

# Twenty-One Genome Sequences from *Pseudomonas* Species and 19 Genome Sequences from Diverse Bacteria Isolated from the Rhizosphere and Endosphere of *Populus deltoides*

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**To aid in the investigation of the *Populus deltoides* microbiome, we generated draft genome sequences for 21 *Pseudomonas* strains and 19 other diverse bacteria isolated from *Populus deltoides* roots. Genome sequences for isolates similar to *Acidovorax*, *Bradyrhizobium*, *Brevibacillus*, *Caulobacter*, *Chryseobacterium*, *Flavobacterium*, *Herbaspirillum*, *Novosphingobium*, *Pantoea*, *Phyllobacterium*, *Polaromonas*, *Rhizobium*, *Sphingobium*, and *Variovorax* were generated.**

Plant-microbe interactions within the rhizosphere have been shown to have important roles in plant health and productivity (1, 4, 8, 20). As part of an ongoing effort to better understand the microbial communities associated with native *Populus deltoides* (Eastern cottonwood), we have under taken both cultivation-independent and cultivation-dependent assessments of microbial communities from the *P. deltoides* rhizosphere and endosphere (3, 5, 25). Our goal is to understand the diversity of the *Populus* microbiome and to elucidate the metabolic and molecular mechanisms responsible for shaping *Populus*-microbe root interactions.

We sampled *P. deltoides* at sites along the Caney Fork River in central Tennessee and at the Yadkin River in North Carolina. These sites represent ecotypes and soil conditions that are common to this region. Approximately 1,100 diverse bacterial strains were collected to investigate phylogenetic and functional diversity. The isolates comprise 7 classes and 85 genera of bacteria, including *Actinobacterium* (14%), *Bacillus* (17%), *Flavobacterium* (6%), *Sphingobacterium* (3%), *Alphaproteobacteria* (22%), *Betaproteobacteria* (16%), and *Gammaproteobacteria* (22%). A number of our isolates were *Pseudomonas* species, which have considerable genetic and phenotypic variability and include pathogenic, biocontrol, and plant growth-promoting bacteria (14, 21). *Pseudomonads* were also found to be one of the most common operational taxonomic units (OTUs) using direct rRNA gene sequencing of *P. deltoides* endosphere and rhizosphere samples (5). While representatives were chosen for genome sequencing based on overall phenotypic traits and phylogeny, a special emphasis was placed on sequencing *P. fluorescens*-like organisms. In all, 23 strains of *Gammaproteobacteria*, 5 of *Betaproteobacteria*, 8 of *Alphaproteobacteria*, 2 of *Bacteroidetes*, and 2 of *Firmicutes* were sequenced.

Paired-end DNA libraries with an average insert size of 500 bp were created and draft genome data were generated using

Illumina (2) HiSeq2000 technology. CLC Genomics Workbench (version 4.7.1) and FASTQC (13) were applied to trim reads for quality sequence data. Trimmed Illumina data were assembled mostly using the CLC Genomics Workbench (version 4.9), although better assemblies for isolates AP49, BC25, CF314, GM16, and GM49 were generated with Velvet (version 1.2) (26). Draft genome sequences were annotated using the U.S. Department of Energy (DOE) Joint Genome Institute (JGI) integrated microbial genomes database and comparative analysis system (IMG) (15), and contigs of 500 bp or greater were deposited at the National Center for Biotechnology Information GenBank database. The median value for the largest contig in each genome was 249,964 bp, and key attributes for the genome sequences are summarized in Table 1.

Recently, a number of genome sequences for plant growth-promoting and biocontrol bacteria have been reported (6, 7, 9–12, 16–19, 22–24, and 27). The genome sequences reported in this study will facilitate comprehensive comparisons of bacteria involved in plant-microbe interactions.

**Nucleotide sequence accession numbers.** The nucleotide sequences have been deposited in DDBJ/EMBL/GenBank under the accession numbers provided in Table 1, and the versions described in this paper are the first versions. The entire DNA sequence data set has been deposited in the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA) database (accession number SRA050017).

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TABLE 1 Summary of genome sequences for 40 rhizosphere and endosphere bacteria

Organism	Origin <sup>a</sup>	Coverage (fold)	No. of contigs	% GC	N <sub>50</sub>	No. of CDS	Genome size (bp)	Accession no.
<i>Acidovorax</i> sp. strain CF316	E	310	315	67	37,104	7,206	7,086,227	AKJX00000000
<i>Bradyrhizobium</i> sp. strain YR681	E	250	351	64	37,719	8,302	7,831,714	AKIY00000000
<i>Brevibacillus</i> sp. strain CF112	E	560	172	54	76,367	5,272	5,271,824	AKKB00000000
<i>Brevibacillus</i> sp. strain BC25	E	650	140	47	68,877	6,021	6,279,079	AKIX00000000
<i>Caulobacter</i> sp. strain AP07	R	390	326	69	30,563	5,373	5,615,958	AKKF00000000
<i>Chryseobacterium</i> sp. strain CF314	E	1,200	119	37	80,113	4,125	4,484,672	AKJY00000000
<i>Flavobacterium</i> sp. strain CF136	E	2,721	113	34	89,762	4,366	5,102,016	AKJZ00000000
<i>Herbaspirillum</i> sp. strain CF444	E	520	125	60	82,125	5,004	5,594,732	AKJW00000000
<i>Herbaspirillum</i> sp. strain YR522	E	530	168	63	54,530	4,949	5,113,042	AKJA00000000
<i>Novosphingobium</i> sp. strain AP12	R	430	187	66	54,713	5,532	5,611,617	AKKE00000000
<i>Pantoea</i> sp. strain GM01	R	680	102	54	91,591	4,998	5,320,548	AKIU00000000
<i>Pantoea</i> sp. strain YR343	R	700	128	55	94,033	4,900	5,314,049	AKIT00000000
<i>Phyllobacterium</i> sp. strain YR531	E	990	41	53	257,533	4,901	4,997,302	AKIZ00000000
<i>Polaromonas</i> sp. strain CF318	E	620	159	65	61,518	4,828	5,008,816	AKIV00000000
<i>Pseudomonas</i> sp. strain GM16	E	2,300	128	59	122,673	5,888	6,550,518	AKJV00000000
<i>Pseudomonas</i> sp. strain GM84	R	256	384	63	24,795	5,295	5,818,772	AKJC00000000
<i>Pseudomonas</i> sp. strain GM24	E	3,200	399	59	32,656	5,885	6,517,063	AKJR00000000
<i>Pseudomonas</i> sp. strain GM102	E	440	159	59	88,165	6,039	6,657,346	AKJB00000000
<i>Pseudomonas</i> sp. strain GM33	E	440	205	60	61,913	6,102	6,727,223	AKJO00000000
<i>Pseudomonas</i> sp. strain GM78	E	469	235	60	57,174	6,724	7,287,561	AKJF00000000
<i>Pseudomonas</i> sp. strain GM80	E	474	282	59	39,805	6,245	6,786,162	AKJD00000000
<i>Pseudomonas</i> sp. strain GM17	E	480	280	63	44,590	6,105	6,786,964	AKJU00000000
<i>Pseudomonas</i> sp. strain GM79	E	486	126	59	96,213	6,062	6,707,010	AKJE00000000
<i>Pseudomonas</i> sp. strain GM67	E	509	183	60	68,050	6,003	6,502,113	AKJH00000000
<i>Pseudomonas</i> sp. strain GM74	R	512	180	60	75,201	5,562	6,104,277	AKJG00000000
<i>Pseudomonas</i> sp. strain GM30	E	520	180	60	59,627	5,611	6,140,967	AKJP00000000
<i>Pseudomonas</i> sp. strain GM41	E	520	164	59	75,073	6,066	6,615,479	AKJN00000000
<i>Pseudomonas</i> sp. strain GM50	E	520	155	59	68,220	6,068	6,692,143	AKJK00000000
<i>Pseudomonas</i> sp. strain GM25	R	530	91	61	137,130	5,758	6,350,607	AKJQ00000000
<i>Pseudomonas</i> sp. strain GM49	R	530	345	60	31,212	6,253	6,589,890	AKJL00000000
<i>Pseudomonas</i> sp. strain GM60	E	540	181	60	62,804	5,911	6,424,244	AKJI00000000
<i>Pseudomonas</i> sp. strain GM21	E	570	210	58	57,752	6,072	6,609,272	AKJS00000000
<i>Pseudomonas</i> sp. strain GM55	E	574	163	60	77,637	5,985	6,489,331	AKJJ00000000
<i>Pseudomonas</i> sp. strain GM18	E	580	140	60	106,048	5,711	6,297,618	AKJT00000000
<i>Pseudomonas</i> sp. strain GM48	R	580	200	59	59,542	5,902	6,443,787	AKJM00000000
<i>Rhizobium</i> sp. strain CF142	E	445	150	60	85,172	7,240	7,457,089	AJWE00000000
<i>Rhizobium</i> sp. strain CF122	E	543	130	60	117,778	6,090	6,142,299	AKKA00000000
<i>Rhizobium</i> sp. strain AP16	E	555	96	60	123,519	6,143	6,497,619	AJVM00000000
<i>Sphingobium</i> sp. strain AP49	E	665	99	63	89,526	4,585	4,479,274	AJVL00000000
<i>Variovorax</i> sp. strain CF313	E	2,200	173	67	65,214	5,674	6,029,174	AKIW00000000
Median		530	166	60	68,549	5,895	6,387,426	

<sup>a</sup> E, endosphere; R, rhizosphere.

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