Draft Genome Sequence of *Lysobacter capsici* AZ78, a Bacterium Antagonistic to Plant-Pathogenic Oomycetes

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*Lysobacter capsici* AZ78, isolated from tobacco rhizosphere, effectively controls *Phytophthora infestans* and *Plasmodiophora viticola* on tomato and grapevine plants, respectively. We report the first draft genome sequence of the *L. capsici* species.

The bacterial genus *Lysobacter* (1) represents a source of biocontrol agents capable of protecting plants against diseases caused by pathogenic microorganisms (2). The species *Lysobacter capsici* encompasses a few bacterial strains that effectively control different plant-pathogenic bacteria, fungi, nematodes, and oomycetes (3–6). Recently, we demonstrated that applications of *L. capsici* AZ78 can control *Phytophthora infestans* and *Plasmodiophora viticola*, which are two remarkable plant-pathogenic oomycetes of tomatoes and grapevines, respectively (7). AZ78 will help elucidate the mechanism of action of this bacterial strain against plant-pathogenic oomycetes and will give background knowledge that is useful for the registration of *L. capsici* AZ78 as an active ingredient in plant protection products.

As expected, the *L. capsici* AZ78 genome contains a high number of genes coding for lytic enzymes (2). Specifically, the lytic weaponry of *L. capsici* AZ78 encompasses chitinases, glucanases, lipases, xylanases, and several enzymes with proteolytic activity.

The availability of the draft genome of *L. capsici* AZ78 will help elucidate the mechanism of action of this bacterial strain against plant-pathogenic oomycetes and will give background knowledge that is useful for the registration of *L. capsici* AZ78 as an active ingredient in plant protection products.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. JAIAC00000000. The version described in this paper is version JAIAB000000.

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**REFERENCES**


