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Czech Journal of Animal Science

Molecular profiling of bacterial species in the geese cecum

Liu B.Y., Wang Z.Y., Wang H.R., Hu P., Xu D., Wang Q.:

Czech J. Anim. Sci., 56 (2011): 192-203

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The purpose of this study was to analyse the microbial diversity in the caecum of geese using a 16S ribosomal RNA gene (rRNA) clone library approach. A total of 160 clones and 124 clones were sequenced and phylogenetically analysed

from the contents and mucosa of the caecum of Yang Zhou geese, respectively. The result indicated that there was a rich variety of bacteria in the caecum contents. Forty-six operational taxonomic units (OTUs) based on a 98% similarity criterion were classified in the contents of goose caecum, as compared to 29 OTUs based on a 97% similarity criterion in the mucosa of goose caecum. The sequences were assigned to 7 and 5 groups in the contents and mucosa of goose caecum, respectively. Contents of goose caecum were dominantly occupied by *Clostridia*-related species (58.7%) with other abundant sequences being related to *Bacteroidetes* (26.9%) and *Erysipelotrichi* (11.2%).

Gammaproteobacteria (59.6%) and *Clostridia* (20.1%) were predominant in the mucosa of goose caecum.

Keywords:

geese; caecum; microbiota; phylogenetic analysis

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