



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

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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.

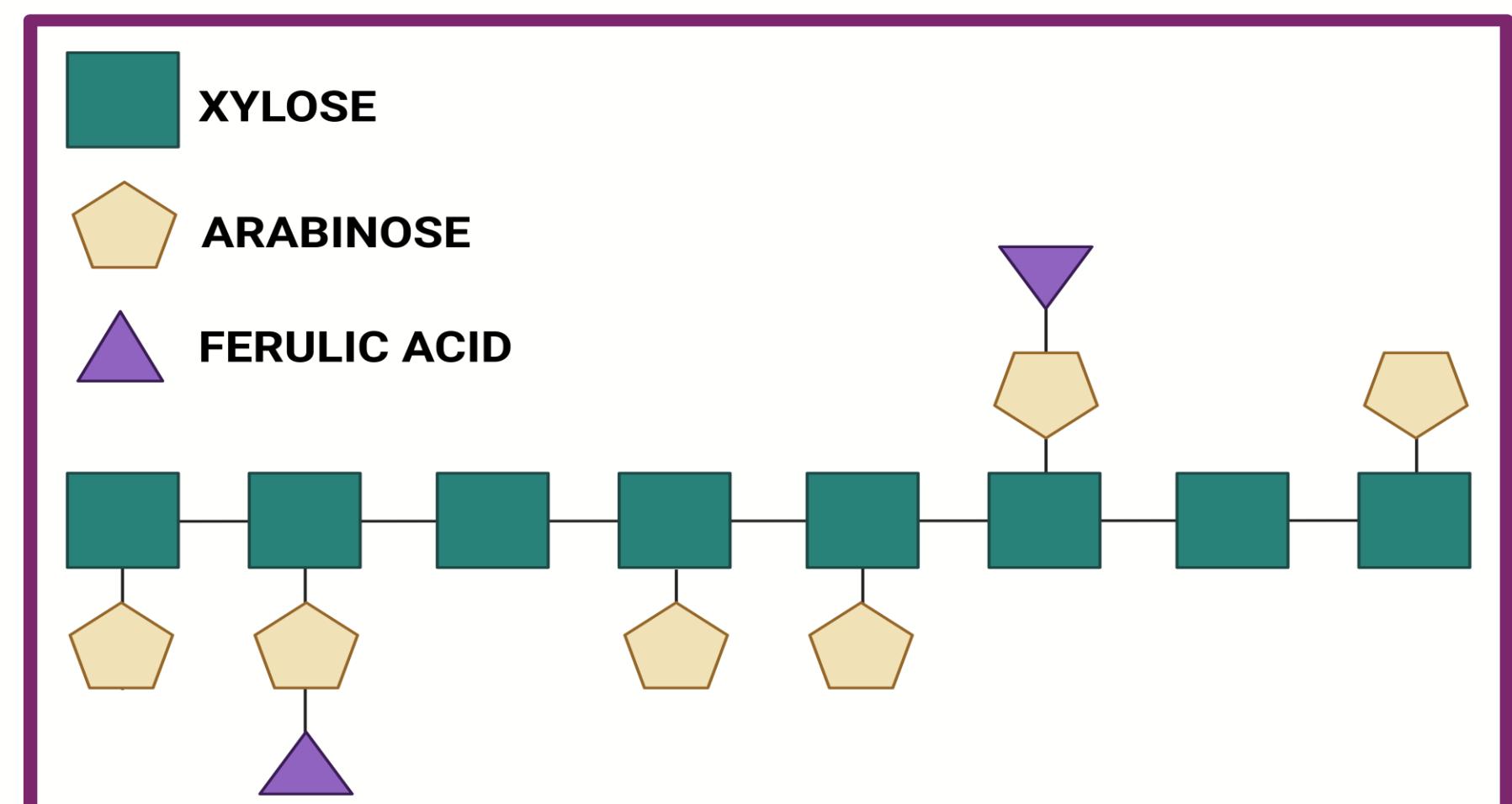


Figure 1. General Structure of arabinoxylan fiber consists of a xylose backbone, arabinose sidechains, and ferulic acid cross linkages.

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:

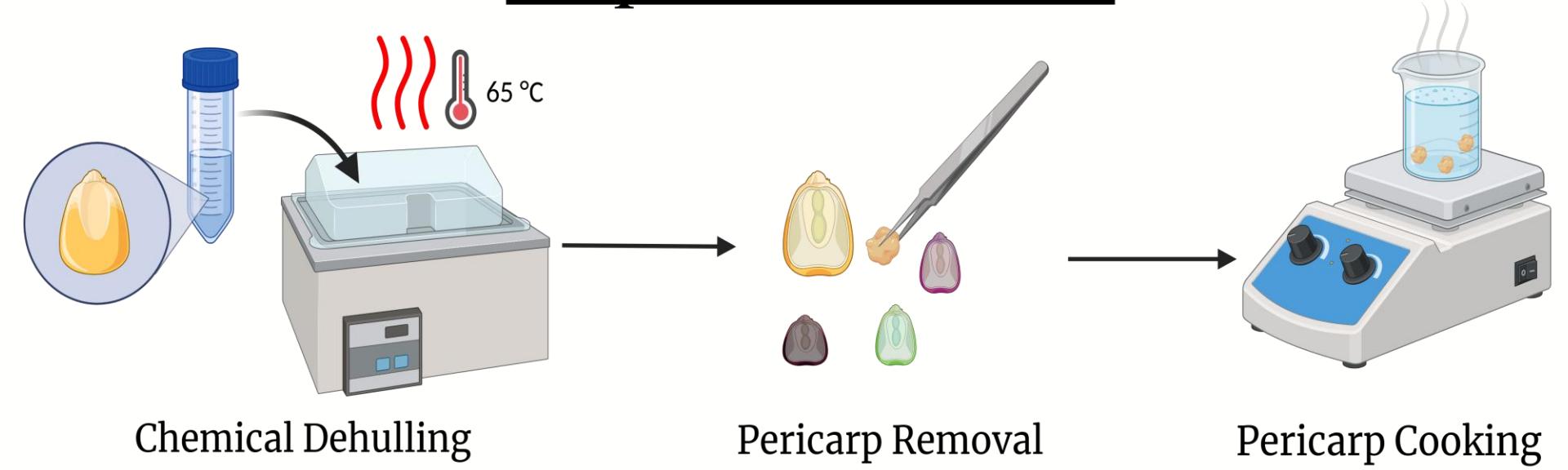


Figure 2. Procedure to remove pericarp from maize. 9 maize lines were chosen based on variation in arabinoxylan RNA expression.

METHODS (cont.)

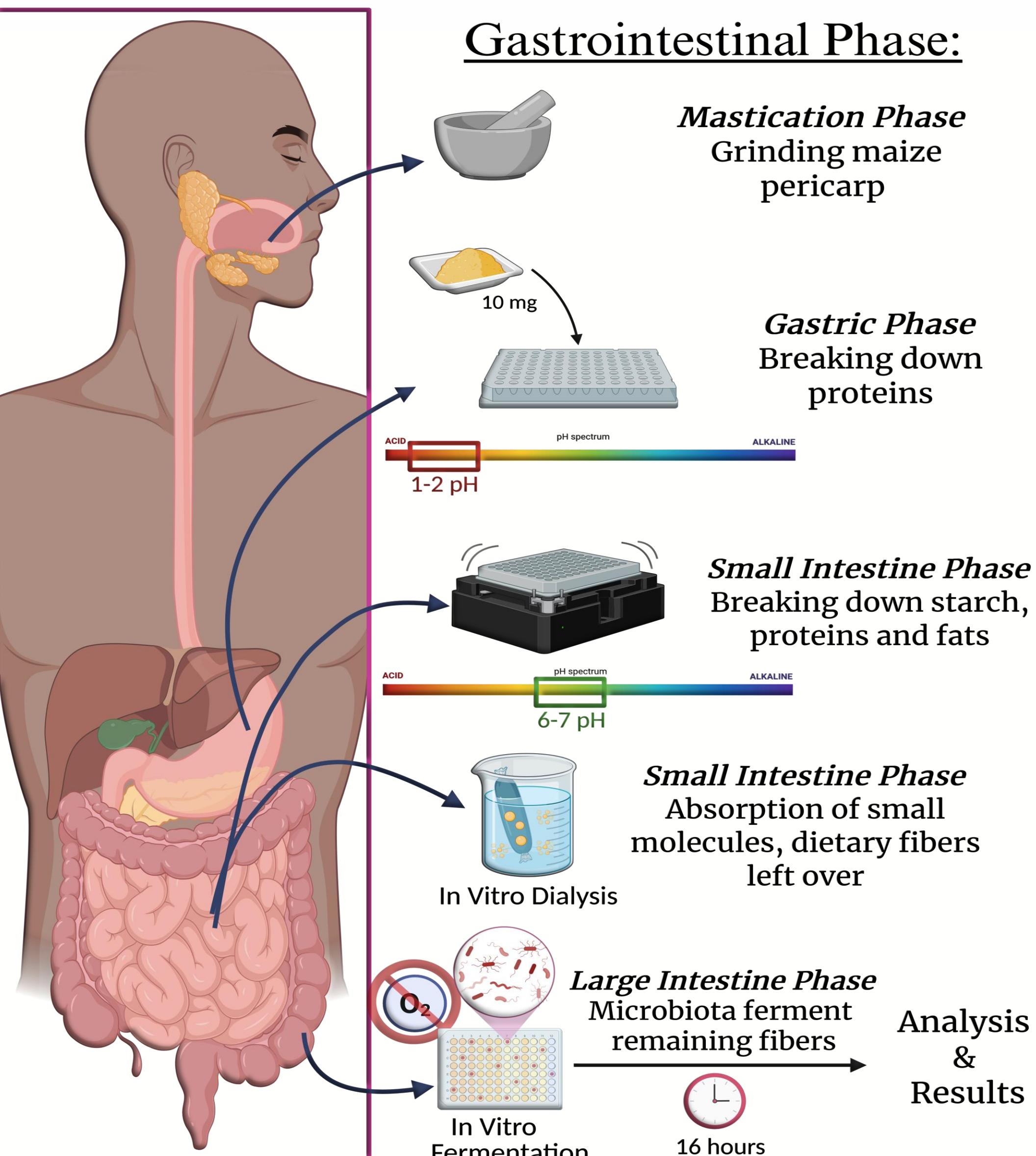


Figure 3. Workflow for fermenting arabinoxylan fiber from maize pericarp to support human gut microbiota growth. A total of 19 distinct human microbiome samples were selected for this experiment.

RESULTS (qPCR)

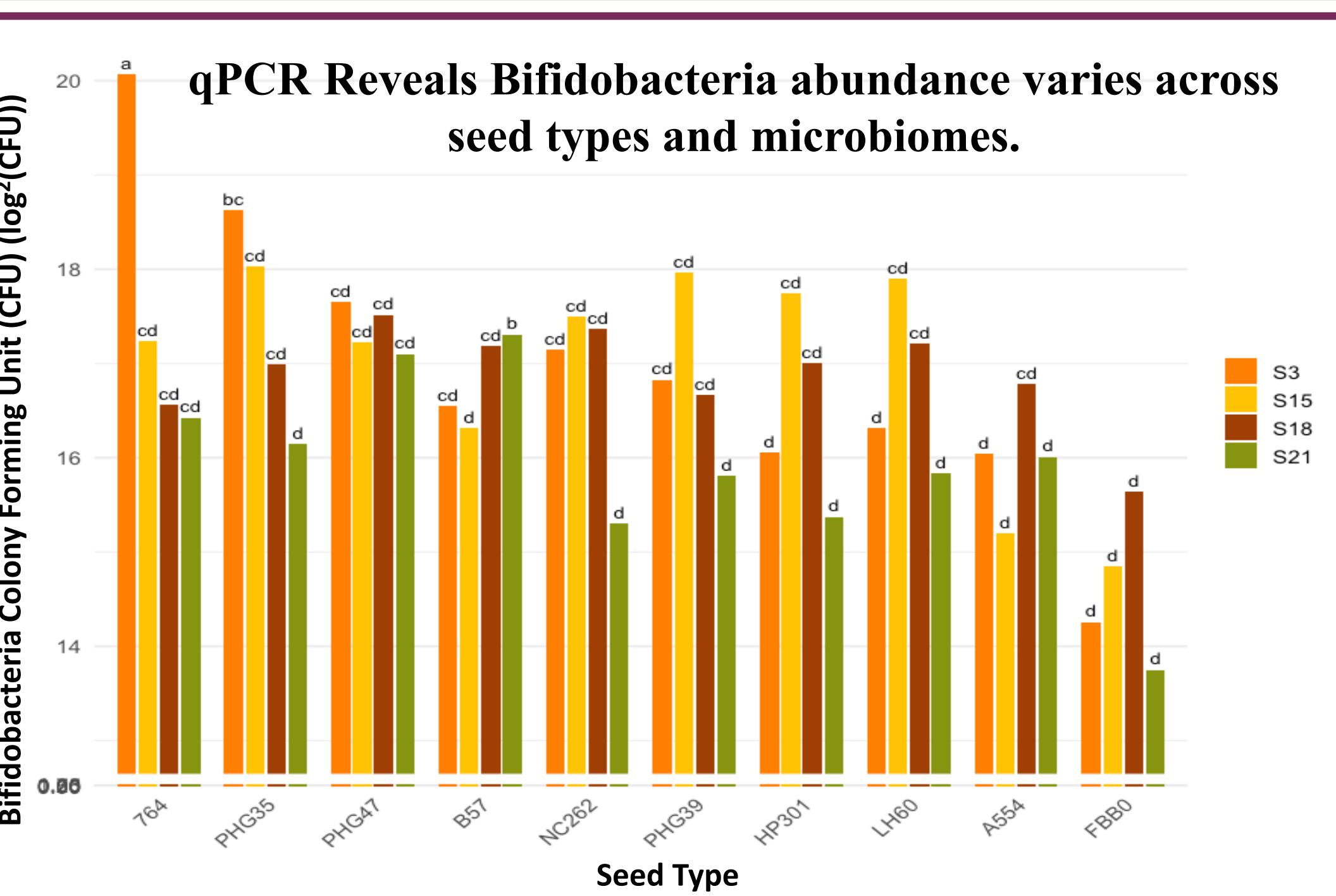


Figure 4. qPCR analysis of Bifidobacteria abundance in microbiomes across seed treatments. Groups not sharing a letter differ significantly ($p < 0.05$, Duncan's test).

RESULTS (16S Sequencing)

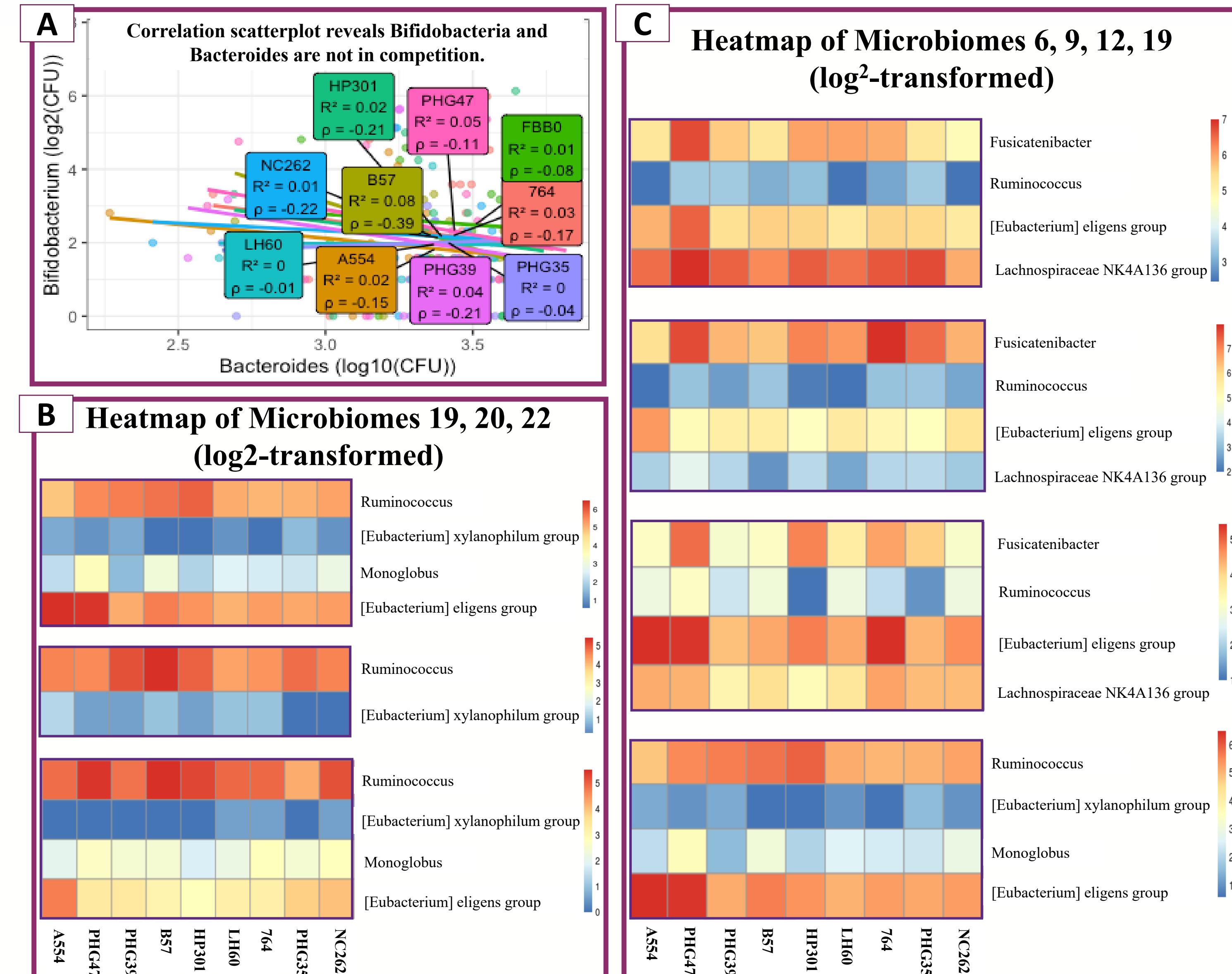


Figure 5. Figure A displays a weak negative correlation between Bifidobacteria and Bacteroides genera. Figure B & C displays relative abundance of different microbiota taxa across the corn lines, with many taxa behaving similarly across the microbiomes.

CONCLUSIONS & 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 in maize lines which showed a response.
- Identify Amplicon Sequence Variants (ASV) of Bifidobacteria and Bacteroides that significantly responds to maize arabinoxylans.

ACKNOWLEDGMENTS & REFERENCES

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