

# Microbial consortium effect depends on poplar genotype

## Background

- Beneficial microbes, such as mycorrhizal fungi and plant-promoting bacteria, can improve plant access to nutrients, increase plant growth, and enhance plant resilience. These microbes when applied as bioinoculants, may create synergistic effects that increase plant productivity, but little is known about the role of plant genetics and root exudation underlying these interactions.

## Approach

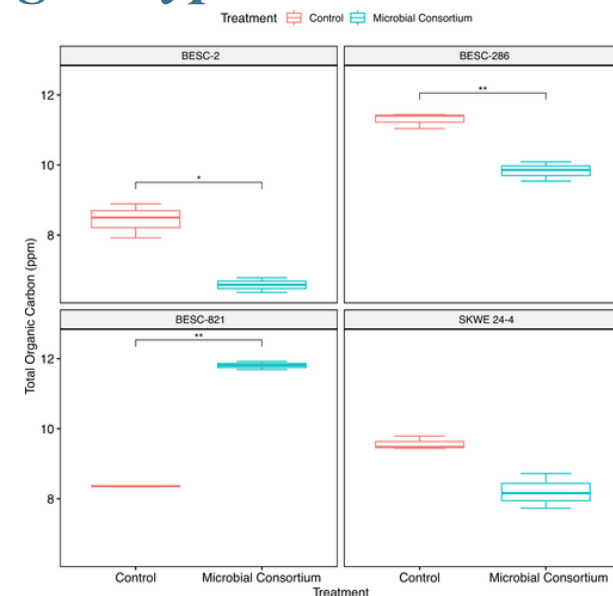
- The study aimed to understand the influence of an added microbial consortium, comprising ectomycorrhizal fungi and the beneficial *Pseudomonas* sp. strain GM41, on *Populus trichocarpa* physiology and root exudate profiles across four different *P. trichocarpa* genotypes in a laboratory setting over 7 weeks post-inoculation.

## Results

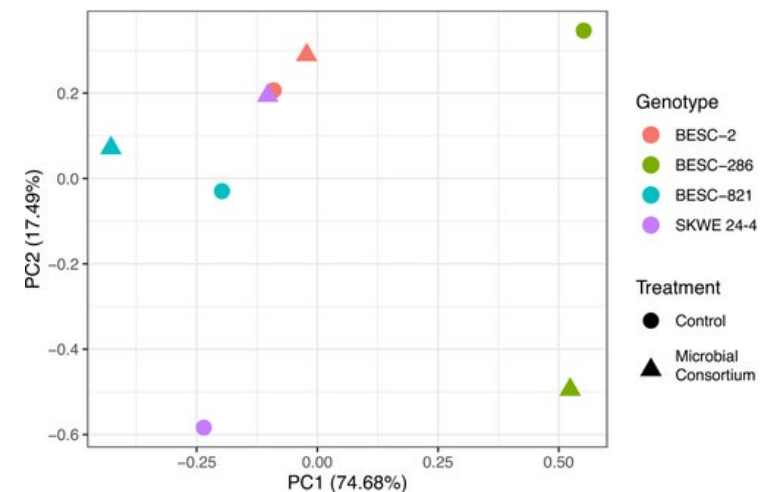
- P. trichocarpa* growth parameters such as growth rate, diameter, height, biomass, and root growth varied across poplar genotypes but were not directly correlated to the microbial inoculants.
- Total organic carbon in plant roots correlated to addition of the microbial consortium but was *P. trichocarpa* genotype dependent.
- The microbial consortium altered exometabolite profiles in a genotype-specific manner.

## Significance

- These results suggest that this microbial consortium may play a pivotal role in initiating early signaling mechanisms within poplar. This interaction appears to significantly impact the plant's metabolic processes that are vital for its subsequent growth, development, and resilience to environmental stresses.



Total organic carbon differed across *P. trichocarpa* genotypes and microbial consortium treatment. \* $P \leq 0.05$ , \*\*  $P \leq 0.01$ , \*\*\* $P \leq 0.001$ .



Principal component analysis (PCA) plot of pooled exometabolites show exudation varied by *P. trichocarpa* genotypes and microbial consortium treatments.