

calis (15.77%) *C. parapsilosis* (8.87%) and *C. akabanensis* (13.09%) respectively. The molecular characterization of the different *Candida* spp. and their phylogenetic relationships were confirmed using the Bayesian analysis. All the *Candida* spp. revealed varying degrees of susceptibilities to voriconazole, fluconazole and nystatin. However, *C. albicans* showed 29.0% resistance to fluconazole, *C. tropicalis* showed 46.0% and 14.0% resistance to nystatin and voriconazole while *C. akabanensis* showed 100% resistance to voriconazole and fluconazole, respectively. Kruskal-Wallis Chi-square test using 'R' (Version 3.2.2) showed nystatin as the most effective antifungal agent (Kruskal-Wallis $\chi^2 = 786.03$, $df = 2$, $P < 0.001$) against *Candida* spp. Also, resistant gene *Erg11* was identified in all the *Candida* spp. resistant to the antifungal agents tested.

Conclusion: Women using contraceptive devices in central Nigeria harbour phylogenetically diverse *Candida* spp. including *C. akabanensis* an uncommon cause of vulvovaginal candidiasis. Out of these *Candida* spp. *C. albicans*, *C. tropicalis* and *C. akabanensis* are notable for multidrug drug resistance as well as harbouring resistant gene *Erg11*.

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Multi-strain Probiotics Upregulated Anti-inflammatory Properties and Reduced *Pasteurella multocida* Mortality in Broilers

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Purpose: *Pasteurella multocida* is the highly contagious and zoonotic pathogen of a broad range of animal diseases causing devastating ecological and economic challenges globally. While about 80.5% of *P. multocida* infections have shown high degree of resistance to broad range of commonly used antibiotics, dietary inclusion of probiotics may become a suitable alternative in mitigating *P. multocida* infections in animals, hence reducing human spread as well as safeguarding the environment. It was hypothesized that dietary supplementation with multi-strain probiotics consisting of *Lactobacillus plantarum*, *L. fermentum*, *Pediococcus acidilactici*, *Enterococcus faecium* and *Saccharomyces cerevisiae* would mitigate *P. multocida* infection in broilers as well as improving gut health, haemato-biochemical parameters and growth performance.

Methods & Materials: A total of 120 birds were randomly allocated to 6 treatments with 2 replicates each, and were fed with a basal diet supplemented with multi-strain probiotics (10^8 CFU/kg) and then orally challenged with 10^8 CFU/mL of *P. multocida*. Clinical manifestations of *P. multocida* infection and mortality were recorded as well as the expression of anti-inflammatory genes, haemato-biochemical parameters, gut microbiota and growth performance.

Results: Probiotics supplementation significantly ($P < 0.05$) improved growth performance and feed efficiency as well as reducing ($P < 0.05$) the population of intestinal *P. multocida*, enterobacteria, and mortality. Haemato-biochemical parameters including total cholesterol, white blood cells (WBC), proteins, glucose, packed cell volume (PCV) and lymphocytes improved ($P < 0.05$) among probiotics fed birds when compared with the controls. Also, transcriptional profiles of anti-inflammatory genes including hypoxia inducible factor 1 alpha (HIF1A), tumor necrosis factor- (TNF) stimulated gene-6 (TSG-6) and prostaglandin E receptor 2 (PTGER2) in

the intestinal mucosa were upregulated ($P < 0.05$) in probiotics fed birds.

Conclusion: The dietary inclusion of the multi-strain probiotics improves growth performance, feed efficiency and intestinal health while attenuating inflammatory reaction, clinical signs and mortality associated with *P. multocida* infection in broilers, and these suggest that the probiotics can be used as alternative against *P. multocida* infections.

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Antimicrobial Resistance Dynamics in the Chicken Gut after Amoxicillin and Thiamphenicol Treatments

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Purpose: the aim of the study was to investigate the selective pressure exerted by amoxicillin (beta-lactam) and thiamphenicol (phenicol) administration on the abundance of antimicrobial resistance genes (ARGs) in the chicken gut.

Methods & Materials: eighteen broiler chicks were allocated in three groups and reared without treatment or treated with either amoxicillin or thiamphenicol at 5 days of age for three consecutive days. Cloacal swabs were taken from all birds at 1 day of age, as reference, and then on days 8, 19, and 28. At the end of the rearing cycle, birds were slaughtered and the caecal content was aseptically collected. Swabs ($n = 72$) and caecal contents ($n = 13$) were analysed by quantitative PCR assays to generate data on the abundance of fourteen ARGs conferring resistance to beta-lactams ($n = 8$) and phenicols ($n = 6$). Difference in ARGs abundance over time points within the same group was assessed using Friedmann test with Dunn's test for multiple comparisons, while Spearman's rank correlation was used to assess the co-occurrence of beta-lactam and phenicol ARGs.

Results: increased abundance of ARGs conferring resistance to phenicols was observed in the groups treated with either amoxicillin or thiamphenicol ($p < 0.05$). In detail, the abundance of *floR* and *cmlA* genes was significantly increased ($p < 0.05$) after treatment with either of the two antimicrobials up to 21 days post-treatment (d.p.t.). Amoxicillin treatment enhanced the abundance of *bla_{SHV}* at 1 d.p.t. ($p < 0.05$). Positive correlations between *bla_{TEM-1}* and *floR* ($p < 0.05$; $r = 0.245$) and *cmlA* ($p < 0.0001$; $r = 0.325$) were also observed.

Conclusion: the results of the study seem to suggest an increasing trend of abundance of *bla_{TEM-1}*, conferring resistance to beta-lactams, and *cmlA* and *floR*, conferring resistance to phenicols, under the selective pressure exerted by amoxicillin and phenicols.

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