

BACTERIOLOGICAL EVALUATION OF POULTRY FEEDS IN EKPOMA, NIGERIA

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ABSTRACT

Aim: Poultry feed is one of the major vector for the transmission of microbial agents to poultry farms and processing plants. This study aims at the evaluation and identification of bacteria and fungi agents in Ekpoma poultry feed.

Methods: Bacteriological investigation was carried out on five different poultry feed samples from poultry farmers in Ekpoma, Edo State from January to June 2015. The samples were examined using standard bacteriological plate culture method.

Results: The highest microbial isolates was *Candida albicans* 66.4%, followed by *Proteus sp.* 18.6%, *Escherichia Coli* 10.6% and *Pseudomonas sp.* 4.4% in descending order. The lowest microbial growths was recorded in grower marsh 14.2%, layer and broiler finish marsh 15.9% each, chick marsh 25.7% and broiler starter marsh 28.3% in ascending order.

Conclusion: This study shows that microbial contamination of poultry feed still constitute one of the problem affecting poultry production.

Key words: Isolation, Bacteria, Fungi, Poultry feed

INTRODUCTION

Poultry feed can serve as a carrier for a range of microbial contaminants such as moulds, mycotoxins and bacteria (Maciorowki et al., 2007). Poultry refers to all birds that have been domesticated by man. The birds include domestic fowl, duck, geese, turkey, guinea fowl, pigeons and ostriches (Barakat, 2004). Many bacteria are associated with environmental contamination of feed ingredients from the family enterobacteriaceae. This family comprises of many established genera including *Escherichia*, *Enterobacter*, *Salmonella* etc (Anon, 2001; Veldman et al., 1995). Common constituents of feeds include whole cereals, soya beans, vitamins and vegetables such as water leaf, tridax and amaranthus spp. The protein contents of the feed vary depending on the purpose of keeping the birds. The protein contents of 13%, 16%, 18%, 21% and 23% is usually a standard measurement for chicks marsh, layers marsh, growers marsh, broiler starter and broiler finish respectively (Barakat, 2004). Feed has been shown to be a major vector for transmission of salmonella and other bacteria to the farm and processing plant.

Crump et al., (2002) compared the number of salmonella serovous found in the feed mill of two integrated companies against those isolates found at their respective processing plants. The percentage isolates found at the processing plant and feed mill were 56.3% and 54.5% respectively. In a Danish study, looking at the health impact of contaminated feed, Hald et al., (2006) also found that 82 salmonella serotypes were isolated from both production animals and humans, 45 of these were those isolated in feed. While attention has been focused on salmonella, feed can also introduce other pathogens into the poultry house and food chain, such as *Escherichia*, *Listeria* and *Clostridia*. Some authors have suggested that these bacteria in feed may be higher than that of *Salmonella* (White et al., 2003). Feed and feed ingredients are also known to be extensively contaminated with antibiotic resistant bacteria. Multi-antibiotic resistant strains of *Salmonella* (MAFF 1993) *Streptococcus* (Morris et al., 1999), *Escherichia* and *Enterococcus* have been found in feed. High level of bacteria in feed have been shown to be associated with productivity problems in poultry (Tabib et al., 1981; Anderson and Richardson 1999 and Derouchey

et al., 2004) and this was thought to be as a result of their effect on the gut. Ekperigin et al., (1990) reported that for successful control of *Escherichia* and *Salmonella*, feed must be exposed to a temperature of 85.7°C because of the heat resistance of spores (Green ham et al., 1987; Macioroski et al., 2004). Chemical disinfection can control bacteria and prevent recontamination. Treatments with organic acid, organic salt and formaldehyde/organic acid blend (Vanderval, 1979) demonstrated that a level in excess of 10kg/tonne of organic acid is needed to control bacterial levels satisfactorily. Control of bacteria in feed has been shown to improve production performances in poultry and to reduce the incidence of salmonella in breeding animals in the farm environment, on carcasses and in eggs. Therefore, this study was carried out to determine the prevalence and identification of bacterial isolates from poultry farm feed.

MATERIALS AND METHODS

Area of Study

A total of 5 different samples of feed were collected from poultry farmers in Ekpoma, Edo State. The samples collected were; Chicks marsh 18% protein form 1st-6th weeks, Grower marsh 13% protein form 7th-20th weeks, Layer marsh 16% protein, Broiler starter (for broiler) 21% protein and Broiler finish (for broiler) 23% protein.

Collection of Samples

Samples were collected aseptically into sterile universal containers and labelled according to the feed after informed consent from the poultry farmers. The five samples collected were taken to the laboratory immediately for bacteriological examination.

SAMPLE ANALYSIS

Samples were inoculated into sterile glucose broth and incubated aerobically at 37°C for 18-24 hours. The broth culture were then sub-culture onto Chocolate agar, Blood agar, Saboraud dextrose agar and MacConkay agar. All the plates were incubated aerobically at 37°C for 18-24 hours.

Identification of Isolates

All bacteria isolates obtained were identified on the basis of their morphological, physiological and biochemical characteristics using standard

procedures (Cheesbrough, 2000; Cruickshank et al., 1975; Sanders, 1994; Cowan and Steel, 1974).

Statistical Analysis

Data obtained were presented in tables, figures and percentages.

RESULTS

Five (5) different poultry feed samples were examined and a total of 113 microbial isolates was recorded. The highest microbial isolates recorded was *Candida albicans* 66.4% followed by *Escherichia coli* 18.6%, *Proteus sp.* 10.6% and *Pseudomonas sp.* 4.4% in descending order (Table 1). Table 2 shows the lowest microbial growths in Grower marsh 14.2%, layer and broiler finish marsh 15.9% each, chick marsh 25.7% and broiler starter marsh 28.3% in ascending order.

Table 1: Prevalence of some microbial isolates in poultry feeds

Microbial isolates	Microbial isolates	% of isolates
<i>Candida albicans</i>	75	66.4%
<i>Proteus sp.</i>	21	18.6%
<i>Escherichia coli</i>	12	10.6%
<i>Pseudomonas sp.</i>	5	4.4%
Total	113	

Table 2: Some microbial isolates from different poultry feeds

Feed	Microbial isolates	% Prevalence
Chick marsh	29	25.7
Grower marsh	16	14.2
Layer marsh	18	15.9
Broiler starter marsh	32	28.3
Broiler finish marsh	18	15.9
Total	113	100

DISCUSSION

Crumps et al., (2002) stated that poultry feed is a major vector for transmission of *Salmonella* and other bacteria to poultry farms and processing plants. This study has shown that most poultry feeds are contaminated with various microbes in Ekpoma environment. The 113 microbial isolates recovered were higher

than the 82 *Salmonella* serotypes isolates reported by Hald et al., (2006), out of which 45 was isolated from feeds. This is however not comparable with our study because of the differences in the microbial isolates. In our study, we did not isolate *Salmonella sp.* and the 113 isolates obtained were a cumulative value of all microbial isolates observed namely; *Candida albicans*, *Proteus sp.*, *Escherichia coli* and *Pseudomonas sp.* Our finding shows that *Candida albicans* was the leading aetiological agent of poultry feed infections. This disagrees with the earlier observation made by Crumps et al., (2002) that *Salmonella* was the major contaminants of poultry feeds. The high percentage of *Candida albicans* obtained agreed with the findings of White et al., (2003) who opined that other microbial contaminants in poultry feeds may be higher than *Salmonella sp.* as earlier reported by Hald et al., (2006). Other bacteria isolates obtained were *Proteus sp.*, *Escherichia coli* and *Pseudomonas sp.* This is inconsonance with the reports of Anon (2001) and Veldman et al., (1995) who stated that the family enterobacteriaceae are the common contaminants of poultry feeds. The isolation of *Escherichia coli* may be attributed to faecal contamination during the preparation of these feeds; while the presence of *Proteus sp.* and *Pseudomonas sp.* may be due to the exposure of the feeds to the unsanitary environment which allowed such organisms with pathetic potential to proliferate and contaminate the feeds. In this study, broiler starter and chick marsh grew the highest percentages of microbes 28.3% and 25.7% respectively. This may be attributed to high protein contents of these marshes which also serve as growth factors for the contaminating organisms. Poor exposure of poultry feed to low temperature and organic acid has been found to enhance bacteria growth in feeds which results to poor production in poultry. Ekperigin et al., (1990), Green ham et al (1987) and Macioroski et al., (2004) have earlier reported that exposure of feeds to a temperature of 85.7oc will successfully eliminate the heat resistance bacterial spores. Vanderwal (1979) has also demonstrated that 10Kg/tonne of organic acid can reduce bacterial level in feeds efficiently. Thus our findings have shown a relatively high level of microbial contamination of poultry feed in the studied area. It therefore becomes imperative to carryout routine microbiological examination on poultry feed in other to improve production performances in poultry management.

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