

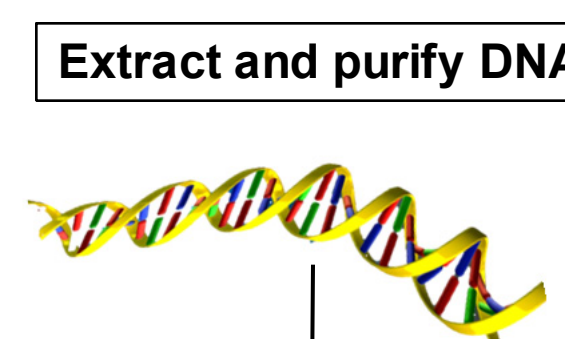


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- Gastrointestinal (GI) disease represents one of the most common medical problems encountered by horse owners and veterinarians. This fact is not surprising in light of the fact that the horse's large intestine (and its microbiome) is crucial for the health of this herbivorous species (a hind gut fermenter). In a majority of cases of equine GI disturbance (colic, diarrhea), a specific etiological explanation cannot be established.
- Next Generation Sequencing offers the potential to better understand diverse microbial perturbations that lead to GI disease in this species.
- Increased knowledge of the equine microbiome promises improved therapeutic and diagnostic methods, especially for common diseases such as colic, diarrhea, and laminitis.
- We sought to determine whether results of microbiome analysis of feces is representative of the microbiome at more proximal aspects of the GI tract of healthy adult horses. Moreover, we also determined whether microbiota samples obtained from the lumen of the GI tract are representative of epithelial-associated microbiota throughout the equine GI tract.

Luminal and mucosal samples were collected from horses (n=9) subjected to euthanasia for reasons unrelated to the project, and determined to be free of gastrointestinal disease via physical and histopathological examination.



Amplify V4 region of microbial 16S rRNA gene via polymerase chain reaction



Annotate sequence data using database of 16S rRNA gene sequences

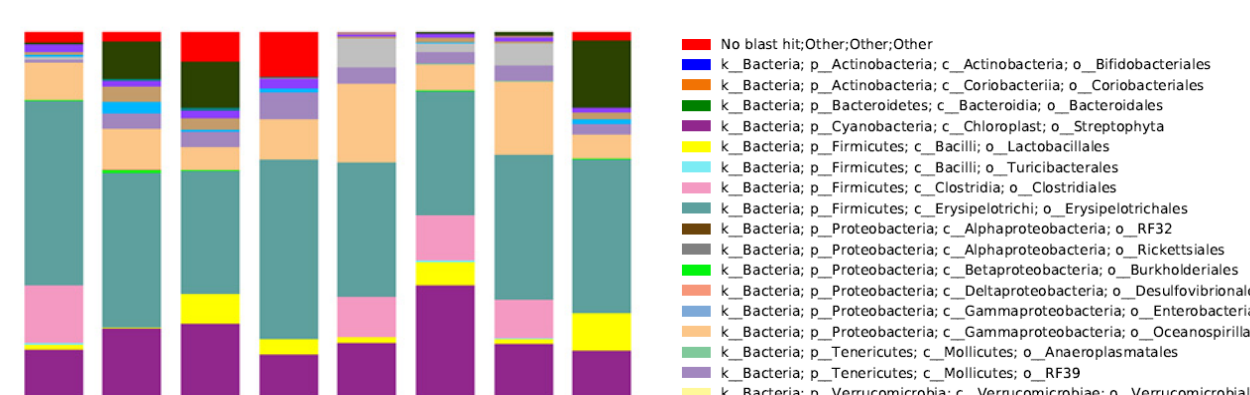


Figure 1: Bar charts showing the relative abundance of microbiota at the family level in each region of the equine GI tract. Blank bars denote regions where inadequate data were available.

Figure 2: Principle component analysis of samples shown in Figure 1, demonstrating clear separation between upper and lower GIT bacterial populations, and tight clustering of lower GIT samples.

Mean number OTUs $\pm$ SEM

Region	Mean number OTUs $\pm$ SEM	Significance Group
Stomach, dorsal	~150 $\pm$ 15	a
Stomach, antral	~160 $\pm$ 10	a
Jejunum	~140 $\pm$ 15	b
Ileum	~150 $\pm$ 15	a
Cecum	~120 $\pm$ 5	b
Colon, asc.	~115 $\pm$ 5	a
Colon, desc.	~125 $\pm$ 5	b

Figure 3: Bar chart showing mean microbial richness of different regions of the GIT. Letters above bars denote a statistically significant difference ($p \leq 0.05$, ANOVA on ranks).

- A “core microbiota” exists in the equine GI tract.
- Differences in the composition of the microbiota along the length of the GI tract were much greater than identified differences between horses.
- Luminal contents were not representative of mucosa-associated microbes at each sampled location.
- Microbiome composition of feces was not representative of the microbiome of the more oral aspects of the GI tract.
- Both luminal and mucosal bacterial communities normalize and become less variable between horses in distal relatively aboral regions of the GI tract.

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