



Draft Genome Sequences of Two *Xanthomonas euvesicatoria* Strains from the Balkan Peninsula

Taca Vancheva, Pierre Lefeuvre, Nevena Bogatzevska, Penka Moncheva, Ralf Koebnik

► To cite this version:

Taca Vancheva, Pierre Lefeuvre, Nevena Bogatzevska, Penka Moncheva, Ralf Koebnik. Draft Genome Sequences of Two *Xanthomonas euvesicatoria* Strains from the Balkan Peninsula. *Genome Announcements*, 2015, 3 (1), pp.e01528-14. 10.1128/genomeA.01528-14 . hal-03625220

HAL Id: hal-03625220

<https://hal.science/hal-03625220>

Submitted on 12 Jan 2023

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 Attribution 4.0 International License

Draft Genome Sequences of Two *Xanthomonas vesicatoria* Strains from the Balkan Peninsula

Taca Vancheva,^{a,b} Nevena Bogatzevska,^c Penka Moncheva,^a Pierre Lefevvre,^d  Ralf Koebnik^b

Faculty of Biology, Sofia University St. Kliment Ohridski, Sofia, Bulgaria^a; UMR 186 IRD-Cirad-Université Montpellier 2 Résistance des Plantes aux Bioagresseurs, Montpellier, France^b; Institute of Soil Science, Agrotechnologies, and Plant Protection Nikola Poushkarov, Sofia, Bulgaria^c; CIRAD, UMR PVBMT, Pôle de Protection des Plantes, Saint-Pierre, Ile de la Réunion, France^d

***Xanthomonas vesicatoria* causes bacterial spot disease of pepper and tomato plants. We report here the first genome sequences of *X. vesicatoria* strains that have been isolated from pepper plants. These data will be used for comparative genomics and will allow the development of new detection and typing tools for epidemiological surveillance.**

Received 29 December 2014 Accepted 5 January 2015 Published 12 February 2015

Citation Vancheva T, Bogatzevska N, Moncheva P, Lefevvre P, Koebnik R. 2015. Draft genome sequences of two *Xanthomonas vesicatoria* strains from the Balkan Peninsula. *Genome Announc* 3(1):e01558-14. doi:10.1128/genomeA.01558-14.

Copyright © 2015 Vancheva 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/4.0/).

Address correspondence to Ralf Koebnik, koebnik@gmx.de.

Xanthomonas vesicatoria is one of the causal agents of bacterial spot disease on pepper and tomato plants (1). The disease symptoms include chlorotic and necrotic lesions on leaves, stems, petioles, fruits, and flowers, as well as defoliation. Bacterial spot disease is present worldwide where environmental conditions are suitable for the pathogen. The disease is one of the economically most important plant diseases on the Balkan Peninsula (2, 3), with annual losses reaching 10 to 20% (4). Bacterial spots of tomato were first recorded in Bulgaria in 1936 (5). Later, the disease was also reported on pepper plants in Bulgaria (6). The first report of bacterial spot disease in Macedonia dates back to 1999 (3). Current control of the disease is mainly based on agricultural practices and the use of copper compounds. In order to develop new molecular markers for epidemiological surveillance, such as variable-number tandem repeats (VNTR) (7), we sequenced the genomes of two strains from the Balkan Peninsula.

Strain 15b, isolated from *Capsicum annuum* in Sofia, Bulgaria, in 2005, and strain 53M, isolated from *C. annuum* in Strumitsa, Macedonia, in 2005, were chosen as representative *X. vesicatoria* strains from the Balkan Peninsula based on their pathogenic, physiologic, and genetic characteristics (8). Their genomes were sequenced using the Illumina HiSeq 2500 platform (Fasteris SA, Switzerland). The shotgun sequencing yielded 2,163,782 100-bp paired-end reads (541 Mb) for strain 15b and 2,007,779 paired-end reads (502 Mb) for strain 53M, with insert sizes ranging from 250 bp to 1.5 kb. The draft genome sequences were assembled using the Edena algorithm version 3.131028 (9), yielding 303 contigs of >500 bp (N_{50} , 31,449 bp) for strain 15b and 320 contigs (N_{50} , 29,340 bp) for strain 53M. The contigs were annotated with GeneMarkS+ release 2.9 (revision 452131) (10), as implemented in the NCBI Prokaryotic Genome Annotation Pipeline (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/), which predicted a total of 4,601 genes for strain 15b and 4,624 genes for strain 53M.

Combined with the draft genome sequence of the New Zealand strain *X. vesicatoria* ATCC 35937, which was isolated from *Lycopersicon*

lycopersicum (11), these genomic resources will aid in the development of new diagnostic tools, such as multilocus VNTR analyses (MLVA), which have been proven to be powerful tools for studying bacterial phytopathogen populations (12–15). In addition, these genome sequences may give new insight into the pathogen-host interaction. For instance, a comparison of the predicted repertoires of type III effectors with the effector repertoire of the tomato isolate *X. vesicatoria* ATCC 35937 revealed that both pepper isolates appear to lack *xopD*, *xopE2*, and *xopJ2*. Contrariwise, the pepper isolates possess homologs of *avrBs1* and *xopH*, which were not found in strain ATCC 35937. Both genes are in tandem arrangement and might be located on a plasmid, as in *Xanthomonas euvesicatoria* strain 85-10 (16). More sequencing and pathotyping are required to assess the importance of these effectors with respect to the host plants.

Nucleotide sequence accession numbers. These whole-genome shotgun projects have been deposited at DDBJ/EMBL/GenBank under the accession numbers JSXZ00000000 (strain 15b) and JSYJ00000000 (strain 53M). The versions described in this paper are the first versions, JSXZ01000000 and JSYJ01000000.

ACKNOWLEDGMENTS

This work was supported by grant BG051PO001-3.3.05-000, financed by Operational Program “Human resources development” and cofinanced by the European Social Fund of the European Union.

T.V. thanks the European Union Erasmus+ Program for support.

REFERENCES

1. Jones JB, Lacy GH, Bouzar H, Stall RE, Schaad NW. 2004. Reclassification of the xanthomonads associated with bacterial spot disease of tomato and pepper. *Syst Appl Microbiol* 27:755–762. <http://dx.doi.org/10.1078/0723202042369884>.
2. Bogatzevska N, Stoimenova E, Mitrev S. 2007. Bacterial and virus diseases spread in Bulgaria and Macedonia on field and greenhouse pepper. *Plant Protect* 18:17–21.
3. Mitrev S, Pejcinovski F. 1999. Characterization of *Xanthomonas campestris* pv. *vesicatoria*, causal agent of bacterial spot of pepper, cv. *Kurtovska*

- kapija*, p 151–163, vol X. In Yearbook for plant protection. Society of Plant Protection of Republic of Macedonia, Skopje, Macedonia.
4. Mitrev S. 2001. Phytopathogenic bacteria of pepper in Macedonia. PSI Institute of Southern Crops Strumica, Strumica, Macedonia.
 5. Kovachevski I. 1936. New parasitic fungi in Bulgaria. *Trudove na Bulgarskoto prirodoizpitvatelno druzhestvo* 7:13–24.
 6. Karov S. 1965. *Xanthomonas vesicatoria* (Doidge) Dowson of pepper, p 245–250, vol 14. Scientific Publishing, High Agricultural Institute, Plovdiv, Bulgaria.
 7. van Belkum A. 2007. Tracing isolates of bacterial species by multilocus variable number of tandem repeat analysis (MLVA). *FEMS Immunol Med Microbiol* 49:22–27. <http://dx.doi.org/10.1111/j.1574-695X.2006.00173.x>.
 8. Kizheva Y, Vancheva T, Hristova P, Stoyanova M, Bogatzevska N, Moncheva P. 2011. Diversity of *Xanthomonas* spp. causal agents of bacterial spot on pepper and tomato plants in Bulgaria. *Biotechnol Biotechnol Equip* 25:98–104. <http://dx.doi.org/10.5504/BBEQ.2011.0126>.
 9. Hernandez D, Tewhey R, Veyrieras JB, Farinelli L, Østerås M, François P, Schrenzel J. 2014. *De novo* finished 2.8 Mbp *Staphylococcus aureus* genome assembly from 100 bp short and long range paired-end reads. *Bioinformatics* 30:40–49. <http://dx.doi.org/10.1093/bioinformatics/btt590>.
 10. Borodovsky M, Lomsadze A. 2014. Gene identification in prokaryotic genomes, phages, metagenomes, and EST sequences with GeneMarkS suite. *Curr Protoc Microbiol* 32:7. <http://dx.doi.org/10.1002/9780471729259.mc01e07s32>.
 11. Potnis N, Krasileva K, Chow V, Almeida NF, Patil PB, Ryan RP, Sharlach M, Behlau F, Dow, Potnis N, Krasileva K, Chow V, Almeida NF, Patil PB, Ryan RP, Sharlach M, Behlau F, Dow JM, Momol M, White FF, Preston JF, Vinatzer BA, Koebnik R, Setubal JC, Norman DJ, Staskawicz BJ, Jones JB. 2011. Comparative genomics reveals diversity among xanthomonads infecting tomato and pepper. *BMC Genomics* 12: 146. <http://dx.doi.org/10.1186/1471-2164-12-146>.
 12. Pruvost O, Magne M, Boyer K, Leduc A, Tourterel C, Drevet C, Ravigné V, Gagnevin L, Guérin F, Chiroleu F, Koebnik R, Verdier V, Vernière C. 2014. A MLVA genotyping scheme for global surveillance of the citrus pathogen *Xanthomonas citri* pv. *citri* suggests a worldwide geographical expansion of a single genetic lineage. *PLoS One* 9:e98129. <http://dx.doi.org/10.1371/journal.pone.0098129>.
 13. Trujillo CA, Arias-Rojas N, Poulin L, Medina CA, Tapiero A, Restrepo S, Koebnik R, Bernal AJ. 2014. Population typing of the causal agent of cassava bacterial blight in the eastern plains of Colombia using two types of molecular markers. *BMC Microbiol* 14:161. <http://dx.doi.org/10.1186/1471-2180-14-161>.
 14. Bühlmann A, Dreö T, Rezzonico F, Pothier JF, Smits TH, Ravnika M, Frey JE, Duffy B. 2014. Phylogeography and population structure of the biologically invasive phytopathogen *Erwinia amylovora* inferred using minisatellites. *Environ Microbiol* 16:2112–2125. <http://dx.doi.org/10.1111/1462-2920.12289>.
 15. Poulin L, Grygiel P, Magne M, Gagnevin L, Rodriguez R, LM, Forero Serna N, Zhao S, El Rafii M, Dao S, Tekete C, Koita O, Pruvost O, Verdier V, Vernière C, Koebnik R. 2014. New multilocus variable-number tandem-repeat analysis tool for surveillance and local epidemiology of bacterial leaf blight and bacterial leaf streak of rice caused by *Xanthomonas oryzae*. *Appl Environ Microbiol* 81:688–698. <http://dx.doi.org/10.1128/AEM.02768-14>.
 16. Thieme F, Koebnik R, Bekel T, Berger C, Boch J, Büttner D, Caldana C, Gaigalat L, Goesmann A, Kay S, Kirchner O, Lanz C, Linke B, McHardy AC, Meyer F, Mittenhuber G, Nies DH, Niesbach-Klösgen U, Patschkowski T, Rückert C, Rupp O, Schneiker S, Schuster SC, Vorhölter FJ, Weber E, Pühler A, Bonas U, Bartels D, Kaiser O. 2005. Insights into genome plasticity and pathogenicity of the plant pathogenic bacterium *Xanthomonas campestris* pv. *vesicatoria* revealed by the complete genome sequence. *J Bacteriol* 187:7254–7266. <http://dx.doi.org/10.1128/JB.187.21.7254-7266.2005>.