Genome Sequence of *Xanthomonas campestris* JX, an Industrially Productive Strain for Xanthan Gum

Fei Tao,^a Xia Wang,^b Cuiqing Ma,^b Chunyu Yang,^b Hongzhi Tang,^a Zhonghui Gai,^a and Ping Xu^{a,b}

State Key Laboratory of Microbial Metabolism & School of Life Sciences and Biotechnology, Shanghai, People's Republic of China,^a and State Key Laboratory of Microbial Technology, Shandong University, Jinan, People's Republic of China^b

***Xanthomonas campestris* JX, a soil bacterium, is an industrially productive strain for xanthan gum. Here we present a 5.0-Mb assembly of its genome sequence. We have annotated 12 coding sequences (CDSs) responsible for xanthan gum biosynthesis, 346 CDSs encoding carbohydrate metabolism, and 69 CDSs related to virulence, defense, and plant disease.**

Xanthan gum is a natural anionic polysaccharide and an important industrial biopolymer derived from the bacterial coat of *Xanthomonas campestris* (3). It is made up of pentasaccharide subunits, forming a cellulose backbone with trisaccharide side chains composed of mannose(β 1,4)glucuronic-acid(β 1,2)mannose attached to alternate glucose residues in the backbone by α 1,3 linkages (6). This biopolymer is of great commercial significance because of its superior pseudoplasticity, thixotropy, viscosity, and biosafety (2, 4, 7). Currently, it is widely used as a thickener or viscosifier in both food and nonfood industries and is used as a stabilizer for a wide variety of suspensions, emulsions, and foams (2).

X. campestris is used in producing xanthan gum by fermentation, and its relevant fermentation conditions and metabolic pathways have been well studied (3–5, 8, 10). However, there are still certain points that need to be investigated, such as the regulation of xanthan gum biosynthesis (8, 9, 11). Moreover, *X. campestris* is a plant pathogen that can infect many plants, including those of agricultural interest (e.g., cabbage, alfalfa, and beans) (4). Genomic analysis is a powerful approach to investigate bacterial genetics. For example, comparative genomics can be used to efficiently discover bacterial genetic features and to understand gene functions relevant to adaptation (9). Therefore, investigation of *X. campestris* strains by using genome sequencing and bioinformatics is desired.

Since 2005, China has become one of the largest xanthan gum production bases in the world. The industrially productive strain *X. campestris* JX (CCTCC M2012178), which was isolated by Boying Jiang (Shandong University) 25 years ago, has contributed to the gum industry. The isolated strain produced more than 20 g of xanthan gum per liter (unpublished data). Here we present the draft genome sequence of strain JX, which was obtained using the Illumina GA system. The reads were assembled with VELVET (12), and the sequence was annotated using the RAST annotation server (1).

The sequence contains 5,023,003 bases, 4,323 predicted coding sequences (CDSs), and 55 RNAs with a G+C content of 65%, which consists of 155 large contigs (>200 bp in size). A large gene cluster responsible for the xanthan gum biosynthesis was predicted, which consists of 14 open reading frames (ORFs), including *gumB*, *-C*, *-D*, *-E*, *-F*, *-G*, *-H*, *-I*, *-J*, *-K*, *-L*, and *-M*, a gene encoding a hypothetical protein, and a gene whose function is unknown, *gumN*, which is similar to that of other *X. campestris* strains (9). Genes *xanA* and *xanB*, which are involved in xanthan gum biosynthesis, were also annotated. Meanwhile, 346 CDSs en-

coding carbohydrate metabolism were annotated, which should be further investigated for substrate utilization. There are 69 CDSs being annotated as the genes related to virulence, defense, and plant disease. About 5 CDSs were annotated as the genes encoding the BarA-UvrY (SirA) two-component system, which is responsible for regulation of virulence. Moreover, we annotated 23 CDSs related to capsular and extracellular polysaccharides, which also correspond to genes involved in virulence.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. [AJVO00000000](https://doi.org/10.1093/nucleotide/AJVO0000000). The version described in this paper is the first version, [AJVO01000000](https://doi.org/10.1093/nucleotide/AJVO01000000).

ACKNOWLEDGMENTS

We acknowledge Huajun Zheng and colleagues for genome sequencing performed at Chinese National Human Genome Center at Shanghai. We also acknowledge Boying Jiang (Shandong University, China) for providing strain JX.

This work was supported in part by the Chinese National Natural Science Foundation (31100078 and 30821005).

REFERENCES

1. Aziz RK, et al. 2008. The RAST Server: rapid annotations using subsystems technology. *BMC Genomics* 9:75. doi:10.1186/1471-2164-9-75.
2. Becker A, Katzen F, Puhler A, Ielpi L. 1998. Xanthan gum biosynthesis and application: a biochemical/genetic perspective. *Appl. Microbiol. Biotechnol.* 50:145–152.
3. Casas JA, Santos VE, Garcia-Ochoa F. 2000. Xanthan gum production under several operational conditions: molecular structure and rheological properties. *Enzyme Microb. Technol.* 26:282–291.
4. Garcia-Ochoa F, Santos VE, Casas JA, Gomez E. 2000. Xanthan gum: production, recovery, and properties. *Biotechnol. Adv.* 18:549–579.
5. Harding NE, Cleary JM, Cabanas DK, Rosen IG, Kang KS. 1987. Genetic and physical analyses of a cluster of genes essential for xanthan gum biosynthesis in *Xanthomonas campestris*. *J. Bacteriol.* 169:2854–2861.
6. Jansson P, Kenne L, Lindberg B. 1975. Structure of the extracellular polysaccharide from *Xanthomonas campestris*. *Carbohydr. Res.* 45:275–282.

Received 1 June 2012 Accepted 19 June 2012

Address correspondence to Ping Xu, pingxu@sjtu.edu.cn.

F.T. and X.W. contributed equally to this article.

Copyright © 2012, American Society for Microbiology. All Rights Reserved.

doi:10.1128/JB.00965-12

7. Katzbauer B. 1998. Properties and applications of xanthan gum. *Polym. Degradation Stab.* 59:81–84.
8. Katzen F, Becker A, Zorreguieta A, Puhler A, Ielpi L. 1996. Promoter analysis of the *Xanthomonas campestris* pv. *campestris* gum operon directing biosynthesis of the xanthan polysaccharide. *J. Bacteriol.* 178:4313–4318.
9. Lu H, et al. 2008. Acquisition and evolution of plant pathogenesis-associated gene clusters and candidate determinants of tissue-specificity in *Xanthomonas*. *PLoS One* 3:e3828. doi:10.1371/journal.pone.0003828.
10. Tseng YH, et al. 1999. Chromosome map of *Xanthomonas campestris* pv. *campestris* 17 with locations of genes involved in xanthan gum synthesis and yellow pigmentation. *J. Bacteriol.* 181:117–125.
11. Yoon KH, Cho JY. 2007. Transcriptional analysis of the *gum* gene cluster from *Xanthomonas oryzae* pathovar *oryzae*. *Biotechnol. Lett.* 29:95–103.
12. Zerbino DR, Birney E. 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. *Genome Res.* 18:821–829.