Plant growth-promoting capacity. An analysis of its 4.5-Mb draft genome will enhance the understanding of DDE degradation persistent organic pollutants (3) and are of concern to human and animal health because of their toxicity and hormone-disrupting properties (4). Endophyte-enhanced phytoremediation using Cucurbita pepo, a DDE-accumulating plant (5), is being explored for a role in the remediation of DDE-contaminated soils. A DDE-degrading bacterial strain was isolated from the roots of C. pepo plants exposed to 100 mg·liter$^{-1}$ DDE. Identified as Enterobacter aerogenes by partial 16S rRNA gene sequencing and phenotypic profiling, the closest related 16S rRNA sequence (87%) was from Enterobacter aerogenes (NCBI) (6), and the annotation was completed using the Mauve (8) was used to order contigs using the genome of E. aerogenes EA1509E (GenBank accession no. FO203355.1) (6), and the annotation was completed using the PGAP (NCBI) pipeline (9). The genome of E. aerogenes consists of a single circular chromosome (53.8% G+C content), which includes 4,191 coding genes that were arranged into 309 pathways using Pathway Tools (10, 11), 260 pseudogenes, 40 rRNAs (5S, 16S, 23S), 77 tRNAs, and 7 noncoding RNAs (ncRNAs).

This E. aerogenes strain showed increased growth when exposed to DDE in comparison to that under control conditions. Analyses of the draft genome showed the presence of dioxygenases and hydroxylases that have been associated with DDE degradation (12–15). Genes for plant growth-promoting capacities, 1-aminoacyclopropane-1-carboxylate deaminase activity, siderophore production, auxin biosynthesis, and phosphorous solubilization, are present, corroborating the results from phenotypic tests. These characteristics make E. aerogenes a promising strain for DDE phytoremediation.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/Genbank under the accession no. JXTQ00000000. The version described in this paper is version JXTQ01000000.

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