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# High-Quality Draft Genome Sequence of *Xanthomonas alfalfae* subsp. *alfalfae* Strain CFBP 3836

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**We report the high-quality draft genome sequence of *Xanthomonas alfalfae* subsp. *alfalfae* strain CFBP 3836, the causal agent of bacterial leaf and stem spot in lucerne (*Medicago sativa*). Comparative genomics will help to decipher the mechanisms provoking disease and triggering the defense responses of this pathogen of the model legume *Medicago truncatula*.**

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*Xanthomonas alfalfae* subsp. *alfalfae* (formerly *Xanthomonas axonopodis* pv. alfalfae) is the causal agent of bacterial leaf and stem spot of lucerne (*Medicago sativa*) (1, 2). While lucerne is the main host of *X. alfalfae* subsp. *alfalfae*, other hosts, such as soybean (*Glycine max*), clover (*Trifolium* spp.), and vetch (*Vicia* spp.), have been reported (3). *X. alfalfae* subsp. *alfalfae* is also pathogenic on the model legume *Medicago truncatula* (4). Lesions first appear on the leaf as water-soaked spots surrounded by a diffuse chlorotic area, which then turns dry, yellow-brown, and papery. Severe defoliation is a common result of leaf infection. Postemergence damping off, stunting of seedlings, and damage of lucerne stands are other symptoms. This seed-borne disease may cause severe losses in hot, moist environments (3). To better understand the molecular basis of legume-bacterium interactions, we sequenced the genome of the *X. alfalfae* subsp. *alfalfae* strain CFBP 3836. This strain is the pathotype strain of the former pathovar *X. axonopodis* pv. alfalfae (5). This strain originates from the Sudan (http://www.angers-nantes.inra.fr/cfbp/resultnum_e.php?r0=3836).

This genome was sequenced using the Illumina HiSeq 2000 platform (GATC Biotech, Germany). Shotgun sequencing yielded 116,576,062 read pairs (37,799,928 100-bp paired-end reads with an insert size of ca. 250 bp and 78,776,134 bp mate-pair reads with an insert size of approximately 3 kb). A combination of Velvet (6), SOAP*denovo*, and SOAP Gapcloser (7) yielded 22 contigs $>$500 bp ($N_{50}$, 763,181 bp), with the largest contig being 2,433,808 bp, for a total assembly size of 5,077,532 bp. Multilocus sequence analyses of seven housekeeping genes described earlier for xanthomonads confirmed that strain CFBP 3836 belongs to *X. alfalfae* subsp. *alfalfae* (8).

The genome carries the core characteristics shared by most plant-pathogenic xanthomonads, including chemotaxis- and flagellum-encoding genes, many genes encoding two-component systems, and TonB-dependent transporters. This genome sequence displays the genes coding for the six secretion systems (from T1SS to T6SS) that have been identified so far in Gram-negative bacteria and multiple effectors. A minimum repertoire of 23 type III effectors is predicted. It comprises two putative transcription activator-like effectors, the highly repetitive sequence of which could not be completely resolved with this sequencing strategy. This genome sequence will be a valuable tool for transcriptomic and genetic studies to allow for a better understanding of disease development and plant defense triggering in legume-bacterium interactions.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited in GenBank under the accession no. AUWN00000000. The version described in this paper is the first version, AUWN01000000.

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