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Microbial Agents Causing Mortalities in Turkey Flocks in Egypt: An Update on the Epidemiological Situation

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REVIEW ARTICLE
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ABSTRACT

Numerous microbial agents, encompassing viral, bacterial, and parasitic pathogens, contribute to significant mortality in turkey flocks, adversely affecting the global turkey industry. This review presents a comprehensive overview of these microbial threats, with an updated epidemiological perspective focusing on Egypt, while emphasizing their broader implications for the turkey industry worldwide. Viral pathogens, such as the Newcastle disease virus, avian influenza virus, avian metapneumovirus, and turkey hemorrhagic enteritis virus, are associated with mortality rates reaching up to 100% in both young and adult turkeys. Additionally, turkey coronavirus has been reported to cause mortality rates of up to 50% in turkey poults. Bacterial infections, which may act as primary or secondary pathogens, also contribute to significant mortality in turkeys. Key bacterial agents include *Mycoplasma spp., Bordetella avium, Ornithobacterium rhinotracheale, avian pathogenic Escherichia coli (APEC), Pasteurella multocida, and Salmonella spp*. Furthermore, parasitic diseases, particularly histomoniasis and coccidiosis, are responsible for elevated mortality rates in turkey flocks.

Keywords: Bacterial, Mortality, Parasitic, Turkey, Viral

INTRODUCTION

Poultry comprises the majority of domesticated animals worldwide and is a critical component of animal production (Conan et al., 2012). The poultry industry remains extremely important and a chief source of income because it acts as a main source of meat and eggs for humans (Fasina et al., 2012). Turkey rearing is rapidly expanding in Egypt, ranking second to the chicken sector (Taha, 2003). Turkey meat has become more popular nowadays because of its higher protein content (22.19%), lower fat percentage (1.21%), and lower cost (Jukna et al., 2012). However, infectious diseases, particularly viral agents, such as the avian influenza virus *(AIV)* and Newcastle disease virus *(NDV)*, turkey coronavirus *(TCoV)*, avian metapneumovirus *(AMPV*), and turkey hemorrhagic enteritis virus *(THEV)*, have severe negative impacts on the turkey industry (Shehata and Hafez, 2024a). Moreover, several bacterial and parasitic agents cause massive financial losses in turkeys (Hafez and Shehata, 2024; Hernandez-Velasco et al., 2024, Figure 1).

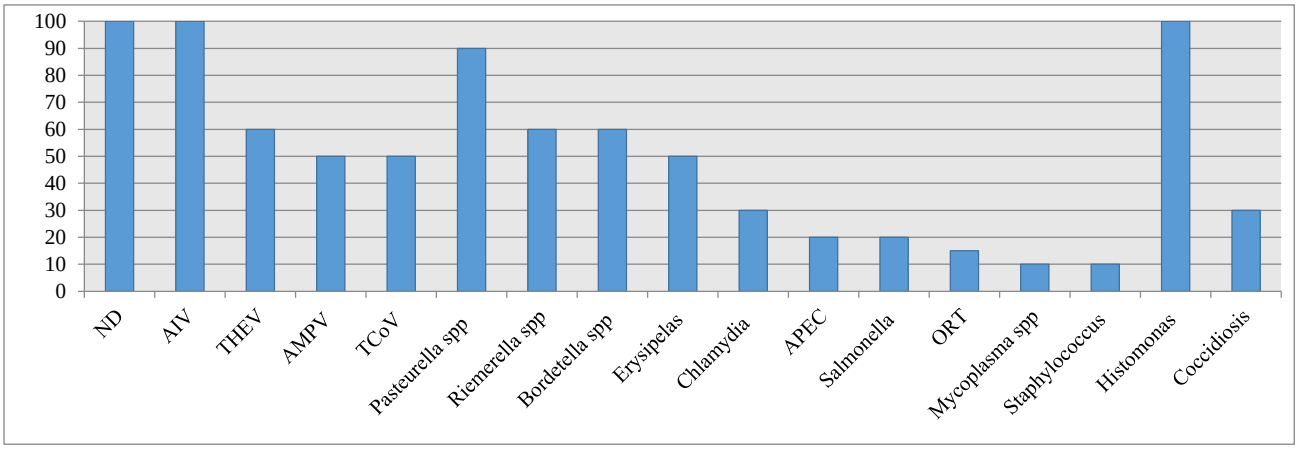

Figure 1. Percentage of mortalities caused by viral, bacterial, and parasitic agents infecting turkeys, showing that the highest mortality percentages are induced by NDV, AIV, Pasteurella spp., and histomonas *ND: Newcastle disease, AIV: Avian influenza virus, THEV: Turkey hemorrhagic enteritis virus, AMPV: Avian metapneumovirus, TCoV: Turkey coronavirus, APEC: Avian pathogenic *E. coli*, ORT: *Ornithobacterium rhinotracheale.* (The figure was created based on data from research results in this review). Source: Shehata and Hafez, 2024a; Hafez and Shehata, 2024; Hernandez-Velasco et al., 2024.

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Due to the limited availability of review articles addressing the microbial etiologies of turkey mortality in Egypt in recent years. Therefore, this review seeks to comprehensively outline the microbial pathogens associated with mortality in turkey flocks and to provide an updated assessment of the epidemiological situation in Egypt.

METHODS

Study design

A systematic literature search was conducted following the guidelines of Preferred Reporting Items for Systematic Reviews and Meta-Analysis (PRISMA, Moher et al. 2009) to identify current literature on microbial agents causing mortalities in turkey flocks, and this allowed the authors of the current study to further highlight relevant search terms and clarify inclusion and exclusion criteria as well as avoid duplication of efforts (Pham et al. 2014). For this review, the authors searched numerous electronic databases, including PubMed, Web of Science, ResearchGate, ScienceDirect, Online Library, and Google Scholar websites for published and unpublished articles (about 1000) in the last 24 years (2000 to 2024). Therefore, 110 articles that included the criteria were reviewed for the study.

The search strategy included Medical Subject Headings and text to look through these databases using the following keywords including avian influenza, antimicrobial, Bordetella, bacteria, Egypt, *Escherichia coli* (*E. coli)*, mycoplasma, mortality, Newcastle, *ornithobacterium rhinotracheale*, parasite, PCR, *salmonella*, staph, signs, sequence, turkey, turkey rhinotracheitis**,** turkey hemorrhagic enteritis, turkey coronavirus, virus, etc. Duplicates were removed, and then a screening of titles and abstracts was performed, followed by a collection of the full texts.

Selection criteria

Articles reporting microbial agents causing mortalities in turkey flocks were included. Studies were included or excluded following predefined criteria. Inclusion criteria were peer-reviewed articles and reviews published between 2000 and 2024, molecular studies on microbial agents causing mortalities in turkey flocks, recent studies of these agents in Egypt, abstracts, and full texts that are available in English. While exclusion criteria were reports published before 2000, reports of mortality in species other than turkey, studies with unclear information on turkey mortality, and studies related to other pathogens were not included in the review.

MORTALITIES CAUSED BY VIRAL AGENTS

Newcastle disease

Newcastle disease *(ND)* is an extremely contagious viral illness that is fatal to 250 species of domestic and wild birds of different ages (Afonso et al., 2016). Newcastle disease virus is an (APMV-1) that belongs to the genus Avulavirus and the family Paramyxoviridae (Miller et al., 2010). The virus is a single serotype with multiple genotypes and sub-genotypes (Diel et al., 2012). Regarding the F protein sequences, NDV is classified into 2 classes (I and II) (Liu et al., 2009). Class I strains comprise a single genotype, but class II strains comprise 21 different genotypes (Dimitrov et al., 2019).

Newcastle disease virus is a negative-stranded, non-segmented RNA with a total genome size of 15198 bp (Czeglédi et al., 2006). There is a variation in the amino acid in the F protein cleavage site between low and virulent strains. Low virulent NDV strains contain monobasic amino acids. They are cleaved by extracellular proteases in the gastrointestinal and respiratory systems. In contrast, highly virulent NDV strains have multibasic amino acids. They are cleaved by all furin-like intracellular proteases found throughout the body (Adam, 2012).

Five ND pathotypes depend on clinical signs and post-mortem (PM) lesions (Marks et al., 2014). Velogenic viscerotropic ND is a very virulent form with an elevated morbidity and mortality rate of up to 100% in young and old age (Falcon, 2004; Miller and Koch, 2013). Infected turkeys with this form of NDV showed blood-tinged diarrhea, dyspnea, and incoordination. Postmortem examination reveals conjunctivitis, hemorrhage in the small intestine, tracheal and splenic necrosis. Histopathological examination reveals atrophy of lymphoid organs and an ulcer in the intestine. While velogenic neurotropic ND causes respiratory and nervous symptoms. Infected turkeys show rapid respiration, periorbital edema, and leg and wing paralysis. Histopathological examination reveals Purkinje fiber necrosis and perivascular cuffing (Piacenti et al., 2006; Wakamatsu et al., 2006; Eid et al., 2022).

Mesogenic ND is related to respiratory and nervous symptoms and has a relatively low mortality rate. Its symptoms include mild respiratory signs and egg production problems (Getabalew et al., 2019). Lentogenic and quiescent enteric ND are both associated with little to no clinical symptoms. Histopathological inspection of infected turkeys reveals mild lymphocytic infiltration in the trachea, air sacs, and eyelid (Piacenti et al., 2006). NDV may be isolated in (SPF) chick embryos and chicken embryo fibroblasts. Serological tests include HI, ELISA, and immunofluorescence assay (Mao et al., 2022).

During 2019-2020, NDV was detected in 47-day-old converter turkeys in Sharkia government in Egypt using RT-PCR targeting the F gene, and the strains belonged to class II genotype VII. 1.1 (Eid et al., 2022). NDV was also detected in Turkey and Egypt in 2019 using PCR targeting the F gene. Pathotyping of the isolates showed velogenic NDVs with 1.90 ICPIs. Characterization using partial F gene sequencing demonstrated that the isolates have 112GRRQKR↓F117 at the fusion protein cleavage site and are grouped with Genotype VII. 1.1 (Lebdah et al., 2022). Moreover, NDV was detected by real-time RT-PCR targeting the F gene of the virulent strains in 443 flocks of turkeys and chickens in Egypt, and most of the isolates are from genotype VII. 1.1 (Abozaid and Abdel-Moneim, 2022).

Avian influenza

Avian influenza (AI) viruses are members of the Orthomyxoviridae family, which has a negative-sense, single-stranded, segmented genome that is 13.5 kb in size (Sangsiriwut et al., 2018). Avian influenza viruses are divided into 16 subtypes depending upon hemagglutinin and 9 subtypes depending upon neuraminidase (Fouchier et al., 2005). AI viruses are classified into HPAI and LPAI (Collins et al., 2002). HPAI is a multi-organ systemic disease produced by several subtypes of H5 and H7. Meanwhile, LPAI H9N2 causes subclinical infections, including those of the respiratory or reproductive systems (Swayne and Pantin-Jackwood, 2008).

The first HPAI H5N1 detection in poultry in Egypt was in 2006, and the disease became endemic in 2008 (Aly et al., 2008). The bobwhite quail was the source of the first LPAI H9N2 isolation in Egypt in 2011 (El-Zoghby et al., 2012). The situation became more challenging with the appearance of HPAIV H5N8 (clade 2.3.4.4b) in Egypt in 2016 (Hassan et al., 2021). Domestic ducks and wild birds were the source of the first HPAI H5N1 clade 2.3.4.4b detection in Egypt in 2021 (El-Shesheny et al., 2023).

Infected turkeys with HPAI may be found dead without any signs. Other clinical signs include depression, sinusitis, erythematous lesions around the head, diarrhea, hemorrhages on the shanks, nervous signs, and mortality up to 100% in young and old ages (Elbers et al., 2004a; Capua and Marangon, 2006). PM lesions of HPAI include tracheitis, neck edema, and hemorrhage in a diversity of organs, including the spleen, liver, kidneys, and intestines. In addition, atrophy of lymphoid organs, splenic necrosis, and mottled pancreas (Elbers et al., 2004b).

Low pathogenic avian influenza (LPAI) viruses often induce significantly less severe clinical manifestations compared to highly pathogenic avian influenza viruses (HPAIVs). Clinical manifestations observed in turkeys include lethargy, varying degrees of respiratory distress, diarrhea, and adverse effects on egg production. LPAI PM lesions are infraorbital sinusitis and fibrino-necrotic exudate in the bronchi, trachea, and lung (Corrand et al., 2012). Infected turkey layers and breeders showed ovarian regression and rupture of mature ova, resulting in egg yolk peritonitis (Studniski, 2024).

Histopathological inspection of HPAI in turkeys reveals edema, congestion in the lungs, and lymphoid depletion (Burcham et al., 2017). While LPAI reveals fibrino-necrotic inflammation in the trachea, bronchi, and lung with leucocytic infiltration (Corrand et al., 2012).

In 2007, HPAI H5N1 was detected by real-time PCR targeting M, H5, and N1 genes in backyard turkeys in Egypt (Hafez et al., 2010). Furthermore, in 2016, real-time PCR was used for the detection of HPAI H5N1 in turkey flocks aged 10-12 weeks in Egypt with previous vaccination against H5N2 and H5N1 at 8 and 34 days, respectively. According to phylogenetic analysis, the virus was a member of clade 2.2.1.2 (Salaheldin et al., 2017). Recently, AIV subtype H5N8 was detected by real-time PCR from a backyard turkey flock with 100% mortality and categorized under clade 2.3.4.4.b. (Hussein et al., 2024). While H9N2 was detected from turkey flocks in 2014 in Egypt by real-time PCR, the isolates belong to the G1-like lineage (Nagui et al., 2015).

Turkey rhinotracheitis (TRT)

Avian metapneumovirus is a member of the Paramyxoviridae family and genus Metapneumovirus. The virus has a non-segmented genome with a total size of 13 kb (Abdel-Azeem et al., 2014). The AMPV genome encodes 8 genes, including fusion, phosphoprotein, nucleocapsid, matrix, second matrix, polymerase, small hydrophobic, and surface glycoprotein (Banet-Noach et al., 2005). Based on genomic examination and viral antigenic features, many isolates are classified into 4 subtypes, including A, B, C, and D (Cook and Cavanagh, 2002).

The virus multiplies in the genital and respiratory tracts of infected turkeys (Turpin, 2002). AMPV causes congestion of the upper airway, foamy conjunctivitis, rales, infraorbital sinusitis, a decrease in egg production, a change in the quality of the eggshell, and a mortality rate of 50% in young and old ages (Jones and Rautenschlein, 2013).

The gross pathology of AMPV includes tracheitis, laryngitis, and rhinitis. Microscopic lesions include submucosal lymphoid cell infiltration and intracytoplasmic inclusion bodies in conjunctival epithelial cells, turbinate, and trachea (Cha et al., 2007). The virus may be isolated in embryonated chicken eggs and tracheal organ cultures (Jones and

Rautenschlein, 2013). Serological methods used for the identification of AMPV are ELISA and virus neutralization tests (Cook and Cavanagh, 2002; Kapczynski et al., 2008).

During 2008-2009, AMPV was detected by RT-PCR from tracheal swabs of white turkey flocks with respiratory distress in the north of Turkey, and sequencing of the glycoprotein revealed that all positive samples were subtype B, with 95% similarity with the reference strain aMPV subtype B (Ongor et al., 2010). Moreover, during 2014-2015, AMPV subtype B was detected by RT-PCR from 26 samples representing 3 out of 63 unvaccinated turkey flocks at 102-163 days old in Iran (Mayahi et al., 2017).

In Egypt, AMPV subtype A was detected in turkeys by real-time PCR, and sequencing of the glycoprotein gene revealed a high level of identity with Nigerian strains (96.4%) (Abdel-Azeem et al., 2014). During 2021-2022, AMPV was also detected by RT-PCR targeting the M gene in turkey flocks in Egypt, with a death rate ranging from 7-23% (Hussein et al., 2024).

Turkey hemorrhagic enteritis (THE)

Turkey hemorrhagic enteritis virus is a dsDNA virus from the genus *Siadenovirus* and family Adenoviridae with a total genome of 25.5 kb (Beach, 2006). Hemorrhagic enteritis virus was detected by conventional PCR targeting the HEV hexon gene from 4-8-week-old turkey flocks in Germany from 2008 to 2012. According to phylogenetic analysis, HEV field isolates exhibited a high degree of sequence similarity (Alkie et al., 2017).

During 2017-2018, HEV was detected by real-time PCR from the spleen of 4-week-old turkeys in Canada, and phylogenetic analysis of the viral genomes revealed that only two out of nine sequences were vaccine-like strains, while seven out of nine were classified as field strains (Palomino-Tapia et al., 2020). Moreover, HEV was detected by PCR from the spleen of 10-week-old commercial turkeys in California with elevated mortality (Ramsubeik et al., 2023).

Turkey coronavirus

Turkey corona (TCOV) enteritis is a significant disease that causes diarrhea in poults, resulting in massive financial losses (Gomaa et al., 2009). It is believed that TCoV is the primary cause of PEMS, or poult enteritis mortality syndrome (Spackmanet al., 2010), which is characterized by watery diarrhea, dehydration, and a mortality rate of 10 to 50% in turkey poults and induced by a combination of several pathogens such as TCoV, adenovirus, Astrovirus (TAstV), and *E. coli* (Barnes et al., 2000).

Turkey coronavirus belongs to the genus CoV and subgenus Igacovirus (Jackwood et al., 2010). The main way of TCoV transmission is the fecal-oral pathway (Gomes et al., 2010). Symptoms of TCoV include watery droppings and severe dehydration (Moura-Alvarez et al., 2014). On necropsy, the intestines are pale and dilated, and the contents are gaseous and watery (Ismail et al., 2003). Microscopic lesions include heterophilic and mononuclear inflammatory cell infiltration in the lamina propria, villus atrophy, and atrophy of the bursa of Fabricius (Brown et al., 2019).

In Canada, TCoV was detected by PCR from turkey poults' intestinal tracts during an outbreak of diarrhea (Hemida et al., 2008). Moreover, TCoV was detected by PCR targeting nucleocapsid genes from turkey flocks with diarrhea and enteritis in Egypt (Gomaa and Mansour, 2009). Finally, the RT-PCR targeting the nucleoprotein (N) gene was used for the detection of TCoV in turkey flocks in Iran with diarrhea, and the daily mortality rate varied from 0.2 to 1.2%. The virus was detected in 8 out of 18 turkey flocks. Phylogenetic analysis of 7 positive samples revealed that there is a close relationship between TCoV and the infectious bronchitis virus (Kashi et al., 2021).

The genome of TCoV comprises 4 structural proteins: spike (S), envelope (E), matrix (M), and nucleocapsid (N), and 15 nonstructural proteins with a total size of 28 kb (Jackwood et al., 2010; Brown et al., 2016).

MORTALITIES CAUSED BY BACTERIAL AGENTS

Mycoplasma

Mycoplasmas are facultative intracellular pathogens with a genome of 600 kbp. Mycoplasmas only have a cell membrane around them and lack a cell wall (Shehata and Hafez, 2024b). Mycoplasma causes ciliostasis and hyperplasia of epithelial cells of the upper airway in turkeys (Sid et al., 2016), impairs the immune system's defense against other pathogens (Papazisi et al., 2003), and causes a mortality rate of 5-10% in young and old ages (Yadav et al., 2022).

Infectious sinusitis in turkeys is caused by *Mycoplasma gallisepticum (MG)* and manifests as coughing, sinusitis, and rales. While *Mycoplasma synoviae (MS)* infections impact the tendon sheaths and joint synovial membranes. Moreover, *Mycoplasma iowae (MI)* causes embryonic death in turkeys, and *Mycoplasma meleagridis (MM)* causes airsaculitis (Shehata and Hafez, 2024b).

During 2017-2018, MG and MS were detected by real-time PCR targeting *mgc2* and *vlhA* genes from tracheal samples isolated from turkey and chicken flocks suffering from respiratory distress in Egypt (Abd El-Hamid et al.,

2019). Moreover, *MG* and *MS* were detected by PCR targeting 16S ribosomal RNA and *mgc2* genes from turkey and chicken flocks in Egypt during 2016-2018 (Marouf et al., 2020).

In Egypt, both *MM* and *MG* were detected by PCR targeting the 16S ribosomal RNA and *mgc2* genes from turkey flocks with sinusitis, and sequencing of the *mgc2* gene of MG isolates revealed 93.1-97.6% identity with each other and 84.9-95.9% with reference strains, while sequencing of 16S rRNA of *MM* isolates reveals 100% identity with each other and 99.7% with *MM* reference strains (Mourad, 2023). While *MG* was detected by PCR from tracheal swabs from non-vaccinated backyard flocks of turkey and chicken with respiratory symptoms in Bandirma, Turkey (Ardıçlı et al., 2024). Finally, *MM* and *MG* were detected by RT-PCR targeting *Mgc2* and 16s from turkey flocks with a mortality range of 7-23% in Behira, Egypt, during 2021-2022 (Hussein et al., 2024).

Bordetella

Avian bordetellosis (turkey coryza) is an extremely infectious bacterial respiratory illness that mostly affects turkeys (Ehsan et al., 2020). It affects turkeys of all ages and is linked to significant morbidity (100%) and mortality rates of 10-60% in turkey poults (Jackwood and Saif, 2008). Although *B. avium* affects turkeys of any age, turkey poults between two and six weeks old are particularly susceptible (Śmietanka et al., 2014).

Turkey coryza is characterized by respiratory distress such as coughing, sneezing, and submaxillary edema. Postmortem lesions include tracheitis, bronchitis, airsaculitis, and pneumonia (Jackwood and Saif, 2008).

In 2016, *B. avium* was detected by PCR targeting *ompA*, *bvgA*, *fimA*, and *fhaB* genes in 2–24-week-old turkeys with respiratory symptoms in Egypt, with a prevalence rate of 22.95% (Eldin et al., 2020). Moreover, PCR targeting the *recA* gene was used for the detection of two strains of *B. avium* from turkeys in Egypt, and sequencing of the *recA* gene demonstrated that the amplified portion of the recA gene exhibited 100% similarity with the American strain 197N and the German strain ATCC 35086 (Erfan et al., 2018).

Ornithobacterium rhinotracheale

Ornithobacterium rhinotracheale (ORT) infection is an extremely infectious bacterial respiratory illness that mostly affects turkeys and chickens (Barbosa et al., 2019). Symptoms of ORT in turkeys include sinusitis, sneezing, coughing, arthritis, a 2-5% decrease in egg production, and variable mortality (1-15%). Postmortem lesions of ORT in turkeys are conjunctivitis, tracheitis, arthritis, meningitis, fibrinous exudate in the air sacs, and lung edema. Heterophilic or mononuclear cell infiltration is the most predominant histopathological abnormality in the infraorbital sinus and trachea (Shehata and Hafez, 2024c).

During 2009-2010, ORT was detected by PCR targeting the 16S RNA gene from the trachea and lung of turkeys in Iran, and sequencing of the 16S rRNA fragment revealed 98% to 100% similarity with other GeneBank sequences (Mirzaie et al., 2011). Moreover, ORT was detected by PCR from 197 out of 481 tracheal swabs (41%) from turkey flocks with respiratory symptoms during 2008-2011 (Numee, 2013). Additionally, ORT was detected in 133 turkey flocks in Poland during 2015-2020 by real-time PCR and conventional PCR with a prevalence of 30.83% and 28.57%, respectively (Kursa et al., 2022). Recently, ORT was detected by PCR in 12 out of 17 turkey flocks in Egypt with a prevalence of 70.59% during 2020-2021 (Mourad et al., 2023).

***Pasteurella multocida* (Fowl cholera)**

Fowl cholera is an extremely infectious bacterial disease that causes massive financial losses in the poultry industry worldwide. *Pasteurella multocida* is the etiological agent of fowl cholera and has 4 capsular serogroups, including A, B, D, and F. The primary serogroup of fowl cholera is serogroup A (Christensen et al., 2008).

There are 3 distinct forms of the disease: Per-acute, acute, and chronic. The per-acute form manifests by sudden death; the acute form is characterized by snood cyanosis, greenish diarrhea, and septicemia with an elevated morbidity and mortality rate of up to 90%, especially in old age. The chronic form is characterized by pneumonia, peritonitis, meningitis, and arthritis (Christensen et al., 2008). Impression smears from infected liver and heart reveal the characteristic bipolarity of *P. multocida* (Abood et al., 2021). During 2011-2012, *Pasteurella multocida* was detected by PCR from turkey flocks in Australia with a history of previous fowl cholera outbreaks (Singh et al., 2013).

Chlamydia

Chlamydia is an obligatory intracellular gram-negative bacterium that belongs to the family Chlamydiaceae, order Chlamydiales (Cheong et al., 2019). Symptoms of chlamydiosis in turkeys include rhinitis, sinusitis, and conjunctivitis, while PM lesions include tracheitis, airsacculitis, pneumonia, enteritis, and a mortality range of 10-30%, especially in young ages (Vanrompay, 2020). *Chlamydia* was detected by PCR targeting the ompA gene in 12 turkey flocks in Egypt, and an impression smear from the infected yolk sac revealed inclusion bodies (Hegazy et al., 2014).

Erysipelothrix rhusiopathiae

There are 2 forms of erysipelas, including acute and chronic. The acute form is characterized by septicemia, congestion in all carcasses, and mortality up to 50%, especially in old age, while the chronic form is distinguished by localized inflammations of the joints, heart valves, and snood (Malik et al., 2021). During 2014-2015, *Erysipelothrix rhusiopathiae* was detected by real-time PCR targeting 16S rRNA from 70-day-old turkeys with septicemia and high mortality in Brazil (Hoepers et al., 2019).

Riemerella anatipestifer

Riemerella anatipestifer infection is an extremely contagious pathogen that mainly affects domestic ducks, geese, and turkeys, with massive financial losses because of weight loss, downgraded carcass, and mortality up to 60%, especially in young birds (Sandhu, 2008).

Riemerella anatipestifer was detected in 24-day-old turkey poults with respiratory distress and high mortality in Croatia using PCR targeting the 16S rRNA gene (Lozica et al., 2021).

Avian pathogenic *Escherichia coli*

Colibacillosis is among the main contributing factors to global financial losses in the poultry industry (Dziva and Stevens, 2008). Symptoms include greenish diarrhea, respiratory distress, arthritis, and mortality. PM lesions include airsacculitis, perihepatitis, pericarditis, pneumonia, enteritis, septicemia, and mortality up to 20% in young and old ages (Nolan et al., 2013). The *E. coli* isolates were detected by PCR from 17-week-old turkey flocks with cellulitis in Iowa, with a prevalence of 88% (De Oliveira et al., 2020). During 2020-2021, *E. coli* was also identified by a MALDI-TOF biotype in 3 out of 51 turkey samples in Spain (Martínez-Laorden et al., 2023). Moreover, 10 *E. coli* isolates were detected by PCR in Egypt. The *iss* and *iutA* genes were detected in 100% of the isolates, while 30% of the isolates had the *eaeA* gene. Serotyping of the isolates revealed the presence of six serotypes: O1, O11, O2, O141, O21, and O78. *E. coli* isolates (Hussein et al., 2024).

Salmonella

Salmonella has a negative impact on the turkey industry worldwide due to decreased egg production, fertility, hatchability, growth rate, and mortality rate of 20% in young and old ages (Hafez, 2013). In 2006/2007, the average *Salmonella* prevalence in all EU member states was 30.7% and 13.6% in fattening and breeding turkey flocks, respectively, whereas the UK had a prevalence of 32.2% and 4.4% (EFSA, 2008). In Egypt, *Salmonella spp*. was detected by PCR targeting the *Salmonella*-specific invA gene from ducklings and turkey poults, and the prevalence rate was 22.5% (Osman et al., 2010). Also, *Salmonella* isolates from turkeys were detected by PCR targeting the oriC gene in Ankara, Turkey, and the result revealed that 110 out of 240 samples were positive (Iseri and Erol, 2010).

Staphylococcus

Staphylococcus (*S.*) infection is among the septicemic diseases in turkey flocks, which is characterized by arthritis, osteomyelitis, septicemia, and a mortality range of 5-10% in young and old ages (Alfonso and Barnes, 2006; Swayne, 2013). In Germany, *Staphylococcus* was detected by real-time PCR targeting the *mec*A gene from 18 out of 20 14-20-week-old turkey flocks with a 4-10% mortality rate in 2009 (Richter et al., 2012). *S. aureus* was identified in Algeria using conventional culture methods during 2011-2018, and the highest prevalence rate was from turkeys (75.6%), breeding hens (52.8%), broilers (48.4%), and laying hens (48.8%) (Benrabia et al., 2020).

MORTALITIES CAUSED BY PARASITIC AGENTS

Histomonas meleagridis is the etiological agent of histomoniasis, a blackhead disease in turkeys. It causes significant financial losses in turkey flocks and a mortality rate of up to 100%, especially at young ages. Clinical signs include reduced appetite, diarrhea, weight loss, and anemia. Postmortem lesions include the cecal core and circular necrotic regions in the liver. Coccidiosis causes significant financial losses due to damage to the intestinal mucosa, malabsorption, weight loss, and mortality up to 30%, especially in young animals. Coccidiosis in turkeys is caused *mostly by E. meleagrimitis* and *E. adenoeides* (Hernandez-Velasco et al., 2024).

CONCLUSION

The global turkey industry is negatively impacted by a variety of pathogens, either viral, bacterial, or parasitic agents. In Egypt, Newcastle disease and avian influenza are the most common pathogens incriminated in turkey mortalities, either in vaccinated or non-vaccinated flocks, which leads to massive economic losses in the Egyptian turkey industry

nowadays. The scarcity of recent data about fowl cholera in Egypt may be due to medication, vaccination, or the stable epidemiological situation of the pathogen. Other pathogens cause economic losses in other countries rather than Egypt, such as turkey hemorrhagic enteritis and erysipelas.

Therefore, routine surveillance of more flocks is essential to identify different pathogens implicated in turkey mortalities and study other infectious and managemental problems. Annual continuous surveillance is recommended to follow up on the evolution of new subtypes of Egyptian viruses. Sequencing of identified pathogens is essential to obtain more data about the pathogens that threaten the turkey industry. A strict program for the prevention and control of these pathogens is necessary to minimize their drawbacks.

DECLARATIONS

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Availability of data and materials

The data presented in this review are available upon reasonable request from the corresponding author.

Authors' contributions

Ashraf Hussein and Hossam Adam contributed to writing, revision, data analysis, and responding to reviewers' comments. Ahmed Mohamed Al-Baqir and Mohamed M. Megahed collected data from the available published papers and reviewed revisions. All authors revised and approved the final manuscript.

Competing interests

The authors have not declared any conflicts of interest.

Ethical considerations

All authors have reviewed and confirmed the content of the review before submission to this journal

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