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Genome Sequence of the Potato Plant Pathogen *Dickeya dianthicola* Strain RNS04.9

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***Dickeya dianthicola* is one of the causative agents of soft rot and blackleg diseases, which are currently identified in European countries in a wide range of crops. Here, we report the draft genome sequence of *D. dianthicola* strain RNS04.9, which was isolated from a potato plant with blackleg symptoms in 2004.**

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Pectinolytic bacteria of the genera *Pectobacterium* and *Dickeya* are causative agents of soft rot and blackleg diseases that affect a wide range of field crops and ornamental plants (1–5). In Europe, *Pectobacterium atrosepticum, Pectobacterium carotovorum* subsp. *carotovorum, Dickeya dianthicola*, and *Dickeya solani* are the main pectinolytic pathogens of potato in the field stage or during storage (6–8). Two *Dickeya* species emerged recently: *D. dianthicola* in the 1970s and *D. solani* in the 2000s (9). The pathogens may propagate from tubers to stems or leaves and reciprocally from aerial parts to progeny tubers (10–13).

Our team has already reported the genome sequences of other blackleg and soft rot diseases agents, *P. atrosepticum* strain CFBP6276 (14) and *D. solani* strain PRI3337 (15, 16). *D. dianthicola* strain RNS04.9 was isolated and characterized in 2004 from a potato plant with blackleg symptom sampled in a French field during the epidemiological annual survey monitored by the FN3PT/RD3PT. This strain has been investigated in several former studies (17–19) and used to develop a valuable greenhouse pathosystem, which allowed the assessment of a biocontrol strategy (20).

Genomic DNA of *D. dianthicola* RNS04.9 was subjected to next-generation Illumina HiSeq 2000 version 3 technology. Two libraries were constructed: a paired-end library with a fragment size of 150 to 500 bp and a shotgun long-jumping-distance mate-pair library with an insert size of 8,000 bp. Sequencing of the libraries was carried out using a 2 × 100 bp paired-end read module by Eurofins Genomics. Assembly was performed by CLC Genomics Workbench version 5.5 (from CLCbio). Sequence reads were trimmed based on quality (threshold 0.05), and minimum size (above 60 nucleotides). Scaffolding of the contig was processed using SSPACE basic version 2.0 (21). A total of 46 contigs were generated by *de novo* assembly and clustered in 2 scaffolds. The first scaffold (3,366,760 bp) comprised 35 contigs, the 11 remaining ones being included in the second scaffold (1,343,990 bp). The *in silico* closure 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. Following this treatment, 36 gaps were elucidated. Then, the collected reads were used for *de novo* local assembling (read length of 0.5 and similarity of 0.8). This allowed the generation of one scaffold with 10 gaps, from 28 bp to 3,271 bp in size. Some gaps were resolved by Sanger sequencing of PCR amplicons.

At the end, the genome sequence of *D. dianthicola* strain RNS04.9 revealed a circular chromosome consisting of 4,721,506 bp and comprised 7 contigs. No plasmid was detected. The G+C content was ~56%. Gene prediction using the RAST version 4.0 automated pipeline (22, 23) revealed the presence of 4,351 coding sequences and 97 RNA-assimilated regions. These features are in accordance with other data of the *Dickeya* spp. genomes and draft genomes that are available in public databases.

Nucleotide sequence accession numbers. This draft genome sequence has been deposited at DDBJ/EMBL/GenBank under the accession number APVF00000000. The version described in this paper is the first version, APVF01000000.

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