

Evaluation of fecal microbiota of dogs fed extruded diets containing white and red sorghum as primary carbohydrate sources.

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ABSTRACT:

- All animal procedures were approved by the University of Illinois Institutional Animal Care and Use Committee
- Three diets containing 30% of corn (CON), 30% white sorghum (WSH), or 30% red sorghum (RSH) were formulated to meet or exceed the AAFCO (2018) nutritional requirements for adult dogs
- Nine intact adult female beagles were randomly assigned to one of the 3 dietary treatments using a replicated 3x3 Latin square design
- Experiment periods consisted of 14 d (10 d of diet adaption + 4 d of total and fresh fecal and total urine collection)
- All diets were highly digested by dogs, and had similar ($P > 0.05$) apparent total tract nutrient digestibility
- Overall, fecal metabolite concentrations and microbiota were similar among treatments

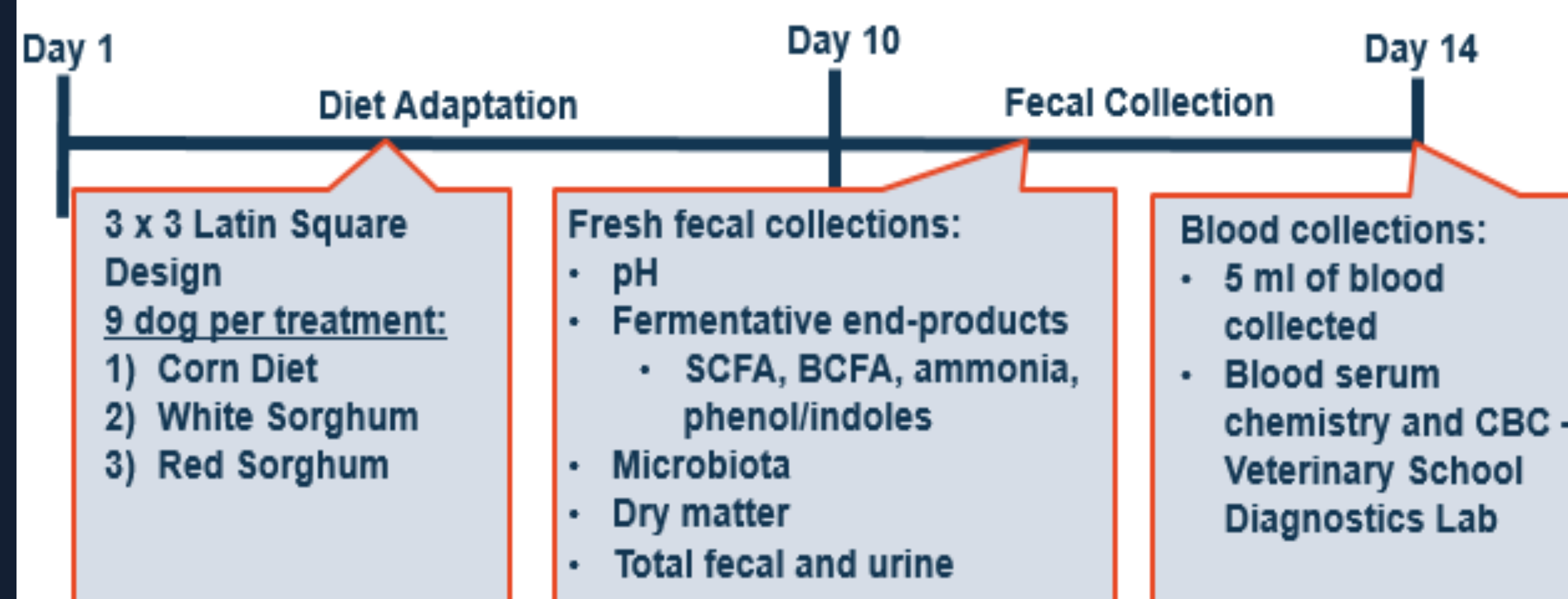
BACKGROUND:

- Sorghum (*Sorghum bicolor*) is a cereal grain consisting of either white, yellow, red, brown or black endosperms
- Human interest of ancient grains replacing modern carbohydrate sources has reached the pet-food market, leading to an increased focus on corn-free, non-GMO, and gluten-free diets in pet foods
- As sorghum is considered an ancient grain and novel ingredient in pet food products, it holds potential as an alternative carbohydrate source in companion animal nutrition
- Depending on the geographical location, sorghum can be more affordable than rice or corn (the common carbohydrate sources in pet foods)
- However, there is not sufficient scientific research regarding the effect of this cereal grain and its varieties on the gastrointestinal microbiome and host health of pet animals

OBJECTIVES:

- The objective of this research was to evaluate the effect of dietary supplementation of a novel sorghum grain (red or white):
 - As the main carbohydrate source on fecal microbiota and metabolites in dogs
 - And how the novel grains compared against a traditionally carbohydrate-only source, corn

EXPERIMENTAL DESIGN:



MATERIALS AND METHODS:

- Nine intact female beagles, avg. age 4.2 yrs; assigned to one of three dietary treatments per period, with three total 14 d periods
- Dogs were housed individually in metabolic crates during collection periods with fresh fecal samples collected and allocated for microbial analysis
- Illumina 16S rRNA sequencing from V4 region was completed using MiSeq and analyzed using QIIME 2
 - Over 1.8 million sequences were generated
- Samples were rarified to 42,160 reads for analysis of diversity and species richness
- Statistical analysis done using SAS 9.4 using MIXED model procedures (diet fixed effect, animal random effect) with significance set at P - and Q -values < 0.05 , linear models were used to evaluate the main effect of treatment

RESULTS:

Figure 1: Fecal microbial composition - phylum level

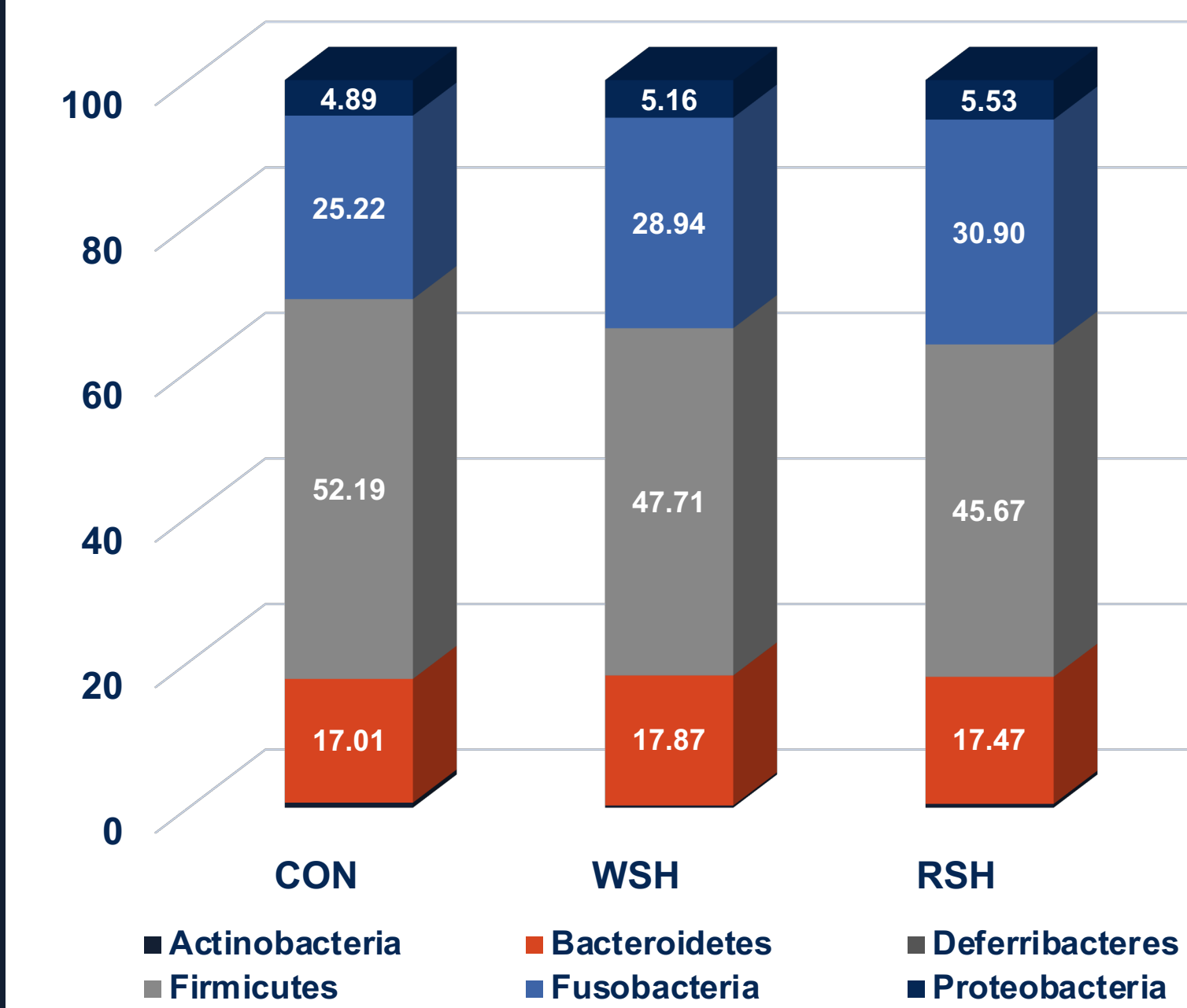


Figure 3: Unweighted (A) and weighted (B) beta-diversity based on UNIFRAC analysis

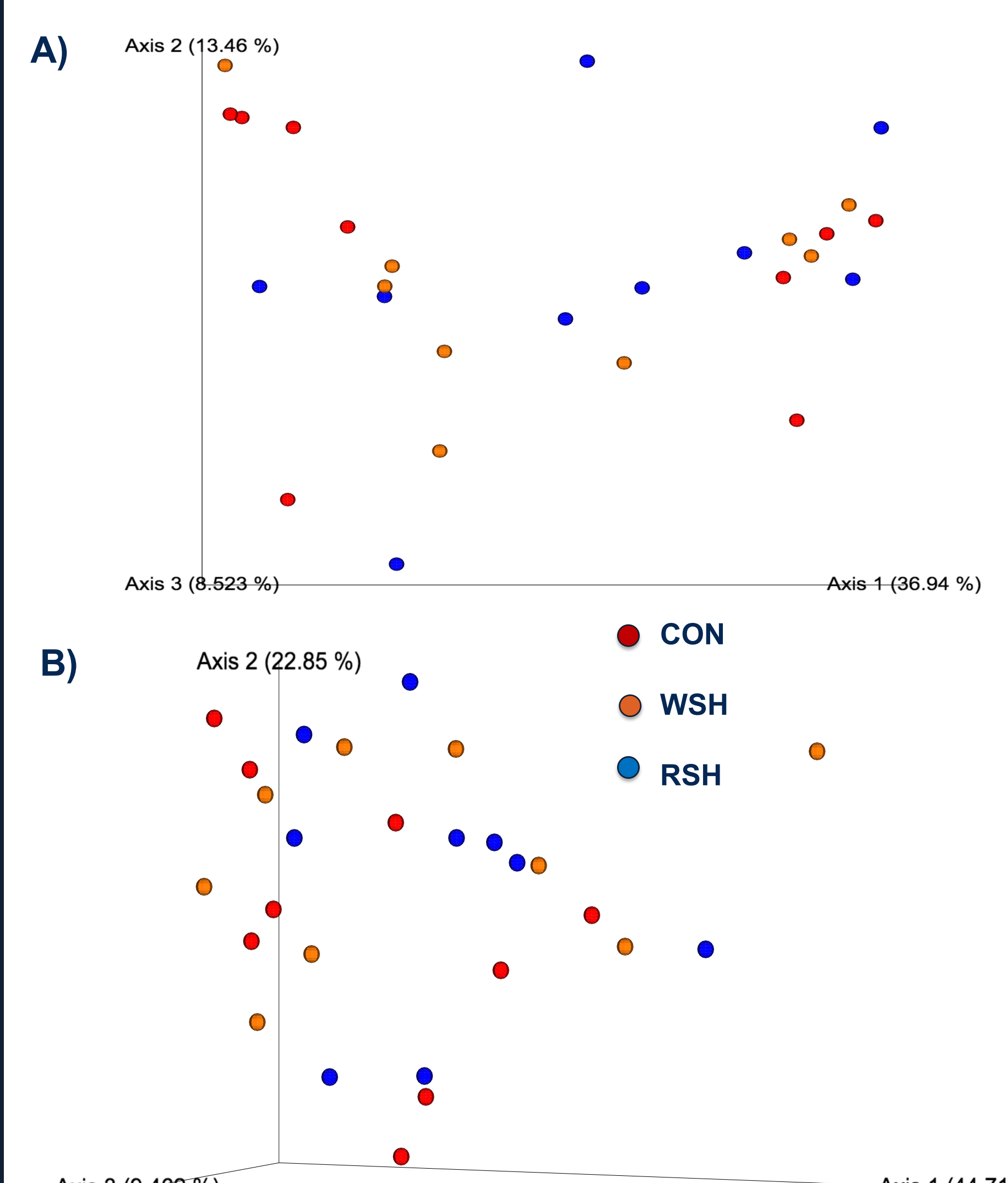


Figure 2: Fecal microbial composition - family level

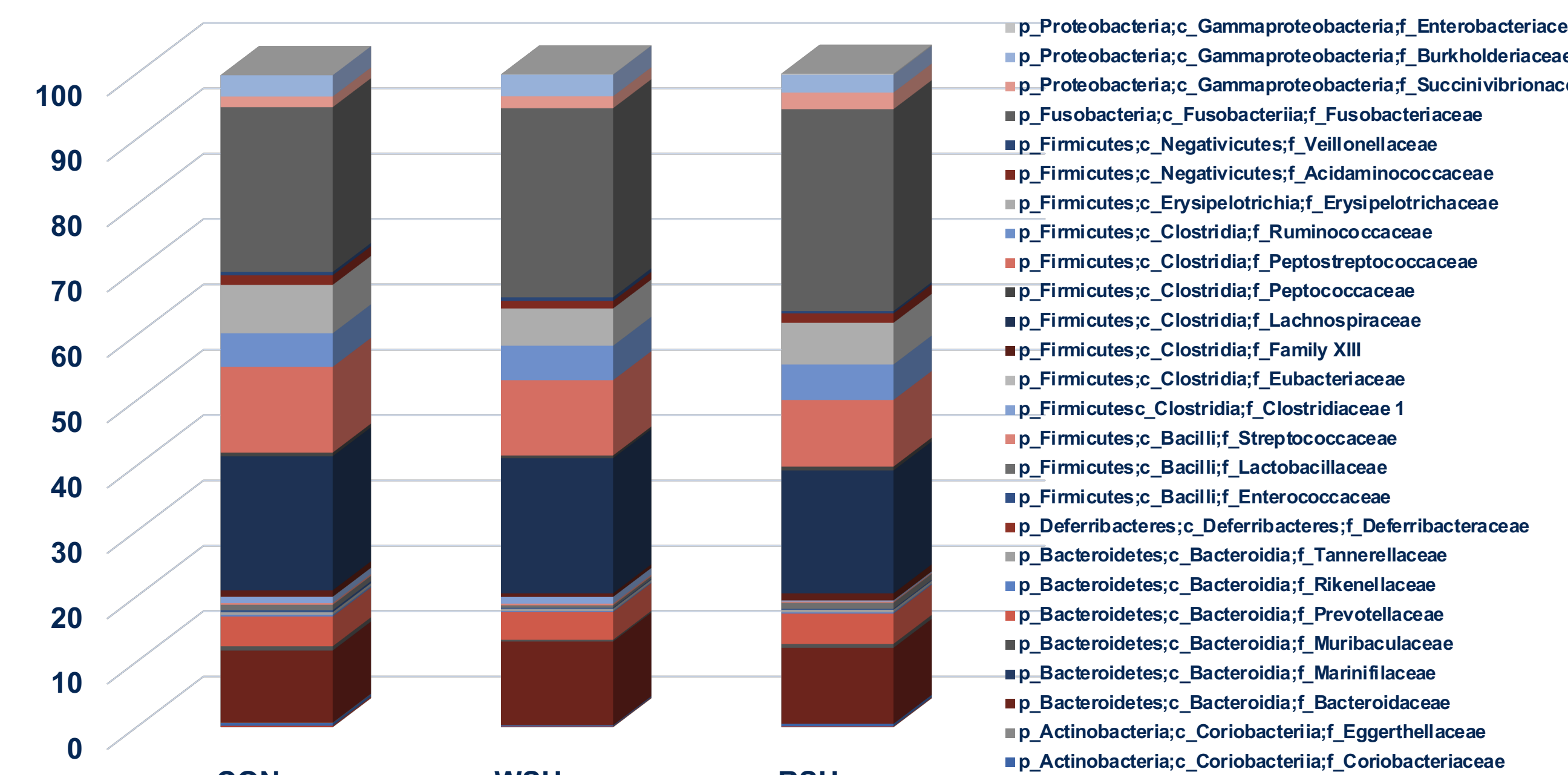


Figure 4: Erysipelotrichaceae and Family XIII

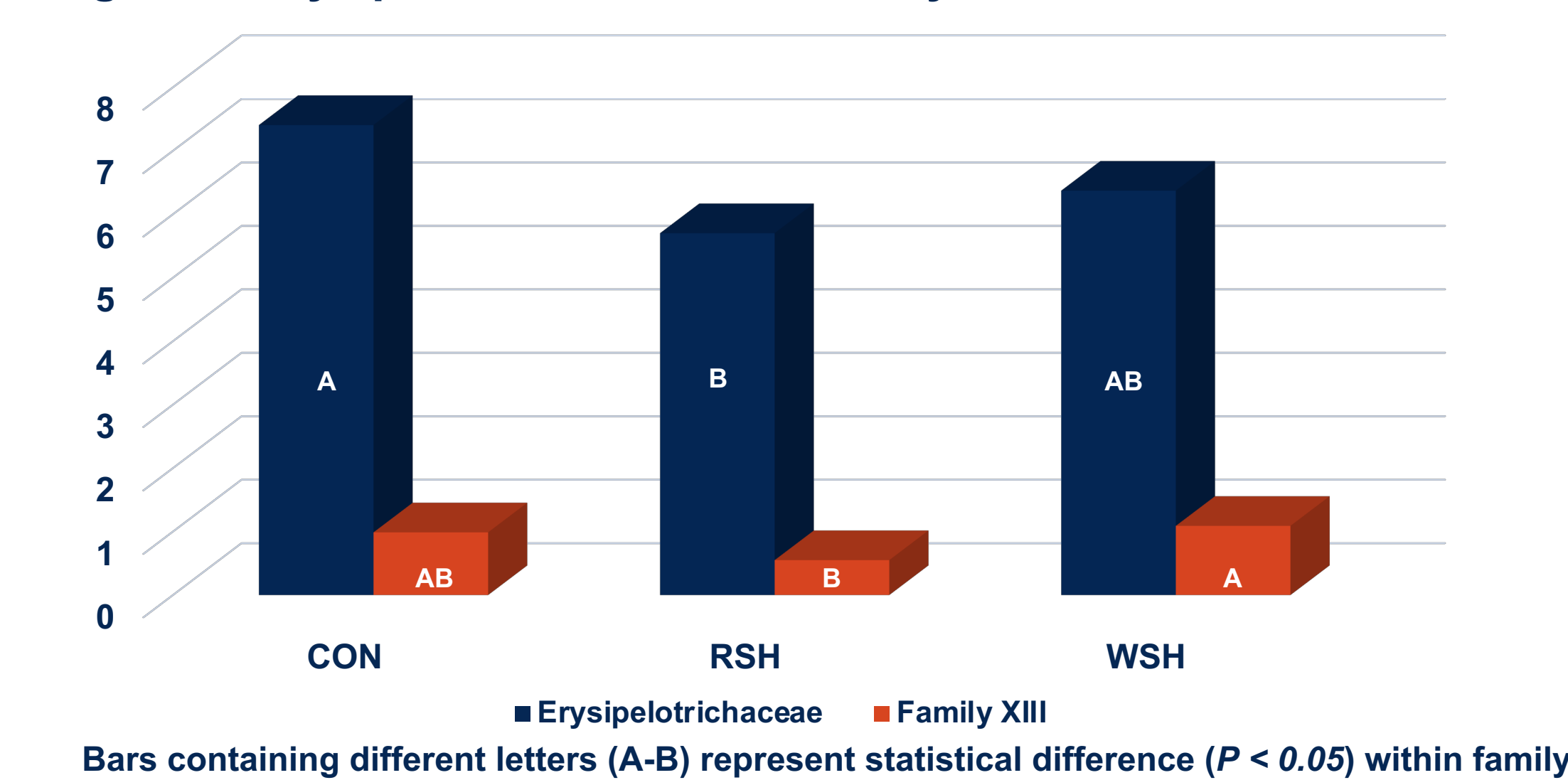
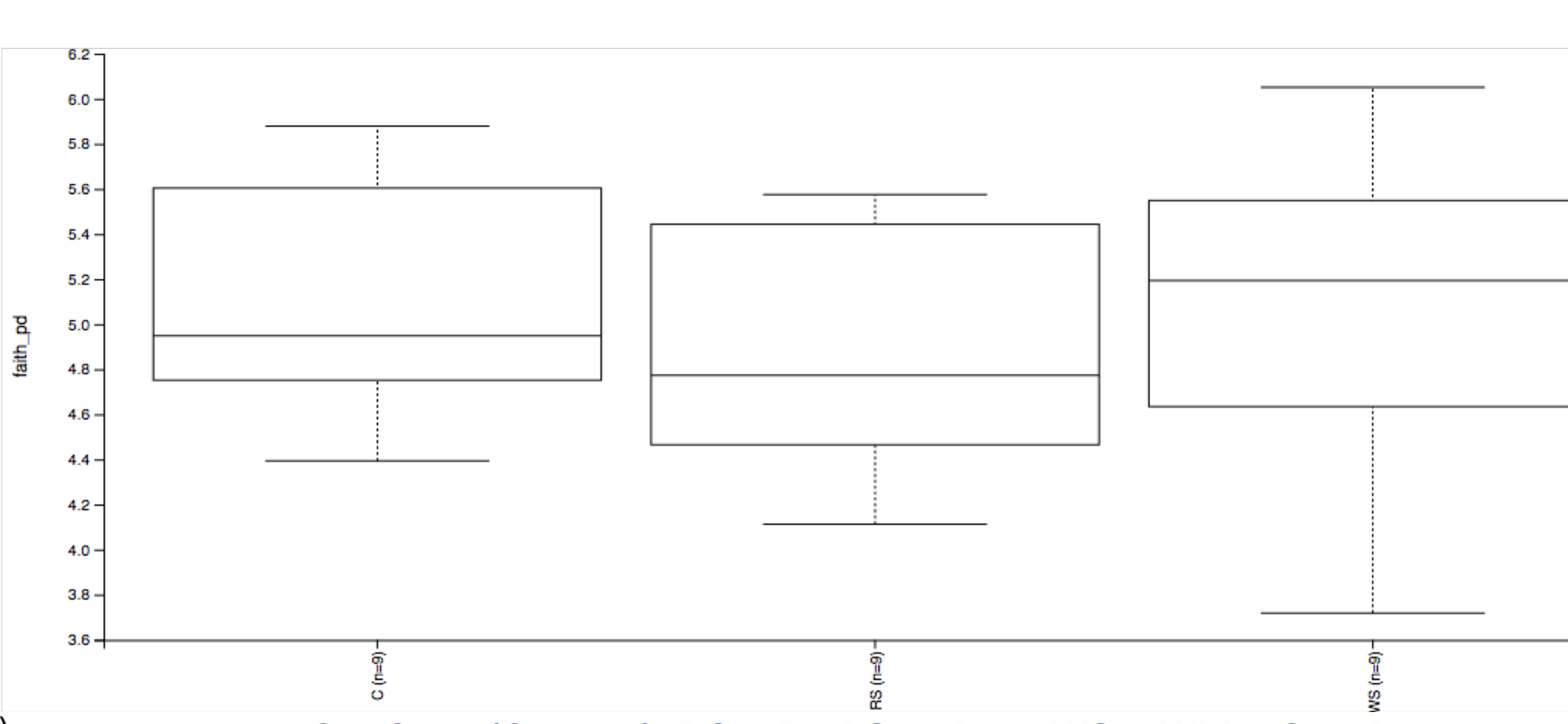


Figure 5: Alpha-diversity based on Faith's phylogenetic diversity



RESULTS:

Table 1: Total tract apparent macronutrient digestibility by adult canines fed dietary treatments

Item	Treatments ¹			SEM ²
	CON	WSH	RSH	
Digestibility, %				
Dry matter	81.3	83.1	82.3	0.91
Organic matter	86.7	88.2	87.5	0.68
Total dietary fiber	52.1 ^b	62.7 ^a	57.8 ^{ab}	2.30

¹ CON = Corn (Control); WSH = White Sorghum; RSH = Red Sorghum

² Standard error of the mean

^{a-b} Superscripts with different letters in a row represent statistical differences ($P < 0.05$)

Figure 6 (A-B): Fecal phenol and indole concentrations of dogs fed selected carbohydrate sources.

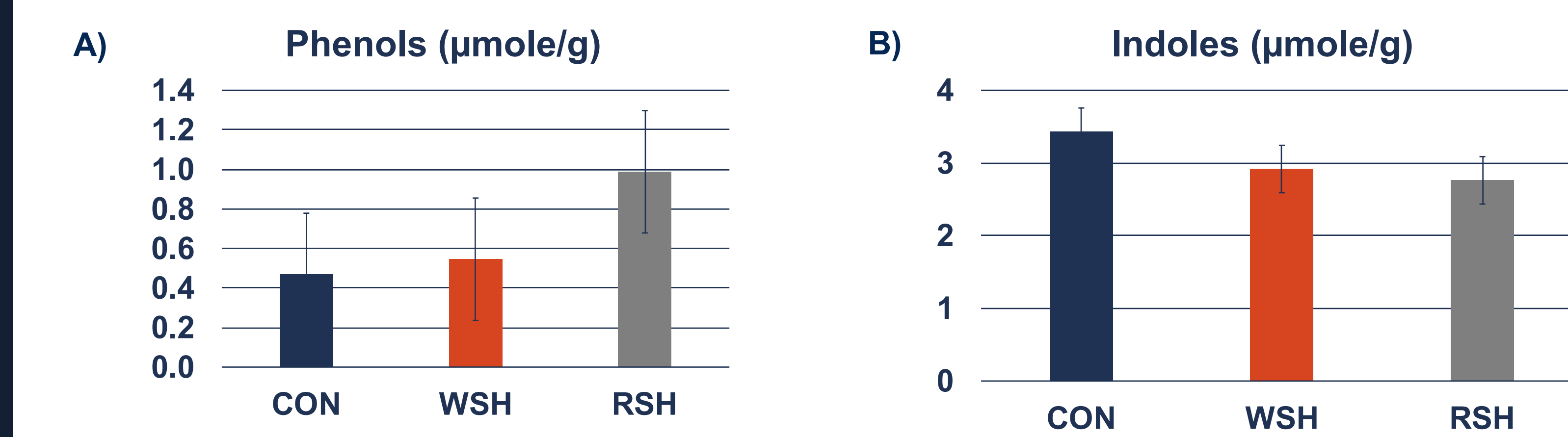
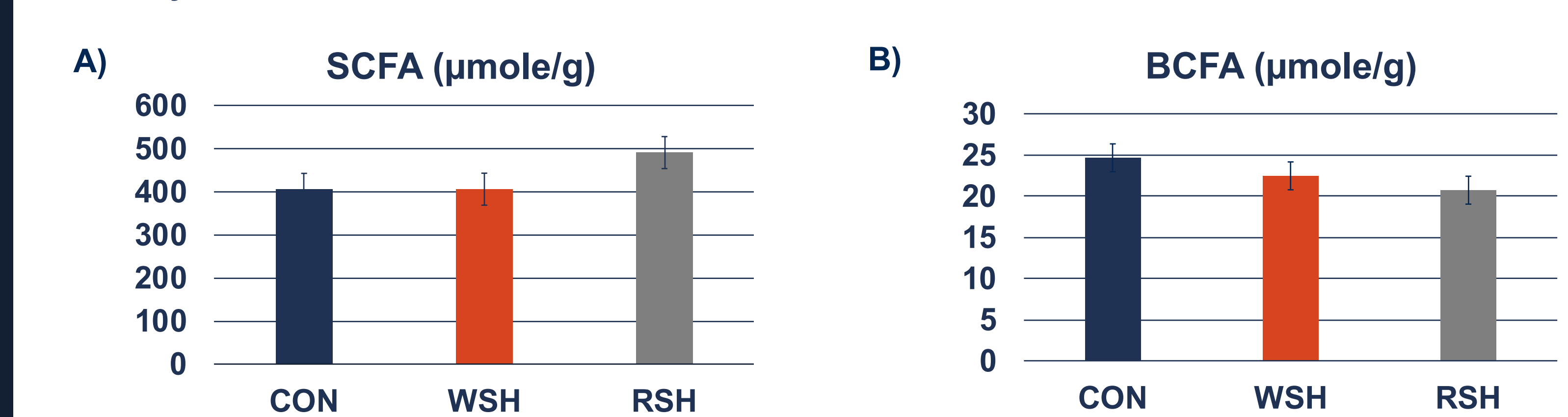


Figure 7 (A-B): Fecal short- and branched chain fatty acid concentrations of dogs fed selected carbohydrate sources.



CONCLUSIONS:

- β -diversity did not differ among dogs fed CON, WSH, or RSH diets (q - and p -values > 0.05)
 - Similarly, microbial richness was also not affected by treatment
- Overall, fecal metabolite concentrations were similar among treatments and did not have a strong correlation with microbial taxa
- Only the families – *Erysipelotrichaceae* and *Family XIII* were significantly different ($P < 0.05$) amongst treatments
- Our findings indicate that extruded diets using these sorghum varieties as a substitute for corn as the main dietary carbohydrate result in similar fecal metabolite profile and microbiota in adult dogs

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