

Feeding enzymatically digested food waste altered fecal microbiota of growing-finishing pigs

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ABSTRACT

Enzymatic digestion converted food waste from supermarkets into pasteurized liquid pig feed. This study was conducted to observe the fecal microbiota of growing-finishing pigs fed with enzymatically digested food waste. Fifty-six crossbred pigs (approximately 32.99 kg BW) were randomly assigned to one of the 2 dietary treatments with 7 replication pens and 4 pigs per pen. A 3-phase feeding program was used with d 0 to 28 as Phase 1, d 28 to 53 as Phase 2, and d 53 to 79 as Phase 3. The 2 dietary treatments were: a corn-soybean meal control diet, and a liquid diet produced from enzymatically digested food waste. Pigs were fed control or liquid diet in phases 1 and 2, while all pigs were fed with control diet in phase 3. Fecal samples were collected on d 0, 28, 53, and 79 from the same pig per pen and fecal microbiota was analyzed using 16S rRNA gene sequencing at the V4 hypervariable region and compositional data was analyzed using QIIME2 (2018.6). Observed species and Shannon diversity indexes were similar in both treatment groups on d 0, but pigs fed with food waste had greater ($P < 0.05$) Shannon diversity than control pigs on d 28, 53, and 79. Feeding food waste tended ($P < 0.10$) to decrease the relative abundance of *Firmicutes* compared with pigs fed control diet. Within this phylum, the abundance of *Lachnospiraceae* and *Ruminococcaceae* was increased ($P < 0.05$) and the abundance of *Streptococcaceae* and *Clostridiaceae* was decreased ($P < 0.05$). The analysis of Bray Curtis PCoA displayed a separate cluster between food waste and control groups on d 28 and 53. In summary, these results demonstrated that feeding enzymatic digested food waste modified the gut microbiome community of growing-finishing pigs.

Keywords

enzymatic digested food waste, fecal microbiota, pigs

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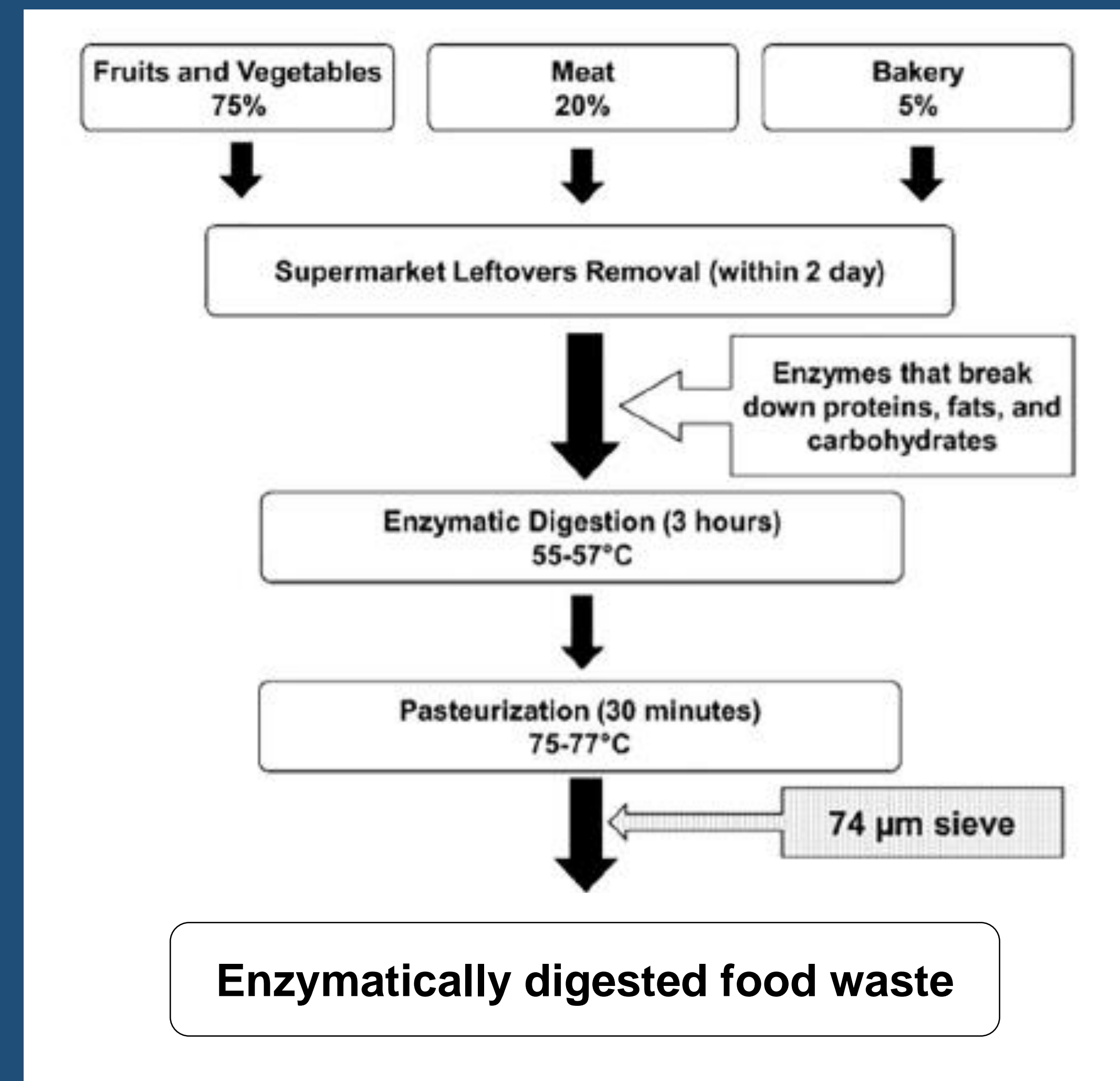
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INTRODUCTION

- Food waste
 - Discarded food that is still considered safe and nutritious for consumption (FAO, 2019)
 - Nearly 50% of food waste is landfilled or incinerated in the U.S. (Buzby, 2014)
- Enzymatic digestion breaks down large nutrient components in food waste to make them easily digestible
- No difference observed in carcass characteristic and meat quality of growing-finishing pigs fed with enzymatically digested food waste (Jinno et al., 2018)



Procedure used to produced enzymatically digested food waste

Chemical Composition

% , DM-basis	Food waste
Dry matter	24.2
Crude protein	29.0
Crude fat	27.2
ADF	5.1
NDF	9.6

Ideal Amino Acid Profile

DM-basis	Food waste	Growing pigs
Lysine	1.62	1.00
Methionine	0.29	0.30
Threonine	0.60	0.65
Tryptophan	0.13	0.18
Arginine	0.78	0.42
Histidine	0.41	0.32
Isoleucine	0.67	0.55
Leucine	1.10	1.00
Phenylalanine	0.66	0.50
Valine	0.74	0.70

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Jinno et al., 2018
Animal Feed Science and Technology





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OBJECTIVE

To determine the fecal microbiota of growing-finishing pigs fed with enzymatically digested food waste.

MATERIALS AND METHODS

- **56 pigs:** 32.99 kg, 7 replicate pens per treatment (2 barrows and 2 gilts per pen)
- **2 dietary treatments:**
 - **Corn-soybean meal diet** (Control) or **liquid enzymatically digested food waste** (Food waste)
- **3-Phase feeding program:**
 - **Phase 1:** d 0 to 28; pigs were fed with Control or FW
 - **Phase 2:** d 28 to 53; pigs were fed with Control or FW
 - **Phase 3:** d 53 to 79; pigs were fed with Control
- **16S rRNA sequencing at V4 region:**
 - **FastQC (v. 0.11.8) and Trimmomatic (v. 0.38):** Quality evaluation and trimming
 - **QIIME2 (2018.6):** Compositional analysis
 - **R program:** Calculate and visualize data
- **Measurements from fecal samples:**
 - **Relative abundance:** phylum, *Firmicutes* & *Bacteroidetes* family
 - ***Firmicutes*:*Bacteroidetes* ratio**
 - **Alpha diversity:** Observed & Shannon indices
 - **Beta diversity:** Bray Curtis PCoA
- **Statistical analysis:** Relative abundance and alpha diversity were analyzed by ANOVA using the PROC MIXED of SAS. Beta diversity was analyzed with Adonis and betadisper {vegan 2.5-4} in the R program (v. 3.5.2).

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DIET COMPOSITIONS

*Limestone, monocalcium phosphate, lysine HCL, DL-methionine, and threonine included Item, %	Control		
	Phase 1	Phase 2	Phase 3
Corn	68.2	74.4	77.7
Soybean meal	27.0	21.0	18.0
Soy oil	2.0	2.0	2.0
Salt	0.4	0.4	0.4
Vitamin-mineral	0.3	0.3	0.3
Other ingredients*	2.1	1.9	1.6

Item, %	Food waste
Enzymatically digested food waste	99.3
Salt	0.4
Vitamin-mineral	0.3

Analyzed nutrients, DM %	Control	Food waste
Dry matter	86.0	24.2
Crude protein	21.4	29.0
ADF	4.5	5.1
Crude fat	4.4	27.2
Ca	0.8	0.7
P	0.6	1.0

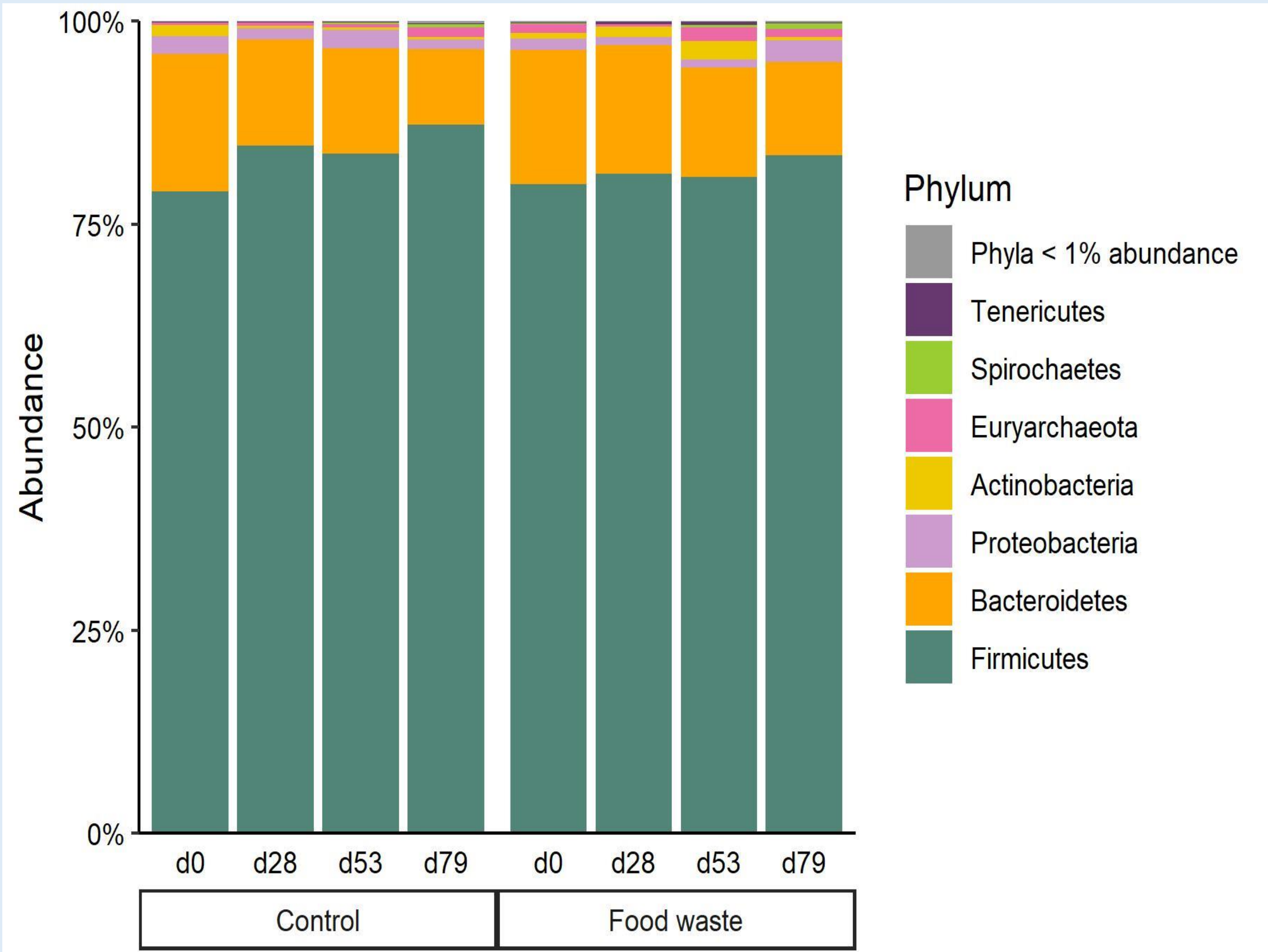
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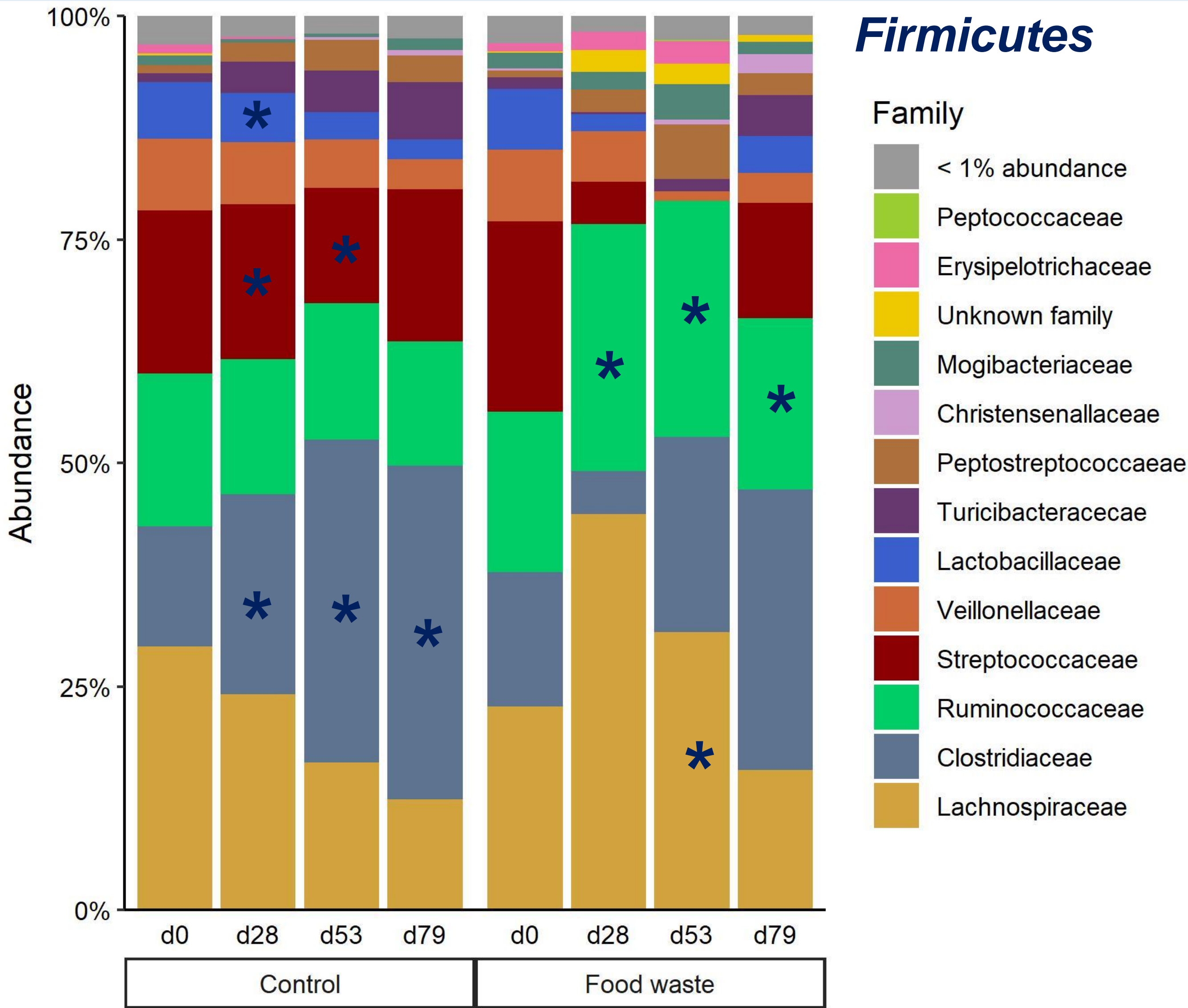
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RELATIVE ABUNDANCE: PHYLUM

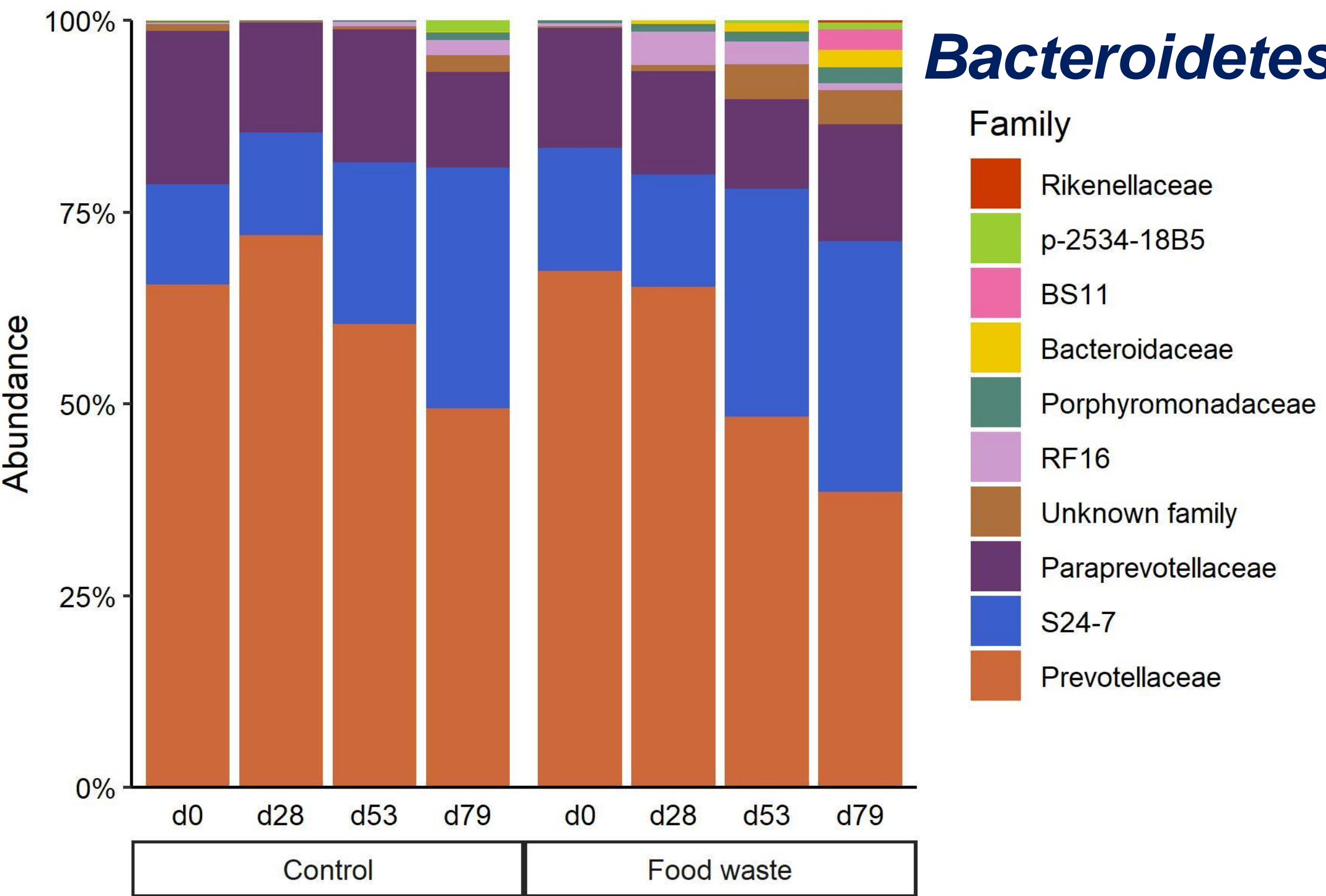
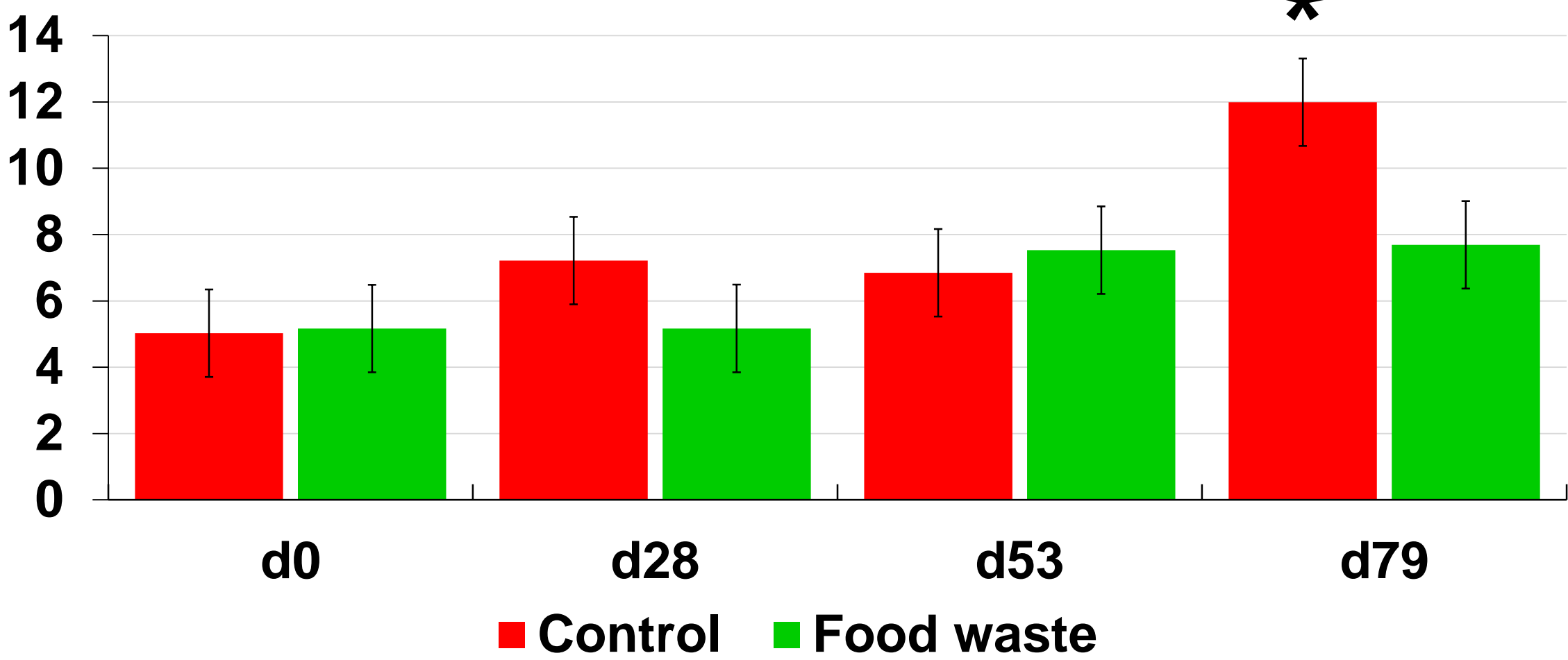


RELATIVE ABUNDANCE: FAMILY



**P* < 0.05

Firmicutes:Bacteroidetes



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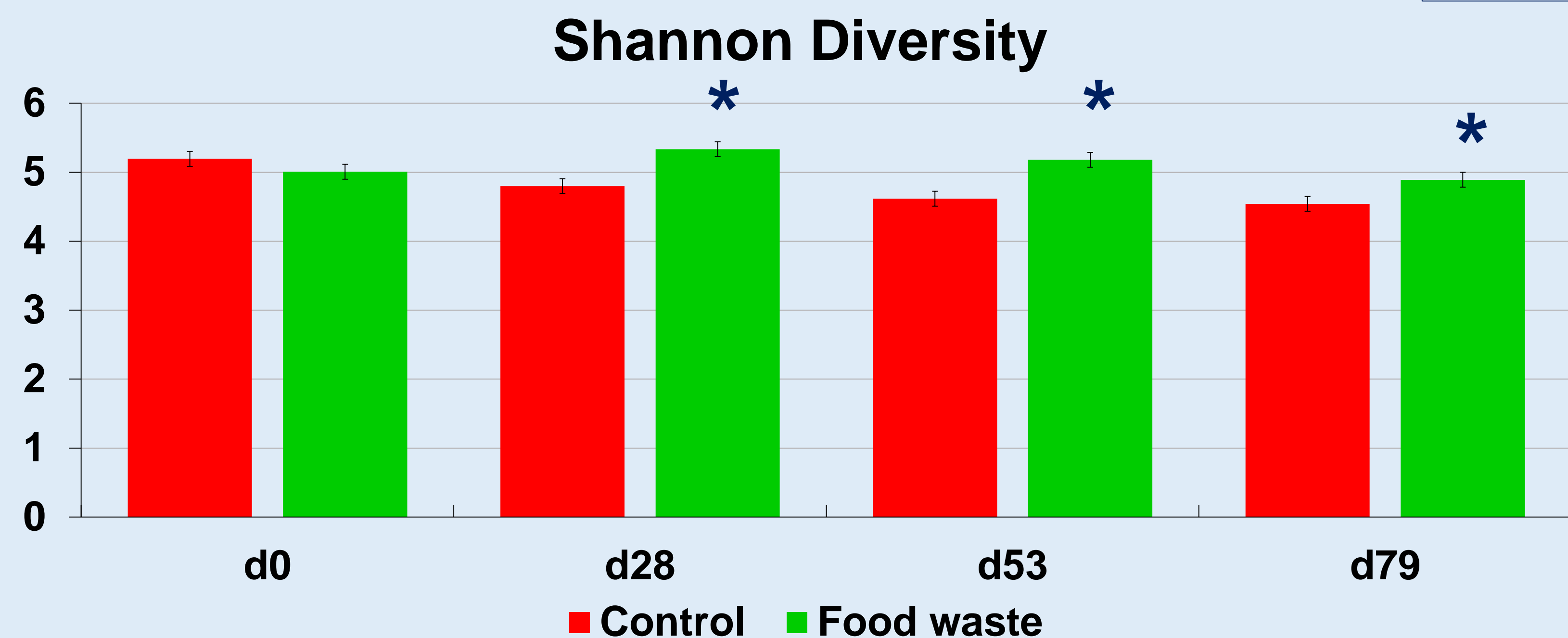
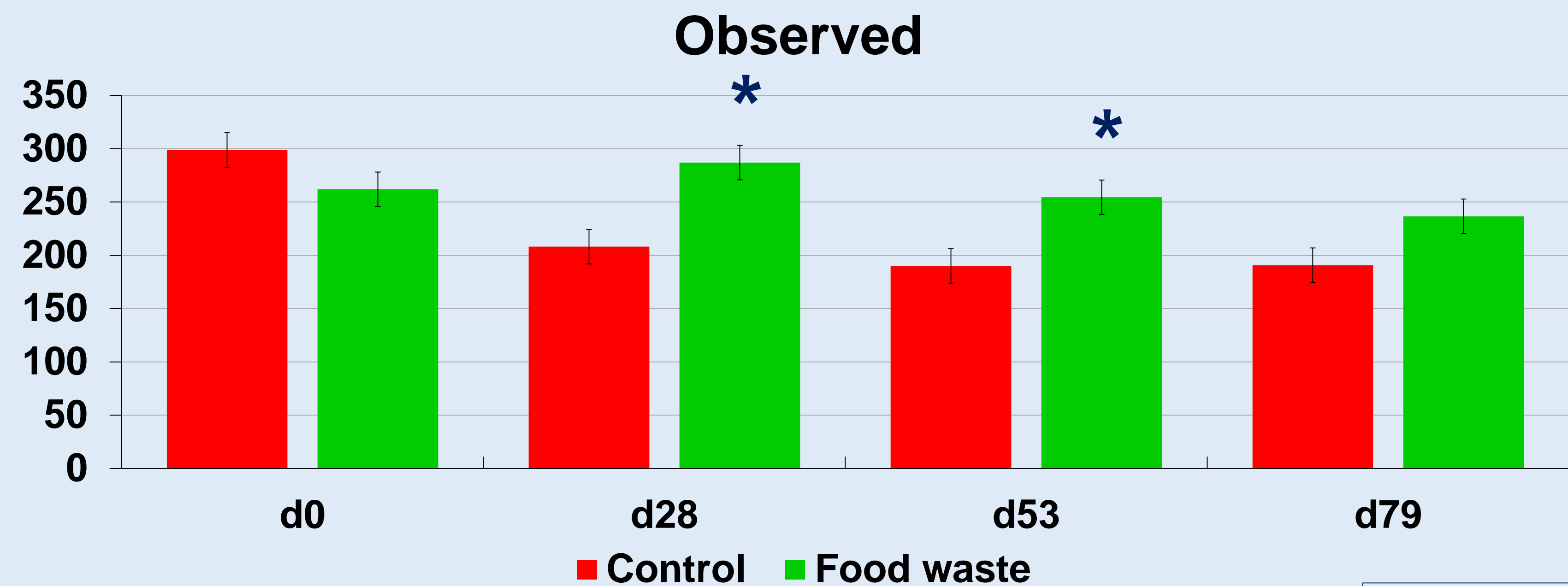
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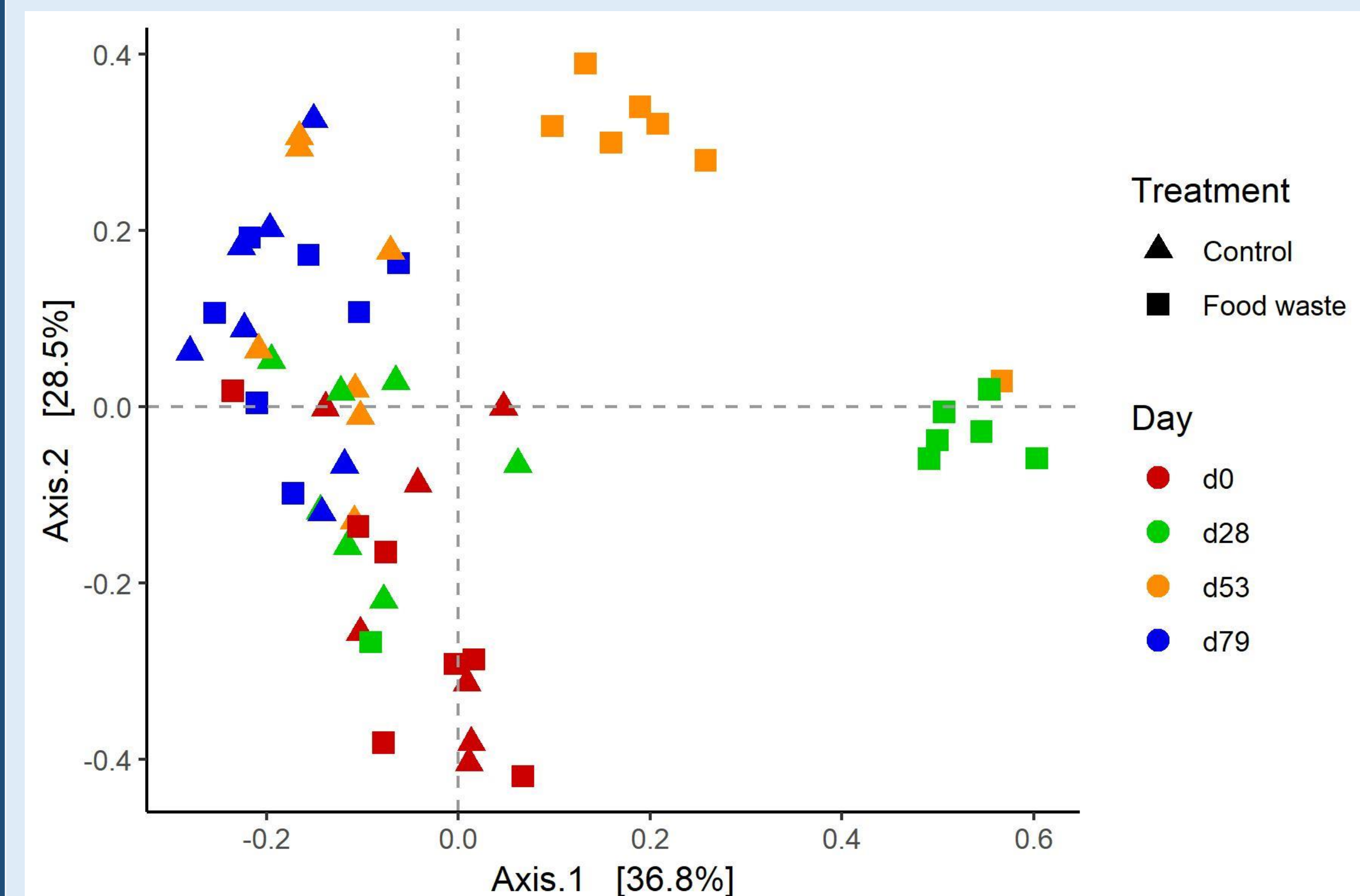
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ALPHA DIVERSITY



* $P < 0.05$

BETA DIVERSITY



Treatment and day
 $R^2 = 0.52$
Adonis $P < 0.05$
Betadisper $P > 0.05$

CONCLUSIONS

- Feeding enzymatically digested food waste alters microbial diversity within the gastrointestinal tract of growing-finishing pigs
- Different nutrient components in food waste diet most likely altered the microbial diversity
- Further analysis will evaluate the metagenomic of the microbiota of growing-finishing pigs fed with enzymatically digested food waste.

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