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Suberin is a potential **preformed barrier** deposited in plant roots. Suberization in response to the microbiome occurs in a **species-specific** manner.

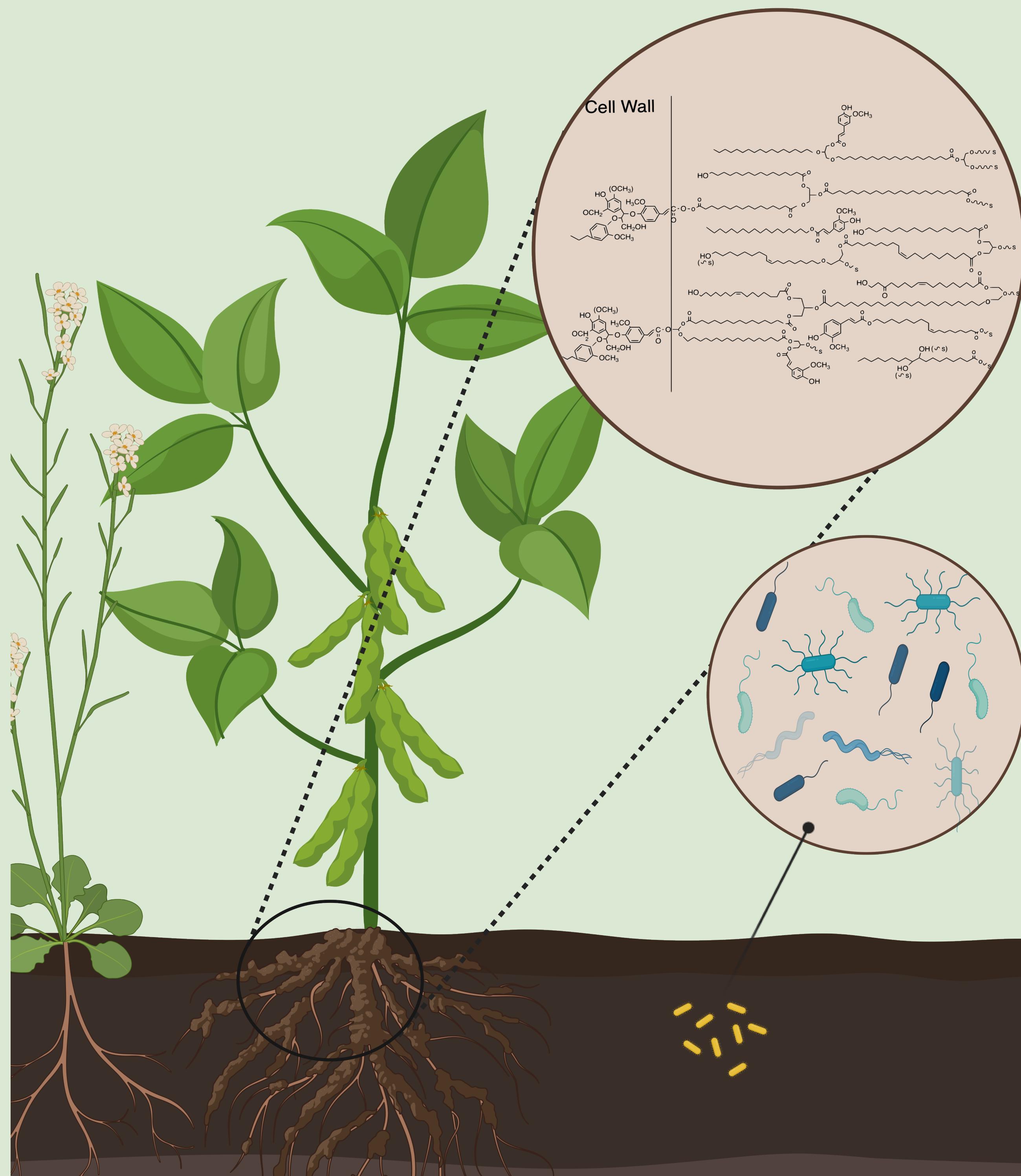


Figure 1 Diagram depicting the appearance of two study species (*Arabidopsis thaliana* and *Glycine max*), in addition to the chemical structure of suberin.

ACKNOWLEDGEMENTS

We thank Agriculture and Agri-Food Canada - Ottawa Research and Development Centre for supplying the soybean seeds for this project and the Natural Sciences and Engineering Research Council (NSERC) for their financial support.

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Introduction

- The rhizosphere is a community of epiphytic microorganisms living in the soil surrounding a plant's roots that may support plant health.¹ Endophytes are microorganisms that colonize a plant's tissues, such as root endophytes that promote plant growth.
- Suberin is a **hydrophobic heteropolymer** that limits what exits (e.g., exuded metabolites) and enters (e.g., microorganisms, nutrients) the root.² The suberin heteropolymer includes phenolic and aliphatic domains, whose exact organization are an area of debate.³
- Current models of the suberin heteropolymer do not yet consider microbiomes. These microorganisms may have an important role in how minerals get taken up by the plant via radial transport in the context of suberin.²
- **We hypothesized** that the rhizosphere microbiome regulates suberization and that suberin composition controls root microbiome composition.

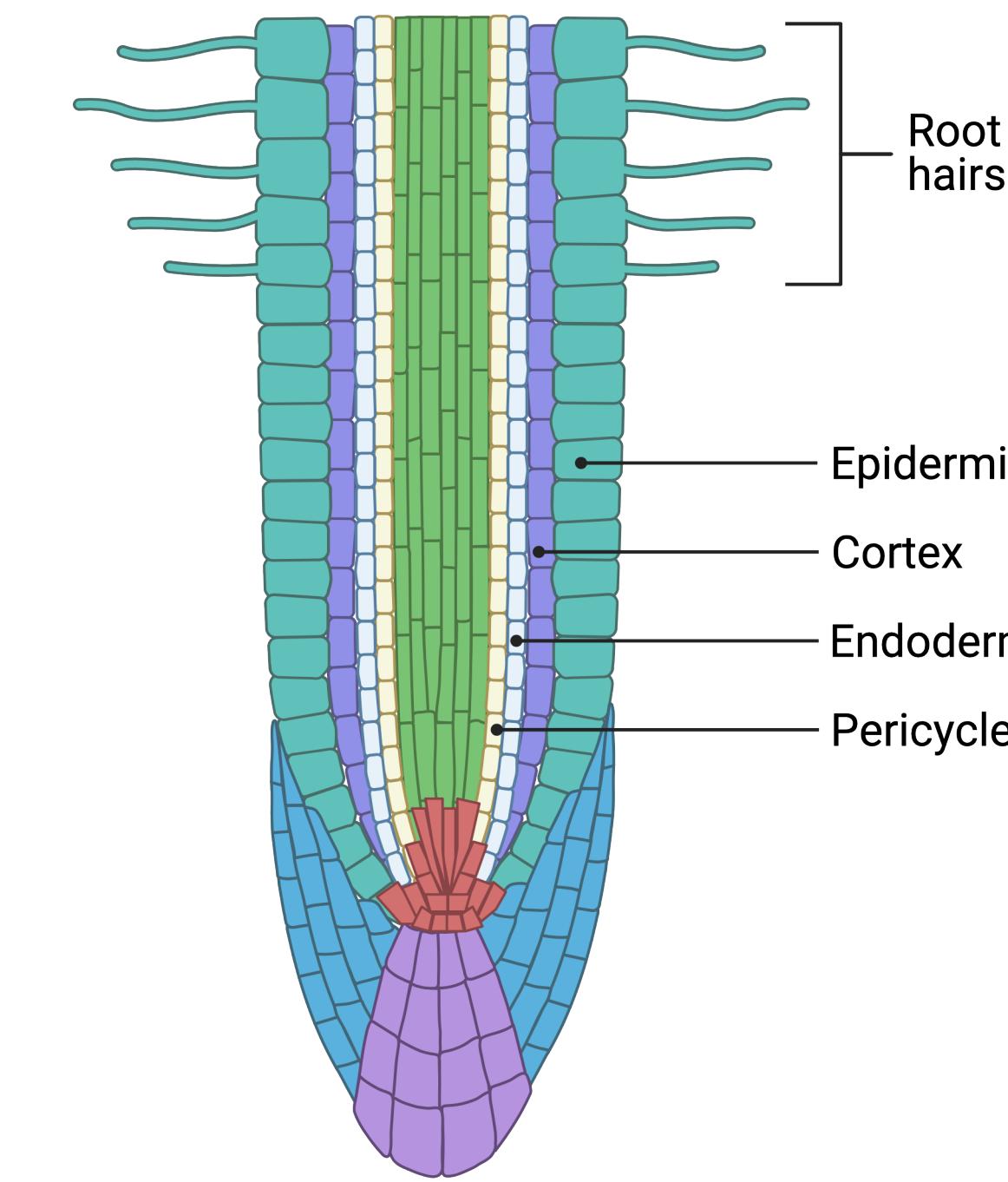


Figure 2. Primary (young) root anatomy. In the primary root, suberin is deposited in the endodermis. Endodermal suberization may initially influence root microbiome (and vice versa). In secondary (mature) roots, suberin is deposited in the periderm. Periderm is derived from the pericycle, not endodermis, during the secondary growth of eudicots. In this study, we are mostly measuring periderm suberin, which may have a different role than endodermal suberin.

Results and Figures

- *A. thaliana* suberin deposition in roots is delayed by microbiome treatment ($p < 0.05$ at 6 weeks, Figure 4), while there is little change in suberin deposition ($p > 0.05$) in response to the microbiome in the related species, *Camelina sativa* (Figure 5).
- Root suberization in the pathogen-tolerant soybean cultivar 'Conrad' is unresponsive to microbiome treatment (Figure 6).
- Plant root and soil samples yielded sufficient DNA for microbial amplicon sequencing.

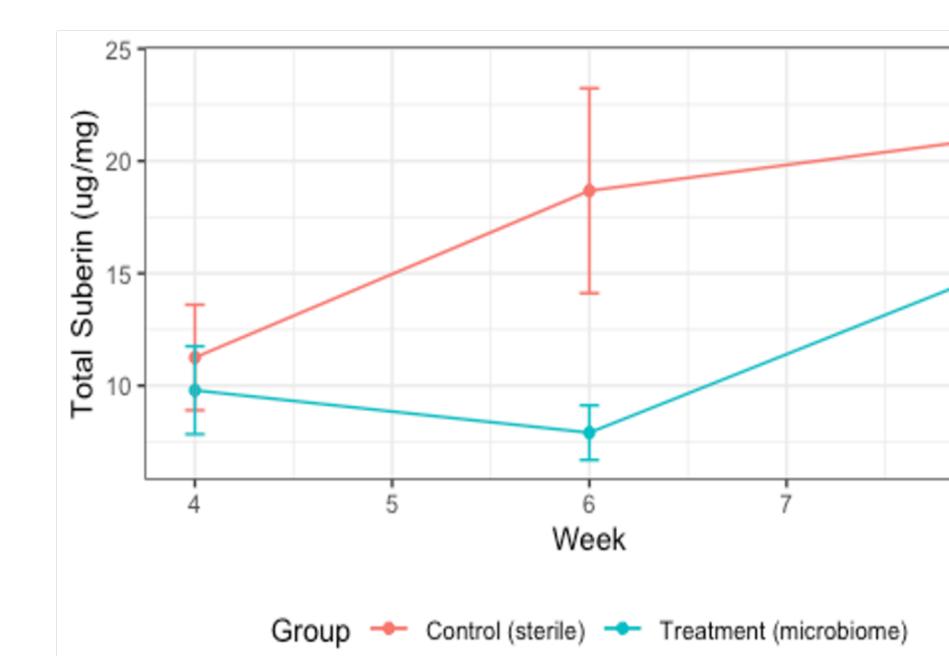


Figure 4 Total suberin content in *Arabidopsis thaliana* with and without a microbiome over time.

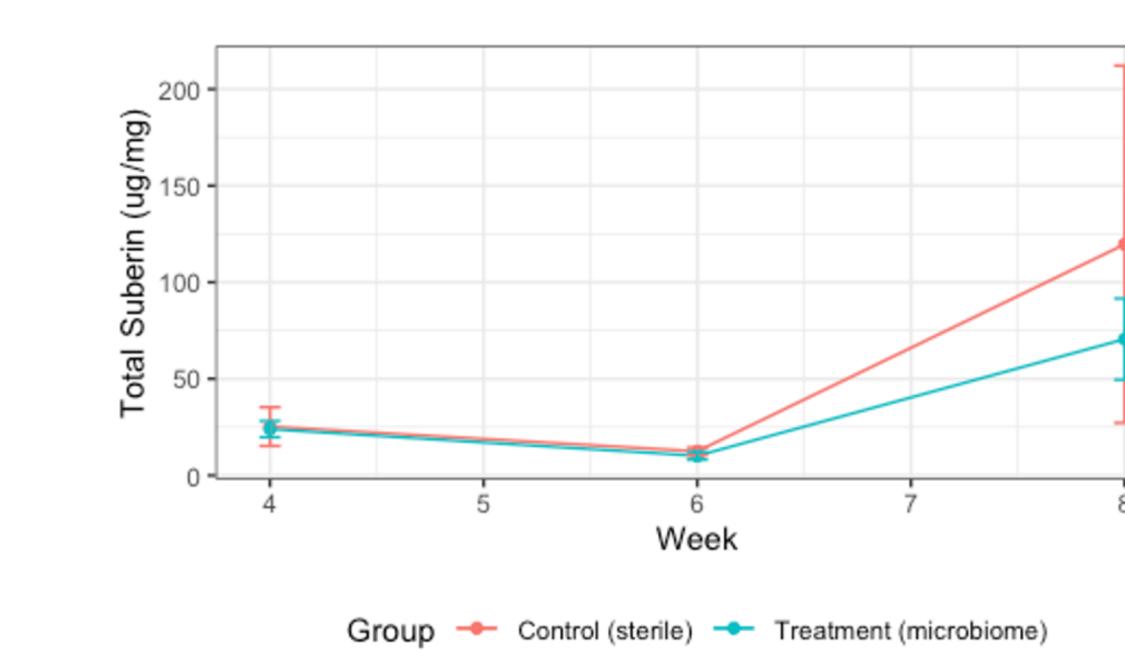


Figure 5 Total suberin content in *Camelina sativa* with and without a microbiome over time.

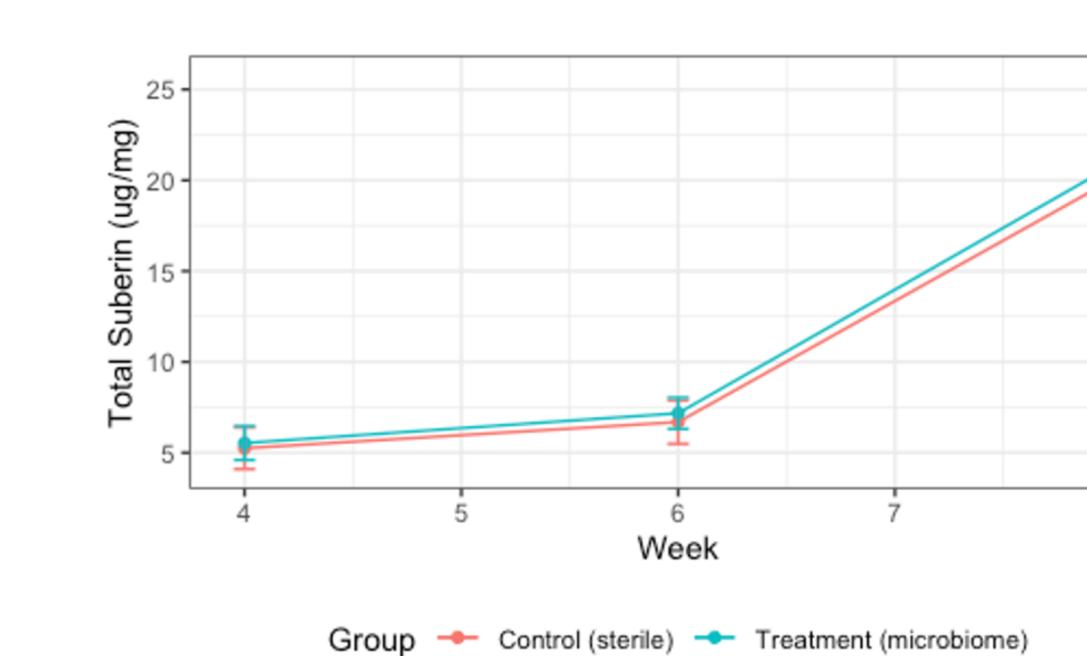
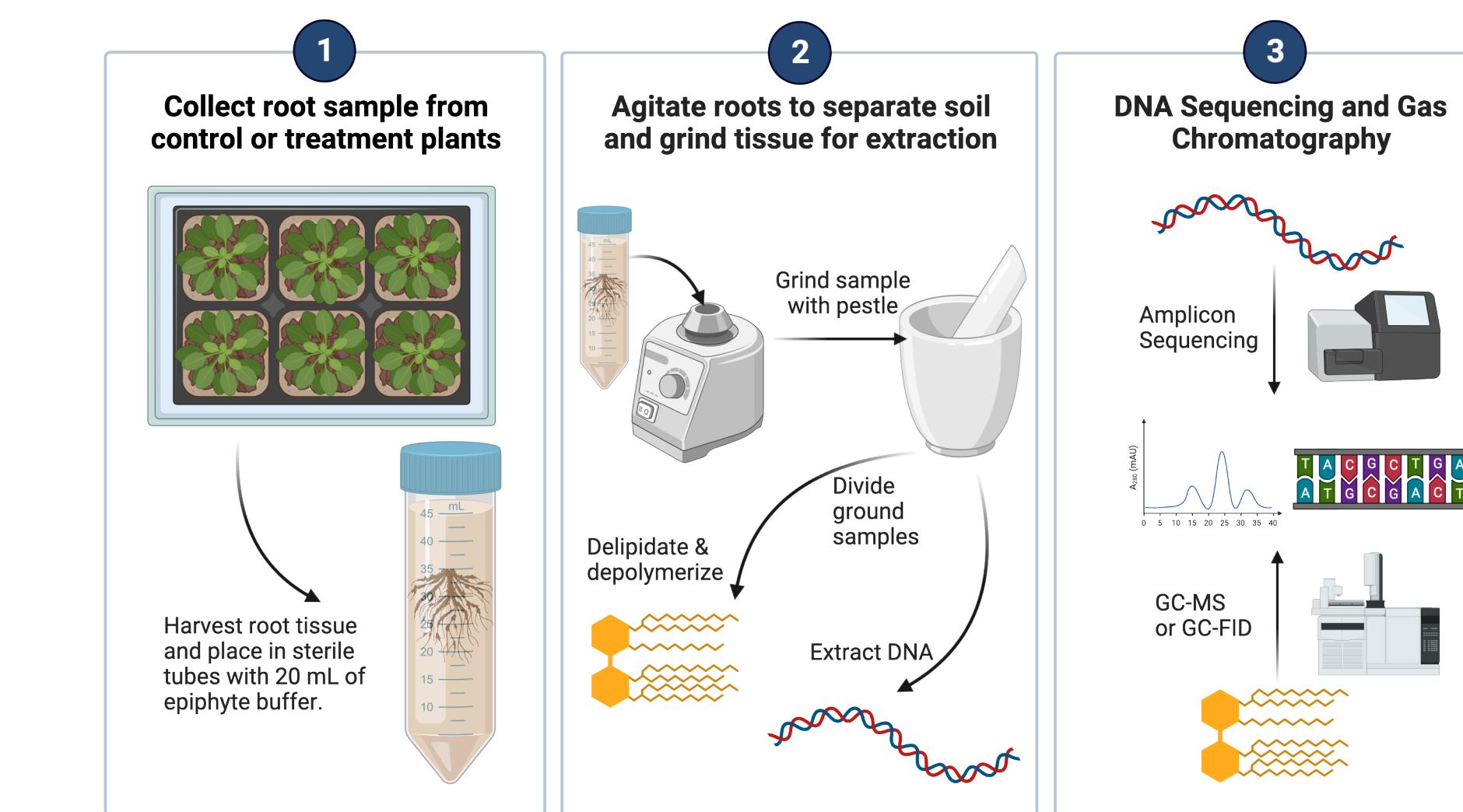


Figure 6 Total suberin content in *Glycine max* with and without a microbiome over time.

Methodology

- We grew three plant species (*Arabidopsis thaliana*, *Camelina sativa*, *Glycine max*) in a peat-based soil with and without a microbiome treatment.
- We collected plant roots from these species after 4, 6, and 8 weeks of plant growth. We also collected the soil from immediately surrounding the roots.
- We then processed the roots for suberin analysis via gas chromatography and extracted DNA for sequencing.



Conclusions

- A method to collect and prepare root samples for both microbiome and analytical chemical analysis has been **validated in three species**.
- The rhizosphere microbiome regulates root suberin in a species-specific manner. This regulation may be mediated by phytohormones.²
- **Varying responses** in root suberin to the microbiome suggests some species can tolerate or resist biotic stressors (e.g., microbial or pathogen invasion) better than others.⁴
- Collected microbial DNA samples (root and rhizosphere) will be sequenced via Illumina MiSeq to identify bacteria and fungi present.
- The response of either *Arabidopsis* suberin mutants (up or down regulated) or different soybean cultivars to microbiome treatment will be tested in future experiments.