

# Metagenomic Analysis of Microbial profile of Guinea Fowls and Chickens

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## Abstract

Probiotics are live microbial feed supplements that promote growth and health to the host by minimizing non-essential and pathogenic microorganisms in the host's gastrointestinal tract (GIT). The campaign to minimize excessive use of antibiotics in poultry production has necessitated development of probiotics with broad application in multiple poultry species. Design of such probiotics requires understanding of the diversity or similarity in microbial profiles among avian species of economic importance. Therefore, the objective of this research was to establish and compare the microbial profiles of the GIT of Guinea fowl and chicken and to establish the microbial diversity or similarity between the two avian species. A metagenomic approach consisting of the amplification and sequence analysis of the hypervariable regions V1-V9 of the 16S rRNA gene was used to identify the GIT microbes. Collectively, we detected more than 150 microbial families. The total number of microbial species detected in the chicken GIT was higher than that found in the Guinea Fowl GIT. Our studies also revealed phylogenetic diversity among the microbial species found in chicken and guinea fowl. The phylum *Firmicutes* was most abundant in both avian species whereas Phylum *Actinobacteria* was most abundant in chickens than Guinea fowls. The diversity of the microbial profiles found in broiler chickens and Guinea fowls suggest that the design of effective avian probiotics would require species specificity.

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