Herein, we report a draft genome sequence of the endophytic Curtobacterium sp. strain ER1/6, isolated from a surface-sterilized Citrus sinensis branch, and it presented the capability to control phytopathogens. Functional annotation of the ~3.4-Mb genome revealed 3,100 protein-coding genes, with many products related to known ecological and biotechnological aspects of this bacterium.

The plant environment is an important habitat for Curtobacterium species that may interact with their host plant, inducing disease symptoms or controlling phytopathogens. This genus was first described by Yamada and Komagata (1) and includes eight recognized Curtobacterium species (C. albium, C. ammonigenes, C. citreum, C. flaccumfaciens, C. ginsengisoli, C. herbarum, C. luticum, and C. pusillum) within the phylum Actinobacteria. The citrus endophytic Curtobacterium sp. strain ER1/6 was isolated from Citrus sinensis (sweet orange) and previously identified by fatty acid methyl ester (FAME-MIDI) as C. flaccumfaciens (2). Further analysis showed that this strain is a divergent genotype which lacks the ability to induce disease symptoms in beans and ornamental seedlings. In addition, a previous study showed that this endophytic bacterium may inhibit the citrus variegated chlo-

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