EVALUATION OF IN VITRO AND IN VIVO EQUINE MICROBIAL POPULATION
SHIFTS IN RESPONSE TO COLIC CONDITIONS

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Abstract

We designed two continuous culture experiments to test the effects of starch
dosage and starvation upon equine fecal microflora. Diets were designed containing
fructooligosaccharides and mannanoligosaccharides in order to investigate treatment
effects on VFA and NH₃ concentration, and pH following starvation or starch overload.

This research indicated that total volatile fatty acid (VFA) concentration may be
affected by treatment following starch overload. Additionally, branched chain VFA, and
butyric acid concentrations were different across treatment in both experiments. This
research indicated that following an abrupt change in the starch content of the diet, or a
starvation period, those effects may be ameliorated by diet.

In our third experiment, we performed pyrosequencing in order to
phylogenetically characterize the shifts in the microbial populations observed in the feces
of eight horses collected from both the colic (large intestinal-nonsurgical) and healthy
states. Healthy samples were collected by the attending/referring veterinarian 60 days (±
30) post discharge. DNA was extracted from the fecal samples and the V1, V2, and V3
region of the 16S rDNA was amplified via emulsion PCR.

When ubiquitous microbes were ranked colic > healthy, four were significant. All
sick horses had greater reads of Clostridium phytofermentans, an uncultured Clostridiales
bacterium, and Bacteroidetes as well as an uncultured bacteroidetes bacterium. These
data suggest there is a need for broad bacterial diversity in the healthy equine gut.