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MYCOLOGICAL AND BACTERIOLOGICAL ASSESSMENT OF POULTRY DROPPINGS FROM POULTRY PENS WITHIN ILORIN, KWARA, NIGERIA

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ABSTRACT
Mycological and bacteriological assessment of poultry droppings from poultry pens within Ilorin metropolis, Kwara, Nigeria and the incidence of antibiotic resistance pattern of the bacterial isolates were investigated. The bacterial and fungal counts ranged from 3.9 x 10^6 - 2.5×10^9 and 1.0 x10^4 - 1.6 x 10^7 CFU/g respectively. The counts of total coliform, faecal coliform, *Salmonella* sp. and *Staphylococcus aureus* ranged from 1.9 x 10^2 – 3.9×10^7, 0.0 - 1.0 x10^6, 1.0 x10^2 - 1.4 x 107, and 0.0 - 2.0 x 10^5 CFU/g respectively. The count of *Pseudomonas aeruginosa* was zero in all the poultry droppings. The bacteria characterized and identified were *Micrococcus holobium, Pseudomonas picketti, Bacillus pumilus, Enterobacter agglomerans, Staphylococcus alrettae, Staphylococcus aureus, Staphylococcus saprophyticus, Salmonella enteritidis, Streptococcus pluranimalium* and *Cellobiococcus sciuri*. The fungal species isolated were *Candida tropicalis, Saccharomyces* sp*., Sporendonema* sp*., Aspergillus fumigatus, Fusarium oxysporum, Kloeckera* sp*., Zygosaccharomyces* sp*., Candida* sp*., Aspergillus niger*, and *Saccharomycopsis*. All the Gram negative bacteria were resistant to ceftazidime, gentamcin and Amoxycillin-clavulinate while all the Gram positive bacteria were resistant to ceftazidime, cefuroxime, ceftriaxone, cloxicillin and Amoxycillin-clavulinate. *S. aureus* and *Microbacterium holobium* were resistant to all the antibiotics used. It was concluded from this study that the poultry droppings harboured pathogenic bacteria some of which were multiple antibiotics resistant. It is recommended that poultry droppings should be prevented from contaminating poultry feed, and the trough containing feed and water. There should be regulation on the use of antibiotics for growth promotion and disease prevention in poultry birds.

Keywords: Poultry, faecal droppings, pathogens, hazard

INTRODUCTION

Poultry refers to all birds of economic usefulness to man including chickens, pigeon, duck, pheasant, quail, guinea fowl and ostrich. They belong to the zoological class aves (Linda, 2016). Droppings can be in form of semisolid or watery. The colour of droppings varies among the species of birds. Some are whitish, ashes and dark brown in colour (Adegunloye, 2005).

The major components of poultry litter include the bedding material, feather, manure and remnant of feed. Man over time has come to recognize the value of chicken droppings as a source of nutrients for crops by enhancing soil fertility (Bolan *et al.,* 2010). The dried chicken dropping is the closest in nutrient profile to NPK fertilizer among the faeces of livestock species. Poultry litter is often used as an organic nutrient to fertilize the soil during forage, cereal and fibre crop production. A number of other potential uses of poultry manure have been indicated; these include gas production and feeds for livestock especially fish and cattle (Musa *et al*., 2012).

Dropping is a complete nuisance especially in this modern 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 flies. The manure is often a source of odour caused by the production of ammonia, dimethylamine and trimethylamine (Nowak *et al*., 2017; Singh *et al*., 2018). Due to the nuisance and health hazard that flies create through dropping, some urban centers enact laws banning Poultry keeping in residential areas.

Pathogenic microorganisms can thrive in poultry wastes. These constitute environmental and health hazards to livestock and the teeming population. The presence of these microorganisms cause various diseases in fowl. Some of these microorganisms include *Escherichia coli*, *Staphylococcus* and *Bacillus* species (Adegunloye, 2005). Diseases that can be transmitted to bird flock through drinking water may originate from contaminated faeces and secretions of sick birds, or by utilization of water already contaminated by pathogenic organisms (Linda, 2016).

Many of the antibiotics used in the industry have been used to cure human illness. Rise in antibiotics resistance have been reported many years ago and it still remains a global problem today. There is regulation on the indiscriminate use of antibiotics in poultry management except if recommended by a veterinarian (Smith, 1999; DANMAP, 2007).

The aim of this study was to assess the mycological and bacteriological profile of poultry droppings from poultry pens within Ilorin, Kwara, Nigeria

MATERIALS AND METHODS

Collection of samples

A total of 10 poultry dropping samples were collected across different poultry farms within Ilorin metropolis. The farms were designated A to J. The faecal materials were collected into sterile black polythene bag aseptically. It was transported to the laboratory for immediate analysis.

Isolation and enumeration of bacteria and fungi in the poultry droppings

One gram of the poultry dropping was serially diluted up to 10^{-7}. Aliquots (0.1ml) were plated from different dilutions. The pour plate technique was employed for the enumeration of bacteria

using nutrient agar while the counts of fungi was enumerated on Potato dextrose agar supplemented with 30mg/l of streptomycin (Fawole and Oso, 2007).

Isolation and enumeration of total and faecal coliforms
Plating of the sample was done from 10^{-1} and 10^{-2} dilutions using spread plate technique. MacConkey agar and eosin methylene blue agar were used for the isolation of total and faecal coliforms respectively. At the end of incubation, typical colonies were counted (Willey *et al*., 2011).

Isolation and enumeration of specific pathogenic bacteria
Pathogenic bacteria such as *S. aureus, Salmonella* spp., *and Pseudomonas aeruginosa* were isolated using Mannitol salt agar, *Salmonella - Shigella* agar and Cetrimide agar respectively. Spread plate technique was used. After the incubation period, the number of typical colonies were counted. These colonies were further confirmed by biochemical tests (Collins and Lyne, 1970; Willey *et al*., 2011).

Isolation of pure culture and preservation of isolates
This was done by subculturing until a pure culture was obtained. The pure isolate was kept in a refrigerator until it is needed (Fawole and Oso, 2007).

Characterization and identification of bacterial isolates
The bacteria were characterized and identified based on their colonial, cellular and biochemical characteristics and then making reference to standard texts (Cowan and Steel, 1985). Similarly, the fungi were characterized and identified by their macroscopic and microscopic features. Then, reference was made to Onions *et al*. (1981) in order to identify the fungi.

Antimicrobial susceptibility test of bacterial isolates
Normal saline broth culture of each isolate was standardized with 0.5 MacFarland's standard (CLSI, 2005). Then, set plate of Mueller Hinton agar was inoculated with the bacterial isolate followed by placing the antibiotic disc (made by Rapid lab) on the agar surface and incubated at 37^{o}C for 24h after which zone of inhibition in millimetre was measured.

RESULTS

Bacteriological counts of the poultry droppings
The bacterial and fungal counts ranged from $3.9 \times 10^6 – 2.5 \times 10^9$ and $1.0 \times 10^4 – 1.6 \times 10^7$ CFU/g respectively (Table 1). The counts of total coliform, faecal coliform, *Staphylococcus aureus*, and *Salmonella* sp. ranged from $1.9 \times 10^2 – 1.4 \times 10^7$, $0.0 – 1.0 \times 10^4$, $0 – 2.0 \times 10^5$, and $1.0 \times 10^2 – 1.38 \times 10^7$ CFU/g respectively. *Pseudomonas aeruginosa* count was zero in all the samples (Table 2).

Characterization and identification of bacterial and fungal isolates
The following bacteria were obtained after characterization: *Micrococcus holobium, Pseudomonas picketti, Bacillus pumilus, Enterobacter agglomerans, Staphylococcus alrettae, Staphylococcus aureus, Staphylococcus saprophyticus, Salmonella enteritidis, Streptococcus pluranimalium and Cellobiococcus sciuri* (Table 3). The fungi isolated were *Candida tropicalis, Saccharomyces* sp.*, Sporendonema* sp.*, Aspergillus fumigatus, Fusarium oxysporum, Kloeckera* sp.*, Zygosaccharomyces* sp.*, Candida* sp.*, Aspergillus niger*, *and Saccharomycopsis* (Table 4).

Occurrence of bacterial and fungal isolates
The occurrence of the bacteria isolated across the poultry farms showed that *Streptococcus pluranimalium and Staphylococcus saprophyticus* were the most common bacteria followed by *Staphylococcus aureus*. *Salmonella enteritidis* was the least bacteria isolated from the poultry farms (Table 5). The occurrences of the fungi isolated across the poultry farms showed that *Candida tropicalis* was the most common fungi followed by *Fusarium oxysporum* and while *Aspergillus fumigatus, Kloeckera* sp., Saccharomyces sp., and Sporendonema sp. were the least (Table 6).

Antimicrobial susceptibility patterns of bacterial isolates
The antibiotics employed showed varying levels of activity with respect to the bacterial isolates whose susceptibility were tested. Ceftazidime, Gentamicin, and Ampicillin had no inhibitory effect on all the Gram negative isolates: *Pseudomonas picketii*, *Enterobacter agglomerans*, and *Salmonella enteritidis*. Ciprofloxacin and nitrofurantoin were able to inhibit all the Gram negative bacteria. Among the Gram positive antibiotic disc ceftazidime, ceftriazone, Cloxacillin and Amoxycillin/Clavulinate were least effective in inhibiting the Gram positive bacterial isolates (Table 7)

Table 1: Microbial counts of poultry droppings

S/No	Poultry pens	Counts (cfu/g)							
		Bacteria	Fungi	Total coliform	Faecal coliform	*Salmonella* spp.	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*S.aureus*
1	A	1.0×10^8	2.0×10^6	3.0×10^6	1.0×10^4	2.0×10^6	0	2.0×10^5	2.0×10^5
2	B	2.5×10^9	1.3×10^7	1.0×10^7	0	4.06×10^6	0	0	
3	C	9.2×10^7	1.1×10^7	1.4×10^7	0	1.4×10^7	0	0	0
4	D	2.5×10^8	9.1×10^5	3.9×10^7	0	4.9×10^6	0	0	0
5	E	2.8×10^7	5.0×10^6	1.0×10^4	0	2.0×10^6	0	0	0
6	F	3.9×10^6	1.6×10^7	1.0×10^4	1.0×10^2	1.0×10^2	0	8.0×10^2	8.0×10^2
7	G	1.3×10^8	3.0×10^5	2.0×10^6	0	1.0×10^3	0	0	0
8	H	1.1×10^7	3.0×10^5	8.2×10^3	2.0×10^3	3.1×10^6	0	0	0
9	I	2.6×10^7	1.0×10^4	2.7×10^4	1.0×10^6	5.7×10^6	0	0	0
10	J	1.5×10^7	2.0×10^6	1.9×10^2	0	6.4×10^6	0	3.0×10^4	3.0×10^4

Table 2: Characterization and identification of bacterial isolates

	Gram staining																													TSI							
Bacterial isolates	Gram reaction	Cell shape	Cells' arrangement	Motility	Spore staining	Oxidase	Catalase	Coagulase	Haemolysis	Starch hydrolysis	Citrate	Indole	Urease	Glucose	Lactose	Sucrose	Maltose	Mannitol	D-arabinose	VP	MR	Nitrate	Sorbitol	Cellobiose	Trehalose	D-xylose	Fructose	Adonitol	OF	Slope	Butt	Gas	H_2S	D-raffinose	Probable identity	
1	+	c	ch	-	-	+	-	-	α	+	-	+	-	A	A	-	A	A	-	-	-	-	A	A	A	A	A	-	f	k	-	-	-	A	*Streptococcus pluranimalium*	*Bacillus sphaericus*
2	+	c	s	-	-	+	+	+	ß		+	+	+	AG	-	A	A	AG	A	-	-	-	A	A	A	A	A	A	f	k	-	+	-	A	*Staphylococcus aureus*	*Staphylococcus aureus*
3	+	c	ch	-	-	+	+	-	γ		+	-	+	A	A	A	A	AG	A	-	-	-	A	A	A	-	A	A	f	k	-	-	-	A	*Micrococcus* sp.	*Micrococcus* sp.
4	-	r	Cl	+	-	-	+	-	γ	-	-	+	+	A	AG	A	A	AG	A	-	-	-	A	-	A	A	A	-	f	A	A	-	-	A	*Pseudomonas picketti*	*Streptococcus* sp.
5	+	c	s	-	-	+	+	-	α	-	-	-	+	A	AG	A	A	AG	A	-	-	-	A	-	A	A	A	A	f	-	-	-	-	A	*Cellobiococcus sciuri*	
6	+	r	Cl	-	+	+	+	-	γ	-	+	+	+	A	A	A	A	AG	A	-	-	-	A	A	A	A	A	-	f	A	-	-	-	A	*Bacillus pumilus*	
7	-	r	s	-	-	+	+	-	γ	-	+	+	-	A	AG	A	A	AG	A	-	-	-	A	A	A	A	A	-	f	A	A	-	-	A	*Enterobacter agglomerans*	
8	+	c	ch	-	-	+	+	-	ß		-	-	+	A	A	A	A	AG	A	-	-	-	A	-	A	A	A	-	f	k	-	-	-	A	*Staphylococcus arlerttae*	
9	+	c	s	-	-	+	+	-	ß		+	-	+	A	A	A	A	AG	A	-	-	-	A	A	A	A	A	-	f	-	-	-	-	A	*Staphylococcus saprophyticus*	
10	-	r	s	-	-	+	+	-	γ		+	-	-	AG	-	A	A	AG	A	-	+	-	-	-	A	A	A	-	f	A	A	+	-	-	*Salmonella enteritidis*	

Key: +, Positive; -, Negative; s, single; ch, chain; cl, cluster, A, acid production; AG, acid and gas; OF, Oxidation-fermentation; f, Fermentative reasction; VP, Voges proskauer, MR, Methyl red, TSI, Triple sugar Iron agar

Table 6: Characterization and identification of fungal isolates

Fungal isolates	Macroscopic features	Microscopic features	Probable fungi
F1	Creamish glistering yeast, reverse of the plate creamish at 72 hours.	The asci exist in clusters; some paired up in bean shape.	*Saccharomypcosis* sp.
F2	A medium sized filamentous mould with white margin and black spores seen at 72 hours; reverse of plate grey.	Presence of double walled conidiophores which was smooth and hyaline. The conidia were warty in nature.	*Aspergillus niger*
F3	A white yeast, big in size, non-mucoid with irregular edge, no spore seen, reverse of plate whitish creamish.	The yeast cells varied in shape some were oval, pointed at one end and arranged in clusters; some of the asci of the yeast were bean shaped and elongated.	*Zygosaccharomyces* sp.
F4	A creamish colonial fungus. The yeast cell was mucoid; the reverse of the plate creamish after 72 hours.	The yeast colonies were spindle shaped, long, thin walled, pointed at both ends. No ascospores seen.	*Kloeckera* sp.
F5	A fungus growth with pinkish pigmentation at the reverse of the plate; appearance of woolly growth on the surface.	The conidiospore breaks into arthrospore. The arthrospores are joined together.	*Sporendonema* sp.
F6	A fungus with creamy edge and with green colouration at the centre; the reverse of plate was dark green after 72 hours incubation.	The conidial heads typically columnar, conidiophores short, smooth walled, green typically in the upper part, conidia globose to subglobose.	*Aspergillus fumigatus*
F7	A creamy irregular growth with whitish tint on the surface. Reverse side of plate was creamish after 72 hours.	The yeast cells were round or spherical; cylindrical or egg shaped	*Saccharomyces* sp.
F8	A big woolly mould with rough edges; reverse side of plate dark at 72hours	The macroconidia were hyaline and sickle shaped; Microconidia were also produced.	*Fusarium oxysporum*
F9	A creamish colony with rough edges; the colony was concave; reverse of plate also creamish at 72 hours	The pseudohyphae were present; the blastospores were ellipsoidal to the cylindrical shape	*Candida* sp.
F10	The colony was creamish with glossy appearance; the reverse of the plate was also glossy after 72 hours.	The hyphae broke into rod shaped chains or arthrospores. The arthrospores were spherical and also in chains.	*Candida tropicalis*

Table 4: Antibiotics susceptibility patterns of bacteria isolated from poultry droppings

	Diameter of zone of inhibition (mm)							
Gram bacteria negative	**CAZ**	**CRX**	**GEN**	**CPR**	**OFL**	**AUG**	**NIT**	**AMP**
Pseudomonas picketti	-	-	-	18	30	-	20	-
Enterobacter agglomerans	-	10	-	10	-	8	15	-
Salmonella enteritidis	-	-	-	25	22	-	25	-
Gram bacteria positive	**CAZ**	**CRX**	**GEN**	**CTR**	**ERY**	**CXC**	**OFL**	**AUG**
Streptococcus pluranimalium	-	-	17	-	20	-	27	-
Staphylococcus aureus	-	-	-	-	-	-	-	-
Microbacterium holobium	-	-	-	-	-	-	-	-
Cellobiococcus sciuri	-	-	-	-	22	-	-	-
Bacillus pumilus	-	-	10	-	-	-	-	-
Staphylococcus alrettae	-	10	5	-	10	-	30	-
Staphylococcus saprophyticus	-	-	-	-	-	-	-	-

Key: -, No inhibition; CAZ, Ceftazidime 30µg ; CRX, Cefuroxime 30µg; GEN, Gentamicin10µg; CTR, Ceftriazone 30µg; CPR, Ciprofloxacin 5 µg; ERY, Erythromycin 5µg; CXC, Cloxacillin 5µg; OFL, Ofloxacin 5µg; AUG, Amoxycillin/Clavulinate 30µg; NIT, Nitrofurantoin 300 µg; AMP, Ampicillin 10 µg

Table 5: Occurrence of bacterial isolates in the poultry droppings

Bacterial isolates	Sampling locations									
	A	B	C	D	E	F	G	H	I	J
Streptococcus pluranimalium	+	-	+	+	+	+	+	+	+	+
Staphylococcus aureus	-	+	+	+	+	+	-	-	+	-
Micrococcus holobium	+	+	-	-	+	-	+	-	+	+
Pseudomonas picketti	-	-	+	-	-	-	-	+	+	-
Cellobioscoccus sciuri	+	+	-	+	+	+	-	+	+	-
Bacillus pumilus	-	-	-	-	+	+	+	-	+	+
Enterococcus agglomerans	-	-	-	-	-	-	+	+	+	+
Staphylococcus alrettae	+	+	+	+	-	-	+	-	+	+
Staphylococcus saprophyticus	+	+	+	+	-	+	+	+	+	+
Salmonella enteritidis	-	-	-	-	-	-	-	-	+	-

Key: +, Isolated; -, Not isolated

Table: Occurrence of fungal isolates in the poultry droppings

Fungal isolates	Sampling locations									
	A	B	C	D	E	F	G	H	I	J
Saccharomycopsis sp.	+	-	+	+	+	+	-	-	-	-
Aspergillus niger	-	+	+	+	+	-	-	-	-	-
Zygosaccharomycopsis sp.	-	-	+	+	+	+	-	+	-	-
Kloeckera sp.	-	+	+	+	-	-	-	-	-	-
Sporendonema sp.	-	-	-	-	+	-	+	+	-	-
Aspergillus fumigatus	-	-	-	-	-	+	+	-	-	+
Saccharomyces sp.	+	-	-	-	-	-	+	-	-	+
Fusarium oxysporum	+	+	+	+	+	+	-	+	-	-
Candida sp.	+	+	+	+	-	-	-	-	+	-
Candida tropicalis	-	+	+	+	+	+	+	+	-	+

Key: +, Isolated; -, Not isolated

DISCUSSION

The bacterial and fungal counts revealed the high microbial contamination of poultry faeces from commensal to pathogenic microorganisms. This could be as a result of high level of contamination of the feeds or water source given to poultry birds. The occurrence of enterobacteriaceae family in the poultry droppings may not be abnormal owing the prevalence of faecal coliforms in the gut of humans and animals. The prevalence of coliforms in the poultry faeces could come from the environment.

Enterobacter agglomerans was isolated from the poultry droppings analysed in this study. In a similar research done by Jemilehin *et al*. (2015), on the enteric bacteria in rats co-habiting with poultry birds, *Enterobacter agglomerans* was isolated as part of the enteric organisms affecting poultry. However, this preponderance can pose a great threat to the health of poultry birds as a number of infections of poultry have been linked to pathogenic *Enterobacter agglomerans*. This infection could be extended to the consumers of meat that are not properly cooked or poorly handled before eating.

Salmomnella spp. Is one of the widely distributed pathogens in chicken litter, with poultry and eggs remaining as the predominant reservoir. Its prevalence level can range from 0 to 100% (Chenz and Jiang, 2014). Furthermore, Omoya and Ajayi (2016) reported that poultry dropping is one of the sources of Gram negative antibiotic resistant pathogens such as *E.coli, Citrobacter* spp., *Enterobacter aerogenes, Klebsiella* spp*., Salmonella* spp*., Serratia marcescens, Shigella dysenteriae, Proteus* spp*., and Pseudomonas aeruginosa*. They also observed that Gram positive cocci, *S. aureus*, and *Micrococcus luteus* were 100% sensitive to streptomycin and 100% resistant to augmentin and cotrimoxazole.

The presence of *Staphylococcus* species in the faeces could be as a result of the people entering the poultry house and giving feed to the fowls. This agrees with the finding of Adegunloye (2005) who reported the incidence of Staphylococci in poultry faeces. The presence of *Staphylococcus aureus* in poultry faeces can cause food poisoning in man when poultry meat contaminated with this organism is taken (Poultrysite, 2014). Transmission of *Staphylococcus* occurs in the hatchery, in the general farm environment and through formites. Other predisposing factors include chronic stress, trauma, and imunosuppression.

Infection of streptococci in poultry droppings could be from the respiratory route. Streptococcal and enterococcal infections in poultry can cause acute septicaemia and chronic infections in affected birds. Members of the genus *Streptococcus* and *Enterococcus* are commensal organisms, primarily of the gastrointestinal tract and mucosal surfaces, in both animals and humans. The majority of infections from these pathogens are opportunistic. *Streptococcus pluranimalium* is associated with valvular endocarditis and septicaemia in adult broiler.

Poultry dropping can be used as feed for fish and cattle because of their ability to utilize the uric acid produced from the dropping. Sharma and Sihag (2013) reported that one of the organism isolated in this study, *Cellobiococcus sciuri* is pathogenic to fishes that are feed with poultry droppings. *C. sciuri* is capable of causing descaling on the lateral side of fish and also depigmentation and whitening of fish.

In this study, Gram positive bacteria represent 70% of the bacterial isolates. Some of the bacteria isolated belong to the

genera: *Streptococcus* and *Staphylococcus*. Chicken litter contains a large and diverse population of microorganisms. Zhoa and Xuiping (2014) obtained microbial populations in chicken litter up to 10^{10} CFU/g, and the predominance of Gram-positive bacteria which account for nearly 90% of the microbial diversity.

There are growing concerns about the presence of antibiotic-resistant pathogens in animal manures from both on-farm exposure and off-farm contamination. Omojowo and Omojasola (2013) have reported the presence of antibiotic resistant bacteria in poultry manure used to fertilise ponds in New Bussa, Nigeria. Widespread dispersal of chicken litter or chicken litter-based organic fertilizers harbouring antibiotic-resistant food borne pathogens can be a serious environmental hazard. Furthermore, horizontal transfer of mobile antibiotic resistance genes from one bacterium to another can possibly occur under some conditions. Nandi *et al*. (2004) reported that Gram-positive bacteria were found to be the major reservoir of Class 1 antibiotic resistance integrants in poultry litter. Isolation of antibiotic-resistant food borne pathogens from chicken litter or chicken litter based-organic fertilizers raises concerns about possible transmission of these bacteria to fresh produce after land application since these pathogens can potentially transfer to the arable land from contaminated chicken litter or chicken litter-based organic fertilizers, and can also further contaminate surface and ground water through runoffs (Mwambete and Stephen, 2015).

The fungi species isolated in this study were *Candida tropicalis, Candida* sp.*, Saccharomyces* sp.*, Sporendonema* sp.*, Aspergillus fumigatus, Fusarium oxysporum, Kloeckera* sp.*, Zygosaccharomyces* sp., *Aspergillus niger and Saccharomycopsis.* In a similar research on diversity of fungi in fresh and aged poultry litter, *Penicillium, Alternaria, Cladosporium, Aspergillus, Scopulariopsis* and *Trichosporon* were isolated (Viegas *et al*., 2012).

The occurrence of *Saccharomyces cerevisiae* is encouraged as studies have shown that these organisms have beneficial effects to poultry birds. Panda *et al*. (2011) reported that *Saccharomyces cerevisiae* apart from being an excellent source of amino acids for poultry is also a good source of mineral and vitamin B complex.

In the genus *Candida*, most species exist as commensals in most healthy individuals or birds. Pathogenic *Candida* species is a growing problem in medical science. *Candida albicans* is the most common species causing human infections. The emergence of non-albicans species such as *C. krusei, C. parapsilosis, C. tropicalis* and *C. glabrata* has been reported in the last decade as human pathogens, mainly among immuno-suppressed individuals and hospitalized patients (Kemoi *et al*., 2013).

Aspergillus fumigatus is commonly found in decomposing compost and on hay. It can cause spoilage of materials. It is the causative agent of a disease of birds, known as aspergillosis. *Aspergillus niger* can also cause aspergillosis. *Fusarium oxysporium* can produce mycotoxin in foodstuffs, and damage of the materials. *F. oxysporum* as a plant pathogens and it occurs in soils (Onoins *et al*., 1981).

Conclusion

It is concluded from this study that poultry droppings contain diverse groups of bacteria and fungi. Some of these isolates have been reported to be pathogenic with multiple antibiotic resistance patterns.

Recommendations

It is recommended that the stock of birds should be maintained at an average level to prevent over-crowding which could facilitate disease transmission in birds. Feed and water bowls should be cleaned daily and fresh feed and water should be supplied. The poultry industry should follow prudent management options and safety precautions by establishing more effective disinfection guidelines to reduce the population of antibiotic-resistant pathogens and monitoring the potential infection of subsequent flocks with resistant bacteria. Incessant use of antibiotics should be avoided by poultry farmers to check the increasing antibiotic resistance to diseases in poultry.

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