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Complete Genome Sequence of the Barley Pathogen *Xanthomonas translucens* pv. translucens DSM 18974^T (ATCC 19319^T)

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We report here the complete 4.7-Mb genome sequence of *Xanthomonas translucens* pv. translucens DSM 18974^T, which causes black chaff disease on barley (*Hordeum vulgare*). Genome data of this *X. translucens* type strain will improve our understanding of this bacterial species.

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The Gram-negative gammaproteobacterium *Xanthomonas translucens* pv. translucens is the causal agent of a bacterial wilt on *Hordeum vulgare* (barley) (1) that is often called black chaff. The strain DSM 18974^T (ATCC 19319^T) was isolated from its host plant in Minnesota, USA. It is the type strain of the species *X. translucens* (2). *X. translucens* strains occur worldwide and infect a broad range of cereals and forage grasses. At the same time, *Xanthomonas* strains are applied in biotechnology to synthesize the exopolysaccharide xanthan (3), a commercial thickening agent. Despite gradually rising numbers of publications, our knowledge about *X. translucens* genomes is still fragmentary. Hence, detailed genome data of *X. translucens* pv. translucens are suitable to advance functional research and deepen our phylogenetic understanding of *X. translucens* and related xanthomonads.

Initially, genomic DNA of *X. translucens* pv. translucens DSM 18974^T was extracted (4) to generate a paired-end library that was shotgun-sequenced with a Genome Sequencer FLX (GS FLX) system by means of the 454 Titanium technology (Roche) as described earlier (5). However, the assembly of the resulting data produced a large number of contigs, possibly pointing to the presence of repetitive IS elements. To address this deficiency, a combination of single-molecule real-time (SMRT) and Illumina sequencing technologies was applied. Genomic DNA was extracted applying Qiagen Genomic-tips 100/G according to the manufacturer's instructions and sequenced on a PacBio RSII instrument (Pacific Biosciences) using P5 chemistry. Genome assembly was performed with the "RS_HGAP_Assembly.3" protocol included in SMRT Portal version 2.3.0, utilizing 49,791 post-filtered reads with an average read length of 12,646 bp. One complete chromosomal contig was obtained and trimmed, circularized, and adjusted to the beginning of the *dnaA* gene. To improve the sequence quality, additional genome data were obtained by sequencing a

paired-end TruSeq PCR-free DNA fragment library with an average size of 719 ± 226 bp on a MiSeq instrument (Illumina) in a 2 × 300-bp run. This provided a total of 1,021,089,076 bp in 4,490,068 reads, among them 2,129,085 paired-ends reads. The Illumina reads were mapped with the Burrows–Wheeler aligner (6) onto the contig to obtain the consensus sequence of a circular chromosome of 4,715,357 bp with an average coverage of 223× and a G+C content of 67.7%. Automated genome annotation carried out by means of the GenDB platform (7) with the Prodigal gene prediction software (8) revealed 3,736 protein-coding genes, 54 tRNAs, and two rRNA operons.

Comparative analysis employing the EDGAR software (9) facilitated the identification of a CRISPR array in addition to virulence factor genes, which encoded protein-secretion systems like a *hrp* type III secretion system with transcription activator-like effectors (10) and the polysaccharide xanthan.

Accession number(s). This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession number LT604072. The version described in this paper is the first version, LT604072.1.

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REFERENCES

1. **Duveiller E, Maraite H**. 1993. *Xanthomonas campestris* pathovars on cereals: cause of leaf streak or black chaff diseases, p. 76–79. *In* Swings JG, Civerolo EL (ed), Xanthomonas. Chapman and Hall, London, United Kingdom.

2. **Rademaker JL, Norman DJ, Forster RL, Louws FJ, Schultz MH, de Bruijn FJ**. 2006. Classification and identification of *Xanthomonas translucens* isolates, including those pathogenic to ornamental asparagus. Phytopathology **96**:876–884. http://dx.doi.org/10.1094/PHYTO-96-0876.

3. **Becker A, Katzen F, Pühler A, Ielpi L**. 1998. Xanthan gum biosynthesis and application: a biochemical/genetic perspective. Appl Microbiol Biotechnol **50**:145–152. http://dx.doi.org/10.1007/s002530051269.

4. **Hopwood DA, Bibb MJ, Chater KF, Kieser T, Bruton CJ, Kieser HM, Lydiate DJ, Smith CP, Ward JM, Schrempf H**. 1985. Genetic manipulation of streptomyces—a laboratory manual. John Innes Foundation, Norwich, United Kingdom.

5. **Arnold M, Wibberg D, Blom J, Schatschneider S, Winkler A, Kutter Y, Rückert C, Albersmeier A, Albaum S, Goesmann A, Zange S, Heese-mann J, Pühler A, Hogardt M, Vorhölter FJ**. 2015. Draft genome sequence of *Pseudomonas aeruginosa* strain WS136, a highly cytotoxic ExoS-positive wound isolate recovered from pyoderma gangrenosum. Genome Announc **3**(4):. http://dx.doi.org/10.1128/genomeA.00680-15.

6. **Li H, Durbin R**. 2010. Fast and accurate long-read alignment with Burrows–Wheeler transform. Bioinformatics **26**:589–595. http://dx.doi.org/10.1093/bioinformatics/btp698.

7. **Meyer F, Goesmann A, McHardy AC, Bartels D, Bekel T, Clausen J, Kalinowski J, Linke B, Rupp O, Giegerich R, Pühler A**. 2003. GenDB—an open source genome annotation system for prokaryote genomes. Nucleic Acids Res **31**:2187–2195. http://dx.doi.org/10.1093/nar/gkg312.

8. **Wichmann F, Vorhölter FJ, Hersemann L, Widmer F, Blom J, Niehaus K, Reinhard S, Conradin C, Kölliker R**. 2013. The noncanonical type III secretion system of *Xanthomonas translucens* pv. *graminis* is essential for forage grass infection. Mol Plant Pathol **14**:576–588. http://dx.doi.org/10.1111/mpp.12030.

9. **Blom J, Albaum SP, Doppmeier D, Pühler A, Vorhölter FJ, Zakrzewski M, Goesmann A**. 2009. EDGAR: a software framework for the comparative analysis of prokaryotic genomes. BMC Bioinformatics **10**:154. http://dx.doi.org/10.1186/1471-2105-10-154.

10. **Boch J, Bonas U, Lahaye T**. 2014. TAL effectors—pathogen strategies and plant resistance engineering. New Phytol **204**:823–832. http://dx.doi.org/10.1111/nph.13015.