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## Foundational Genomics Research, Plant-Microbe Interfaces

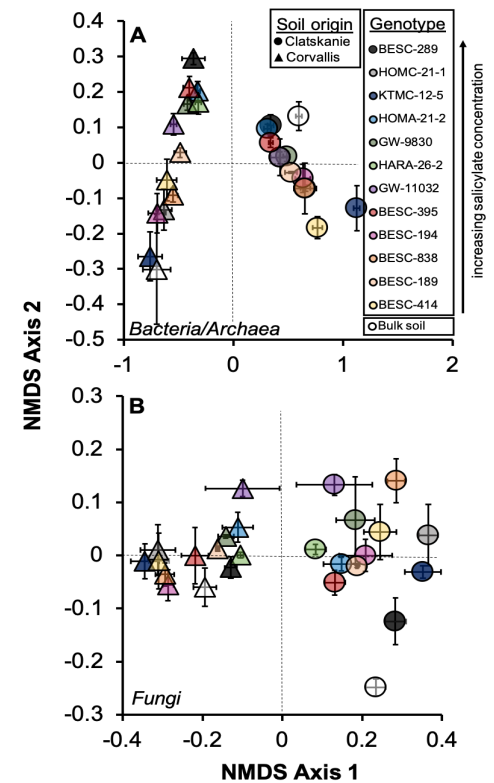


**Novel approach:** Used a combined analysis of plant microbiome composition, secondary metabolome variation, and host plant growth and physiology to understand the effects of their interactions in the rhizosphere.

Objective	<ul style="list-style-type: none"><li>Understand how amount and form of salicylate secondary chemistry effects rhizosphere microbial communities in <i>Populus trichocarpa</i> genotypic variants</li></ul>
New science	<ul style="list-style-type: none"><li>Bacterial and fungal community composition, differed first by soil origin, but are secondarily shaped by <i>Populus</i> genotype and their resulting chemotypes</li><li>Within a soil type, bacteria/archaea and fungi diversity shifted in response to specific metabolites (populin, tremuloidin, salicylic acid) and overall salicylate levels</li><li>Bacterial responses to individual metabolites were stronger whereas fungal communities tended to respond more to overall levels</li></ul>
Impact	<ul style="list-style-type: none"><li>Illustrates how the host plant may help shape the local rhizosphere microbiome via genotypes that vary in secondary metabolisms</li></ul>

Rhizosphere microbiomes diverge among *Populus trichocarpa* plant-host genotypes and chemotypes, but it depends on soil origin.

Veach AM, Morris R, Yip DZ, Yang ZK, Engle NL, Cregger MA, Tschaplinski TJ, Schadt CW  
Microbiome. DOI: 10.1186/s40168-019-668-8.



**Microbiome divergence across soils and genotypes.** Bacteria/archaea (A) and fungal (B) community composition among plant genotypes grown in two different soil origins (Clatskanie, Corvallis).