

Structural Variations in Maize Arabinoxylans Influence Gut Microbiota Colonies, Highlighting Effects on Bifidobacteria

Favor Igwilo¹, Bo Peng², Tricia King², Tieling Zhang², James Schnable² Andrew Benson²
 Department of Chemistry, Texas Christian University¹; Nebraska Food for Health Center, University of Nebraska-Lincoln²

INTRODUCTION

"You are what you eat", applies not only to humans, but also to the trillions of microbes living in our gut.

Bifidobacterium, an important genera of gut microbiota, is essential for maintaining gut health, digestion, and providing immunity to diseases.

Arabinoxylan, a major dietary fiber present in corn pericarp, acts as an important food source for Bifidobacteria and can vary structurally across different maize lines.

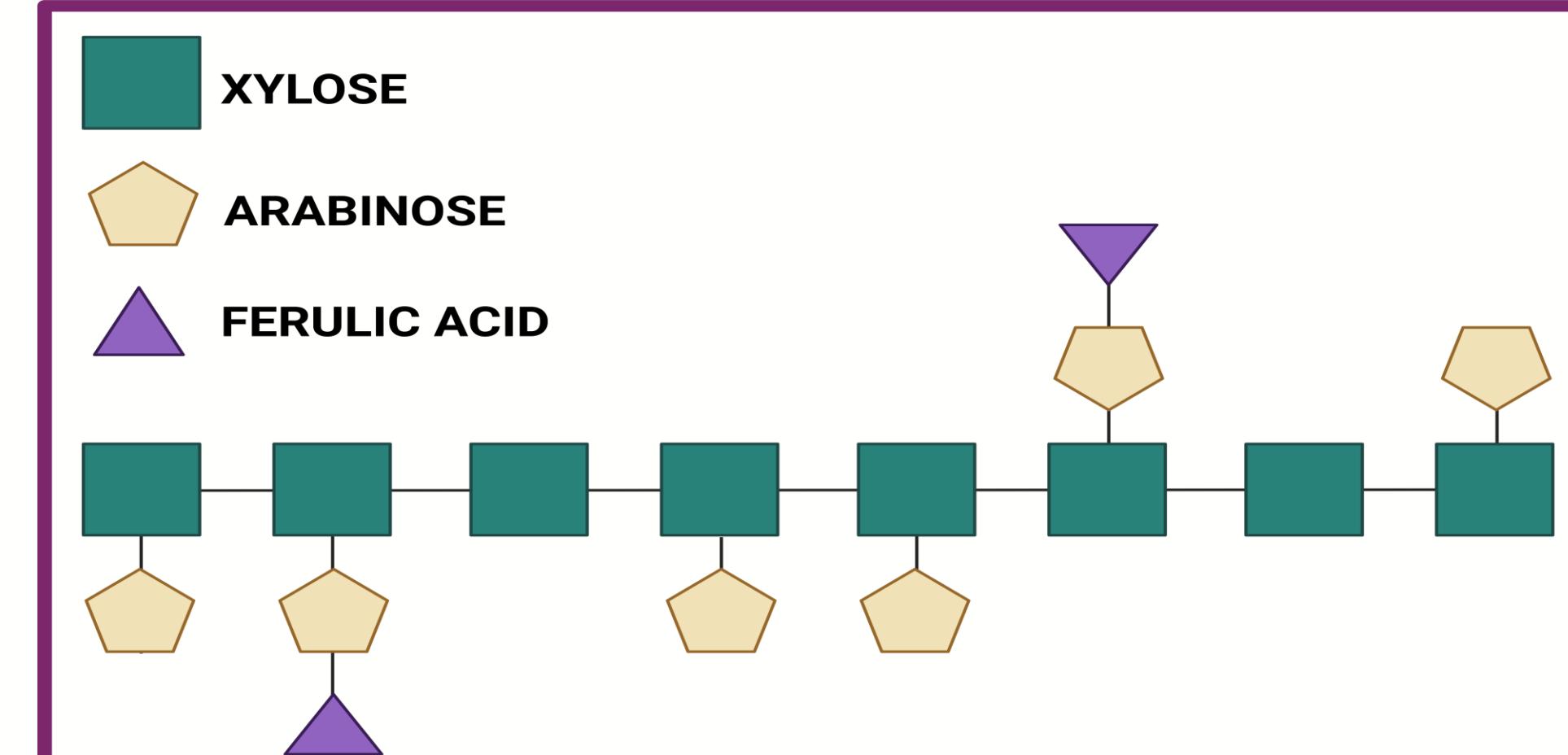


Figure 1. General Structure of arabinoxylan fiber consists of a xylose backbone, arabinose sidechains, and ferulic acid cross linkages.

HYPOTHESIS

Structural variations in maize arabinoxylans influences the composition and abundance of human gut microbiota, with distinct effects on the growth and activity of Bifidobacteria.

METHODS

Preparation Phase:

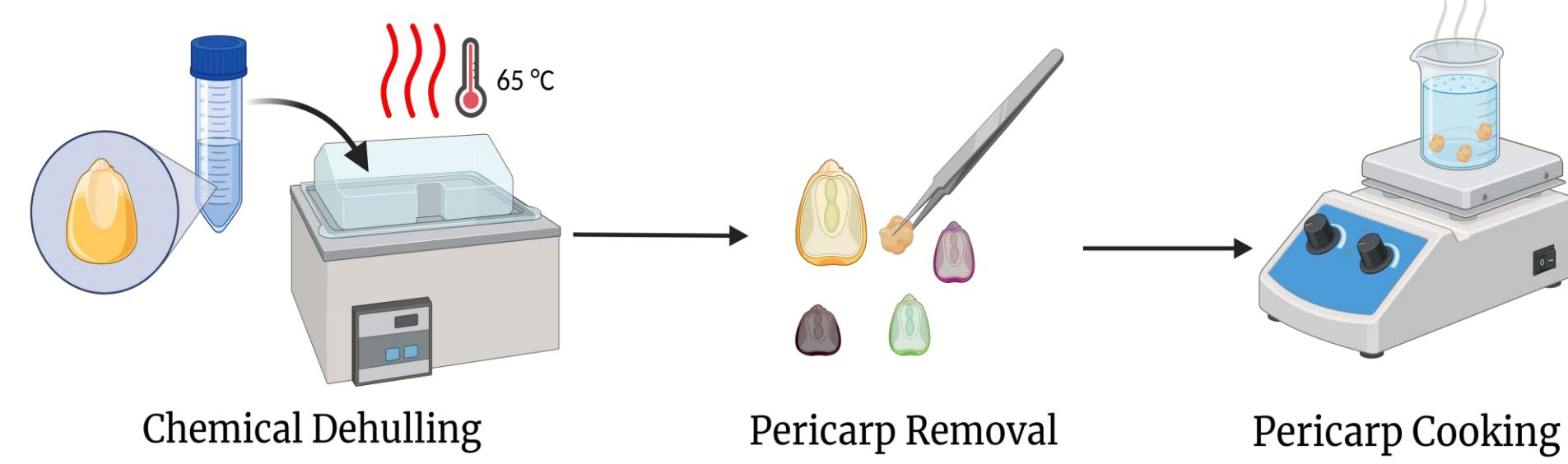


Figure 2. Procedure to remove pericarp from maize.

METHODS (cont.)

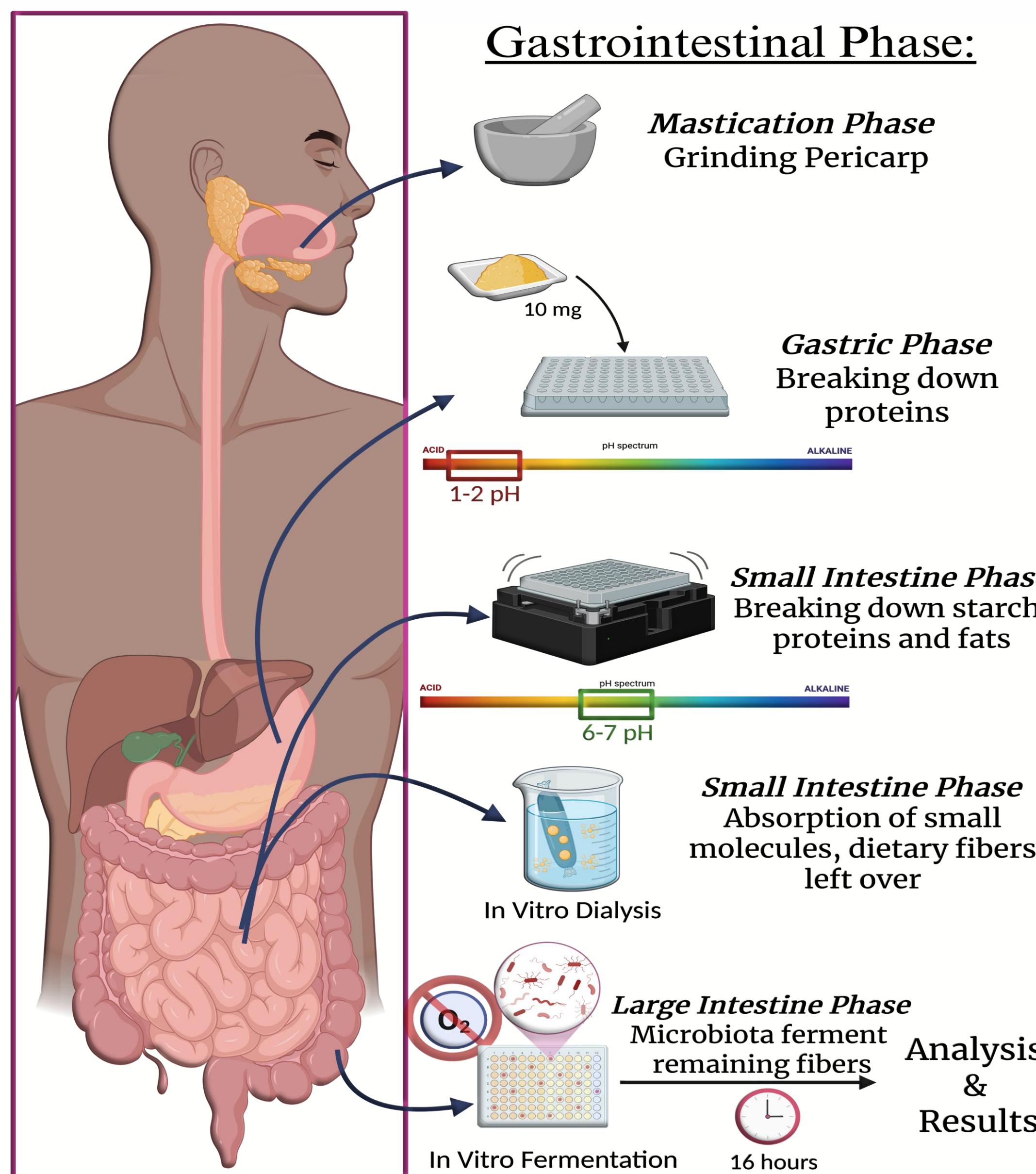


Figure 3. Procedure to ferment arabinoxylan fiber in pericarp for microbiota colony growth.

RESULTS

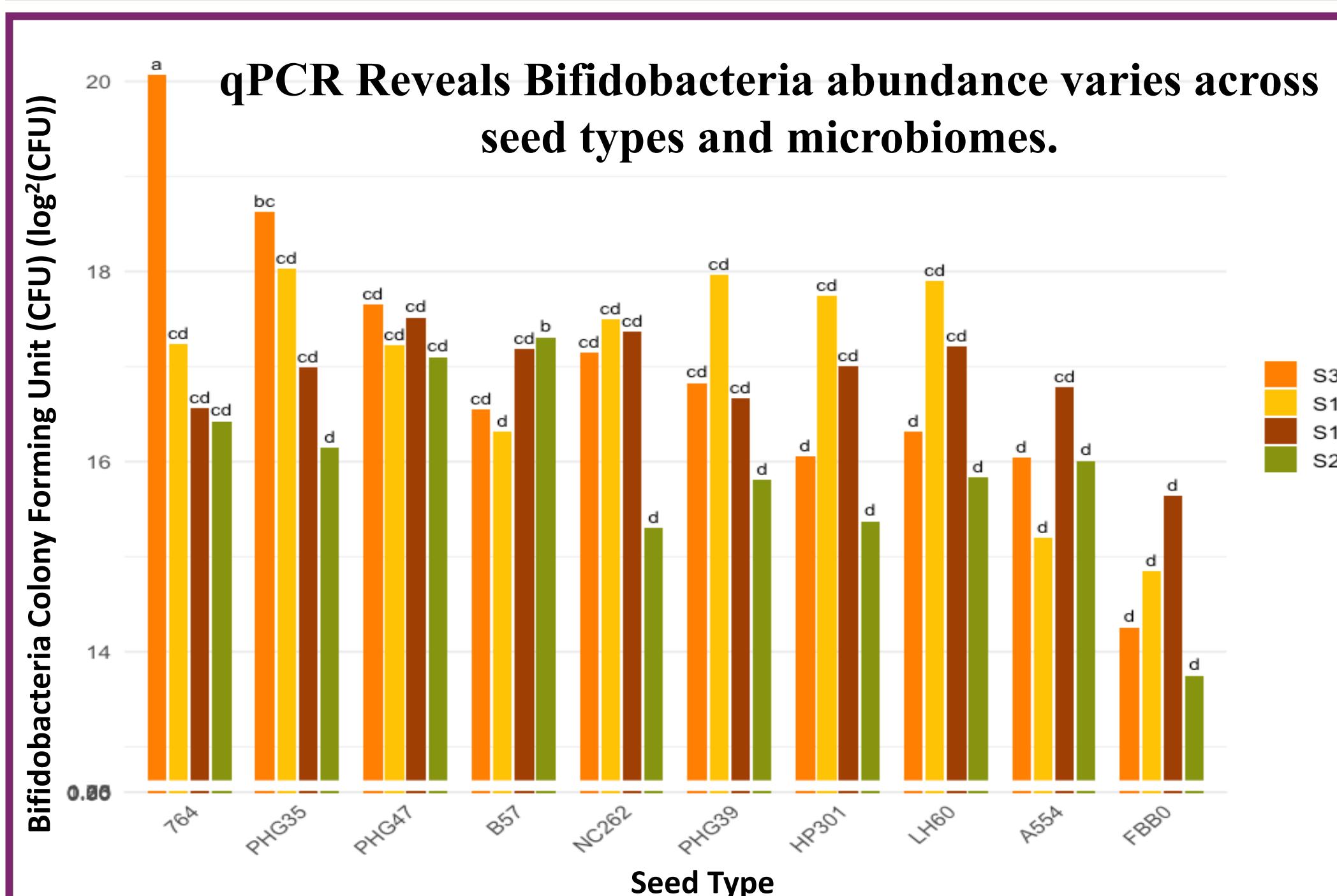


Figure 4. qPCR analysis of Bifidobacteria abundance in microbiomes across seed treatments. Groups not sharing a letter differ significantly ($p < 0.05$, Duncan's test).

RESULTS (cont.)

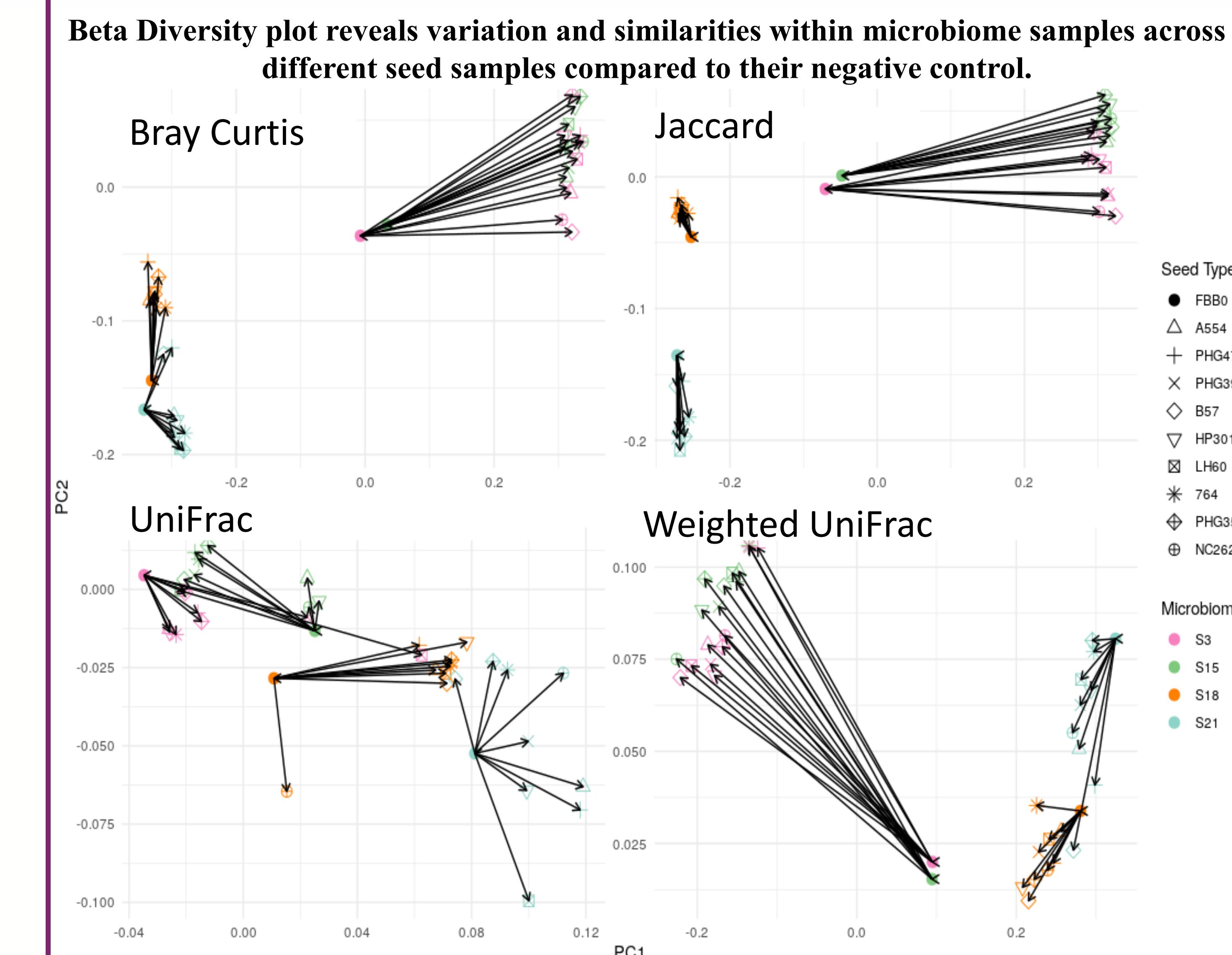


Figure 5. β -diversity was used to assess microbial community differences based on presence/absence (Jaccard, UniFrac), abundance (Bray-Curtis, Weighted UniFrac), and phylogenetic relationships (UniFracs).

CONCLUSION & FUTURE WORK

Analyses reveals variation in Bifidobacteria abundance and overall microbiome composition, likely driven by structural differences in maize arabinoxylans that may selectively enrich beneficial microbes.

Future Work:

- Correlate microbial taxa with known arabinoxylan degradation pathways.
- Characterize arabinoxylan structure across maize lines.
- Determine what % of Bifidobacteria and Bacteroidetes strains utilize arabinoxylans.

ACKNOWLEDGMENTS & REFERENCES

Nebraska Food for Health Center USDA-NIFA REEU grant 2022-67037-36616.



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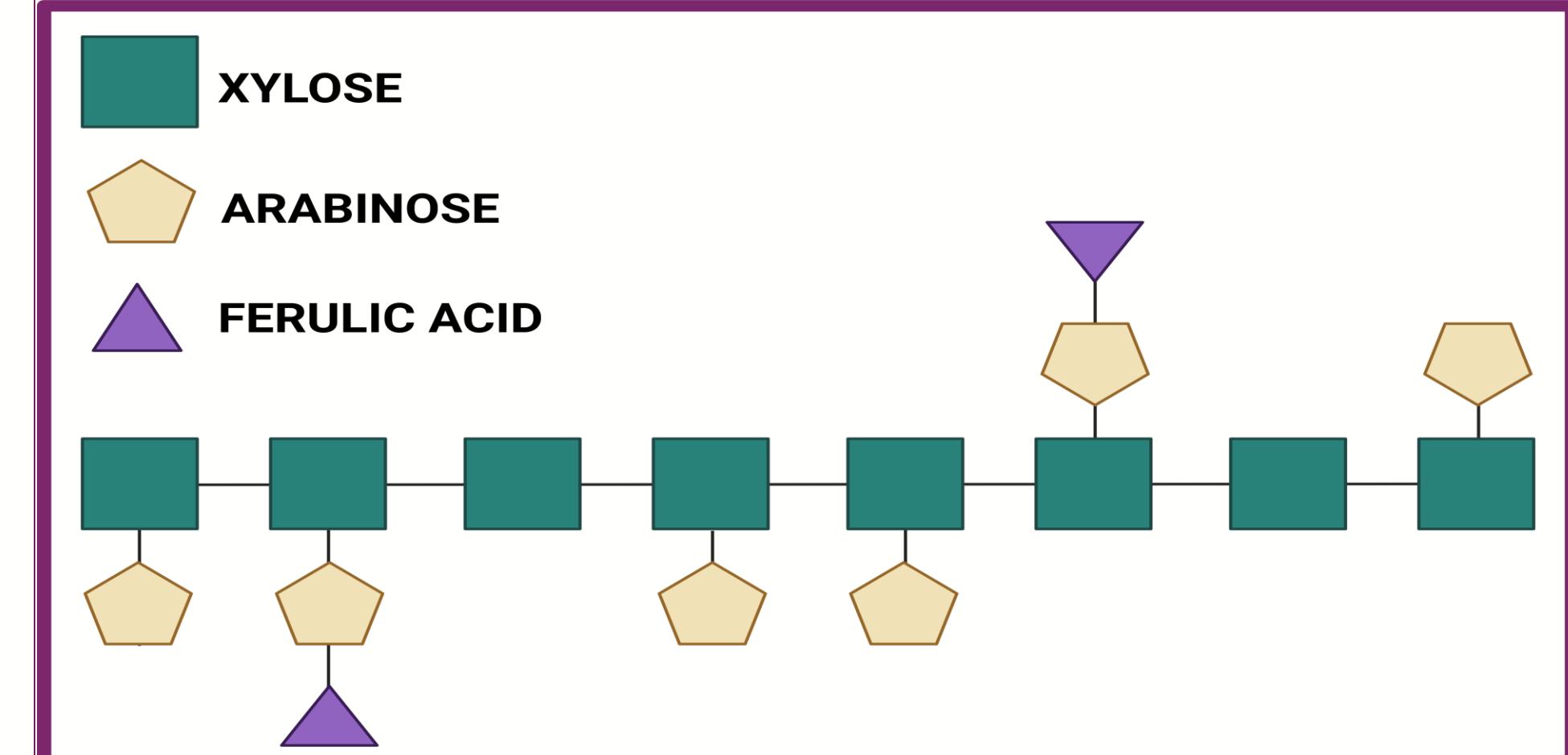


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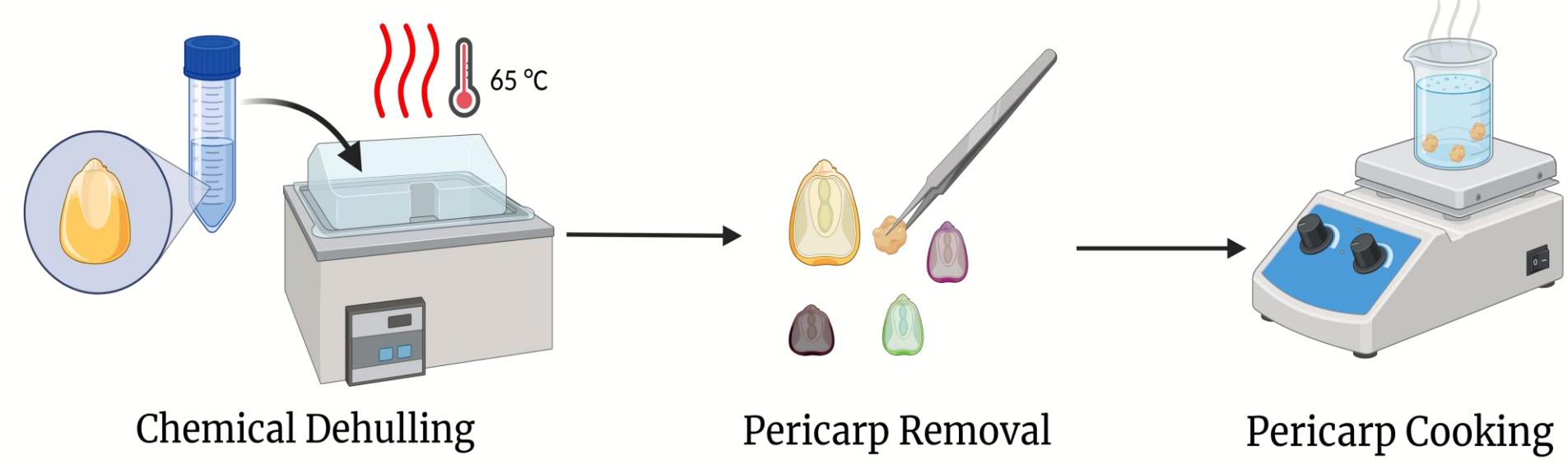


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METHODS (cont.)

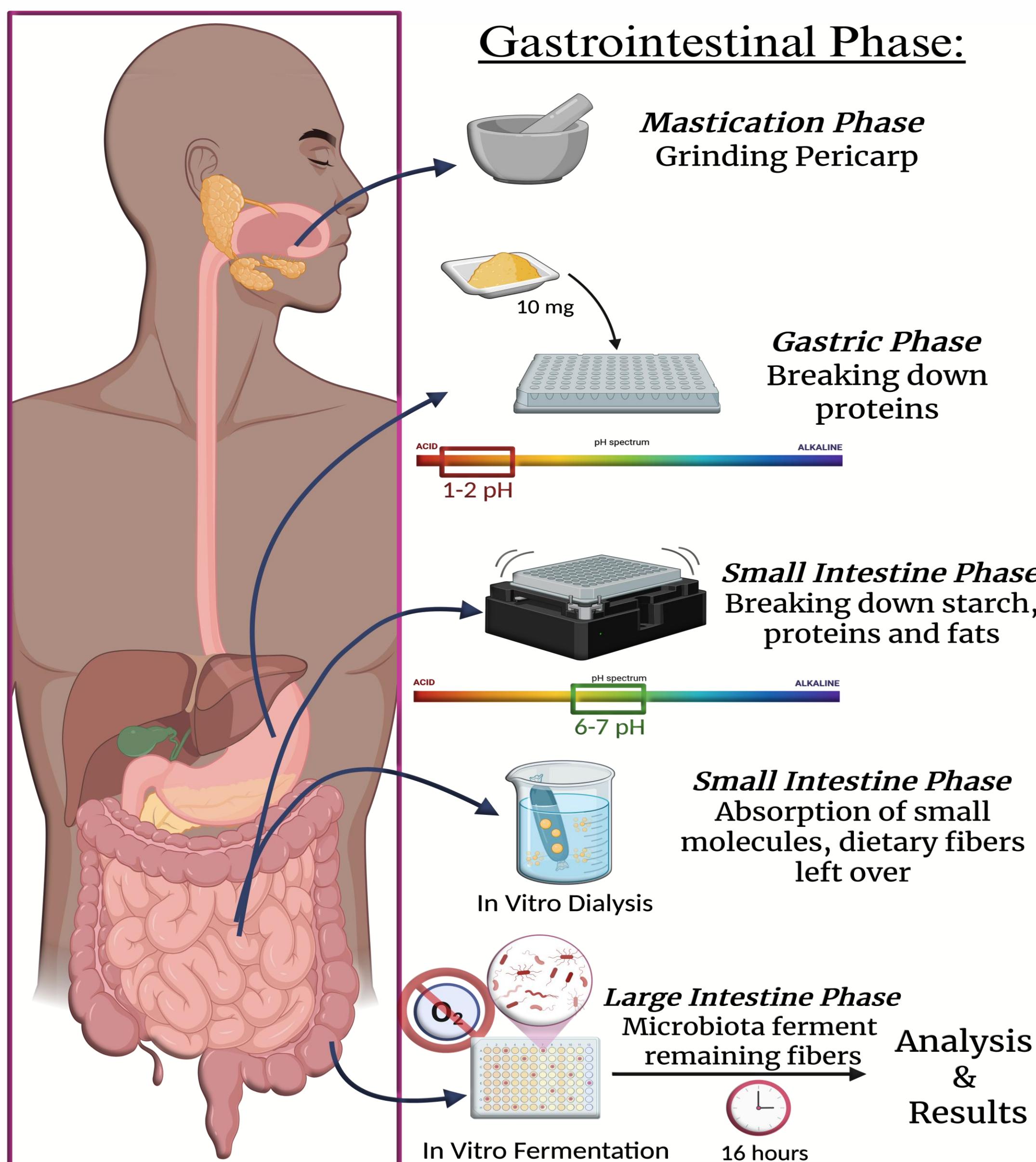


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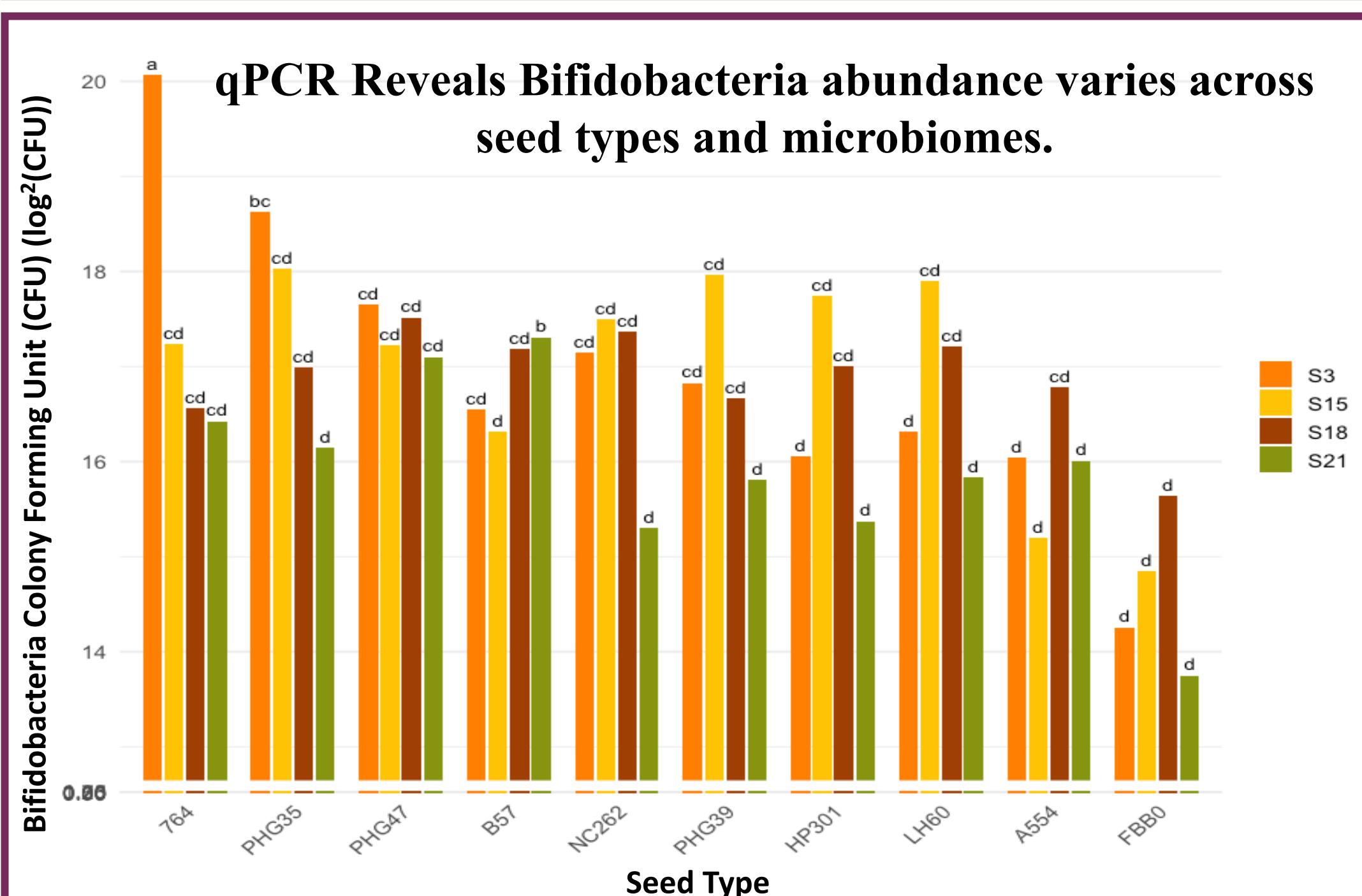


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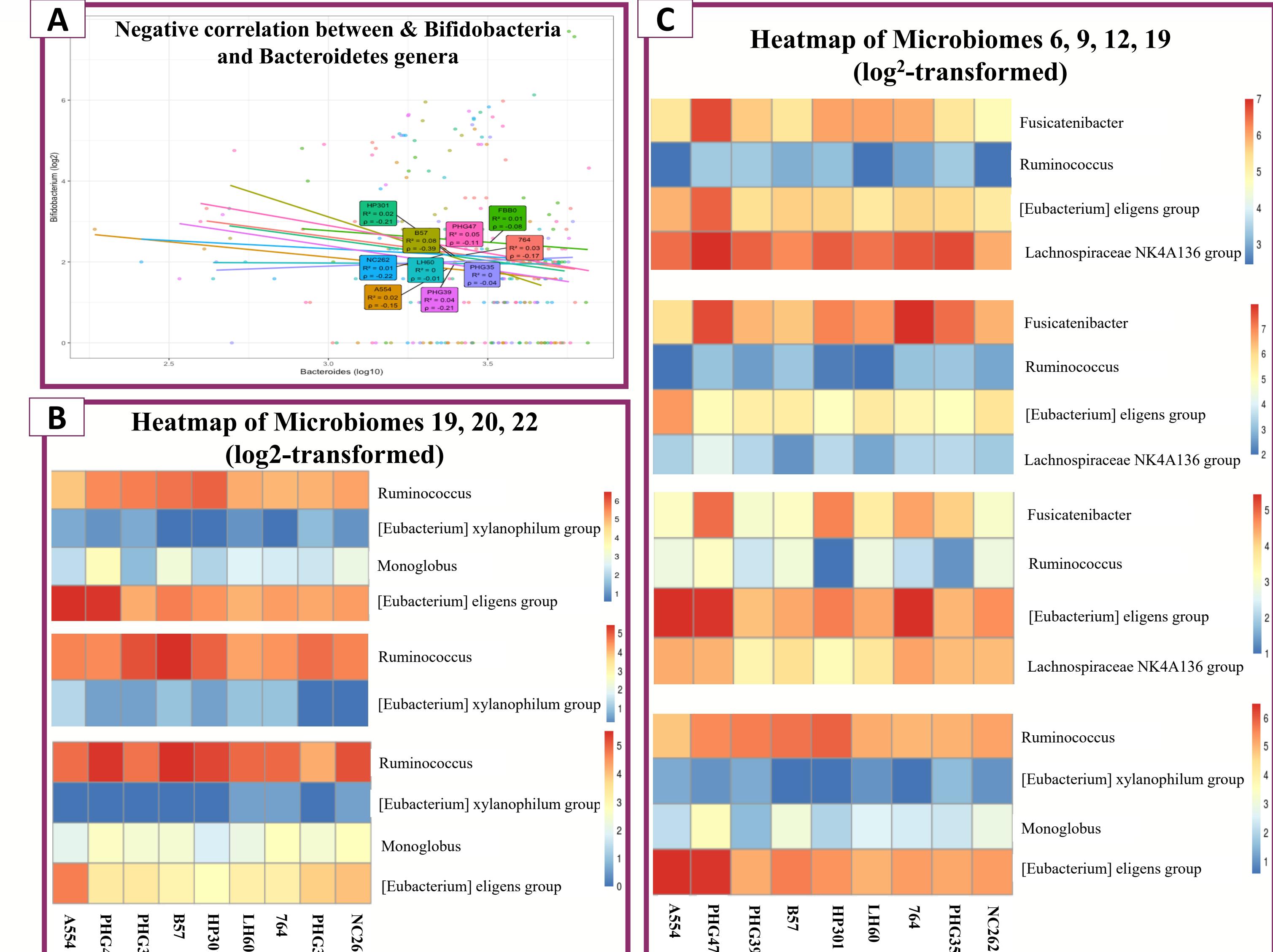


Figure 5. A displays correlation between Bifidobacteria and Bacteroidetes genera. B&C displays relative abundance of different bacterial species across various samples within each of our microbiome sets.

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