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Assessment Microbiological Quality for Wild Birds Carcasses in Aswan Governorate, Egypt

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LITTLE information is available about the microbial hazards of game bird's meats. Therefore this study aimed to assess the bacteriological quality of meat cuts obtained from various species of game birds: pintail (*Anas acuta*), shoveler (*Spatula clypeata*), Eurasian wigeon (*Mareca penelope*) and Egyptian goose (*Alopochen aegyptiacus*).The mean counts of aerobic bacteria, *Enterobacteriaceae*, *Staph. aureus*, total Coliform and *E. coli* were 4.91, 4.35, 3.44, 3.94 and 3.76 in breast meat, while the corresponding counts in thigh meat were 5.19, 4.47, 3.42, 4.07 and 3.90 log CFU/g.A few counts of *Pseudomonas* and *Clostridium perfringens* (<10 CFU/g) were found, whereas yeasts and molds ranged from 10 to 2.2 $\times 10^2$ CFU/g in all the examined meat samples. Aerobic bacteria, *staph. aureus*, yeasts and molds were high observed in pintail and shoveler than wigeon and Egyptian goose birds ($p< 0.05$). Neither *Salmonella* spp. nor *Listeria monocytogenes* could be isolated from the examined game bird carcasses. The public health aspects for the estimated and isolated microorganisms were discussed.

Keywords: Bacteriological Quality, Health Situation, Game bird's meats.

Introduction

Several European countries are currently observing an increase in small gamebirds harvest, but in African countries, this industry was not significantly contributing and thus it is continuing development. Game meat the greater original source of animal protein in human nutrition for poorer countries and the more developed countries, as well as game consumption was a popular activity in many communities (Ahl et al., 2002). The annual consumption of game meat in many countries differ from 0.6 to 1.0 kg per / person in Austria, France, Germany and Switzerland (Atanassova et al., 2008; Membré et al., 2011). Meanwhile, it was 3.3 kg per/person in Norway (Lillehaug et al., 2005), or in hunters' families up to 4.0 kg per/person in Northern Italy (Ramanzin et al., 2010). In many countries game meat exported or imported in substantial amount such as Germany.

Game birds may load zoonotic bacteria in their skin or intestines and transfer them to hunters through handling and cause contaminated meat. Therefore, good manufacturing practices (GMPs) throughout game bird handling and good cooling requirements of harvesting meat as specified in European union (EU) legislation at ≤4 °C (EC, 2004) and appropriate heat treatment are needed to reduce the health risk for hunters and consumers (Sauvala et al., 2021).

Meat from wild animals is similar to meat from domestic animals in foodborne infections, therefore, the aerobic bacterial count and *Enterobacteriaceae* count and presence or absence of pathogenic bacteria is all important factors in evaluating the sanitary quality of game meat (Atanassova et al., 2008). General indicators used in meat and poultry industries include mesophilic aerobic counts and *Enterobacteriaceae*, coliforms, *Pseudomonas* spp., lactic acid bacteria, yeasts and

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molds for evaluation of the potential shelf-life (Capita et al., 2001; Álvarez-Astorga et al., 2002; Capita et al., 2002).

Presence of Coliforms bacteria and *E. coli* in raw meat indicates unsanitary conditions, however, they are indicators of fecal contamination at slaughter house during evisceration intestinal contents and washing (Duffy et al., 2003). High level of *Enterobacteriaceae* and aerobic bacterial counts in poultry carcasses can be employed as indicators of poor hygiene during processing and storage (Roberts et al., 1995; Zweifel et al., 2005). Moreover, *Staph. aureus* is one of the most common food poisoning bacteriadue to the synthesis of toxins (Collins, 1967). *Pseudomonas* spp. found in everywhere and isolated from various sources, including drinking water, domestic and wild animals, humans, plants, and a variety of foods. Moreover, decrease the shelf life of food productsby creating lipolytic and proteolytic enzymes, which are responsible for most of the food degradation during storage. (Arnaut-Rollier et al., 1999; Adams & Maurice, 2008; Franzetti & Scarpellini, 2007). *Salmonella* spp. commonly settle in gastrointestinal tract of animals, though preventative procedures, the meat of animals contaminated with *Salmonella* during slaughter of skin or gastrointestinal tract (Arthur et al., 2008; Garrido et al., 2014; Wu et al., 2014). Presence *Listeria monocytogenes* expected in wild avian species and also be a part of the resident microflora in food plants (Klinth-Jensen et al., 2004).

In North Africa particularly Egypt, a large number of wild ducks are hunted and sold as live birds in several governorates through the period of September to March every year. Despite the presence of many studies on domestic poultry, only few studies are devoted to the microbial quality of game bird meats with only one scientific paper on wild duck meats (Khalifa & Nassar, 2001) in Egypt. Therefore, the aim of this study was to evaluate the microbiological quality of meat cuts obtained from various species of game birds namely Pintail (*Anas acuta*), Shoveler (*Spatula clypeata*), Eurasian wigeon (*Mareca Penelope*) and Egyptian Goose (*Alopochen aegyptiacus*) which are known in Egypt with the local names Balbol, Kish,Al-Sawaa and pharaony goose, respectively.

Materials and Methods

Birds

Birds were obtained in live and healthy forms directly from hunters, where they were hunted using net instrument,and were procured of Lake Nasser hunters from Gerf Hussein south Aswan city during September and November 2020. Almost 68 birds were studied, 24 Pintail (*Anas acuta*), 24 shoveler (*Spatula clypeata*), 12 Eurasian wigeon (*Mareca Penelope*), eight Egyptian Goose (*Alopochen aegyptiacus*), each group comprised of male and female's ratio (1:1). The birds were slaughtered according to Islamic law and left to bleed freely for 5 minutes and then hand plucked and eviscerated. The carcass was cut into four quarters and washed with tap water. The pieces of meat and skin of each of the breast and thigh were minced, then packed in sterile polyethylene bags, and then stored at -20 ° C until microbiological analysis was performed.

Microbiological analysis procedures

Twenty-five gm of minced breast and thigh meats was taken under antiseptic conditions. The appropriate samples were transferred to aseptic stomacher bag, mixed with 225 ml of 0.1% sterile peptone waterand a homogenate in stomacher lab blender at 2000 rpm for 1-2 min to give 10^{-1} (APHA, 1992). Serial dilutions prepared in ten-fold using sterile peptone water were spread or mixed on appropriate media for each microbe for enumeration and isolation of targeted microorganism in the present study. Samples were analyzed at Animal Health Research Institute, Food Microbiology Unit, Giza, Egypt.

Enumeration of Aerobic bacterial count

The total aerobic bacterial count of all the studied samples were determined according to the method of (ISO, 2013) as follow: One ml of three suitable serial dilutions of each sample were poured into sterile petri dish and thoroughly mixed with 15-20 ml of nutrient agar medium. Plats were incubated at (30±1) °C for (72±3) hours, then the total number of colonies was counted and multiplied by the conforming dilution to obtain the total number of bacterial colonies per gram sample. Values obtained were compared to guidelines of Egyptian organization for standardization (EOS, 2005).

Enumeration of Staph. aureus count

According toFDA (2001) using Barid-parker Agar (BPA), briefly, 1mL of required serial dilutions was poured into Barid-parker Agar plate, the plates were incubated at (37±1) °C for 24 – 48 hr. All typical colonies, characterized by gray to jet-blackcolor with light-colored (off-white)

margin and 2-3 mm in diameter were examined and recorded as total *staph. aureus* count.Values obtained were compared to guidelines of EOS (2005).

Enumeration of coliform bacteria and E. coil

According to FDA (2002), the method was performed through three stages. First stage: Presumptive test for coliform, three tubes of lauryl tryptosesulfate (LTS) broth were inoculated with 1 ml of the serial dilutions formerly prepared 10^{-1}, 10^{-2} and 10^{-3}. The tubes were then incubated at 37°C, positive tubes produced gas, therefore, all tubes display turbidity with gas were considered as Presumptive positive for total coliforms. Second stage: Confirmatory test. Tubes containing brilliant green lactose bile (BGBL) brothwere inoculated with three loopful of presumptive positive tubes and incubated at 35-37 °C for 24-48 hr. Tubes showing turbidity and gas at 37°C after 48 hr were registered as positive for total coliform. Whereas tubes display turbidity and gas production after 48 hr at 44±0.2 °C were registered as positive for fecal coliform. Third stage: complementary test for *E. **coli***, Chromocult Coliform Agar (CCA) plates were inoculated by positive tubes from fecal coliform and incubated for 24 ht at 37°C. All typical colonies, characterized by blue-black colonies with a green metallic sheen were specified as *E. coli*, values obtained of total coliforms were compared to guidelines of EOS (2005).

Enumeration of Enterobacteriaceaecount

According to APHA (2015) using Violet Red Bile Glucose (VRBG) Agar, briefly, 1mL of required serial dilution was pour plated ontoviolet, red bile glucose ager, the plates were incubated at 37±1°C for 24 – 48 hr. All typical colonies, characterized by red or purple colorwere examined and recorded as total *Enterobacteriaceae* count; values obtained were compared to guidelines of European commission (EC, 2005).

Enumeration of Clostridium perfringens count

According to ISO (2004) using Sulfite Polymyxin Sulfadiazine (SPS) Agar medium, plates were incubated at 37 °C for 72 hr in an aerobically conditions. All typical colonies, characterized by form black colonies on SPS medium were examined and recorded as total *Clostridium perfringens* count, values obtained were compared to guidelines of EOS (2005).

Enumeration of Pseudomonas count

According to Rita Ramalho et al. (2002) using Pseudomonas Agar Base (PAB) supplemented with CFC (Pseudomonas) Supplement contains Cetrimide, Fusidic Acid and Cefaloridin, briefly, 1mL of required serial dilution was poured plated onto PAB, plates were incubated at 41.5 °C for 24 and 48 hr.

Enumeration of yeasts and molds count

According to ISO (2008) using Dichloran Rose-Bengal Chlortetracycline (DRBC) Agar and then the plates were incubated at 25 °C for 5-7 days; values obtained were compared to guidelines of EOS (2005).

Detection of Salmonella spp.

25 g of sample with Buffered peptone water and incubated at 34 °C and 37 °C for 24 hr (non-selective enrichment) stage, in the enrichment stage 0.1 ml of non-selective enrichment broth was transferred into Rappaport-Vassiliadis Soya (RVS) broth and incubated at 37 °C for 24 hr. From the cultures obtained enrichment stage broth inoculated with Xylose Lysine Deoxycholate (XLD) Agar and incubated at 37 °C for 24 hr, then Confirmation of *Salmonella* spp.was made using biochemical tests according to ISO (2017a).

Detection ofListeria monocytogenes

25 g of sample with Buffered Listeria enrichment broth (BLEB) and incubated at 30 °C for 24 hr to 26 hr (selective enrichment) stage, in the isolation stage take one loop full of the enriched broth using sterile inoculating loop and streak on Oxford Agar (OXA) and incubated at 35 °C for 24-48 hr, then after incubation typical Listeria species colonies are gray to black colonies surrounded by a black halo (ISO, 2017b).

Statistical analysis

Results were expressed as the mean ± standard error. Statistical differences between genotype and sexes were specified by tow-way analysis of variance (ANOVA) using the Duncan's Multiple Range test atsignificant level of 0.05 using SPSS program (SPSS, 2001). for windows software, version 25. The significance difference was set at ($p< 0.05$).

Results and Discussion

Microbial analysis of meat samples taken from breast and thigh of wild birds (male and female) was carried out and the obtained results were tabulated in Tables 1 & 2. Data revealed that total of aerobic bacterial count ranged between 3.98 – 5.80 and 4.28 – 5.90 CFU/g for meat samples of breast and thigh, respectively. It could be concluded that

there was a significant difference in total aerobic bacterial count between the different birds from breast and leg meats at (P< 0.05). Therefore, the higher aerobic bacterial count was observed in breast of Pintail and Shoveler birds (5.46 to 5.80 logCFU/g),while the lower count was in breast of wigeon and Egyptian goose birds (3.96 to 4.47 log CFU/g) (Table 1). The same trend was observed in thigh muscles, where aerobic bacterial count recorded (5.72 to 5.90 log CFU/g) and (4.28 to 5.02 log CFU/g) for Pintail, Shovelerbirds and wigeon, Egyptian goose birds, respectively. These findings agree with that recorded by Abdallaha et al. (2014) which calculated the total count of aerobic bacteria in domestic duck carcasses in Egypt by about 4.97 and 5.49 CFU/g for breast and thigh meat, respectively. Also, El-Ghareeb et al. (2009) determined the aerobic bacterial count in breast and thigh meat of wild partridges, quails and pheasants by about (4.19 and 5.30), (6.48); (5.48 and 5.48) log CFU/g, respectively. However, it was lower compared to the findings obtained by Edris et al. (2015) in chicken meat 7.94 log CFU/g. According to the safe permissible limit specified by EOS (2005) for total aerobic bacterial count, it was clear that, the result of Pintail and Shoveler meats was not compatible to EOS that recommended aerobic bacterial counts not exceed 10^5, whilst wigeon and Egyptian goose meats agree with EOS limits.The higher microbial load of examined wild bird carcasses samples may be accredited to those live birds loading great numbers of bacteria on their faces, feet, and feathers. In addition to cross contamination through scalding and defeathering processes and the unsanitary hygienic conditions through handling particularly during evisceration which play a main role in microbial contamination.

Numbers of *Staph. aureus* generally ranged from <10 CFU/g to 3.69 log CFU/g in breast and thigh meats. On the other hand,there was a highly significant difference of *Staph. aureus* between the different birds from breast and thigh meats at (P< 0.05). Results in Tables 1 & 2, revealed that the higher count was in breast and thigh meat of Pintail and Shoveler birds 3.23 to 3.69 log CFU/g, while the lower count was recorded in breast and thighmeat of wigeon and Egyptian goose birds <10 CFU/g except breast meat of Egyptian goose male recorded 3.03 log CFU/g. These results came in accordance with those of other investigators in duck carcasses 3.34log CFU/g (Abdallaha et al., 2014), in wild birds <2.00 to 5.90log CFU/g (El-Ghareeb et al., 2009) and in wild quail 3.30log CFU/g (El-Dengawy & Nassar, 2001), while higher count reported by Buzón-Durán et al. (2017) in raw poultry-based meat preparations 4.07 log CFU/g.According to the safe permissible limit specified by EOS (2005) recommended that,*Staph. aureus*(didn'texceed 10^2 cfu/g), therefore, samples ofPintail and Shoveler birds were unaccepted (exceeded >2.00 log CFU/g), but wigeon and Egyptian goose bird samples were accepted (didn't exceeded <2.00 log CFU/g).The highestcount of *Staph aureus*may be due to sample meat minced with skin and the presence of *Staph. aureus*in a food marker contamination from workers handling, skin and nose or mouth. The wide variation in*Staph aureus* countsbetween different bird meats meat may be attributed to environmental conditions for birds, feeding variation (herbivorous, carnivorous, and omnivorous) andpotential differences in handling by personnel.

Presence of Coliforms and *E.coli* in raw meat was due to serious deficiencies in sanitary conditions, however, they are indicators of fecal contamination at slaughter house during evisceration "intestinal contents" and washing (Duffy et al., 2003). The coliforms and *E. coli* counts were achieved in Tables 1 & 2. The results revealed that *E. coli* and Coliforms ranged from 2.95 to 4.48 and 3.57 to 4.84 log CFU/g in breast and thigh meats, respectively. Moreover, it was clear that, there was no significant difference of Coliforms and *E. coli* counts between the different birds from breast and thigh meats at (P> 0.05). The present results are also in agreement with values observed by El-Ghareeb et al. (2009) in wild partridges, pigeons, quails and pheasants in Egypt *E. coli* recorded 4.12 log CFU/g and Paulsen et al., (2008) in uneviscerated wild pheasant in the Slovak Republic *E. coli* recorded 2.0 to4.1 log CFU/g, in contrast, lower coliforms loads were observed by El-Dengawy & Nassar (2001) for wild quail carcasses in Egypt 6×10^2 CFU/g and Cordero et al. (2019) for domestic and wild pigeon breast meats in Spain 2.11 and 1.10 log CFU/g, respectively. According to the safe permissible limit specified by EOS (2005) recommended that, coliforms (didn't exceed 10^2 CFU/g), therefore, samples of all examined muscles were unaccepted (exceeded >2.00 log CFU/g). The contamination with Coliforms may be from water as sources of Coliforms in meat and during slaughtering and dressing of carcasses and cutting carcasses into various parts. Moreover, the presence of *E. coli* in the examined samples is an indicator for carcass may be contaminated with intestinal microflora of animals.

TABLE 1. Microbial counts of breast meat samples from pintail and shoveler, Eurasian wigeon, Egyptian geese(Mean± standard error).

	Northern Pintail		Northern Shoveler		Eurasian wigeon		Egyptian Geese		P-Value	
Microorganisms	**Male**	**Female**	**Male**	**Female**	**Male**	**Female**	**Male**	**Female**	**Genotype (G)**	**Sex (S)**
Aerobic bacterial count	5.8 ± 0.2	5.7± 0.2	5.6± 0.6	5.46 ± 0.3	3.98± 0.5	4.31 ± 0.2	4.47± 0.3	3.96± 0.12	0.001	0.823
Staph. aureus	3.51± 0.6	3.53± 0.3	3.47± 0.3	3.23± 0.6	<10	<10	3.03± 0.3	<10	*0.000*	*0.425*
Escherichia coli	3.92± 0.1	4.84± 0.5	3.90± 0.8	3.27± 0.7	3.63± 0.3	3.01± 0.4	3.68± 0.2	3.83± 0.5	*0.193*	*0.896*
Total coliform	4.03± 0.1	4.6± 0.8	3.99± 0.3	3.48± 0.6	4.03± 0.4	3.51± 0.4	3.89± 0.0	4± 0.7	*0.649*	*0.815*
Enterobacteriaceae	4.08± 0.3	4.91± 0.5	4.30± 0.6	3.70± 0.4	4.68± 0.1	3.74± 0.2	4.81± 0.8	4.60± 0.4	0.455	0.493
Clostridium perfringens	2.1	2.27	<10	<10	<10	<10	<10	<10	_	_
Pseudomonas	<10	<10	<10	<10	<10	<10	<10	<10	_	_
Yeasts	2.1×10^{r}	3x10	$2.2x10^{2}$	<10	<10	<10	<10	<10		
Molds	7×10	1x102	7x10	6x10	<10	<10	<10	<10		
***Salmonella* spp.**	ND	ND	ND	ND	ND	ND	ND	ND		
Listeria monocytogenes	ND	ND	ND	ND	ND	ND	ND	ND		

Abbreviations:**log (CFU/g)** log colony forming units per gram (CFU/g), <10 means lower count than colony forming units per gram (CFU/g), (**ND**) No detected, Yeast and Molds calculated as (CFU/g), (p-value) of > 0.05 non-significant (NS) difference, p-value < 0.05 significant difference.

TABLE 2. Microbial counts of thigh meat samples from pintail and shoveler, Eurasian wigeon, Egyptian geese leg meats. (Mean± standard error).

	Northern Pintail		Northern Shoveler		Eurasian wigeon		Egyptian Geese		P-Value	
Microorganisms	**Male**	**Female**	**Male**	**Female**	**Male**	**Female**	**Male**	**Female**	**Genotype (G)**	**Sex (S)**
Aerobic bacterial count	5.79± 0.2	5.72± 0.1	5.73± 0.7	5.90± 0.1	4.28± 0.6	4.70± 0.5	5.02 ± 0.1	4.41± 0.5	0.008	0.946
Staph. aureus	3.3 ± 0.4	3.69± 0.2	3.39± 0.4	3.30± 0.6	<10	<10	<10	<10	0.000	0.720
Escherichia coli	3.89± 0.6	4.76± 0.3	4.02± 0.6	4.24± 0.3	3.09± 0.3	4.31± 0.4	3.96± 0.6	2.95 ± 0.9	0.376	0.399
Total coliform	3.95± 0.6	3.85± 0.5	4.06± 0.1	4.28±0.3	3.57± 0.2	4.43± 0.4	4.48± 0.4	3.91± 0.6	0.881	0.731
Enterobacteriaceae	4.07± 0.2	4.89± 0.5	4.87± 0.3	4.28± 0.7	3.76± 0.8	4.38± 0.1	5.57± 0.5	3.95± 0.9	0.676	0.644
Clostridium perfringens	<10	<10	<10	<10	<10	<10	<10	<10	_	_
Pseudomonas	<10	<10	<10	<10	<10	<10	<10	<10	_	_
Yeasts	1.7×10^3	10×3	2.1×10^2	5×10	<10	<10	1×10	1×10		
Molds	1×10	7×10	7×10	7×10	<10	<10	1×10	1×10		
***Salmonella*spp.**	ND	ND	ND	ND	ND	ND	ND	ND		
Listeria monocytogenes	ND	ND	ND	ND	ND	ND	ND	ND		

Abbreviations:**log (CFU/g)** log colony forming units per gram (CFU/g), <10 means lower count than colony forming units per gram (CFU/g), (**ND**) No detected, Yeast and Molds calculated as (CFU/g), (p-value) of > 0.05 non-significant (NS) difference, p-value < 0.05 significant difference.

Total plate count of *Enterobacteriaceae* especially *E. coli* are generally used as indicatorfor deficiencies in hygiene programs according to EC (2005). These bacteria may occur during unsatisfactory hygienic measures of handling, processing, and storage. The *Enterobacteriaceae* counts of wild birds' meat are presented in Tables 1 & 2, The results revealed that, *Enterobacteriaceae* ranged from 3.70 to 4.91 and 3.76 to 5.57 log CFU/g in breast and thigh meats, respectively. No significant differences were observed on *Enterobacteriaceae* counts between the different birds from breast and thigh meats at (P> 0.05). The number of *Enterobacteriaceae* isolated from wild birds' meat in the present study was almost like that obtained by previous investigators.

El-Ghareeb et al. (2009) reported that the number of *Enterobacteriaceae* isolated from fresh breast and thigh muscles of hunted partridges and pigeons were (4.00; 4.48) and (3.48; 4.00) log CFU/g, respectively. The same value was recorded by Mousa et al. (2016). Also, Abdallah et al. (2014) found that the mean values of total *Enterobacteriaceae* isolated from frozen breast and thigh duck meat were 7.85×10^3 and 9.13×10^4 CFU/g, respectively. On the other hand, lower values (2.60 to 3.74 log CFU/g) were found in breast, thigh and liver cuts of farm and hunted wild pheasants (Buňková et al., 2016). Also,2.06 and 1.35 log CFU/g were recorded by Cordero *et al*. (2019) for breast meat of domestic and wild pigeon, respectively. According to the safe permissible limit specified by Center for Food Safety (CFS, 2014), which recommended that, *Enterobacteriaceae* should not exceed (10^2 CFU/g), and also EC (2005) which recommended that, *Enterobacteriaceae* should not exceed 2,5 log CFU/ cm2), therefore, samples of all samples examined in the current study were unaccepted (exceeded >2.00 log CFU/g).

Pseudomonas species are linked with spoilage of meat producing off-odors, off-flavors, discoloration and gas production (Borch et al., 1996; Arnaut-Rollier et al., 1999). More recent, Franzetti & Scarpellini (2007) reported that *Pseudomonas* spp. reduce the shelf life and thus the quality of food products by releasing lipolytic and proteolytic enzymes, which are the most common causes of food spoilage during storage.

However, examination of breast and thigh meat samples of the studied wild birds for the presence of *Pseudomonas* bacteria indicated that total counts of *Pseudomonas* spp. were <10 log CFU /g of all examined samples, as shown in Tables 1 & 2. According to Mead (2005), the initial count of *Pseudomonas* species on poultry products should not exceed 100 CFU/g under aerobic conditions to provide optimal storage life and sensory qualities. Therefore, *Pseudomonas* count obtained in the present study was lower than the recommended limits.

Poultry carcass and meat cuts may be contaminated with *Clostridium perfringens* from intestinal contents through slaughter house process especially during evisceration (Voidarou et al., 2011). Thus, numbers of *Clostridium Perfringens* in the present study were found to be <10 CFU/g for all examined muscles or may not be exist, as shown in Tables 1 & 2, except breast muscles of Pintail male and females recorded 2.1 and 2.27 log CFU/g. Refer to some previous studies, (Khalifa & Nassar, 2001; El-Dengawy & Nassar, 2001) it found that, *Clostridium perfringens* could not be detected in breast and thigh of wild duck and quails, but in other studies Shaltout et al. (2017) found that total count of vegetative form of *Clostridium perfringens* in raw and cooked chicken meat samples were 1.15 x 10^4 and 2.7 x 10^2 CFU/g, respectively. Shaltout et al. (2017) found that, total count of vegetative form of *Clostridium perfringens* in rawbreast and thigh chicken meat samples were $9.1x10^3$ and $2.5x10^4$ CFU/g, respectively. According to the safe permissible limit specified by EOS (2005) recommended that, *Clostridium Perfringens* (didn't exceed 10^3CFU/g).

Regarding mold and yeast counts in tested wild birds' meat samples data in Tables 1&2 revealed that, pintail and shoveler samples showed higher contamination levels than wigeon and Egyptian goose samples. The breast samples of pintail and shoveler recorded 30 to 220 and 60 to 100 CFU/g for yeasts and molds, respectively. Leg samples of the same two types of birds contained 30 to 210 CFU/g for yeasts and10 to 70 CFU/g for molds. In contrast, the contamination levels of wigeon and Egyptian goose samples with yeasts or molds recorded<10 CFU/g in all examined samples. The present results were consistent with that observed by Mahdy et al. (2019) (10 to 1.1 x 10^3 CFU/g) in chilled and frozen duck meat, and by Odetunde et al. (2011) (1.3×10^1 to1.5×10^2 CFU/g in chilled chicken meat. Meanwhile, Abdallaha et al. (2014) recorded 7.57×10^2 and 1.12×10^3 CFU/g in duck

breast and thigh meat. In contrast, Almorshidy (2013) found that, raw poultry samples were free from fungi. According to the maximum permissible limits stipulated by EOS (2005) which recommended that the contamination level should not be exceed than 10^2 CFU/g. On the other hand, most of the studied samples especially of wigeon and Egyptian goose proved to be acceptable.

Salmonella spp. and *Listeria monocytogenes* were not detected in all examined samples. it is evident that the *Salmonella* Spp. are in the permissible limit of (EOS, 2005) for raw poultry meat (sample should be free), so that, these samples are accepted according to the EOS (2005). The obtained results are similar to that obtained by Sidorov et al. (2021) they found that, *Salmonella* was not detected in wild wigeon, shoveler and scoter duck carcasses samples, except for mallard duck carcass. Also, Paulsen et al. (2008) and El-Dengawy & Nassar (2001) found that, *salmonella* was not recovered from any sample of wild pheasant and wild quail carcasses in Egypt.

Conclusion

From the presented results it could be concluded that birds' meats were highly contaminated with *Enterobacteriaceae,* Coliform and *E. coli*, therefore, this indicates that higher microbial load in wild birds may be accredited to those live birds loading great numbers of bacteria on their faces, feet, feathers, and skin, as well as lack of hygiene measures during handling and processing by hunters.Wigeon and Egyptian goose birds showed safe for human consumption than pintail and shoveler birds, because its lower count of aerobic bacterial count, *Staphylococcus auras,* molds and yeasts. Therefore, there is an urgent need to improve health situation of wild bird game meats, hence, good manufacturing practices (GMPs) during game bird handling, good cooling requirements, appropriate heat treatment (cooking) and E-beam irradiation applications must be enforced to reduce microbial load.

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