

Draft Genome Sequence of *Flavobacterium* sp. Strain F52, Isolated from the Rhizosphere of Bell Pepper (*Capsicum annuum* L. cv. Maccabi)

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Here we report the draft genome sequence of *Flavobacterium* sp. strain F52, isolated from the rhizosphere of bell pepper (*Capsicum annuum* L. cv. Maccabi). *Flavobacterium* spp. are ubiquitous in the rhizospheres of agricultural crops; however, little is known about their physiology. To our knowledge, this is the first published genome of a root-associated *Flavobacterium* strain.

Members of the genus *Flavobacterium* are widespread in freshwater, marine, and terrestrial environments and are believed to play a significant role in the degradation and turnover of organic matter (2). Flavobacteria are often characterized based on the presence of a yellow-orange pigment, flexirubin (2), gliding motility (4), and a unique *Bacterioidetes*-associated Por secretion system (PorSS) (9, 11). Isolation-based and culture-independent analyses have determined that *Flavobacterium* spp. are often highly abundant in the rhizospheres of agricultural crops (5–8), and certain evidence suggests that they are associated with the stimulation of plant resistance to disease (3, 7, 10). However, genomic properties providing for *Flavobacterium* species fitness in the highly competitive root environment are currently not well known.

We recently isolated a large number of *Flavobacterium* spp. from the rhizosphere of mature bell pepper (*Capsicum annuum* L. cv. Maccabi) plants grown in potting mixtures amended with citrus wood-derived biochar in an experimental greenhouse (3, 7). *Flavobacterium* sp. strain F52 tested positive for many biochemical assays associated with plant growth promotion and protection, including NH₃ production, hydrogen cyanide (HCN) production, and extracellular chitinase activity. Integrative analyses of these traits led us to select *Flavobacterium* sp. F52 as a model strain for studying *Flavobacterium*-root interactions. The draft genome sequence of *Flavobacterium* sp. F52 was determined by *de novo* assembly of paired-end Illumina sequence data. A library of genomic DNA from *Flavobacterium* sp. F52 was prepared for sequencing using the Nextera library preparation kit (Epicentre, Madison, WI), with subsequent size selection for fragments of 400 to 800 bp using a Pippin Prep automated electrophoresis system (Sage Scientific, Beverly, MA). A total of 26 million paired-end reads were acquired, and a *de novo* assembly was performed using the software package CLC genomic workbench (version 5.0; CLC bio A/S, Denmark), yielding 54 contigs with more than 400× average coverage. Annotation was performed in RAST (1) and in the CG-Pipeline before being submitted to NCBI.

The *Flavobacterium* sp. F52 draft genome is roughly 5.3 Mbp, with an overall GC content of 34.4%, encompassing approximately 4,800 protein-coding genes. The genome contains all of the known proteins associated with both gliding motility and the PorSS that have been comprehensively defined in the soil-isolated

model strain *F. johnsoniae* UW101^T (4, 9). In addition, over 20 genes associated with chitin degradation were identified, as were a myriad of genes involved in the metabolism of other complex plant-related sugars, proteins, and fatty acids. Functional gene- and 16S rRNA gene-based phylogenetic analyses of sequenced *Flavobacterium* genomes revealed two environmentally distinct clusters: a soil/rhizosphere clade comprised of *F. johnsoniae* UW101^T and *Flavobacterium* sp. F52 and an aquatic-associated *Flavobacterium* clade encompassing the strains *F. frigoris* PS1, *F. branchiophilum* FL-15, *F. columnare* ATCC 49512, *F. psychrophilum* JIP02/86, and *F. indicum* GPTSA100-9. Interestingly, the genomes of the soil/rhizosphere flavobacterial clade were nearly twice the size of the genomes of the marine flavobacterial strains. This significant difference in genome size may be associated with the fact that the terrestrial strains require significantly higher metabolic flexibility than their aquatic counterparts.

Nucleotide sequence accession numbers. The *Flavobacterium* sp. F52 genomic assembly and annotation were deposited in GenBank under the accession number [AKZQ000000000](https://www.ncbi.nlm.nih.gov/nuccore/AKZQ000000000) and the BioProject accession number [PRJNA169163](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA169163).

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