Anaerobic fungal communities differ along the horse digestive tract.

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Abstract

Anaerobic fungi are potent fibre degrading microbes in the equine hindgut, yet our understanding of their diversity and community structure is limited to date. In this preliminary work, using a clone library approach we studied the diversity of anaerobic fungi along six segments of the horse hindgut: caecum, right ventral colon (RVC), left ventral colon (LVC), left dorsal colon (LDC), right dorsal colon (RDC) and rectum. Of the 647 ITS1 clones, 61.7 % were assigned to genus level groups that are so far without any cultured representatives, and 38.0 % were assigned to the cultivated genera Neocallimastix (35.1 %), Orpinomyces (2.3 %), and Anaeromyces (0.6 %). AL1 dominated the group of uncultured anaerobic fungi, particularly in the RVC (88 %) and LDC (97 %). Sequences from the LSU clone library analysis of the LDC, however, split into two distinct phylogenetic clusters with low sequence identity to Caecomyces sp. (94-96 %) and Liebetanzomyces sp. (92 %) respectively. Sequences belonging to cultured Neocallimastix spp. dominated in LVC (81 %) and rectum (75.5 %). Quantification of anaerobic fungi showed significantly higher concentrations in RVC and RDC compared to other segments, which influenced the interpretation of the changes in anaerobic fungal diversity along the horse hindgut.

These preliminary findings require further investigation.

Involved units

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