

Detection of *Balantidium coli* and fecal microbiome dysbiosis in horses affected with fecal water syndrome

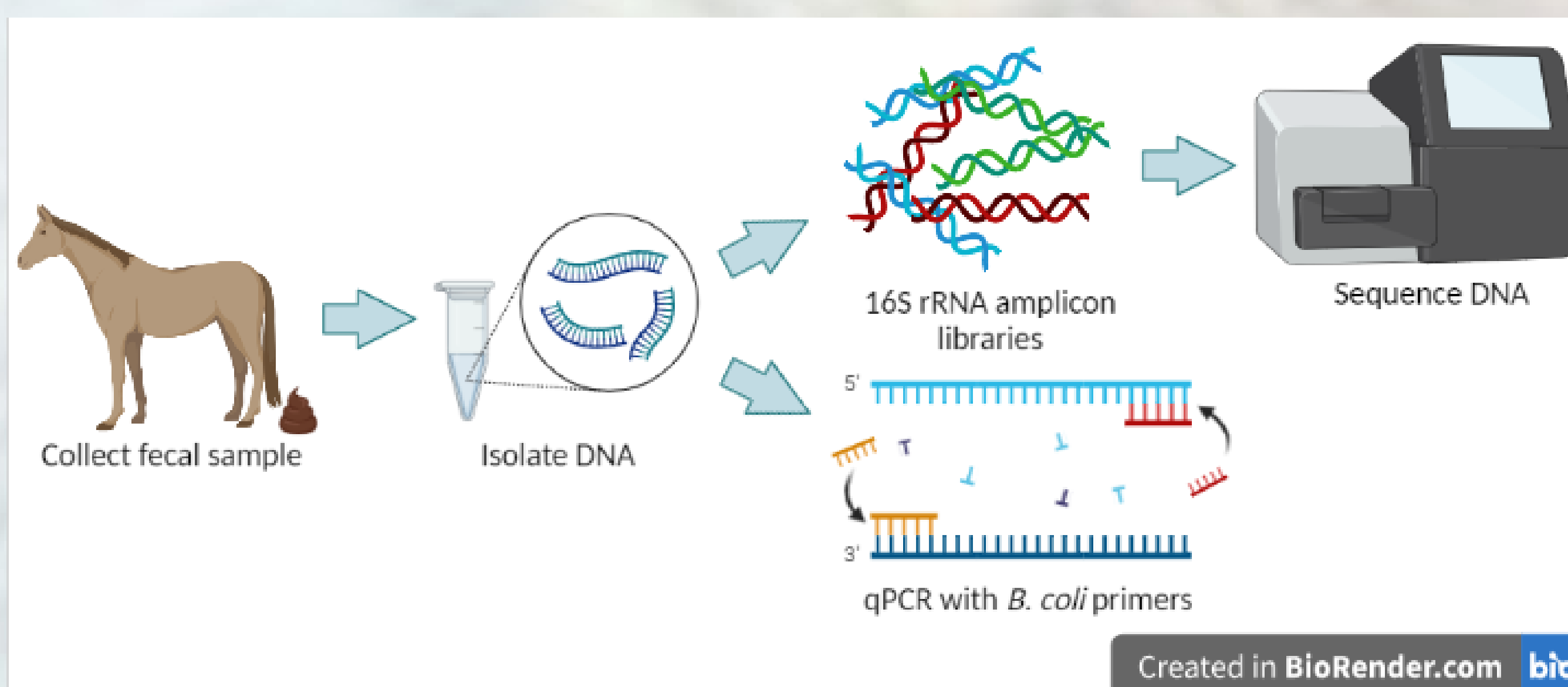
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Introduction

- Fecal water syndrome is characterized by the passage of formed stool accompanied with or followed by excessive fecal water
- FWS can lead to soiling of the legs, discomfort while defecating, and sanitary concerns for owners
- Causes of FWS are largely unknown, but previous research has suggested the following risk factors: type of hay fed, social standing, changes in the microbiome, age and gender
- There have been previous novel observations of *B. coli* in the feces of horses with FWS and elimination of *B. coli* following coccidiostat treatment sometimes in resolution of FWS
- Balantidium coli* is a parasitic protozoan found in the colon of many species and is most prevalent in tropical or sub-tropical regions
- The objective of this project is to identify any differences in fecal bacterial microbiomes of horses with FWS and determine if the protozoan *Balantidium coli* is overrepresented in affected horses

Methods



Conclusions and Future Studies

- Significant changes in the gut bacterial microbiome could be creating conditions that favor *B. coli* overgrowth
- Anti-protozoal medications may be helpful for the management of FWS symptoms as *B. coli* is overrepresented in fecal samples from horses with symptoms of FWS
- What is the abundance of *B. coli* in the United States?
- Do the symptoms of FWS resolve following treatment with a coccidiostat?
- What are the mechanisms behind FWS?

Acknowledgments

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Similar phyla abundance in FWS and controls

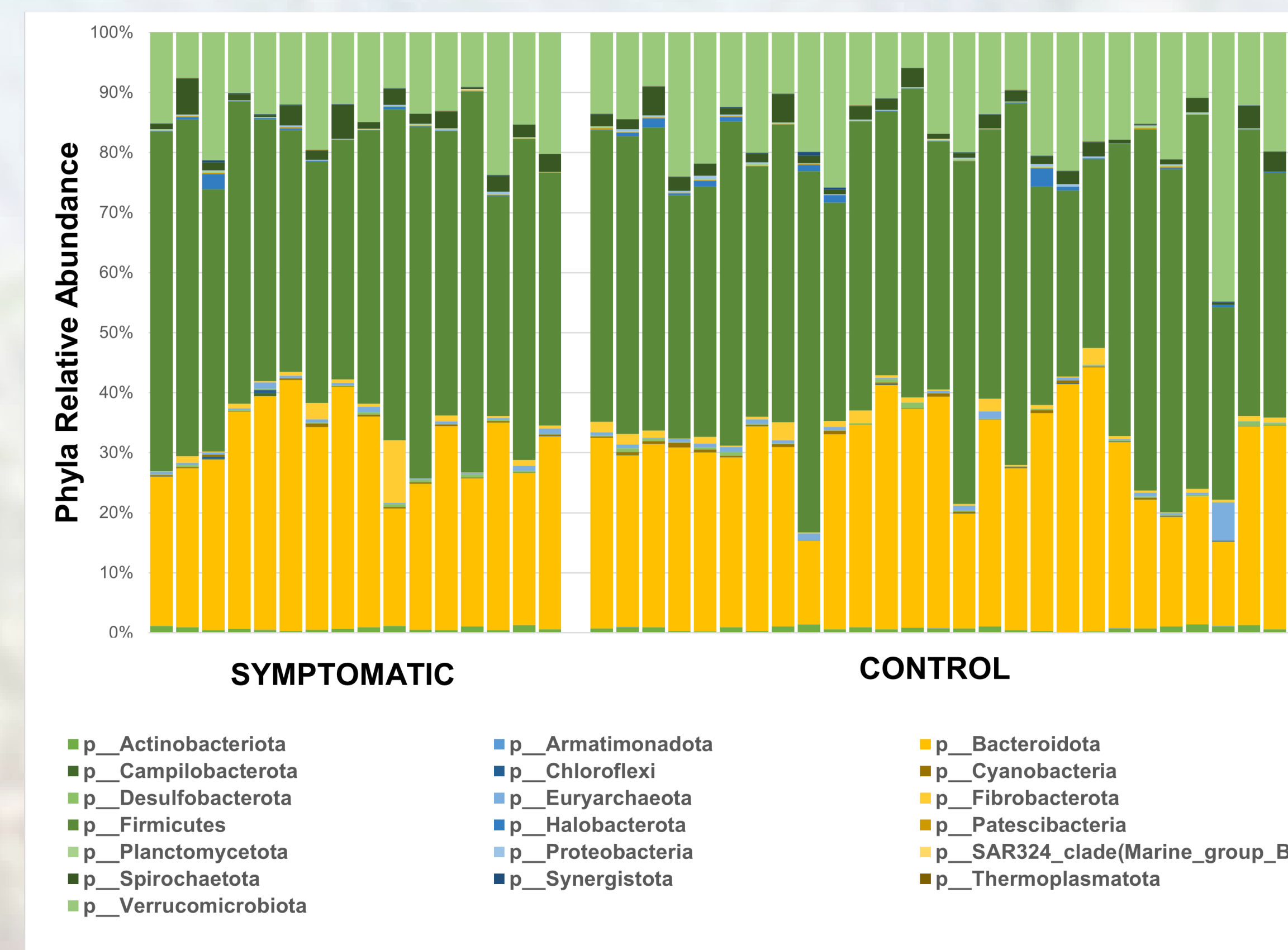


Figure 1. Stacked bar chart showing phyla Relative abundance of symptomatic (n=16) and unaffected controls (n=28). The three most abundant phyla in both groups are Bacteroidota (yellow), Firmicutes (dark green), and Verrucomicrobiota (pale green).

Samples cluster by status when considering a subset of ASVs

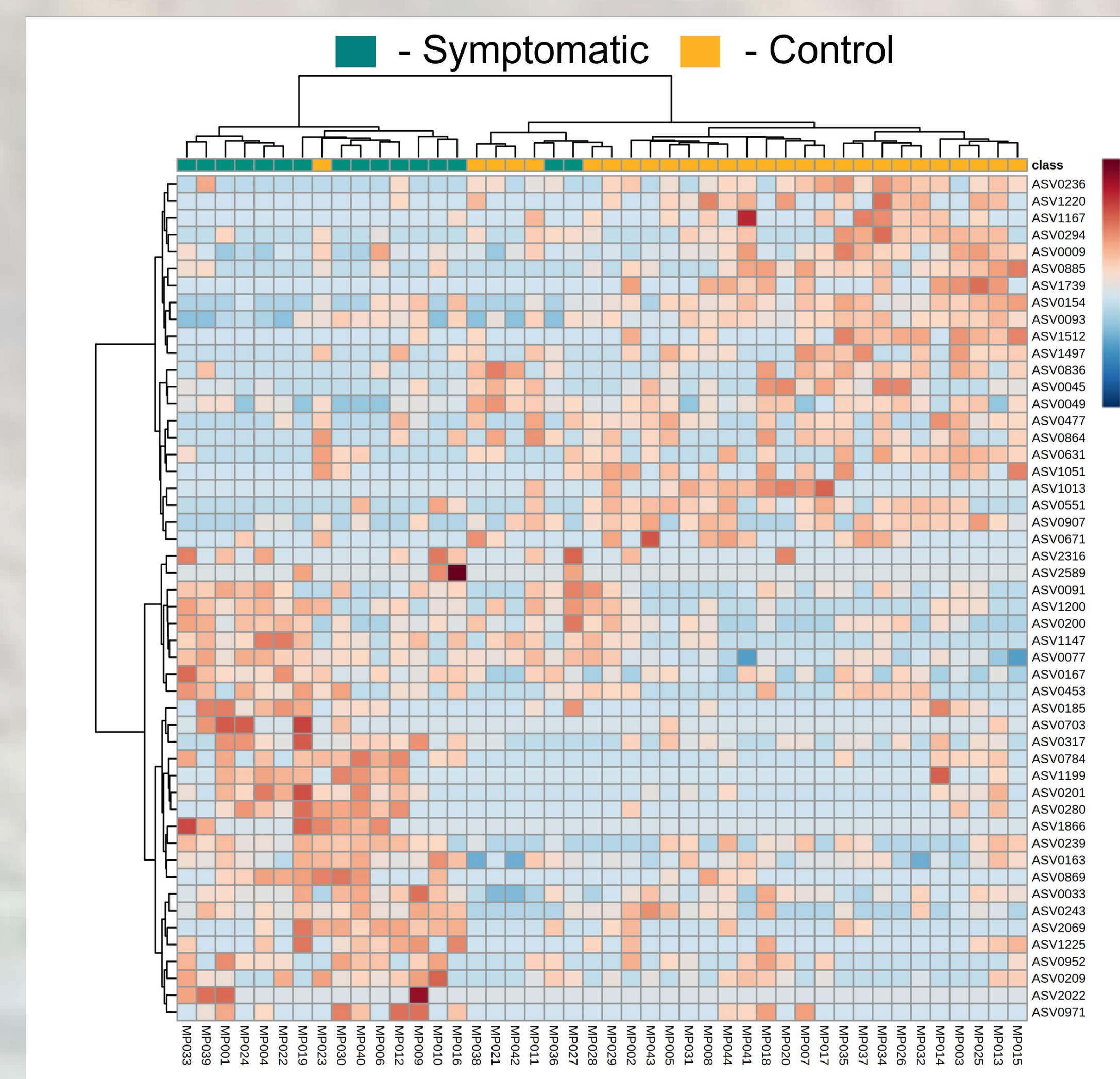


Figure 3. Heatmap generated using hierarchical clustering algorithm (UPGMA) using 50 ASVs with the lowest P value. Samples are arranged in columns with ASVs arranged in rows. Color indicates relative abundance within each ASV, legend at right.

Changes in fecal composition associated with FWS

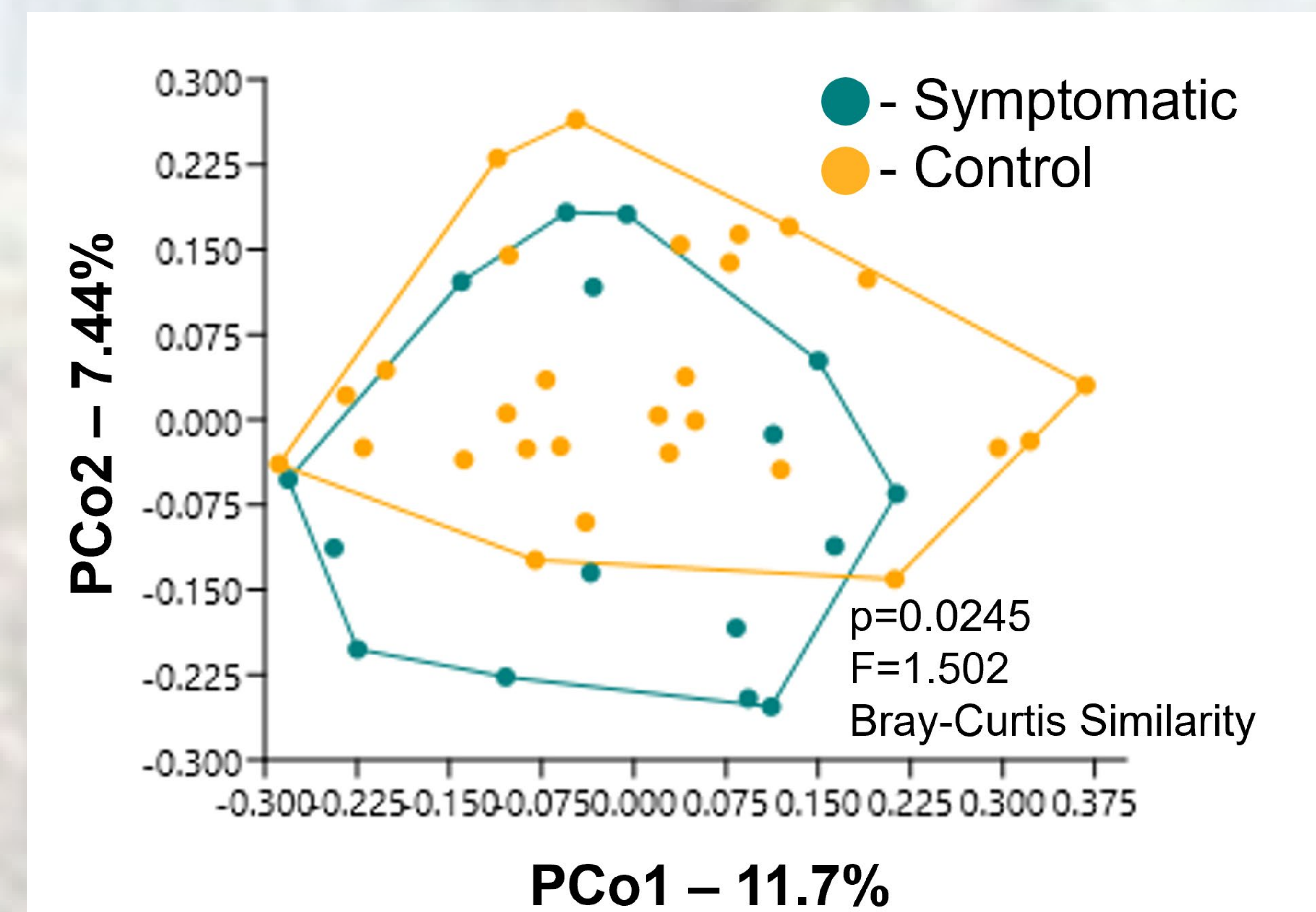


Figure 2. Principal coordinate analysis (PCoA) plot showing differences in composition between fecal microbiome in horses with FWS and controls. A one-way PERMANOVA was performed to determine statistical significance.

Differences in *B. coli* abundance in horses with FWS

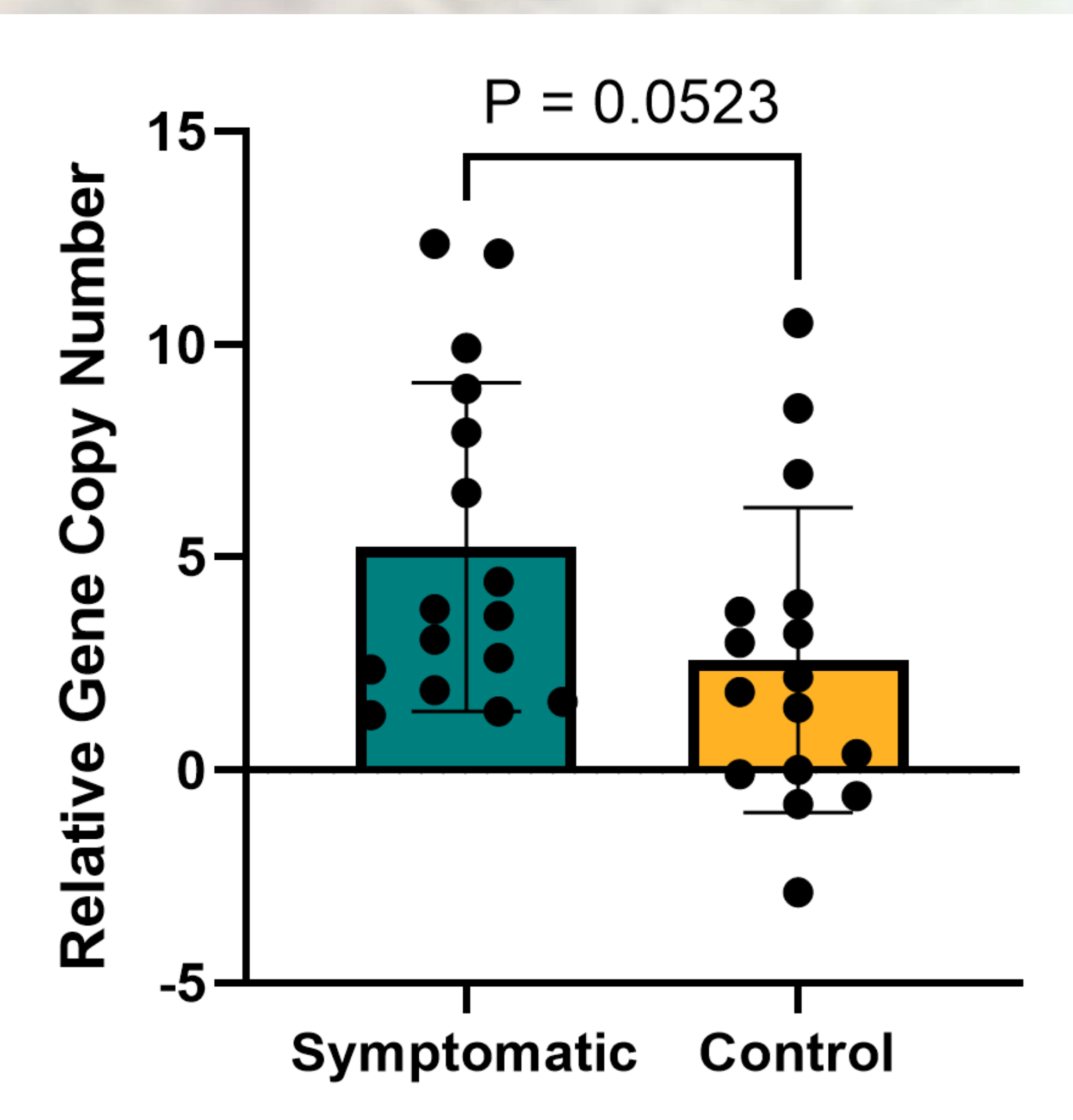


Figure 4. Relative gene copy number of *B. coli*-specific 18S gene in symptomatic horses and controls. A t-test was performed to determine statistical significance.