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HYPOTHESIS ON THE PATHOPHYSIOLOGY OF SMALL INTESTINAL STRANGULATION BY PEDUNCULATED LIPOMAS

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Background: To explain the pathogenesis of pedunculated lipoma strangulation, many authors stated that it moves around a loop of intestine wrapping it with its stalk. Why the lipoma should move around the loops of intestine and why it then became entangled is not explained, making this hypothesis not fully convincing.

Objectives: To propose an explanation of strangulation by pedunculated lipomas that accounts for the many aspects this pathology involves.

Methods: Analysis of the anatomical features of 11 cases of lipoma strangulation in horses.

Results: We hypothesised that the stalk is tensioned by the weight of the lipoma or by the fact that the lipoma is trapped between portions of intestine. This produces a slit-like aperture formed by the stalk and the mesentery. One (or multiple) loop of intestine pass lateral to the stalk before turning into this aperture either because of lack of space in the abdominal cavity or by effects of the peristalsis. The weight of the intestine itself causes a 'fall' of the loop. This causes a modification of the whole system similar to that done by a surgeon when making a half-hitch knot: the falling of the loop cause a movement of the 'post' formed by the stalk of the lipoma that turns in a half-hitch that strangulates the loop of intestine.

Conclusions: This hypothesis, as opposed to previously proposed ones, can explain strangulation by short and long stalk pedunculated lipomas, by lipomas of different weights and shape and of multiple loops of bowel simultaneously.

Ethical animal research: No ethical approval required.

Source of funding: None.

Competing interests: None.

Objectives: The purpose of this project was to compare the faecal microbiome and metabolome in three populations of horses: those receiving antimicrobial therapy that developed diarrhoea (AAD), those on antibiotics that did not develop diarrhoea (ABX) and a healthy control population not exposed to antibiotics (CON). Horses were matched for diet and antimicrobial agent including dose, route of administration and duration.

Methods: Illumina sequencing of 16S rRNA genes was performed and QIIME 2.0 was used to generate alpha and beta diversity metrics. Untargeted metabolomics using GC-MS platforms was performed and data analysed using Metaboanalyst 5.0.

Results: Faecal samples were collected from horses with AAD (n = 17), ABX (n = 15) and CON (n = 31). ANOSIM analysis of microbiome composition was significantly different in AAD compared to CON (R = 0.568, p = 0.001), but not to ABX (R = 0.121, p = 0.0012). AAD and ABX horses had significantly decreased richness and evenness compared to CON horses (p < 0.05). AAD showed decreased abundance of Actinobacteria, Armatimonadetes, Fibrobacteres, Spirochaetes, Synergistetes, and TM7 and increased abundance of Bacteroidetes compared to CON (p < 0.05). Only Verrucomicrobia was markedly decreased in AAD compared to ABX and CON horses (p < 0.05). Untargeted analysis yielded a total of 1398 compounds including 127 names metabolites. PCA plots indicated separation of metabolomic profiles between AAD and ABX, CON groups. Seven metabolites were found to be significantly different between groups from the following pathways (p < 0.05): amino acid metabolism (L-tyrosine, kynurenic acid, xanthurenic acid, 5-hydroxyindole-3-acetic acid, N-acetyltyramine), lipid metabolism (docosahexaenoic acid) and biosynthesis of secondary metabolites (daidzein).

Conclusions: Horses with AAD have a dysbiosis compared to CON horses, and show minor differences in bacterial community composition compared to ABX horses. Metabolite profiles of horses on antimicrobials, especially those with AAD, are altered compared to CON horses.

Ethical animal research: No ethical approval required.

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Diagnostics

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ALTERATIONS IN THE FAECAL MICROBIOME AND METABOLOME OF HORSES WITH ANTIMICROBIAL ASSOCIATED DIARRHOEA COMPARED TO ANTIBIOTIC-TREATED AND NON-TREATED HEALTHY CASE CONTROLS

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Background: Diarrhoea is an adverse effect of antimicrobial therapy in horses. The microbiome and metabolome of horses with antimicrobial associated diarrhoea (AAD) has not yet been described or compared to horses that did not develop diarrhoea on antibiotics.

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THE VALUE OF TRANSABDOMINAL ULTRASOUND IN HORSES THAT PRESENT WITH WEIGHT LOSS, RECURRENT BOUTS OF ABDOMINAL PAIN, PYREXIA OF UNKNOWN ORIGIN AND CHRONIC DIARRHOEA

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