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Title: Comparison of faecal microbiota of horses suffering from atypical myopathy and healthy co-grazers

Authors: Simona Cerri[1], Bernard Taminiau[2], Dominique Votion[3], Helene Amory [1], Georges Daube [2], Carla Cesarini[1]

1 Clinique Vétérinaire Universitaire et Département Clinique des Animaux de Compagnie et des Equidés, Faculté de Médecine vétérinaire, Université de Liège

2 FARAH Center, Department of Food Sciences – microbiology, University of Liege, B43b Quartier Vallée 2, Avenue de Cureghem 10, 4000 Liège Belgium

3 Equine Pole, FARAH Center, Faculty of Veterinary Medicine, Avenue de Cureghem, 7A (B42), Quartier Vallée 2, Sart Tilman, Liège, B-4000, Belgium.

Corresponding author:

Carla Cesarini, DVM, PhD, Dip.ECEIM, Dip.ACVIM

Clinique Vétérinaire Universitaire - Pôle Equin

Avenue de Cureghem 5D, B41 Quartier Vallée 2, 4000 Liège 1 (Sart Tilman), BELGIQUE

Tel: + 32 4 366 4107, + 32 4 242 7545

Email: ccesarini@ulg.ac.be

Key words: microbiota, atypical, myopathy, equine, gastrointestinal

Objectives: To characterize faecal microbiota of horses with atypical myopathy (AM) compared with healthy co-grazers (HcG).

Methods: Fresh faecal samples were obtained from 6 horses (1 stallion, 3 geldings and 2 females; mean age of 11.8±10 years) with confirmed AM and 6 HcG (4 geldings and 2 females; mean age of 13.6±8 years) during autumn-2016 and spring-2017 AM outbreaks in Belgium.

Bacterial taxonomy profiling obtained by 16S amplicon sequencing of faeces was used to identify differentially distributed bacterial taxa between AM and HcG. Results were statistically compared using Welch's t-test with STAMP software.

Results: A total of 90,407 sequences were analysed and clustered to 8,066 operational taxonomic units. Bacterial populations were distributed between 17 phylas, although 20% of sequences could not be attributed to an existing phylum.

Horses with AM harboured a significantly higher relative abundance of *Ruminococcaceae* family with a significantly lower *Lachnospiraceae* when compared to HcG.

Discussion: AM is caused by hypoglycin A intoxication, but only a part of horses pasturing in the same toxic environment develops the pathology, suggesting that there may be protective factors at the horse level. The results of this study show significant differences in faecal microbiota between AM cases and HcG, which could suggest that microbiota could play a role in the development or prevention of clinical disease.

Conclusions: Results demonstrate that microbiota of AM affected horses is significantly different compared to HcG.

Significance: Microbiome could influence the development of AM, but this role deserves further investigation.