Draft Genome Sequence of *Xanthomonas axonopodis* pv. allii Strain CFBP 6369

L. Gagnevin,[a] S. Bolot,[b,c] J. L. Gordon,[d] O. Pruvost,[a] C. Vernière,[a] I. Robène,[a] M. Arlat,[b,c,e] L. D. Noël,[b,c] S. Carrère,[b,c] M.-A. Jacques,[f,g,h] R. Koebnik[i]

CIRAD, UMR Peuplements Végétaux et Bioagresseurs en Milieu Tropical (PVBMT), Saint-Pierre, La Réunion, France[a]; INRA, Laboratoire des Interactions Plantes Micro-Organismes (LIPM), UMR 441, Castanet-Tolosan, France[b]; CNRS, Laboratoire des Interactions Plantes Micro-Organismes (LIPM), UMR 2594, Castanet-Tolosan, France[c]; Université de la Réunion, UMR Peuplements Végétaux et Bioagresseurs en Milieu Tropical (PVBMT), Saint-Pierre, La Réunion, France[d]; Université de Toulouse, Université Paul Sabatier, Toulouse, France[e]; INRA, Institut de Recherche en Horticulture et Semences (IRHS) and UMR 1345 SFR 4207 QUASAV, Beaucouzé, France[f]; Université d'Angers, Institut de Recherche en Horticulture et Semences (IRHS) and UMR 1345 SFR 4207 QUASAV, Beaucouzé, France[g]; Agrocampus Ouest, Institut de Recherche en Horticulture et Semences (IRHS), UMR 1345 SFR 4207 QUASAV, Beaucouzé, France[h]; IRD, UMR 186 IRD-CIRAD-Université Montpellier 2 Résistance des Plantes aux Bioagresseurs, Montpellier, France[i]

L.G. and S.B. contributed equally to this study.

We report here the draft genome sequence of *Xanthomonas axonopodis* pv. allii strain CFBP 6369, the causal agent of bacterial blight of onion. The draft genome has a size of 5,425,942 bp and a G+C content of 64.4%.

Address correspondence to L. Gagnevin, lionel.gagnevin@cirad.fr.

*X*anthomonas axonopodis* pv. allii is the causal agent of bacterial blight of onion (*Allium cepa*) and other *Allium* species (1, 2). First reported in 1978 (3), the disease has been emerging since the 1990s. It is included in the A1 list of pathogens of the European and Mediterranean Plant Protection Organization (EPPO). Lesions on leaves infected with this pathogen begin as small water-soaked spots that enlarge into chlorotic lesions and collapse at the point of initial infection, causing a reduction in bulb size. The bacterium can contaminate seeds, which are a major source of inoculum (4, 5), together with diseased plants and plant debris, epiphytically polluted *Allium* or weed species, and irrigation water. Seed trade is responsible for long-distance dissemination (6, 7). Yield losses can reach 50% and are favored by high temperature and humidity. The control of the disease can be partially achieved through integrated pest management (8, 9) and should improve with better knowledge of the bacterium and its interaction with its host species. *X. axonopodis* pv. allii strains are more genetically diversified and less host specialized than is usually expected for a *Xanthomonas* pathovar. They belong to the genetically diverse group 9.2 of *X. axonopodis* (1) and are probably polyphyletic (10). Strain CFBP 6369, isolated in 1996 in Réunion Island, France, was chosen because its genetic, physiologic, and pathogenic characteristics are representative of the pathovar (1).

Strain CFBP 6369 was sequenced using the Illumina HiSeq 2000 platform (GATC Biotech, Germany). The shotgun sequencing yielded 35,091,791 read pairs (21,359,123 100-bp paired-end reads with an insert size of ca. 250 bp, and 13,732,668 50-bp mate-pair reads with an insert size of ca. 3 kb). A combination of Velvet (11), SOAP*denovo*, and SOAPGapCloser (12) yielded 13 contigs >500 bp (N_{50}, 1,415,587 bp), with the largest contig being 1,460,767 bp, for a total assembly size of 5,425,942 bp. The G+C content was 64.4%. Genomic contigs were annotated using the EuGene-P annotation pipeline to identify RNAs and protein-coding genes (13). The draft genome of strain CFBP 6369 was predicted to contain 4,963 coding sequences (CDSs).

The genome of strain CFBP 6369 has an average nucleotide identity (ANI) close to 99% (14) with other xanthomonads in the 9.2 group, while it shares <95% ANI with strains from groups 9.5 and 9.6. *X. axonopodis* pv. allii has a gene content similar to those of other xanthomonads, with a large representation of two-component system sensor and regulatory proteins, methyl-accepting chemotaxis proteins, ATP-binding cassette (ABC) transporters, major facilitator superfamily (MFS) transporters, TonB-dependent receptors, and transcriptional regulators. It contains a complete set of genes coding for the hypersensitive response and pathogenicity (HRP) type III secretion system and a minimal repertoire of 22 putative type III effector genes: *avrBs2*, *xopA*, *xopAD*, *xopAE*, *xopAJ*, *xopAK*, *xopC2*, *xopE1*, *xopF1*, *xopF2*, *xopI*, *xopJ*, *xopK*, *xopL*, *xopN*, *xopP*, *xopQ*, *xopR*, *xopV*, *xopX*, *xopZ1*, and *xopAP*. This resource will be instrumental for dissecting the genetic and molecular basis of *X. axonopodis* pv. allii pathogenicity on *Alliaceae*, investigating the natural genomic diversity of this emerging plant pathogen, and improving diagnostics.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in GenBank under the accession no. JOJQ00000000. The version described in this paper is the first version, JOJQ01000000.

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