

# Modifying chicken microbiomes to improve performance and reduce *Campylobacter*

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## Video Byte

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# Abstract

Chickens are an important source of proteins for humans. Chicken diets are therefore formulated to enhance production efficiency and human health. But few studies have explored how industrial production system parameters affect certain pathogens in the chicken gut, such as *Campylobacter*, the leading cause of human foodborne bacterial gastroenteritis. A recent study examined how the presence of *Campylobacter* in the chicken gut microbiome varied across three different production systems, one based on a normal production system, and two based on higher welfare with and without omega-3. The standard production system produced a significantly different microbial composition than the other systems, with bacteria of the genus *Alistipes* playing a more prominent role in the gut microbiome of chickens from the normal production system, and *Eisenbergiella* playing a more prominent role in the other two production systems. These bacteria play active roles in energy metabolism and nutrient uptake. *Campylobacter*, meanwhile, was linked to increased microbial diversity and increased environmental pressure on microbial community structure. The findings demonstrate that distinct microbial communities arise from different industrial production systems, offering clues on how to manipulate diet to improve performance and combat the presence of *Campylobacter* in the food chain.