

# DOMESTICATED EQUINES DIFFER IN THEIR FAECAL MICROBIOTA COMPOSITION

V. Free communications

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## Background

Comparative studies aiming to identify differences in the fibrolytic potential of the hindgut microbiome between different types of equines are lacking, particularly as donkeys are known to degrade fibre more effectively than horses and ponies. This study was therefore conducted to assess differences in faecal microbiota composition of ponies, donkeys and donkey × pony hybrids.

## Methods/Approach

Animals (n=8 per equine type) were fed the same haylage and straw based diet for four weeks. Faecal samples were then collected and DNA extracted. Quantitative PCR was used to determine faecal concentrations of bacteria, archaea and anaerobic fungi. Universal 16S ribosomal RNA gene barcoded amplicon sequencing was used to characterise the faecal bacterial/archaeal community composition.

## Results

Microbial concentrations were not affected by equine type ( $P > 0.25$ ). Microbiota composition significantly differed between donkeys and ponies ( $P = 0.01$ ), with hybrids not differing from donkeys or ponies ( $P > 0.15$ ). At the genus level, two taxa were affected by equine type: *Lachnoclostridium* 10 ( $P = 0.03$ ) and *Lachnospiraceae* probable genus 10 ( $P = 0.01$ ). The relative abundance of both taxa was significantly higher in donkeys compared to both ponies and hybrids ( $P < 0.01$ ), with no significant difference between ponies and hybrids ( $P > 0.73$ ).

## Conclusions

Donkey faecal microbiota differed from that of ponies and hybrids in terms of only two bacterial genera. It is speculated that these genera may contribute to the ability of donkeys to degrade fibre more effectively compared to other domesticated equines, as both genera are known to contain species/isolates with fibrolytic activity.