Advances in Microbiology, 2014, 4, 774-779
Published Online September 2014 in SciRes. http://www.scirp.org/journal/aim
http://dx.doi.org/10.4236/aim.2014.412085

Scientific Research

Microbial Assessment of Turkey (*Meleagris ocellata* L.) and Duck (*Anas platyrhynchos* L.) Faeces (Droppings) in Akure Metropolis

Deke Victoria Adegunloye, Felix Abiodun Adejumo

Department of Microbiology, Federal University of Technology, Akure, Nigeria
Email: adegunloyedeke@yahoo.com

Received 13 June 2014; revised 12 July 2014; accepted 9 August 2014

Abstract

This study was carried out to determine the occurrence of bacteria and fungi in populations of turkey and duck faeces. The prevalence of bacteria and fungi in the faeces of domesticated turkey and ducks (*Meleagris ocellata* and *Anas platyrhynchos*) in the City of Akure (Nigeria) was investigated. Five different locations were sampled in Akure Metropolis in April for each of turkey and duck faeces using standard microbiological methods. The microbial load for bacteria ranged from 16.23×10^5 to 30.04×10^5 cfu/g and 12.60×10^5 to 46.01×10^5 cfu/g for turkey and duck faeces respectively while the fungal count ranged from 12.38×10^5 to 28.05×10^5 s/g and 10.60×10^5 to 34.09×10^5 s/g for turkey and duck faeces respectively. The following bacteria were isolated from turkey faeces: *Azomonas agilis*, *Bacillus cereus*, *Escherichia coli*, *Proteus vulgaris*, *Sarcina maxima*, *Thiocapsa lumicola*, *Staphylococcus aureus*, *Enterococcus* spp., *Xanthomonas fragariae* and *Streptococcus* spp. while *Aeromonas hydrophila*, *Bacillus cereus*, *Echerichia coli*, *Proteus vulgaris*, *Lactobacillus* spp., *Sarcina maxima*, *Streptobacillus moniliformis*, *Staphylococcus aureus*, *Enterococcus* spp and *Streptococcus* spp. were isolated from duck faces. Bacteria common to both turkey and duck faeces are *Bacillus cereus*, *Escherichia coli*, *Proteus vulgaris*, *Sarcina maxima*, *Staphylococcus aureus*, *Enterococcus* spp. and *Streptococcus* spp. The fungal species isolated includes *Mucor* spp., *Cladosporium* spp., *Aspergillus fumigatus* and *Aspergillus flavus*, *Alternaria* sp., *Candida* spp., *Fusarium* spp., *Varicosporium elodea* and *Penicillium* spp. Some of the isolated microorganisms are of major importance in the natural environment as well as food and drug production. It could be concluded that turkey and duck faeces are a potential human health hazard and that accumulation of their droppings may pose a public health risk and can cause illness.

Keywords

Assessment, Duck, Microbial, Turkey

How to cite this paper: Adegunloye, D.V. and Adejumo, F.A. (2014) Microbial Assessment of Turkey (*Meleagris ocellata* L.) and Duck (*Anas platyrhynchos* L.) Faeces (Droppings) in Akure Metropolis. *Advances in Microbiology*, **4**, 774-779.
http://dx.doi.org/10.4236/aim.2014.412085

1. Introduction

A turkey is either of two or three living species of large birds in the genus *Meleagris*. One species, *Meleagris gallopavo*, commonly known as the Wild Turkey, is native to the forests of North America. The other species, *Meleagris ocellata*, known as the Ocellated Turkey, is native to the forests of the Yucatán Peninsula. The domestic turkey is a descendant of the Wild Turkey [1]. Duck is the common name for a number of species in the Anatidae family of birds. The ducks are divided between several subfamilies in the Anatidae family; they do not represent a monophyletic group but a form taxon, since swans and geese are not considered ducks. Ducks are mostly aquatic birds, mostly smaller than the swans and geese, and may be found in both fresh water and sea water (The American Heritage Dictionary of the English Language [2]).

Poultry faeces are waste products excreted by poultry fowls such as chickens, ducks, turkey and geese. It can also be defined as the by-product that resulted from the digestion of food intake by poultry birds. Faeces can be in form of semi-solid or water and the colour varies among the species of birds. Some are whitish, ashes and dark brown in colour. There are several billions of bacteria present in poultry faeces including pathogenic and non-pathogenic species, the normal flora and the opportunistic ones [3]. The nutrient composition of poultry faeces varies with the type of bird, the feed ration, the proportion of litter droppings, the manure handling system, and the type of litter. They also vary in both physical and chemical composition and the factors affecting the composition includes: the types of birds, number of birds per unit area, nutrient density of the feed, environmental factors and other management factors [4]. The chemical composition of faeces consists of water, nitrogen, phosphorus and potassium with some other minerals. The chemical composition supports the growth of billion of microorganisms which contaminate various poultry products e.g. eggs and meat. Poultry faeces contain three important elements that make it to be used as manure. Its organic matter content makes it suitable to be used as soil conditioner [3].

Poultry faeces are a complete nuisance in an age where there is concern with pollution of the environment. It is moist and because of its nutrient and organic matter content, the manure is a suitable breeding ground for pestiferous flies like houseflies, flesh flies, black garbage flies and biting stable flies. The manure is also a source of odour, caused by the production of fatty acids such as butyric, valeric, capronic and caprylic acids [3].

The high nutrient content of bird excrement provides an excellent sanctuary for potentially harmful organisms. Bird droppings do pose a public health risk and cause illness. Humans become infected by inhaling dust containing dried faeces, urine, or respiratory secretions of infected birds [5]. Other sources of exposure include a bite from an infected bird and handling the plumage and tissues of infected birds. Poultry droppings cause corrosion on roofs around the dumpsite due to accumulation of droppings while the birds are resting on them [6]. The study was carried out to isolate and identify microorganisms that are associated with turkey and duck faeces in Akure metropolis; and to determine the pathogenic microorganisms present as well as their potential transmission and health implications on the human environment.

2. Materials and Methods

2.1. Collection of Samples

The research targeted five locations (Lafe, Danjuma, Adebowale, Oke ogba, Aule) during the month of April in Akure metropolis. Faecal samples of fresh droppings were scooped in triplicates into sterile sampling bottles and labeled appropriately with the source, time and date of collection. They were transported to the laboratory for analysis. Samples were collected from domesticated turkey and ducks.

2.2. Detection of Aerobic Bacteria and Fungi

Bacteriological and mycological examinations were carried out using standard methods for aerobic bacteria and fungi [7]. For the detection of aerobic bacteria, all samples were serially diluted and plated on Nutrient agar and subsequently incubated aerobically at 37˚C for 24 hours. Typical bacterial colonies were randomly selected, examined microscopically for their morphology and re cultivated to obtain pure cultures.

2.3. Cultivation of Bacteria

About 1 g of fresh droppings was thoroughly mixed in 10 ml of normal saline. Aliquot (1.0 ml) was transferred

into the next test tube and diluted serially in one-tenth stepwise to 10^5 dilution. From the dilution of 10^5 of dropping sample, 0.1 ml aliquot was transferred aseptically onto freshly prepared nutrient agar plates and spread with a sterile bent glass rod. The inoculated plates were inverted and incubated at 37˚C for 24 hours after which the plates were examined for growth. Pure cultures of bacteria were obtained by aseptically streaking representative colonies of different morphological types, which appear on the cultured plates onto freshly prepared nutrient agar plates from the incubator. Discrete bacteria colonies that developed were sub cultured on nutrient agar slopes and incubated at 37˚C for 24 hours. The identification of isolated bacteria was based on colony morphology, microscopic examination and biochemical characteristics.

2.4. Cultivation of Fungi

For the detection of fungi, the serially diluted samples were plated on Sabouraud Dextrose Agar and incubated at 24˚C for 4 - 10 days. Fungi were identified macroscopically based on colony morphology, and microscopically using lactophenol staining. Colonies that developed were observed macroscopically for distinguishing characteristics. They were later sub cultured to obtain pure cultures. The following standard characterization tests were performed in duplicates: macroscopic examination was done by observing the colony morphology diameter, color (pigmentation), texture and surface appearance. Microscopic examination was done. Observations were made for the sexual and asexual reproductive structures like sporangia, conidial head, arthrospores and the vegetative mycelium. The complete identification of fungal isolates was by comparing the result of their cultural and morphological characteristics with those of known taxa [8].

2.5. Statistical Analysis

The results obtained were statistically analysed using analysis of variance (ANOVA), and tests of significance carried out by Duncan's multiple range test at $P \leq 0.05$.

3. Results

Prevalence of Microbial Contamination

Mean total bacterial viable counts are shown in **Table 1**. The bacterial population isolated from turkey and duck faeces showed a range of 16.33 to 30.00 × 10^5 cfu/g and 12.67 to 46.00 × 10^5 cfu/g respectively while the fungal population mean values (as shown in **Table 2**) were 21.8 cfu/spore and 21.2 cfu/spore for duck and turkey faeces respectively. A total of 12 bacteria isolates were isolated and identified from turkey and duck faeces which are highlighted in **Table 3**. Bacterial colony count was done to determine the total number of microorganisms present in the duck and turkey faecal samples collected. The colony forming units were established as: Colony forming unit (cfu) = (number of colonies per plate) (dilution factor).

4. Discussion

Numerous Bacterial and Fungal species were identified in the fecal sample obtained from the turkey and duck faeces. The bacterial population isolated from turkey and duck faeces showed a range of 16.23 to 30.04 × 10^5 cfu/g and 12.60 to 46.01 × 10^5 cfu/g respectively while the fungal population mean values were 21.80 cfu/ spore

Table 1. Bacterial counts in turkey and duck faeces.

	Turkey faeces	Duck faeces
Sample location	Bacterial count (cfu/g)	Bacterial count (cfu/g)
A	$16.23 \pm 0.09^a \times 10^5$	$38.56 \pm 0.02^a \times 10^5$
B	$25.40 \pm 0.07^b \times 10^5$	$29.31 \pm 0.05^b \times 10^5$
C	$27.10 \pm 0.09^c \times 10^5$	$12.60 \pm 0.06^c \times 10^5$
D	$28.47 \pm 0.22^d \times 10^5$	$19.64 \pm 0.09^d \times 10^5$
E	$30.04 \pm 0.59^e \times 10^5$	$46.01 \pm 0.36^e \times 10^5$

KEY: A—Lafe, B—Danjuma, C—Adebowale, D—Oke ogba, E—Aule. Values are means of triplicates ±SD. Values in the same column carrying the same superscript are not significantly different according to Duncan's multiple range test at ($P \leq 0.05$).

Table 2. Fungal counts in turkey and duck faeces.

	Turkey faeces	Duck faeces
Sample location	Fungal count (spore/g)	Fungal count (spore/g)
A	$26.59 \pm 0.05 \times 10^5$	$34.09 \pm 0.12 \times 10^5$
B	$18.44 \pm 0.11 \times 10^5$	$17.56 \pm 0.12 \times 10^5$
C	$12.38 \pm 0.06 \times 10^5$	$10.60 \pm 0.13 \times 10^5$
D	$22.77 \pm 0.11 \times 10^5$	$19.38 \pm 0.33 \times 10^5$
E	$28.05 \pm 0.06 \times 10^5$	$30.03 \pm 0.03 \times 10^5$

KEY: A—Lafe, B—Danjuma, C—Adebowale, D—Oke ogba, E—Aule. Values are means of triplicates ±SD. Values in the same column carrying the same superscript are not significantly different according to Duncan's multiple range test at ($P \leq 0.05$).

Table 3. Microorganisms isolated from turkey and duck faeces.

	Microorganisms isolated	Percentage occurrence (%)
Turkey faeces	*Azomonas agilis*	5.53
	Bacillus cereus	9.94
	Escherichia coli	15.55
	Proteus vulgaris	5.77
	Sarcina maxima	3.23
	Thiocapsa lumicola	4.02
	Staphylococcus spp.	13.74
	Enterococcus spp.	4.01
	Xanthomonas fragariae	6.72
	Streptococcus spp.	3.23
	Mucor spp.	4.22
	Cladosporium spp.	2.34
	Aspergillus fumigates	3.48
	Aspergillus flavus	8.08
	Alternaria spp.	2.45
	Candida spp.	3.22
	Fusarium spp.	4.47
Duck faeces	*Aeromonas hydrophila*	10.03
	Bacillus cereus	8.77
	Escherichia coli	20.05
	Proteus vulgaris	6.34
	Sarcina maxima	4.20
	Lactobacillus spp.	8.89
	Staphylococcus spp.	11.2
	Enterococcus spp.	6.37
	Streptococcus spp.	6.64
	Streptobacillus monoliformis	2.23
	Penicillium spp.	3.45
	Varicosporium elodea	1.22
	Fusarium spp.	2.55
	Aspergillus flavus	4.02
	Mucor spp.	1.04
	Aspergillus niger	3.00

and 21.20 cfu/spore for duck and turkey faeces respectively. The microbial population of the faeces varies from one location of sampling to another. Differences in environmental conditions such as water activity, pH, oxidation-reduction potential, nutrient content may be responsible for the difference in the microbial population [9].

The identified bacterial species from turkey faeces includes *Azomonas agilis*, *Bacillus cereus*, *Escherichia coli*, *Proteus vulgaris*, *Sarcina maxima*, *Thiocapsa lumicola*, *Staphylococcus aureus*, *Enterococcus* spp., *Xanthomonas fragariae* and *Streptococcus* spp. (**Table 3**). These identified bacterial species was in accordance with the findings of Jingrang and Domingo [10], Ksenija *et al*. [11] and Adegunloye [3] as they also isolated a large group of bacteria from turkey droppings. The identified bacteria from duck faeces (**Table 3**) includes *Aeromonas hydrophila*, *Bacillus cereus*, *Echerichia coli*, *Proteus vulgaris*, *Lactobacillus* spp., *Sarcina maxima*, *Streptobacillus moniliformis*, *Staphylococcus aureus* and *Enterococcus* spp. This finding correlates with that of Murphy *et al*. [12], Ksenija *et al*. [11] and Aguirre *et al*. [13]. Bacteria found out to be common to both turkey and duck faeces are *Bacillus cereus*, *Staphylococcus aureus*, *Proteus vulgaris*, *Escherichia coli and Enterococcus* spp. This could be due to the similar nature of the food/feed intake and digestive tract of both turkey and duck [14]. The microorganisms present in the turkey and duck faeces can be traced to a few sources-feed, cage or nest, normal intestinal flora, feeding water and air borne organisms [9].

The study suggests that turkey and ducks can harbour *E. coli* isolates, probably reflecting the presence of such isolates in their sources of food and/or water in the environment. Brittingham *et al*. [15] and Kocijan *et al*. [16] reported that *Staphylococcus* spp. and *Streptococcus* spp. are ubiquitous and of low pathogenicity and usually found in poultry feed. Birds (such as turkey and ducks) excrete these bacteria via the alimentary tract. The same authors assume that *E. coli* is pathogenic specie. Hinsworth *et al*. [17] implicated *Streptococcus monoloformis* with rat bites, fever, bacteremia as well as drinking water diseases. In addition, bird faeces can easily contaminate areas where aerosols are produced and the aerosols can carry the bacteria in a similar way to contaminate foods and air. It is also possible that many of the bacterial entities when disseminated to humans and other animals could also cause subclinical respiratory illnesses [18].

In contrast, some of the isolated microorganisms are of major importance in the natural environment as well as food and drug production. Members of the genus *Aspergillus* are sources of natural products that can be used in the development of medications to treat human diseases. The largest application of *Aspergillus niger* is as the major source of citric acid and is commonly used for the production of native and foreign enzymes, including glucose oxidase and hen egg white lysozyme [19]. Members of the genus *Penicillium* produce penicillin, a molecule that is used as an antibiotic, which kills or stops the growth of certain kinds of bacteria in human body [20].

In accordance with this research, Hubálek [21] also reported a large number of fungal species isolated from poultry birds. He proved the presence of 41 species of fungi isolated from 858 samples (feathers, nests, pellets, and droppings) collected from different species of free-living birds. In addition, data on alimentary microflora may be indicative for an assessment of potential public health risks. Further microbiological investigations are needed, to define the health status of these birds, in order to estimate the real risks of the cohabitation of turkey and ducks with humans.

5. Conclusion

A survey of the natural microflora of turkey and duck faeces identified both bacteria that are potentially human pathogenic and non pathogenic ones and that both turkey and ducks are possible reservoirs of pathogenic bacteria. The pathogenic ones are potential human health hazards as they can contaminate products such as eggs and meat as well as air and water in surrounding environment and eventually lead to different types of infections. Their presence in the air could also cause negative health effects. In conclusion, the contribution of each reservoir of bacterial species identified to the incidence of human infection is still unknown and needs to be investigated. In recommendation, observing good and hygienic measures can reduce the diseases caused when an individual comes into contact with the turkey and duck droppings.

References

[1] Smith, A.F. (2006) The Turkey: An American Story. University of Illinois Press, Champaign, 17.

[2] (2006) The American Heritage Dictionary of the English Language. Houghton Mifflin Company. 4th Edition. http://dictionary.reference.com/browse/duckling

[3] Adegunloye, D.V. (2006) Microorganisms Associated with Poultry Faeces. *Journal of Food, Agriculture and Environment*, **4**, 41-42.

[4] Vest, L., Merka, B. and Segars, W.I. (2004) Composition of Poultry Waste. The University of Georgia, Georgia College of Agric and Environmental Sciences, Athens.

[5] Chang, W.N., Huang, C.R., Lei, C.B., Lee, P.Y., Chien C.C. and Chang, H.W. (2004) Serotypes of Clinical Cerebrospinal Fluid *Cryptococcus neoformans* Isolates from Southern Taiwan and Their *in Vitro* Susceptibilities to Amphotricin B, Fluconazole, and Voriconazole. *Japanese Journal of Infectious Diseases*, **57**, 113-115.

[6] Horta, J.A., Staats, C.C., Casali, A.K., Ribeiro, A.M., Schrank, I.S. and Schrank, A. (2002) Epidemiological Aspects of Clinical and Environmental *Cryptococcus neoformans* Isolates in the Brazilian State Rio Grande do Sul. *Medical Mycology*, **40**, 565-571. http://dx.doi.org/10.1080/714031150

[7] Brown, A.E. (2005) Benson's Microbiological Applications: Laboratory Manual in General Microbiology (Reidy, P.E. and Fornango, J.S., Eds.). McGraw-Hill, Inc., New York.

[8] Barnett, H.L. and Hunter, B.B. (1972) Illustrated General of Imperfect Fungi. 3rd Edition, Burgrees Publishing Co., 193.

[9] Frazier, W.C. and Westhoff, D.C. (2003) Food Microbiology. 18th Edition, Tata McGraw Hill, Inc., New York.

[10] Jingrang, D.A. and Domingo S.S. (2008) US Environmental Protection Agency. Office of Research and Development, National Risk Management Laboratory, Cinicinnati, 387.

[11] Vlahović, K., Prukner-Radovčić, E., Horvatek, D., Pavlak, M., Gomerčić, T., Rumiha, Z. and Dovc, A. (2010) Bacterial and Fungal Flora in Faecal Samples from Rooks (*Corvus frugilegus*) in the City of Zagreb, Croatia. *Veterinarski Arhiv*, **80**, 81-92.

[12] Murphy, J., Devane, M.L., Robson, B. and Gilpin, B.J. (2005) Genotypic Characterization of Bacteria Cultured from Duck Faeces. *Journal of Applied Microbiology*, **99**, 301-309. http://dx.doi.org/10.1111/j.1365-2672.2005.02590.x

[13] Aguirre, A.A., Quan, T.J., Cook, R.S. and McLean, R.G. (1992) Cloacal Flora Isolated from Wild Black-Bellied Whistling Ducks (*Dendrocygna autumnali*) in Laguna La Nacha, Mexico. *Avian Diseases*, **36**, 459-462. http://dx.doi.org/10.2307/1591530

[14] Bryan, F.L. (1980) Poultry and Poultry Meat Products. In: Silliker, J.H., *et al.*, Eds., *Microbial Ecology of Foods, Volume II. Factors Affecting Life and Death of Microorganisms*, Academic Press, Inc., New York, 410-458.

[15] Brittingham, M.C., Lemaitre, J.P. and Rousset, A. (1998) Prevalence of Listeria sp. in Droppings from Urban Rooks (*Corvus frugilegus*). *Journal of Applied Microbiology*, **82**, 641-647.

[16] Kocijan, I., Prukner-Radovčić, E., Beck, R., Galov, A., Marinculić, A. and Sušić, G. (2009) Microflora and Internal Parasites of the Digestive Tract of Eurasian Griffon Vultures (*Gyps fulvus*) in Croatia. *European Journal of Wildlife Research*, **55**, 71-74. http://dx.doi.org/10.1007/s10344-008-0209-4

[17] Hinsworth, C.G., Parsons, K.L. and Jardine, C. (2013) Rats, Cities, People and Pathogens: A Systematic Review and Narrative Synthesis of Literature Regarding the Ecology of Rat-Associated Zoonoses in Urban Centres. *Vector-Borne and Zoonotic Diseases*, **13**, 349-359. http://dx.doi.org/10.1089/vbz.2012.1195

[18] Strong, T., Dowd, S., Gutierrez, A.F. and Coffman, J. (2013) Amplicon Pyrosequencing of Wild Duck Eubacterial Microbiome from a Fecal Samples. *F*1000*Research*, **2**, 224.

[19] Arabatzis, M. and Velegraki, A. (2013) Sexual Reproduction in the Opportunistic Human Pathogen *Aspergillus terreus*. *Mycologia*, **105**, 71-79. http://dx.doi.org/10.3852/11-426

[20] Kirk, P.M., Cannon, P.F., Minter, D.W. and Stalpers, J.A. (2009) Dictionary of the Fungi. 10th Edition, CABI, Wallingford, 505.

[21] Hubalek, Z. (2004) An Annotated Checklist of Pathogenic Microorganisms Associated with Migratory Birds. *Journal of Wildlife Diseases*, **40**, 639-659. http://dx.doi.org/10.7589/0090-3558-40.4.639

Scientific Research Publishing (SCIRP) is one of the largest Open Access journal publishers. It is currently publishing more than 200 open access, online, peer-reviewed journals covering a wide range of academic disciplines. SCIRP serves the worldwide academic communities and contributes to the progress and application of science with its publication.

Other selected journals from SCIRP are listed as below. Submit your manuscript to us via either submit@scirp.org or Online Submission Portal.