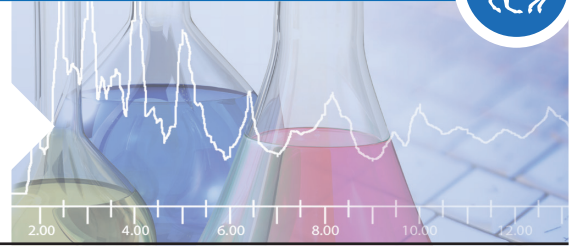




# FOCUS ON RESEARCH



## A Postbiotic from *Saccharomyces cerevisiae* Fermentation Improves Microbiome Robustness in Young Stress-Challenged Horses in Training

In this study, Diamond V™ TruEquine™ C, a *Saccharomyces cerevisiae* fermentation postbiotic was hypothesized to improve the robustness of the gut microbiome in stress-challenged horses.<sup>1</sup>

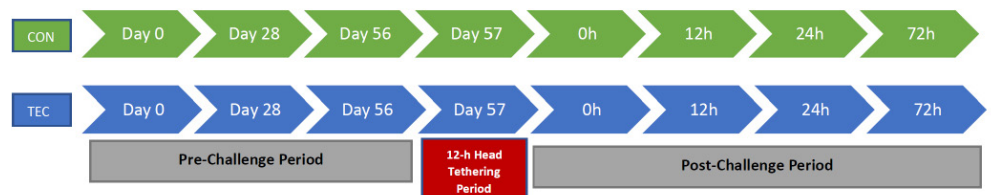
### Study Background

Horses are subjected to various stressors on a daily basis. Nutritional and environmental stressors can disturb the gut microbiome of horses which may ultimately decrease their health and performance. Diamond V TruEquine C, a *Saccharomyces cerevisiae* derived postbiotic, has been shown to help balance indicators of immunity and inflammation in horses. The objective of this study was to evaluate changes in the gut microbiome of horses subjected to a stressor that horses commonly encounter during trailering and transport.

### Experimental Overview

- Twenty Quarter Horses (22 months old; BW 438.17 kg) were randomly allotted to two daily dietary treatments consisting of 60% forage and 40% a standard non-postbiotic supplemented concentrate (CON; n=10) or supplemented with Diamond V TruEquine C (TEC; 47.8 mg/kg BW; n=10)
- Both treatment regimens were fed throughout the 60-d study.
- From Day 1-56 (pre-stress challenge), horses were exercised four days/week for 30-45 minutes at a light to moderate level of intensity.
- On Day 57, horses were placed in individual stalls and tethered with their heads restrictively elevated 14 inches above wither height for 12 hours to simulate a safety practice commonly imposed during trailering and transport.
- Gut metagenomic changes were characterized from fecal samples collected at Days 0, 28, 56 (pre-stress challenge, and at 0, 12, 24 and 72 hours once untethered (Figure 1).
- DNA extraction and Nanopore shotgun metagenomics were applied to all fecal samples.
- Alpha-diversity and microbial abundances were compared using non-parametric Wilcoxon-Rank-Sum test with Benjamini-Hochberg FDR correction.

### Figure 1: Experimental Design and Fecal Sampling Timepoints



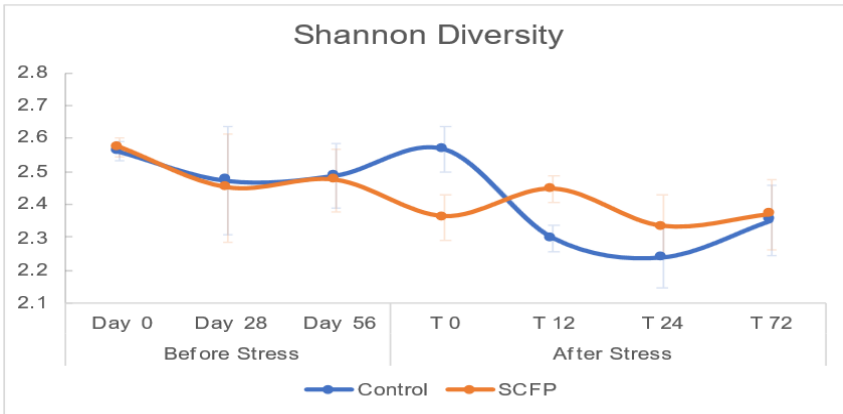
### Results

- The gut microbiome of CON horses displayed larger and persistent changes in alpha-diversity compared to the TEC group which was more stabilized alpha-diversity across all time points. Significant differences were noted between CON and TEC at 0 and 12 h ( $P < 0.05$ ; Figure 2).

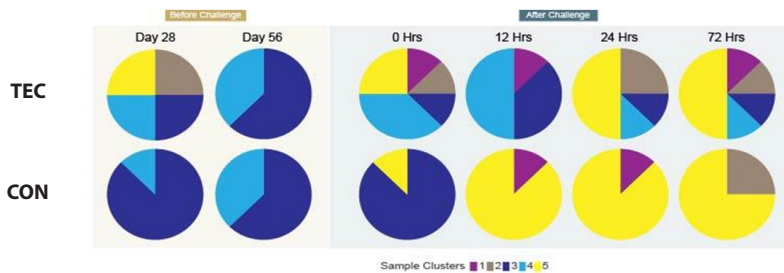
## Results - continued

- During the post-challenge period compositional clusters in the microbiome of CON horses were characterized by low abundances ( $P < 0.05$ ) of several beneficial commensal species versus TEC (Figure 3).
- No difference in beta-diversity were observed between CON and TEC on d 56 prior to head-tying, however, at 12 h post-challenge TEC horses maintained higher abundances of fibrolytic taxa ( $P < 0.05$ ).
- From this analysis, two distinct clusters of carbohydrase enzyme function (CAZy) were identified, both of which were retained in TEC horses following head-tying while only one was retained at any time from 0-72 h post-stress in CON horses (Figure 4).

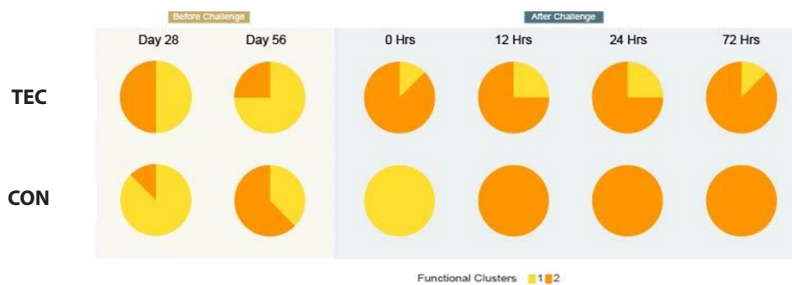
**Figure 2: Alpha-Diversity Changes Over Time in Response to Treatment and Stress**



**Figure 3: Community Compositional Clusters**



**Figure 4: Community Functional Clusters**



## Summary

These data demonstrate that dietary inclusion of Diamond V™ TruEquine™ C postbiotic improves microbiome robustness in horses indicating an ability to resist change due to stress.

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