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

^{1,2}Daniels S.P., ²Leng J., ³Ellis R., ⁴Swann J.R., ¹Moore-

Colyer M.J.S. and ²Proudman C.J.

¹Centre of Equine Management and Science, Royal Agricultural University, Cirencester, Gloucestershire GL9 6JS; ²School of Veterinary Medicine, University of Surrey, Guildford, Surrey GU2 7TE; ³Animal & Plant Health Agency, Addlestone, Surrey KT15 3NB; ⁴Faculty of Medicine, Department of Surgery & Cancer, Imperial College, London SW7 2AZ. 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 aut fermentation kinetics.

Methods: Seventeen horses, mean 12 3.5 years, kept at pasture, with haylage provided and no concentrat**G**. 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.

Ethical animal research: Ethical approval obtained from University of Surrey Animal Welfare and Ethical Review Board NASPA-2015-008-SVM. Owner consent obtained. Source of funding: None. Competing interests: None.

References

Escalona, E.E., Leng, J., Dona, A.C., Merrifield, C.A., Holmes, E., Proudman, C.J. and Swann, J. (2015). Dominant Components of the Thoroughbred Metabolome characterised by (1) H-Nuclear Magnetic Resonance Spectroscopy: A Metabolite Atlas of Common Biofluids. *Equine Veterinary Journal*. 47 (6): 721-730.

Hillyer, M.H., Taylor, F.G.R., Proudman, C.J., Edwards, G.B., Smith, J.E. and French, N. P. (2002). Case control study to identify risk factors for simple colonic obstruction and distension colic in horses. Equine Veterinary Journal. 35(5): 455-463.

Murray, J. M.D., Longland, A. and Moore-Colyer, M.J.S. (2006). *In vitro* fermentation of different ratios of high-temperature dried lucerne and sugar beet pulp incubated with an equine faecal inoculum. *Animal Feed Science and Technology*. 129: 89-98.

Segata, N., Izard, J., Waldren, L., Gevers, D., Miroplosky, L., Garrett, W.S. and Huttonhower, C. (2011) Metagenomic biomarker discovery and explanation. *Genome Biology*. https://doi.org/10.1186/gb-2011-12-6- r60.