## Diversity of *Pseudomonas* Genomes, Including *Populus*-Associated Isolates, as Revealed by Comparative Genome

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**Background** 

The *Pseudomonas* genus, a metabolically versatile group influences the phylogenetic diversity and heterogeneity of the microbial communities associated in the endosphere and rhizosphere of plants.

• Comparative genome analysis of 1073 *Pseudomonas* genomes, including 21 PMI isolates from the roots of *P. deltoides*, was performed in order to provide insights into the interactions of these woody plants and *Pseudomonas* spp.

**Approach** 

 Various comparative genomic tools, (AAI, pan and core genome analysis, pathway analysis) were used for phylogenomic diversity assessment, systematic functional analysis, and classification into genomic species clusters.

## **Outcomes**

- All the *Pseudomonas* genomes fall into 9 major groups and 131 robust and reproducible genomic clusters of 'species'.
- The *Populus* isolates contribute to 14 genomic species and formed 3 distinct subgroups within the major *P. fluorescens* group; each being identified by genomic similarity (AAI).

## **Significance**

• This study highlights the need to sequence multiple isolates, especially from the *P. fluorescens group,* and reveals the extensive genomic variation within a single OTU. We find more than 200,000 different gene families within the *Pseudomonas* genus.

Pseudomonas sp R62 Pseudomonas moraviensis R28 Pseudomonas sp GM25 \* Pseudomonas fluorescens Pf01 <sup>9</sup>seudomonas sp GM80 <sup>3</sup> Pseudomonas fluorescens NZ01 Subgroup 1 seudomonas chlororaphis 1 Pseudomonas sp GM24 \* Pseudomonas so H1h Pseudomonas fluorescens R124 Pseudomonas sp URIL14HWK12I6 Pseudomonas sp GM30 3 Pseudomonas sp Ant303 Pseudomonas putida 1 Pseudomonas sp G5 Subgroup 2 Pseudomonas sp GM55 \* Pseudomonas sp GM33 \* Pseudomonas sp UW4 Pseudomonas sp GM74 \* Pseudomonas sp GM49 \* Pseudomonas sp GM48 \* Pseudomonas sp GM21 \* Pseudomonas so QTF5 Subgroup 3 eudomonas mandelii 36MECvi11 Pseudomonas umsongensis 20MFCvi11

A tree of *Populus*-associated *Pseudomonas* isolates (indicated by asterisks) and related strains as identified by comparative genomic analyses, which formed three distinct OAK subgroups.

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