

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

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Funding Source: DOE Office of Biological and Environmental Research, Genomic Science Program

## 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

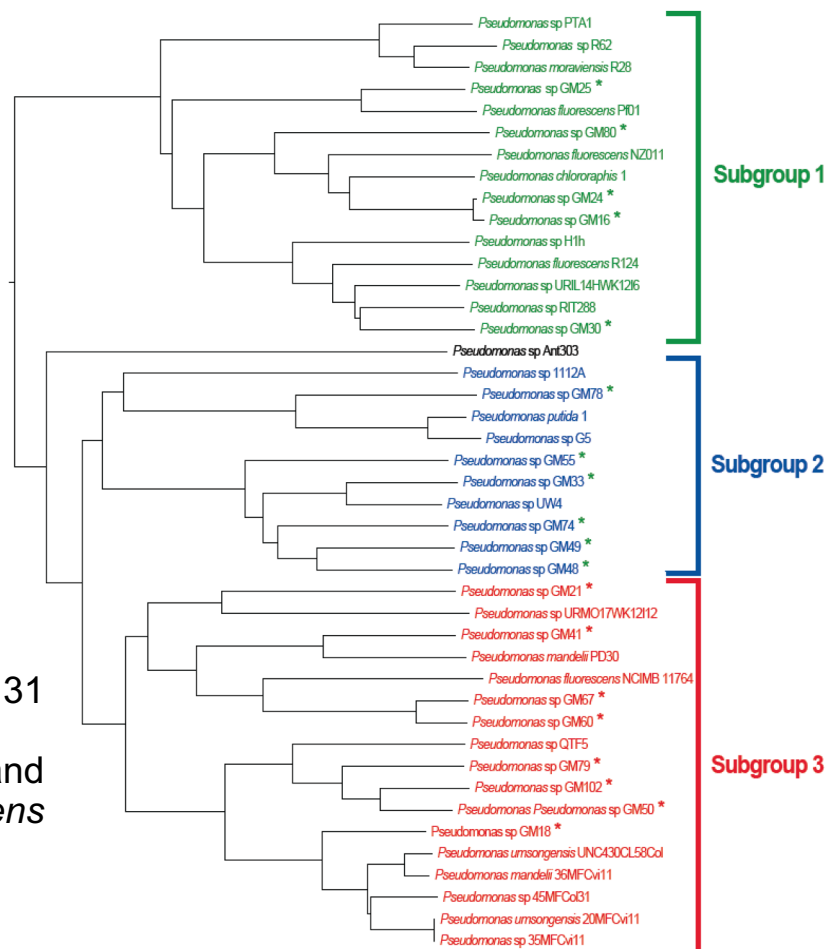
- Various comparative genomic tools, (AAI, pan and core genome analysis, pathway analysis) were used for phylogenomic diversity assessment, systematic functional analysis, and classification into genomic species clusters.

## 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.



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