly they can transmit the disease widely (Aradilla, 2009). The control of larvae is the key strategy of vector-borne disease control programs caused by vectors around the world because it can prevent larvae to become adults. The larvae stadium has the longest lifespan of about 10-15 days so that the exposure is also longer, adult stage or adult mosquitoes can also fly so that it can spread the disease widely. The use of insecticide as larvacide can be the most commonly used way for people to control the growth of the vector (Manimegalai and Sukanya, 2014). Control of mosquito larva that has been often used is chemical control, namely by using synthetic chemicals. It can suppress vector populations rapidly. However, control in this way when done repeatedly is less effective because it can cause resistance to larvae, death for animal predatory predators and environmental pollution (Yasmin and Fitri, 2013). Biolarvasida of a plant (vegetable) is considered quite potential replacing synthetic insecticide. Plant insecticides are generally more selective than chemical insecticides because they are directly targeted at the target insect species, but also do not pollute the environment because it is easily degraded by nature and its use is quite safe (Aktar et al., 2009). More than 2400 plant types that belong to 255 families are reported to contain pesticide ingredients. Basil, germanium,

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and zodia belong to a group of mosquito repellent plants due to their distinctive aroma. The plant contains compounds, such as methyl eugenol and some microelements, such as Linalool, Terpincol, Eugenol, Sincol, and Geraniol. In addition, there are other types of mosquito repellent including lavender, zodia, rosemary, fragrant lemongrass, and citrus kaffir lime (Kardinan, 2005). *C. hystrix* is a plant that is found easily by people. Plants derived from this genus of *Citrus* have chemical compounds that have biological activities, such as flavonoids, carotenoids, and Limonoids (Nurhaifah and Sukesi, 2015). Limonoid compounds are the teranoriterpen found in the leaves of Citrus lime which is potentially antifeedant to insects, growth regulator, and toxic substances in rice lice, larvacide, antimicrobial, insect repellent, and reproductive inhibitors (Li, 2001). The limonoid compound is an analog of juvenile hormones on insects that serve as a regulator of the growth of larval cuticles (Tunaz and Uygun, 2004). Saponin is also able to become biolarvasida. Saponin compounds in extracts that are eaten by the larvae of *Cx. quinquefasciatus* may irritate the digestive tract of *Cx. Quinquefasciatus*, and damage the cell membrane of the larva *Cx. Quinquefasciatus* (Pelah et al., 2002). In addition, limonoid has the ability to inhibit the formation of cancer cells, reducing the formation of low-density lipoproteins (LDL) as well as being able to suppress the appetite from insects (Murthy et al., 2021). Therefore, this research is done to find out the benefits of citrus leaves that are thought to have effects on larvae of *Cx. quinquefasciatus*.

MATERIALS AND METHODS

The research was conducted in the entomology laboratory of The Institute of Tropical Disease (ITD), Airlangga University, and the Department of Medicine of Veterinary Faculty of Universitas Airlangga, Surabaya, Indonesia. The material used consists of 420 larvae instar III *Cx. quinquefasciatus* obtained from the laboratory of ITD. Each treatment group used a sample of 20 larvae.

The current study utilized experimental research methods of laboratories with the experimental design using a completely randomized design using simple random sampling. The study was conducted in several phases, namely the rearing phase of the larva of Cx. quinquefasciatus, the manufacturing stage of citrus leaf extract of C. hystrix, the manufacturing stage of larvacidal material, and the observation phase after treatment. In rearing the larvae of Cx. quinquefasciatus, selection was based on the body length (5-6 millimeters, determined by a compound microscope with calibrated eyepiece graticule) and the day after the eggs hatch (four to six days). There was a triangular thickening consisting of many comb-shaped scales, had complete its morphological structure, and clearly, the body could be divided into a part of the head, chest, and abdomen. Prior to the study, the larvae were restored in advance in order to prove that the administration proved optimal. Subsequently, 420 larvae of instar III of Cx. quinquefasciatus were divided into seven treatment groups, namely the control group (+) consisting of Temephos 1 ppm + aquadest AD 100 ml solution, the control group (-) consisting of a solution of aquadest 100 ml, treatment 1 entailing 25 mg of citrus leaf extract of kaffir lime + aquadest AD 100 ml, treatment 2 consisting of 50 mg of kaffir lime citrus leaf extract + aquadest AD 100 ml, treatment 3 having 100 mg Citrus leaf extract of kaffir lime + aquadest AD 100 ml, treatment 4 including 200 mg citrus leaf extracts of kaffir lime + aquadest AD 100 ml, treatment 5 consisting of 400 mg of citrus leaf extracts of kaffir lime + aquadest AD 100 ml. The larvacide extract of the kaffir lime citrus leaves was then poured into plastic cups. Then, into the plastic cups that have been contained treatment solution inserted larvae of 20 tails of each glass. Observations were performed every 4 hours for 24 hours to see the dead larvae.

The physical factors measured in the room used during the study included the pH of water, water temperature, and room temperature. Measured water pH ranges from 7.0 to 7.2. The condition is a neutral pH and qualifies for the life of larvae in water. The measured room temperature is 25°C, which is the temperature suitable for larvae growth.

RESULTS

Result of soaking larvae Instar III of *Cx. quinquefasciatus* in various concentrations of treatment for 24 hours obtained the average value and standard deviation of the number of Instar larva III *Cx. quinquefasciatus* every 4 hours observation that can be seen in Table 1.

Based on Table 1 above, it can be noted that there is a significant difference in each treatment of the percentage of mortality of Instar-III Larva ($p \le 0.05$). However, the results of a comparison of immersion treatment in solution Temephos with extracts N-hexane citrus leaves of 4000 ppm concentrations do not show a noticeable difference. It is different from the immersion comparison of Temephos solution 1 ppm with the N-hexane extracts of citrus leaves with the concentrations of 2000, 1000, 500, and 250 ppm which show noticeable different results. Extract N-hexane citrus leaves of 4000 ppm concentrations at a 4-hour observation have shown an average death of as much as 19 tails so that it can be known that the value (LC_{90}) of extract n-hexane lime leaf is 4000 ppm. More details can be seen in Figure 1.

Based on Figure 1 of the comparative mortality ratio of Larva Cx. quinquefasciatus on the observation every 4 hours for 24 hours obtained the result that the relationship between the concentration of N-hexane extracts of citrus

leaves with larvae instar-larva III *Cx. quinquefasciatus* have a positive direction, meaning the higher concentrations of citrus leaf extract kaffir lime, the higher the power of the larva of mosquitoes *Cx. quinquefasciatus*. The increased immersion time at the concentrations of P1, P2, P3, and P4 showed an increase in the number of deaths each time of observation, it showed the time of immersion of N-Hexsan extract material affecting the death process of the mosquito larva *Cx. quinquefasciatus*. In negative control does not encounter the death of larvae it indicates there is no reaction of the use of aqueous solutions.

The results in the experiment indicated a significant difference in each treatment. This means that the death of the larvae of instar III Cx. quinquefasciatus was due to the immersion of the larvae in the kaffir lime citrus leaf extract. Insignificant differences in the positive control and the highest concentration of citrus leaf extract kaffir lime resulted from the equation of the effectiveness of citrus leaf extract in the killing of larvae.

Mortality (%)			Average ± star	ndard deviation		
error! Bookmark - not defined. Groups	4 hours	8 hours	12 hours	16 hours	20 hours	24 hours
K (+)	88.33 ± 2.88	100 ± 0	100 ± 0	100 ± 0	100 ± 0	100 ± 0
K (-)	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0
P1	11 ± 5.77	21.66 ± 5.77	25 ± 5	30 ± 5	38.33 ± 7.63	41.66 ± 7.63
P2	15 ± 5	28.33 ± 7.63	36.66 ± 5.77	38.33 ± 7.63	48.33 ± 10.40	51.66 ± 7.63
P3	30 ± 13.22	45 ± 13.22	56.66 ± 14.43	66.66 ± 10.40	76.66 ± 5.77	78.33 ± 7.63
P4	55 ± 5	63.33 ± 7.63	68.33 ± 10.40	73.33 ± 7.63	80 ± 10	91.66 ± 10.4
P5	93.33 ± 2.88	100 ± 0	100 ± 0	100 ± 0	100 ± 0	100 ± 0

Table 1. The results of soaking larvae every four hours

K+: Temephos, K-: Aquadest, P1: 250 ppm, P2: 500 ppm, P3: 1000 ppm, P4: 2000 PPM, and P5: 4000 ppm



Figure 1. Comparative mortality of Larva *Cx. quinquefasciatus* on observation every 4 hours in a day, K+: Temephos, K-: Aquadest, P1: 250 ppm, P2: 500 ppm, P3: 1000 ppm, P4: 2000 PPM, and P5: 4000 ppm

DISCUSSION

The results of soaking larvae on the negative control (k-) of the larvae mortality rates were 0% for every four hours (Table 1). This means that the larvae were still alive and the addition of aquadest in control treatment did not show any effect on the mortality of larvae. In positive control (k+), the death of Larva instar III *Cx. quinquefasciatus* resulted from the administration of Temephos 1 ppm solution. Temephos is an organophosphate larvicide used to treat water infested with disease-carrying insects. This larvide has a residual power of approximately one month in the water shelter. As with other organophosphates, temephos affects the central nervous system through inhibition of cholinesterase. In larvae, this results in death before reaching the adult stage. The function of the enzyme cholinesterase is to hydrolyze acetylcholine into choline and sour vinegar (acetic acid) so that if the enzyme is inhibited then hydrolyze acetylcholine does not occur so that the muscles will remain contracted for a long time and will occur continuously, and the insect will eventually die (Nugroho, 2011). So as with other organophosphate compounds, Temephos acts as an anticholinesterase (Nugroho,

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2011). Chemical compounds in plants that are potentially biolarvicides, are flavonoids, saponins, tannins, alkaloids, and essential oils (Kristanti et al., 2008). The *C. hystrix* leaf extract has high toxicity of lime leaves (*Citrus aurantifolia*), lime leaves (*c. amblycarapa*), and Balinese citrus leaves (*c. maxima*; Adrianto et al., 2014). The kaffir lime leaves contain essential oils, flavonoids, alkaloids, terpenoids, saponins, and limonoids (Adrianto et al., 2014).

Limonoid compounds are an important natural active component consisting of oxidized triterpenoid components (Khalil et al., 2003). Limonoid causes a bitter taste in orange and has the most potent larvacide effects. The larva cannot be transformed into a pupa because the title of the juvenile hormone in the larvae is not reduced but increases. To be a pupa, larva needed lower amounts of Juvenile hormones. Although the larvae make the skin change to instar IV, the larva will not be able to metamorphosis into the pupa and eventually die (Prijadi et al., 2014). Limonoida can enter into the body of the mosquito larva (*Aedes aegypti*) as a stomach poison. Limonoida goes into digestion through the concentration of the eaten extract concentrations. Insecticides will enter into the digestive organs of insects and are absorbed by the intestinal wall then circulate with blood that will interfere with the metabolism of mosquitoes so that it will lack energy for his life activities that will result in mosquitoes it is seizure and eventually dies (Baskar et al., 2020).

Another substance contained in the leaves of lime that can interfere with insects in digesting food is saponin. Saponin can lower the surface tension of the mucous membrane of the digestive tract larvae. The interaction of the saponin molecules with a layer of larval cuticle will result in damage to the cuticle (Chapagain and Wiesman, 2005). Saponins can also lower the enzyme activity of proteases in the gastrointestinal tract as well as interfere with food absorption (Afidah et al., 2014).

This alkaloid content acts as a stomach poison and contact poison. The alkaloid is a grain of salt so that it can degrade the cell membrane of the digestive tract to enter into and damage cells and can also interfere with the nervous system work of larvae by inhibiting the enzyme work of acetylcholinesterases. Where this enzyme cannot execute its duties in the body mainly forward the delivery of orders to the digestive tract larvae (midgut) so movement cannot be controlled. The occurrence of discoloration in the body of larvae becomes more transparent and the movement of larvae slows down when the touch is stimulated and always bends the body also caused by alkaloid compounds (Ahdiyah and Purwani, 2015).

Tannins are polyphenol compounds that can form complex compounds with proteins. Tannins cannot be digested in the stomach and have a connective power with proteins, carbohydrates, vitamins, and minerals. Tannins can interfere with insects in digesting food because tannins will bind to proteins in the digestive system that required insects for growth so that the digestive process is estimated that become disturbed to the larva *Cx. Quinqufasciatus* (Yunita et al., 2009).

The death of Larva instar III *Cx. quinquefasciatus* not only was resulted from the compounds of limonoid but this can also be caused by various ingredients contained in the extract N-hexane lime leaves such as materials that have been mentioned above which can affect the death of larva *Cx. Quinqufasciatus*. Therefore, The higher the concentration, the higher the content of the active ingredient contained in the extract of N-hexane lime leaves, which can cause a decrease in digestive activity, causing seizures and disrupt the nervous system and suppress the rate of growth of larvae (Minarni et al., 2013). The content of essential oils that are the secondary metabolite of extracts that are dissolved with aquadest will cause an oil layer to be formed due to differences in polarity. This coating will cover the water surface and siphon. The presence of oil will prevent larvae from taking oxygen, even the coating of oil will stick to the siphon will prevent the diffusion of oxygen towards the tissues, so that oxygen transport is interrupted. The nature of this essential oil can be respiratory poison (Hedayat, 2008).

After soaking the extract of N-hexane citrus leaf, the following kaffir lime signs were observed. In the first 15 minutes, the larvae *Cx. quinquefasciatus* showed a rapidly rising movement, convulsive movements, such as forming the U, weakened body movements, at 2 hours of observation time at concentrations of 4000 ppm and 2000 ppm has begun to show the situation where the larvae are unable to move, stiff, and subsequently die. The results of soaking larvae every 4 hours were observed. Larvacida contact poison can kill enough larva when exposed to external body parts. Then larvae show the sign of ascending movement rapidly (telescopic movement).

The results of the research on the concentration of the extract of N-hexane lime leaves at all treatments except the negative control (k-) were the death of larvae. The mortality rate of larvae at a concentration of 4000 ppm was 93.33%. This concentration is the best concentration of N-hexane extracts of citrus leaves as larvacide. The difference between the numbers of larvae deaths is caused by the concentration of each treatment. This indicates that the higher the concentration and duration of observations of N-hexane citrus leaves of the purut, the higher the active content and the larvasidal power to kill the larva of quinquefasciutus mosquitoes.

When compared, concentration 4000 ppm extract N-hexane citrus leaves are equally effective with a solution Temephos 1 ppm in killing the larva instar III *Cx. quinquefasciatus* is the same as indicating the death of 100%. But for the efficiency of the solution temephos is higher in killing the larvae *Cx. Quinqufasciatus* then extract N-hexane citrus leaves of kaffir lime with a concentration of 4000 ppm because it only takes 1 ppm (mg/l) of Temephos solution, compared to 4000 ppm (mg/l) extract N-hexane lime leaves to kill 100% larvae for 8 hours in a 24-hour time.

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CONCLUSIONS

The findings of this study have confirmed that extracts of N-hexane lime leaves contain active substances that can be larvicidal. Therefore, the results larvacides are considered good when the test material shows the value of mortality between 90-100% of test larvae. In conclusion extract of N-hexane kaffir lime orange leaves have a larvicidal effect on the larva *Cx. quinquefasciatus* in vitro. The optimal concentration of N-hexane extracts of citrus leaves that cause the larval mortality of *Cx. quinquefasciatus* in vitro amounted to 93.33% on 4 hours of observation with a concentration of 4000 ppm.

DECLARATIONS

Competing interests

Authors declare no competing interests.

Authors' contribution

The authors have participated in this study equally.

Ethical consideration

Ethical issues (Including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by the authors.

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Effect of Processed Lemon Pulp with *Saccharomyces cerevisiae* in Zaribi Goats Diet on Milk Production, Nutrients Digestibility, Blood Parameters, and Reproductive Performance

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ABSTRACT

The aim of the present study was to evaluate the effect of replacing concentrate feed (CFM) mixture with different levels of treated lemon pulp (TLP) on milk production and composition, nutrients digestibility, and blood parameters of Zaribi goats. A total of 24 Zaribi female goats at the end of the pregnant period were divided into three groups of eight according to live weight. Concentrate feed mixture and clover hay at a rate of 50:50 were offered twice a day. Treatedlemon pulp replaced CFM at rates 0%, 25%, and 50 % in diets of R1, R2, and R3 treatment groups, respectively. The feeding trial lasted 90 days. Dry matter digestibility and Nitrogen free extract digestibility were significantly raised by the increased level of TLP in groups R2 (72.37% and 70.36%) and R3 (72.28% and 70.30%), compared to (70.99% and 68.51%) in R1, respectively. The same trend was observed for organic matter digestibility (OMD), crude protein digestibility (CPD), crude fiber digestibility (CFD), and ether extract digestibility (EED) with R3, compared with either R1 or R2. However, there were insignificant differences between R1 and R2 in terms of OMD, CPD, and EED but CFD was significantly higher in R2, compared to R1. There was a significant increase in the milk yield by the increased level of TLP in the diet and for R2 (1448.4g/h/d) and R3(1558.7g/h/d), while it was reported as 1377.6 g/h/d in the control group. Feeding dams on the R3 diet had a significant effect on improving total antioxidant capacity by 63.5%, compared with control. The results of the present study indicated that the replacement of CFM by TLP decreased the costs of feed and increase milk production for the replacement level by 50% (R3). Moreover, no adverse effects were noticed on nutrient digestibility and blood parameters of the investigated samples.

Keywords: Blood parameters, Lemon pulp, Milk production, Saccharomyces cerevisiae

INTRODUCTION

Traditional feedstuffs are very expensive so the use of agro-industrial by-products in animals diets has been introduced as the best way to decrease the cost of the feed. In Egypt, there is a shortage of animal feeds which had a negative effect on increasing animal production. Ruminant animals can depend on by-product feedstuffs (BPF) in their diets because the rumen microorganisms can use BPF which contains high levels of crude fiber and low protein content to cover their requirements for growth, reproduction, and production.

Adding citrus by-products to ruminants' diet is suitable because the rumen microorganism has the ability to ferment high fiber feeds (Grasser et al.,1995). The citrus residues of the juice industry (oranges, tangerines, lemons, or grapefruits) are called the citrus pulp. The citrus pulp can be used in animal feeding either fresh or after ensilage or dehydration. The nutritional value of citrus pulp is high owing to its high content of readily fermentable carbohydrates and contains a variety of energy substrates for ruminal microbes (Habeeb et al., 2017). The high content of easily fermentable carbohydrates and different energy sources found in the citrus pulp which are available for ruminal microorganisms can increase its nutritional value (Habeeb et al., 2017).

This important bioprocess is characterized by microbial growth in the insoluble substrate, in the presence of small amounts of free fluid, using the nutrients and residual elements present in these residues (Pinto et al., 2005). The microbial growth in this insoluble substrate, which contains small amounts of free fluid, depends on residual elements (Pinto et al., 2005). Micro-fungi solid substrate fermentation of this pulp could increase the protein content, antioxidant activity, and digestibility of the pulp. In fact, the citrus pulp is an energy source for rumen micro-organisms.

Protein enrichment of these by-products by microorganisms improves the nutritional value of the forage palm for ruminants (Vendruscolo et al., 2009). Residues of fruits and vegetables have been good substrate for protein enrichment and bioconversion into value adds products as enzymes and other metabolites. Using *Saccharomyces cerevisiae* (*S. Cerevisiae*) and fungi to bioconvert these agro-industrial by-products in raising their protein content. Fermented pineapple wastes by *S. cerevisiae* for 48 hours caused an increase in protein from 6.4% to 16.1% (Roberta et al., 2007).

Improving protein content by processing wet citrus pulp increases their efficiency in livestock nutrition. Some studies indicated that processing citrus pulp with microorganisms increases the crude protein contents as a result of converting lignocelluloses and easily-digestible materials into energy, protein, and CO2 by their extracellular enzymes (Scerra et al., 1999). Using pectin, digestible fiber, and soluble carbohydrates, which are found in citrus pulp residues, as a source of energy are easily and extensively degraded instead of starch led to producing acetic acid, which does not cause a pH drop like lactic acid and result in acidosis. Long rumination period and high fiber content cause large quantities of saliva buffering rumen ph. Lemon pulp is considered as a safer feed than cereals for animals fed low-roughage and high-concentrate diets in high-yielding dairy cows (Crawshaw, 2004). So, the use of agro-industrial by-products in ruminant diets might be an alternative to replace food energy and protein concentrates, increasing the efficiency and reducing the economic costs of the production system and consequently, making it more competitive. Also, the citrus family (Citrus lemon) contains an antioxidant component. The antioxidant activity of phenolic compounds such as flavonoids and phenols in lemons can improve in reducing the risk of cardiovascular disease (Ghasemi et al., 2009).

The objective of this study was to evaluate the impact of partial replacing of CFM by lemon pulp fermented with *S*. *Cerevisiae* on chemical composition, digestion coefficients, blood parameters, and milk production performance of the Zaribi goats.

MATERIALS AND METHODS

This experiment was carried out at Sakha, Animal Production Research Station of Animal Production Research Institute, Agriculture Research Center during the summer season of 2020.

Ethical approval

This study was approved by the Scientific Committee of Animal Production Research Institute (protocol no: 1-2-2-924).

Preparing lemon pulp

Lemon pulps were collected from the Elmarowa factory in Sixth of October City, Egypt, and sun-dried for 7 days, then, the dried lemon pulp was mixed with water at 1:2 ratio (pulp: water). Then, temperature, humidity, and acidity of lemon pulp were adjusted to be suitable for yeast growth, whereas the optimal humidity and pH for yeast growth are 85% and 5.6, respectively, according to Dadvar et al. (2015), so, bicarbonate was added by 6.4% to the media to adjust the pH. Samples of prepared lemon pulp were put in polyethylene bags and inoculated with4% yeast and incubated at 35°C for 24 hours. After the incubation period, the samples were sun-dried for 4 days, then, kept for chemical analysis. Feed ingredients, *S. cerevisiae* powder, Concentrate Feed Mixture (CFM), Clover Hay (CH), and feces were analyzed for proximate analysis according to AOAC (1995) whereas Nitrogen Free Extract (NFE) was calculated by difference.

Items (%)	DM	ОМ	CF	СР	EE	NFE	ASH
ULP	90.98	91.22	13.59	8.90	5.03	63.70	8.78
TLP	89.80	87.68	10.86	13.92	3.46	59.44	12.32
Relative change	-1.3	- 3.9	-20.1	+56.4	- 31.2	- 6.69	+40.3

Table 1. Chemical composition of untreated lemon pulp and treated lemon pulp on dry matter basis

DM: Dry matter, OM: Organic matter, CF: Crud fiber, CP: Crud protein, EE: Ether extract, NFE: Nitrogen free extract, ASH: Ash, ULP: Untreated lemon pulp, TLP: Treated lemon pulp

Experimental diets and animals

A total of 24 Zaribi female goats at the end of the pregnant period were divided into three groups of eight according to live weight for 90 days trial. Goats in each group were fed CFM consisting of 35% decorticated cottonseed cake, 25% corn grain, 30% wheat bran, 5% molasses, 2% limestone, 1.5% salt, and mineral, and 1.5% vitamins mixture, clover hay, CH, and treated lemon pulp (TLP). Feed was offered twice a day at 8 am and 4 pm and the remaining amounts from the previous day were measured. Water is offered freely all day round. The CFM is adjusted biweekly according to the body weight changes and milk production. Daily feed intakes, milk production, were recorded and feed efficiency (g feed/g milk) was calculated. Kids weighed biweekly before morning feeding. According to live body weight and milk production goats were fed the experimental diets as 50 % CFM and 50% clover hay.

The efficiency of dams was measured by litter weight at birth, which was calculated by total kids birth weight per dam. Litter weight at weaning was measured by total kids weight at weaning per dam, and total litter weight gain was estimated by total kids birth weight minus total kids weight at weaning per dam. Finally, the average daily gain was

calculated by the differences between total kids birthweight per dam and total kids weight at weaning divided on suckling period. On the other hand, the first group (control, R1) received experimental diets while, (R2) and (R3) experimental groups received the experimental diets by replacing 25% and 50% of CFM with treated lemon pulp, respectively. The chemical composition of raw materials and different experimental diets are presented in Table 2.

Parameters (%)	DM	OM	CF	СР	EE	NFE	ASH
Tested materials							
СН	89.93	87.59	25.22	12.80	2.57	47.00	12.41
CFM	91.53	89.97	11.62	14.02	2.96	61.37	10.03
TLP	90.98	87.68	13.59	13.92	3.46	56.71	12.32
Experimental diets							
R1(control)	90.73	88.78	18.42	13.41	2.77	54.19	11.22
R2	90.66	88.50	18.67	13.40	2.83	53.6	11.50
R3	90.60	88.21	18.91	13.39	2.89	53.02	11.79

Table 2. Chemical composition of concentrate feed mixture, clover hay, treated lemon pulp, and experimental diets on a dry matter basis.

DM: Dry matter, OM: Organic matter, CF: Crud fiber, CP: Crud protein, EE: Ether extract, NFE: Nitrogen free extract, ASH: Ash, TLP: Treraterd lemon pulp, CFM: Concentrate feed mixture, CH: Clover Hay, R1: Control diet (50% concentrate feed mixture + 50% clover hay), R2:37.5% concentrate feed mixture + 50% clover hay+12.5 % treated lemon pulp, R3:25% concentrate feed mixture + 50% clover hay+25 % treated lemon pulp.

Digestibility trials

Three animals from each group were used in digestibility trials using the acid insoluble ash (AIA) technique as an internal marker according to Van-Keulen and Young (1977) to determine the nutrients digestibility and feeding values of the experimental diets. Fecal samples of nearly 100 g were taken from the rectum twice daily at 8 a.m and 6 p.m for 3 days collection period. Representative samples of feed and feces from the whole collection period were prepared for proximate analysis according to AOAC (1995).

Blood and milk sample analyses

The blood samples were taken at the end of the termination of the experiment from the jugular vein in dry clean glasses tubes. Blood samples were collected into sterile blood tubes and immediately placed on ice before centrifuging to obtain serum. The serum was immediately frozen for subsequent biochemical analysis. Blood parameters, including total protein, urea-N, triglycerides, cholesterol, high-density lipoprotein, and low-density lipoprotein, were measured using enzymatic procedures and commercial kits. Daily milk yield was recorded and milk samples were collected at first, middle, and end of the experiment for analysis of milk composition using Milko Scan (model 130 series, type 10900 FOSS electric, Denmark). Body weight changes were individually determined biweekly before morning feeding. The growth of kids was also measured biweekly.

Statistical analysis

Analysis of variance (one-way, ANOVA) was performed to compare between different groups. Statistical analysis was carried out using SAS (2001) and Duncan's multiple range test (Duncan, 1955) was used to separate the means when the main effect was statistically significant at p < 0.05.

RESULTS AND DISCUSSION

The obtained results of Table 1 indicated that treating lemon pulp with yeast caused a decrease in dry matter, organic matter, ether extract, and nitrogen-free extract by 1.3%, 3.9%, 31.2%, and 6.69%, respectively. These decreases might be due to the internal metabolism and respiration of yeast, some amounts of carbon in lemon pulp are lost as carbon dioxide. Moreover, crude fiber content was a decrease by 20.1% after treatment and this may be due to the possible secretion of some extracellular enzymes, such as amylase and cellulose into the substrates which break the starch and other polysaccharides into simpler sugars easily metabolized by yeast as a source of carbon (Dadvaret al., 2015). However, there was an increase in crude protein (CP) and ash content with that treatment by 56.4% and 40.3%, respectively. These results were in agreement with the findings of Ezekiel et al. (2010) that there was an increase in ash content when cassava peels were fermented with *Trichoderma viride*. There was an increase in CP content since sugar could be an appropriate substrate for single-cell protein leading to the considerable final protein content of bioprocesses product *S. cerevisiae*. These results were in agreement with the findings of Roberta et al. (2007) who treated pineapple waste with *S. cerevisiae* leading to a significant increase in crude protein content of pineapple waste after processing. This increase can be attributed to high residual sugar as an appropriate substrate for single-cell protein leading to the considerable for single-cell protein leading to the considerable for single-cell protein final protein content of pineapple waste with *S. cerevisiae* leading to a significant increase in crude protein content of pineapple waste after processing. This increase can be attributed to high residual sugar as an appropriate substrate for single-cell protein leading to the considerable final protein leading to the considerable final protein leading to the considerable final

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protein content of bioprocesses product *S. cerevisiae*, which did not produce fungal toxins excreted by some filamentous fungi, such as *aspergillus*. Generally, yeasts have been shown to convert starchy materials, such as sweet potatoes and cassava peels, to protein. The increase in the ash content may not be a product of fermentation (Oboh, 2006).

Data in Table 2 represents the chemical composition of feedstuff and the similarity in chemical composition among the experimental diets used in the current experiment. The chemical composition of clover hay and concentrate feed mixture is in agreement with the findings of Sayed and Ghobashy (2018).

Nutrients digestibility and feeding values

Data in Table 3 showed that there was a significant increase in dry matter digestibility and NFE digestibility (p < 0.05) when TLP feed in R2 or R3 was reported as (72.37 and 70.36%) and (72.28 and 70.30%), respectively, compared to (70.99 and 68.51%) for R1. The same trend was observed for organic matter digestibility (OMD), crude protein digestibility (CPD), crude fiber digestibility (CFD), and ether extract digestibility (EED) with R3, compared to either R1 or R2. However, there were insignificant differences between R1 and R2 in OMD, CPD, and EED (p > 0.05) but CFD was significantly higher in R2 (p < 0.05), compared with R1.

These results might be due to the highly digestible NFE and high content of nonstructural carbohydrates of TLP diets, compared with control (Habeeb et al., 2017), or might be improving the rumen digestion environment with the TLP as mentioned by McDonald et al. (2011). This is due to yeast and its enzymes improving the rumen condition for fermentation. Miron et al. (2002) indicated that replacing 11% dry citrus pulp with corn seeds resulted in better conditions for rumen microorganisms and improved the digestion of crude protein. Moreover, treated lemon pulp with *S. cerevisiae* increased the digestibility of crude protein leading to an increased crude protein in the rumen for microorganism utilization. Additionally, yeast caused an increase in fibrolytic bacteriain rumen (Habeeb et al., 2017). This positive effect for TLP might be due to replacing starchy concentrates with feeds rich in easily degradable cell walls had generally been associated with a more favorable rumen condition for cellulolytic bacteria (Arthington et al., 2002).

The results of nutrient digestibility were reflected on the nutritive value of the experimental diets where R3 recorded the highest significant total digestible nutrient (TDN) followed by R2 then R1 as 62.15%, 60.98%, and 59.35%, respectively (p < 0.05). However, there was an insignificant difference among groups regarding digestible crude protein (DCP) value (p > 0.05). These results agreed with the finding of Kim et al. (2007) that citrus pulp supplementation might improve TDN and DCP.

Donomotors		Tre	eatments	
rarameters	R1	R2	R3	SEM
Digestibility coefficients (%)				
DM	70.99 ^b	72.37 ^a	72.28 ^a	0.35
OM	69.19 ^b	69.25 ^b	70.76 ^a	0.42
СР	69.44 ^b	69.77 ^b	73.90 ^a	0.76
CF	58.57 ^c	62.76 ^b	67.13 ^a	0.37
EE	76.60 ^b	77.60 ^b	79.13 ^a	0.44
NFE	68.51 ^b	70.36 ^a	70.30 ^a	0.37
Feeding values on DM basis (%)				
TDN	59.35°	60.98 ^b	62.15 ^a	0.44
DCP	9.31	9.35	9.90	0.055

Table 3. Digestion coefficients and nutritive values of the experimental Zaribi goats' diet

^{a,b,c} Means different superscripts in the same row are significantly different (p < 0.05). DM: Dry matter, OM: Organic matter, CF: Crud fiber, CP: Crud protein, EE: Ether extract, NFE: Nitrogen free extract, ASH: Ash, TDN: Total digestible nutrient, DCP: Digestible crude protein, R1: Control diet (50% concentrate feed mixture + 50% clover hay), R2: 37.5% concentrate feed mixture + 50% clover hay + 12.5 % treated lemon pulp, R3: 25% concentrate feed mixture + 50% clover hay + 25% treated lemon pulp, SEM: Standard error mean.

Milk yield and composition

According to Table 4, milk yield significantly increased (p < 0.05) by increasing the level of TLP in the diet as 1448.4 and 1558.7 g/h/d for R2 and R3, compared to 1377.6 g/h/d for R1. This increase might be due to the high TDN content in these diets, compared with the control diets (Schingoethe et al., 2004). Citrus pulp (dehydrated or ensiled) in diets for lactating ewes give conflicting results whereas some authors found no effect (Volanis et al., 2004), others reported a positive effect on daily milk yield (Piquer et al., 2011). Milk composition of T3 showed a significant increase in fat yield by 6.40%, compared with control, this agrees with the finding of (Volanis et al., 2004) who found a significant increase in milk fat percentage in ewes fed ensiled citrus pulp attributed their results to the easily digestible fiber in citrus pulp silage, which modified condition in the rumen and improved microbial activity, which leads to fiber degradation and subsequent higher production of acetic acid (Piquer et al., 2009), and promotes milk fat synthesis in the mammary glands.

Opposite results were seen by Piquer et al. (2011) when studied the effect of adding the citrus pulp to the diet of dairy ewes on the composition of milk. The results obtained by these authors showed that the use of 30% citrus pulp in the diet led to a reduction in milk fat content, while protein content was increased for ewes with 10% of citrus in the diets. The protein content of T3 had the highest value compared with control, this may result from supplementation of ruminant diets with citrus pulp may improve N utilization (Kim et al., 2007; Piquer et al., 2009), reducing the ruminal NH3-N escape, and consequently, the milk urea level, which several studies support this hypothesis in dairy ewes (Scatassa et al., 2006). Highly degradable carbohydrates led to the higher digestibility of the LP diets (Piquer et al., 2009), increased level of nitrogen absorption, and therefore, increased level of nitrogen excreted in milk. All treatments showed a significant increase in lactose and solid not fat, compared with control by increasing the level of TLP into the diets.

As can be seen in Table 5, there was a significant decrease between treatments in glucose concentration in the blood of goats fed LP this disagrees with the findings of Ali et al. (2016). Furthermore, blood serum cholesterol and TG levels decreased (p < 0.05) in R2 and R3, compared with control, which disagrees with the findings of a study by Alnaimyet al. (2017) reporting that blood cholesterol concentration increased in cows fed with a diet containing dried citrus pulp. This decrease in cholesterol content might result from the prevention of cholesterol formation by Trippine in lemon pulp (Takarada et al., 2002).

Description of any		Treatr	nents	
Parameters	R1	R2	R3	SEM
Daily milk yield (g/h/d)	1377.6 ^c	1448.4 ^b	1558.7 ^a	
Daily 4%-FCM (g/h/d)	1243.3 ^c	1313.7 ^b	1359.9 ^a	2.48
Milk composition				
Fat (%)	3.35 ^a	3.38 ^a	3.15 ^b	0.14
Fat yield (g)	46.14 ^b	48.95 ^a	49.09 ^a	0.75
Protein (%)	2.45	2.59	2.77	0.37
Protein yield (g)	33.75 ^c	37.5 ^b	43.17 ^a	1.08
Lactose (%)	3.94	3.45	3.44	0.54
Lactose yield (g)	54.27 ^c	49.96 ^b	53.61 ^a	1.44
Total solids (%)	10.5 ^a	10.31 ^b	10.29 ^b	0.78
Total solids yield (g)	144.78 ^c	149.33 ^b	160.39 ^a	1.84
Solids not fat (%)	7.16	6.93	7.14	0.74
Solids not fat yield (g)	98.63 ^b	100.37 ^b	111.29 ^a	1.71
Ash (%)	0.76	0.88	0.93	0.14

Table 4. Effect of different experimental of Zaribi goats diet on milk yield and its composition

^{a,b,c} Means different superscripts in the same row are significantly different (p < 0.05). R1: Control diet (50% concentrate feed mixture + 50% clover hay), R2: 37.5% concentrate feed mixture + 50% clover hay + 12.5% treated lemon pulp, R3: 25% concentrate feed mixture + 50% Clover hay + 25% treated lemon pulp, SEM: Standard error mean, Fat corrected milk (4%) for goats calculated according to gains equation: 4% FCM = 0.4 milk yield + 15 fat yield

Table 5. Biochemical	parameters in blood	serum of Zaribi goats	as affected by feedin	g experimental diet
			1	

Paramatars		Treatm	ents	
T at an etc 15	R1	R2	R3	SEM
Tp (g/dl)	6.45 ^c	7.33 ^b	7.84 ^a	0.92
Alb (g/dl)	3.94	3.97	4.17	2.38
Glo (g/dl)	2.51	3.36	3.67	3.77
Ur (mg/dl)	6.24	6.44	6.78	2.55
Cr mg/dl	1.14	1.12	1.18	0.17
Glu (mg/dl)	94.47 ^a	80.15 ^b	72.55 [°]	0.58
ALT (U/L)	15.74 ^a	14.33 ^b	14.77 ^b	0.13
AST (U/L)	26.79 ^a	24.16 ^b	22.48 ^b	0.91
Cho (mg/dl)	141.19 ^a	124.22 ^b	108.45 ^c	2.96
HDL	77.72^{a}	71.67 ^b	65.43 ^c	0.57
LDL	44.13 ^a	35.03 ^b	26.55 ^c	0.27
TAC	0.52^{b}	0.58^{ab}	0.85^{a}	0.24
TG (mg/dl)	96.71 ^a	87.56 ^b	82.35 ^c	1.68

^{a,b,c} Means different superscripts in the same row are significantly different (p < 0.05), TP: Total protein; Alb: Albumin, Glo: Globulin; Glu: Glucose, Cr: Creatinine, Ur: Urea-N Cho: Cholesterol, TG: Triglycerides, ALT: Alanine transaminase, AST: Aspartic transaminase, TAC: Total antioxidant capacity, SEM: Standard error mean, R1: Control diet (50% concentrate feed mixture + 50% clover hay), R2: 37.5% concentrate feed mixture + 50% clover hay + 12.5% treated lemon pulp, R3: 25% concentrate feed mixture + 50% Clover hay + 25% treated lemon pulp

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Data showed that there were no significant (p < 0.05) differences among groups in blood concentrations of albumin, globulin, urea, and creatinine. However, feed TLP in R2 and R3 significantly decreased blood concentration of glucose, ALT, AST, HDL and LDL (p < 0.05), compared with control. Feeding dams on diets contained TLP improved total antioxidant capacity insignificantly for R2 (p > 0.05) and significantly for R3 (p < 0.05) by 11.5% and 63.5%, respectively, compared with control. These results agreed with the findings of Ali et al. (2016), while lemon increased the concentrations of high-density lipoprotein (HDL) increased, but the concentration of cholesterol and triglycerides declined. The increase in total antioxidant capacity with R2 and R3 might be due to the fact that lemon had a strong antioxidant activity of its essential oil on the removal of free radicals; this may be related to phenolic and flavonoids compounds (Ghasemi et al., 2009).

According to Table 5, blood total protein significantly increased linearly with the increasing TLP (p < 0.05). These results are in agreement with those of Oni et al. (2008) that total plasma protein increased linearly with the increasing levels of citrus pulp. Table 6 shows the development of the body weight of kids and goats throughout the experimental period. Diets (R3) had a higher birth weight of kids, followed by those born from goats fed R2 diets, and less birth weight was obtained for goats in the control group (R1). This indicated that the diets improve the weight of the kids because the goat fed these diets at the last period of pregnancy.

Goats showed an increase in body weight after the parturition period in R3 followed by R2 indicating that an increase in digestion coefficient of TLP caused an increase in body weight for those groups. At the end of the experiment, kids in the group fed R3 showed the highest body weight and average daily gain, compared to the control (R1). This may be the result of an increase in milk yield so the kids had the best values of 280.3 and 226.3g/day for R3 and R2, respectively. Bueno et al. (2002) reported that different levels of orange pulp on Saanen kids' diets led to an increase in ADG, and kids fed a diet containing 42.3% orange pulp had the highest value. This finding is in agreement with that of Castollo-Gonzalez (2014) who concluded that the ruminal microflora improved production. The reason is that ruminal microorganisms are very important for ruminant animals, so, it is necessary to increase information about microbial ecosystems to improve the rumination process. Therefore, using additives in ruminant diet improves the efficient nutrients digestibility and reduces the production cost.

Data in Table 8 indicates the prices of experimental materials and average daily feed intake. The results revealed that daily milk yield increased by 1558.7g/ dam/day for R3 which might result from replacing 50% pf CFM with TLP. This led to an increase in nutrient digestion, TDN, and modification of rumen fermentation which causes high improvement in milk yield. When comparing the total feed cost (LE/dam/day), it was found that R3 had the lowest price being 5.20 while the highest value was found in R1 being 5.63 LE. However, there was a decrease in feed cost/kg milk by 18.38% and 7.10% for R3 and R2, compared with control, respectively. This represented that treatment LP with yeast could decrease the cost of production.

According to Table 7, feeding TLP in R2 and R3 respectively improved feed efficiency of DMI/FCM being 1.06 and 1.02 as well as DCPI/ FCM being 0.099 and 0.1 compared to 1.10 and 0.103 for R1.

Demonsterre		Experimental diets				
Parameters	R1	R2	R3	- SEM		
Dams performance						
No. of dam kidded	8	8	8	-		
Initial weight at Late-pregnancy (kg)	34.22	33.88	34.15	3.75		
Body weight at parturition (kg)	28.34	31.17	32.38	2.41		
Body weight at 1st month before parturition (kg)	22.49°	24.88^{b}	26.33 ^a	0.17		
Body weight two months before parturition (kg)	26.12	28.13	31.04	3.44		
Body weight three months before parturition (kg)	29.71	31.85	32.79	2.18		
Offspring performance						
Total number of kids	14	15	17	-		
Litter size/ dam at birth	1.75	1.87	2.12	-		
Birth weight (kg)	2.63	2.48	2.35	0.47		
weaning weight (kg)	13.44	13.37	14.25	2.48		
Total weight gain (kg)	10.81	10.89	11.90	-		
Average daily gain (g/ day)	120.11 ^b	121.00 ^b	132.22 ^a	2.86		
Relative improve (%)	100	100.7	110.1	-		
Dam production						
Litter weight at birth (kg)	4.60	4.63	4.98	2.46		
Litter weight at weaning (kg)	23.52 ^b	25.00 ^b	30.21 ^a	1.67		
Total litter weight gain (kg)	18.92	20.37	25.23	-		
Average daily gain (g/day)	210.2	226.3	280.3	-		

Table 6. Effect of feeding different experimental diets on dams and their offspring performance

^{a,b} Means different superscripts in the same row are significantly different (p < 0.05). SEM: Standard error mean, NO: Number, R1: Control diet (50% concentrate feed mixture + 50% clover hay), R2: 37.5% concentrate feed mixture + 50% clover hay + 12.5 % treated lemon pulp, R3: 25% concentrate feed mixture + 50% clover hay + 25 % treated lemon pulp

Table 7. Feed intake, milk yield, feed conversion, and feed efficiency of milk production of dams during the suckling period (90 days)

Devenuetore	Experimental diets				
Farameters	R1	R2	R3	SEM	
Total DM intake (g/ dam/day)	1370	1390	1380	-	
TDNI (g/dam/day)	813	848	858	-	
DCPI (g / dam /day)	128	130	137	-	
Daily 4%FCM (g/ dam/day)	1243.3 ^c	1313.7 ^b	1359.9 ^a	2.48	
Feed conversion ratio					
DM intake, g/g (4% FCM) milk	1.10	1.06	1.02	-	
TDNI, g/g (4% FCM) milk	0.65	0.65	0.63	-	
DCPI, g/g (4% FCM) milk	0.103	0.099	0.100	-	

^{a,b,c} Means different superscripts in the same row are significantly different (p < 0.05). SEM: Standard Erro Mean, FCM: Fat corrected Milk, TDN: Total digestible nutrient, DCP: Digestible crude protein, TDNI: Total digestible nutrient intake, DCPI: Digestible crude protein intake

Table 8.	Feed	intake	and	economical	evaluat	ion of	dams	during	the suc	kling	period	of 90	day	/S

	0 01	2		
Poromotors	Ex	perimental diets	5	
1 ai ameter s	R1	R2	R3	
Average daily feed intake, g/dam/day (feed)				
CFM	712.5	550	347	
Clover hay (CH)	818.75	830	848	
Treated lemon pulp (TLP)	-	180	365	
Daily milk yield (g/ dam/day)	1377.6 °	1448.4 ^b	1558.7 ^a	
Economical evaluation				
Average total feed cost (LE/dam/day)				
CFM	3.34	2.58	1.63	
Clover hay (BH)	2.29	2.32	2.37	
Treated lemon pulp (TLP)	-	0.59	1.20	
Total feed cost (LE/dam/day)	5.63	5.49	5.20	
Price of average daily milk (LE/dam/day)	8.26	8.69	9.35	
Feed cost (L.E) / milk (kg)	4.08	3.79	3.33	

^{a,b,c} Means different superscripts in the same row are significantly different (p < 0.05). Prices of concentrate feed mixture (CFM), Treated Lemon Pulp (TLP), and Clover Hay (CH) were reported as 4700 L.E./ton, 3300 L.E./ton, and 2800 L.E./ton, respectively. Based on the market price in 2020 and 6 LE/kg raw milk. R1: Control diet (50% concentrate feed mixture + 50% clover hay), R2: 37.5% concentrate feed mixture + 50% clover hay + 12.5 % treated lemon pulp, R3: 25% concentrate feed mixture + 50% clover hay + 25 % treated lemon pulp, Total daily feed cost (L.E.): Cost of CFM + TLP + clover hay, SEM: Standard error mean.

CONCLUSION

It could be concluded that replacement of concentrate feed mixture by lemon pulp treated by *Saccharomyces cerevisiae* in dairy goats diets can decrease the costs of feed and increase milk production by 50% without any adverse effect on milk yield, its composition, and animals health with high economic efficiency.

DECLARATION

Authors' contributions

Dr. Haiam A. Sayeddesigned the study, performed the chemical analysis and wrote the manuscript. Dr.Mouhmed M. Elmaghraby and Dr. Mohamed M. Elbadwy carried out the practical part of the experiment, collected samples from animals, and reviewed the manuscript. All authors read and approved the final manuscript

Competing interests

The authors declare that they have no competing interests.

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Ethical considerations

Ethical issues (including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by the authors.

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SHORT COMMUNICATION

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The Effects of Different Concentrations of Bay Leaf Extract on Shelf Life of Preserved Scad Fish

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ABSTRACT

Scad fish (Decapterus kurroides) is the most productive fish species. To provide the added value, fishermen can process scad fish into various forms of processed products, such as preserved fish, which extend the shelf life. In order to extend the shelf life of canned fish, natural preservatives could be used that contain antimicrobial agents, such as bay leaves. The present study aimed to determine the effects of bay leaf extract in different concentrations on the shelf life of preserved scad fish. In the present study, the completely randomized design was used as an experimental research method. The treatments given differed in terms of the concentration of the bay leaf extract. The groups were treated as the scad fish without bay leaf extract (A), scad fish soaked in 6% of bay leaf extract (B), scad fish soaked in 7% of bay leaf extract (C), scad fish soaked in 8% of bay leaf extract (D), and scad fish soaked in 9% of bay leaf extract (E). The analyzed parameters included the total plate count, pH, and water level test using Analysis of Variance (ANOVA). The supportive parameters observed included an organoleptic test. The results indicated that the lowest total bacterial count from the beginning to the end of the experiment (18 hours) occurred on treatment C (7% of bay leaf extract addition), which was 1.54×103 to 5.85×106 . Regarding the water level test from the beginning to the end of the experiment, treatment A (control) was not significantly different from other treatments. The difference in the concentration of bay leaf extract on scad fish effectively inhibited the growth of bacterial colonies. In conclusion, adding bay leaf extract to scad fish could inhibit bacteria for up to 12 hours. Treatment C (7% of bay leaf extract) gave the best results since this concentration level could inhibit the bacteria on scad fish.

Keywords: Bay leaf, Preservation, Scad fish, Shelf life

INTRODUCTION

Scad fish (*Decapterus kurroides*) is the most productive fish species, accounting for 52% of the total catch of approximately 2323365 tons per year. In addition, scad fish comes at a relatively low price. To achieve added value, fishermen process scad fish into various forms of processed products, such as *petis* (fish paste) and preserved fish. Preserved fish is one of the most famous marine products in Indonesia due to a combination of boiling and salting. The resulting product is a preserved fish with low salt content. The traditional preservation process of boiling the fish in the salt solution is called *pindang cue* (Triarso, 2012; Junianingsih, 2015).

Pindang cue uses scad fish, which can be found in traditional markets and are commonly placed in *paso* or *naya* (small woven tray) without any packaging. Thus, microbial contamination occurs during the sales process. The shelf life of scad fish is approximately 1-2 days, and safety is not guaranteed. Scad fish contain high water (60%) and protein (27%), which are suitable for the microorganisms' growth. The maximum limit for the microorganism in food products is 5.0×105 cells/gram (Ariyani, and Yennie 2008).

Preservation is an appropriate way to extend the shelf life of scad fish. Fish preservation is a process that is aimed at developing high-quality processed fish products (in terms of color, odor, texture), offering a wide range of food and varietal products on the market, increasing the economic value of the product, as well as enhancing the shelf life of fish. Since these preserved scad fish had a limited shelf life and are prone to deterioration, fish should be stored longer to provide benefits to traders while increasing consumers' appeal. Conservation also is used to inhibit the activities of enzymes and microorganisms (Herawati, 2008).

Preservation with hazardous chemicals, such as formalin, is mostly used because the price is lower than safe preservation. The use of formalin has been constantly increasing. Thus, natural preservations are required to inhibit the growth of spoilage bacteria (Hastuti, 2010; Nafisyah, 2015). Herbs and spices native to Indonesia contain active antimicrobial substances that potentially can be used as natural preservatives. Bay leaf is one of the natural ingredients

that can be used as a preservative, and also has many benefits to be utilized in cooking as a seasoning because of its distinctive aroma and odor, as well as its low price and easy procurement (Purwani and Muwakhidah, 2008).

Bay leaf is an ingredient that can be used as a fish preservative since it contains flavonoid, terpenoid, and tannin, which have antibacterial properties. Flavonoids inhibit bacterial growth by forming complex compounds with extracellular proteins through hydrogen bonds, that damage the cell membrane. Tannin inhibits bacterial growth by denaturating bacterial cell proteins in the cell membrane. The terpenoid inhibition mechanism for bacterial growth is to react with porin (transmembrane protein) on the external membrane of the bacterial cell wall. Bay leaf indicated good antibacterial activity against *Staphylococcus aureus* (Roslizawaty, 2013; Nurwijayanti, 2016). Based on the fact that bay leaf indicated sufficient antibacterial activity against Staphylococcus aureus, the present study was conducted to investigate the effects of bay leaf extract with different concentrations on the shelf life of scad fish.

MATERIALS AND METHODS

The current research used an experimental research method and the experiment design of a completely randomized design. The following is the bay leaf treatments on scad fish, scad fish without bay leaf extract treatment (A), scad fish soaked in 6% of bay leaf extract (B), scad fish soaked in 7% of bay leaf extract (C), scad fish soaked in 8% of bay leaf extract (D), and scad fish soaked in 9% of bay leaf extract (E).

The variables included in the present study were independent, dependent, and control variables. The independent variable was the bay leaf extract. The dependent variables of the study were the Total Plate Count (TPC), organoleptic value, pH, and water level of scad fish. The control variables of the research were bay leaves, preserved scad fish, and bay leaves boiled at 90°C for 30 minutes.

The research procedure was divided into two stages of preparation and implementation. The preparatory stage consisted of fish processing, sterilization of tools and materials, bay leaf extraction, and preparation of Plate Count Agar (PCA) media. The implementation stage included the treatment of scad fish, marked with the letter A, B, C, D, and E. Then, the treatment was performed by mixing bay leaf extracts with the preserved scad fish. In treatment A, the scad fish were not soaked in the bay leaf extract. In treatments B, C, D, and E, the scad fish were soaked in bay leaf extract with concentrations of 6%, 7%, 8%, and 9%, respectively, for 30 minutes. Furthermore, the soaked scad fish were then placed into the oven for 30 minutes at a temperature of 50°C. Then, the fish were transferred to clean containers and stored at room temperature. Afterward, the total number of bacteria, the pH value, water content, and the organoleptic value were observed before storage and after 3, 6, 9, 12, 15, and 18 hours of storage.

The research parameters were the main parameters and supporting parameters. The main observed parameters entailed the TPC test, pH, and water level. The supporting parameters observed included the organoleptic tests. The research result data were analyzed in the terms of TPC, pH, and water level using Analysis of Variance (ANOVA) to determine the difference in the different concentrations of bay leaf extracts on the shelf life of scad fish. Duncan's Multiple Range Test was then performed to determine the differences between treatments. The data analysis for organoleptic tests used descriptive methods. The distinction between the two approaches to sensory evaluation of fish products was made to first emphasize that both of these approaches were necessary for the evaluation of this commodity. Secondly, these two aspects of sensory evaluation of fish products were not mutually exclusive but rather acted as a mutual information resource. Sensory assessment of fish products would continue to be essential in quality testing, even as with time, useful chemical tests are developed which are as efficient and cost-effective as sensory testing. In product grading, standard chemical and physical tests can only measure what is already known. The sensory assessor can measure both the known attributes of the product and assess the presence of new attributes, especially in the area of measurement of 'taint' in fish products. The factor of sensory testing is part of the definition of taint in a product ['fish that is rancid or has an abnormal odor or flavor (DFO, 1978). However, chemical testing can accurately assess the level of a particular compound in a sample, it cannot by itself, indicate what this number means relative to the final quality of the product and the action that needs to be taken as to whether the product will continue to be used as a food, or whether it has deteriorated to a point where it is no longer usable. The definition of the 'cut-off' point for taint will always be based on a human definition of this level for the particular culture in which the product is being used (York and Sereda, 2014).

RESULTS

Total bacterial count

The highest mean total bacterial count from the beginning of the experiment until the end of the experiment (18 hours) occurred in treatment A (control), which was 1.57×103 to 8.55×106 . Meanwhile, the mean value of the lowest total bacterial count occurred from the beginning to the end in treatment C (7% of bay leaf extract), which was 1.54×103 to 5.85×106 (Table 1).

Water level test

The water level test utilized a moisture analyzer. The average value of the water content found in the redtail scad at the beginning of the experiment and the end of the experiment of each treatment decreased during storage at room temperature until the end of the study. The results of the ANOVA test showed that the mean value of the water level at the beginning and in hour 18 of the experiment in treatment A (control) did not significantly differ (p > 0.05) from the other treatments (Table 2).

PH level test

The results of the ANOVA test showed that the mean value of the water level at hour 12 in group D and hour 15 in group C, and E was significantly different (p < 0.05) from the other treatments (Table 3).

Table 1. Total bacterial count (CFU/gram) of Staphylococcus aureus and bacterias in Scad fish meat

Observation	bservation Treatment (Average ± SD)					
Time (hour)	A (0%)	B (6%)	C (7%)	D (8%)	E (9%)	
1	$1.57{\times}10^{3a}\pm0.11$	$1.52{\times}10^{3a}\pm0.15$	$1.54{ imes}10^{3a}{\pm}0.17$	$1.82 \times 10^{3a} \pm 0.12$	$1.43 \times 10^{3a} \pm 0.14$	
3	$8.25{\times}10^{3a}\pm0.04$	$6.85{\times}10^{3ab}\pm0.05$	$5.1 \times 10^{3c} \pm 0.07$	$5.95 \times 10^{3bc} \pm 0.04$	$6.45 \times 10^{3b} \pm 0.07$	
6	$2.58{\times}10^{4a}\pm0.04$	$2.22{\times}10^{4ab}\pm0.13$	$1.72{\times}10^{4b}{\pm}0.07$	$2.22{\times}10^{4ab}{\pm}0.12$	$2.11{\times}10^{4ab}\pm0.11$	
9	$6.60 {\times} 10^{4a} \pm 0.04$	$6.65{\times}10^{4a}\pm0.03$	$5.11{\times}10^{4b}{\pm}0.03$	$6.50\!\!\times\!\!10^{4a}\!\pm 0.05$	$5.94{\times}10^{4a}{\pm}0.02$	
12	$2.78{\times}10^{5a}\pm0.02$	$2.23{\times}10^{5b}\pm0.10$	$1.47{\times}10^{5c}{\pm}0.02$	$1.87{\times}10^{5b}\pm0.03$	$2.18{\times}10^{5b}{\pm}0.08$	
15	$2.35{\times}10^{6a}\pm0.08$	$2.12{\times}10^{6a}\pm0.07$	$1.45{\times}10^{6b}\pm0.05$	$1.94{\times}10^{6a}{\pm}0.06$	$2.08{\times}10^{6a}{\pm}0.08$	
18	$8.55{\times}10^{6a}\pm0.04$	$7.17{\times}10^{6ab}\pm0.04$	$5.85{\times}10^{6b}{\pm}0.06$	$6.1{\times}10^{6b}\pm\!0.08$	$6.57{\times}10^{6b}\pm0.07$	

The different superscript letters in the same column shows a significant difference (p < 0.05). CFU: Colony-forming unit, SD: Standard deviation.

Table 2. Water level test of scad fish meat

Treatment (%)	The water level at the beginning of the study (%)	The water level at the end of the study (%)
A (0%)	$45.97^{a} \pm 1.34$	$34.74^{a} \pm 6.87$
B (6%)	$48.6^{a} \pm 4.49$	$34.133^{a} \pm 8.88$
C (7%)	$47.41^{a} \pm 2.44$	$33.78^{a} \pm 11.02$
D (8%)	$43.08^{a} \pm 5.89$	$37.81^{a} \pm 9.25$
E (9%)	$45.94^{a} \pm 5.42$	$36.51^{a} \pm 7.62$

Remarks: The notation indicated by different superscript letters in the same column shows a significant difference (p < 0.05).

Table 3. PH Level of scad fish meat

Treatment					
	A (0%)	B (6%)	C (7%)	D (8%)	E (9%)
Observation time					
1	$7.05^{a} \pm 0.40$	$6.99^{a} \pm 0.42$	$6.78^{a} \pm 0.24$	$6.78^{a} \pm 0.21$	$6.73^{a} \pm 0.09$
3	$6.89^{a}\pm0.57$	$6.88^{a} \pm 0.40$	$6.73^{a} \pm 0.12$	$6.7^{a} \pm 0.23$	$6.6^{a} \pm 0.11$
6	$6.92^a\pm0.48$	$6.95^{a} \pm 0.34$	$6.75^{a} \pm 0.10$	$6.7^{a} \pm 0.21$	$6.7^{a} \pm 0.08$
9	$6.85^a\pm0.35$	$6.7^{a} \pm 0.18$	$6.65^a \pm 0.24$	$6.53^{a} \pm 0.17$	$6.53^{a}\pm0.05$
12	$6.78^a \pm 0.28$	$6.7^{ab} \pm 0.00$	$6.63^{ab}\pm0.22$	$6.5^{b}\pm0.08$	$6.53^{ab}\pm0.05$
15	$6.73^{a}\pm0.09$	$6.55^{ab}\pm0.10$	$6.5^b \pm 0.14$	$6.6^{ab} \pm 0.11$	$6.5^{b}\pm0.18$
18	$6.45^a\pm0.13$	$6.45^{a} \pm 0.24$	$6.28^{a} \pm 0.17$	$6.3^{a} \pm 0.00$	$6.3^{a} \pm 0.23$

Remarks: The notation indicated by different superscript letters in the same column shows a significant difference (p < 0.05). A: Scad fish without bay leaf extract treatment, B: Scad fish soaked in 6% of bay leaf extract, C: Scad fish soaked in 7% of bay leaf extract, D: Scad fish soaked in 8% of bay leaf extract, E: Scad fish soaked in 9% of bay leaf extract.

Organoleptic test

The organoleptic tests on preserved scad fish included five parameters, including visual, aroma, odor, texture, and mucus parameters that create an individual experience via the senses including taste, sight, smell, and touch. The minimum acceptable score was 6. The results of the organoleptic tests were provided at the beginning of the experiment and after 18 hours of preservation time.

Visual parameter

The results of the visual parameters at the beginning of the trial indicated the preserved scad fish in treatment A, B, C, D, and E experienced organoleptic values until the end of the storage period (18 hours). The average visual score of the beginning of the experiment in treatments A, B, C, D, and E ranged from 7.39 to 8.35. Furthermore, the average visual score at the 18 hours in treatments A, B, C, D, and E ranged from 5.48 to 6.97 (Figure 1).

Aroma parameter

The results of the aroma parameter of scad fish at the beginning of the experiment up to hour 18 of all treatments A, B, C, D, and E indicated a decrease in the organoleptic score. The average odor score at the beginning of the

experiment in all treatments was between 7.33 and 8.31. Furthermore, the average aroma value in all treatments at hour 18 ranged from 5.8 to 6.89 (Figure 2).

Odor parameter

The results of the odor parameter of the scad fish at the beginning of the experiment in all treatments indicated a decrease of the organoleptic values after 18 hours of storage period. The average odor value in all treatments at the beginning of the experiment was between 7.28 and 8.03 (Figure 3). The odor parameter results at the 18 hours were not assessed because the total value of the bacteria exceeded the limit of microorganisms.

Texture parameter

The results of the texture parameter at the beginning of the experiment at all treatments indicated a decrease in the organoleptic values by the end of 18 hours of the storage period. The average texture value at the beginning of the experiment was between 7.18 and 8.3 for all treatments. Furthermore, the average texture value was between 6.27 and 6.92 for all treatments after 18 hours (Figure 4).

Mucus parameter

The results of the mucus parameter at the beginning of the experiment for all treatments indicated a decrease in the organoleptic values by the end of 18 hours of the storage period. The average mucus value at the beginning of the experiment for all treatments was between 7.18 and 8.3. Furthermore, the average mucus value was between 6.13 and 6.87 for all treatments after 18 hours (Figure 5).



Figure 1. The results of the visual parameters of scad fish at the beginning of the experiment and after 18 hours of the storage period.



Figure 2. The results of the aroma parameters of scad fish at the beginning of the experiment and after 18 hours of storage period.

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Figure 3. The results of the odor parameters of the scad fish at the beginning of the experiment and after 18 hours of the storage period.







Figure 5. Mucus parameter of scad fish at the beginning of the experiment and after 18 hours of the storage period.

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DISCUSSION

Shelf life is the period in which the quality of fresh food is impaired and becomes inedible. In the present research, the shelf life was determined using the TPC of the microbiological tests, chemical tests (water level and pH), and sensory tests (organoleptic test). The food product quality is influenced by the microbial content of the product as it determines consumption safety. The shelf life of food is determined by the total bacterial count in the product using a method called the TPC. The results of total bacteria calculation on the scad fish in all treatments increased constantly from the beginning of the experiment up to after 18 hours since the storage time could increase the total bacteria count. The test results of bay leaf extract on scad fish from the beginning up to 12 hours indicated that the number of microorganisms was still at the maximum growth limit of 5×105 Colony-Forming Unit (CFU)/gram (Buckle, 1987; Herawati, 2008).

Various factors that influenced microbial growth in the food products included intrinsic factors such as acidity (pH), water activity, nutrient content, biological structure, and antimicrobial content, while the extrinsic factors included storage temperature, humidity, type and amount of gases in the environment, and preparation and processing errors. All the treatments indicated that the bay leaf extract could inhibit the bacteria for up to 12 hours. The best treatment was obtained in treatment C (7% of bay leaf extract) because it had the lowest bacterial count among all treatments. The current result is in line with the previous study conducted by Buckle (1987) and Sahputra (2015) which suggested that a combination between 7% of bay leaf extract treatment and 8% of salt can inhibit bacteria in the milkfish (Buckle, 1987; Sahputra, 2015).

Bay leaf extract contained antibacterial compounds with high tannin, terpenoid, and flavonoid contents. These compounds could inhibit the growth of microbes. Flavonoid compounds have an important role in the inhibition of bacteria by forming complex compounds with extracellular proteins through hydrogen bonds that degrade bacterial cell membranes. Hydrogen and flavonoid bonds cause unstable cell wall structure and cell membrane and cellular deterioration. Tannin compounds play a role in shrinking cell walls and membranes to interfere with cell permeability. The impaired cell permeability means that the cell cannot perform living activities. Thus, it could inhibit bacterial growth and kill the bacteria. In addition, terpenoid compounds act as antibacterial compounds on the outer membrane of terpenoid cell walls by reacting with porin (transmembrane protein) to form strong polymer bonds. The polymer bonds caused the porin to deteriorate as a connecting gateway to reduce the permeability of the bacterial cell walls; and that caused bacterial cells to lack in the nutrient, whereby the bacterial growth is inhibited (Roslizawaty, 2013).

The water level is a factor that affects the shelf life of processed food and determines the freshness of food against microbes. The high water content causes bacteria, mold, and yeast to multiply easily. So there will be changes in the food. When stored in-room temperature, water level changes would be caused by the free water formed as a result of protein denaturation by microorganisms (Nirmala, 2016). Based on the results of the present study, the water level decreased from the beginning to the end of the storage process. This condition was caused by the evaporation of most of the water as the storage process was only stored at room temperature. The low water content led to a decrease in bacterial activity. However, based on the current research, the water level and the TPC indicated the opposite results, where the water level decreased, while the TPC increased. This phenomenon was caused by the still good water level, which allowed the bacteria to grow well. More than 30% of the water content in the food could affect bacterial growth. Elevated microbes could damage the hydrophilic protein, resulting in a reduced ability to hold water when the water level finally decreased (Siskos, 2007).

The pH value is an indicator that is measured to chemically determine the freshness level of fishery products. The optimal pH for bacterial growth is 6.5-7.5. The pH value of scad fish decreased from the beginning up to 18 hours. The pH change was caused by several factors, such as poor storage and storage temperature. The pH values obtained indicated that the scad fish marinated in bay leaf extract had an acidic pH value. The bay leaf boiling time affected the pH value of the leaf extract because the longer the leaves were boiled, the more organic acids from the leaves were extracted, resulting in a decrease in the pH value of the bay leaf. The pH value is closely related to the growth of microbes in fishery products. Fresh fish has a neutral pH, making it an ideal medium for bacterial growth (Junior, 2010). The organoleptic test on the scad fish, with and without adding bay leaf extract, included the visual, aroma, odor, texture, and mucus parameters. The result showed that at the starting hour, the quality of the fish was still acceptable by the panelists according to the Indonesia Nasional Standard with a minimum organoleptic value of 6. At the starting hour, the appearance of the scad fish received an average value in the range of 7.39 to 8.35. Meanwhile, the results of the organoleptic test at the 18 hours of storage suggested that the visual score of the scad fish decreased from 5.48 to 6.97. The results also indicated that there was an increasing bacterial count by hour 18. The appearance change was caused by the growth of microbe that could damage the products as the microbe were highly destructive to food.

The odor of the scad fish averaged between 7.33 to 8.31 at the beginning of the experiment. The odor value indicated that the fish was still fresh and smelled good. The fish smelled fresh since the bay leaves contained terpenoid compounds containing essential oils, which produced a distinctive but less sharp aroma. After 18 hours, the average result of the odor value decreased and was between 5.8 and 6.89. Therefore, the aroma parameter of scad fish at the

beginning of the experiment up to hour 18 of all treatments A, B, C, D, and E indicated a decrease in the organoleptic score. Treatment A gave the lowest score, reaching 5.8 at hour 18. The lowest odor score parameter on treatment A was also supported by the result indicating the high bacterial count found in the fish, which was 8.55×106 . A decrease in the organoleptic matter could occur because the room temperature could accelerate the disintegration process during the storage of the fish. These bacteria could carry out a perfect metabolism that produced a bad odor.

Initially, the scad fish began to smell an average value of between 7.28 to 8.03, indicating that the fish was tasty, savory, or less savory. Meanwhile, after 18 hours, the odor test was not carried out by the organoleptic test due to the high TPC level of enzyme in the scad fish. In addition, the texture of the scad was given an average value in the range of 7.18 to 8.3, indicating that the fish were solid and elastic or less elastic. This texture was caused by the salt that was added in the process of making preserved scad fish since salt could improve the texture of fish. The salt used in the process of making scad fish reduced the water contents in the fish, which made the texture more solid and firm. Meanwhile, after 18 hours, the texture of scad fish decreased from 6.27 to 6.92. Treatment A had the lowest score, 6.27 at the 18 hours. The texture parameter of treatment A was also indicated by the high bacterial count found in the fish, which was 8.55 \times 106, compared to the other treatments. The high bacterial count was caused by microorganism activity affecting the texture changes. The protein denaturation produced a simple protein, and also decreased the protein capacity to hold water so that the texture of fish became less solid and firm.

At the starting hour, the mucus of the scad fish obtained an average score from 7.18 to 8.3, indicating that the fish had thin and more neutral mucus and was odorless. Meanwhile, at 18 hours, the mucus content of scad fish fell from 6.13 to 6.87. The mucus parameter of the treatment is considered treatment with the lowest value of 6.13. The mucus parameter of treatment A was also indicated by the high bacterial count found in the fish, reaching 8.55×106 , compared to other treatments. Mucous could be caused by bacteria. The mucus found in the fish's skin could be used as a parameter to determine the freshness level of the scad fish by focusing on the clearness and thickness of the mucus. The mucus changes were caused by the increasing number of spoilage bacteria activity on the fish after 18 hours (Lougovois and Kyrana, 2005).

CONCLUSION

Adding bay leaf extracts to preserved scad fish indicated that the total bacterial count was lesser than the Indonesian National Standard (SNI), of 5×105 CFU/gram, which could inhibit bacterial development by 12 hours. The best result was with treatment C (7% of bay leaf extract addition), as the concentration at this percentage could inhibit bacteria in preserved scad fish.

DECLARATIONS

Authors' contribution

Fuaidah designed the study, Triastuti collected the data and Pramono wrote the manuscript. Finally, all of the authors approved the final draft of the manuscript for submission.

Competing interests

The authors have not declared any conflict of interest.

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Effects of Laying Cycle Periods on Egg Quality, Egg Chemical Composition, and Reproductive Performance of Japanese Quail Breeders Reared in Northern Algeria

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ABSTRACT

Egg quality traits in quail breeders depend on various factors which may influence embryo survival during incubation, affecting the chicks' production and quality. The current study aimed to determine the effect of the laying period on the external and internal quality of the egg, the chemical composition of albumen, yolk, and eggshell as well as the reproductive parameters of quail breeders. A total of 450 quails (Coturnix japonica) obtained from the same hatchery, were reared in a battery cage with a sex ratio of 1 male to 3 females. All the quails were subjected to standard breeding conditions and fed a balanced laying diet. A total of 960 eggs were collected at two different periods of the laying cycle, the beginning period of the laying (BP indicating 10 weeks of quail age) and the peak period of laying (PP showing 20 weeks of quail age). At each laying period, 30 eggs were used to analyze the various parameters of egg quality, and 450 eggs were randomly selected to assess the reproductive performances. Overall, no differences in the external quality of eggs, such as egg length, egg width, and the egg shape index, were recorded between the two laying periods. Apart from albumen weight that tended to be higher at the peak laying period, the shell and the yolk weights were not affected by the period of laying. Additionally, Japanese quail tend to deposit similar proportions of shell, albumen, and yolk at the two periods of laying. Likewise, the rate of dry matter of the three egg components, shell mineral concentrations, and yolk fat concentrations did not show any noticeable variation with the laying period. The most significant effect of the laying period was related to the potential reduction in the total protein content of the albumen and the yolk of eggs laid at the peak period of laying. Finally, the laying period did not significantly affect the fertility and hatchability rate of the incubated quail eggs but slightly improved the embryonic mortality rate during the peak laying phase.

Keywords: Albumen, Coturnix japonica, Eggshell, Fertility, Quail

INTRODUCTION

To fight against food insecurity that increasingly threatens the growing world population, identifying alternative food resources is a key intervention to improve and ensure dietary protein. The integration of game birds, such as geese, guinea fowl, pheasant, and quail in FAO food security programs, has been recommended, especially for developing countries (Geldenhuys et al., 2013). As in several African countries, Algeria must be oriented towards the diversification of its animal protein resources due to its demographic growth, which may reach 74 million in 2050, and change consumers' eating habits, which is becoming more and more demanding. The development of quail farming could make it possible to improve the population's consumption of animal proteins (eggs and meat) at a lower cost (Kaci, 2015).

Hatching egg quality is a matter of great importance in the production of living and healthy chicks. Indeed, the physical and chemical properties of an egg play an essential role in the proper development of embryos by protecting them and ensuring their nutritional needs (Bai et al., 2016; D'Alba et al., 2016; Chen et al., 2019) and even serve as a food source during the first days of the chick's life (Abanikannda, 2007). However, as Zita et al. (2013) mentioned, several factors affect the reproductive performances and egg quality of Japanese quails. Some are directly linked to the animal (genetics, age of breeders, laying cycle), and others depend on the quails' rearing conditions, such as nutrition, rearing system, light, and temperature (Yambayamba and Chileshe, 2019, Ratriyanto et al., 2020), the sex ratio (Ipek et al., 2004) as well as the storage and incubation conditions of the eggs (Kuurman et al., 2002).

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The quail egg-laying period ranges from 8 to 12 months for breeders (Chelmonska et al., 2008) and could continue to 14 months for laying hens. This reproductive cycle is characterized by a beginning period of laying that lasts from the time when quails start laying (6 weeks) (Daikwo et al., 2014) to the time when quails lay maximum eggs, namely the peak laying period (17-22 weeks of age, Sauveur, 1988). The start of laying is a very critical period for female breeders. Their transfer from the grower house to the breeders' house could lead to stressful conditions for females, which results in poor laying start-up, and consequently low productivity and economic losses. Furthermore, it is well known that the weight of a bird determines its sexual maturity. Thereby, the variability of body weight within female breeders causes flock heterogeneity which may result in unsynchronized sexual maturity (delayed ovary development) and consequently failure in the mating process and performance.

Indeed, in the hen species, the beginning-laying phase of the breeders is characterized by high variability in egg quality, such as weight and egg fertility, most often attributed to the lack of uniformity of the flock (Pedroso et al., 2005).

The effects of breeder age were observed on the eggs' external and internal characteristics (Zita et al., 2013; Nasri et al., 2020), the eggs' fertility (Majhi et al., 2016), and embryonic development (Pokhrel et al., 2018). Several studies have revealed that during a laying period the weight of the eggs increases with the age of the breeders (Nasri et al., 2020). On the other hand, the weight and thickness of the shell decrease (Travel et al., 2010), and the proportion of yolk increases at the detriment of the albumen and shell proportions (Suarez et al., 1997). The beginning-laying period usually leads to the production of many small eggs. However, the component proportions of the hatching egg are affected by egg size. At the same breeders' age, smaller eggs contain more proportion of yolk than larger eggs (Vieira and Moran, 1998). It is well known that the egg yolk provides the nutrients for the developing embryo. However, the larger eggs, with a smaller proportion of yolk provide less nutrient content which could negatively affect embryo development and, consequently, incubation performance by increasing early and late embryo mortality. Moreover, the eggshell quality greatly influences the viability of the embryo and the hatchability of the eggs (Portugal et al., 2014; Ergun and Yamak, 2017).

Few studies have reported the effect of the laying period on Japanese quail reproductive parameters and quail egg quality so far. The objective of this study was to evaluate the effects of two laying periods of the breeders' quail, the beginning-laying period (BP) and the period of maximum production called the peak laying period (PP) on the external and internal quality of the hatching eggs as well as the variation of reproductive parameters.

MATERIALS AND METHODS

Ethical approval

The study was approved by the scientific council of the Superior National Veterinary School of Algeria with certificate reference 255/FDCS/2021.

Quails (Coturnix japonica) and protocol design

The current study was conducted at the farm of the technical institute of breeding, department of monogastric, Ministry of agriculture and rural development, BABA ALI, Algeria. A total of 960 eggs were obtained from 450 Japanese quail breeders, housed in a five-story battery cage. Each story was divided into 3 cages of 30 quails each, with a sex ratio of 3 females to 1 male. All the quails were subjected to the same standard breeding conditions and fed the same layer diet containing 2700 kcal.Kg-1 of metabolic energy, 19.01% of crude protein, 4% of calcium, and 0.7% phosphorous (ITELV, 1988).

All the eggs were collected at two different periods of the laying cycle, namely BP (at week 5 of egg production, representing 10 weeks of quail age) and PP (week 10 of egg production, representing 20 weeks of quail age). At each laying phase, 30 eggs were used to assess egg quality traits, and 450 eggs were randomly selected from eggs laid during one week to analyze the reproductive and hatching performances. For both laying phases (BP and PP), each egg was given individual identification and weighed by an electronic precision scale with 0.01g accuracy. The length and width egg measurements were recorded by a caliper, and the egg shape index was calculated (SI = width/length \times 100; Smai et al., 2018). At the end of the egg collection, the eggs for external and internal quality determination were transferred to a feed analysis laboratory of the Superior National Veterinary School. However, those used for reproductive traits assessment were set in a vertical incubator (La Nationale, France. Serial Number:4391) at a temperature of 37.7°C, relative humidity of 60 %, and automatic egg-turning every 8 hours.

Measurements of egg quality

In the first step, each egg was broken. Afterward, eggshell, albumen, and yolk were carefully separated and weighed by a scale with 0.0001 g accuracy to determine their fresh weights and then expressed them as a percentage of whole egg weight (Zita et al., 2013). The dry matter (DM) of the three separated structures was determined by drying the

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samples at 80°C in a ventilated oven until constant weight (3 days). The chemical composition of each part of the quail egg was determined according to the methods of AOAC (1990), namely, eggshell mineral matter, yolk and albumin crude proteins, and yolk fat matter. Thus, the mineral matter of each dehydrated eggshell was determined by gradual incineration (550°C) in a muffle furnace until all organic material was destroyed. The dry ash was weighed and then expressed as a DM percentage. The crude proteins of the albumen and yolk were determined using the Kjeldahl method by measuring the total nitrogen content and then using a factor of 6.25 to convert total nitrogen into crude proteins (CP = total nitrogen \times 6.25). The total fat of the yolk was determined by the Soxhlet method using petroleum ether as a solvent. The extraction process lasted for 18 hours. After completion of the extraction, the solvent was evaporated, and the mass of lipid remaining was dried in an oven, weighed, and then expressed as a DM percentage.

Reproductive performances determination

On day 14 of incubation, the eggs were removed from the incubator and candled to detect infertile eggs. On day 15 of incubation, the eggs were transferred to a hatcher where the temperature and relative humidity were maintained as 36.7° C and 80%, respectively. After hatching, the unhatched eggs were broken to investigate fertility that was expressed as the fertile eggs/ incubated eggs×100. The hatchability of fertile eggs was determined as a number of chicks hatched/fertile eggs ×100. The hatchability of incubated eggs was calculated as the number of chicks hatched /number of incubated eggs ×100. Embryo mortality was obtained as the proportion of dead embryos out of the number of fertile eggs (Hegab and Hanafy, 2019).

Statistical analysis

Data were descriptively presented as means and subjected to one-factor variance analysis (ANOVA) performed with the Statview software (Abacus Concepts, 1996, Inc., Berkeley, CA94704-1014, USA). Version 4.57.0.0. Student-Newman-Keuls test was used to detect the differences. The statistical significance was set at $p \le 0.05$.

RESULTS AND DISCUSSION

Egg external traits

The external qualities of Japanese quail breeders' eggs laid at BP and PP are presented in Table 1. The results indicated that the laying period of Japanese quails did not affect the weight of the eggs (p > 0.05). Also, no variation in the eggs' length, width, and shape index was associated with periods of the laying cycle (p > 0.05). These findings are consistent with those obtained by some previous research (Moula et al., 2014; Smaï et al., 2018). In an experiment by Smaï et al. (2018), no difference in the egg weight of Japanese quails was observed between the two periods of laying (10.2 vs 11.1 g, p > 0.05 at BP and PP, respectively). In contrast, other authors have reported different egg weights of Japanese quail in various phases of the reproductive cycle. Some studies revealed an increase in egg weight during the breeding cycle of Japanese quails (Nazligul et al., 2001). Zita et al. (2013) have reported that the egg weight increased in quails by 18 % (p < 0.05) from the beginning phase of laying (week 9 of age) to the age of 21 representing the same peak laying phase in the current study. Moreover, it has been found that the egg shape index changes with the breeders' age (Molnar, 2016; Rakib et al., 2016; Kraus et al., 2020). In the present study, the shape index of eggs laid by the quail breeders remained unchanged on average over the two experimented periods of laying (77% vs 76% for BP vs PP, respectively). These results are consistent with those reported by Zita et al. (2013) and Moula et al. (2014) but did not agree with those of Orhan et al. (2001), who recorded a significant decrease in the form index of Japanese quail eggs by their age. Investigations in breeder hens and Peking ducks indicated a higher egg form index towards the end of the breeding season rather than the beginning (Romanoff and Romanoff, 1949; Kokoszynski et al., 2007). It is often acknowledged that at the beginning of production, the smaller eggs have a rather spherical shape, which tends to lengthen gradually during the laying period showing an ellipsoidal form for larger eggs (Gonzalez et al., 1982). This change in egg shape is thought to result from a weakening of the muscle tone of the shell gland in older hens (Travel et al., 2010).

Table 1. The effects of beginning and peak of laying periods on the ex	xternal quality of eggs in Japanese quail bre	eders
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Trait	Laying period	BP	РР	SEM	p-value*
Weight (g)		10.72	11.18	0.20	0.12
Length (cm)		2.95	2.98	0.03	0.43
Width(cm)		2.28	2.28	0.02	0.89
Shape Index (%)		77.53	76.82	0.53	0.35

BP: Beginning laying period, PP: Peak laying period. SEM: Standard Error of the Mean. *Significant differences ($p \le 0.05$).

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Egg components

The effects of the laying period (BP and PP) of Japanese quail breeders on the shell, albumen, and yolk weights, as well as their proportions in relation to the weight of whole quail eggs, are presented in Table 2. The laying periods (BP and PP) did not affect the weight of the different egg components, namely shell, albumen, and yolk (p > 0.05). Moreover, the current results have revealed that the proportions of the different quail egg components, such as eggshell, albumen, and yolk, do not change significantly with variations in the laying period (p > 0.05). Eggs tended to have the same proportions of shell, albumen, and yolk at BP and PP periods. In contrast, Zita et al. (2013) recorded an increase in the weight of all three egg components over the variation in quail laying periods. Similarly, Moula et al. (2014) reported an impact of the laying period on the weights of the two nutritive components of the Japanese quail egg, namely albumen, and yolk. An increase of +3 and +4 % was recorded for quail eggs laid at 20 weeks of age for albumen and yolk, respectively. However, the same authors did not reveal any effect of the laying period on eggshell weight, whereas Curtis et al. (1986) reported that the percentage of shell in hens' eggs decreased throughout the production periods. During the laying period spanning from the beginning to the peak, albumen proportion increased from 61.10% to 62.10%, however, the yolk proportion decreased from 30.97% to 29.75% during the same period (Nowaczewski et al., 2010). Hegab and Hanafy (2019) attribute this variation in weight and proportion of the different egg constituents with the laying period to the increase in weight, length, and width of the egg with the age of the breeders. Similarly, Cook et al. (2005) reported a tendency in yolk proportion to be lower in large eggs than smaller ones.

As the egg size increases, the relative amount of yolk decreases. Flock age and egg size are major factors that determine the albumen and yolk content in eggs (Nangsuay et al., 2011). Furthermore, Nasri et al. (2020) reported that as breeders become older, ovulation intervals increase. This results in equal quantities of yolk synthesized by the liver being deposited in fewer follicles causing higher yolk weights (Zakaria et al., 1983).

The effect of the laying period (BP and PP) of Japanese quail breeders on the shell, albumen, and yolk dry matter is presented in Figure 1. The effect of the laying period of Japanese quail breeders on mineral eggshell content, total protein albumen and yolk contents, and total yolk lipids is presented in Figure 2. No effect of laying period was noted for the rate of dry matter of the shell, the albumen, and the yolk of Japanese quail eggs (p > 0.05). These results contrasted with the finding of Ulmer-Franco et al. (2009), who reported that dry shell percentage was greater in eggs laid by younger commercial broiler breeder hens than those laid by older hens. Similarly, Cook et al. (2005) and Nasri et al. (2020) found that whites from eggs produced by older hens had lower solids content than those obtained from younger hens. However, the latter authors showed that contrary to albumen DM, yolk DM percentage increased with breeder age.

The eggshell is the major source of minerals during the latter stages of embryonic development (Ono and Wakasugi, 1984; Solomon, 2010). Thus, this component should be considered when setting eggs for incubation to achieve successful hatching. In the current study, the laying period of Japanese quail breeders did not affect mineral deposition in the eggshell, the mineral matter percentage remained constant throughout the two periods of laying. These results are in agreement with the findings of Crosara et al. (2019), who reported that the contents of mineral eggshells are the same throughout the broiler breeders' life. Proteins are present primarily in egg albumen and egg yolk, while lipids are almost exclusively in the yolk (Nangsuay et al., 2011). In the present study, the crude protein concentrations in each of the albumen and yolk of quail eggs were influenced by the laying period. Both the yolk and albumen of eggs laid at the BP of laying contained +28 % and +36 % more crude proteins, respectively, than those of eggs laid at the PP of laying (p < 0.05). However, the laying period did not affect the concentration of the total lipid of the breeder quail egg yolk. Thus, a similar lipids deposition was recorded at the two periods of egg production. These results were consistent with those reported by Curtis et al. (1986), who noted a significant period effect on the percentage of albumen protein with a gradual decline over the production period and those that reported no effect of flock age on the lipids contents of hen egg yolk (Cook et al., 2005). In contrast, no variation in the yolk protein contents of eggs was observed to be associated with hens' ages (Cook et al., 2005).

Egg components	T	Laying	Laying period		n voluo*
Egg components	Trait	BP	PP	SEM	p-value.
	Weight (g)	5.33	5.74	0.16	0.07
Albumen	Weight proportion (%)	49.57	51.17	0.87	0.20
T 7 11	Weight (g)	3.47	3.54	0.08	0.55
Yolk	Weight proportion (%)	32.39	31.60	0.48	0.26
	Weight (g)	1.52	1.58	0.15	0.75
Shell	Weight proportion (%)	14.25	14.33	1.49	0.97

Table 2. The effects of beginning and peak of laying periods on the shell, albumen and yolk weights, and their proportions in relation to the weight of whole eggs in Japanese quail breeders

BP: Beginning laying period, PP: Peak laying period. SEM: Standard Error of the Mean. * Significant differences (p \leq 0.05).

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Figure 1. The effects of beginning and peak of laying periods on shell, albumen and yolk dry mater in Japanese quail breeders. BP: beginning laying period, PP: peak laying period, significant differences ($p \le 0.05$).



Figure 2. The effects of beginning and peak of laying periods on mineral eggshell content, total protein albumen and yolk contents and total yolk lipids in Japanese quail breeders. BP: beginning laying period, PP: peak laying period, significant differences ($p \le 0.05$).

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Reproduction parameters: Fertility, hatchability, and embryo mortality

The effect of the laying period (BP and PP) of Japanese quail breeders on the fertility, hatchability, and embryo mortality of the incubated and fertile eggs is shown in Table 3. The current results indicated that the laying periods did not affect the fertility of the incubated eggs (p > 0.05). These results agreed with the findings of Ipek et al. (2004) regarding Japanese quail and those of Santos et al. (2015) concerning European quail. According to these authors, the laying period had no effect on egg fertility throughout the reproductive life of European quails. In contrast, Ipek et al. (2004) have shown that the fertility of eggs in Japanese quails was lower at ages of 7-10 weeks than those of 15-18 weeks. This inconsistency in results may be due to a difference in the experimental protocol, such as the applied malefemale ratio. In poultry, the male is one of the main factors limiting the fertility of flocks (Farooq et al., 2018). In fact, any delayed growth and sexual maturity in males affect sexual behaviors in young flocks, often caused by nutritional factors or inappropriate light stimulation (Brillard, 2003). Previous studies have explained the improvement of fertility rate at the peak of laying of quails by the acquiring of a greater number of mature ovarian follicles (Bagh et al., 2016). The laying period of the Japanese quail breeders did not significantly affect the hatchability of the incubated and fertile eggs (p > 0.05). However, statistical analysis revealed that the numerical values of hatchability rates tended to be slightly higher, with +3.5% (p = 0.14) for incubated eggs and +3% (p = 0.06) for fertile eggs during the peak laying period, compared to the beginning laying ones. Similarly, previous studies have reported that the laying period, which is closely related to the age of the breeders, has no effect on the hatching capacity of incubated eggs (Ipek et al., 2004; Smaï et al., 2018). Likewise, Smaï et al. (2018) did not detect any significant variation in the hatchability of incubated eggs during the breeding season of domestic quails. These authors recorded a numerical improvement in the hatching rate of the incubated eggs of +7% (p > 0.05) between the period of the beginning of laying (8-12 weeks of age) and the period when the maximum eggs are laid (16th and 26th weeks of age). However, the recorded hatchability rate values remain lower (70% vs. 75%, respectively, BP and PP), compared to the results of the current study. These low rates could be explained by the sex ratio applied (1/2) by these researchers, which probably affected the fertility of the eggs and, consequently, their hatchability rate. Some contradictory findings were also reported. Elibol and Brake (2006) recorded better hatchability of incubated eggs in laying hens at the early-laying period, compared to the other periods of the reproductive cycle. Seker et al. (2004) reported a higher hatchability rate of fertile eggs at the peak of laying (93.33%) than at the beginning of laying (81.53 %). The variation in the hatching rate of fertile eggs during a reproductive cycle is most often attributed to a variation in the quality of the eggs during that cycle (Sahan et al., 2014; Boleli et al., 2016). In the current study, the laying period did not affect the embryo mortality rate of the incubated eggs (p > 0.05). A similar result was reported by Santos et al. (2015) in European quail. However, a significant decrease of -40 % in the mortality rate for the fertile eggs during the PP of laying is recorded (p = 0.05).

However, Majhi et al. (2016) and Amiar et al. (2017) noted a gradual decrease in embryo mortality of incubated eggs from the beginning to the peak period of laying. In the same trend, Seker et al. (2004) recorded an improvement in the embryonic mortality rates of fertile eggs over the two periods of the reproductive cycle. This is in contrast with Wilson et al. (2003), who suggested an opposite effect of quail age on embryonic mortality due to the poor positioning of the embryos before hatching. It should be noted that in poultry, several physiological parameters change with flock age (O'Sullivan et al 1992). The most noticeable change is the increasing egg weight (North and Bell, 1991). Indeed, Hegab and Hanafy (2019) reported that the embryonic mortality rate is lower for heavy eggs, compared to lighter eggs, which is explained by the richness of heavy eggs in sufficient nutrient reserves, compared to lighter eggs.

Thur 14	Description	Laying period		CEM	1 *
Iralt	Parameters	BP	PP	SEM	p value*
Fertility (%)	Incubated egg	95.11	94.89	1.03	0.88
Hatchability (%)	Incubated egg	86.89	90.00	1.50	0.14
	Fertile egg	91.36	94.61	1.22	0.06
Mortality (%)	Incubated egg	12.67	9.33	1.47	0.11
	Fertile egg	8.18	4.92	1.18	0.05

Table 3. The effects of beginning and peak of laying periods on the fertility, hatchability, and embryo mortality of the incubated and fertile eggs in Japanese quail breeders

BP: Beginning laying period, PP: Peak laying period. SEM: Standard Error of the Mean. *Significant differences (p ≤ 0.05).

CONCLUSION

In conclusion, the laying period shows stability in egg external quality, their overall composition, and in the most of chemical components of albumen, yolk, and shell. Nevertheless, the peak of laying has a large negative impact on the protein rate of albumen and yolk but without affecting the threshold egg quality needed for the successful development

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of the embryo. Eggs laid by quail breeders at the beginning and the peak periods of laying were of equal fertility and hatchability performances. However, the low proteins could affect negatively chicks' quality at hatch and their growth performances. Further research must be conducted to draw more clear conclusions, determining the effect of quality of eggs on growth performances of chicks hatched from eggs of different periods of laying cycle and examining the possible interaction effects of the laying period with other factors such as egg storage duration.

DECLARATIONS

Authors' contribution

Z Berrama and H Mefti-Korteby designed the experiment, Z Berrama, S Souames, and R Merati curated the data. Laboratory analyses were done by MS Chirane, N Negab, H Idris, K Hettab, and Z berrama. Z Berrama wrote the manuscript. S Temim, S Souames, and N Morzouglal revised the manuscript. All authors confirmed the manuscript's final draft and data analysis.

Competing interests

The authors have not declared any conflict of interest.

Ethical consideration

Ethical issues (including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by all the authors.

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The Role of Salinity in Histopathology Description of Jatim Bulan Tilapia Juvenile (*Oreochromis niloticus*) Exposed by Lead (PB)

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ABSTRACT

The decrease in the number of lands for aquaculture will cause the freshwater fish aquaculture, especially tilapia is reared. As one of the efforts to survive, the breeders use the coastal area to anticipate, so the freshwater fish can adapt to the sea waters. Heavy metal pollution near the coasts (or in the coastal waters) has great potential impacts on the environment. The present study aimed to find out the effect of Lead (Pb, heavy-metal) exposure on the Jatimbulan Juvenile tilapia with the different salinity towards histopathology description of the gill, intestine, and the skin tissues. The method used was an experimental method with a completely randomized design using six treatments and three times repetition. The observed parameters included the changes in histopathology description of gill, intestine, and skin organs of Jatimbulan juvenile tilapia. Kruskal-Wallis scoring method was used for data analysis and was continued by Mann-Whitney. The result of the current study showed the effect of changes was proven with the histopathology description in the form of the damage of edema, hyperplasia, and necrosis on the gill tissue; the damage of edema, atrophy, and necrosis on the gill tissue as well as the damage of edema, atrophy, hemorrhagic and necrosis on the gill tissue. From the result of the current study which has been conducted, it can be concluded that the heavy-metal exposure by lead was 0.03 ppm on the salinity of 10 ppt and 20 ppt. given the significant effect on the histopathology description of gill, intestine, and skin of Jatimbulan juvenile tilapia.

Keywords: Histopathology, Lead, Metal, Oreochromis niloticus, Salinity

INTRODUCTION

One of the superior commodities in fisheries aquaculture activities was tilapia aquaculture (*Oreochromis niloticus*). Tilapia has some superiority over other fish for some features; for example, it has rapid growth, is easy to breed, and is efficient for additional feeding, thus it can be a favorite commodity in an aquaculture activity. Along with the increase in the number of tilapia breeders, the need for lands as the aquaculture area highly increases. Based on the data, the potential pond area in East Java in 2014 was decreased by 64% from the previous year to 129518 hectares (FAO, 2005). The decrease in the number of lands for aquaculture threatens the freshwater fish aquaculture business, especially tilapia. As an effort to survive, the breeders utilize the coastal areas to anticipate whether freshwater fish can be adapted to sea waters (Tuiyo, 2016).

Shrimp and milkfish ponds can be used for tilapia aquaculture activities because it has a euryhaline characteristic, thus tilapia can be used as a substitution in the shrimp or milkfish pond that is less productive (Hosseini Aghuzbeni et al., 2017). Nevertheless, coastal waters have a high potential for environmental impacts. The environmental impact meant is heavy metal pollution due to human activities. Heavy metal pollution in coastal areas has a high potential for aquatic toxicity due to industrial waste discarded into the river. One of the heavy metals usually found is Lead (Pb). Water sources, the most vulnerable to the Lead threats, are the rivers which are usually close to the residential areas and the agriculture, and residue of industrial waste that is not favorable and sufficient (Ritonga and Yunasfi, 2014).

Lead (Pb) is a dangerous heavy metal because it is indestructible (non-degradable) for living organisms, and it can accumulate into the environment. Lead settles to the bottom of waters to form complex compounds together with organic and inorganic materials. The Lead continues to enter the tissues of living organs through the respiratory tract, digestion, and skin. Lead dissolved in fat will penetrate the cell membrane, thus the Lead ions will pile up in the cells and organs (Jaishankar et al., 2014; Okereafor et al., 2020).

The presence of salinity in waters has also an impact on the level of Lead toxicity. Salinity is the total volume of K +, Na +, Mg2 +, NO3-, Ca2 +, SO₄ 2-, Cl-, and HCO3- in the water. If there is a decrease in salinity due to the desalination process, it will cause an increase in the toxic power of heavy metals, and will cause a greater level of bioaccumulation of heavy metals (Okereafor et al., 2020). Therefore, it is required to conduct a study to determine the

effect of Lead as a heavy-metal exposure on Jatimbulan juvenile tilapia with different salinity for organ damage, especially in the gill, intestine, and skin.

MATERIALS AND METHODS

The present study was conducted at the Faculty of Fisheries and Marine, Universitas Airlangga (Surabaya, Indonesia) according to the ethical rules of Universitas Airlangga for animal studies. The materials used in this study consisted of Jatimbulan Juvenile tilapia obtained from the Technical Implementation Unit for Freshwater Aquaculture Development, Umbulan, Pasuruan, Indonesia. The selected Jatimbulan Juvenile tilapia was a juvenile which had a body length of 3-7 cm and weighs \pm 13 grams as many as 200 fishes. The Lead used was the Lead (II) Nitrate, and the salinity of the water was 0 ppt, 10 ppt, and 20 ppt, distilled water, and nitric acid.

The current study was experimental using a complete randomized design method. Three treatments and six times repetition were used in this study, thus there were 18 test units. Data collection technique was carried out by direct observation, namely by observing directly the behavior of tilapia juvenile after being exposed to Lead (heavy-metal), and histological observation was conducted to determine the description of gill, intestine, and skin tissue due to the effect of salinity on heavy metal exposure. In this study, there were three treatments with six times repetition, namely A (Salinity 0 ppt and using 0.03 mg/l of Pb), B (Salinity 10 ppt and using 0.03 mg/l of Pb), and C (Salinity 20 ppt and using 0.03 mg/l of Pb).

The dose of lead used in the present study was 0.03 mg/l by as suggested by Tarigan and Rozak (2003). The Lead nitrate was weighed, then mixed using distilled water and 60% nitric acid (HNO₃), and after that stored in a bottle; thus the Lead dissolved easily in the water. The water was mixed with the Lead, then aerated, and waited for 2 hours to be mixed properly because the Lead could cause poisoning effects on the fish after the fish has been exposed to the Lead for two hours (Musthapia and Sunarno, 2006). Furthermore, water salinity was made using seawater which was diluted with fresh water from *Perusahaan Daerah Air Minum* (PDAM, Regional Water Company) to obtain the required salinity concentration. The experiment fish that would be used in this study was previously acclimatized so that the fish would not experience stress with the new environment (Rosdianasari and Perbedaan, 2015).

The next stages carried out in this study were measuring the water quality, calculating the survival rates, also making and observing histopathology preparations. The main observed parameter was the histopathology description of the gill, intestine, and the skin of the Jatimbulan tilapia which was exposed to the Lead (heavy-metal) at a different salinity. Supporting the observed parameter was water quality and survival rate. The water quality for observed parameters included pH, temperature, dissolved oxygen, and salinity. The present study used salinity as the independent variable, dose of Lead as a control variable, and the histopathology description of the gill, intestine, and the skin as a dependent variable.

The result in the form of scoring data from the histopathology was then analyzed using analysis of Kruskal-Wallis one-way ranking variant to determine the differences between samples (Dalgaard, 2008), marking real population differences or the differences (p value less than 0.05) due to accidental variation between random samples from the same population. Furthermore, the Mann-Whitney test was carried out to examine whether two independent groups have been drawn from the same population.

RESULTS

The result of the survival rate of Jatimbulan juvenile tilapia (*Oreochromis niloticus*) after exposure to the Lead heavy metal showed that there was no significant difference in each treatment (Table 1). The lowest survival rate was found in treatment B (10 ppt + 0.03 mg/l Pb), while the highest survival rate was found in the control treatment (0 ppt + 0 mg/l Pb). The observation result of gill tissue damage on the Jatimbulan Juvenile tilapia exposed to the Lead at different salinity for 30 days can be seen in Table 2.

Based on the data above, the most severe value of edema was found in treatment A (0 ppt + 0.03 mg/l Pb) with the high level of damage which was 2.6, while the small value of damage of edema was found in the control with the low level of damage (that was 1.4). Considering hyperplasia, the highest damage value was found in treatment A (0 ppt + 0.03 mg/l Pb) with the medium level of damage which was 1.5, while the smallest average of hyperplasia was found in the control treatment with the normal level of damage which was 0.5. While the highest damage value of necrosis was found in treatment A (0 ppt + 0.03 mg/l Pb) with the medium level of damage which was 0.5. While the highest damage value of necrosis was found in treatment A (0 ppt + 0.03 mg/l Pb) with the medium level of damage which was 0.7, the smallest damage value of necrosis was found in the treatment C (20 ppt + 0.03 mg/l Pb) with the normal level of damage which was 0.1.

Histopathological description of the tilapia's gill organ exposed to the Lead (heavy-metal) showed the change in gill tissue structure in Figure 1. In the gill of the tilapia fish, there was a report of edema, hyperplasia, and necrosis. Edema in histopathology was characterized by the rounded shape, and there was liquid in the circle. Hyperplasia was characterized by the finding of thickening or enlargement in an organ. In the gill, it could be recognized by the

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enlargement of the secondary lamella. Meanwhile, the damage of necrosis occurred due to excessive hyperplasia, thus the gill tissue cells were no longer intact. The observation results of the intestinal tissue damage on the Jatimbulan Juvenile tilapia exposed to the Lead at different salinity for 30 days can be seen in Table 3.

Table 1. Survival rate of Jatimbulan Juvenile tilapia exposed to the lead at different salinity

Treatments		Repetition					
Treatments	1	2	3	4	5	$= \operatorname{Inealis}(70) \pm \mathrm{SD}$	
Control (0 ppt + 0 mg/1 Pb)	90	100	90	100	100	96 ± 4.89	
A (10 ppt + 0.03 mg/1 Pb)	100	100	80	80	70	86 ± 12	
B (20 ppt + 0.03 mg/1 Pb)	30	100	100	100	90	84 ± 27.27	
C (30 ppt + 0.03 mg/1 Pb)	90	100	70	100	100	92 ± 11.66	

*SD: Standard error of the means

Table 2. The histopathology damage of gill in each treatment

Treatment	Edema	Hyperplasia	Necrosis
Control (0 ppt + 0 mg/1 Pb)	1.4 ± 0.73	0.5 ± 0.70	0.4 ± 0.51
A (10 ppt + 0.03 mg/1 Pb)	2.6 ± 0.51	1.5 ± 0.70	1.7 ± 0.67
B (20 ppt + 0.03 mg/1 Pb)	2.1 ± 0.87	1.3 ± 0.48	0.6 ± 0.69
C (30 ppt + 0.03 mg/1 Pb)	1.6 ± 0.96	1.4 ± 0.84	0.1 ± 0.31

*p < 0.05, Normal: 0-0.75, Low: 0.75-1.5, Medium: 1.5-2.25, High: 2.25-3



Figure 1. The Histopathologic Description of the gill of Jatimbulan Juvenile Tilapia in the magnification of $400 \times$. **1:** Normal gill, **2:** Treatment A (0 ppt + 0.03 mg/l Pb), **3:** Treatment B (10 ppt + 0.03 mg/l Pb), **4:** Treatment C (20 ppt + 0.03 mg/l Pb); A: Edema, B: Hyperplasia, C: Necrosis, Pb: lead

Table 3.	The	histopatl	nological	damage	of the	intestine	in	each	treatment
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Treatment	Edema	Atrophy	Necrosis
Control (0 ppt + 0 mg/1 Pb)	1.1 ± 0.73	0.4 ± 0.51	1 ± 0.81
A (10 ppt + $0.03 \text{ mg}/1 \text{ Pb})$	2.1 ± 0.99	0.7 ± 0.67	0.9 ± 0.99
B (20 ppt + $0.03 \text{ mg}/1 \text{ Pb})$	1.6 ± 0.96	0.4 ± 0.51	1.3 ± 0.94
C (30 ppt + 0.03 mg/1 Pb)	1.5 ± 0.70	0.4 ± 0.69	0.9 ± 0.99

p < 0.05, Normal: 0-0.75, Low: 0.75-1.5, Medium: 1.5-2.25, High: 2.25-3

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Based on the data above, the most damage value of edema was found in treatment A (0 ppt + 0.03 mg/l Pb) with the medium level of damage which was 2.1, while the smallest damage value of edema was found in the control treatment with the low level of damage which was 1.1. The most damage value of atrophy was found in treatment A (0 ppt + 0.03 mg/l Pb) with the low damage rate of 0.7, while the average atrophy damage in the control treatment B (10 ppt + 0.03 mg/l Pb) and C (20 ppt + 0.03 mg/l Pb) had the same value of 0.4, and fallen into a normal category. Furthermore, the most damage value of necrosis was found in the treatment B (10 ppt + 0.03 mg/l Pb) with the low level of damage value of necrosis was found in the treatment A (0 ppt + 0.03 mg/l Pb) with the low level of damage which was 1.3, while the smallest damage value of necrosis was found in treatment A (0 ppt + 0.03 mg/l Pb) with the low level of damage which was 0.9.

The histopathologic description of the intestinal organs of tilapia exposed to the Lead (heavy-metal) revealed the presence of edema, atrophy, and necrosis (Figure 2). Edema was characterized by its rounded shape in an organ due to the liquid entering the cell tissue. Atrophy was characterized by shrinking cells. Meanwhile, the necrotic damage could be found with the characteristic of cells which was blurred or lost because of the inability of these cells to absorb the color when histology staining was done.



Figure 2. The Histopathologic Description of the intestinal Organs of Jatim Bulan Juvenile Tilapia in the magnification of $100\times$. **1:** Normal Intestine, **2:** Treatment A (0 ppt + 0.03 mg/l Pb), **3:** Treatment B (10 ppt + 0.03 mg/l Pb), **4:** Treatment C (20 ppt + 0.03 mg/l Pb). A: Edema, B: Hyperplasia, C: Necrosis, D: Hemorrhage, E: Atrophy, Pb: lead

The result of observation of the skin tissue damage on the Jatimbulan Juvenile tilapia exposed to the Lead at different salinity for 30 days can be seen in Table 4 below.

Based on the data above, the highest damage value of edema was found in treatment A (0 ppt + 0.03 mg/l Pb) with the low level of 1.4, while the smallest edema damage was found in the treatment B (10 ppt + 0.03 mg/l Pb) with the normal level of damage which was 0.2. The most hemorrhagic and atrophic damage values were found in the control treatment with the normal level of damage which was 0.6. The most damage value of necrosis was found in treatment A (20 ppt + 0.03 mg/l Pb) with the medium damage level of 1.5, while the smallest damage value of necrosis was found in treatment A (20 ppt + 0.03 mg/l Pb) with the low level of damage which was 0.9.

Histopathologic description of the tilapia's skin organ exposed to the heavy-metal Lead found the presence of edema, atrophy, hemorrhage, and necrosis (Figure 3). Edema was characterized by swelling of cells or excessive accumulation of fluid in the skin tissue. Atrophic damage was characterized by the reduced size of the skin tissue cells. Hemorrhagic damage was characterized by the release of cells from the blood vessels in the skin tissue. Meanwhile, the damage of necrosis was found by the death of skin tissue cells because of the inability to absorb the color when the histology staining was being done.

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Table 4. The histopathological damage of the skin in each treatment

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Treatment	Edema	Atrophy	Hemorrhage	Necrosis
Control (0 ppt + 0 mg/1 Pb)	$0.9\pm0{,}87$	0.6 ± 0.82	0.6 ± 0.69	1.1 ± 0.73
A (10 ppt + 0.03 mg/1 Pb)	$1.4 \pm 0,69$	0.5 ± 0.91	0.5 ± 0.70	1.5 ± 0.52
B (20 ppt + 0.03 mg/1 Pb)	$0.2 \pm 0,94$	0.4 ± 0.69	0.4 ± 0.51	1.3 ± 0.82
C (30 ppt + 0.03 mg/1 Pb)	1.1 ± 0.99	0.4 ± 0.51	0.4 ± 0.51	0.9 ± 0.96
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p < 0.05, Normal: 0-0.75, Low: 0.75-1.5, Medium: 1.5-2.25, High: 2.25-3



Figure 3. The Histopathologic Description of the skin organ of Jatim Bulan Juvenile Tilapia in the magnification of 400×. **1:** Normal Skin, **2:** Treatment A (0 ppt + 0.03 mg/l Pb), **3:** Treatment B (10 ppt + 0.03 mg/l Pb), **4:** Treatment C (20 ppt + 0.03 mg/l Pb), A: Edema, B: Hyperplasia, C: Necrosis, D: Hemorrhage, E: Atrophy, Pb: lead

The water quality observed in the study included temperature (°C), pH, ammonia (mg/l), and salinity (ppt). The result of the observation of water quality parameters can be seen in Table 5. Based on the data above, it could be seen that the temperature in each treatment had the same range of values among treatments which ranged from 27.5-33°C. In the observation of pH during the maintenance, it was known that the pH among treatments was not significant. In the control treatment and treatment A (0 ppt + 0.03 mg/l Pb), the obtained pH value was the same ranging from 7.7 to 9.1 in the treatment B (10 ppt + 0.03 mg/l Pb), and the lower limit value of the pH was slightly higher than the control treatment and the treatment A (0 ppt + 0.03 mg/l Pb), however the highest value of pH in the treatment B (10 ppt + 0.03 mg/l Pb) was the same as the control treatment (0 ppt) and the treatment A (0 ppt + 0.03 mg/l Pb) which was 7.8-9.1. In the treatment C (20 ppt + 0.03 mg/l Pb), the pH value was higher than the control treatment (0 ppt), A (0 ppt + 0.03 mg/lPb) and B (10 ppt + 0.03 mg/l Pb), however the pH value from the treatment C (20 ppt + 0.03 mg/l Pb) was not much different from other treatments which was 7.9-9.3. Considering the result of observation of salinity during the maintenance, it was known that the salinity value has increased. It was due to the evaporation during the study. The increase occurred in the treatment B (10 ppt + 0.03 mg/l Pb) and C (20 ppt + 0.03 mg/l Pb). The increase in salinity in both treatments; B (10 ppt + 0.03 mg/l Pb) was 10-12 ppt, treatment C (20 ppt + 0.03 mg / l Pb) was 20-22. From the result of observation of ammonia during the maintenance, it was known that the ammonia value in each treatment was the same as 0-0.5 mg/l, there was no difference at all amongst the treatments.

Table 5. The observation result of the water qu	aality
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Treatment Water Quality Parameter	Control	Α	В	С
Temperature (°C)	27.5-33	27.5-33	27.5-33	27.5-33
pH	7.7-9.1	7.7-9.1	7.8-9.1	7.9-9.3
Salinity (ppt)	0	0	10-12	20-22
Ammonia (mg/l)	0-0.5	0-0.05	0-0.05	0-0.05

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DISCUSSION

The results of histopathological examination of gills, intestines, and skin organs in the present study showed the damage caused by exposure to heavy-metal lead with different salinity. The damage in the gill organ included edema, hyperplasia, and necrosis. The initial damage that occurred in the gill was found in the presence of edema, then developed into hyperplasia and necrosis. This could be seen from the histopathologic changes in Jatimbulan Juvenile tilapia during the exposure to the heavy-metal lead at a different salinity. In the intestinal tissue, the changes were found in histopathology in the form of edema and atrophy which then were developed into necrosis. Meanwhile, in the skin tissue, the presence of edema, atrophy, hemorrhage, and necrosis was also found. These conditions indicated that absorption and bioaccumulation of the heavy metal could be stored well in the tissues of skin, gill, stomach, muscles, intestine, liver, brain, kidney, and reproductive organs (Chen and Chen, 2001; Bawuro et al., 2018).

Exposure to the heavy metal lead in treatment A (0 ppt + 0.03 mg/l Pb) had the highest damage effect on the gill organs when being compared with the skin and intestine, especially for edema and necrosis damage. This was because the reaction of the Lead in low salinity resulted in the lead toxicity level became higher (Sullivan, 1977). Besides, the gill was also the first organ to filter water that would enter the body of the fish. Gills were also the organs which were very sensitive to the effect of metal toxicity which would disrupt the normal function of metalloenzyme and metabolism of cells (Darmono , 2006). Therefore, if there was heavy metal in the water sources, the gill would react to the heavy metal.

Edema damage was also found in the intestinal tissue and skin. The highest edema damage to the intestinal tissue and skin occurred when treatment A (0 ppt + 0.03 mg/l Pb) was given. However, from the three tissues, the edema damage was the highest which occurred in the gill with treatment A (0 ppt + 0.03 mg/l Pb) which was 2.6 ± 0.51 . Edema was a swelling of cells caused by the entering of the lead into the tissue, thus it resulted in an excessive accumulation of fluid, and was considered as the initial stage of histological damage. The presence of the lead diffused into the gill cells and bounded to the plasma membrane of the lamella epithelial gill cells in synergy, and it caused the lack of Adenosine triphosphate (ATP). The low levels of oxygen in the blood could cause the cells to have insufficient ATP. The low amount of ATP in the cells caused the accumulation of Na + in the cells. This was due to the lack of energy to secrete Na + ions outside the cell. A large amount of Na + could cause osmotic pressure changes, thus water, Ca2 + and Na + could enter and cause swelling or edema (Catron et al., 2015). The high damage value of edema in the gill tissue, intestine, and skin tissue in treatment A (0ppt + 0.03mg/l Pb) with the low salinity value proven that the lower salinity would increase the level of toxicity in the heavy-metal lead toxicity.

The presence of edema in the gill, intestine, and skin was the initial stage of tissue damage and caused other histological damage. As in the gill, hyperplasia and necrosis were found, atrophy and necrosis were found in the intestine, and atrophy, finally hemorrhage, and necrosis were also found in the skin tissue. Excessive edema could cause hyperplasia due to red blood cells coming out of the capillaries, and the cells would be separated from the supporting tissue. Hyperplasia occurred at the lower level of irritation and was usually accompanied by an increase in the number of mucous cells at the base of the lamella, thus resulting in a lamella fusion. The presence of hyperplasia indicated a mechanism of adaptation of gill tissue to protect the tissue from irritants such as heavy metals. The mechanism was as protection and inhibitor of the gill function as a respiratory system because of the process of epithelial cells' cleavage, and excessive chloride cells that disrupted the respiratory system. In this study, the incidence of hyperplasia was found in almost every treatment on the gill tissue. An excessive lead in the gill tissue of Jatimbulan Juvenile tilapia also caused necrosis damage in the gill tissue. The highest necrosis damage was found in treatment A (0 ppt + 0.03 mg/l Pb). This could occur because of the concentration of heavy-metal lead in the water causing continuous absorption into the gill tissue, and causing necrosis (Mulyani et al., 2014).

The lower value of the damage was found in the intestinal and skin tissues. Lead exposure to intestinal tissue caused the damage of edema, atrophy, and necrosis. The intestine has experienced the damage because lead ion was bounded to the food. The results of intestinal histopathology after exposure to the heavy-metal lead did not show a significant difference in each treatment. This occurred because lead exposure entered the intestine through the water and food absorption, where food containing lead was more easily excreted from the body of the fish. Metal absorption through the respiration was usually quite large, while in the digestive tract of fish which most of the metal penetration came from food such as small fishes, aquatic plants, and plankton that have been bound to lead metal ion may not be absorbed by fish and excreted through feces (Darmono , 2006; Kasumyan, 2018).

In the skin tissue which was the outer part of the fish, and at the same time served as a protection against physical, chemical, and biological changes, when it was exposed to the heavy metal lead, it caused damages to edema, atrophy, hemorrhage, and necrosis. The skin experienced damages due to lead exposure that entered through the diffusion process. Histopathological results of the skin observation after the exposure to the heavy-metal lead did not show a significant difference in each treatment. The presence of lead in the skin tissue was able to damage to the necrosis stage or cell death, although Lead was able to cause necrosis, but only with the low value of the damage. This was because the skin had a mechanism for detoxification and excretion so that the toxic effect could still be tolerated (Yulaipi et al.,

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2013). Lead entered the skin organ through the circulatory system, but it took a long time in the distribution process, so only a little Lead and the damage of the skin was found.

The highest mortality rate in Jatimbulan Juvenile tilapia due to exposure to the heavy-metal Lead occurred after getting the treatment B (10 ppt + 0.03 mg/l Pb) with a mortality percentage of 84%, while the highest survival rate occurred after obtaining the control treatment (0 ppt) with a percentage of 96%. This happened because of the efficiency of fish in the utilization of feed, so it did not disrupt the body's metabolic system of fish. The survival rate of fish was also influenced by the condition of water quality which included temperature, pH, salinity, and ammonia. In the result, it could be seen that the parameter of temperature during the study showed an average value of 27.5° C to 33° C. The temperature was in accordance with the condition of the Jatimbulan tilapia fish habitat which was able to grow optimally at the temperature of 14°C to 38° C (FAO, 2018). The result of pH parameter during the study showed an average value ranging from 7.7 to 9.3, which was higher than the optimal PH value which was good for tilapia growth (PH 6 - 8.5; FAO, 2018). Nevertheless, the PH condition did not affect the condition of fish, because Jatimbulan tilapia had a high tolerance to PH. Meanwhile, the results of the ammonia parameter showed the value of 0-0.5, which meant that the waters had a normal ammonia level.

Salinity was also one of the factors highly considered during the study. Salinity is the weight of inorganic halogen salts in gram dissolved in 1kg of water. In this study, the salinity influenced the description of the damage in the gill, intestine, and skin of Jatimbulan Juvenile tilapia. The decrease in salinity caused an increase in the toxicity of heavy metals. The salinity influenced the toxic power of Lead in the body of tilapia which was when the tilapia was placed in the salinity water, then the osmoregulation process of fish tended to maintain the fluid in the body against the changes in salinity. If it was found that Lead has exceeded the limit and could not be tolerated by the body of the fish itself, it would be excreted the xenobiotic substances. The xenobiotic substances in the body of the fish would stimulate the fish to take the physiological resistance to minimize the impact of the poison caused (Yulaipi et al., 2013; Kasumyan, 2018).

CONCLUSION

From the results of the study which has been conducted, it can be concluded that the exposure of heavy-metal Lead was 0.03 ppm at the salinity of 10 ppt and 20 ppt, giving a significant effect on the histopathologic description of the gill, intestine, and the skin of Jatimbulan Juvenile tilapia. The effect of these changes was known with the presence of histopathologic description in the damage of edema, hyperplasia, and necrosis in the gill tissue, the damage of edema, atrophy, and necrosis in the intestinal tissue, and the damage of edema, atrophy, hemorrhage, and necrosis in the skin tissue.

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In Vitro Antibiotic Activity of Red Shallot (*Allium ascalonicum*), Mulberry (*Morus indica*), and Marigold (*Tagetes erecta*) Extracts against Streptococcus pyogenes

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ABSTRACT

Bacterial infection is a major global health concern. One of the critical problems is the widespread of antimicrobialresistant bacteria from inappropriate and prolonged use of antimicrobial agents in both humans and animals. Plant extracts might afford the chance to replace antibiotic drugs and reduce the emerging of antimicrobial-resistant bacteria. This study aimed to examine the antibiotic activity of ethanolic crude extracts of some Thai medicinal plants grouping in their parts as whole onions of red shallot (Allium ascalonicum), petals of marigold (Tagetes erecta), mulberry leaves, and root barks (Morus indica) to inhibit the growth of Streptococcus pyogenes. The antibiotic activities of the crude extract of three Thai medicinal plants using absolute ethanol were trialed against Streptococcus pyogenes using the disk diffusion method. Erythromycin and Ceftriaxone discs were chosen to be positive control standards as the representative of antibiotic drugs. Each dried plant extracts was prepared to test the inhibition with a concentration at 25, 50, and 75 mg/mL stock solution. The results showed that three groups from all testing groups of Thai medicinal plant extracts had the potential of antibiotic activity against S. pyogenes. The highest antibiotic activity against S. pyogenes was detected from whole onion extract red shallot followed by the extract of the mulberry leaves and root barks of mulberry strain Nakhon Ratchasima 60 (Nak 60) while the extract of marigold petal did not present antibiotic activity. The results revealed that crude extract of those two Thai medicinal plants, including red shallot and mulberry, had antibiotic activity against bacterial growth of S, pyogenes in the experiment and these medical Thai plants had potential benefits for developing as alternative treatment agents for S. pyogenes infections in both humans and animals in the future.

Keywords: Antibiotic activity, Ethanolic crude extract, Thai medicinal plants, Streptococcus pyogenes

INTRODUCTION

Streptococcus pyogenes (S. pyogenes) is known as an important Gram-positive bacteria which display oxidase negative, catalase-negative, and β -hemolytic on blood agar. It is a facultative anaerobe bacteria that usually grows in 5-10% carbon dioxide and forms colonies on blood agar. It is grouped as Group A Streptococci (GAS) by Lancefield serological grouping system (Spellerberg, 2016). In humans, *S. pyogenes* normally colonizes in the throat, skin epithelial surfaces, anus, genital mucosa, and pharynx (Cunningham, 2000), while it was reported to be found in the eye discharge of a dog with conjunctivitis, feces of a dog with colitis, free-living European hedgehog, free-ranging non-human primates and bovine mastitis (Vela et al., 2017). However, the spread of the bacteria to typically sterile body sites can induce invasive conditions that lead to high morbidity and mortality. Therefore, *S. pyogenes* is pathogenic to humans and animals with its contagious infections. *S. pyogenes* can transmit through various routes, including direct contact, droplets, nasal discharge, fomites or surfaces contaminated with this bacteria, skin contact with a contaminated lesion, and by oral route from contaminated foods (Vela et al., 2017).

Currently, the increasing antimicrobial resistance (AMR) is becoming the most important problem for both animal and human health as well as the potential zoonotic infection. The problem can challenge the public health system, cause economic loss, and increase the morbidity rate of infected cases and also the mortality rate of the patients who might not be cured by any antibiotic medications (Shuster et al., 2013). The increase of AMR in *S. pyogenes* has been observed worldwide (Lai et al., 2021). The highest rate of resistance is usually found in erythromycin which was reported in Europe, including Finland, Spain, Italy, Netherlands, Germany, and also the USA (Arvand et al., 2000).

At present, there are many attempts to reduce the usage and for the rational use of antibiotic drugs to treat bacterial infections. Then, the development of alternative agents, including effective natural agents is necessarily required to replace antibiotic drugs. Many studies have addressed the antibiotic activity of plant extracts against the growth of bacteria that could be developed into antibacterial agents or therapeutic drugs (Abiala et al., 2016; Elisha et al., 2017). Marigold petal)*Tagetes erecta*(has revealed a large amount of flavonoids biologically content, especially for patulitrin that is the dominant active substance in the flavonoids containing anti-inflammatory effect and also effective antibiotic

activity to destroy bacterial cells (Rhama and Madhavan, 2011; Dasgupta et al., 2012). An earlier study has reviewed the bulbs of red shallot (*Allium ascalonicum* Hort.) entailing a high level of quercetin can inhibit bacterial growth (Fattorusso et al., 2002). The mulberry (*Morus alba* L.) extract was found to have bioactive components, such as flavonol quercetin 3-(6-Malonylglucoside) substance which could inhibit both Gram-negative and Gram-positive bacterial pathogens, including *Escherichia Coli, Bacillus subtilis, Bacillus cereus, Pseudomonas aeruginosa,* and *Staphylococcus aureus* (Salem et al., 2013; Grajek et al., 2015; Gunjal et al., 2015) and quercetin which could destroy the membranes of bacteria leading to growth inhibitation (Wang et al., 2018). Therefore, the current research aimed to evaluate the antibiotic activity of ethanolic crude extracts from potential Thai medicinal plants, such as red shallot (*Allium ascalonicum*), mulberry leaves and root (*Morus indica*) strain Nakhon Ratchasima 60 (Nak 60), and marigold (*Tagetes erecta*) against *Streptococcus pyogenes* for the potential of usage as an antibiotic agent to reduce the problem of antibiotic resistance in the future.

MATERIALS AND METHODS

Ethical approval

Ethical approval was not required for this research. All experiments and procedures in the current study did not certainly interrupt both humans and animals. All of the experiments and procedures were prepared and processed One Health research unit and Veterinary Public Health (VPH) laboratory room, Faculty of Veterinary Sciences, Mahasarakham University, Maha Sarakham province, Thailand.

Medicinal plant materials

All Thai medicinal plants in this study were identified, housed, harvested, and collected at Mahasarakham University, Maha Sarakham, Northeastern Thailand. Ethanolic crude extracts were prepared from three Thai medicinal plants as were shown their external characteristic in Table 1 and their antibiotic activities were investigated. The selected medicinal plants which used in this research included root barks and leaves of mulberry (*Morus indica*) strain Nakhon Ratchasima 60 (Nak 60), marigold petal (*Tagetes erecta*), and whole onions or bulbs of red shallot (*Allium ascalonicum*) as shown in Figure 1. All medicinal plants were weighed, washed with purified and distilled water, then, they were dried at room temperature for 5 days. After that, they were chopped into 1x1 cm pieces and desiccated in a drying oven for 24 hours at 65°C. The dried medicinal plants were weighed after drying and extracted by soaking with absolute ethanol in a plant-ethanol ratio of 1:5 for 24 hours at room temperature within the cabinet. The medicinal plant extracts were then sieved using a filter paper and concentrated to yield ethanolic crude extracts via evaporation by vacuum rotary evaporator (Heidolph, Germany) at 289 mbar, 60 rpm, and 60°C in a water bath as shown in Figure 2. Each Thai medicinal plant extracts was then dissolved in dimethyl sulfoxide (DMSO) as solvent before measuring the antibiotic activity test. Each dried plant extracts in this study were used three different concentration tests (low, medium, and high) at 25 mg/ml, 50 mg/ml, and 75 mg/ml, respectively.

Thai medicinal plants		Part used	Weight before	Weight after	
Common name	Scientific name	I alt used	drying (g)	drying (g)	
Red shallot	Allium ascalonicum	Whole onions	3226	557.5	
Mulberry	Manua in dia n	Root barks	345.65	286	
	<i>Morus inaica</i>	Leaves	340.45	101.78	
Marigold	Tagetes erecta	Petals	557.5	201.31	

Table 1. Thai medicinal plants and their part used for antibiotic activity test

Target bacterial strain

This study used a reference strain of *Streptococcus pyogenes* (ATCC19615) as a target microorganism. The bacterial strain was maintained in the Veterinary Public Health Laboratory at the Faculty of Veterinary Sciences, Mahasarakham University, Thiland. *S. pyogenes* was subcultured from the original bacterial culture, stored at -20°C, and streaked on nutrient agar plates (Oxoid, UK) to maintain at 4°C. It was used to test for antibiotic susceptibility by disc diffusion protocol. *S. pyogenes* was cultured on tryptone soy agar (Oxoid, UK) in aerobic incubation at 37°C for 24 hours. Antibiotic activity testing protocol was processed following the methods for antimicrobial dilution and disk susceptibility testing CLSI guidelines M45 (CLSI, 2017). The *S. pyogenes* colony had cultured overnight, then, it was suspended in sterile saline water and the suspension has adjusted the turbidity to equal that of a standard value of 1.5x 10⁸ CFU/ml by 0.5 McFarland.

Evaluation of antibiotic activity

Disk diffusion method was processed in triplicate for root barks of mulberry, leaves of mulberry, marigold petal, and whole onions of red shallot ethanolic crude extracts in each concentration. The bacterial suspension was spread onto the surface of the Muller Hinton agar; MHA (Oxiod, UK) that was used to determine the antibiotic activity by sterile cotton swabs. Each dried plant extracts was prepared a concentration at 25, 50, and 75 mg/mL stock solution in DMSO. Wells which were used to place the medicinal plant extracts testing were cut into MHA. The volume of stock solutions

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about 5 μ l in each concentration was loaded to the wells in MHA plates which the target bacterial strain was spread along with representative antibiotic drugs as selected antibiotic assay discs including erythromycin and ceftriaxone (Oxoid, UK) which used as the positive control, then incubated the plates in aerobic incubation for 24 hours at 35°C together with DMSO which was utilized as the solvent control or negative control in this trial. The zone of the inhibition diameters in each plate was interpreted following the recommendation of CLSI guidelines M100 (CLSI, 2020).



Figure 1. Thai medicinal plants used in the experiment, Whole onions of red shallot (A), Mulberry leaves (B), Root barks of mulberry (C), Petals of marigold (D)



Figure 2. The extraction methods of Thai medicinal plants

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Statistical analysis

The experimental data were statistically analyzed using differentiation of disk diffusion results by descriptive statistics analysis and one-way analysis of variance (ANOVA) and the least significant difference (LSD) post hoc tests at 95% confidence level. The significance statistical difference was set at p < 0.05. The IBM SPSS statistic version 21.0 was used for analysis.

RESULTS

The experimental result from the antibiotic activity trial for inhibiting the growth of *S. pyogenes* by the ethanolic crude extracts of Thai medicinal plants is demonstrated in Table 2 .Ethanolic crude extracts of red shallot and mulberry showed the antibiotic activities on the reference strain of *S. pyogenes*. From the result of inhibition zone performed by the lowest concentration at 25 mg/ml, the average diameters of inhibition zone of whole onions of red shallot extract, root barks of mulberry extract, leaves of mulberry extract, and marigold petal extract were 7.1, 5.17, 5.33, and 2 mm, respectively. At 50 mg/ml concentration, the average diameters of the inhibition zone were 7.83, 6.17, 6.67, and 2.5 mm, respectively. At least, the average diameters of the inhibition zone of the highest concentration at 75 mg/ml were 8.67, 7, 7.83, and 3 mm, respectively.

Thai medicinal plant extracts comprising red shallot, root bark, and leaves of mulberry showed good antibiotic activity against *S. pyogenes*, while marigold extract rarely had antibiotic activity. Red shallot ethanolic extracts appeared the most antibiotic activity following by the crude extract of mulberry leaves and root bark of mulberry extract, respectively. The inhibition zones of erythromycin and ceftriaxone which were used as the positive control in this trial were 15.67 mm and 24.42 mm in diameter, respectively. There were statistically significant differences among the four categories of Thai medicinal plant extracts in all concentration tests when analyzed through one-way ANOVA and the least significant difference (LSD) post hoc tests at 95% confidence level. The obtained results from LSD post hoc test indicated that the ethanolic extracts of red shallot bulbs were the most effective against *S. pyogenes*, while the ethanolic extracts of marigold showed the lowermost antimicrobial activity at all concentration tests.

	Zone of inhibition diameter (mm) Plant extracts concentration)mg/ml)					
Thai medicinal plants extract						
	25	50	75			
	7	7.5	8.5			
Red shallot	7.5	8	8.5			
	7	8	9			
Average	7.16	7.83	8.67			
	5	6	7.5			
Mulberry (root bark)	5	6	6.5			
	5.5	6.5	7			
Average	5.17	6.17	7			
	6	7	8			
Mulberry (leaves)	5	6	7.5			
	5	7	8			
Average	5.33	6.67	7.83			
	2	2.5	3			
Marigold	2.5	3	3.5			
	1.5	2	2.5			
Average	2	2.5	3			

Table 2. Antibiotic activity of Thai medicinal plant ethanolic crude extracts demonstrated as the diameter of inhibition zone

DISCUSSION

The outcomes of the study revealed the potential antibiotic activity derived from ethanolic crude extracts of Thai medicinal plants comprising red shallot, mulberry leaves, and mulberry roots strain Nakhon Ratchasima 60 (Nak 60) inhibiting the growth of *S. pyogenes*. Ethanolic crude extracts of bulbs or whole onions part of red shallot expressed the highest potential inhibitory activity against *S. pyogenes* which is consistent with a previous study from Mekvimol et al. (2020) that mentioned the high antibiotic activity of red shallot and mulberry leaves extracts against the growth of Grampositive bacteria, such as *Streptococcus agalactiae*. The findings of the current research indicated that the bulbs or whole

onions part of red shallot and the leaves and rook barks part of mulberry ethanolic crude extracts have the possibility to inhibit the growth of S. pyogenes in all concentrations. Some previous studies reported that the shallot bulbs and mulberry leaves contain a high level of active phenolic compound which demonstrated to have antimicrobial activities, including flavonoid substance which can inhibit the growth of bacteria (Butkhup et al., 2013; Mozin et al., 2015). The major active ingredient of flavonoid substances from these herb extracts is quercetin with a bactericidal effect by demolishing bacterial cell membranes (Mozin et al., 2015). Therefore, this result is consistent with many previous studies indicating that quercetin was a crucial bioactive compound and plays a role in inhibiting Gram-positive and Gram-negative bacteria by prohibiting the activity of extracellular proteins (Koo and Jeon, 2009; Mozin et al., 2015; Fredotović et al., 2021). Nevertheless, some reports revealed that quercetin could not inhibit the growth of some Gramnegative organisms include E. coli and Salmonella typhi (Souza et al., 2010; Mozin et al., 2015). The bioactivity compounds of red shallot and mulberry which were revealed the potential antibiotic activity on S. pyogenes were likely more effective to inhibit bacterial growth, while ethanolic extract of marigold seemed to have no effect on the bacterial growth. The *in vitro* study of antibiotic activity from Thai medicinal plant extracts is a crucial phase for the alternative treatment strategy as surrogate antibacterial agents replacing antibiotic drugs for several bacterial pathogens, including S. pyogenes. The findings of the current in vitro study can be well used for alternative medicine. These medicinal plants in urban communities can be developed into therapeutic drugs as plant-based antimicrobial agents. This evidence is in accordance with many previous studies that revealed the success of herbal medicine in curing bacterial infectious diseases (Palombo, 2011; Abiala et al., 2016; Elisha et al., 2017). More than that, the current research seems to be the first investigation that discovered ethanolic crude extracts from various Thai medicinal plants, including whole onions of red shallot, root bark, and leaves of mulberry had antibiotic activity against the growth of S. pyogenes.

CONCLUSION

The current *in vitro* study revealed that red shallot (*Allium ascalonicum*), leaves part and root barks part of mulberry (*Morus indica*) strain Nakhon Ratchasima 60 (Nak 60) ethanolic extracts expressed the antibiotic activity against *S. pyogenes*. Thus, the future development of red shallot and mulberry leaves ethanolic extracts as an alternative treatment for *S. pyogenes* infections in both humans and animals are recommended for resolving the antimicrobial resistance in the prospect. Ethanolic crude extract of red shallot exhibited strong activity against *S. pyogenes* reference strain ATCC19615. Further investigation should be aimed to analyze the quantity of active ingredients and action mode of these plant extracts against bacterial clinical strains. It would be interesting to evaluate *in vivo* trial for developing and applying these medicinal plants as natural therapeutic products for both humans and animals for medical and veterinary use.

DECLARATIONS

Competing interest

The authors declare that they have no competing interests.

Authors' contribution

Natapol Pumipuntu designed and supervised the research project, supported in the experimental study and data analysis. Tanawadee Mekvimol, Chayanit Chaipunna, and Gannika Poonthong designed the research experiment and collected the data. All authors interpreted the data, wrote the manuscript, and approved the final version.

Ethical consideration

Ethical issues (including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by all the authors.

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Controlling Food Poisoning Bacteria in Fermented Chicken Sausage Using *Lactobacillus plantarum*

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ABSTRACT

Lactobacillus plantarum (L. plantarum) bacteria is generally recognized as safe and widely used in the food industry. The current study aimed to study the antimicrobial effects of L. plantarum against some food poisoning microorganisms, such as Staphylococcus aureus (S. aureus), Bacillus cereus (B. cereus), and Escherichia coli (E. coli) in oriental fermented chicken sausage for 18 days of storage at 4° C. The L. plantarum has broad-spectrum antimicrobial effects that enhance the quality and safety of food products. L. plantarum reduced the count of S. aureus, B. cerus, and E. coli to 1.54, 4.26, and 3.03 Log₁₀, respectively, after 18 days of refrigerated storage. Moreover, there were significant effects of L. plantarum on pH, thiobarbituric acid, total volatile basic nitrogen, and sensory attributes of fermented sausage samples during storage time. It was revealed that L. plantarum enhanced the physic-chemical, sensory attributes, and shelf life of fermented chicken sausage. Moreover, L. plantarum inhibited to use L. plantarum in fermented meat products as a starter and a bio-preservative to enhance the quality of the fermented chicken sausage.

Keywords: Chicken sausage, Food safety, Lactobacillus plantarum, Probiotic

INTRODUCTION

Food safety is a key concern in the food industry since it has serious and long-term consequences for public health, particularly when people consume food contaminated with harmful bacteria (FDA, 2020). Moreover, meat products with functional ingredients are considered a demand in the meat industry to reduce the risk of food-borne diseases and enhance health conditions (Sirini et al., 2020). In this regard, fermented sausages fortified with probiotic bacteria are considered a functional food with several health-promoting benefits (Lafarga and Hayes, 2017).

Probiotics, such as lactic acid bacteria are generally recognized as safe and are widely used in the food industry (Oleksy and Klewicka, 2018). It has been applied in human medicine for treatment or alternative in the treatment of chronic inflammation, cancer, cardiovascular diseases, and Alzheimer's disease (Woo et al., 2014; Kurhan and Çakir, 2016), as it can enhance individuals' health, physiology, and immunity (Arasu et al., 2016). Moreover, it is used for food fermentation, improving the texture and flavor of sausages, suppressing the spoilage bacteria of food, and prolonging the shelf-life (Lin and Pan, 2017).

Lactobacillus plantarum is one of the Lactic acid bacteria, that has promising characteristics to be applied in the commercial fermented meat industry as well as it has a great antioxidant effect in the fermentation of camel sausages (Ayyash et al., 2019).

Although the effect of *L. plantarum* inoculation on the quality of fermented meat products was evaluated before (Sun et al., 2016), the current study aimed to focus on the evaluation of not only the antimicrobial effect of *L. plantarum* against some food poisoning microorganisms, such as *Staphylococcus aureus* (*S. aureus*), *Bacillus cereus* (*B. cerus*), and *Escherchia coli* (*E. coli*) but also changes in physicochemical and sensory attributes of inoculated oriental fermented chicken sausage stored at refrigerated temperature for 18 days.

MATERIALS AND METHODS

Ethical approval

The present study did not involve either humans or animals as an experimental setup. The experiment was conducted at Animal Health Research Institute, Egypt.

Bacterial strains

Referenced pathogenic bacterial strains, including *E. coli* (Lot No: 020090, Des: NCTC: 12241 and ATCC: 25922), *S. aureus* (Lot No: 460074, Des: NCTC: 10788 and ATCC: 6538), *B. cereus* (Lot No: 02900402, Des: NCTC: 10400 and ATCC: 6633), and *L. plantarum* local strain used in the current study were obtained from Media Unit, Food Hygiene Department, Animal Health Research Institute, Dokki, Giza, Egypt.

Pathogenic strains were adjusted to obtain a count of $6 \log_{10} \text{CFU mL}^{-1}$ and *L. plantarum* was adjusted at $8 \log_{10} \text{CFU mL}^{-1}$.

Assessment of in vitro antimicrobial activity of L. plantarum against different food poisoning bacteria

Disc diffusion method was used following Toure et al. (2003) to assess the inhibitory range of *L. plantarum* (10^6 , 10^7 , and 10^8 CFU ml⁻¹) against *E. coli, S. aureus*, and *B. cereus* at 10^6 CFU ml⁻¹ concentration.

Preparation of chicken sausage

Minced chicken breast meat was purchased from markets in Elminofia governorate, Egypt. The sausage formulations were prepared according to the formulae detailed by Mejri et al. (2017) with minor modifications using chicken meat instead of camel meat. Briefly, sausage batters were prepared for each experiment based on chicken meat content, mincing it with a meat mincer (MK-G20NR-W, Panasonic, Osaka, Japan). The added ingredients to the minced meats included 25 g kg⁻¹ NaCl, 10 g kg⁻¹ garlic, 4 g kg⁻¹ sucrose, and mixed spices 30 g kg⁻¹.

Before the experiment, the meat was surface treated with ultraviolet light (UV) (wavelength 385 nm) for 15 minutes to minimize background micro-flora according to Morsy et al. (2018).

Challenge study

The prepared mixture was divided into seven groups, then inoculated with cultured bacteria adjusted at 10^6 for pathogenic bacteria and 10^8 for *L. Plantarum*. The first group named control entailed UV treated but not inoculated, the second group included *E. coli* inoculated group, the third group had *E. coli* + *L. plantarum*, the fourth group composed of *S. aureus* included group, the fifth group was *S. aureus* + *L. plantarum*, the sixth group contained *B. cereus* infected group, and the seventh group included *B. cereus* + *L. plantarum* inoculated group. After inoculation, samples were kept at room temperature (22°C) for 15 minutes for cell attachment and then stuffed into a sterile polyethylene sausage casing using a handheld sausage filling machine. Samples were kept at $4 \pm 1^\circ$ C for 18 days, and they were analyzed at the beginning of the study as well as days 3, 6, 9, 12, 15, and 18 for remaining microbial populations. The current experiment was repeated three times for each group to obtain mean values for statistical analysis (n = 3).

Microbiological assay

At each sampling day, samples were opened and then 10 g from each one of them was aseptically transferred into 90 mL of 0.1% buffered peptone water (BPW, Biolife) and stomached (model G-560E, Bohemia) for 1 minute. Ten-fold serial dilutions were made in BPW (Biolife) and 1 ml was poured on Eosin methylene blue (EMB, Biolife) for *E. coli* (ISO 21150, 2006), Baird parker (LO, Biolife) for *S. aureus* (ISO 6888-1, 2003) and *B. Cereus*, agar base-MYP (BC-MYP, Biolife) with polymyxin B sulphate supplement (Code 4240001) and egg yolk emulsion (Code 42111601) for *B. cereus* (ISO 7932, 2004). Colonies were counted after 24 hours of incubation at 37°C and expressed as log10 CFU gm⁻¹.

Physico-chemical evaluation

The measured parameters were included pH value using a digital pH-meter (model P107, Consort, Belgium), total volatile base nitrogen (TVB-N, N/100 g of sample), and Thiobarbituric acid reactive substances (TBARS, MDA kg-1) using spectrophotometric (CE 599Universal, USA, AOAC, 2005).

Sensory evaluation

Sensory evaluation of fermented sausage (control and inoculated groups) was performed under the controlled conditions of temperature 22 °C and humidity 55% by seven well-trained panelists who were working in Food Hygiene and Control Department, Animal health research institute, Egypt. The criteria used as the basis of the descriptive organoleptic assessment (color, odor, and texture) with triangle test and the hedonic rating system to score on numerical and continuous scales from 0 (the lowest score for each attribute, very bad) to 9 (the highest score for each attribute, very good). The scale points were used according to ISO 13299 (2003).

Statistical analysis

Results of physicochemical properties and sensory attributes were tested for normality and homogeneity. Then, a one-way analysis of variance was applied to evaluate the statistical significance of differences between groups followed by an LSD test as post hoc for making multiple comparisons by the Statistical Package for Social science Software (Version 25, SPSS Inc.; Chicago, IL, USA). The values were expressed as the mean \pm standard error. A significant difference was used at the p \leq 0.05 probability level. Statistical analysis of concerning results of the effects of *L*. *plantarum* on food poisoning bacteria was carried out using student's T-test according to Steel and Torrie (1980). Significant differences were calculated at degree of freedom at p values 0.05.

RESULTS AND DISCUSSION

Natural bio-control demand has raised with varying efficacy and impacts on food quality and consumer health (Al-Juhaimi et al., 2018). Minimum inhibitory concentration of *L. plantarum* was evaluated *in vitro*, results in Table 1 showed that zones of inhibition differed according to the use of *L. plantarum* concentration. It was found 10^8 CFU ml⁻¹ concentration had the widest inhibitory zone against *S. aureus*, *B. cereus*, and *E. coli*.

Challenge study

Based on the results in Table 2 *L. plantarum* showed antimicrobial effect against *S. aureus, B. cerus*, and *E. coli* selected for the challenge study, there was a significant difference between groups inoculated with pathogenic bacteria only and those treated with *L. plantarum* ($p \le 0.05$). It was found the pathogenic bacteria of inoculated groups reached a count of 8.61, 7.94, and 8.61 log₁₀ for *S. aureus, B. cereus*, and *E. coli* over the course of the experiment, respectively. *L. plantarum* decreased count of *S. aureus, B. cereus*, and *E. coli* in treated groups to reach 1.54, 4.26, and 3.03 log₁₀ respectively, after day 18 of refrigerated storage. The *L. plantarum* reduced the microbial load of inoculated pathogens mainly against *S. aureus*, followed by *E. coli*, and *B. cereus*. The *L. plantarum* showed antimicrobial properties in fermented chicken sausage (Yadav and Pipaliya, 2017). This might be due to the low pH level of the product that affects directly inoculated bacteria or the metabolites secreted as organic acids, fatty acids, exopolysaccharides, and bacteriocins (Oleksy and Klewicka, 2018).

Table 1. Antimicrobial activity assessment of Lactobacillus plantarum against Staphylococcus aureus, Bacillus cerus,and Escherichia coli using disc diffusion method

	Lactobacillus plantarum					
Pathogenic bacteria	106	10 ⁷	10 ⁸			
Staphylococcus aureus (10 ⁶)	8 ± 0.22	12 ± 0.10	18 ± 0.15	mm		
Bacillus cereus (10 ⁶)	ND*	9 ± 0.23	13 ± 0.11	mm		
Escherichia coli (10 ⁶)	ND	10 ± 0.10	15 ± 0.14	mm		
ND*: Not detected						

ND*: Not detected

Table 2. Effect of *Lactobacillus plantarum* on different food poisoning bacteria (log CFU/gm) inoculated in chicken sausage stored at 4°C

Chound	Storage period (day)								
Groups	1	3	6	9	12	15	18		
Staphylococcus aureus (10 ⁶)	6.38 ± 0.09	6.89 ± 0.02	7.12 ± 0.05	7.56 ± 0.06	7.88 ± 0.07	8.20 ± 0.04	8.61 ± 0.06		
Staphylococcus aureus (10 ⁶) + Lactobacillus plantarum	6.35 ± 0.05	5.60 ± 0.09 ****	5.12 ± 0.03 ***	$4.81 \pm 0.03 ^{***}$	4.00 ± 0.08 ***	3.73 ± 0.09 ****	1.54 ± 0.13 ****		
Bacillus cereus (10 ⁶)	6.50 ± 0.08	6.79 ± 0.02	7.07 ± 0.03	7.36 ± 0.04	7.71 ± 0.04	7.81 ± 0.02	7.94 ± 0.03		
Bacillus cereus (10 ⁶) + Lactobacillus plantarum	6.40 ± 0.05	$6.20 \pm 0.00^{***}$	$5.99 \pm 0.02^{\ast \ast \ast}$	$5.55 \pm 0.03^{***}$	$5.13 \pm 0.03^{***}$	$4.99 \pm 0.07^{***}$	$4.26 \pm 0.02^{***}$		
Escherichia coli (10 ⁶)	6.38 ± 0.09	6.89 ± 0.02	7.12 ± 0.05	7.56 ± 0.06	7.88 ± 0.07	8.20 ± 0.04	8.61 ± 0.06		
Escherichia coli (10 ⁶) + Lactobacillus plantarum	6.28 ± 0.15	$5.83 \pm 0.08^{\ast \ast \ast}$	$5.37 \pm 0.04^{***}$	$4.86 \pm 0.03^{***}$	$4.92\pm 0.03^{***}$	$3.54 \pm 0.08^{***}$	$3.03 \pm 0.12^{***}$		

Data are presented as (Mean \pm S.E). S. E: Standard error. *** Represents statistical significance at p ≤ 0.05

Physico-chemical evaluation

In this phase of the study, the effect of *L. plantarum* on freshness, shelf life time, and chemical quality of chicken sausage was evaluated. Results in Table 3 revealed that pH values in groups that inoculated with *L. plantarum* were significantly different ($p \le 0.05$) than the control one. Moreover, there was a significant difference ($p \le 0.05$) in the pH value over the storage period (18 days) in the same group. The *L. plantarum* decreases pH values in sausage due to the growth of lactic acid bacteria (Slima et al., 2017). This acidification is a straightforward metric for assessing a starter's effectiveness. Organic acids formation during fermentation reduces pH and prevents pathogens' growth (Mataragas et al., 2015). Moreover, it has positive effects on the flavor, as it strengthens the perception of aroma (Bonomo et al., 2009).

Concerning TVB-N results during challenge study in Table 4 revealed that TVB-N increased gradually during chilling storage at 4°C with significant difference ($p \le 0.05$) between groups inoculated with pathogenic bacteria and

those treated with *L. plantarum* due to bacterial or enzymatic actions on protein degradation. There was also a significant difference ($p \le 0.05$) in TVB-N values over the storage period (18 days), with prolonged storage time the TVB-N values increased in groups inoculated with pathogenic bacteria, whereas in those treated with *L. plantarum* decreased. *L. plantarum* maintains lipid oxidation in fermented sausage (Slima et al., 2017).

Regarding Thiobarbituric acid (TBA), a typical indicator of lipid rancidity in meat products provides useful information on lipid oxidation (Tornuk et al., 2015). Results in Table 5 revealed that TBA increased gradually during extended chilling storage at 4 °C with significant difference ($p \le 0.05$) between groups inoculated with pathogenic bacteria and those treated with *L. plantarum* due to oxidative action effect on fatty acids. There was a significant difference ($p \le 0.05$) in TBA values over the refrigerated storage period, with prolonged storage time TBA values increased in groups inoculated with pathogenic bacteria, compared to *L. plantarum* treated groups. The *L. plantarum* in camel sausages (Ayyash et al., 2019) and chicken sausages (Yadav and Pipaliya, 2017) has a significant antioxidant effect.

Physico-chemical properties, including pH, TBA, and TVN, in all pathogenic bacteria inoculated groups were evaluated until nine days of storage While, those groups treated with *L. plantarum* were evaluated till 18 days of refrigerated storage (4° C) when samples undergo spoilage.

Table 3. Effect of Lactobacillus plantarum on pH of chicken sausage stored at refrigerator temperature 4°C

Croups	Storage period (day)							
Groups	1	3	6	9	12	15	18	
Control	5.90 ± 0.04	6.34 ± 0.04	6.97 ± 0.07	S	S	S	S	
Staphylococcus aureus (10 ⁶)	5.86 ± 0.02	6.51 ± 0.05^a	7.01 ± 0.16	S	S	S	S	
Staphylococcus aureus (10 ⁶) + Lactobacillus plantarum	5.74 ± 0.01^{ab}	4.87 ± 0.03^{ab}	4.50 ± 0.04^{ab}	4.47 ± 0.04	4.23 ± 0.06	5.00 ± 0.06	5.35 ± 0.07	
Bacillus cereus (10 ⁶)	5.90 ± 0.03	$6.51\pm0.05~^a$	7.01 ± 0.16	S	S	S	S	
Bacillus cereus (10 ⁶) + Lactobacillus plantarum	5.79 ± 0.02^{ab}	$4.67\pm0.03^{\ ab}$	4.55 ± 0.04^{ab}	4.48 ± 0.04	4.26 ± 0.06	5.00 ± 0.06	5.32 ± 0.16	
Escherichia coli (10 ⁶)	5.97 ± 0.03	$6.60\pm0.05~^a$	7.22 ± 0.08	S	S	S	S	
Escherichiacoli (10 ⁶) + Lactobacillus plantarum	$5.84\pm0.03^{\ b}$	$4.80\pm0.03^{\ ab}$	$4.76\pm0.03^{\ ab}$	4.46 ± 0.04	4.20 ± 0.05	5.51 ± 0.07	5.80 ± 0.08	

Data are presented as (Mean \pm S.E). S.E: Standard error, S: Spoilage depending on sensory evaluation. Significance at $p \le 0.05$.^a Significant in the control group, ^b Significant within corresponding bacterial groups

Channa	Storage period (day)											
Groups	1	3	6	9	12	15	18					
Control	1.65 ± 0.03	18.33 ± 0.33	27.72 ± 0.67	S	S	S	S					
Staphylococcus aureus (10 ⁶)	1.71 ± 0.05	19.60 ± 0.32^{a}	30.26 ± 0.65^{a}	S	S	S	S					
Staphylococcus aureus (10 ⁶) + Lactobacillus plantarum	1.57 ± 0.03	$4.80\pm0.20^{\ ab}$	$9.47\pm0.25~^{ab}$	13.66 ± 0.26	16.01 ± 0.51	19.19 ± 0.34	27.72 ± 0.67					
Bacillus cereus (10 ⁶)	$1.79 \pm 0.05^{\ a}$	21.00 ± 0.55 ^a	32.06 ± 0.63^{a}	S	S	S	S					
Bacillus cereus (10 ⁶) + Lactobacillus plantarum	1.63 ± 0.03 ^b	$5.54\pm0.28^{\ ab}$	10.25 ± 0.36^{ab}	14.39 ± 0.33	17.26 ± 0.36	19.93 ± 0.47	29.67 ± 1.41					
Escherichia. coli (10 ⁶)	$2.09\pm0.07^{\ a}$	21.66 ± 0.66^{a}	32.95 ± 0.53^{a}	S	S	S	S					
Escherichiacoli (10 ⁶) + Lactobacillus plantarum	$1.78\pm0.04^{\ b}$	$6.10\pm0.10^{\ ab}$	10.93 ± 0.33^{ab}	15.06 ± 0.59	18.20 ± 0.39	20.88 ± 0.61	32.95 ± 0.53					

Table 4. Effect of Lactobacillus plantarum on TVB-N of chicken sausage stored at 4°C

Data are presented as (Mean \pm S.E). S.E: Standard error, S: Spoilage depending on sensory evaluation. Significance at $p \le 0.05$. ^a Significant in the control group, ^b Significant within corresponding bacterial groups

Table 5.	Effect of	E Lactobacillus	plantarum o	on 🛛	Thiobarbituric	acid of	chicken	sausage	stored a	at refrigerated	temperature
4ºC.											

0	Storage period (day)											
Groups	1	3	6	9	12	15	18					
Control	0.05 ± 0.00	0.81 ± 0.03	1.07 ± 0.06	S	S	S	S					
Staphylococcus aureus (10 ⁶)	0.05 ± 0.00	0.90 ± 0.02	1.23 ± 0.07	S	S	S	S					
Staphylococcus aureus (10 ⁶) + Lactobacillus plantarum	0.04 ± 0.01	0.14 ± 0.02^{ab}	$0.32\pm0.04^{\ ab}$	0.49 ± 0.04	0.66 ± 0.04	0.81 ± 0.03	1.07 ± 0.06					
Bacillus cereus (10 ⁶)	0.06 ± 0.01	0.97 ± 0.04	1.37 ± 0.06^{a}	S	S	S	S					
Bacillus cereus (10 ⁶) + Lactobacillus . plantarum	0.05 ± 0.01	0.19 ± 0.03^{ab}	$0.40\pm0.06^{\ ab}$	0.57 ± 0.06	0.74 ± 0.04	0.88 ± 0.04	1.37 ± 0.06					
Escherichia coli (10 ⁶)	0.06 ± 0.01	$1.05\pm0.07^{\:a}$	1.34 ± 0.09^{a}	S	S	S	S					
Escherichia coli (10 ⁶) + Lactobacillus plantarum	0.05 ± 0.00	0.35 ± 0.14^{ab}	$0.53\pm0.05^{\ ab}$	0.64 ± 0.07	0.79 ± 0.05	1.00 ± 0.07	1.49 ± 0.07					

Data are presented as (Mean \pm S.E). S.E: Standard error, S: Spoilage depending on sensory evaluation. Significance at p \leq 0.05. ^a Significant in the control group, ^b Significant within corresponding bacterial groups

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Sensory evaluation

Sensory evaluation performed to assess the overall acceptability (odor, texture, and color) of chicken sausage during storage at 4°C is shown in Table 6. Results showed that there was a significant difference ($p \le 0.05$) between samples inoculated with pathogenic bacteria only and treated groups with *L. plantarum* on overall acceptability (odor, texture, and color). Inoculated pathogenic bacteria groups in the current study spoiled at day nine.

Over the refrigerated storage period, there was a significant difference ($p \le 0.05$) in overall acceptability values between the first group (control one) and groups inoculated with pathogenic bacteria and that inoculated with pathogenic bacteria and *L. Plantarum*. During storage, fermented chicken sausage became unaccepted or rejected in groups without *L. plantarum* at day 9 of storage and still acceptable in those treated with *L. plantarum* until day 18. Generally, all organoleptic data were in agreement with microbiological, physical, and chemical quality indices present in Tables 1, 2, 3, and 4. Changes in color, odor, and texture during refrigerated storage occurred due to lipid oxidation and protein degradation (Sirocchi et al., 2017). Changes can also be attributed to the ability of lactic acid bacteria to produce small organic substances prevent oxidation mechanism, so enhance the aroma and give specific organoleptic attributes of the products (Tagg et al., 1976). Consumers' demand for foods depends mainly on sensory attributes (Fernández-López et al., 2005). The current study results were in agreement with Slima et al. (2017) who used *L. plantarum* to evaluate the enhanced quality and safety of beef sausages stored at 4°C for 10 days.

Carrier			St	orage period (da	ay)		
Groups	1	3	6	9	12	15	18
Control	9.11 ± 0.14	6.44 ± 0.13	3.80 ± 0.21	R	R	R	R
Staphylococcus aureus (10 ⁶)	$8.44\pm0.21~^a$	6.44 ± 0.13	3.80 ± 0.21	R	R	R	R
Staphylococcus aureus (10 ⁶) + Lactobacillus plantarum	9.22 ± 0.18^{b}	8.70 ± 0.10^{ab}	7.23 ± 0.07^{ab}	6.91 ± 0.02^{ab}	$6.14\pm0.08^{\ ab}$	5.30 ± 0.14^{ab}	4.93 ± 0.18^{ab}
Bacillus cereus (10 ⁶)	9.01 ± 0.09	6.44 ± 0.13	3.47 ± 0.13	R	R	R	R
Bacillus cereus (10 ⁶) + Lactobacillus plantarum	9.06 ± 0.06	8.81 ± 0.04^{ab}	7.74 ± 0.10^{ab}	7.31 ± 0.12^{ab}	$6.84\pm0.06^{\ ab}$	$6.06\pm0.05^{\ ab}$	5.07 ± 0.09^{ab}
Escherichia coli (10 ⁶)	9.47 ± 0.20	6.10 ± 0.46	$2.80\pm0.39^{\rm \ a}$	R	R	R	R
Escherichia coli (10 ⁶) + Lactobacillus plantarum	9.22 ± 0.18	$8.70\pm0.10^{\ ab}$	$7.73\pm0.13^{\ ab}$	$6.91\pm0.02^{\ ab}$	$6.14\pm0.08^{\ ab}$	$5.30\pm0.14^{\ ab}$	4.62 ± 0.14^{ab}

Table 6. Effect of Lactobacillus plantarum on sensory attributes of chicken sausage stored at 4°C

Data are presented as (Mean \pm S.E). S.E: Standard error, R: Rejected depending on sensory evaluation. Significance at $p \le 0.05$.^a Significant in the control group, ^bSignificant within corresponding bacterial groups

CONCLUSION

Results of the present study revealed that *L. plantarum* has broad *in vitro* and *in vivo* antimicrobial effects against *S. aureus, B. cereus*, and *E. coli*. The use of *L. plantarum* in chicken sausage enhances shelf lifetime, physicochemical properties, sensory attributes, and safety until day 18, whereas infected groups inadmissible at day 9 of storage 4°C. It is recommended to use *L. plantarum* in fermented meat products as a starter and a bio-preservative to enhance the quality.

DECLARATION

Authors' contributions

Rasha Elsabagh designed the plan of study, revised the research article. Shaimaa M. Nada and Elsayed M. Abd-Elaaty analyzed the data, performed laboratory experiments, and drafted the manuscript. Rasha Elsabagh provided the experimental tools. All authors checked the statistical results and approved the final version of the article.

Competing interests

The authors declare no conflicts of interest.

Ethical considerations

Ethical issues (including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by the authors.

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SHORT COMMUNICATION

The Effect of the Different Artificial Insemination Time Periods on the Pregnancy Rate of Sapudi Ewes

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ABSTRACT

Artificial insemination is required to increase the reproduction rate in ruminant breeding. The artificial insemination success rate in sheep only reaches 47.6%, whereas the proposed ideal rate is 70%. One of the factors influencing the artificial insemination success rates in sheep is improper estrus detection, resulting in no fertilization. The present study aimed to determine the effect of different artificial insemination time periods on the pregnancy rates of Sapudi ewes. The research design was based on a completely randomized design. A total of 20 female Sapudi sheep were divided into four treatment groups with five repetitions (for each group). In addition, the observed variables were artificial insemination time in Sapudi ewes. Estrus synchronization in ewes was conducted by injecting PGF_{2a}. The results of the research indicated that ewes subjected to artificial insemination 6, 12, 18, and 24 hours after estrus had a pregnancy rate of 20%, 100%, 60%, and, 60%, respectively. It can be concluded that the time differences in artificial insemination significantly influence the pregnancy rate in Sapudi ewes'.

Keywords: Artificial insemination, Estrus, Pregnancy rate, Sapudi ewes

INTRODUCTION

Sapudi sheep is a family of native Indonesian sheep with the characteristics of a larger tail size than other sheep strains. This different characteristic provides benefits to farmers during the dry season, since Sapudi sheep can reserve energy in their tails (Tanziila, 2018). However, the big size of Sapudi sheep's tails is also one of the problematic factors to conduct natural mating. Therefore, human assistance is required to conduct artificial insemination in order to improve the reproduction rate (Hafez, 2000).

Artificial insemination is a reproductive bio-technique that relies on improving livestock genetic quality, controlling reproductive infectious diseases, and optimizing the reproductive appearance (Ramadhani, 2016). However, the insemination success rate of sheep only reaches 47.6%, whereas the ideal rate is believed to be 70% (Rizal, 2006). This situation can be affected by many factors, including the quality of the frozen semen which experiences a quality decrease after thawing, incorrect implementation of artificial insemination, and incorrect estrus detection which results in a fertilization failure (Abebe and Alemayehu, 2021). The estrus period detection is highly complicated to perform, which results in difficulties in determining the ovulation period (Miguel-Cruz et al., 2019). The length of ewes' estrus period is around 24-36 hours, and the sheep's ovulation period begins approximately 24-30 hours from the beginning of the estrus time (Miguel-Cruz et al., 2019). Determining the ovulation period is considered important for an exact time for artificial insemination (Ramadhani, 2016).

One of the alternative methods to overcome the problems above is conducting an estrus synchronization. Estrus synchronization is a method to hormonized insemination (insemination at the same time), within a short period of time, so can be estimated in animal models (Mirshamsollahi, 2016). As a result, livestock can be inseminated at the same time. The estrus synchronization commonly is achieved using prostaglandin F2a or PGF_{2a} hormone (Mirshamsollahi, 2016; Miguel-Cruz et al., 2019). The hormone acts by lysing the *corpus luteum*, which leads to a decreased level of the progesterone hormone (Ferrag et al., 2017). The low progesterone is followed by an FSH increase, which stimulates the development of matured follicles causing the heat in sheep (Stenbak et al., 2001). The PGF_{2a} hormones can only regress the active corpus luteum rather than starting or growing corpus luteum (Sudarmaji et al., 2004). The implementation of massive estrus synchronization will improve the reproductive efficiency of the livestock, optimize the artificial insemination implementation, and increase the group fertility (Sardi, 2011).

Pregnancy failure often occurs due to an inappropriate estrus detection, which results in incorrect artificial insemination time (Sigit et al., 2014). Based on the background above, the present study was done for determining the effects of insemination time on the pregnancy rate of Sapudi ewes.

MATERIAL AND METHODS

The research design in this study was a completely randomized design. The current study was conducted at Dinas Peternakan Provinsi Jawa Timur, Garahan, Jember from April to June 2017.

Ethical approval

All processes and experiments of the present study (*in vivo* and *in vitro*) were approved by the ethical committee of Universitas Airlangga.

Estrus detection and synchronization

This research comprised of 20 unfertilized Sapudi ewes, which were examined with Ultrasound guided (USG) device. Estrus detection was done using USG according to the method of Macías et al. (2017). The estrus synchronization is achieved by intramuscular administration of prostaglandin F2 α or PGF2 α at the dose of 7.5 mg/sheep. In addition, the PGF2 α injection in the current study was carried out twice to obtain simultaneous sheep estrus with an interval of 11 days. The sheep would be sexually excited two days after PGF_{2 α} injection (Srianto et al., 2010).

Artificial insemination

The artificial insemination was carried out by employing the frozen semen of Sapudi sheep obtained from Farm animal Institute, Universitas Airlangga of Indonesia. In addition, this research utilized 0.25 ml of mini straws with the concentration of each straw \pm 50x106 spermatozoa (Hardijanto et al., 2010). The number of straws was adjusted to the required spermatozoa concentration for artificial insemination on the ewes. Afterward, the straw was thawed on the water at room temperature for 30 seconds, and then it was inserted into the artificial insemination gun. Next, the straw tip was cut using a pair of scissors. After that, the plastic sheath was installed on an artificial insemination gun, which already contained the straw (Hardijanto et al., 2010).

The 20 ewe samples were divided into four groups. The artificial insemination in the first group was carried out 6 hours after the estrus occurred (P1). Meanwhile, artificial insemination in the second group was conducted 12 hours after the estrus was detected (P2). The artificial insemination of the third group was performed 18 hours after the sheep were in estrus (P3). Finally, the artificial insemination in the fourth group was carried out 24 hours after the estrus signs appeared (P4). Furthermore, the semen was sprayed in the area before the uterine cornua branch with a sperm concentration of approximately $\pm 50 \times 10^6$ on each spraying (Satiti et al., 2014). The ewes' pregnancy diagnosis was conducted when the pregnancy reached 60 days by employing Carelife portable USG device.

Data analysis

The research data were the pregnancy rate analyzed by using F-test or One-way Factorial ANOVA, and followed by Duncan's Multiple Range Test if there were differences in the ANOVA Factorial test (p < 0.05).

RESULTS

The pregnancy diagnosis of the examined Sapudi ewes was performed using a USG device with different artificial insemination times generated the pregnancy rate (Table 1). The results identified there was a significant difference between P1, where the artificial Insemination was conducted 6 hours after the initial estrus, and P2, where the artificial Insemination was administered 12 hours after the initial estrus, on the pregnancy success rate. On the other hand, the results obtained from P2, and from P3 where the artificial insemination was performed 18 hours after the initial estrus, were not significantly different in affecting the pregnancy success rate. Similarly, the results achieved from the P2 group and the P4 group where the artificial insemination was carried out 24 hours after the initial estrus, were not significantly different regarding the pregnancy success rate. As can be seen in Table 1, Sapudi ewes in P1 exhibited a pregnancy rate of 20%. Meanwhile, the ewes in P2 were fertilized 100% after being inseminated artificially 12 hours after the estrus. The artificial insemination conducted in Sapudi sheep 18 hours after the estrus (P3) resulted in the pregnancy rate of 60%. In addition, the pregnancy rates of the ewes artificially inseminated 24 hours after estrus (P4) amounted to 60%.

Table 1	1. Pregnancy	Rates of Sa	apudi Ewes [†]	with different	artificial	insemination	times
	0 1		1				

Group	Repetition	Pregnancy Rate (%)
P1	5	(20%) ^a
P2	5	(100%) ^b
P3	5	(60%) ^{ab}
P4	5	(60%) ^{ab}

P1: Artificial Insemination was conducted 6 hours after estrus, P2: Artificial Insemination was conducted 12 hours after estrus, P3: Artificial Insemination was conducted 18 hours after estrus, P4: Artificial Insemination was conducted 24 hours after estrus

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Figure 1. The result of Ultrasound-guided examination on Sapudi ewes 60 days after artificial insemination. A: Amniotic fluid is black, **B**: The fetus appears white in amniotic fluid

DISCUSSION

Findings demonstrated that the highest pregnancy rate appeared if the artificial insemination was carried out 12 hours (P2) after the estrus was detected. The results of pregnancy diagnosis employing USG device in Sapudi sheep is illustrated in Figure 1.

The PGF_{2 α} Injection was carried out on day 1 and day 11 with the same dose, according to Toelihere (1981), stating that PGF_{2 α} injection can be performed with one injection or two injections with an interval of 11-12 days. The PGF_{2 α} injection can lyse the corpus luteum, causing a follicular period process. It causes estrus and ovulation symptoms on the ewes. The ewes will be in estrus one to three days after the hormone treatment was administered (Martinez-Ros et al., 2018). Ewes indicate the signs of estrus if they keep bleating frequently, and it can be identified through the physical condition where transparent mucus comes from their genital organs, the vulva looks swollen, and the vulvar mucosa appears purplish-red and warm when touched. Moreover, if they are grouped with other ewes, they indicate standing heat (Martinez-Ros et al., 2018).

The high pregnancy success rate can be influenced by controlled estrus and the insemination time. The number of ovulatory follicles increases estrogen levels in serum, and this condition can prolong the estrus (Setiatin, 2015; Martinez-Ros et al., 2018). Estrus synchronization in ewes is carried out by injecting PGF2 α , which can lyse the corpus luteum, and cause a follicular period. These factors cause estrus and ovulation symptoms of the ewes. One to three days after being administered with hormonal treatment, the ewes will be in estrus (Martinez-Ros et al., 2018).

The artificial insemination conducted 12 hours after the initial estrus signs resulted in a higher pregnancy rate, compared to the other treatments (Table 1). It implies that the proper artificial insemination timing is 12 hours after the initial estrus signs are detected (Srianto et al., 2010). The ewes' estrus period is around 24-36 hours, and the ovulation period begins approximately 24-30 hours after the estrus (Srianto et al., 2010). The artificial insemination in the other treatments identified imperfect pregnancy results because, in the first treatment, where artificial insemination was conducted 6 hours after estrus, the fusion between spermatozoa and egg cells was too early. The spermatozoa cells can only survive in the female genital tract for 12-24 hours, while ovulation occurs 24- 30 hours after the initial estrus signs appear (Table 1). Hence, fertilization cannot occur. At the third treatment where the artificial insemination was conducted 18 hours after estrus, and the fourth treatment where the artificial insemination was conducted 24 hours after estrus, the pregnancy rate was lower. It occurred because the spermatozoa cells stayed in the female genital tract for 30 hours with a capacitation period of 1.5 hours in the oviduct (Bedford, 1970). Moreover, ovulation happens 24 hours after the initial estrus sign; therefore, the possibility of fertilization is not strong.

The samples of the experiment were limited to 20 ewes of productive age so that the expected value obtained was less than or equal to five (\leq 5). This fact might be caused by the feed given, the estrus time, the estrus period, and the

individual response of the Sapudi ewes to each different treatment. Each animal may respond differently to the treatment provided due to the livestock conditions and feed given (Toelihere, 1981; Thornton, 2010).

CONCLUSION

The difference in artificial insemination time influenced Sapudi sheep pregnancy rate. The highest pregnancy rate was obtained in the second treatment, namely Sapudi sheep, received artificial insemination 12 hours after estrus signs appeared. Therefore, the best time to carry out artificial insemination seems to be12 hours after the estrus signs were detected.

DECLARATION

Author's contribution

All authors had equal roles in conducting, writing, and editing the manuscript.

Competing interests

The author did not report any conflicts of interest in the current research.

Ethical considerations

Ethical issues (including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by the authors.

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Milk Production and Reproductive Performance of Retained and Culled Cows in a Large Holstein Herd in Egypt

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ABSTRACT

The study aimed to identify the culling reasons of Holstein cows raised in a large commercial herd in Egypt with emphasis on the performance of retained and culled cows. A total of 31534 complete lactation records for 10994 cows calved from 2008 to 2019 were used. The overall rate of culling per lactation was 61.1%. Involuntary culling represented 92% of all culling cases. The reasons for culling included mastitis and udder problems (24.2%), reproductive disorders (18.7%), metabolic and digestive disorders (13.6%), lameness (13%), endemic diseases (10.8%), low milk yield (8.1%), respiratory diseases (4.3%) and unknown causes (7.3%). Means of 305-day milk yield and daily milk yield were significantly lower in culled cows than the retained ones. On the other hand, no significant differences were observed between culled and retained cows for days open and the number of services/conception. The high involuntary culling rate of Holstein under the Egyptian conditions revealed that management practices regarding mastitis prevention and reproductive efficiency should be improved.



Keywords: Culling reasons, Egypt, Holstein, Milk production, Reproductive performance

INTRODUCTION

Culling refers to the process of removing animals from the herd. Culling could be voluntary due to low milk production or sale of excess animals or could be involuntary, as a result of illness, injury, infertility, or death. Both types of culling are applied to keep herd economics high. However, a high rate of involuntary culling reduces the herd profit, particularly for high-yielding cows. Replacement of heifers necessitates replacing culled cows. which adds a financial load on the dairy unit where rearing replacement of heifers represents about 20% of total variable costs (Karszes, 2014).

Culling strategies vary from one farm to another. These strategies can be also modified within the same farm over time. Culling decision is a complicated process since one should consider the price of culled cows, availability of replacement heifers within the farm, and the cost of rearing replacement heifers. Pinedo et al. (2010) studied cows calved between 2001 and 2006 in the Eastern United States and found that the main culling causes were death (20.6%), reproductive problems (17.7%), injury/other (14.3%), low production, and mastitis (12.1% for each). However, in the Polish population of Holstein, Adamczyk et al. (2017) found that the primary reasons for culling were reproductive disorders (39.6%) and udder problems (15.5%). In Spanish dairy cattle farms (2006-2016), Armengol and Fraile (2018) found that reproductive disorders were the most frequent reason for cow removal (30.2%), followed by low milk yield (23.4%), accidents (7.7%), diseases (7.2%), locomotor disorders (2.4%), and obstetrics (2.4%). Doornewaard et al. (2018) also stated that the main reasons for culling dairy cows in Wageningen, Netherland were reproduction failure, mastitis udder health, low production, and leg diseases. The rate of culling varies due to parity, stage of lactation, breed, and management strategies (Pinedo et al., 2014). De Vries (2017) reported that the rate of culling was within the range of 28-64%.

In Egypt, Holstein cattle are the main dairy cattle in commercial farms which supply the local market with milk stably and steadily. Egypt lies in the semi-arid subtropical zone where the temperature and humidity are high mainly in the summer season, besides, there are limited feed and water resources. Thus, dairy farms in Egypt have to pay for imported feeds and vaccinations and also for installing and maintaining cooling systems. These harsh conditions markedly increase culling rates, shorten Holstein's longevity, and rise the cost of raising replacement heifers. Breeding programs should take into consideration the way to diminish the causes of involuntary culling. Therefore, it is necessary to identify the reasons for culling Holstein cows raised in Egypt.

Although the performance of Holstein in Egypt has been intensively studied, few available reports are found concerning culling reasons, therefore, the objective of this study was to identify the culling reasons, as well as, investigating the performance of retained and culled cows in large Holstein herds in Egypt.

MATERIALS AND METHODS

Source of data

Data used in the present study were collected from Dina farm, one of the largest commercial dairy farms in Egypt. This farm is placed in the Menoufia governorate in northern Egypt. The geographical coordinates of the farm are 30.14°N, 30.33°E. The location is characterized by a subtropical climate with humid summers and relatively mild winters. Data of 38060 lactation records for 12259 Holstein cows were obtained from the herd management software of Dairy Comp 305 (Valley Ag Software, Tulare, CA). A total number of 31534 records of complete lactations for 10994 cows, calved from 2008 to 2019 were extracted from the whole data and used in the current study.

Herd management

Cows were housed in shaded free stall barns with a concrete floor. Heifers were served for the first time at about 370 kg body weight and frozen semen was used in insemination. Machine-milking three times/day was performed at eight-hour intervals and cows were dried off two months before the expected calving dates. The farm was provided with a cooling system. All cows were housed, fed, and milked under the same conditions and received the same management.

Studied traits

The productive traits: included the standard lactation length (305-dMY, kg) and daily milk yield (DMY, kg). The reproductive traits: included days open; the days from calving until conception (DO, days), and the number of services per conception for each cow (NSPC).

Data analysis

The statistical analysis was performed using the XLSTAT version 2020.3.1. The following model was applied to analyze productive and reproductive traits:

$$Y_{ijklm} = \mu + L_i + P_j + Y_k + S_l + (L_i X P_j) + b (x_{ijklm} - \bar{X}) + e_{ijklm}$$

Where, Y_{ijklm} is an observation of productive or reproductive trait, μ denotes the overall mean, L_i refers to the fixed effect of the ith longevity class, (i=1,2), 1 explains cows have subsequent record(s) (retained), and 2 means cows have no subsequent records (culled), P_j is the fixed effect of the jth parity order, (j = 1, 2,..., and 6), 1=1st, 2=2nd, 3=3rd, 4=4th, 5=5th and 6=6th, Y_k serves as the fixed effect of the kth period of calving, (k = 1, 2, 3), 1 = 2008-2011, 2 = 2012-2015, and 3 = 2016-2019, S₁ stands for the fixed effect of the season of calving (1 = 1, 2, 3, 4), 1 refers to Winter (December-February), 2 denotes Spring (March-May), 3 explains Summer (June-August) and 4 indicates Autumn (September-November), L_iXP_j is the interaction between longevity class and parity order, b accounts for the linear regression coefficient of the studied trait on age at first calving, x_{ijklm} shows the age at first calving, \bar{X} signifies the overall average of age at first calving (AFC, month), and e_{iiklm} is random residual effect.

All possible interactions were tested, but only the interaction between longevity class and parity order was significant, therefore, the used model included only this interaction.

RESULTS AND DISCUSSION

Culling rate per lactation

The numbers and percentages of retained and culled cows across parities are shown in Table 1. The overall average culling rate was high (61.1%). The semi-arid subtropical climate prevailing in the farm location, particularly in summer times, may cause heat stress as well as adverse fertility and milk production process, and encourage causes of various diseases. Haine et al. (2017) and Rilanto et al. (2020) reported lower culling rates (35% and 26.2%, respectively) than that obtained in the present study. Bahrampour et al. (2016) stated that culling risk was clear in warm, dry, and semi-arid regions, compared to temperate or cold and wet regions. Moreover, cows in large herd sizes are more exposed to be culled as a result of stressful mechanization, less individual care, and greater levels of physiological pressure. Jankowska et al. (2014) stated that culling rates were mainly high (92%) in herds keep > 100 cows.

The culling rate increased with the parity order until the fourth one (58.1%, 59.9%, 63.4%, and 68% in the first four parities). Culling rates in the fourth to the sixth parities were higher than those in the first to third parities. The high culling rate in older cows found in the present study was also declared by Mostafa (2009), Ansari-Lari et al. (2012), and Bahrampour et al. (2016). Old cows are more susceptible to culling since they gradually consume the energy reserve in

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their bodies during milk synthesis, and pregnancy as well as overcoming diseases until they become unable to continue in the herd.

Culling reasons across parities

Table 2 presents the culling reasons across parities. The involuntary reasons formed about 92% of total culling cases. Mastitis and udder problems, as well as reproductive disorders, were the primary reasons forcing to cull cows, representing about 43% of culling cases. The same results were reported by Ansari-Lari et al. (2012) although the overall value of culling was lower (17.5%). Metabolic and digestive disorders and lameness had almost the same contribution in culling cases (about 13%). Endemic diseases were responsible for one-tenth of culling cases, whereas culling due to respiratory diseases was the lowest (4.3%). Reproductive disorders were the primary reasons for culling in the first and second lactations indicating 27.2% and 21.5% of culling cases, respectively.

Regardless of the parity order, reproductive disorders represented the second main reason for culling in this study (18.7%). The same result was obtained by Boujenane (2017) and Karrar et al. (2017). They stated that reproductive disorders were responsible for 12.5-47% of culling cases. The high risk of culling due to reproduction failure in dairy cattle has increased throughout the world as a result of intensive selection for milk yield for decades. An increase in milk yield is accompanied by a reproduction decrease due to the negative correlation between production and reproduction (Knob et al., 2016). In the present study, the proportion of culling due to reproduction disorders decreased with the increase in parity number. It is similar to the finding of Armengol and Fraile (2018) who declared that the role of reproductive failure as a culling reason greatly decreased after the third lactation. This is because cows with reproductive problems are gradually excluded from the herd.

Mastitis and udder problems were the first reasons for culling in the third till the sixth parity. The culling due to mastitis and udder problems increased as the cows got older, representing one-third of total culling in the sixth parity. The increase of culling due to mastitis and udder problems with parities was also stated by Esslemont and Kossaibati (1997). The culling of cows infected with frequent mastitis aims to reduce the risk of new infections within the herd. Mastitis is not only accompanied by a reduction in milk yield and quality, but also by its negative effects on reproduction (Pinedo et al., 2016). As it is associated with long DO, high NSPC, decrease in conception rate, and increase in early abortion (Kumar et al., 2017). The change in percentage of culling due to low milk yield or respiratory diseases across parities was narrow. The percentage of culled cows due to metabolic and digestive disorders was almost constant throughout lactations, ranging from 13% to 15%. Metabolic disorders as a reason for culling were also reported by Chiumia et al. (2013) and Rilanto et al. (2020). High milk-producing cattle are challenged by high metabolism which could put stress on these cattle causing metabolic disorders.

Lameness is the second reason for culling in the fifth and sixth parities. It is highly related to the number of parity. Similarly, Egger-Danner et al. (2015) and Gross et al. (2016) reported lameness as a reason causing culling. In the present study, the overall percentage of culls that occurred due to lameness (13%) was higher than 9.9%, 3.5%, and 2% reported by Olechnowicz and Jaskowski (2011), Ansari-Lari et al. (2012), and Karrar et al. (2017), respectively. The high rate of lameness may be rooted in the high humidity in stall barns and poor hygienic conditions surrounding cows, where cows stand in the slurry for a time on the concrete floor. The increase of culling due to lameness in old cows was also observed by Olechnowicz and Jaskowski (2011). They reported that culling due to lameness increased from 3.5% in the first lactation to 9% in the seventh one. Lameness and locomotive disorders make cows unable to perform their daily activities. So, it negatively affects milk production and reproductive performance (Pinedo et al., 2016).

Endemic diseases are viral infectious diseases. They are represented by lumpy skin disease (LSD, 42%), bovine ephemeral fever (BEF, 39%), and foot and mouth disease (FMD, 19%). They recorded the greatest percentage (16.5%) in the first parity and reached the lowest in the sixth one (6.3%). The endemic diseases are one of the causes that raise the involuntary culling rates in dairy herds in endemic countries, compared with other countries as the case in the current study. Outbreaks of these diseases occur in summer when the weather is hot and humid. The LSD and BEF are transmitted by biting insects (Sprygin et al., 2019) and FMD is spread by contact, polluted farming equipment, vehicles, clothing, or feed, and by domestic and wild predators (Salam et al., 2015). They greatly cause economic losses due to decrease in milk yield and fertility, increase in abortions, and embryo losses as well as difficulty in animal movement, vaccination, and treatment cost, all in all, may sometimes cause mortality induced by secondary bacterial infections (Ahmed and Dessouki, 2013; Knight-Jones and Rushton, 2013). Although vaccination is obligatory in Egypt, outbreaks of LSD and FMD still occur. The vaccine used against LSD depends on using strains derived from sheep. It was confirmed that these strains are not effective enough to beat the virus (Allam et al., 2020). Moreover, with the import of animals from endemic African countries and the high mutation rate, there is a possibility to develop new strains of FMD that could resist the currently used vaccine. Until developing proper vaccines for endemic diseases, management procedures should prevent the spread of infections. Applying programs that include biosafety and insect control could help in reducing the infection rate.

	0	Parity												
Longevity class	(%)	First		Second		Third		Fourth		Fifth		Sixth		-
	(/0) -	Ν	%	Ν	%	Ν	%	Ν	%	Ν	%	Ν	%	Total
Retained	38.9	1583	41.9	1345	40.1	775	36.6	338	32	166	34.7	66	31.9	4273
Culled	61.1	2199	58.1	2009	59.9	1342	63.4	718	68	312	65.3	141	68.1	6721
Total	100	3782	100	3354	100	2117	100	1056	100	478	100	207	100	10994

Table 1. Numbers and percentages of retained and culled Holstein cows raised in a large herd in Egypt during 2008-2019

Table 2. Culling reasons across parities for Holstein cows raised in a large herd in Egypt during 2008-2019

	Overall	Parity												
Culling reason	average (%)	Fi	First		ond	Th	nird	Fou	ırth	Fifth		Si	xth	•
		Ν	%	Ν	%	Ν	%	Ν	%	Ν	%	Ν	%	Total
-Mastitis and udder problems	24.2	320	14.5	424	21.2	336	25.1	201	28.1	79	25.3	44	31.2	1404
-Reproductive disorders*	18.7	598	27.2	433	21.5	230	17.2	120	16.7	50	16.1	19	13.5	1450
-Metabolic & digestive disorders	13.6	289	13.1	285	14.3	176	13.1	95	13.2	41	13.2	21	14.8	907
-Lameness	13.0	178	8.1	188	9.3	162	12.1	83	11.5	55	17.6	27	19.2	693
-Endemic diseases**	10.8	362	16.5	246	12.2	129	9.6	82	11.4	27	8.6	9	6.3	855
-Respiratory diseases	4.3	110	5.1	83	4.2	62	4.6	32	4.4	16	5.2	3	2.3	306
-Unknown	7.3	179	8.1	174	8.6	129	9.6	44	6.2	18	5.7	8	5.6	552
Subtotal	91.9	2036	92.6	1833	91.3	1224	91.3	657	91.5	286	91.7	131	92.9	6167
-Low milk yield	8.1	163	7.4	176	8.7	118	8.7	61	8.5	26	8.3	10	7.1	554
Total	100	2199	100	2009	100	1342	100	718	100	312	100	141	100	6721

*Reproductive diseases included dystocia, metritis, pregnancy toxemia, uterus prolapse, uterus adhesion, and repeat breeder. **Endemic diseases included lumpy skin disease (LSD), Bovine ephemeral fever (BEF), and Foot and mouth disease (FMD)

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		305-di	МҮ	DM	IY	DO)	NSPC		
Classification	Ν	LSM	SE	LSM	SE	LSM	SE	LSM	SE	
Overall mean	10994	9321	28	26.2	0.05	161	1.0	3.4	0.03	
Longevity class		***		**	***		NS		S	
Retained	4273	9465 b	49	26.4 b	0.12	162 a	2.7	3.5 a	0.07	
Culled	6721	9177 a	29	26.1 a	0.09	160 a	2.0	3.4 a	0.05	
Parity order		***	:	**	*	**	*	**	**	
1	3782	9063 a	28	27.9 b	0.09	216 d	1.9	4.6 d	0.05	
2	3354	9080 a	26	25.9 a	0.08	183 c	1.8	4.0 c	0.05	
3	2117	9308 b	33	25.8 a	0.10	163 b	2.2	3.6 b	0.06	
4	1056	9364 bc	109	26.2 a	0.15	141 a	3.4	3.0 a	0.09	
5	478	9509 с	49	26.2 a	0.22	140 a	4.9	3.0 a	0.13	
6	207	9605 c	71	25.7 a	0.34	124 a	7.5	2.5 a	0.20	
Period of calving		***	:	***		***		***		
2008-2011	1833	9163 a	40	25.7 a	0.12	168 b	2.8	3.2 a	0.07	
2012-2015	4620	9270 b	29	25.8 a	0.09	177 a	2.0	4.0 b	0.05	
2016-2019	4541	9530 c	36	27.3 b	0.11	138 c	2.5	3.1 a	0.06	
Season of calving		***	:	**	*	**	*	**	:*	
Winter	2873	9192 a	35	25.9 a	0.11	163 b	2.4	3.4 b	0.06	
Spring	2350	9266 a	36	25.9 a	0.11	174 c	2.5	3.8 c	0.06	
Summer	2535	9393 b	35	26.5 b	0.11	160 b	2.5	3.5 b	0.06	
Autumn	3236	9435 b	36	26.7 b	0.11	147 a	2.3	3.0 a	0.06	
Longevity class X Parity		***	:	**	*	**	*	**	:*	
Reg. on AFC		***	:	**	k	**	*	*	*	

Table 3. Least squares means of productive and reproductive traits for retained and culled Holstein cows raised in a large herd in Egypt during 2008-2019

LSM: Least squares means, SE: Standard error, 305-dMY: 305-day milk yield, DMY: Daily milk yield, DO: Days open, NSPC: Number of services per conception, AFC: age at first calving. Within each classification in the same column means followed by different letters differ significantly, **: (p < 0.001) and ***: (p < 0.0001).

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Milk production and reproductive performance of retained and culled cows

According to Table 3, culled cows recorded significantly lower means of 305-dMY and DMY than retained ones (p < 0.0001). All productive and reproductive traits were significantly affected by parity order (p < 0.0001). Primiparous cows recorded the lowest values of 305-dMY (9063 kg), then the value increased gradually till reached 9605 kg at the sixth lactation. The DMY decreased by an increase in parity, the primiparous had the highest value (27.9 kg/day), compared to those in the other parities. The effect of year and season of calving and the regression on age at first calving were significant on all investigated productive and reproductive traits.

Although the productive performance of culled cows was significantly lower than retained ones (Table 3), there were no significant differences in either DO or NSPC. Kalantari and Cabrera (2015) proposed that the relationship between infertility level and farm economics may not be linear and many aspects are included when estimating the losses. Moreover, the increase in NSPC and DO which result in longer calving intervals may lead to prolonged lactations as it is a herd management approach followed in the intensive dairy system in hot regions (Flores et al., 2019). The reason is that the hot climate adversely affects the conception rate and more services are needed for conception (Mellado et al., 2016). In this case, extending the calving interval may not negatively influence the profits of the farm (Inchaisri et al., 2011). Conversely, the extension of calving intervals may offer economic advantages and permits the herd managers an option for decisions regarding high-yielder cows having reproductive disorders. This could reduce the involuntary cow culling (Rodríguez-Godina et al., 2021). With the progress of parity, lower NSPC and shorter DO were recorded which was similar to the results reported by Wondossen et al. (2018). This may explain the decrease in the proportion of cows culled due to reproductive disorders with the increase of parity number. Wondossen et al. (2018) attributed the longer DO in younger cows to the requirements needed for maintenance, growth, and milk production at an early age.

The interaction effect of longevity \times parity order

Effects of longevity class × parity on productive and reproductive traits are presented in Figures 1-4. In the first parity, significant differences appear clearly between retained and culled cows for all the studied traits. Figure 1 shows that values of 305-dMY of retained cows were higher than those of culled ones in all parities except for the sixth one. The same trend is also displayed in Figure 2 for DMY. Figures 3 and 4 show the traits of DO and NSPC, respectively. Their values were both significantly higher in the first parity in culled cows, compared to the retained ones (p < 0.0001). Their values became almost similar in the subsequent lactations compared to retained ones. Significantly greater values of DO and NSPC in culled cows were also reported by Mostafa (2009). Moreover, it is observed that curves for both productive (Figures 1 and 2) and reproductive traits (Figures 3 and 4) belonging to retained cows show more fluctuations than curves of culled cows. This may express the effort done by retained cows to overcome challenges using different internal mechanisms to keep their performance high. So, Adriaens et al. (2021) reported that perturbation in production curves is a good approach to measure how cows respond to challenges.



Figure 1. The interaction effect of longevity class x parity order on 305-day milk yield of Holstein cows raised in a large herd in Egypt during 2008-2019

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Figure 2. The interaction effect of longevity class \times parity order on daily milk yield of Holstein cows raised in a large herd in Egypt during 2008-2019



Figure 3. The interaction effect of longevity class \times parity order on days open of Holstein cows raised in a large herd in Egypt during 2008-2019



Figure 4. The interaction effect of longevity class \times parity order on the number of services per conception of Holstein cow raised in a large herd in Egypt during 2008-2019

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CONCLUSION

In Egypt, the culling rate for Holstein cows was higher than expected. Mastitis and udder problems and reproductive disorders were the primary causes for involuntary culling. Milk production performance of culled cows was significantly lower than that of retained ones. However, there was no significant difference between retained and culled cows regarding reproductive performance. To reduce the culling rate, it is important to set management programs that include good farming practices for mastitis prevention and improvement of reproductive efficiency.

DECLARATIONS

Authors' contribution

Nadia H. Fahim analyzed the results and wrote the manuscript, M. A. M. Ibrahim performed the statistical analysis, A. H. Amin collected the data and R. R. Sadek suggested the topic and revised the manuscript.

Competing interests

The authors certify that there is no conflict of interest.

Ethical consideration

Ethical issues (including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by all the authors.

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The Effects of Borax (NA₂B₄O₇10H₂O) on Histopathology of Wistar Rats' Cerebrum (*Rattus norvegicus*)

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ABSTRACT

The present study aimed to determine the effects of borax ($Na_2B_4O_7.10H_2O$) addition on the changes of histological cerebrum imaging in the brains of white mice (*Rattus norvegicus*). The current research was an experimental study with randomization of 24 white mice that were divided into four treatment groups with five replications. Borax was dissolved for each treatment with a dose of 19 mg/mouse/day, 26 mg/mouse/day, and 37 mg/mouse/day, and it was administered orally for 14 days. Then, it was analyzed statistically using the Kruskal-Wallis test. The statistical analysis results suggested that there were significantly different results in each treatment group. The control treatment with an administration dose of 26 mg/rat/day had a significantly different result in the worst cloudy swelling degeneration of cerebrum in histopathology imaging on Wistar rats (*Rattus norvegicus*). Using the Mann-Whitney test, it was found that the dose of borax at 37 mg/rat/day led to significant difference, compared to the other treatment groups, which means that 37 mg/rat/day of borax caused the worst pyramidal cell necrosis in histopathology imaging of the cerebrum on white mice. Borax exposure on Wistar rats (*Rattus norvegicus*) can cause cloudy swelling at a dose of 26mg/head/day, and pyramidal cell necrosis at a dose of 37 mg/head/day.

Keywords: Borax, Cerebrum, Cloudy swelling, Necrosis

INTRODUCTION

Borax is a component of many detergents, cosmetics, and enamel glazes. It is used to make buffer solutions in biochemistry, as a fire retardant, as an anti-fungal compound, in the manufacture of fiberglass, as a flux in metallurgy, neutron-capture shields for radioactive sources, a texturing agent in cooking, as a cross-linking agent in slime, as an alkali in photographic developers, as a precursor for other boron compounds, and is useful as an insecticide (similarly to boric acid, Levy and Lisensky, 1978). The use of borax on a large scale as a food preservative can be profitable in terms of production since borax can be purchased at a relatively cheap price. However, the negative impact resulting from excessive use can cause health problems. Borax is used excessively as preservatives in the food-making process of some foods, such as in *bakso*, noodles, and dumplings (Sugiyatmi, 2015). In a small amount, borax can create a chewy effect in the food, making the food stickier, long-lasting, and feel tasty. Compared to other preservatives, borax can maintain the food texture, which results in the longer maintenance of food without any change in chewiness and appearance. Borax can also maintain acidity causing the food not to spoil quickly.

The use of borax on a large scale as a food preservative can certainly be profitable in production since borax can be purchased at a relatively cheap price, compared to other harmless preservatives. In fact, even non-hazardous preservatives must be used in the right dosage. Borax even needs more cautious treatment since people cannot estimate the dosage used as a food preservative (Meacham et al., 2010).

The direct danger caused by the excessive use of borax or the residual left can have a systemic impact on the body (Dourson et al., 1998). Visible effects of borax include skin hardening or dead skin. The more dangerous effects of borax include making damage to the liver, stomach, small intestine, large intestine, testicular, and ovarian organ infertility, and it stimulates cancer cell growth (Nasution, 2009). Borax attacks cells, especially in the mitochondria, and it is accumulated in the cytoplasm and can disturb the cells' metabolism function. The study aimed to determine the effects of borax (Na₂B₄O₇.10H₂O) addition on the changes of the histological imaging of cerebrum in Wistar rats' brains (*Rattus norvegicus*).

MATERIALS AND METHODS

Ethical approval

All experimental protocols and procedures were approved by the Institutional Animal Care of Indonesia. The present research was conducted in experimental animal cages in the Faculty of Veterinary of Universitas Airlangga in Indonesia. The making of histopathological preparations of mice brains was carried out at the Veterinary Pathology Laboratory of the Faculty of Veterinary of Universitas Airlangga.

Research material

The experimental animals used in the current research were 24 healthy male Wistar rats (*Rattus norvegicus*) aged 1.5 months old and weighed approximately 100 grams. The rats were obtained from the Faculty of Medicine, Universitas Airlangga, Indonesia. The equipment used in the current study included 40 cm \times 25 cm \times 12 cm plastic cages, wire mesh for cage cover, feeding and drinking places, digital scales, feeding needles, surgical scissors, sterile scalpel, sterile tweezer, object glass, cover glass, tray as a container, small pot, lid as organ storage, Bunsen burner, oven, aluminum foil, microtome, staining jar, refrigerator, camera, and Eclipse C® 140 with NIS application (Nikon imaging system) BR40. The materials of the current study consisted of borax (Na₂B₄O₇.10H₂O) obtained from a chemical store on Jalan Tidar (Surabaya), sterile aqua dest as a borax solvent, 511 pellet chicken feed from PT Charoen Pokphand (Surabaya), drinking water, husk as the base for an individual cage, sterile cotton, ketamine, and 10% formalin.

Research design

The current study employed a laboratory experimental method. The research design used was a completely randomized design of various borax doses of 19 mg/rat/day, 26 mg/rat/day, and 37 mg/rat/day (Wagner and Wolff, 1976). The treatment groups were defined as P0 including Wistar rats treated with 0.5 ml/rat/day sterile aqua dest, P1 entailing Wistar rats treated with 0.5 ml/rat/day sterile aquadest + 19 mg/mouse/day borax, P2 having Wistar rats treated with 0.5 ml/rat/day sterile aquadest + 26 mg/mouse/day borax, and P3 including Wistar rats treated with 0.5 ml/rat/day sterile aquadest + 37 mg/mouse/day borax.

On day 15 of the experiment, the rats were intramuscularly anesthetized using ketamine. After that, fixation and dissection were conducted to separate the cerebrum from the brain organ. Furthermore, the pathology of anatomy was observed and histopathology preparation of the cerebrum was performed. The observed changes on the histopathologic imaging included cloudy swelling and pyramidal cell necrosis aspects (Sairazi et al., 2017). The damage level scoring (cloudy swelling and necrosis degenerations) in one visual field can be seen in Table 1 as follows (Purnima et al., 2013):

Score	Degeneration	Necrosis
0	If the degenerative cloudy swelling of the pyramidal cell was not found at a third of the observed visual field of the cerebrum.	If the pyramidal cell necrosis was not found at a third of the observed the visual field of the cerebrum.
1	If the cloudy swelling degeneration of the pyramidal cell was found at a third of the observed visual field of the cerebrum.	If the pyramidal cell necrosis was found at a third of the observed visual field of cerebrum.
2	If the cloudy swelling degeneration of the pyramidal cell was found at a third until two-third of the observed visual field of the cerebrum.	If the pyramidal cell necrosis was found at a third until two-third of the observed power field of the cerebrum.
3	If the cloudy swelling degeneration of the Pyramidal cell was found at two-third until the whole of the observed visual field of the cerebrum.	If the pyramidal cell necrosis was found at two-third until the whole of the observed power field of the cerebrum.

Table 1. Histopathological scoring of Borax exposure in the cerebrum of rats

Data analysis

The present study was analyzed using the Kruskal-Wallis test (p < 0.05). If significant differences were found, it would be continued with the Mann-Whitney test (Purnima et al., 2013).

RESULTS

The results of statistical analysis with the Kruskal-Wallis test suggested that there was a significantly different cloudy swelling degeneration in each treatment group (p < 0.05). Based on the results of statistical analysis with the Kruskal-

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Wallis test, it was found that there were significantly different results in each treatment group (p < 0.05). In the Mann-Whitney test, it was found that P0, P1, and P3 were not significantly different statistically; values of P0 and P2 were significantly different; values of P1, P2, and P3 were not significantly different (p > 0.05); and values of P2 and P3 were not significantly different either (p > 0.05). In Table 2, it was identified that most cloudy swelling degeneration occurred in P2, whereas, the pyramidal cell that had cloudy swelling degeneration was hardly found in P3, whom the highest dose was used since more than two-thirds of the whole of the pyramidal cell had necrosis in one visual field of the Wistar rats.

Meanwhile, the results of the statistical analysis of the Kruskal-Wallis test indicated that there were significantly different results of necrosis in the pyramidal cell of Wistar rats' cerebrum in each treatment group. Regarding the Mann-Whitney test, P3 was significantly different (p<0.05), compared to the whole treatment groups. An insignificant difference (p > 0.05) only occurred in P1 and P2.

Table 2. Histopathological Imaging Analysis of the Cloudy Swelling Level and Necrosis of the pyramidal Cell of Cerebrum in each treatment group of Wistar rat (*Rattus norvegicus*)

Treatment	Cloudy Swelling Degeneration Mean ± SD	Necrosis Mean ± SD
P0: Control of 0.5ml/rat/day sterile aquadest	0. $10^{a} \pm 0$	$1^a \pm 0$
P1: 0.5 sterile aquadest + 19 mg/rat/day borax	$0.33^{abc} \pm 0.516$	$1.5^{b} \pm 0.54$
P2: 0.5 sterile aquadest + 26 mg/rat/day borax	$0.83^{\circ} \pm 0.408$	$1.5^{\rm bc} \pm 0.548$
P3: 0.5 sterile aquadest + 37 mg/rat/day borax	$0.38^{\rm acd} \pm 0.495$	$1.63^{d} \pm 0.71$

Different superscript in the same column indicates that there were significant differences (p < 0.05), SD: Standard deviation

DISCUSSION

Brain damage caused by borax exposure can pass through various pathophysiological ways. Borax which is orally got into the stomach would react with hydrochloric acid (HCl) causing faster synthesis to become boric acid (Sugiyatmi, 2015). Furthermore, the boric acid would be absorbed by the intestines, then it gets into the blood circulation until reaching the organs, and causes some damages including brain damage.

Boric acid attacks cells from the body's systemic process, especially mitochondria (Dourson et al., 1998). Normally, mitochondria function to produce energy for cell activities through the oxidative phosphorylation process (Nielsen, 1994; Pizzorno, 2015). Boric acid will inhibit H^+ ion that makes a co-enzyme bound between NAD⁺ and H^+ ion. The H+ ion which bounds with boric acid will cause the failure of reduction-oxidation reaction in mitochondria (Litovitz et al., 1988). In addition, boric acid is bounded with proteins and lipids causing malfunction and forming Reactive Oxygen Species (ROS, Tanaka et al., 2016). The failure of reduction-oxidation reaction in mitochondria and the increase of ROS can cause a decrease in neuron cell viability caused by the inhibition of the electron transport chain. That process could disturb Adenosine triphosphate (ATP) formation that causes cell degeneration or even necrosis. The ATP is required for the fluency of sodium (NA⁺) and potassium (K⁺) pumps.

The mechanism of the sodium-potassium pump's disturbance starts with the shifting of sodium ion. Then, H_2O and calcium (Ca⁺) get into the cell, while potassium and magnesium (Mg+) move out from the cell increasing the intracellular fluid influx, changes of the cell form, and acute cell swelling (Price and Wilson, 1986). The process of cloudy swelling degeneration occurs due to the failure of ATP formation as the implication of mitochondria function experiencing energy synthesis disturbance (Jamison, 1974). The failure of energy synthesis is caused by the boric acid and co-enzyme bond of NAD⁺ and H⁺ ion. Therefore, it inhibits the sodium-potassium pump to maintain intracellular stability. The cells which are supposed to release metabolic energy to pump sodium ion out of the cells cannot function properly. This situation increases sodium ion concentration inside the cells followed by water entrance causing cell inflammation and cloudy cytoplasm. If the influence of toxic substances can be removed, the cell would return to its normal situation (Nielsen, 1994).

Necrosis is the cell destruction caused by pathological damage, such as toxin exposure (Kumar, 2007). Some biochemical mechanisms of necrosis include ATP depletion, oxygen deprivation, or the formation of Reactivated Oxygen Species, the loss of calcium homeostasis, the defect in plasma membrane permeability, and mitochondrial damage (Heindel et al., 1992). The cerebrum pyramidal cell necrosis of the Wistar rats' brains with borax exposure started with boric acid and co-enzyme bound of NAD⁺ and H⁺ ion. It led to the failure of a reduction-oxidation reaction inside the mitochondria (Nielsen, 1994). The manifestations of failure in mitochondrial function would disturb glycolysis, energy synthesis, and ATP formation. The ATP is required to ease the sodium-potassium pump. If ATP formation is obstructed, water accumulation will occur inside the cytoplasm since sodium absorbs water. Next, cloudy swelling occurs in the cell. Extended and continuous effects of toxic substances make the cell unable to metabolize resulting in cell death or necrosis (Price and Wilson, 1986).

Extended cell degeneration disruption and the relatively large effect of toxic substances in cells will surpass the interference compensation limit causing necrosis to take place. Necrosis is marked by the morphological changes of the cell nucleus, including pyknosis, karyorrhexis, and karyolysis. Pyknosis is the depreciation and compaction process of the cell nucleus causing it to be more basophilic with bluer cell color with H & E coloring. Microscopically, it was marked by the cell nucleus looking more compact and darker. Karyorrhexis is marked by the spread of broken nucleus and chromatin fragments formation, while karyolysis is marked by the nucleus dissolution (Kumar, 2007). Necrosis process also increases the bloodstream, and is followed by capillary vasodilation that occurs actively inside the microcirculation. Cell swelling around the capillary will press and cause lumen narrowing, causing the blood unable to stream smoothly, commonly referred to as congestion (Bezabeh et al., 2004).

In imaging pyramidal cells of the cerebrum caused by borax exposure, the cells experienced widespread necrosis that caused systemic damage or cell injury around it, followed by an inflammatory reaction. The capillary was blocked by cell inflammation-causing blood vessel dilatation, followed by increasing blood amount. In this stage, the erythrocytes would accumulate in the capillary as congestion. If the capillary is broken, it will be followed by the spread of erythrocytes around the cell, resulting in hyperemia (Bezabeh et al., 2004). Borax can also cause brain, heart, fat, and kidney disturbance. In addition, borax can cause comma, central nervous system disruption, depression, and even mortality (Murray, 1998). The exposure of 20.8 mg/kg BW of borax in Wistar rats for 14 days increased the dehydrogenase inside the cerebrum (Parks and Edwards, 2005). Histologically, degeneration, congestion edema in the brain, meninges, perivascular hemorrhage, and intravascular thrombosis may occur.

CONCLUSION

Borax addition can cause cerebrum cloudy swelling on Wistar rats (*Rattus norvegicus*) at the dose of 26 mg/rat/day. Meanwhile, borax addition at the dose of 37 mg/rat/day can cause necrosis in the pyramidal cells of Wistar rats' cerebrum.

DECLARATION

Authors' contribution

All authors contributed equally to conduct this study.

Competing interest

The authors declare that there are no conflicts of interest regarding the publication of this manuscript.

Ethical considerations

Ethical issues (including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by the authors.

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Evaluation of Milk Yield and Reproductive Performance of Pure Holstein and Its F1 Crossbreds with Montbeliarde in Egypt

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ABSTRACT

The present study was carried out to compare the milk yield and reproductive performance of pure Holstein (HO) cows with those of their first generation (F1) crossbreds with Montbeliarde cows (MO) in four commercial dairy herds under Egyptian conditions. Data used in the current study comprised 2268 records for the first four lactations of 531 HO and 536 MO × HO F1 crossbred cows during the period between 2012 and 2020. Data were analyzed using the least squares method by XLSTAT software. The MO × HO crossbred cows were significantly superior compared with pure HO cows for 305-day milk yield, scoring 9210 ± 96 kg versus 7987 ± 149 kg. Moreover, MO × HO F1 crossbred cows had a significantly higher daily milk yield (30.0 ± 0.45 kg) than pure HO cows (25.9 ± 0.52 kg). However, pure HO cows had significantly greater days in milk (399 ± 6 days) than MO × HO crossbred cows (341 ± 5.2 days). With regard to reproductive performance, MO × HO F1 crossbred cows had significantly less number of services per conception and days open than pure HO cows (2.6 ± 0.16 vs. 3.7 ± 0.18) and (132 ± 5.2 days vs. 190 ± 6 days), respectively. However, the statistical difference between MO × HO F1 crossbred cows and pure HO cows for age at first calving was not significant (22.9 ± 0.11 vs. 23.1 ± 0.15 months, respectively). It can be concluded that under Egyptian subtropical conditions, the first generation of MO × HO crossbred cows exhibit better performance, compared to pure HO cows in milk yield and reproductive traits. These findings could provide an effective strategic option for the genetic improvement of dairy cattle in hot subtropical regions.

Keywords: Crossbreeding, Egypt, Holstein, Milk Yield, Montbeliarde, Reproduction

INTRODUCTION

Over the last decades, worldwide milk production has been dominated by the Holstein (HO) breed due to the intensive continuous selection for milk production (Heins et al., 2012). However, the superiority in milk production had direct negative effects on other functional traits related to survival and reproduction as a result of consistent increases of inbreeding leading to higher rates of culling and reduction of profitability (Heins et al., 2012; Puppel et al., 2018).

To overcome these challenges, dairy cattle holders have tended to use the crossbreeding between pure Holstein and other dairy breeds. Crossbreeding dairy breeds may be a feasible way to achieve significant improvement in milk yield, fertility, and health characteristics more quickly than pure breeding (Dezetter et al., 2017). Crossbreeding seeks to take advantage of positive heterosis effects and complementarity between dairy breeds by introducing the desirable genes and decreasing the rate of inbreeding (Sørensen et al., 2008; Knob et al., 2020; Clasen et al., 2021).

Several previous studies have been conducted to compare the performance of pure Holstein with their first generation (F1) crosses, including HO × Simmental cows (Knob et al., 2020; Knob et al., 2021), HO ×Viking Red cattle (Hazel et al., 2017a), HO × Nordic Red cattle (Clasen et al., 2018), HO × Jersey cows (Prendiville et al., 2010), and HO × Brown Swiss (Blöttner et al., 2011; El-Tarabany et al., 2016). These studies had shown positive outcomes of crossbred cows compared with pure HO cows especially for fertility, health, and survival traits with the possibility to increase the rate of genetic gain for these economically valuable traits (Shonka-Martin et al., 2019; Clasen et al., 2021).

Recently, the Montbeliarde (MO) breed has received considerable interest as the best complement with Holstein in crossbreeding programs (Hazel et al., 2017a). Montbeliarde is a French breed that was subjected to heavy selection for fertility, health traits, body condition, and milk quality traits (Heins and Hansen, 2012; Hazel et al., 2017a). Numerous comparative studies have been conducted between pure HO and MO \times HO crossbreds to assess their productive and reproductive performances. The productive traits in terms of milk, fat, and protein yields were very close between the two genetic groups with slightly higher estimates for pure HO cows (Hazel et al., 2013; Buckley et al., 2014; Hazel et al., 2014).

However, MO × HO crossbred cows revealed superiority compared to pure HO cows for fertility traits in terms of first-service conception rates, days open, days to first breeding, and a number of services per conception (Hazel et al., 2014; Hazel et al., 2017a). Likewise, MO × HO crossbred cows had advantages over pure HO cows for survival traits, including survival of subsequent calving and mortality rates (Heins et al., 2012; Hazel et al., 2014; Hazel et al., 2017a). Consequently, MO × HO crossbred cows had greater longevity and lower total health cost per cow than pure HO cows which means greater profitability for crossbreds. Furthermore, the calves resulted from the mating of Montbeliarde sires with Holstein dams had significantly greater birth weight than calves from pure HO with no significant increase in calving difficulty and stillbirth rate (Heins et al., 2010). Also, milk from MO × HO crossbred cows exhibits a lower somatic cell score compared with milk from pure HO cows (Heins and Hansen, 2012).

In Egypt, the performance of HO and its crosses with different breeds has been intensively studied (Ibrahim et al., 2009; Rushdi, 2015; El-Tarabany et al., 2016). But, no available studies were found concerning the milk yield or reproductive traits on $MO \times HO$ crosses. Therefore, this work is considered the first study on the Montbeliarde cows in Egypt. The objective was to compare the milk yield and reproductive performance of pure Holstein cows with those of first generation crossbreds of Montbeliarde with Holstein cows in four commercial dairy herds in Egypt.

MATERIALS AND METHODS

Ethical approval

The study was carried out with existing records from four commercial dairy herds and did not involve animal handling.

Data collection

Data of productive and reproductive traits used in the current study were collected from 2268 records for the first four lactations of 531 pure HO and 536 first generation crossbred MO × HO cows. These records covered the period from 2012 to 2020. Pure Ho cows were daughters of 42 sires, whereas, MO × HO crossbred cows were daughters of 23 Montbeliarde sires. Cows in this study either pure HO or MO × HO crossbred were generated from artificial insemination (AI) proven bulls from the United States for both HO and MO breeds mated to locally born pure Holstein dams. The locally born HO cows originated from European HO dams. Data used were provided from four commercial dairy herds where pure HO and MO × HO crossbred cows were kept together all the time. These herds were located at four different governorates namely (herd one: Helaly farm, Dakahlia governorate, herd two: Osama Nigm farm, Gharbia governorate, herd three: Elyosr farm, Ismailia governorate, and herd four: Shash farm, Sharkia governorate). Table 1 indicates the distribution of the two genotypes among the four herds. All the data for the four herds were entered using Dairy Live 0.3 software (Version, 5.208A, USA) manually by the managers and owners.

		8 8		
Herd	НО	$MO \times HO$	Total	
Helaly farm, Dakahlia governorate	25	64	89	
Osama Nigm farm, Gharbia governorate	64	73	137	
Elyosr farm, Ismailia governorate	412	270	682	
Shash farm, Sharkia governorate	30	129	159	

531

536

106

Table 1. Distribution of Holstein cows and Montbeliarde × Holstein F1 crossbred cows among the four herds

HO: Holstein cows, MO × HO: Montbeliarde × Holstein F1 crossbred cows

Herd management

Total

All cows in the four herds were fed an *ad libitum* total mixed ration (TMR) diet consisting of 50 % forage and 50 % concentrate and was adjusted monthly to account for dry matter. The ingredients consist of corn silage, Alfalfa hay or Egyptian clover, soybean meals, ground corn, vitamins and minerals, yeast, and other additives. Cows were fed 4-5 times a day by a TMR mixer. Cows were machine milked three times per day and housed in open yards equipped with a cooling system in groups depending on milk production level and lactation number. Automated recording of milk yield was conducted on daily basis to calculate the aggregated total milk production for each cow. Cows were dried off two months before the expected calving dates. The crossbred heifers have inseminated artificially for the first time when reached 12-13 months and 350-370 Kg. The pregnant cows were determined via ultrasound at 28-33 days after insemination, follow-up confirmation via rectal palpation at approximately 60 and 100 days after inseminated.

Studied traits

The milk yield traits were total milk yield (TMY, kg) calculated by the cumulated amount of milk yield in kilograms of a cow throughout the lactation period, 305-day milk yield (305-dMY, kg) calculated using the International Committee for Animal Recording equation (ICAR, 2000) as follows:

The 305-dMY = [(TMY+405) / (100+LP)]

where, TMY is the total milk yield and LP signifies lactation period, days in milk (DIM, days) is defined as a number of days in milk from calving to drying-off date, and daily milk yield (DMY, kg) is calculated by dividing total milk yield in kilograms by lactation period length in days. The reproductive traits included age at first calving (AFC, months) which is defined as the number of months from birth to first calving date of the cow, number of services per conception (NSPC) denotes the number of artificial insemination times required for each cow to be pregnant, and days open (DO, days) is estimated by the number of days from calving date to conception date. The descriptive statistics of the milk yield and reproductive studied traits dataset are presented in Table 2.

Table 2. Descriptive statistics of the milk yield and reproductive studied traits for Holstein cows and Montbeliarde \times Holstein F1 crossbred cows in Egypt

Variable	Ν	Minimum	Maximum	Mean	SD
Milk yield traits					
Total milk yield (kg)	2268	2131	22491	9597	2226
305-day milk yield (kg)	2268	1833	21376	8544	2299
Days in milk (days)	2268	230	1071	358	99.3
Daily milk yield (kg)	2268	5.6	72.5	28.3	8.61
Reproductive traits					
Age at first calving (months)	1045	20	33	24	2.7
Number of services per conception	2268	1	18	3.2	2.7
Days open (days)	2268	23	866	151	99.1

N: Number of observations, SD: Standard deviation

Statistical analysis

Data were analyzed using the least square means technique as applied in XLSTAT 2020.3.1.27 program with the following two statistical models.

To analyze TMY, 305-dMY, DIM, DMY, NSPC, and DO, model 1 was used as follows:

 $Y_{ijklmn} = \mu + G_i + H_j + P_k + S_l + Y_m + (G \times H)_{ij} + e_{ijklmn} \pmod{1}$

Where, Y_{ijklmn} is the observations on TMY, 305-MY, DIM, DMY, NSPC, and DO, μ refers to the overall mean, G_i stands for the fixed effect of the ith genotype (i=1, 2), in which, 1: pure HO cows and 2: HO × MO F1 crossbred cows, H_j signifies the fixed effect of the jth herd (j:1, 2, 3 and 4), where, 1: Helaly farm, Dakahlia governorate; 2: Osama Nigm farm, Gharbia governorate; 3: Elyosr farm, Ismailia governorate and 4: Shash farm, Sharkia governorate, P_k is the fixed effect of the kth parity (k:1, 2, 3 and 4), S_1 refers to the fixed effect of the lth season of calving (l:1, 2, 3 and 4), where, 1: winter (December to February), 2: spring (March to May), 3: summer (June to August), and 4: autumn (September to November), Y_m signifies the fixed effect of the mth year of calving, starting from 2012 and ending by 2020, (G × H)_{ij} is the effect of the fit hand used and the part of the ball $D(0, \pi^2)$.

the effect of the interaction between i^{th} genotype and j^{th} herd, and e_{ijklmn} is residual error assumed to be N I D (0, $\sigma^2 e$).

To analyze AFC, model 2 was employed.

 $Y_{ijkmn} = \mu + G_i + H_j + S_k + Y_m + e_{ijkmn}$ (Model 2)

Where, Y_{ijkmn} is the observations of AFC, μ refers to the overall mean, G_i stands for the fixed effect of the ith genotype (i:1, 2), where, 1: pure HO cows and 2: HO × MO F1 crossbred cows, H_j signifies the fixed effect of the jth herd (j:1, 2, 3 and 4), where, 1: Helaly farm, Dakahlia governorate; 2: Osama Nigm farm, Gharbia governorate; 3: Elyosr farm, Ismailia governorate and 4: Shash farm, Sharkia governorate, S_k is the fixed effect of the kth season of birth (1:1, 2, 3 and 4), where, 1: winter (December to February), 2: spring (March to May), 3: summer (June to August), and 4: autumn (September to November), Y_m is the fixed effect of the mth year of birth, starting from 2011 and ending by 2017, and e_{ijkmn} is residual error assumed to be N I D (0, $\sigma^2 e$).

RESULTS AND DISCUSSION

Milk yield

The least squares means (LSM) and standard errors (SE) for TMY, 305-dMY, DIM, and DMY are presented in Table 3. It could be observed that MO × HO crossbred cows have higher TMY (9827 ± 119 kg), compared with pure HO cows (9616 ± 138 kg) but the difference was not statistically significant (p > 0.05). On the other hand, MO × HO crossbred cows had significantly (p < 0.05) higher 305-dMY (9210 ± 96 kg) than pure HO (7987 ± 149 kg). Pure HO cows had significantly greater DIM (399 ± 6 days) than MO × HO crossbred ones (341 ± 5.2 days). Crossbred cows showed significantly superior milk yield performance, compared to pure HO cows due mainly to their higher DMY (30.0 ± 0.45 kg versus 25.9 ± 0.52 kg, respectively).

The herd had a significant effect on TMY, 305-dMY, and DMY (p < 0.05) with the highest values observed for herd one (Helaly farm, Dakahlia governorate, Egypt), scoring 10195 ± 179 kg, 9003 ± 191 kg, and 29.4 ± 0.67 kg for

TMY, 305-dMY, and DMY, respectively. While the lowest values were recorded for herd three (Elyosr farm, Ismailia governorate, Egypt), having 8933 ± 161 kg, 7910 ± 148 kg, and 25.6 ± 0.61 kg for TMY, 305-dMY, and DMY, respectively. However, the length of DIM was not significantly different across herds.

The interaction of the genotype and herd was significant for all productive traits (p < 0.05, Table 4). The LSM of TMY, 305-dMY, DIM, and DMY for genotype by herd revealed that MO × HO crossbred cows exhibited significant superiority than pure HO cows under the same management system for TMY, 305-dMY, and DMY across herds one, two, and four with significantly longer DIM for pure HO cows. Among the different herds, MO × HO crossbred cows located in herd one had a magnitude advantage for TMY and DMY over other crossbreds herds. However, pure HO cows exhibited a significant superiority over MO × HO crossbred cows for TMY in herd three with relatively higher LSM of 305-dMY and DMY for MO × HO cows, compared to HO cows without any significant differences for 305-dMY and DMY between the two genotypes.

Table 3. Least squares means and standard errors of milk yield traits for Holstein cows and Montbeliarde \times Holstein F1 crossbred cows in Egypt

			Traits		
Classification	Ν	TMY (kg)	305-dMY (kg)	DIM (days)	DMY(kg)
		LSM±SE	LSM±SE	LSM±SE	LSM±SE
The overall mean	2268	9722 ± 47	8598 ± 48	370 ± 2.1	27.9 ± 0.18
Genotype		NS	*	*	*
НО	1096	$9616^{a} \pm 138$	$7987^{a} \pm 149$	$399^{b} \pm 6$	$25.9^{a} \pm 0.52$
$MO \times HO$	1172	$9827^{a} \pm 119$	$9210^{b} \pm 96$	$341^{a} \pm 5.2$	$30.0^{b} \pm 0.45$
Herd		*	*	NS	*
1	236	$10195^{\circ} \pm 179$	$9003^{b} \pm 191$	$370^{a} \pm 7.8$	$29.4^{b} \pm 0.67$
2	311	$10094^{\circ} \pm 153$	$8923^{b} \pm 178$	$372^{a} \pm 6.6$	$28.8^{b} \pm 0.57$
3	1338	$8933^{a} \pm 161$	$7910^{a} \pm 148$	$369^{a} \pm 7$	$25.6^{a} \pm 0.61$
4	383	$9664^{b} \pm 182$	$8557^{b} \pm 193$	$368^{a} \pm 7.9$	$28^{b} \pm 0.68$
Parity		*	*	NS	*
1	1052	$9384^a\pm109$	$7999^{a} \pm 106$	$377^{a} \pm 4.7$	$26.6^{a} \pm 0.41$
2	768	$9603^{b} \pm 121$	$8735^{b} \pm 108$	$367^{a} \pm 5.2$	$27.8^{b} \pm 0.45$
3	344	$9714^{bc} \pm 152$	$8748^b \pm 150$	$366^{a} \pm 6.6$	$28.1^{b} \pm 0.57$
4	104	$10185^{\circ} \pm 237$	$8910^{b} \pm 263$	$370^{a} \pm 10.3$	$29.3^{b} \pm 0.89$
Season of calving		*	*	*	*
Winter	736	$9522^a \pm 123$	$8622^{b} \pm 110$	$363^b \pm 5.4$	$28.3^b\pm0.46$
Spring	243	$9783^{ab} \pm 181$	$8221^{a} \pm 166$	$397^{d} \pm 7.8$	$26.5^a\pm0.68$
Summer	427	$9731^{ab} \pm 145$	$8503^{ab} \pm 128$	$375^{c} \pm 6.3$	$27.1^{a} \pm 0.54$
Autumn	862	$9850^{b} \pm 119$	$9047^{c} \pm 101$	$345^{a} \pm 5.2$	$29.9^{\circ} \pm 0.45$
Year of calving		*	*	*	*
2012	13	$8866^a \pm 622$	$7223^{a} \pm 589$	$348^{b} \pm 27$	$26.1^{bc} \pm 2.33$
2013	69	$8575^a \pm 288$	$7112^{a} \pm 214$	$417^{e} \pm 12.5$	$22.5^{a} \pm 1.08$
2014	145	$8907^a \pm 212$	$7457^{\mathrm{a}} \pm 202$	$406^{de} \pm 9.2$	$23.6^{ab} \pm 0.80$
2015	200	$9282^{a} \pm 181$	$7953^{b} \pm 188$	$385^{cde} \pm 7.9$	$26^{bc} \pm 0.68$
2016	317	$10146^{b} \pm 140$	$8569^{\circ} \pm 146$	$382^{cd} \pm 6.1$	$28.4^{cd} \pm 0.53$
2017	348	$10656^{b} \pm 137$	$9522^{d} \pm 142$	$371^{bc} \pm 6$	$30.7^{de} \pm 0.51$
2018	553	$10382^{b} \pm 137$	$9106^{d} \pm 141$	$361^{bc} \pm 5.9$	$30.5^{de}\pm0.51$
2019	572	$10185^{b} \pm 141$	$9283^{d} \pm 145$	$346^{b} \pm 6.1$	$30.6^{de} \pm 0.53$
2020	51	$10495^{b} \pm 333$	$9323^{d} \pm 374$	$313^a\pm14.5$	$33.5^{e}\pm1.25$
Genotype and herd interaction	2268	*	*	*	*

Means followed by different superscripts within each column are significantly different (*p < 0.05), LSM±SE: Least squares means ± standard errors, N: Number of observations, NS: Non-significant, TMY: Total milk yield, 305-dMY: 305-day milk yield, DIM: Days in milk, DMY: Daily milk yield, HO: Holstein cows, MO × HO: Montbeliarde × Holstein F1 crossbred cows, herd 1: Helaly farm, Dakahlia governorate, herd 2: Osama Nigm farm, Gharbia governorate, herd 3: Elyosr farm, Ismailia governorate, herd 4: Shash farm, Sharkia governorate

Tuble 1 Deast squares means and standard errors of mendered between genetypes and eow nere	Table 4. Least	t squares means and	l standard errors of	interaction between	genotypes and	l cow herds
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	Herd 1		Her	Herd 2		Herd 3		Herd 4	
Traits	HO (n=25)	MO × HO (n=64)	HO (n=64)	MO × HO (n=73)	HO (n=412)	MO × HO (n=270)	HO (n=30)	MO × HO (n=129)	
TMY (kg)	$10001^{cd}\pm283$	$10389^{d} \pm 189$	$9800^{\rm c}\pm200$	$10388^{d} \pm 192$	$9166^{\text{b}}\pm163$	$8700^{a}\pm182$	$9498^{bc}\pm293$	$9830^{\rm c}\pm158$	
305-dMY (kg)	$8102^{a}\pm300$	$9904^{c}\pm196$	$7908^{a}\pm239$	$9938^{c} \pm 207$	$7790^{a}\pm161$	$8030^{a}\pm183$	$8146^a \pm 325$	$8967^b \pm 151$	
DIM (days)	$415^{\text{de}}\pm12.3$	$326^{a}\pm8.2$	$416^{\text{e}}\pm8.7$	$327^a \!\pm 8.4$	$382^{\rm c}\pm7.1$	$356^{b}\pm7.9$	$382^{cd}\pm12.7$	$354^{b}\pm 6.8$	
DMY(kg)	$26^{a}\pm1.06$	$32.9^{c}\pm0.71$	$25.2^{a} \pm 0.75$	$32.4^{\rm c}\pm0.72$	$25.4^{a}\pm0.61$	$25.7^{a}\pm0.68$	$26.9^{ab}\pm1.10$	$29.1^{\text{b}}\pm0.59$	
NSPC	$3.9^{cd} \pm 0.34$	$2.1^{a}\pm0.23$	$3.8^{cd}\pm0.25$	$2.0^{\rm a}\pm0.24$	$4.1^{\rm d}\pm0.26$	$3.8^{cd}\pm0.28$	$3.2^{bc}\pm0.39$	$2.4^{ab}\pm0.20$	
DO (days)	$204^{\text{d}} \pm 12.3$	$116^{a} \pm 8.2$	$205^d \pm 8.7$	$116^a \pm 8.4$	$176^{\rm c}\pm7.1$	$149^{b}\pm7.9$	$175^{c}\pm12.7$	$145^{\rm b}\pm 6.8$	

Means within a row with different superscript are significantly different (*p < 0.05), Results are expressed as mean value ± standard error, HO: Holstein cows, MO × HO: Montbeliarde × Holstein F1 crossbred cows, TMY: Total milk yield, 305-dMY: 305-day milk yield, DIM: Days in milk, DMY: Daily milk yield, NSPC: Number of services per conception, DO: Days open, n: Number of cows, herd 1: Helaly farm, Dakahlia governorate, herd 2: Osama Nigm farm, Gharbia governorate, herd 3: Elyosr farm, Ismailia governorate, herd 4: Shash farm, Sharkia governorate

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Parity had a significant effect (p < 0.05) on TMY, 305-dMY, and DMY. The three traits increased gradually with increasing parity order. The LSM of TMY, 305-dMY, and DMY were the highest (10185 \pm 237 kg, 8910 \pm 263 kg, and 29.3 \pm 0.89 kg, respectively) at the fourth lactation. The length of DIM was not significantly different across parities.

Season of calving explained a significant variation for all productive traits (p < 0.05). The LSM highest estimates for TMY, 305-dMY, and DMY (9850 ± 119 kg, 9047 ± 101 kg, and 29.9 ± 0.45 kg, respectively) were observed in autumn. However, the lowest estimate for TMY (9522 ± 123 kg) was observed in winter, whereas the lowest estimates for 305-dMY (8221 ± 166 kg) and DMY (26.5 ± 0.68 kg) were observed in spring. The length of DIM was significantly different across seasons. The DIM was significantly longer in spring and shorter in autumn.

Year of calving significantly affected all the studied productive traits (p < 0.05). Cows calved in 2013 had significantly longer DIM (417 \pm 12.5 days), compared with other years. On the contrary, the LSM for TMY (8575 \pm 288 kg), 305-dMY (7112 \pm 214 kg), and DMY (22.5 \pm 1.08 kg) were significantly lower for cows calving in 2013. On the other hand, DIM (313 \pm 14.5 days) was significantly shorter for dams that calved in 2020. However, cows that calved in 2017 had significantly greater TMY (10656 \pm 137 kg), 305-dMY (9522 \pm 142 kg), and DMY (30.7 \pm 0.51 kg). It could be observed from Table 3 that the LSM of TMY for calving years (2012 to 2015) was significantly different from the other years.

In contrast to the findings of the present study, many studies have shown that pure Holstein cows tended to have higher total milk yield, and consequently higher daily milk yield than MO × HO crossbred cows during a uniformed lactation period of 305 days. Heins et al. (2006) reported that pure Holstein cows had significantly higher 305-days milk yield (9757 kg) than MO × HO cows (9161 kg) during the first lactation. Likewise, Heins and Hansen (2012) found that pure Holstein cows had significantly higher 305-day milk yield (11417 kg), compared to MO × HO crossbred cows (10744 kg) across the first five lactations. Hazel et al. (2014) observed higher 305-dMY for pure HO cows versus MO ×HO crossbreds without significant difference during their first five lactations. Furthermore, Hazel et al. (2013) reported that MO × HO crossbred cows had significantly lower total milk yield, compared to pure HO cows during the first 150 days of the first lactation. Likewise, 305-dMY was lower for MO × HO crossbred, compared to HO cows without significant difference.

The higher trend of TMY, 305-dMY, and DMY for MO \times HO crossbred cows than pure HO cows in the current study could be attributed to the positive heterotic effect for these traits. According to Sørensen et al. (2008), the heterosis effect for yield traits was approximately 3% depending on the average production of the parental purebreds that were crossed as well as environmental conditions. Furthermore, the pure Montbeliarde breed is genetically adapted to hot climates and has a higher heat stress tolerance than pure HO cows (Allouche et al., 2018; Ouarfli and Chehma, 2018). Consequently, MO \times HO crossbred cows were able to produce more efficiency under Egyptian subtropical environmental conditions than pure HO cows.

Reproductive performance

Table 5 shows the LSM of NSPC and DO. The effect of genotype on NSPC and DO was significant (p < 0.05). Crossbred cows (MO × HO) had significantly lower (p < 0.05) NSPC and DO than pure HO cows (2.6 ± 0.16 vs. 3.7 ± 0.18 for NSPC) and (132 ± 5.2 days vs. 190 ± 6 days for DO), respectively with significant advantages of approximately one dose fewer for NSPC and 58 days fewer for DO.

Herds differed significantly (p < 0.05) in NSPC which was significantly greater (3.9 ± 0.25) in herd three (Elyosr farm, Ismailia governorate, Egypt). However, DO estimates were not significantly different across herds. The interactions of genotype and herd were significant (p < 0.05) for NSPC and DO traits (Table 4). The MO × HO crossbred cows showed significantly lower NSPC and DO, compared to pure HO cows within the same herd with a magnitude advantage for crossbreds found in the first two herds than in the third and fourth herds. Parity had no significant effect on both NSPC and DO. Season of calving explained a significant variation for the two reproductive traits. The NSPC was significantly greater in winter and spring (3.4 ± 0.17 and 3.8 ± 0.27 , respectively) compared to summer and autumn (2.7 for both). Dams calved in autumn had significantly shorter DO (136 ± 5.2 days), while cows calved in spring and summer had longer DO (188 ± 7.9 and 165 ± 6.3 days, respectively). Year of calving was a significant source of variation in both NSPC and DO. Cows calved in 2013 had significantly greater NSPC (3.7 ± 0.36) and longer DO (206 ± 12.5 days) compared with other years. Cows calved in 2012 scored the lowest NSPC (2.5 ± 0.74), and those calves in 2020 had significantly the shortest DO (105 ± 14.5 days).

Many studies arrived at the same results of the current study concerning the superiority of MO \times HO crossbred cows compared to pure Holstein cows in reproductive traits. Hazel et al. (2017a) reported that the MO \times HO cows had fewer bred times (2.07) than pure HO cows (2.30) during the first lactation in eight high-performance dairy herds in the United States. Furthermore, Malchiodi et al. (2014) found that the MO \times HO cows were inseminated fewer times (2.02) than the first lactation pure HO cows (2.53). However, Walsh et al. (2008) observed no significant difference in the NSPC between MO \times HO cows (1.97) and pure Holstein-Friesian cows (1.98) in Ireland. The results of DO were in

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accordance with those of Hazel et al. (2014) who reported that MO × HO cows had significantly shorter DO (128 days), compared with that of pure HO cows (167 days) during their first five lactations. Similarly, Hazel et al. (2017a) found that MO × HO cows had fewer DO (113 days) than pure HO cows (125 days) during the first lactation. The same trend was observed by Malchiodi et al. (2014) who found that DO was 83.7 days for MO × HO cows versus 109.1 days for HO cows in the first lactation. Heins et al. (2012) also found that DO was 19 days longer for pure HO cows compared with MO × HO crossbred. Furthermore, the current findings agreed with those of Heins and Hansen (2012) who observed that the advance of parity in MO × HO crossbred cows led to a significantly fewer DO ranging from 131 days in the first lactation to 110 days in the fifth lactation. On the other hand, the authors of this study found that pure HO cows tended to have greater DO with the advance of parity with a range from 148 days in the first lactation to 157 days in the fifth lactation.

		Tr	aits
Classification	Ν	NSPC	DO (days)
		LSM±SE	LSM±SE
The overall mean	2268	3.2 ± 0.06	161 ± 2.1
Genotype		*	*
НО	1096	$3.7^{b} \pm 0.18$	$190^{\rm b} \pm 6$
$MO \times HO$	1172	$2.6^{a} \pm 0.16$	$132^{a} \pm 5.2$
Herd		*	NS
1	236	$3.0^{a} \pm 0.22$	$160^{a} \pm 7.8$
2	311	$2.9^{a}_{a} \pm 0.19$	$161^{a} \pm 6.6$
3	1338	$3.9^{b} \pm 0.25$	$162^{a} \pm 7$
4	383	$2.8^{a} \pm 0.24$	$160^{a} \pm 7.9$
Parity		NS	NS
1	1052	$3.4^{bc} \pm 0.15$	$168^{a} \pm 4.7$
2	768	$3.4^{\circ} \pm 0.17$	$158^{a} \pm 5.2$
3	344	$3^{ab} \pm 0.21$	$157^{a} \pm 6.6$
4	104	$2.8^{a} \pm 0.32$	$160^{a} \pm 10.3$
Season of calving		*	*
Winter	736	$3.4^{b} \pm 0.17$	$154^{\rm b} \pm 5.4$
Spring	243	$3.8^{b} \pm 0.27$	$188^{d} \pm 7.9$
Summer	427	$2.7^{a} \pm 0.20$	$165^{\rm c} \pm 6.3$
Autumn	862	$2.7^{a} \pm 0.16$	$136^{a} \pm 5.2$
Year of calving		*	*
2012	13	$2.5^{a} \pm 0.74$	$138^{b} \pm 27$
2013	69	$3.7^{\circ} \pm 0.36$	$206^{e} \pm 12.5$
2014	145	$3.6^{bc} \pm 0.27$	$196^{de} \pm 9.2$
2015	200	$3.1^{abc} \pm 0.23$	$174^{cde} \pm 7.9$
2016	317	$3.0^{abc} \pm 0.19$	$173^{bcde} \pm 6.1$
2017	348	$2.7^{ab} \pm 0.19$	$162^{bcd} \pm 6$
2018	553	$3.4^{abc} \pm 0.22$	$153^{bc} \pm 6$
2019	572	$3.4^{abc} \pm 0.23$	$138^{b} \pm 6.1$
2020	51	$2.9^{abc} \pm 0.53$	$105^{a} \pm 14.5$
Genotype and herd interaction	2268	*	*

Table 5. Least squares means and standard errors of number of services per conception and days open for Holstein cowsand Montbeliarde \times Holstein F1 crossbred cows in Egypt

Means followed by different superscripts within each column are significantly different (*p < 0.05), LSM±SE: Least squares means ± standard errors, N: number of observations, NS: Non-significant, NSPC: Number of services per conception, DO: Days open, HO: Holstein cows, MO × HO: Montbeliarde × Holstein F1 crossbred cows, herd 1: Helaly farm, Dakahlia governorate, herd 2: Osama Nigm farm, Gharbia governorate, herd 3: Elyosr farm, Ismailia governorate, herd 4: Shash farm, Sharkia governorate

Table 6 shows the LSM of age at first calving (AFC). The values of AFC for the two genotypes were very closed (22.9 \pm 0.11 and 23.1 \pm 0.15 months for MO × HO and pure HO cows, respectively) and the difference was not significant (p = 0.156). A similar trend was recorded by Hazel et al. (2017b) who found that there was no significant difference for AFC between MO × HO crossbred cows and pure HO cows (23.8 vs. 23.9 months, respectively). All herds could significantly affect AFC (p < 0.05) with the highest value observed for Shash farm, Sharkia governorate (25.7 \pm 0.20 months). While heifers of herd two (Osama Nigm farm, Gharbia governorate, Egypt) had the lowest AFC with 21 \pm 0.19 months. The effect of the season of birth was significant (p < 0.05) on AFC. Heifers born in spring had significantly lower AFC (22.6 \pm 0.16 months) and calved for the first time 0.7 months earlier than those born in summer (23.3 \pm 0.16 months). Also, the year of birth affected significantly AFC (p < 0.05). Heifers born in 2015 significantly showed the highest AFC of 24.1 \pm 0.18 months, compared with other years.

In the current study, despite $MO \times HO$ crossbred cows scored a high mean of milk yield, they revealed better and significant reproductive performance than that of pure HO ones. This result showed the positive heterosis direction for

fertility along with milk yield traits for the first generation of MO \times HO crossbred cows under Egyptian subtropical conditions.

Table 6. Least squares means and standard errors of age at first calving for Holstein cows and Montbeliarde \times Holstein F1 crossbred cows in Egypt

		Trait
Classification	N	AFC (months)
		LSM±SE
The overall mean	1045	22.9 ± 0.08
Genotype		NS
НО	524	$23.1^{a}\pm0.15$
$MO \times HO$	521	$22.9^{a}\pm0.11$
Herd		*
1	87	$21.1^{a} \pm 0.26$
2	136	$21^{a} \pm 0.19$
3	152	$24.2^{b} \pm 0.14$
4	670	$25.7^{\circ} \pm 0.20$
Season of birth		*
Winter	317	$23.1^{bc} \pm 0.13$
Spring	172	$22.6^{a} \pm 0.16$
Summer	177	$23.3^{\circ} \pm 0.16$
Autumn	379	$22.9^{ab} \pm 0.13$
Year of birth		*
2011	61	$22.7^{\rm a} \pm 0.26$
2012	105	$22.7^{\rm a} \pm 0.21$
2013	75	$22.6^{a} \pm 0.23$
2014	172	$23.1^{a} \pm 0.17$
2015	218	$24.1^{b} \pm 0.18$
2016	271	$23.1^{a} \pm 0.19$
2017	143	$22.8^{a} \pm 0.23$

Means followed by different superscripts within each column are significantly different (*p < 0.05), LSM±SE: Least squares means ± standard errors, N: Number of observations, NS: Non-significant, AFC: Age at first calving, HO: Holstein cows, MO × HO: Montbeliarde × Holstein F1crossbred cows, herd 1: Helaly farm, Dakahlia governorate, herd 2: Osama Nigm farm, Gharbia governorate, herd 3: Elyosr farm, Ismailia governorate, herd 4: Shash farm, Sharkia governorate

The reasons behind the superiority of MO × HO crossbred cows, compared to pure Holstein cows, for fertility traits were explained in several previous studies. Hazel et al. (2013) and Hazel et al. (2014) found that the body traits of MO × HO crossbred cows were characterized by significantly greater body weight and body condition score (BCS) without consuming extra dry matter intake than pure HO cows across the first five lactations. The larger body characteristics for MO × HO crossbred cows were attributed to continuous selection for BCS and feed efficiency for pure MO breed that was in contrast to breeding goal for HO breed to enhance angularity features. Greater BCS at the time of calving or less loss in BCS after calving increases the reproductive ability for cows in the next parity (Hazel et al., 2014). Likewise, greater BCS for MO × HO crossbred cows was associated with enhancement of immunity and a lower rate of health problems, and consequently, improved the reproductive performance for MO × HO crossbred cows than pure HO cows (Walsh et al., 2008; Hazel et al., 2013; Hazel et al., 2017a).

Furthermore, Sørensen et al. (2008) stated that the heterosis estimate for fertility traits was at least 10% for the first generation crosses when unrelated two breeds are mating involving HO cows. The power of the heterosis for fertility traits could be generated from the new combinations of additive genetic effects in the F1 crosses. Moreover, crossing between unrelated breeds contributed to significant changes in genes interaction within and among loci in terms of non-additive genetic effects of dominance and epistasis (Sørensen et al., 2008). In addition, crossbreeding between genetically different breeds leads to an increase in the proportion of animals with heterozygous loci over the animals with homozygous loci especially when the two breeds had a greater genetic distance; and consequently, obtain crossbred with better performance compared with the average of the purebred parental breeds (Sørensen et al., 2008). According to Malchiodi et al. (2014), the intensive selection for high milk production that HO cows were subjected to, may alter their metabolic physiology to use the energy for production over reproduction; however, MO × HO crossbred cows may have a different metabolic mechanism that allows to better respond to the physiological process of production, reproduction, and survival at the same time in early lactation.

The magnitude of economic advantages for reproductive superiority of $MO \times HO$ crossbred cows is due to lower costs required for hormonal treatment for synchronization programs, lower rate of culling for fertility problems, lower replacement costs, and a faster return to peak production at second lactation (Hazel et al., 2017a).

CONCLUSION

Under Egyptian subtropical conditions, the first generation of $MO \times HO$ crossbred cows showed better performance compared to pure HO cows for milk yield and reproductive traits. Crossing pure Holstein with Montbeliarde may provide an effective strategic option for the genetic improvement of dairy cattle raised in hot subtropical climates. Further studies are required to define the best gene combination (s) for crossing and also, phenotypic, genetic, and molecular characterization of the crossbreds are needed.

DECLARATIONS

Authors' contribution

R. R. Sadek, S. Abou-Bakr and A. A. Nigm designed the study. M. A. A. Awad and M. M. Badr collected the data. M. A. M. Ibrahim and M. A. A. Awad performed the editing and statistical analysis of data. M. A. A. Awad interpreted the results and wrote the manuscript. R. R. Sadek, S. Abou-Bakr and A. A. Nigm edited and revised the manuscript. All authors read and approved the final manuscript.

Competing interests

The authors have not declared any conflict of interest.

Ethical consideration

Ethical issues including plagiarism, consent to publish, data fabrication, and double publication have been checked by all the authors.

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Intensity and Predilection of Helminth Parasites of the Red Snapper (*Lutjanus argentimaculatus*)

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ABSTRACT

Marine fish, particularly the red snappers, are often exposed to helminth parasitic infestation. As a result of the parasitic infestation, the fish population, the fish weight, and the morphological changes in the fish are shrinking. The present research aimed to find out the intensity and predilection of the helminth ectoparasites over the infection of the red snapper (*Lutjanus argentimaculatus*) and employed the survey method for this purpose. The sampling was carried out by the purposive sampling technique. The sample obtained consisted of 30 fish, 20% of the total red snapper population of 150 fish reared in the floating net cages of Balai Besar Perikanan Budidaya Laut Lampung. The intensity of the fish infestation by a mixture of *Haliotrema epinepheli* and *Benedenia epinepheli* was 132.5 individuals/fish. *Neobenedenia girellae* and *Haliotrema epinepheli* infected fish with an intensity of 149.41 individuals/fish. The 66.7% of *Benedenia epinepheli* had a predilection for the dorsal fin, and 33.3% for the anal fin. In *Neobenedenia girellae*, 57.1% had a predilection for the body surface, 37.2% for the head surface, and 5.7% for the dorsal fin. In conclusion, all sampled fish were positively infected with helminth ectoparasites, including *Neobenedenia girellae*, Haliotrema epinepheli, and Benedenia epinepheli.

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INTRODUCTION

One of the main problems and challenges in red snapper cultivation is disease control (Hussan et al., 2016; Oliveira et al., 2020). Diseases of red snapper could occur in water due to imbalances in the environment, host, and pathogenic organisms (Engering et al., 2013; Hussan et al., 2016; Oliveira et al., 2020). Parasitic infestation and infection might also be attributed to high fish density and inadequate nourishment in fish, as well as poor water and environmental quality (Yadollahi et al., 2013; Hussan et al., 2016).

In nature, red snappers might be susceptible to a number of diseases or parasites (Cable et al., 2017; Oliveira et al., 2020). In the culture environment, the parasites might even be present in far greater numbers and could be lethal to fish (Omeji et al., 2011). Marine fish, particularly the red snappers, are often exposed to parasitic helminth infestation (Montoya-Mendoza et al., 2014; Oliveira et al., 2020). Visual results indicated that the most prevalent ectoparasitic worm in the red snapper was *Benedenia epinepheli*, which was found on the fin and skin (Jithendran et al., 2005; Loh et al., 2020). Meanwhile, *Neobenedenia girellae* (Kishimori et al., 2015), *Hatschekia poche* (Justine et al., 2012), *Haliotrema* species, and *Diplectanum squamatum* N. (Santos et al., 2002) were encountered on the gill.

A parasitic infestation could lead to economic losses. The economic impacts of parasites in fish include reduced fish population for consumption, decreased fish weight, and changes to fish morphology (Iwanowiez, 2011). The prevention and treatment of diseases had thus developed into an important cultivation component. Diseases might be caused by stress, pathogens (e.g., protozoans, bacteria, and viruses), environmental changes (e.g., algae bloom), overdose, and malnutrition (Pikarsky et al., 2004). Different causes could produce distinctive external symptoms of illness in fish, including sudden death, changes in behavior, loss of appetite, and bleeding in places where scales have peeled off (Madhun et al., 2015). Parasites infest or infect the red snapper in a number of ways by, for instance, parasitic contamination of the water in which red snappers are cultivated, direct contact, or rubbing with red snappers contaminated with parasites. In this case, the spread of the sick red snappers would have negative effects, especially if the density is too high. Furthermore, the equipment previously used to hand or transport parasite-contaminated red snappers would also cause parasite infestation or infection (Melianawati and Aryati, 2012).

Helminths are classified according to the International code. Every parasite belongs to particular phylum, class, order, genus, and species. Helminths per se are assigned to four different phyla, namely Platyhelminthes, Nemathelminthes, Acanthocephala, and Annelida (Gibson et al., 2014; Morand et al., 2015).

The phylum Platyhelminthes is characterized by a dorsoventral flattening of the body and bilateral symmetry, whereby its organs are embedded within the parenchyma tissues, and there are no respiratory and circulatory systems. The phylum Platyhelminthes is composed of two classes, namely Trematode and Cestode (Hahn et al., 2014; Morand et al., 2015). The parasites of the Trematode class have an ovoid, leaf-like, unsegmented body, and an incomplete digestive tract (a sac with one or two suckers for attachment). Worms in this class have a hermaphrodite reproductive system. This class is divided into three subclasses of Monogenea, Aspidogastrea, and Digenea (Crotti, 2013). Parasites of the order Dactylogyridae of the class Trematode are parasites of aquatic vertebrates, for example, the Reptiles (crocodiles), Amphibians (frogs), and Pisces (fishes). The majority of the parasites in the order Dactylogyridea are ectoparasites with a direct life cycle. The order Dactylogyridea of the class Trematoda has a distinctive feature on its posterior part of the body, that is, a haptor with a pair of hooks to attach itself to its host (Gibson et al., 2014).

There are a number of ectoparasitic worm types that infect the red snapper, namely Benedenia, Neobenedenia, and Diplectanum. These three worms are described as follows. Benedenia is a colorless ectoparasite that attacks the surface of the body. In particular, Benedenia causes fish to lose their appetite and have abnormalities in the way they swim on the bottom or surface of the container or floating net cage. Severe infection with Benedenia could cause wounds or ulcers (a pus-like liquid) on the skin and eventually secondary bacterial and fungal infection (Zhang et al., 2017). *Neobenedenia girellae* shows a higher degree of pathogenicity than *Benedenia epinepheli*because *Neobenedenia girellae* infects not only the skin but also the eye and causes blindness. Severely infected fish lose their appetite, have dark body colors, and have irregular swimming patterns and movements (Zhang et al., 2017). *Neobenedenia melleni* shows clinical symptoms in the skin, such as hyperemia and bleeding, and often infects the eye, causing damages to the cornea and blindness of the fish (Trujillo-González et al., 2015). Diplectanum disrupts the respiratory function in fish. The resulting wounds would lead to secondary bacterial infection. The growth of fish might be delayed, and the body weight and appetite are reduced. The fish infected by Diplectanum had pale gills, which produced excessive amounts of muccus, and a pale body (Cecchini et al., 1998). These three worms (Benedenia, Neobenedenia, and Diplectanum) are responsible for the diseases that the red snappers suffer from. The present research was then conducted to figure out the intensity and predilection of the helminth ectoparasites of the red snappers.

MATERIALS AND METHODS

Ethical approval

The present research employed the survey method. The sample of red snappers (*L. argentimaculatus*) was obtained by the purposive sampling method according to specified criteria. The sample had sizes specified by the researchers from the location of the floating net cages for one week. In this case, the red snappers were found to be 25–35 centimeters long.

The red snappers enrolled as samples were taken from one of seven floating net cages at Balai Besar Perikanan Budidaya Laut (BBPBL) Lampung with the number 30, or accounting for 20% of the total population of 150 red snappers, which were reared in $1 \times 1 \times 1.5$ m³ polyethylene nets. The extracted sample was transported to the Laboratory of Fish Health and Environment of BBPBL Lampung, Indonesia, for helminth parasites examination.

The current research used a fishing net, a plastic bucket for fish sampling, and a Kemmerer bottle for water sampling. The instruments used to calculate the intensity and predilection of the helminth parasites were a set of surgical instruments (scalpel, surgical scissors, forceps, object-glass, and cover glass), pipette, towel paper, ruler, digital scale, digital camera, label paper, microtube, and trinocular microscope. Instruments used to measure water quality included a pH meter for pH measurement, a refractometer for measuring salinity, a Dissolved Oxygen (DO) meter for measuring dissolved oxygen, and a thermometer for measuring temperature.

The main materials used for the present research were the red snappers (*L. argentiaculatus*) and the seawater sample from the floating net cage location. Meanwhile, 250 mL of 5% glycerin was used to study the helminth parasite. The current research was undertaken from February through March 2016 in the Laboratory of Fish Health and Environment, BBPBL Lampung, and the Education Laboratory of the Faculty of Fisheries and Marine Affairs, Universitas Airlangga, while the sampling was performed at the location of the floating net cages of BBPBL Lampung.

RESULTS

The results of the present research concerned the intensity of the helminth ectoparasites, the predilection of helminth ectoparasites, the distribution of predilection of helminth ectoparasites, and the water quality parameters.

Intensity of helminth ectoparasites

From the investigation of the 30 samples of red snappers (*Lutjanus argentimaculatus*) that were cultivated in a floating net cage of BBPBL Lampung, helminth ectoparasites were found. The results of the sample examination indicated that a single sample fish could be infested with more than one type of helminth ectoparasite. Of the 30 sample

fish examined, 12 were only infested by *Haliotrema epinepheli* (sole infestation), including 1534 worms found with an intensity of 127.83 individuals/fish. Aside from those fish, 6 were infected with a mixture of *Benedenia epinepheli* and *Haliotrema epinepheli*, with 795 worms found with an intensity of 132.5 individuals/fish, and 12 were infested with a mixture of *Neobenedenia girellae* and *Haliotrema epinepheli*, having 1793 worms with an intensity of 149.41 individuals/fish.

Predilection of helminth ectoparasites

Observations on the predilection of the helminth ectoparasites were performed in the Laboratory of Fish Health and Environment of BBPBL Lampung. The observations were carried out on macroscopic and microscopic bases. The predilection test procedure was performed by scraping off all body parts of the fish, followed by observations under a microscope at $100 \times$ and $400 \times$ magnifications. Predilection sites for the helminth ectoparasites were the body surface of the fish and the fins, including the dorsal, pectoral, anal, and pelvic fins. The predilection study on the gills was conducted by observing the histopathological preparations of the fish infested by the ectoparasitic worms. The examination included changes in the structure and appearance of the organs infested by the ectoparasitic worms.

According to the examination results of the worms in the red snappers, *Benedenia epinepheli* had a round, elongated body with a length of 2.06 to 3.05 mm, a width of 0.67 to 1.51 mm, and a diameter of 0.50 to 0.78 mm. *Benedenia epinepheli* had attachment organs 0.16-0.25 mm long and 0.12 to 0.27 mm wide, a pharynx of 0.16-0.35 mm long and 0.18-0.25 mm wide, accessory sclerites of 0.07 to 0.11 mm long, anterior hamuli of 0.08 to 1.21 mm long, and posterior hamuli of 0.04 to 0.07 mm long.

Neobenedenia girellae was found to have a round elongated body with a length of 4.6 to 5.7 mm, and a width of 1.5 to 2.5 mm. In addition to an opisthaptor of 1.2-1.5 mm in size, *Neobenedenia girellae* also had a pair of attachment organs with the length of 0.14 to 0.22 mm and width of 0.17 to 0.29 mm, a pharynx with a length from 0.51 to 0.71 and a width of 0.39 to 0.42 as well as accessory sclerites with a length of 0.25 to 0.31 mm, anterior hamuli of 0.28-0.39 mm long, and posterior hamuli of 0.11-0.18 mm long. Meanwhile, *Haliotrema epinepheli* was found to be 200.8 µm in length and 48.12 µm in width, and also had a pharynx 15.40 to 18.71 µm in diameter.

Distribution of the predilection of helminth parasites

66.7% of the *Benedenia epinepheli* that infest the red snappers preferred the dorsal fin, and 33.3% preferred the anal fin. No *Benedenia epinepheli* infestation was found on the caudal, pectoral, and ventral fins, and head. For the *Neobenedenia girellae* infestation in the red snappers, a majority of 57.1% had a high predilection for the body surface, 37.2% a medium predilection for the head, and 5.7% a low predilection for the dorsal fin. No predilection was indicated for the caudal, pectoral, anal, and ventral fins. Meanwhile, a 100% predilection for *Haliotrema epinepheli* was indicated for the gills and none for other parts of the body. As for the histopathologic observations of the gills, the results indicated that *Haliotrema epinepheli* had a predilection for the lamellae part of the red snapper gills.

Water quality parameters

The measurement of the water quality in terms of pH, DO, and salinity was performed once a week in the morning. The results of the observation of some indicators of water quality in the floating net cages of BBPBL Lampung in 2016 indicated that the water was in a normal condition for the life of the cultivated fish. The data indicated that the values were within normal ranges, where the temperature was between 30°C and 31°C, salinity was reported as 5 ppt, pH was estimated at 7, DO was between 6 and 8.37 mg/L, and the ammonia was also between 0.044 and 0.221 mg/L.

DISCUSSION

Based on the results of the examination of the body surface and the gills of red snappers (*Lutjanus argentimaculatus*), it was found that three parasitic worm species infest the red snappers in the floating net cages of BBPBL Lampung, namely *Benedenia epinepheli*, *Neobenedenia girellae*, and *Haliotrema epinepheli*. The helminth parasites *Benedenia epinepheli* and *Neobenedenia girellae* were encountered on the body surface of the red snappers, while *Haliotrema epinepheli* were found in the gills. The present findings are similar to Kritsky's (2012) review in the Persian Gulf, the eastern, Indo-west Pacific Ocean, and Mexico gulfs snappers.

The helminth ectoparasite *Benedenia epinepheli*, which infested the body surface of the red snappers as estated previously by Ravi and Yahaya (2016), had a predilection, especially on the dorsal and anal fins and in the skin area. When examining the ectoparasitic worms in the red snappers, *Benedenia epinepheli* was found to infest the dorsal fin area of 4 out of 30 sample fish, and infestation on the anal fin was rare.

The present research also discovered an infestation of the ectoparasitic worm *Neobenedenia girellae*. During the investigation, *Neobenedenia girellae* was found on the body surface, especially in the head area, in 13 out of 30 sample red snappers. It can be said that the worms had the highest prevalence on the body surface and rarely showed up on the

dorsal fin. *Neobenedenia girellae* had a predilection for the skin around the head and would also cause blindness, but was not found on the dorsal fin and the remaining body parts such as the gills and the internal organs.

The ectoparasitic worm *Haliotrema epinepheli* was also encountered in the present research. The predilection of the worm was exclusively for the gills. All sample fish infested by *Haliotrema epinepheli* demonstrated clinical symptoms of excessive mucus and swimming on the water surface. A severe infection of *Haliotrema epinepheli* could damage the filaments of the gills and cause the infected fish to suffer respiratory disorders or, in the worst case, die.

Based on the visual results, all sampled fish were infested by *Haliotrema epinepheli* in the gills. The *Benedenia epinepheli* infestation was present on the dorsal and anal fins, while the *Neobenedenia girellae* infestation occurred on the body surface, head, and dorsal fin, suggesting that *Heliotrema epinepheli* predominantly infested fish gills, eliminating competition between worm species in the areas. The fish infested by the helminth ectoparasite *Haliotrema epinepheli* rarely suffered wounds in their gill lamellae.

Although many of the red snappers (*Lutjanus argentimaculatus*) cultivated in the floating net cages at BBPBL Lampung were infested by *Haliotrema epinepheli* in the gills, none of the fish died. *Benedenia epinepheli* and *Neobenedenia girellae* did not leave any serious impact on the red snappers' health in small numbers. However, if *Benedenia epinepheli* and *Neobenedenia girellae* were present in significant numbers, they could be fatal to the fish (Melianawati and Aryati, 2012).

Based on the results of the examination on the 30 sample red snappers, 100% of the fish were positively infested with helminth ectoparasites, suggesting that the infestation intensity in floating net cages was very high. The infestation with helminth ectoparasites in the cultivation of floating net cages occurred due to the poor fish rearing and uncontrolled water quality since the cultivation was weather-dependent. Another factor presumed to decrease the red snappers' physical endurance was the stress resulted from the flow of water and net cages spoilage from the attachment of parasites and other microorganisms which blocked water circulation, which was mentioned by Cooper (2015). In addition, stress could also be caused by high density, which allowed parasites to develop rapidly, with high density triggered competition for space, food, and oxygen. The mortality rate from infestation with helminth ectoparasites at this cultivation location (East Java) was categorized as so high that the red snapper population in these floating net cages was smaller compared to other populations.

CONCLUSION

All of the fish samples were positively infected by helminth ectoparasites, including *Neobenedenia girellae, Haliotrema epinepheli*, and *Benedenia epinepheli*. Therefore, in the East Java region, Ocean fish are most likely to be infected with these parasites. In fish inspections, parasite-related infections should be considered cautiously, especially in marine fish like Red Snapper (*Lutjanus argentimaculatus*).

DECLARATIONS

Authors' contribution

All the authors contributed equally to this study.

Competing interests

The authors have not declared any conflict of interest.

Ethical considerations

Ethical issues (including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by the authors.

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Cross Reaction of Haemonchus contortus Protein with *Toxocara vitulorum* Anti-L2 Serum Using Western Blot Technique

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ABSTRACT

In the adult stage, Haemonchus contortus worms infect the abomasum host causing anemia and even death in animals. However, identifying the H. contortus protein can be used as a reference for the diagnosis of diseases. The diagnosis is performed by serological cross-reaction between H. contortus protein and anti-L2 Toxocara vitulorum (T. vitulorum) serum using the western blot technique. The main purpose of the current research was to identify the cross-reaction between H. contortus proteins and anti-L2 T. vitulorum serum using the western blot technique. T. vitulorum worms were collected from the intestine of cattle and H. contortus worms were collected from the abomasum of goats. The first step was making antibodies by oral infection of rats with infective eggs (L2) of T. vitulorum. The blood was taken 21 days after infection. Then, the blood was centrifuged at 1500 rpm for 10 minutes to get the serum. The second step was making homogenates from the whole worm extract of H. contortus. After crushing the worms, it was centrifuged at 5000 rpm for 15 minutes and the supernatant was taken. The supernatant was then analyzed using Sodium Dodecyl Sulphate Polyacrylamide Gel Electrophoresis (SDS-PAGE) with coomassie brilliant blue staining. The third step was the analysis of H. contortus protein with serum anti-L2 T. vitulorum using the western blot technique. From the H. contortus homogenates analysis using SDS-PAGE, 16 protein bands were obtained. The cross-reactions were 141.3, 81.3, 64. 6, 51.3, 46.8, and 38 kDa. The data from cross-reactions suggested that the H. contortus protein cannot be used as a diagnostic material. It is serologically Haemonchosis because it caused false positives with diagnostic Toxocariasis.

Keywords: Cross reaction, Haemonchus contortus, SDS-PAGE, Toxocara vitulorum, Western blot

INTRODUCTION

Haemonchosis is a parasitic disease caused by a nematode worm infection from the family of Trichostrongylidae and *Haemonchus* genus. The main cause of haemonchosis is *Haemonchus contortus* (*H. contortus*) worm. In the adult stage, this worm infects the abomasum of the host, causing anemia that leads to death (Githigia et al., 2001). Meanwhile, *Toxocara vitulorum* (*T. vitulorum*) is a pathogenic worm in ruminants. Their definitive hosts are buffaloes and they live as an adult within the small intestine lumen of ruminants (Abdelrahman and El-Menyawe, 2015). They can also be found in the calves of bulls (Van der Steen et al., 2014).

The conventional diagnosis of nematodes shows positive results if the infection has passed the prenatal stage (13-16 weeks). The effort which can be done to overcome the problem in diagnosis is developing a sensitive diagnostic technique based on serological examination. Serological testing using ELISA can be used to diagnose the disease. However, this technique has a disadvantage; If the antigen used is not specific, then the test's specificity will be in the low range (Sackey et al., 2003).

The *H. contortus* is the most dangerous and most observed worm in Southeast Asia, including in Indonesia; In North Sumatra, the prevalence of livestock infected by *H. contortus* has reached 40% (Silva et al., 2008). In Nigeria, the prevalence of toxocariasis due to *T. vitulorum* infection in calves is 61.4-91.1% (Sackey et al., 2003). Haemonchosis is a significant threat in tropical, subtropical, and warm regions as warm and moist conditions are favorable for the free-living stages (Besier et al., 2016; Fentahun, 2020). Worm-infected cases result in economic losses because of the decrease in animal productivity, weight loss, diarrhea, and severe cases that even lead to death (Githigia et al., 2001). Conventional diagnosis by finding eggs in a patient's stool is not possible because eggs are only produced by adult worms. For diagnosis, cases of *H. contortus* infected, require an accurate test and one of them is serological testing. Worms are multicellular organisms that have various specific and non-specific proteins that can trigger the host's immune response to form various antibodies so that when a positive diagnosis is made with serological tests, it allows to

conduct cross-reaction (Sackey et al., 2003). Cross reaction between worm species can cause false positives, but proteins that experience the cross-reaction can be developed as vaccine candidates. In proteins that are not cross-reactions, further detentions and evaluations can be carried out on the specificity of the worm antigen (Abdel-Rahman and Abdel Megeed, 2000). Identification of specific proteins plays an important role, which can be used as a reference for the diagnosis of disease. One of the tests recommended to confirm the diagnosis is the serological test. The main principle of serological tests is to react to antigens with appropriate antibodies. In the case of infection, it will result in antibodies that are dissolved in the serum. The formed antibodies will circulate throughout the tissues and blood circulation. The body will mobilize B lymphocyte cells which will differentiate into plasma cells, during the time it deals with infectious agents. Plasma cells will produce antibodies. If the antibodies find an antigen, then the antigen will be bound by antibodies (Slifka and Amanna, 2019).

The present study evaluated *H. contortus* protein along with anti-L2 *T. vitulorum* serum using Western blot technique. This study was conducted to determine the cross-reactions that can occur in worms of the same class, but in different species that were *H. contortus* and *T. vitulorum*. This study aimed to detect blood mononuclear (BM) *H. contortus* proteins that could bind to anti-L2 *T. vitulorum* serum using Western blot techniques.

MATERIALS AND METHODS

The current study was a laboratory exploratory study aimed at describing BM *H. contortus* proteins undergoing crossreaction with anti-L2 *T. vitulorum* serum. The study was conducted at the Parasitology Laboratory of Universitas Airlangga and the Institute of Tropical Disease (ITD), Surabaya, Indonesia, from July until November 2016.

The sample collection process from the intestine of cattle and the abomasum of goats was in accordance with animal ethic regulations announced by the Airlaanga University Ethical committee.

Collection of Haemonchus contortus and Toxocara vitulorum

The *H. contortus* worms were obtained from goat abomasum and *T. vitulorum* worms were taken from the small intestine of male cows. The collected worms were separated from the stool and immediately cleaned using Phosphate Buffer Saline (PBS). The cleaned worms were put in a petri dish containing PBS and then incubated in an incubator at 37°C (Kusnoto et al., 2011).

Isolation of L2 Toxocara vitulorum

Adult *T. vitulorum* worms were incubated for three days in an incubator at 37°C to produce eggs. After three days, the eggs of *T. vitulorum* worm were surgically taken from the reproductive tract. Afterwards, the worm eggs were identified, then fertilized in PBS medium at room temperature for 28 days to obtain *T. vitulorum* L2 (Kusnoto et al., 2011).

Calculation of worm eggs per gram stool

In the current study, egg counting was performed by modifying the calculation of worm eggs per gram stool using the Lucient Brumpt method. Based on the calculation, to identify the number of *T. vitulorum* eggs in each ml suspension of culture media, the following formula was used. The number of drops per ml (N) × number of worm eggs per drop (n) × number of dilutions (Lindstrom, 2003).

Treatment of experimental animals

The experimental animals used in this research were five male rats aged two months old. The rats were infected with L2 *T. vitulorum* at a dose of 10 grains per gram of body weight orally (Kusnoto et al., 2011). Before being infected, the rats were adapted for seven days. After adaptation, the rats were infected with L2 *T. vitulorum*. The purpose of this artificial infection was to obtain a serum containing L2 *T. vitulorum* antibodies.

Blood sampling of rats

The blood of the rats was taken 21 days after infection by cutting the rat's tail. The blood was inserted into a microtube, centrifuged at 1500 rpm for 10 minutes to get the serum (Lee and Goosens, 2015).

Preparation of Haemonchus contortus homogenate

Homogenate was made manually by grinding *H. contortus* worms with a mortar, then it was inserted into the test tube and suspended with 3 ml PBS. The suspension was then centrifuged at 5000 rpm for 15 minutes. Pellets and supernatants were separated. Supernatants were stored for protein analysis with SDS-PAGE and western blotting. Running was conducted on the results using the SDS-PAGE technique (Lindstrom, 2003).

Protein analysis using the SDS-PAGE technique

During SDS-PAGE technique, the protein electrophoresis was done in an ionic detergent which was Sodium Dodecyl Sulfate (SDS). One of the systems in SDS is discontinuation (Laemmli). In this system, protein migrates rapidly through ion solvents on stacking gel and separating gel. Protein is concentrated in a thin band line (Lindstrom, 2003).

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Characterization of proteins using Western blot technique

From the homogenate of *H. contortus* worms which has gone by the running gel process using SDS-PAGE, gel with protein fragments was obtained based on BM. In this process, the protein can be directly transferred to the nitrocellulose membrane using the Bio-rad model. The transfer of protein from the gel to nitrocellulose membrane was carried out by the Electrophoresis technique (Lindstrom, 2003).

Calculation of protein molecular weight

The Relative Molecular mass (MR) of the antigen protein was determined by a regression equation method. It was based on the value of the Retardation factor (Rf) of each band formed by using the western blot technique according to the method of Miletić and Saracević (1984). The MR was determined based on the MR log of the standard protein and the Rf value. Then, the equation was obtained by determining the standard curve of Rf and log MR (Lindstrom, 2003).

The molecular weight of an antigen or antibody was obtained by calculating the Rf value of each band (band) with the following formula:

Rf = Migration distance of the protein

Migration distance of the dye front

Where, distance refers to the distance of protein movement from the initial place, and Length is the distance of color movement from the starting point (dye front).

The relative molecular mass of protein was determined by converting the Rf value data and the relative molecular mass of standard protein to an equation. The logarithmic value of the relative molecular mass of standard proteins indicated the function Y, while X is the value of Rf. After the Rf value of the sample was found, it was entered into the equation. Furthermore, based on the results of the equation, the anti-log value was obtained to get the relative molecular mass value of protein (Kusnoto et al., 2011).

RESULTS AND DISCUSSION

Collection and identification of Haemonchus contortus worms

The *H. contortus* worms were obtained from the goat abomasum. *H. contortus* worms have a very small body size. Male *H. contortus* worms are 10-20 mm in length and red color, while female worms are 18-30 mm in length and red and white colors (it is known as barber's pole). The color produced by the variation of ovaries and intestines is red because of the blood sucked from the host. Identification of *H. contortus* worms is based on their reproductive organs. Male *H. contortus* worms have dorsal rays that are shaped like "Y" and spicules with 0.46-0.506 mm length (Figure 1). In female worms, the vulvars are covered by large and prominent flaps (Vulva flap). Male and female *H. contortus* have been demonstared in Figure 2.

Collection and identification of Toxocara vitulorum worms

The *T. vitulorum* worms were collected from the small intestine of adult male cows. The male *T. vitulorum* worms are 15-26 cm in length and 3-5 mm diameter with a small tail and female *T. vitulorum* worms are 22-30 cm in length with 5-6 mm diameter. Female *T. vitulorum* worms have thin, soft, and transparent cuticles. The identification of the *T. vitulorum* worms is based on the length of the body and the presence of its reproductive organ (Figure 3).

Collection of L2 Toxocara vitulorum

The eggs of *T. vitulorum* are subglobular and brownish. The eggs have thick spotted walls. Stage II (L2) larvae were found in ineffective worm eggs. The details are presented in Figure 4.

Protein analysis using sodium dodecyl sulphate polyacrylamide gel electrophoresis technique

From the protein analysis of Whole Worm Extract (WWE) of *H. contortus* using SDS-PAGE technique, WWE of *H. contortus*, 16 protein bands were prepared. By running SDS-PAGE on WWE of *H. contortus*, 16 proteins bonds with the following BM 141.3, 117.5, 81.3, 64.6, 51.3, 46.8, 42.7, 38, 34.7, 29.5, 26.9, 23.4, 20.9, 15.5, 12.9, and 11.7 kDa were obtained.

Protein characterization using western blot technique

The results from WWE of *H. contortus* analyzed proteins which were reacted with anti-L2 *T. vitulorum* serum by western blot technique indicated that the WWE of *H. contortus* bounded to anti-L2 *T. vitulorum* serum on BM 141.3; 81.3; 64.6; 51.3; 46.8 and 38 kDa.

Results of protein analysis using sodium dodecyl sulphate polyacrylamide gel electrophoresis technique

In SDS-PAGE, the protein is electrophoresed in ionic detergent and SDS. In the discontinuous system (Laemmli), proteins migrate rapidly through ion solvents on stacking gel and separating gel. The protein will be concentrated on a thin line in the form of a thin band (Slifka and Amanna, 2019). In the current study from the results of WWE of *H. contortus* protein analysis, 16 kinds of protein bands with the BM of 141.3, 117.5, 81.3, 64.6, 51.3, 46.8, 42.7, 38, 34.7, 29.5, 26.9, 23.4, 20.9, 15.5, 12.9, and 11.7 kDa were obtained. Meanwhile, from the identification of the other WWE of *H. contortus*, 16 protein bands included the BM of 107.74, 64.68, 51.39, 47.1, 43.52, 38.55, 36.27, 32.97, 28.95, 25.8, 23.25, 20.95, 15.65, 12.85, and 9.93 kDa. Protein bands that were similar to those obtained in this study included 64.6, 51.3, 38, 23.4, 20.9, 15.5, and 12.9 kDa. The difference was related to the calculation and possible relative differences in determining the distance of the protein band and the length, as well as the beginning of the measurement of the gel. It is possible that several protein bands had some differences with the results of other studies (Santos et al., 2014; Tak et al., 2015), but they referred to the same protein (Kusnoto et al., 2011).

The SDS-PAGE is the commonly used analytical method for resolving components of a protein mixture (Grabski and Novagen, 2001). Observations on protein analysis using the SDS-PAGE technique indicated that the success rate of the analysis was influenced by three factors, including homogenate cleanliness, homogenate purity level, and protein content in homogenates. Hygiene cleanliness affects the quality of protein bands formed in the gel where the ribbon could look sharply colored on a bright gel, thus allowing protein analysis and documentation. This technique is also a powerful tool for estimating the molecular weights of proteins (Grabski and Novagen, 2001).

Characterization of proteins using western blot technique

The *H. contortus* and *T. vitulorum* are worm pathogens because they attack internal organs and cause diarrhea in animals and in case the infected animal is not treated intensively, it will even die. One of the techniques that can determine the presence of antigen reactions with antibodies is blotting. Blotting is a technique for transferring macromolecules from the gel medium onto the membrane after the Electrophoresis process. Separate bands can be detected by coloring. The blotting technique is used to detect proteins, carbohydrates, and enzyme activity. One of the used blotting techniques is Western blot.

The basic principle of the Western blot technique is to separate proteins by SDS-PAGE, then transfer the proteins to the appropriate nitrocellulose membrane, followed by labeling the proteins with antibodies and visualizing them by the desired coloring, such as coomassie blue (Slifka and Amanna, 2019). Cross-reactions occurred between *H. contortus* protein and anti-L2 *T. vitulorum* serum on BM 141.3, 81.3, 64.6, 51.3, 46.8, and 38 kDa. The presence of a cross-reaction indicated that the protein is not a good diagnostic agent for haemonchosis because it causes false positives with diagnostic Toxocariasis.



Figure 1. Adult stage of Haemonchus contortus

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Figure 2. Identification of male and female *H. contortus* worms. Male worms (1), A is Spikula and B is dorsal rays. Female worms (2), part of C is vulva flap. The observation was done by using $40 \times$ magnification.



Figure 3. Adult Toxocara vitulorum worms



Figure 4. L2 Toxocara vitulorum (100× magnification).

CONCLUSION

In this research, cross-reactions between *Haemonchus contortus* protein and anti-L2 *Toxocara vitulorum* serum on BM of 141.3, 81.3, 64.6, 51.3, 46.8, and 38 kDa were obtained. The anti-L2 *T. vitulorum* serum can recognize antigens from *Haemonchus contortus*, *Moniezia benedeni*, and *Toxocara canis* on proteins with the same BM of 38 kDa. The presence of a cross-reaction indicates that the protein is not a good diagnostic agent for haemonchosis because it causes false positives with diagnostic toxocariasis.

DECLARATIONS

Authors' contribution

R. Wilujeng Asmorowati, Kusnoto, and H. Eliyani contribute equally in conduction, analysis, and writing of the manuscript. The authors checked and confirmed the final version of article.

Competing interests

The authors have no conflict of interests

Ethical considerations

Ethical issues (including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by the authors.

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A Highlight on Avian Toxoplasmosis: One Health Disease with a Special Reference to the Current Egyptian Situation

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ABSTRACT

This review article was developed to the infection of avian species with Toxoplasma gondii (T. gondii), diagnosis, pet bird and human infection, and control methods with a special reference to the current status of infection among the Egyptian poultry farms and population. Toxoplasmosis is a zoonotic disease caused by a unicellular, protozoan parasite T. gondii. Different domesticated and wild animals, as well as birds can harbor T. gondii and may be a potential source of infection to humans. Avian species could be infected with T. gondii through the ingestion of contaminated food, soil, and water with oocysts shed in the excreta of infected animals, especially cats. Poor sanitation and hygienic conditions increase the risk of infection. Consumption of food or water, as well as undercooked poultry meat or meat products containing the oocysts of the parasite, are the main sources of human infection with T. gondi. Diagnosis of T. gondii in the infected host depends on the serological detection of specific antibodies and molecular detection of the parasite. Microscopic demonstration of the oocysts and other developmental stages of the parasite in the intestine, liver, brain, and skeletal muscles tissues is another means for rapid diagnosis. Generally, a high prevalence of the disease is also reported in pet birds. Toxoplasmosis in humans is associated with abortion, congenital disorders, stillbirth, and other complications, especially in immunocompromised patients. Application of hygienic measures, as well as public awareness, are essential for the prevention and control of toxoplasmosis. In different Egyptian governorates, a high prevalence of T. gondii has been detected in animals, birds, and humans. High incidence of infection was recorded due to the contact with Toxoplasma oocysts shed mainly from infected cats or other carriers. Egyptian chicken and turkey flocks and backyard birds revealed the presence of different developmental stages of the parasite and even its antibodies. In addition, human populations showed signs of toxoplasmosis with severe complications.

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INTRODUCTION

Keywords: Bird, Egypt, Human, Toxoplasma gondii, Zoonosis

Toxoplasmosis is an important zoonotic parasitic disease of public health importance (CDC, 2004) and it is caused by an obligatory intracellular protozoan parasite, Toxoplasma gondii (T. gondii) (Tenter et al., 2000). The disease is of widespread nature and causes significant economic and reproductive losses in animals and serious public health problems in humans (Sukthana, 2006; Pan et al., 2017). Toxoplasmosis is a cosmopolitan zoonotic parasitic disease of nearly all warm-blooded mammals and birds. The infection rate with T. gondii in humans, animals, and birds is influenced by some epidemiological risk factors, such as age, sex, feeding pattern, and geographical distribution (Wilking et al., 2016; Zhang et al., 2016). Strains of T. gondii are transferred through continents mainly by stray cats and other animals, including migratory birds (Can et al., 2014). Most domestic and wild avian species showed infection with T. gondii (Ammar et al., 2020; Mikaeel and Al-Saeed, 2020; Ly et al., 2021). Avian species become infected with T. gondii through ingestion of the infective oocysts contaminated soil, food, and water (Ruiz and Frenkel, 1980; Dubey et al., 2008) as these oocysts may be shed in the feces of host animal's like cats (Yan et al., 2009). The oocysts of the parasite were detected in the liver, brain, and muscles of broiler chickens (Deyab and Hassanein, 2005; Amin et al., 2012). On the other hand, humans get infected with T. gondii through ingestion of undercooked chicken meat containing infective oocysts or other stages of the parasite (Zhang et al., 2016). However, spontaneous abortion, mental, and congenital disorders, as well as stillbirth and other complications were observed in people infected with T. gondii (Krueger et al., 2014; Egorov et al., 2018). Generally, the diagnosis of toxoplasmosis depends mainly on the detection of specific antibodies using serological tests (Li et al., 2020). Microscopic examination and molecular techniques such as Polymerase Chain Reaction (PCR) are other methods used for the diagnosis of toxoplasmosis (Barakat et al., 2012; Ibrahim et al., 2016a).

Egyptian environment enhances the infection and transmission of *T. gondii* due to the presence abundant number of domestic or stray cats that shed oocysts and contaminate the environment. Animals such as sheep, goats, and chickens

are regarded as important intermediate hosts for *T. gondii* and their meat is the main source of the parasite to humans in case consumed unhygienically (El-Massey et al., 1990). Serological tests reveal the presence of *T. gondii* infections with a high prevalence rate either in animal or human populations. In addition, definitive diagnostic procedures of clinical cases with toxoplasmosis in Egypt are still required (Abbas et al., 2020). Regarding the infection of avian species with *T. gondii*, insufficient data are available. Therefore, this review article was developed to highlight the infection of avian species with *T. gondii*, diagnosis, pet birds and human infection, and control methods with a special reference to the current status of infection among the Egyptian poultry farms and population.

The protozoon parasite

There are three morphological stages of toxoplasmosis infection, namely an active multiplying tachyzoite stage, slowly multiplying semi-dormant bradyzoite stage in tissue cysts, and a sporozoite stage within oocysts that present in the environment (Ferguson, 2004; Al-Ammash et al., 2018). It has been reported that sporulated oocysts of *Toxoplasma* spp. can persist and survive in the environment for a long time and can infect all warm-blooded animals, birds, and humans (Frenkel, 2000; Sibley et al., 2009; Abdel-Shafy et al., 2015). Oocysts require 1 to 5 days to sporulate and become infective. Environmental conditions such as warm temperature or high humidity are essential for the survival of oocysts. It has been found that the incidence of toxoplasmosis is higher in humid tropical areas than in arctic areas (Meerburg and Kijlstra, 2009; Simon et al., 2013). Suitable environmental conditions, such as high temperature especially in spring, summer, and early autumn enhance the sporulation of *T. gondii* oocysts.

Genetic polymorphic classification of *T. gondii* strains is based on detection of three major clonal lineage types I, II, and III, additional lineage, and recombinant or atypical genotypes (Shwab et al., 2014; Lorenzi et al., 2016). Type II strains of *T. gondii* were common in Europe (Ajzenberg et al., 2002), while type II and III strains were detected in sub-Saharan and North Africa, the Middle East, and the Peninsula (Al-Kappany et al., 2010a; Dubey et al., 2010; Mercier et al., 2010). In addition, types I, II, and III of *T. gondii* and the recombinant strains were found in North and Central, and South America (Pena et al., 2008; Khan et al., 2011; Rajendran et al., 2012). In some Asian countries such as Iran, the three major clonal lineages of *T. gondii* were also detected (Zia-Ali et al., 2007; Chaichan et al., 2017).

Susceptibility of avian species to toxoplasmosis

Various domestic and farm animals, including birds, showed infection with *T. gondii* (Mose et al., 2016). Direct detection of *T. gondii* oocysts in the environment is difficult, so infected broiler chickens are regarded as an important indicator for severe environmental contamination and poor hygienic conditions in poultry farms (Dubey, 2010; Mahmood et al., 2014). World-wide infection of domestic avian species, such as chickens, turkeys, ducks, and pigeons, with *T. gondii* has been recorded and they are considered as important sources of humans' infection (Dubey, 2010; Guo et al., 2015).

The prevalence rate of *T. gondii* in backyard chickens was 65.1% in Rio de Janeiro (da Silva et al., 2003), 64% in Ghana (Dubey et al., 2008), 11.4% in China (Yan et al., 2009), and 38.4% in Ethiopia (Tilahun et al., 2013). In Iraq, Mohammed and Abdullah (2013) detected *T. gondii* in domestic chickens kept in the house in Sulaimania Province, while Mikaeel and Al-Saeed (2020) found a high prevalence rate of the parasite among free-range local chickens in Duhok Province, and this was indicative for heavy environmental contamination with the parasite. In the same context, some researchers indicated that the infection rate of *T. gondii* was more in free-range chickens when compared with cages reared birds in Nanjing region, China (Liu et al., 2017) and in Egypt (Ibrahim et al., 2009). Moreover, in Pakistan, it has been observed that domesticated chickens could harbor more *T. gondii* than broiler chickens kept in farms which may be attributed to frequent contact of domesticated birds with cats and ground feeding habits (Khan et al., 2020). Besides, broiler chickens kept in farms are reared under a controlled environment, have fast growth, and have low chances of contact with reservoir animals, such as cats (Krueger et al., 2014). The experimental challenge of turkeys with *T. gondii* was successful (Dubey et al., 1993b).

Some reports investigated the presence of toxoplasmosis in pigeons as well as their relation to public health (Dubey, 2002; Tsai et al., 2006). Free-flying birds such as pigeons may act as another reservoir or source of *Toxoplasma* infection for contact birds, animals, or humans (Biancifiori et al., 1986). Besides, successful experimental infection of pigeons with *T. gondii* has been conducted with induction of signs and death (Simitch et al., 1965).

Water fowls, including ducks and geese, are also susceptible to *T. gondii* infection. The first detection of fetal toxoplasmosis in domesticated ducks was in Argentina (Boehringer et al., 1962), then the disease was recorded worldwide in different countries (Zardi et al., 1967; Literák and Hejlícek, 1993; El-Massry et al., 2000). The prevalence's rates of *T. gondii* in ducks were recorded as 56% in Italy (Zardi et al., 1967) and 6% in Florida (Burridge et al., 1979), as well as 20% (Chen et al., 1986), 32.19% (Zhai et al., 1987), 23.33% (Zhang, 1989), and 3.93% (Lv, 1993) in China. Moreover, ToxoDB#9 genotype (Chinese I strain) was found to be predominant in ducks (Including 115 duck muscle samples, Zou et al., 2017). In China, *T. gondii* has been detected molecularly and serologically either in ducks (Lv et al., 2021) or geese (Rong et al., 2014).

Successful oral infection of bobwhite quails (Dubey et al., 1993b) and Japanese quails (Dubey et al., 1994) with 49 strain of *T. gondii* oocysts has been reported. From the previous studies, the oocysts were re-isolated from the brain, heart, and muscles of the inoculated quails, moreover, antibodies to *T. gondii* were detected in quails for 63 days post-infection (PI) using an agglutination test. Experimental inoculation of quails with *T. gondii* tachyzoites revealed distribution and presence of this stage in the liver, lungs, and spleen at the day 7 PI, while the oocysts were detected in the brain the brain and the heart of the birds on day 70 PI (Albuquerque et al., 2001).

Antibodies against *T. gondii* have been demonstrated serologically in ostriches in different localities of the world like Ghana (Dubey et al., 2000), Spain (Martínez-Díaz et al., 2002), Zimbabwe (Hove and Mukaratirwa, 2005), Brazil (Contente et al., 2009) and Egypt (El-Madawy and Metawea, 2013).

Wild birds are regarded as an important source and a reservoir for *T. gondii* for carnivores, besides, some of these birds are migratory and can spread the parasite worldwide (Nardoni et al., 2019). For instance, the prevalence rates of the parasite were 1% in doves, and 6.9% in the wild pigeon (Ammar et al., 2020), as well as 26.5% and 17.5% in sparrows of Iran (Khademvatan et al., 2013) and Brazil (Gondim et al., 2010), respectively. Moreover, the seroprevalences of *T. gondii* in broiler and layer chickens, pigeons, and sparrows using a random-effect model in Iran were 20%, 8%, and 15%, respectively (Shokri et al., 2017). In the same context, Amouei et al. (2018) serologically detected *T. gondii* in 51.4% of 385 free-ranging birds (chicken, ducks, and geese) and migratory birds (*Anas crecca, Anas platyrhynchos*, and *Fulica atra*).

Regarding the age's susceptibility, it has been reported that older hens were more susceptible to *T. gondii* than younger ones in the Thika Region of Kenya (Mose et al., 2016). A recent study by Lv et al. (2021) in China showed that ducks older than one year were more susceptible to the parasite than ducks younger than one year old.

Pathogenicity of parasite

Infection with *T. gondii* is mainly induced lesions in the liver and small intestine. The lesions are represented as congestion of the blood vessels and degenerative changes of the tissues. Congestion of the blood vessels is related to the ability of the parasite to pass from the intestine to the bloodstream and release some protein substances that destruct the blood platelets leading to increased vascular permeability and hemorrhages (Burney et al., 1999). The hyperplasia of the liver and the small intestine's cells were also reported (Amin et al., 2012). Infiltration of the parasite in the intestinal cells leads to apoptosis and deaths of some cells, while other cells show rapid regeneration and hyperplasia (Liesenfeld, 2002).

Diagnosis of toxoplasmosis

Rapid detection of the stages of *T. gondii* infection in avian hosts can be carried out through finding the parasites in stained impression smears or through histopathological sections of the affected organs (Dubey et al., 2007a; Dubey et al., 2007b; Ibrahim et al., 2016a). Moreover, *T. gondii* antigen could be detected using immunohistochemical staining techniques with polyclonal rabbit antibodies (Dubey et al., 2001). Intraperitoneal mouse inoculation (mouse bioassay) of *T. gondii* positive tissues should be done to obtain the tachyzoites stage (Dubey, 2010).

Diagnosis of *T. gondii* infection especially in birds is mainly based on the detection of specific antibodies using serological tests (Cabezón et al., 2011; Li et al., 2020). It has been reported that antibodies to *Toxoplasma* infection in cats could be detected within 3 weeks of infection and persisted in high titers for 5 years even in the absence of re-infection (Dubey, 1995). Enzyme-linked immunosorbent assay (ELISA), competitive-inhibition ELISA, indirect fluorescent antibody test (Nardoni et al., 2019), modified agglutination test (MAT) (Dubey, 2010; Alvarado-Esquivel et al., 2012; Rong et al., 2014), latex agglutination test (Raafat et al., 2011), Sabin-Feldman dye test (Literák and Hejlícek, 1993) and Western blotting are commonly used as serological test for the detection of *T. gondii* infection is MAT as it is specific, sensitive, does not require special equipment, and can be used for all avian species (Dubey, 2002). Tachyzoites of *T. gondii* could be maintained on monkey kidney adherent fibroblasts (Vero cells) cultures supplemented with 8% heat-inactivated fetal bovine serum for further serological detection (Ibrahim et al., 2016a).

The seroprevalences of *T. gondii* in domestic birds vary from one country to another according to the method used in testing, the number of the examined birds, and the type and the hygiene of breeding (Dubey, 2010). Many factor such as the locality, the number of birds, and the type and the hygiene of breeding affect the incidence or seroprevalences of *T. gondii* in domestic avian species (Dubey, 2010). For example, the seroprevalence of *T. gondii* antibodies among free-ranging chickens was 27.1% in Southern Iran (Asgari et al., 2008) and 40.4% in Giza Province of Egypt (Dubey et al., 2003a),

The molecular techniques for the diagnosis of *T. gondii* infection are based on the identification of immunodominant antigens using sera of animals infected with geographically distant isolates and from acute and chronically infected animals. In this regard, the surface antigen 2 of *T. gondii* (TgSAG2) which is expressed in *Escherichia coli* or the insect cells can be used as a useful, highly sensitive, and specific antigen for ELISA (Huang et

al., 2002). Moreover, PCR is a specific, rapid, sensitive, and cost-effective technique that could be used for the detection of *T. gondii* DNA in chickens (Barakat et al., 2012). Howe et al. (1997) and Dubey et al. (2005) a fragment of 94 bp from the B1 gene of the parasite as a target to PCR amplification.

Toxoplasmosis in pet birds

Pet birds are usually kept in close contact with a human for companionship and entertainment. These birds play an important epidemiological role in the transmission and maintenance of many pathogens with public health significance for humans. Pet birds are bred in a semi-free-range system, so the birds have opportunities to contact food or water contaminated with *T. gondii* when they gather together. In addition, wild pet birds could transmit the protozoon in a long distance during flying and migration, and this transmission accelerated the spread of *T. gondii* diffusion. The role of pet birds in the transmission of *T. gondii* should be given more concern because they can serve as an important source of infection for cats (Ruiz and Frenkel, 1980; Dubey and Hamir, 2002). For instance, dead *T. gondii* infected pet birds from parks, pet shops or households are often un-hygienically disposed of and may be eaten by cats, and consequently, cats may become infected with the parasite and shed millions of oocysts. However, the transmission of *T. gondii* from pet birds to humans is not common as they are not bred for meat production (Boseret et al., 2013).

Up to now, some studies have been carried out to investigate the prevalence of T. gondii in psittacines and passerines species (Dubey, 2002; Hartley et al., 2008; Gazzonis et al., 2021). Fetal toxoplasmosis has been reported in parrots in Australia and New Zealand, psittacines in America, and budgerigars in Switzerland and the Netherlands (Dubey et al., 2004; Ferreira et al., 2012; Howe et al., 2014). In Brazil, the anti-T. gondii antibodies (IgY) were found in the serum of 71 adult blue-fronted Amazon parrots with a seropositivity rate of 9.8% (Marietto-Goncalves et al., 2013). Besides, Andrade et al. (2016) serologically examined 67 different psittacine species and found anti-T. gondii antibodies in 1.3% of the examined birds. However, the recent investigation of Sato et al. (2020) revealed the absence of antibodies against T. gondii in wild red-tailed Amazon parrots. For the first time in China, the anti-T. gondii antibodies were found in 13.63% of Cockatiels and 3.85% of Lovebirds (Zhang et al., 2014). Further Chinese study of Cong et al. (2014) demonstrated that the seroprevalences of T. gondii were 11.65%, 11.39%, and 5.26% in Eurasian Siskin, Oriental Skylark, and Black-tailed Grosbeak, respectively, and these birds molecularly showed the presence of T. gondii B1 gene and type II variant (ToxoDB genotype #3). A virulent type II T. gondii strain has been isolated from a black-winged lory in North America (Dubey et al., 2004; Dubey et al., 2011), while type I/III variant T. gondii strain was demonstrated in Valley quail in Brazil (Casagrande et al., 2015). In Australia, based on histopathology, immunohistochemistry, and multilocus DNA typing findings, atypical type II genotype T. gondii strain was found in a pet peach-faced lovebird with nervous signs and lesions in the brain, spleen, liver, and heart (Cooper et al., 2015). Budgerigars are relatively resistant to clinical toxoplasmosis (Dubey and Hamir, 2002; Zhang et al., 2014). However, successful experimental infection of Budgerigars with T. gondii has been carried out (Kajerová et al., 2003). Before the identification of Toxoplasma species in 1908, the Toxoplasma-like parasite was detected in Java sparrows in the 1900s (Tenter et al., 2000), however, antibodies against T. gondii were detected in 34.29% of Java sparrows (Huang et al., 2019).

Toxoplasmosis in human

Recently, there is increasing attention to understand the main sources for human infection with toxoplasmosis (Dubey et al., 2008). Humans could be infected with *T. gondii* through ingestion of contaminated water or consumption of undercooked or raw poultry meat products containing infective oocysts or other stages of the parasite (Dubey and Jones, 2008; Dubey et al., 2010; Zhang et al., 2016). In addition, other problems such as congenital infection as well as blood transfusions and organs transplantation transmission methods have been reported (Tenter et al., 2000). Several factors are associated with infection of humans with *T. gondii* such as food handling and preparation hygiene, eating habits, levels of natural immunity, the oocysts contamination of the environment, and the level of contact with infected animals (del-Castillo and Herruzo, 1998; Swai and Schoonman, 2009).

It has been estimated that one-third of humans could be infected by *T. gondii* (Shokri et al., 2017) leading to different mental and congenital disorders, spontaneous abortion, and stillbirth (Krueger et al., 2014). In the United State of America, about 400-4000 infants are born with congenital toxoplasmosis having some complications like schizophrenia and obsessive-compulsive disorder (Egorov et al., 2018).

Toxoplasmosis is not commonly a significant problem for healthy people, however, it can be a life-threatening problem for congenitally infected young immuno-deficient patients, and primary infected pregnant women resulting in an acute or reactivated infection or even death (Pinard et al., 2003; Montoya and Liesenfeld, 2004; Remington et al., 2006). In Pakistan, the reports showed that the prevalence of *T. gondii* in the human population ranged from 12% to 28% (Majid et al., 2016; Latif et al., 2017; Nazir et al., 2017).

Toxoplasmosis in Egypt

Identification of *T. gondii* infections either in humans, animals, and birds in Egypt is commonly based on serological and molecular techniques. The high prevalence of *T. gondii* infection in Egypt may be related to the presence of an abundant number of homeless cats that live on scraps of garbage to hunt for their food (Abbas et al., 2020). These cats are the main host and source of the parasite that heavily contaminate the environment with oocysts. Animals and birds can get the infection with *T. gondii* from this contaminated environment (Al-Kappany et al., 2010b). The main risk factor associated with *T. gondii* seropositive free-range and wild birds may be the contact with soil-harboring oocysts from street cats (Ibrahim et al., 2009). The high seroprevalence rate of *T. gondii* in free-range and cage chickens may be owing to the contact with soil-harboring oocysts shed from street cats (Ibrahim et al., 2009). Consumption of improperly cooked or grilled meat and meat products of domesticated animals (rabbits and poultry) is a major risk factor for Egyptians, especially those living in rural areas (Abou Elez et al., 2017).

From 2000 until 2020, the seroprevalences of *T. gondii* in birds were variable in different provinces of Egypt based on the geographical location, type of the collected samples, season, and the bird's species, age, and sex. Table 1 shows the incidences and the prevalence rates of *T. gondii* infections in different avian species from different provinces in Egypt in the period from 2000-2020.

Species of birds	The findings	References
Commercial turkeys, chickens, and ducks	The MAT has been done to detect the presence of antibodies against <i>T. gondii</i> in the sera of 173 turkeys, 108 chickens, and 48 ducks from Giza, Egypt. The prevalence rateS of anti- <i>T. gondii</i> antibodies among turkeys, chickens, and ducks were 59.5%, 47.2%, and 50%, respectively.	El-Massry et al. (2000)
Commercial chickens	A high prevalence rate (40.4 %) of <i>T. gondii</i> in chickens from the rural area surrounding Giza (South of Cairo), Egypt was detected using MAT.	Dubey et al. (2003)
House-bred and farm-bred chickens	The seroprevalence of <i>Toxoplasma</i> antibodies was 30.0% (18 out of 60) in house-bred chickens, while it was 11.1% (10 out of 90) in farm-bred chickens by MAT in different Egyptian governorates. The histopathological examination of the tissues revealed lesions induced by <i>T. gondii</i> and the oocysts were detected in the liver, brain, heart, and skeletal muscles of 22 (78.6%) out of 28 positive chickens.	Deyab and Hassanein (2005)
Free-range and caged chickens	Serological detection of <i>T. gondii</i> specific antibodies, as well as tissue oocysts, showed positive percentages of 16.49 and 11.34 % in the free-range chickens and 8.69 and 4.83 % in the caged chickens, respectively in Delta provinces, Egypt.	Ibrahim et al. (2009)
Ducks	The prevalence of <i>T. gondii</i> was detected in ducks from Behera governorate, Egypt using MAT. The prevalence rate of the parasite was 13.9%. The highest prevalence was in the native breed (17.65%) and the 6-8-months age group (19.4%) .	AbouLaila et al. (2011)
Quails	The presence of anti- <i>T. gondii</i> antibodies in the fecal and serum samples of native quails in Giza province, Egypt has been detected. It has been found that <i>T. gondii</i> antibodies prevalence rates were 29.8 and 25.5%, using MAT and LAT, respectively.	Raafat et al. (2011)
Free-range and commercial chickens	The seroprevalence rates of <i>T. gondii</i> in chickens of six Egyptian governorates were compared using ELISA. In addition, the presence of local <i>T. gondii</i> chicken strain was confirmed by PCR. The total prevalence rate was 68.8% comprised of 59.5%, 82.3%, 67.1%, 62.2%, 75%, and 50% in El Sharkia, El Gharbia, Kafr El sheikh, Cairo, Quena, and Sohag governorates, respectively. Moreover, the prevalence rates were higher among free-range (69.5%) than commercial farm chickens (68.5%); while the prevalence rate was less in upper Egypt than lower Egypt governorates and Cairo.	Barakat et al. (2012)
Free-range and farmed chickens	The seroprevalence of <i>T. gondii</i> infection in domestic chickens and humans in Beni-Suef province, Egypt was demonstrated. Serum samples of 215 (90 free-range and 125 farmed) chickens were examined using MAT. In addition, 250 sera samples were collected and examined for IgG using ELISA. The results showed 20% and 9.6% of antibodies of <i>T. gondii</i> in free-range and farmed chickens, respectively. However, antibodies to <i>T. gondii</i> were detected in 37.5% of poultry contact workers and in 30.5% of non-poultry contacts persons. Seroprevalence of 45.0 and 41.66% were observed among persons of ages 41-50 years and >50 years, respectively.	Aboelhadid et al. (2013)
Chickens	A total of 304 blood and brain samples were collected from chickens in the Delta provinces of Egypt. The prevalence rates of <i>T. gondii</i> infection were 11.18%, 6.91%, 6.91% using ELISA, histopathology, and immunohistochemistry methods, respectively. Moreover, significant differences in the prevalence of <i>T. gondii</i> were detected on the basis of season, sex and habitat.	Ibrahim et al. (2016a)
Ostriches	One hundred and twenty serum samples from ostriches in Ismailia province, Egypt were tested for anti- <i>T. gondii</i> antibodies using ELISA and MAT tests. Using enzyme immunoassay, 5 out of 120 birds (4.2%) were positive to IgM, while 11 birds (9.2%) were positive to IgG. However, MAT detected IgG in 15 birds (12.5%). The results of PCR revealed the presence of <i>T. gondii</i> DNA in the blood of 9 birds (7.5%). The results of PCR of the tissues showed positive <i>T. gondii</i> DNA in 5 dead birds either in the heart, brain, and thigh muscles.	El-Madawy and Metawea (2013)
Quails	One hundred samples were collected from 7-37 days old diseased quails in Assiut and El-Menia governorates, Egypt. The results of Giemsa-stained smears revealed the presence of <i>Toxoplasma's</i> tachyzoites in 7% of the examined samples.	Hassan et al. (2020)

Table 1. The incidences and the prevalence rates of *Toxoplasma gondii* infections in different avian species from different provinces in Egypt in the period from 2000-2020.

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The seroprevalences of *Toxoplasma* infections in humans varied from 27 % to 68% in asymptomatic pregnant women (Ghoneim et al., 2010; El Deeb et al., 2012; Ibrahim et al., 2016b), 26% in cerebrospinal fluid of patients with meningoencephalitis (Mabrouk and Dahawi, 1991), and 59.6% in blood donors without signs (Elsheikha et al., 2009). It has been reported a higher percentage of toxoplasmosis among Egyptians with liver cirrhosis (El-Henawy et al., 2015; El-Sayed et al., 2016). In the Province of Sharkia, Egypt, Mostafa et al. (2018) demonstrated a significant correlation between the seroprevalence of *T. gondii* in patients and the presence of different types of tumors as breast cancer, bone's squamous cell carcinoma, and brain tumors. Anti-*Toxoplasma* IgG was found in patients with liver tumors and bladder cancer, while IgM was detected in patients with benign uterine tumors, bone carcinoma, and breast cancer. In addition, *T. gondii* oocysts were detected in immuno-stained brain sections. In another study revealed a significantly higher proportion of seropositive anti-*Toxoplasma* IgG antibodies among type I diabetes mellitus patients (45%) compared with the control group (23.3%) (Khattab et al., 2019).

Prevention and control of toxoplasmosis

Estimation of zoonotic diseases in animals and birds is helpful for monitoring and improving public health in humans. Therefore, a definitive diagnosis of *Toxoplasma* infection in animals is necessary to prevent human zoonose infection (AbouLaila et al., 2011). Definitive diagnosis of zoonotic diseases with public health concerns, such as toxoplasmosis is very helpful for the prevention of human infection (AbouLaila et al., 2011).

Consumption of insufficiently cooked meat of birds should be avoided as well as fecal contamination from birds should be controlled (Raafat et al., 2011). Nardoni et al. (2019) demonstrated the wide distribution of *T. gondii* in game and wild birds and advised accurate estimation of the human infection risks in handling, managing, and eating wild bird species with regard to domestic carnivores and the impact of viscera or offal's in the environment.

Free-ranged and farmed chickens are regarded as a potential risk to the contact resident persons, so, application of strict preventive hygiene measures is a must to avoid transmission of *T. gondii* infection from birds to humans (Aboelhadid et al., 2013; Mikaeel and Al-Saeed, 2020).

It is very essential to implement a high level of education and awareness among populations to reduce the prevalence of toxoplasmosis (Jones et al., 2001). Consumption of undercooked animal products or unwashed raw vegetable/fruit, poor hands hygiene, and un-carful contact with soil, farm animals, and birds should be avoided (El Deeb et al., 2012). Furthermore, periodic exclusion diagnosis of toxoplasmosis in patients with chronic diseases should be done to avoid the possibility of increasing the disease's severity and for possible management of these malignancies.

CONCLUSION

Toxoplasmosis represents a complex problem, not only for animals and birds but also for human health, especially under Egyptian conditions. However, the current situation of avian toxoplasmosis in Egypt still needs more investigation. Therefore, periodical detection of toxoplasmosis prevalence's in living birds or in their products as well as application of hygienic measures in poultry farms are important to avoid the possibility of zoonotic transmission. In addition, periodical testing and examination, as well as public health awareness of human populations, are very critical.

DECLARATIONS

Competing interests

The author has not declared any conflict of interest.

Ethical considerations

Plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy have been checked by the author.

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4. References in the text should be arranged chronologically (e.g. Kelebeni, 1983; Usman and Smith, 1992 and Agindotan et al., 2003). The list of references should be arranged alphabetically on author's surnames, and chronologically per author. If an author's name in the list is also mentioned with co-authors, the following order should be used: Publications of the single author, arranged according to publication dates - publications of the same author with one co-author - publications of the author with more than one co-author. Publications by the same author(s) in the same year should be listed as 1992a, 1992b, etc.

5. Names of authors and title of journals, published in non-latin alphabets should be transliterated in English.

6. A sample of standard reference is " 1th Author surname A, 2th Author surname B , 3th Author surname C. 2013. Article title should be regular and 7 pt . *World Vet. J.*, Add No. of Volume (Issue No.): 00-00."

7. The color of references in the text of article is dark blue. Example: (Preziosi et al., 2002; Mills et al., 2015).

8. At least 35% of the references of any submitted manuscript (for all types of article) should include scientific results published in the last five years.

-Examples (at the text- blue highlighted)

Abayomi (2000), Agindotan et al. (2003), (Kelebeni, 1983), (Usman and Smith, 1992), (Chege, 1998; Chukwura, 1987a,b; Tijani, 1993,1995), (Kumasi et al., 2001).

--Examples (at References section)

a) For journal:

Lucy MC (2000). Regulation of ovarian follicular growth by somatotropin and insulin- like growth factors in cattle. Journal of Dairy Science, 83: 1635-1647. DOI: XXX

Kareem SK (2001). Response of albino rats to dietary level of mango cake. Journal of Agricultural Research and Development. pp 31-38. DOI: XXX

Chikere CB, Omoni VT and Chikere BO (2008). Distribution of potential nosocomial pathogens in a hospital environment. African Journal of Biotechnology. 7: 3535-3539. DOI: XX

b) For symposia reports and abstracts:

Cruz EM, Almatar S, Aludul EK and Al-Yaqout A (2000). Preliminary Studies on the Performance and Feeding Behaviour of Silver Pomfret (Pampus argentens euphrasen) Fingerlings fed with Commercial Feed and Reared in Fibreglass Tanks. Asian Fisheries Society Manila, Philippine 13: 191-199. Link

c) For edited symposia, special issues, etc., published in a journal:

Korevaar H (1992). The nitrogen balance on intensive Dutch dairy farms: a review. In: A. A. Jongebreur et al. (Editors), Effects of Cattle and Pig Production Systems on the Environment: Livestock Production Science, 31: 17-27. Link

d) For books:

AOAC (1990). Association of Official Analytical Chemists. Official Methods of Analysis, 15th Edition. Washington D.C. pp. 69-88. Link

Pelczar JR, Harley JP, Klein DA (1993). Microbiology: Concepts and Applications. McGraw-Hill Inc., New York, pp. 591-603. Link

e) Books, containing sections written by different authors:

Kunev M (1979). Pig Fattening. In: A. Alexiev (Editor), Farm Animal Feeding. Vol. III. Feeding of Different Animal Species, Zemizdat, Sofia, p. 233-243 (Bg). Link

In referring to a personal communication the two words are followed by the year, e.g. (Brown, J. M., personal communication, 1982). In this case initials are given in the text.

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Nomenclature should follow that given in NCBI web page and Chemical Abstracts. Standard abbreviations are preferable. If a new abbreviation is used, it should be defined at its first usage. Abbreviations should be presented in one paragraph, in the format: "term: definition". Please separate the items by ";". E.g. ANN: artificial neural network; CFS: closed form solution...

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Percent	%		

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6. In the English articles, a decimal point should be used instead of a decimal comma.

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