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Yannick Raoul Des Essarts, Samuel Mondy, Valérie Hélias, Denis Faure. Genome Sequence of the Potato Plant Pathogen *Dickeya dianthicola* Strain RNS04.9.. *Genome Announcements*, 2015, 3 (3), pp.e00581-15. 10.1128/genomeA.00581-15 . hal-01433048

**HAL Id: hal-01433048**

**<https://hal.science/hal-01433048>**

Submitted on 11 Aug 2020

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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.**

Received 29 April 2015 Accepted 1 May 2015 Published 4 June 2015

**Citation** Raoul des Essarts Y, Mondy S, Hélias V, Faure D. 2015. Genome sequence of the potato plant pathogen *Dickeya dianthicola* strain RNS04.9. *Genome Announc* 3(3): e00581-15. doi:10.1128/genomeA.00581-15.

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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 treat-

ment, 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.

## ACKNOWLEDGMENTS

We thank the Centre national de la recherche scientifique (CNRS, France), Saclay Plant Sciences LABEX (ANR-10-LABX-0040-SPS and ANR-11-IDEX-0003-02), the Fédération Nationale des Producteurs de Plantes de Pomme de Terre (FN3PT/RD3PT), and the Association Nationale de la Recherche et de la Technologie (ANRT-CIFRE no. 1282/2011) for their financial support.

Y.R.D.E. also thanks Yves Le Hingrat (FN3PT) and Yves Dessaux (CNRS) for editing.

## REFERENCES

- Gardan L, Gouy C, Christen R, Samson R. 2003. Elevation of three subspecies of *Pectobacterium carotovorum* to species level: *Pectobacterium atrosepticum* sp. nov., *Pectobacterium betavasculorum* sp. nov. and *Pectobacterium wasabiae* sp. nov. *Int J Syst Evol Microbiol* 53:381–391. <http://dx.doi.org/10.1099/ijs.0.02423-0>.
- Ma B, Hibbing ME, Kim H-S, Reedy RM, Yedidia I, Breuer J, Breuer J, Glasner JD, Perna NT, Kelman A, Charkowski AO. 2007. Host range and molecular phylogenies of the soft rot enterobacterial genera *Pectobacterium* and *Dickeya*. *Phytopathology* 97:1150–1163. <http://dx.doi.org/10.1094/PHYTO-97-9-1150>.

3. Perombelon MCM, Kelman A. 1980. Ecology of the soft rot erwinias. *Annu Rev Phytopathol* 18:361–387. <http://dx.doi.org/10.1146/annurev.py.18.090180.002045>.
4. Pérombelon MCM. 1992. Potato blackleg: epidemiology, host-pathogen interaction and control. *Neth J Plant Pathol* 98:135–146. <http://dx.doi.org/10.1007/BF01974480>.
5. Samson R, Legendre JB, Christen R, Fischer-Le Saux M, Achouak W, Gardan L. 2005. Transfer of *Pectobacterium chrysanthemi* (Burkholder et al. 1953) Brenner et al. 1973 and *Brenneria paradisiaca* to the genus *Dickeya* gen. nov. as *Dickeya chrysanthemi* comb. nov. and *Dickeya paradisiaca* comb. nov. and delineation of four novel species, *Dickeya dadantii* sp. nov., *Dickeya dianthicola* sp. nov., *Dickeya dieffenbachiae* sp. nov. and *Dickeya zeae* sp. nov. *Int J Syst Evol Microbiol* 55:1415–1427. <http://dx.doi.org/10.1099/ijms.0.02791-0>.
6. Hauben L, Moore ER, Vauterin L, Steenackers M, Mergaert J, Verdonck L, Swings J. 1998. Phylogenetic position of phytopathogens within the *Enterobacteriaceae*. *Syst Appl Microbiol* 21:384–397. [http://dx.doi.org/10.1016/S0723-2020\(98\)80048-9](http://dx.doi.org/10.1016/S0723-2020(98)80048-9).
7. Van der Wolf JM, Nijhuis EH, Kowalewska MJ, Saddler GS, Parkinson N, Elphinstone JG, Pritchard L, Toth IK, Lojkowska E, Potrykus M, Waleron M, de Vos P, Cleenwerck I, Pirhonen M, Garland L, Hélias V, Pothier JF, Pflüger V, Duffy B, Tsrör L, Manulis S. 2014. *Dickeya solani* sp. nov., a pectinolytic plant-pathogenic bacterium isolated from potato (*Solanum tuberosum*). *Int J Syst Evol Microbiol* 64:768–774. <http://dx.doi.org/10.1099/ijms.0.052944-0>.
8. Van der Wolf M, J, De Boer H, S. 2007. Bacterial pathogens of potato, p 595–617. In Vreugdenhil D, Bradshaw J, Gebhardt C, Govers F, Mackerron DKL, Taylor MA, Ross HA (ed), *Potato biology and biotechnology*. Elsevier, Amsterdam.
9. Toth IK, van der Wolf JM, Saddler G, Lojkowska E, Hélias V, Pirhonen M, Tsrör Lahkim L, Elphinstone JG. 2011. *Dickeya* species: an emerging problem for potato production in Europe: *Dickeya* spp. on potato in Europe. *Plant Pathol* 60:385–399. <http://dx.doi.org/10.1111/j.1365-3059.2011.02427.x>.
10. Czajkowski R, Pérombelon MCM, van Veen JA, van der Wolf JM. 2011. Control of blackleg and tuber soft rot of potato caused by *Pectobacterium* and *Dickeya* species: a review. *Plant Pathol* 60:999–1013. <http://dx.doi.org/10.1111/j.1365-3059.2011.02470.x>.
11. Czajkowski R, Grabe GJ, van der Wolf JM. 2009. Distribution of *Dickeya* spp. and *Pectobacterium carotovorum* subsp. *carotovorum* in naturally infected seed potatoes. *Eur J Plant Pathol* 125:263–275. <http://dx.doi.org/10.1007/s10658-009-9480-9>.
12. Czajkowski R, de Boer WJ, van Veen JA, van der Wolf JM. 2010. Downward vascular translocation of a green fluorescent protein-tagged strain of *Dickeya* sp.(biovar 3) from stem and leaf inoculation sites on potato. *Phytopathology* 100:1128–1137. <http://dx.doi.org/10.1094/PHYTO-03-10-0093>.
13. Czajkowski R, de Boer WJ, Velvis H, van der Wolf JM. 2010. Systemic colonization of potato plants by a soilborne, green fluorescent protein-tagged strain of *Dickeya* sp. biovar 3. *Phytopathology* 100:134–142. <http://dx.doi.org/10.1094/PHYTO-100-2-0134>.
14. Kwasiborski A, Mondy S, Beury-Cirou A, Faure D. 2013. Genome sequence of the *Pectobacterium atrosepticum* strain cfbp6276, causing blackleg and soft rot diseases on potato plants and tubers. *Genome Announc* 1(3):e00374-13. <http://dx.doi.org/10.1128/genomeA.00374-13>.
15. Khayi S, Mondy S, Beury-Cirou A, Moumni M, Hélias V, Faure D. 2014. Genome sequence of the emerging plant pathogen *Dickeya solani* strain RNS 08.23.3.1A. *Genome Announc* 2(1):e01270-13. <http://dx.doi.org/10.1128/genomeA.01270-13>.
16. Pédrón J, Mondy S, des Essarts YR, Van Gijsegem F, Faure D. 2014. Genomic and metabolic comparison with *Dickeya dadantii* 3937 reveals the emerging *Dickeya solani* potato pathogen to display distinctive metabolic activities and T5SS/T6SS-related toxin repertoire. *BMC Genomics* 15:283. <http://dx.doi.org/10.1186/1471-2164-15-283>.
17. Hélias V, Hamon P, Huchet E, Wolf JVD, Andrivon D. 2012. Two new effective semiselective crystal violet pectate media for isolation of *Pectobacterium* and *Dickeya*. *Plant Pathol* 61:339–345. <http://dx.doi.org/10.1111/j.1365-3059.2011.02508.x>.
18. Crépin A, Barbey C, Beury-Cirou A, Hélias V, Taupin L, Reverchon S, Nasser W, Faure D, Dufour A, Orange N, Feuilloley M, Heurlier K, Burini J-F, Latour X. 2012. Quorum sensing signaling molecules produced by reference and emerging soft-rot bacteria (*Dickeya* and *Pectobacterium* spp.). *PLoS One* 7:e35176. <http://dx.doi.org/10.1371/journal.pone.0035176>.
19. Crépin A, Beury-Cirou A, Barbey C, Farmer C, Hélias V, Burini J-F, Faure D, Latour X. 2012. *N*-Acyl homoserine lactones in diverse *Pectobacterium* and *Dickeya* plant pathogens: diversity, abundance, and involvement in virulence. *Sensors* 12:3484–3497. <http://dx.doi.org/10.3390/s120303484>.
20. Cigna J, Raoul des Essarts Y, Mondy S, Hélias V, Beury-Cirou A, Faure D. 2015. Draft genome sequences of *Pseudomonas fluorescens* strains PA4C2 and PA3G8 and *Pseudomonas putida* PA14H7, three biocontrol bacteria against *Dickeya* phytopathogens. *Genome Announc* 3(1):e01503-14. <http://dx.doi.org/10.1128/genomeA.01503-14>.
21. Boetzer M, Henkel CV, Jansen HJ, Butler D, Pirovano W. 2011. Scaffolding pre-assembled contigs using SSPACE. *Bioinformatics* 27:578–579. <http://dx.doi.org/10.1093/bioinformatics/btq683>.
22. 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. <http://dx.doi.org/10.1186/1471-2164-9-75>.
23. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the rapid annotation of microbial genomes using subsystems technology (RAST). *Nucleic Acids Res* 42:D206–D214. <http://dx.doi.org/10.1093/nar/gkt1226>.