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# Comparison of Antimicrobial Resistant Genes in Chicken Gut Microbiome Grown in Organic and Conventional Diet

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## Abstract

Antibiotics are widely used in chicken production for therapeutic purposes, disease prevention and growth promotion that may select for drug resistant microorganisms known to spread to humans through consumption of contaminated food. Raising chickens in organic feed regimen, without the use of antibiotics, is getting increasingly popular with the consumers. In order to determine the effects of diet regimen on antibiotic resistant genes in the gut microbiome, we analyzed the phylotypes and identified the antimicrobial resistant genes in chicken, grown under conventional and organic dietary regimens. Phylotypes were analyzed from DNA extracted from fecal samples from chickens grown under these dietary conditions. While gut microbiota of chicken raised in both conventional and organic diet exhibited the presence of DNA from members of *Proteobacteria* and *Bacteroidetes*, organic diet favored the growth of members of *Fusobacteria*. Antimicrobial resistance genes were identified from metagenomic libraries following cloning and sequencing of DNA fragments from fecal samples and selecting for the resistant clones ( $n=340$ ) on media containing different concentrations of eight antibiotics. The antimicrobial resistant genes exhibited diversity in their host distribution among the microbial population and expressed more in samples from chicken grown in conventional diet at higher

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