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Genome Sequence of the Quorum-Quenching *Rhodococcus erythropolis* Strain R138

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***Rhodococcus erythropolis* strain R138 was isolated from the rhizosphere of *Solanum tuberosum* and selected for its capacity to degrade *N*-acyl-homoserine lactones, quorum-sensing signals used as communication molecules by the potato pathogens *Pectobacterium* and *Dickeya*. Here, we report the genome sequence of *Rhodococcus erythropolis* strain R138.**

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Proteobacteria may use quorum-sensing (QS) signals, such as *N*-acyl-homoserine lactones (AHLs), to synchronize the gene expression at a population level. Several bacteria, including *Rhodococcus erythropolis*, are able to degrade AHLs, hence disrupting the expression of the QS-regulated functions (1, 2). These AHL-degrading bacteria were collectively named quorum-quenching bacteria (3). *R. erythropolis* expresses at least three enzymatic activities involved in AHL degradation: lactonase, opening the gamma-butyrolactone ring of the AHLs; amidase, cleaving AHLs into homoserine lactone and fatty acids; and reductase, converting the ketone function at the C-3 position of the fatty chain into hydroxyl (4, 5). Until now, only the lactonase-coding gene *qsdA* was characterized (5). The quorum-quenching *Rhodococcus* strains are proposed to be used as antibiofouling (6) and biocontrol (1, 7) agents. *R. erythropolis* strain R138 was isolated from the potato rhizosphere (7). It is able to degrade AHLs and limit the symptoms induced by the plant pathogen *Pectobacterium atrosepticum* on potato tubers (8). The growth and root colonization of *R. erythropolis* R138 are enhanced in the presence of gamma-caprolactone and gamma-heptanolactone, which are assimilated as a carbon source (9). In *R. erythropolis* R138, the lactonase QsdA is involved in the cleavage of AHLs, as well as that of gamma-caprolactone and gamma-heptanolactone (5, 10).

Here, we report the *de novo* genome assembly of *R. erythropolis* R138 by combining Illumina and 454-Roche technologies. Three genomic libraries were constructed: a 300-bp library used for paired-end 2 × 72 Illumina sequencing (Imagif, France), a 380-bp shotgun library used for single-read 454 sequencing, and a long paired-end library with an insert size of 8 kbp used for 454 sequencing (Eurofins MWG, Germany). Sequence reads with low quality (<0.05), ambiguous nucleotides ($n > 2$), and sequence lengths of <50 (454 mate-paired), 20 (454 single), or 70 (Illumina) nucleotides were discarded for the assembly. Assembly was carried out using the CLC Genomics Workbench version 5.1 (CLC bio, Aarhus, Denmark), with a read length of 0.5 and similarity of 0.8 as parameters. In total, 53,576,242 reads were obtained, corresponding to 4,010,660,803 bases, with an average length of 74.9 bp. The scaffolding was processed using SSPACE basic version 2.0 (11). The *in silico* finishing of the remaining gaps was carried out by mapping mate-pair reads (read length, 0.9; similarity, 0.95) on each of the 5-kbp contig ends. Next, the collected reads were used for *de novo* assembly (read length, 0.5; similarity, 0.8). Some additional gaps were resolved using Sanger sequencing of the PCR amplicons. The published sequence is composed of 12 contigs, with a sequence length from 5.5 kbp to 2.7 Mbp grouped in 3 scaffolds.

The *R. erythropolis* R138 genome consists of one circular chromosome (6,444,743 bp), a linear plasmid (247,675 bp), and a circular plasmid (84,151 bp). The G+C content percentages were homogenous among the replicons (from 60 to 62%). A total of 6,562 coding sequences were predicted using the Rapid Annotations using Subsystems Technology (RAST) version 4.0 automated pipeline (12).

Nucleotide sequence accession number. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. ASKF00000000.

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