Draft Genome Sequence of *Agrobacterium* sp. Strain UHFBA-218, Isolated from Rhizosphere Soil of Crown Gall-Infected Cherry Rootstock Colt

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We report here the draft genome sequence of the alphaproteobacterium *Agrobacterium* sp. strain UHFBA-218, which was isolated from rhizosphere soil of crown gall-infected cherry rootstock Colt. The draft genome of strain UHFBA-218 consists of 112 contigs (5,425,303 bp) and 5,063 coding sequences with a G+C content of 59.8%.

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Species of the genus *Agrobacterium* have been implicated either in the formation of tumors (galls) or for the production of agrocin-like antibiotics that suppress the tumor caused by them (1). We isolated *Agrobacterium* strain UHFBA-218 from rhizosphere soil of crown gall-infected cherry rootstock Colt (April 2010). This strain did not show any gall development on an artificially inoculated stem of a potted tomato plant when tested for pathogenicity (2) and was designated a nonpathogenic isolate belonging to the biovar I division of *Agrobacterium* (genome species G6). Strain UHFBA-218 is available from Microbial Culture Collection, Pune, India (MCC2101), and the current draft genome is listed in Genomes OnLine Database (GOLD) as card Gi23696.

The genome of *Agrobacterium* strain UHFBA-218 was sequenced using Illumina (2-kb paired-end library; 6,733,683 reads) and 454 GS FLX titanium (74,904 reads) platforms. The data were assembled using the Velvet 1.2.03 assembler (3) set at a k-mer length of 55. The assembly generated 112 contigs (N_{50} contigs, 100.18 kb) comprising of 5,425,303 bp. The final (validated pair-end criterion) assembly had 85.67-fold coverage with the largest contig (GenBank accession no. APCC01000003) of 246,613 bp in size and an average G+C content of 59.8%.

The draft genome was annotated using RAST version 4.0 (4), NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html). A total of 5,063 protein-coding sequences and 1,412 hypothetical proteins were predicted on annotation. A single copy of each of the 5S, 16S, and 23S RNA and 56 tRNA genes was predicted using RNAmmer (5) and tRNAscan-SE (6), respectively. The contig 21 (GenBank accession no. APCC01000021) contains an operon which is >97% similar to the characterized RNA operon reported in *A. tumefaciens* MAFF301001 (GenBank Accession no. AB102734.2) and codes for 16S rRNA, tRNA-Ile-GAT, tRNA-Ala-TGC, 23 S rRNA, 5S rRNA, and tRNA-Met-CAT. The draft genome was found to be closely related to *A. tumefaciens* C58 (88% nucleotide identity as determined by using ANI perl script [7]). Contig 26 (GenBank accession no. APCC01000026) of the final (validated)

assembly was found to contain prophage genomic regions (15.3 kb) as predicted using PHAST (8). S1-PFGE analysis (9) of strain UHFBA-218 indicated a possible tripartite genomic makeup, with a primary circular chromosome, a secondary linear chromosome, and the presence of a megaplasmid. Based on BLASTn analysis, a 149-kb cluster of contigs ($n = 12$) represented a megaplasmid that showed 99% homology (51% query coverage) to the tumor-inducing plasmid pTiC58. However, no virulence genes have been found on the putative megaplasmid, which makes it an interesting prospect for future research.

A detailed comparative genomic analysis of strain UHFBA-218 and its phylogenetic neighbors (10) that belong to biovar I is underway. Such analysis is expected to provide further insights into the evolution of the genomic organization pertaining to this biovar designation.

Nucleotide sequence accession numbers. This Whole-Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number APCC00000000. The version described in this paper is the first version, APCC01000000.

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REFERENCES

1. **Escobar MA, Dandekar AM.** 2003. Agrobacterium tumefaciens as an agent of disease. Trends Plant Sci. **8:**380–386.
2. **Gupta A, Gupta AK, Mahajan R, Singh D, Khosla K, Lal R, Gupta V.** 2013. Protocol for isolation and identification of *Agrobacterium* Isolates from Stone Fruit plants and sensitivity of native *A. tumefaciens* isolates against agrocin produced by *A. radiobacter* strain K84. Natl. Acad. Sci. Lett. **36:**79–84.
3. **Zerbino DR, Birney E.** 2008. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. Genome Res. **18:**821–829.

4. **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.

5. **Lagesen K, Hallin P, Rødland EA, Staerfeldt HH, Rognes T, Ussery DW.** 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res. **35**:3100–3108.

6. **Lowe TM, Eddy SR.** 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res. **25**: 955–964.

7. **Richter M, Rosselló-Móra R.** 2009. Shifting the genomic gold standard for the prokaryotic species definition. Proc. Natl. Acad. Sci. U. S. A. **106**: 19126–19131.

8. **Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS.** 2011. PHAST: a fast phage search tool. Nucleic Acids Res. **39**:W347–W352.

9. **Barton BM, Harding GP, Zuccarelli AJ.** 1995. A general method for detecting and sizing large plasmids. Anal. Biochem. **226**:235–240.

10. **Slater S, Setubal JC, Goodner B, Houmiel K, Sun J, Kaul R, Goldman BS, Farrand SK, Almeida N, Jr, Burr T, Nester E, Rhoads DM, Kadoi R, Ostheimer T, Pride N, Sabo A, Henry E, Telepak E, Cromes L, Harkleroad A, Oliphant L, Pratt-Szegila P, Welch R, Wood D.** 2013. Reconciliation of sequence data and updated annotation of the genome of Agrobacterium tumefaciens C58, and distribution of a linear chromosome in genus Agrobacterium. Appl. Environ. Microbiol. **79**:1414–1417.