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Can high dietary copper supplementation co-select antibiotic resistance genes in the swine gut microbiome?

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Abstract

The use of antibiotics in swine production has increased the abundance of antibiotic resistance genes (ARGs) in swine microbiomes, which has resulted in restrictions on the use of antibiotic growth promoters in diets for pigs (1,2). Thus, producers today rely on alternative growth promoters such as elevated levels of dietary copper. We investigated the impacts of copper sulfate (CuSO_4 ; 250 $\mu\text{g Cu g}^{-1}$ feed) versus cuprous oxide (Cu_2O ; 250 $\mu\text{g Cu g}^{-1}$ feed) on the antibiotic resistome, mobilome, and bacterial community composition. Fecal samples were collected at four different growth stages from a total of 40 pigs per treatment (including a control) during a four-month experiment conducted at the University of Illinois (USA). Fecal DNA was extracted and bacterial community composition was investigated by 16S rRNA gene amplicon sequencing. ARGs and mobile genetic elements (MGEs) were quantified using high-throughput quantitative PCR using a total of 384 validated primer sets. Highly abundant and diverse ARGs and MGEs were detected, but only subtle shifts in the bacterial community composition, mobilome, or resistome were observed in response to dietary Cu treatments. By contrast, microbiomes clearly differed between different pig growth stages, indicating gut microbiome maturation over time. ARGs conferring resistance to aminoglycosides, macrolide-lincosamide-streptogramin B (MLSB), and tetracycline were the most abundant. Relative abundance of MGEs was highly dominated by transposases. A significant correlation between bacterial community composition (i.e. bacterial taxa present) and resistome profiles (ARGs present) was displayed by Procrustes analysis, indicating that bacterial community composition was a determining factor of the fecal resistome. In conclusion, results did not provide evidence for dietary copper-induced co-selection of ARGs or MGEs even at a Cu concentration level exceeding the maximal permitted level for pig diets in the EU (25 to 150 $\mu\text{g Cu g}^{-1}$ feed depending on pig age). Nevertheless, we cannot rule out that Cu-induced co-selection of antibiotic resistance may have occurred in specific bacterial species. We also note that ARG levels were consistently high across all treatments and that some dispersal of bacteria may have occurred between pigs fed different levels of dietary Cu.

Keywords

Antibiotic resistance; Co-selection; Copper supplementation; Microbiome modulation; Swine

References

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