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Genome Sequence of the Quorum-Quenching *Agrobacterium tumefaciens* Strain WRT31

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Agrobacterium tumefaciens **strain WRT31 is a quorum-sensing signal-degrading bacterium that has been isolated from the rhizosphere of tobacco plants. This strain belongs to *A. tumefaciens* genomovar G1, is avirulent on various putative host plants, devoid of Ti plasmid, and contains the *blcC* gene encoding a gamma-butyrolactonase.**

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Among the cultured community collected from tobacco rhizosphere, *Agrobacterium tumefaciens* strain WRT31 has been identified as an isolate that efficiently degrades the quorum-sensing (QS) signals of the *N*-acyl homoserine lactone (AHL) class (1, 2). This strain is avirulent on different hosts (*Datura stramonium* and tomato plants). It is defective for the plasmid Ti, and hence for the *traI* gene that encodes the synthesis of the QS signal 3-oxo-octanoyl-homoserine lactone (3-OC8-HSL). However, strain WRT31 harbors the lactonase-encoding gene *blcC* (*attM*) that is involved in the assimilation of gamma-butyrolactone as a carbon source and the cleavage of AHL QS signals, including 3-OC8-HSL (3, 4). In strain WRT31, cleavage of the AHL QS signals occurred even in the absence of known *blcC* inducers, such as gamma-aminobutyric acid, gamma-butyrolactone, and gamma-hydroxybutyric acid (4–6). This feature might suggest a constitutive expression of the lactonase BlcC or the presence of uncharacterized additional quorum-quenching enzymes in WRT31, hence its efficient AHL degradation ability.

Here, we report the *de novo* genome assembly of *A. tumefaciens* strain WRT31. Two libraries were constructed using the TruSeq SBS v3 sequencing kit: a shotgun (SG) paired-end library with a fragment size between 150 and 500 bp and a long jumping distance (LJD) mate-pair library with an average insert size of 7,765 bp. The two libraries were sequenced using a 2 × 100 bp paired-end read module of Illumina HiSeq 2000 by Eurofins Genomics (France). Sequence reads with low quality (<0.05), ambiguous nucleotides ($n > 1$), and a sequence length of <50 nucleotides were discarded prior to assembly. After trimming, 40,155,546 paired-end reads were retained (3,786,667,988 bases) with an average length of 94.3 bp, and 7,117,455 mate-paired reads (590,748,765 bases) with an average length of 83 bp. Sequence assembly was carried out using the CLC Genomics Workbench v5.5 (CLC bio, Aarhus, Denmark), with a read length of 0.5 and a similarity of 0.8. Nineteen contigs were obtained, with lengths ranging from 2 kbp to 844 kbp and an N_{50} value of 596,214 bp. The scaffolding was processed using SSPACE basic v2.0 (7). The *in silico* finishing of some gaps was carried out by mapping (read length of 0.9 and similarity of 0.95) the mate pair reads on each of the 5-kbp contigs ends. The collected reads were used for *de novo* local assembling (read length of 0.5 and similarity of 0.8). The published sequence is composed of 10 contigs (from 2 kbp to 2.17 Mbp) grouped in 4 scaffolds, with a coverage rate ranging from 569- to 827-fold.

The *A. tumefaciens* WRT31 genome consists of one circular chromosome containing 2,938,081 bp, one linear chromosome containing 2,176,692 bp, and two additional scaffolds containing 674,326 bp and 86,649 bp, respectively. The percentages of G+C content are 58.4%, 58.6%, 57.4%, and 54.6% for the circular chromosome (scaffold 1), linear chromosome (scaffold 2), scaffold 3, and scaffold 4, respectively. A total of 5,718 putative coding sequences were predicted using the Rapid Annotations using Subsystems Technology (RAST) v4.0 automated pipeline (8). A BLAST search using scaffold 3 and scaffold 4 as queries indicated that both should be part of a plasmid related to the At plasmid of *A. tumefaciens* strain C58 encoding the lactonase BlcC.

Nucleotide sequence accession numbers. The *A. tumefaciens* WRT31 genome sequence has been deposited at DDBJ/EMBL/GenBank under the accession no. APLP00000000. The version described in this paper is the first version, APLP01000000.

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REFERENCES

1. **D'Angelo-Picard C, Faure D, Carlier A, Uroz S, Raffoux A, Fray R, Dessaux Y.** 2004. Bacterial populations in the rhizosphere of tobacco plants producing the quorum-sensing signals hexanoyl-homoserine lactone and 3-oxo-hexanoyl-homoserine lactone. FEMS Microbiol. Ecol. **51**:19–29.
2. **D'Angelo-Picard C, Faure D, Penot I, Dessaux Y.** 2005. Diversity of *N*-acyl homoserine lactone-producing and -degrading bacteria in soil and tobacco rhizosphere. Environ. Microbiol. **7**:1796–1808.

3. **Zhang HB, Wang LH, Zhang LH.** 2002. Genetic control of quorum-sensing signal turnover in *Agrobacterium tumefaciens*. Proc. Natl. Acad. Sci. U. S. A. **99:**4638–4643.
4. **Carlier A, Chevrot R, Dessaux Y, Faure D.** 2004. The assimilation of gamma-butyrolactone in *Agrobacterium tumefaciens* C58 interferes with the accumulation of the *N*-acyl-homoserine lactone signal. Mol. Plant Microbe Interact. **17:**951–957.
5. **Chevrot R, Rosen R, Haudecoeur E, Cirou A, Shelp BJ, Ron E, Faure D.** 2006. GABA controls the level of quorum-sensing signal in *Agrobacterium tumefaciens*. Proc. Natl. Acad. Sci. U. S. A. **103:**7460–7464.
6. **Cirou A, Mondy S, An S, Charrier A, Sarrazin A, Thoison O, DuBow M, Faure D.** 2012. Efficient biostimulation of native and introduced quorum-quenching *Rhodococcus erythropolis* populations is revealed by a combination of analytical chemistry, microbiology, and pyrosequencing. Appl. Environ. Microbiol. **78:**481–492.
7. **Boetzer M, Henkel CV, Jansen HJ, Butler D, Pirovano W.** 2011. Scaffolding pre-assembled contigs using SSPACE. Bioinformatics **27:**578–579. doi:10.1093/bioinformatics/btq683.
8. **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. doi:10.1186/1471-2164-9-75.