Abstract for ECEIM Congress 2-4 November, 2017

Submission for: oral presentation (preference) or poster

Topic: Musculoskeletal, Metabolic, toxicology

The authors state that the present work is not presented or published elsewhere before the ECEIM Congress 2-4 November, 2017.

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

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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 phyla, although 20% of sequences could not be attributed to an existing phylum.

Horses with AM harboured a significantly higher relative abundance of Ruminococcaeae 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.