Genome Sequence of the Plant Growth-Promoting Rhizobacterium *Pseudomonas putida* S11

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Here we report the genome sequence of a plant growth-promoting rhizobacterium, *Pseudomonas putida* S11. The length of the draft genome sequence is approximately 5,970,799 bp, with a G+C content of 62.4%. The genome contains 6,076 protein-coding sequences.

Plant growth-promoting rhizobacteria (PGPR) colonize the rhizosphere and promote plant growth through either direct or indirect mechanisms. Root colonization is the crucial step that determines the success of the plant growth promotion. *Pseudomonas putida* S11 was isolated from the sugarcane rhizosphere. It efficiently colonizes corn roots and promotes plant growth. This strain was submitted to the Microbial Type Culture Collection and Gene Bank (MTCC), Chandigarh, India, with the accession number MTCC 5670. Earlier, we identified that a mutation of the two-component signal transduction system (*pstSR*) in *P. putida* S11 increased pyoverdine production and iron uptake, which, in turn, results in improved abiotic and biotic surface colonization (4). Whole-genome shotgun sequencing of *P. putida* S11 was done to further understand genes essential for root colonization and survival in the rhizosphere.

Total genomic DNA of *P. putida* S11 was isolated using the Qiagen DNeasy kit by following the manufacturer's instructions. The sequencing was performed by Roche 454 pyrosequencing at the Research and Testing Laboratory, Lubbock, TX. The data generated contained 230,568 reads with an average read length of 588 bp. Altogether, 135,627,871 sequenced bases were obtained with an ~22-fold coverage of the ~5.9-Mb genome. The *de novo* assembly using MIRA (Mimicking Intelligent Read Assembly) version 3.4.0 (2) yielded 346 contigs (N_{50} length = 32,259 bp). The Staden package, version 2.0 (5), was used to visualize contigs and to join the overlapping contigs, which finally yielded 196 contigs (longest contig = 255,672 bp; shortest contig = 349 bp). The consensus length of the draft genome sequence is 5,970,799 bp, with a G+C content of 62.4%. The draft genome was annotated using the Rapid Annotations using Subsystems Technology (RAST; version 4.0) (1) server with the RAST gene caller. A total of 6,076 protein-coding genes and 85 RNA coding regions were predicted.

The bioavailability of iron is low in the rhizosphere. PGPR require efficient iron acquisition mechanisms to compete with other microorganisms and plants for uptake of the essential micronutrient (3). The genome of *P. putida* S11 contains 31 genes with predicted function in siderophore pyoverdine biosynthesis, transport, and regulation. In addition, 25 putative TonB-dependent siderophore receptor genes involved in iron transport are identified. Predicted sigma factor/anti-sigma factor gene pairs are found flanking six of these putative siderophore receptor genes. Further analysis of the functional role of these predicted genes in iron acquisition and metabolism and the influence of iron uptake in root colonization of strain S11 are presently being investigated. The draft genome sequence of *P. putida* S11 provides a framework for further genetic studies to understand the influence of abiotic and biotic stress tolerance mechanisms on rhizosphere colonization and ecological fitness of the PGPR.

Nucleotide sequence accession numbers. The *Pseudomonas putida* S11 whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ALXA00000000. The version described in this paper is the first version, ALXA01000000.

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