Microbial community composition of the ileum and cecum of broiler chickens as revealed by molecular and culture-based techniques - DTU Orbit (17/12/2018)

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The microbial communities of the ileum and cecum of broiler chickens from a conventional and an organic farm were investigated using conventional culture techniques as well as cloning and sequencing of 16S rRNA genes. Eighty-five percent of the 557 cloned sequences were <97% related to known cultured species. The chicken ileum was dominated by lactobacilli, whereas the cecum harbored a more diverse microbial community. The cecum was dominated by a large group of bacteria with hitherto no close cultured relatives but most closely related to Faecalibacterium prausnitzii. Approximately 49 and 20% of the cecal clones belonged to this cluster in conventional and organic broiler chickens, respectively. We were, however, able to recover a number of these phylotypes by cultivation, and the isolates were shown to be butyric acid producers. The investigation was a descriptive rather than a comparative study of 2 different rearing systems; however, several differences were observed. For instance, Clostridium perfringens was found in significantly higher numbers in the birds from the organic farm compared with the conventional broilers, probably due to the addition of salinomycin to the conventional feed. In the ileum, the abundance of the different Lactobacillus species differed between the 2 broiler types. The culture-based and culture-independent techniques complemented each other well. Strengths and limitations of the different methods are discussed.

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