# Genome Sequence of *Enterobacter radicincitans* DSM16656$^T$, a Plant Growth-Promoting Endophyte

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***Enterobacter radicincitans* sp. nov. DSM16656$^T$ represents a new species of the genus *Enterobacter* which is a biological nitrogen-fixing endophytic bacterium with growth-promoting effects on a variety of crop and model plant species. The presence of genes for nitrogen fixation, phosphorous mobilization, and phytohormone production reflects this microbe's potential plant growth-promoting activity.**

Plant beneficial endophytic interactions are characterized by the bacterial production of phytohormones, increased nutritional uptake, and environmental stress control (4). The diazotrophic strain *Enterobacter radicincitans* DSM16656$^T$, formerly *Pantoea agglomerans*, was isolated from the phyllosphere of winter wheat under temperate climatic conditions and was described as a new species of the genus *Enterobacter*. The strain promoted the growth of roots and shoots and increased yields upon the inoculation of various plant species (2, 3, 6). While 10 genome sequences of *Enterobacter* strains have been published to date, only one displays plant growth-promoting characteristics similar to those of DSM16656$^T$, i.e., *Enterobacter* sp. strain 638, which was isolated from a poplar stem (8). The sequence of the *E. radicincitans* DSM16656$^T$ genome, presented in this work, will extend the understanding of regulatory mechanisms of endophytic colonization and host plant interaction.

Bacterial DNA was isolated from 1-day cultures using an extraction kit (Gentra Puregene Yeast/Bact. Kit; Qiagen). Next-generation sequencing technology coupled Genome Sequencer FLX (Roche), HiSeq 2000 (Ilumina), and Sanger technology for long reads, short reads, and gap closure (MWG Eurofins), leading to 20.6-fold coverage depth. The draft genome sequence of *E. radicincitans* DSM16656$^T$ presented two chromosomes with a genome size of 6,041,938 bp and a G+C content of 53%. Genome annotation was performed using the Annotation Engine service (http://ae.igs.umaryland.edu/cgi/index.cgi) (1) and visualized using the Manatee genome curation and browsing tool (http://manatee.sourceforge.net). The analysis revealed a total of 6,124 protein-coding genes, 69 tRNAs, and 9 rRNAs, which equals ~88% of the genome sequence.

Endophytic microorganisms assimilate plant metabolites and have developed mechanisms for their uptake or detoxification. The DSM16656$^T$ genome harbors 174 coding sequences for ABC transporters, 35 genes of the phosphotransferase system family, and 19 transporters from the resistance nodulation and cell division family.

Unlike plant growth-promoting *Enterobacter* sp. strain 638, DSM16656$^T$ is able to biologically fix atmospheric nitrogen (5). Besides the presence of the complete *nif* operon, comprising the *nifUBALMVSNETKDHJ* genes, the genome sequence indicates the dissimilation of nitrate (*narBLXKGHJI*) and nitrite (*nirBD*). The potential application of the strain as a biofertilizer is strengthened by the identification of genes for phosphate transporters (*pstSCAB*) and siderophore production (*fhuFCDBE*), which enhance the availability and uptake of phosphorus and iron for plant growth promotion. DSM16656$^T$ is able to produce auxin (7), and in accordance with that, we have identified genes for indole-3-acetaldehyde synthesis and an auxin efflux carrier. The genome information presented here will allow in-depth functional and comparative genome analyses to provide a better understanding of beneficial plant-bacterial associations.

**Nucleotide sequence accession numbers.** This Whole-Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. AKYD00000000. The version presented in this paper is the first version, AKYD01000000.

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