Plant-Microbe Interfaces: The contribution of host chemotype as a driver of rhizosphere microbial community structure

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Background and Objective

- A diverse consortia of soil bacteria and fungi exist belowground and interact with plant rooting systems under varying contexts. Beyond carbon exchange between roots and associated microbiota, the relative influence of plant chemical properties on rhizosphere microbiome assembly has been understudied[1,2].
- ***Populus*** trees produce high salicylic acid levels complexed into higher-order conjugates that mediate host defense, metabolism, and may also be directly mineralized or inhibitory towards exogenous soil microbiota.
- Our research goal is to understand the relative importance of plant host genotype, chemotype (salicylic acid production), and soil origin (physicochemical differences) on rhizosphere microbiome (archaea, bacteria, fungi) structure within the ***Populus*** root – soil interface.

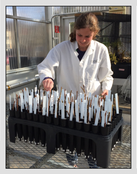
Experimental Design

- Twelve ***P. trichocarpa*** genotype clones were selected for greenhouse assays based on higher-order salicylate profiles (Table 1). These were selected based on past field collected leaf profiles from the GWAS population.
- Five replicate cuttings/genotype grown in two soils (Corvallis, Clatskanie origin) for 4 months after rooted for ~ 1 month.
- At destructive harvest, plant roots and rhizospheres were collected for metabolomics (specifically salicylates), 16S and ITS2 rRNA amplicon-based sequencing.

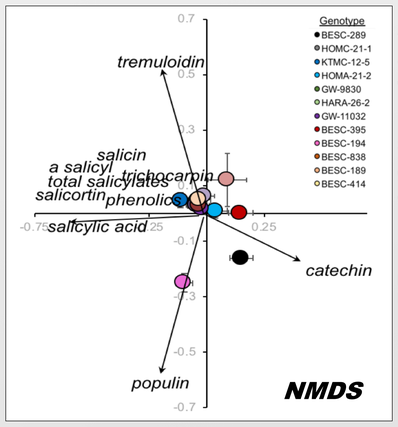
Total Salicylate Rank	Clone Genotype	Rationale for selection
1	HOMC-21-1	High salicortin and total salicylates
2	HARA-26-2	High salicortin and total salicylates
8	KTMC-12-5	High salicortin and total salicylates
3	BESC-289	High salicortin and populin
4	HOMA-21-2	High salicortin and populin
219	BESC-414	Presence of tremuloidin and populin
592	BESC-194	Presence of tremuloidin and populin
1041	GW-9830	Low salicortin and salicin
994	BESC-838	Low salicortin and salicin
975	GW-11032	Low salicortin and salicin
1017	BESC-395	Low salicortin and salicin
1051	BESC-189	Low salicortin and salicin

Table 1. Summary of twelve *P. trichocarpa* genotypes selected for the trap-plant experiment.

Before harvest at ~ 4 months

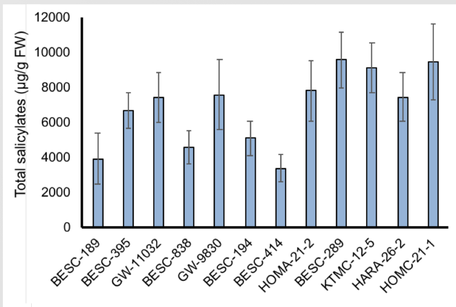


Plant Metabolites



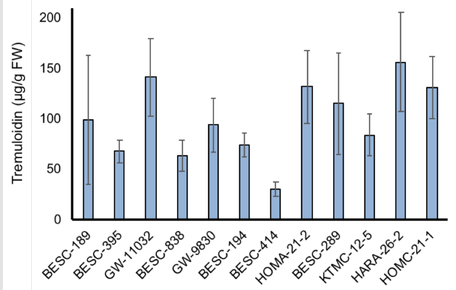
A linear discriminant analysis (LDA) indicates that populin is the only metabolite that signiciantly explained genotypic differences due to high variation among replicates.

Linear discriminants for populin - R^2 = 0.79, p < 0.01

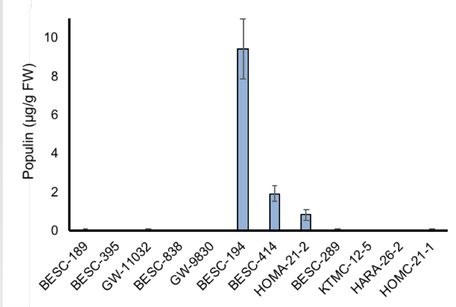


Total salicylates did vary among plants and ranged between 3,000 – 10,000 µg g FW^{-1}

Predicted range of total salicylates from field data did not translate to those observed in greenhouse roots

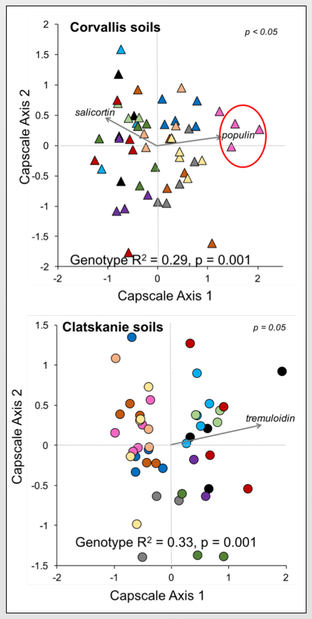


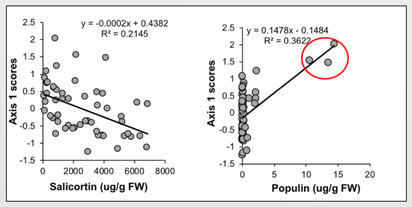
Tremuloidin was present among all genotypes



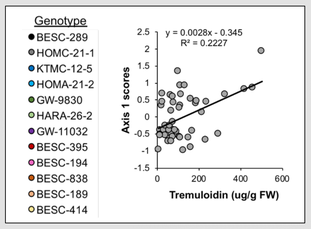
As predicted (Table 1), populin was only > 1 µg/g FW^{-1} in 3 genotypes which varied an order of magnitude

Rhizosphere Archaea/Bacteria

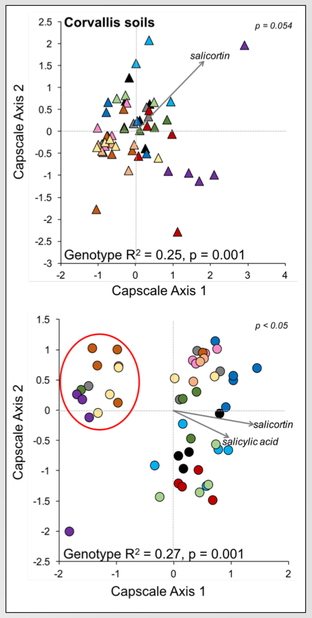


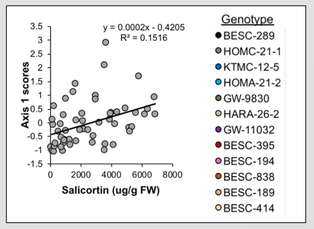


- Soil origin explained most variation in community composition for archaea/bacteria (R^2 = 0.52) and fungi (R^2 = 0.40, p < 0.01).
- Within soil origins, populin, salicortin, and tremuloidin significantly influenced community composition for archaea/bacteria.

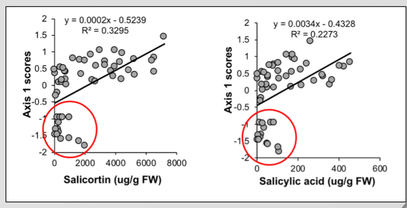


Rhizosphere Fungi





- Conversely to archaea/bacteria, salicorin and salicylic acid (and not populin or tremuloidin) significantly influenced fungal community composition.
- Genotype effects were also less influential in fungi compared to archaea/bacteria.



Conclusions and Future Directions

- Greenhouse root metabolites were more variable and lower in overall salicylates than field grown leaf profiles, although correlated. Populin presence or absence was the only metabolite profile which correctly translated from field to greenhouse
- Overall rhizosphere microbiome community patterns were largely driven by soil origin, but both genotype and chemotype effects were detected.
  - Bacteria/Archaea: sensitive to less abundant compounds (populin, tremuloidin)
  - Fungi: sensitive more abundant salicylates (salicortin, salicylic acid)
- Ongoing analysis will identify major OTUs/groups of taxa differ between low – high metabolite profile environments.
- Our analysis of root endosphere communities failed in this case, so future work will need to address whether these results scale to other plant niches.

References:

[1]**Lebeis SL, Paredes SH, Lundberg DS, Breakfield N, Gehring J, *et al.* (2015) Salicylic acid modulates colonization of the root microbiome by specific bacterial taxa. Science, 10, 860-4.**

[2]**Lareen A, Burton F, Schafer P (2016) Plant root-microbe communication in shaping root microbiomes. Plant Mol Biol 90, 575-587.**

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