

Domesticated equines have fundamental differences in faecal microbial concentrations

J.E. Edwards¹, P. van den Berg¹, F. Burden², D.A. van Doorn^{3,4}, W.F. Pellikaan⁵, J. Dijkstra⁵, H. Everts³ and H. Smidt¹

joan.edwards@wur.nl

¹Laboratory of Microbiology, Wageningen University & Research, 6708 WE Wageningen, The Netherlands

²The Donkey Sanctuary, Sidmouth, Devon, EX10 0NU, United Kingdom

³Division of Nutrition, Department of Farm Animal Health, Faculty of Veterinary Medicine, Utrecht University, 3584 CM Utrecht, The Netherlands

⁴Department of Equine Health, Faculty of Veterinary Medicine, Utrecht University, 3584 CL Utrecht, The Netherlands

⁵Animal Nutrition Group, Wageningen University & Research, 6708 WD Wageningen, The Netherlands

Background: Nutritional studies have shown that donkeys have a higher dry matter digestibility (DMD) of dietary material than horses for a given diet, with the difference between the two equines being more pronounced as diet quality decreases¹. As analysis of the equine gut microbiome to date has primarily focussed on horses, however, it is unclear to what extent these differences in DMD between the equines are mediated by differences in their physiology and/or hindgut microbiota.

Objective: A preliminary study was therefore conducted in order to assess the faecal concentrations of bacteria, archaea and anaerobic fungi in horses, donkeys and donkey hybrids.

Methods: For each equine group, one fresh faecal sample was collected during September & October 2016 from healthy 4-25 year old animals (n=18) with no known history of gut-related problems. For each equine group a representative animal size range was used, with animals sourced from multiple locations. The majority of the animals sampled had a predominantly pasture based diet. Faecal samples were freeze-dried and ground, and then DNA extracted using a customised Maxwell method (Promega). Concentrations of bacteria, archaea and anaerobic fungi were determined using established quantitative PCR methods. Data were analysed on a dry weight basis after Log₁₀ transformation using a one-way ANOVA with equine group as a single independent factor and a Tukey post-hoc test.

Results: The concentrations of all three microbial groups analysed were significantly affected by equine group ($P < 0.05$). The mean bacterial concentration in horses was significantly lower than in donkey hybrids (153% of the horse mean (Hm)), with donkeys (112% of the Hm) not significantly differing from horses or donkey hybrids. Mean archaeal and anaerobic fungal concentrations in horses were significantly lower than in donkeys

(213% and 617% respectively of the Hm) and donkey hybrids (242% and 365% respectively of the Hm), which did not significantly differ from each other.

Conclusion: Whilst all microbial concentrations were affected by equine group, the greatest differences were observed in terms of the anaerobic fungi. A six-fold higher anaerobic fungal concentration in donkeys relative to horses suggests that these potent fibre degrading organisms significantly contribute to the higher DMD of donkeys relative to horses.

¹ Smith & Pearson 2005 Trop. Anim. Health Pro. 37, 1-19.