THE EFFECT OF MOXIDECTIN TREATMENT ON THE EQUINE HIND GUT MICROBIOME, METABONOME AND FEED FERMENTATION KINETICS IN HORSES WITH VERY LOW PARASITE BURDENS

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Background: The equine microbiome is extremely sensitive to change, anthelmintic treatment is a colic risk factor (Hillyer et al., 2002).

Objectives: The aim was three-fold, does moxidectin: (i) alter bacterial composition (ii) get metabolized by bacteria (iii) alter hind gut fermentation kinetics.

Methods: Seventeen horses, mean 12.35 years, kept at pasture, with haylage provided and no concentrates. Faecal Egg Counts were conducted September 2015-March 2016, no eggs seen, no anthelmintic given. Sampling commenced March 2016, points were 0 (prior), 16, 48 and 168 hours post anthelmintic. Treatments were randomized, nine animals dosed orally with Moxidectin 18.92 mg/g at 0.4 mg/kg bw and eight controls. Three horses from each group were randomly assigned for fermentation kinetics.

Sequencing of the 16S rRNA gene was conducted on extracted faecal bacterial DNA, bioinformatics using QIIME assigning operational taxonomic units (OTUs). LEfSe (Segata et al., 2011) was used to identify differentially abundant OTUs. Bacterial metabolic profiles were characterized by 1H NMR spectroscopy (Escalona et al., 2015), from urine, analysed by Principal Components Analysis. Fermentation of hay and oats, separately, were measured by in vitro gas production (Murray et al., 2006), data were analysed by repeated measures ANOVA.

Results: There were 13 differing OTU abundances between groups overall. At 16 hours we found 4 differing OTU abundances between groups. 1H NMR identified no significant metabolite differences. There was a significant reduction in fermentation of both hay (P = 0.04) and oats (P = 0.005) at 16 hours post treatment.

Conclusions: Moxidectin altered fermentation kinetics of hay and oats, but bacterial diversity did not significantly alter. No change in bacterial metabolite output was detected.

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References


