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Draft Genome Sequence of *Xylella fastidiosa* Pear Leaf Scorch Strain in Taiwan

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The draft genome sequence of *Xylella fastidiosa* pear leaf scorch strain PLS229, isolated from the pear cultivar Hengshan (*Pyrus pyrifolia*) in Taiwan, is reported here. The bacterium has a genome size of 2,733,013 bp, with a G+C content of 53.1%. The PLS229 genome was annotated and has 3,259 open reading frames and 50 RNA genes.

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Xylella fastidiosa, a Gram-negative bacterium, causes pear leaf scorch (PLS) disease in Taiwan (1). The disease was observed around 1991 in the area where the low-chilling pear cultivar Hengshan (*Pyrus pyrifolia*) was grown. The pathogen resides in the xylem tissues of the host plant and can be transmitted through grafting. The PLS strain is one of the few *X. fastidiosa* strains reported outside the Americas (1–3). Early serological tests indicated that the PLS strain is unique compared to other known *X. fastidiosa* strains (1). Analyses using DNA-DNA hybridization (4), sequences of 16S rRNA genes and 16S-23S rRNA intergenic transcribed sequences (16S-23S ITS) (5), sequences from 18 genomic loci (6), and randomly amplified polymorphic DNA (RAPD) profiles (7) further confirmed that the PLS strain is distinct from the currently known subspecies, i.e., *X. fastidiosa* subsp. *fastidiosa*, *X. fastidiosa* subsp. *multiplex*, and *X. fastidiosa* subsp. *pauca* (8).

X. fastidiosa is nutritionally fastidious (9). Characterization of the bacterium through the traditional cultivation-based methodologies has yielded limited information. Whole-genome sequencing has been an efficient technique for generating biological information for fastidious prokaryotes. Both complete and shotgun whole sequences of the known subspecies of *X. fastidiosa* have been published (10–17). Here, we report a draft whole-genome sequence of an *X. fastidiosa* PLS strain.

X. fastidiosa strain PLS229 was isolated from the symptomatic pear cultivar Hengshan (*Pyrus pyrifoliae*) at Houli (24°20'14"N, 120°44'11"E), Taiwan, and triple-cloned. To obtain genomic DNA, strain PLS229 was cultured in PD2 broth (18) at 28°C for 5 to 6 days. The bacterial cells were collected by centrifugation. Total genomic DNA was extracted according to a procedure described previously (5). Genome sequencing was carried out on a 454 GS-FLX system using Titanium chemistry (Roche) (19). Paired-end reads were assembled with the Newbler software (version 2.6; Roche Diagnostics). The PLS229 genome consists of 2,733,013 bp (~20× coverage; G+C content, 53.1%) assembled into 85 contigs ranging from 525 bp to 230,364 bp. Annotation

was performed by the RAST server (<http://rast.nmpdr.org/>) (20), which utilized GeneMark, Glimmer, and tRNAscan-SE searches. The PLS229 genome was predicted to have a total of 3,259 open reading frames (ORFs) and 50 RNA genes.

The sequences of *ssr* (16S rRNA) and three housekeeping genes, *gyrB* (DNA gyrase subunit B), *dnaK* (chaperone protein), and *rpoD* (RNA polymerase sigma factor), were selected and compared, using BLAST analyses (21), to the corresponding gene sequences of *X. fastidiosa* strains deposited in GenBank. The *ssr* sequence shares 100% similarity to that of the previously published *X. fastidiosa* PLS strain (5) and 99% similarity to those of *X. fastidiosa* subsp. *fastidiosa* (strains Temecula1 and M23), *X. fastidiosa* subsp. *multiplex* (strain M12), and *X. fastidiosa* subsp. *pauca* (strain 9a5c). All these further confirmed that the sequenced bacterial strain is a member of *X. fastidiosa*. Strain PLS229 is similar to all three subspecies of *X. fastidiosa* (strains 9a5c, M12, M23, and Temecula1), with 88% at locus *gyrB*, 89% at locus *dnaK*, and 88% at locus *rpoD*, suggesting the uniqueness of strain PLS229.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [JDSQ000000000](https://www.ncbi.nlm.nih.gov/nuccore/JDSQ000000000). The version described in this paper is version [JDSQ010000000](https://www.ncbi.nlm.nih.gov/nuccore/JDSQ010000000).

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REFERENCES

1. Leu LS, Su CC. 1993. Isolation, cultivation, and pathogenicity of *Xylella fastidiosa*, the causal bacterium of pear leaf scorch disease in Taiwan. *Plant Dis.* 77:642–646. <http://dx.doi.org/10.1094/PD-77-0642>.
2. Berisha B, Chen YD, Zhang GY, Xu BY, Chen TA. 1998. Isolation of

- Pierce's disease bacteria from grapevines in Europe. *Eur. J. Plant Pathol.* 104:427–433. <http://dx.doi.org/10.1023/A:1008655621235>.
3. Su C-C, Chang C-J, Chang C-M, Shih H-T, Tzeng K-C, Jan F-J, Kao C-W, Deng W-L. 2013. Pierce's disease of grapevines in Taiwan: isolation, cultivation and pathogenicity of *Xylella fastidiosa*. *J. Phytopathol.* 161: 389–396. <http://dx.doi.org/10.1111/jph.12075>.
 4. Mehta A, Rosato YB. 2001. Phylogenetic relationships of *Xylella fastidiosa* strains from different hosts, based on 16S rDNA and 16S–23S intergenic spacer sequences. *Int. J. Syst. Evol. Microbiol.* 51:311–318. <http://ijs.sgmjournals.org/content/51/2/311.full.pdf+html>.
 5. Su CC, Chang CJ, Yang WJ, Hsu ST, Tzeng KC, Jan FJ, Deng WL. 2012. Specific characters of 16S rRNA gene and 16S–23S rRNA internal transcribed spacer sequences of *Xylella fastidiosa* pear leaf scorch strains. *Eur. J. Plant Pathol.* 132:203–216. <http://dx.doi.org/10.1007/s10658-011-9863-6>.
 6. Chen J, Su C, Chang C. 2006. Multigenic sequence comparison of *Xylella fastidiosa* pear leaf scorch strains from Taiwan to strains from Americas. *Phytopathology* 96:S23. <http://apsjournals.apsnet.org/doi/pdf/10.1094/PHYTO.2006.96.6.S1>.
 7. Su CC, Yang WJ, Feng CY, Hsu ST, Tzeng KC. 2008. The application of DNA fingerprintings amplified by arbitrary primers in differentiating pear leaf scorch bacterium from other *Xylella fastidiosa* strains. *Plant. Pathol. Bull.* 17:183–194. (In Chinese with English abstract.) <http://140.112.183.1/cpps/pdf/17-3/183-194.pdf>.
 8. Schaad NW, Postnikova E, Lacy G, Fatmi M, Chang CJ. 2004. *Xylella fastidiosa* subspecies: *X. fastidiosa* subsp. [correction] *fastidiosa* [correction] subsp. nov., *X. fastidiosa* subsp. *multiplex* subsp. nov., and *X. fastidiosa* subsp. *pauca* subsp. nov. *Syst. Appl. Microbiol.* 27:290–300. <http://dx.doi.org/10.1078/0723-2020-00263>.
 9. Wells JM, Raju BC, Huang H-Y, Weisburg WG, Mandelco-Paul L, Brenner DJ. 1987. *Xylella fastidiosa* gen. nov., sp. nov.: gram-negative, xylem-limited, fastidious plant bacteria related to *Xanthomonas* spp. *Int. J. Syst. Bacteriol.* 37:136–143. <http://dx.doi.org/10.1099/00207713-37-2-136>.
 10. Alencar VC, Barbosa D, Santos DS, Oliveira AC, de Oliveira RC, Nunes LR. 2014. Genomic sequencing of two coffee-infecting strains of *Xylella fastidiosa* isolated from Brazil. *Genome Announc.* 2(1):e01190-13. <http://dx.doi.org/10.1128/genomeA.01190-13>.
 11. Chen J, Xie G, Han S, Chertkov O, Sims D, Civerolo EL. 2010. Whole genome sequences of two *Xylella fastidiosa* strains (M12 and M23) causing almond leaf scorch disease in California. *J. Bacteriol.* 192:4534. <http://dx.doi.org/10.1128/JB.00651-10>.
 12. Chen J, Huang H, Chang CJ, Stenger DC. 2013. Draft genome sequence of *Xylella fastidiosa* subsp. *multiplex* strain griffin-1 from *Quercus rubra* in Georgia. *Genome Announc.* 1(5):e00756-13. <http://dx.doi.org/10.1128/genomeA.00756-13>.
 13. Bhattacharyya A, Stilwagen S, Reznik G, Feil H, Feil WS, Anderson I, Bernal A, D'Souza M, Ivanova N, Kapatral V, Larsen N, Los T, Lykidis A, Selkov E, Jr, Walunas TL, Purcell A, Edwards RA, Hawkins T, Haselkorn R, Overbeek R, Kyrpidis NC, Predki PF. 2002. Draft sequencing and comparative genomics of *Xylella fastidiosa* strains reveal novel biological insights. *Genome Res.* 12: 1556–1563. <http://dx.doi.org/10.1101/gr.370702>.
 14. Schreiber HL, IV, Koirala M, Lara A, Ojeda M, Dowd SE, Bextine B, Morano L. 2010. Unraveling the first *Xylella fastidiosa* subsp. *fastidiosa* genome from Texas. *Southwest. Entomol.* 35:479–483. <http://dx.doi.org/10.3958/059.035.0336>.
 15. Simpson AJ, Reinach FC, Arruda P, Abreu FA, Acencio M, Alvarenga R, Alves LM, Araya JE, Baia GS, Baptista CS, Barros MH, Bonaccorsi ED, Bordin S, Bové JM, Briones MR, Bueno MR, Camargo AA, Camargo LE, Carraro DM, Carrer H, Colauto NB, Colombo C, Costa FF, Costa MC, Costa-Neto CM, Coutinho LL, Cristofani M, Dias-Neto E, Docena C, El-Dorry H, Facincani AP, Ferreira AJ, Ferreira VC, Ferro JA, Fraga JS, França SC, Franco MC, Frohme M, Furlan LR, Garnier M, Goldman GH, Goldman MH, Gomes SL, Gruber A, Ho PL, Hoheisel JD, Junqueira ML, Kemper EL, Kitajima JP, Krieger JE, et al. 2000. The genome sequence of the plant pathogen *Xylella fastidiosa*. The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing and Analysis. *Nature* 406:151–159. <http://dx.doi.org/10.1038/35018003>.
 16. Van Sluys MA, de Oliveira MC, Monteiro-Vitorello CB, Miyaki CY, Furlan LR, Camargo LE, da Silva AC, Moon DH, Takita MA, Lemos EG, Machado MA, Ferro MI, da Silva FR, Goldman MH, Goldman GH, Lemos MV, El-Dorry H, Tsai SM, Carrer H, Carraro DM, de Oliveira RC, Nunes LR, Siqueira WJ, Coutinho LL, Kimura ET, Ferro ES, Harakava R, Kuramae EE, Marino CL, Giglioti E, Abreu IL, Alves LM, do Amaral AM, Baia GS, Blanco SR, Brito MS, Cannavan FS, Celestino AV, da Cunha AF, Fenille RC, Ferro JA, Formighieri EF, Kishi LT, Leoni SG, Oliveira AR, Rosa VE, Jr, Sasaki FT, Sena JA, de Souza AA, Truffi D, et al. 2003. Comparative analyses of the complete genomes sequences of Pierce's disease and citrus variegated chlorosis strains of *Xylella fastidiosa*. *J. Bacteriol.* 185:1018–1026. <http://dx.doi.org/10.1128/JB.185.3.1018-1026.2003>.
 17. Zhang S, Flores-Cruz Z, Kumar D, Chakrabarty P, Hopkins DL, Gabriel DW. 2011. The *Xylella fastidiosa* biocontrol strain EB92-1 genome is very similar and syntenic to Pierce's disease strains. *J. Bacteriol.* 193: 5576–5577. <http://dx.doi.org/10.1128/JB.05430-11>.
 18. Davis MJ, Purcell AH, Thomson SV. 1980. Isolation media for the Pierce's disease bacterium. *Phytopathology* 70:425–429. <http://dx.doi.org/10.1094/Phyto-70-425>.
 19. Margulies M, Egholm M, Altman WE, Attiya S, Bader JS, Bemben LA, Berka J, Braverman MS, Chen YJ, Chen Z, Dewell SB, Du L, Fierro JM, Gomes XV, Godwin BC, He W, Helgesen S, Ho CH, Ho CH, Irzyk GP, Jando SC, Alenquer ML, Jarvie TP, Jirage KB, Kim JB, Knight JR, Lanza JR, Leamon JH, Lefkowitz SM, Lei M, Li J, Lohman KL, Lu H, Makhiyani VB, McDade KE, McKenna MP, Myers EW, Nickerson E, Nobile JR, Plant R, Puc BP, Ronan MT, Roth GT, Sarkis GJ, Simons JF, Simpson JW, Srinivasan M, Tartaro KR, Tomasz A, Vogt KA, et al. 2005. Genome sequencing in microfabricated high-density picolitre reactors. *Nature* 437:376–380. <http://dx.doi.org/10.1038/nature03959>.
 20. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <http://dx.doi.org/10.1186/1471-2164-9-75>.
 21. Altschul SF, Madden TL, Schäffer AA, Zhang J, Zhang Z, Miller W, Lipman DJ. 1997. Gapped BLAST and psi-blast: a new generation of protein database search programs. *Nucleic Acids Res.* 25:3389–3402. <http://dx.doi.org/10.1093/nar/25.17.3389>.