



HAL
open science

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

Lionel Gagnevin, Stéphanie Bolot, J L Gordon, Olivier Pruvost, Christian Vernière, Isabelle Robene-Soustrade, Matthieu Arlat, Laurent Noel, Sebastien Carrere, Marie Agnes Jacques, et al.

► **To cite this version:**

Lionel Gagnevin, Stéphanie Bolot, J L Gordon, Olivier Pruvost, Christian Vernière, et al.. Draft Genome Sequence of *Xanthomonas axonopodis* pv. *allii* Strain CFBP 6369.. *Genome Announcements*, 2014, 2 (4), <10.1128/genomeA.00727-14>. <hal-01209994>

HAL Id: hal-01209994

<https://hal.science/hal-01209994v1>

Submitted on 21 Jun 2018

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons CC BY 4.0 - Attribution - International License

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. Koebnikⁱ

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, Beaucauzé, France^f; Université d'Angers, Institut de Recherche en Horticulture et Semences (IRHS) and UMR 1345 SFR 4207 QUASAV, Beaucauzé, France^g; Agrocampus Ouest, Institut de Recherche en Horticulture et Semences (IRHS), UMR 1345 SFR 4207 QUASAV, Beaucauzé, France^h; IRD, UMR 186 IRD-CIRAD-Université Montpellier 2 Résistance des Plantes aux Bioagresseurs, Montpellier, Franceⁱ

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%.

Received 7 July 2014 Accepted 16 July 2014 Published 31 July 2014

Citation Gagnevin L, Bolot S, Gordon JL, Pruvost O, Vernière C, Robène I, Arlat M, Noël LD, Carrière S, Jacques M-A, Koebnik R. 2014. Draft genome sequence of *Xanthomonas axonopodis* pv. *allii* strain CFBP 6369. *Genome Announc*. 2(4):e00727-14. doi:10.1128/genomeA.00727-14.

Copyright © 2014 Gagnevin et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

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

Xanthomonas 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), SOAPdenovo, 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.

ACKNOWLEDGMENTS

This work was supported by the French Agence Nationale de la Recherche (no. ANR-2010-GENM-013, ANR-10-LBX-41, and ANR-11-IDEX-0002-02). Funding was also received from the European Union Seventh

Framework Programme (FP7/2007-2013) under grant agreement no. 263958 (RUN-Emerge project).

REFERENCES

1. Roumagnac P, Gagnevin L, Gardan L, Sutra L, Manceau C, Dickstein ER, Jones JB, Rott P, Pruvost O. 2004. Polyphasic characterization of xanthomonads isolated from onion, garlic and Welsh onion (*Allium* spp.) and their relatedness to different *Xanthomonas* species. *Int. J. Syst. Evol. Microbiol.* 54:15–24. <http://dx.doi.org/10.1099/ijs.0.02714-0>.
2. Gent DH, Schwartz HF, Ishimaru CA, Louws FJ, Cramer RA, Lawrence CB. 2004. Polyphasic characterization of *Xanthomonas* strains from onion. *Phytopathology* 94:184–195. <http://dx.doi.org/10.1094/PHYTO.2004.94.2.184>.
3. Alvarez AM, Buddenhagen IW, Buddenhagen ES, Domen HY. 1978. Bacterial blight of onion, a new disease caused by *Xanthomonas* sp. *Phytopathology* 68:1132–1136. <http://dx.doi.org/10.1094/Phyto-68-1132>.
4. Picard Y, Roumagnac P, Legrand D, Humeau L, Robène-Soustrade I, Chiroleu F, Gagnevin L, Pruvost O. 2008. Polyphasic characterization of *Xanthomonas axonopodis* pv. *allii* associated with outbreaks of bacterial blight on three *Allium* species in the Mascarene archipelago. *Phytopathology* 98:919–925. <http://dx.doi.org/10.1094/PHYTO-98-8-0919>.
5. Roumagnac P, Gagnevin L, Pruvost O. 2000. Detection of *Xanthomonas* sp., the causal agent of onion bacterial blight, in onion seeds using a newly developed semi-selective isolation medium. *Eur. J. Plant Pathol.* 106: 867–877. <http://dx.doi.org/10.1023/A:1008743120242>.
6. Gent DH, Lang JM, Bartolo ME, Schwartz HR. 2005. Inoculum sources and survival of *Xanthomonas axonopodis* pv. *allii* in Colorado. *Plant Dis.* 89:507–514. <http://dx.doi.org/10.1094/PD-89-0507>.
7. Gent DH, Lang JM, Schwartz HF. 2005. Epiphytic survival of *Xanthomonas axonopodis* pv. *allii* and *X. axonopodis* pv. *phaseoli* on leguminous hosts and onion. *Plant Dis.* 89:558–564. <http://dx.doi.org/10.1094/PD-89-0558>.
8. Lang JM, Gent DH, Schwartz HF. 2007. Management of *Xanthomonas* leaf blight of onion with bacteriophages and a plant activator. *Plant Dis.* 91:871–878. <http://dx.doi.org/10.1094/PDIS-91-7-0871>.
9. Robène-Soustrade I, Legrand D, Gagnevin L, Chiroleu F, Laurent A, Pruvost O. 2010. Multiplex nested PCR for detection of *Xanthomonas axonopodis* pv. *allii* from onion seeds. *Appl. Environ. Microbiol.* 76: 2697–2703. <http://dx.doi.org/10.1128/AEM.02697-09>.
10. Gent DH, Al-Saadi A, Gabriel DW, Louws FJ, Ishimaru CA, Schwartz HF. 2005. Pathogenic and genetic relatedness among *Xanthomonas axonopodis* pv. *allii* and other pathovars of *X. axonopodis*. *Phytopathology* 95:918–925. <http://dx.doi.org/10.1094/PHYTO-95-0918>.
11. Zerbino DR, Birney E. 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. *Genome Res.* 18:821–829. <http://dx.doi.org/10.1101/gr.074492.107>.
12. Luo R, Liu B, Xie Y, Li Z, Huang W, Yuan J, He G, Chen Y, Pan Q, Liu Y, Tang J, Wu G, Zhang H, Shi Y, Liu Y, Yu C, Wang B, Lu Y, Han C, Cheung DW, Yiu SM, Peng S, Xiaoqian Z, Liu G, Liao X, Li Y, Yang H, Wang J, Lam TW, Wang J. 2012. SOAPdenovo2: an empirically improved memory-efficient short-read *de novo* assembler. *GigaScience.* 1:18. <http://dx.doi.org/10.1186/2047-217X-1-18>.
13. Sallet E, Roux B, Sauviac L, Jardinaud MF, Carrère S, Faraut T, de Carvalho-Niebel F, Gouzy J, Gamas P, Capela D, Bruand C, Schiex T. 2013. Next-generation annotation of prokaryotic genomes with EuGene-P: application to *Sinorhizobium meliloti* 2011. *DNA Res.* 20: 339–354. <http://dx.doi.org/10.1093/dnares/dst014>.
14. Goris J, Konstantinidis KT, Klappenbach JA, Coenye T, Vandamme P, Tiedje JM. 2007. DNA-DNA hybridization values and their relationship to whole-genome sequence similarities. *Int. J. Syst. Evol. Microbiol.* 57: 81–91. <http://dx.doi.org/10.1099/ijs.0.64483-0>.