

Assessment of Faecal Microbiota Transplantation on Horses Suffering from Free Faecal Water

Louise Laustsen¹, Joan Edwards², Hauke Smidt², David van Doorn³, Nanna Lúthersson⁴

¹ Department of Veterinary Education, Institute of Veterinary Science, University of Liverpool, Neston, United Kingdom.

² Laboratory of Microbiology, Wageningen University & Research, Wageningen, The Netherlands.

³ Faculty of Veterinary Medicine, Utrecht University, Utrecht, The Netherlands.

⁴ Hstedoktoren, Kirke Eskilstrup, Denmark.

Background: Equines suffering from chronic gastro-intestinal tract related disease may undergo faecal microbiota transplantation (FMT). However, there are no validated protocols for the use of FMT in equines. Therefore, this study assessed the effect of a standardised FMT protocol on horses suffering from free faecal water (FFW). This is a clinical and management problem where FFW spontaneously runs out of the horse's anus.

Methods/Approach: FFW horses (n=10) had a history of chronic (>1 year) FFW. Clinically healthy controls were selected from the same barns as FFW horses (n=12). FFW horses were treated with the FMT protocol, including Omeprazole (4mg/kg *per os* SID) before (d-9 to d-5) and during (d-4 to d0) the five consecutive days of FMT. Faeces (500g) from a healthy donor was diluted in 5L of saline and transplanted via naso-gastric tube, followed by a dose of Psyllium (0.5-1g/kg BW) diluted in 3-5L of water. An FFW symptom severity scale (SSS), ranging from 0 (symptom free) to 4 (maximum severity), was used to assess horses before (d-9) and after (d7, d14, d28, d84 and d164) application of FMT.

Results: Compared to d-9 (mean 3.5, SEM 0.16), the SSS significantly decreased in FFW horses by d14 (mean 2.3, SEM 0.51; $P = 0.02$), and then remained decreased ($P < 0.02$). All control horses had an SSS of 0 throughout the study.

Conclusions: The applied FMT protocol significantly decreased FFW symptoms in horses suffering from FFW during the study period. Molecular analyses will provide further insight into the corresponding changes in hindgut microbial composition.