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Genome Sequence of the Quorum-Sensing-Signal-Producing Nonpathogen *Agrobacterium tumefaciens* Strain P4

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***Agrobacterium tumefaciens* P4 is a quorum-sensing-signal-producing bacterium that has been isolated from the tobacco rhizosphere. This strain belongs to genomospecies 1 of the *A. tumefaciens* complex; it is avirulent on various putative host plants, devoid of the Ti plasmid, and contains a *luxI* homolog on the At plasmid.**

Received 4 September 2013 **Accepted** 9 September 2013 **Published** 3 October 2013

Citation Mondy S, Lalouche O, Dessaux Y, Faure D. 2013. Genome sequence of the quorum-sensing-signal-producing nonpathogen *Agrobacterium tumefaciens* strain P4. Genome Announc. 1(5):e00798-13. doi:10.1128/genomeA.00798-13.

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Among the cultured community collected from a tobacco rhizosphere, *Agrobacterium tumefaciens* strain P4 has been identified as an isolate that produces quorum-sensing (QS) signals of the *N*-acyl homoserine lactone (AHL) class (1). However, this strain is avirulent on different hosts (*Datura stramonium* and tomato plants) and defective for the plasmid Ti and, hence, for the *traI* gene that encodes the synthesis of the QS signal 3-oxo-octanoyl-homoserine lactone (3OC8-HSL) in agrobacteria. Using thin-layer chromatography, commercial 3OC8-HSL as a reference, and *A. tumefaciens* NT1(pZLR4) as an AHL biosensor strain (2), we confirmed that strain P4 produces a large amount of a molecule that is not 3OC8-HSL but indeed activates *Agrobacterium* QS-regulated *tra* genes. The exact structure of this molecule is currently being investigated.

Here, we report the *de novo* genome assembly of *A. tumefaciens* strain P4. Two libraries were constructed using the TruSeq SBS version 3 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). Sequences reads with low quality (<0.05), ambiguous nucleotides ($n > 1$), and a sequence length of <50 nucleotides were discarded prior to assembly. After trimming, we retained 49,531,690 paired-end reads (4,695,604,212 bases) with an average length of 94.8 bp and 3,283,394 mate-paired reads (271,536,684 bases) with an average length of 82.7 bp. Sequence assembly was carried out using the CLC Genomics Workbench version 5.5 (CLC bio, Aarhus, Denmark), with a read length of 0.5 and a similarity of 0.8. Eighteen contigs were obtained with a length ranging from 2.4 kbp to 884 kbp, with an N_{50} value of 532,842 bp. The scaffolding was processed using SSPACE basic version 2.0 (3). 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 contig ends. Next, 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 nine contigs (from 53.8 kbp to 1.63 Mbp) grouped in 3 scaffolds, with a coverage rate ranging from 853- to 965-fold.

The *A. tumefaciens* strain P4 genome consists of one circular chromosome containing 2,856,286 bp, one linear chromosome containing 2,052,829 bp, and one circular At plasmid containing 661,825 bp. The G+C contents are 58.8%, 58.6%, and 56.7% for the circular chromosome, linear chromosome, and At plasmid, respectively. A total of 5,379 putative coding sequences were predicted using the Rapid Annotations using Subsystems Technology (RAST) version 4.0 automated pipeline (4). A survey of the P4 genome revealed the presence of a *luxI* homolog on the At plasmid, the function of which remains to be investigated.

Nucleotide sequence accession numbers. The *A. tumefaciens* P4 genome sequence has been deposited at DDBJ/EMBL/GenBank under the accession no. APJV00000000. The version described in this paper is the first version, APJV01000000.

ACKNOWLEDGMENTS

This work was supported by the Centre National de la Recherche Scientifique (CNRS), Gif-sur-Yvette, France, and ANR (Program Blanc ECORUM).

REFERENCES

1. **Haudecoeur E, Tannières M, Cirou A, Raffoux A, Dessaux Y, Faure D.** 2009. Different regulation and roles of lactonases AiiB and AttM in *Agrobacterium tumefaciens* C58. Mol. Plant Microbe Interact. **22:**529–537.
2. **Cha C, Gao P, Chen YC, Shaw PD, Farrand SK.** 1998. Production of acyl-homoserine lactone quorum-sensing signals by Gram-negative plant-associated bacteria. Mol. Plant Microbe Interact. **11:**1119–1129.
3. **Boetzer M, Henkel CV, Jansen HJ, Butler D, Pirovano W.** 2011. Scaffolding pre-assembled contigs using SSPACE. Bioinformatics **27:**578–579.
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. doi:10.1186/1471-2164-9-75.