

# Draft Genome Sequences of 17 Isolates of the Plant Pathogenic Bacterium *Dickeya*

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***Dickeya* (formerly *Erwinia chrysanthemi*) species cause diseases on a wide range of crops and ornamental plants worldwide. Here we present the draft sequences of 17 *Dickeya* isolates spanning four *Dickeya* species, including five isolates that are currently unassigned to a species.**

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Species of the *Dickeya* genus (previously *Erwinia chrysanthemi*) of phytopathogenic bacteria cause disease in a wide range of plant species, including crops, worldwide (1). The *Dickeya* genus is currently described as having six species: *dianthicola*, *dadantii*, *zeae*, *chrysanthemi*, and *paradisiaca* (2, 3) and the newly described *D. solani* (4). Draft genome sequences of eight *D. dianthicola* and *D. solani* isolates were recently described (5), and four complete sequences of *Dickeya* strains, *D. paradisiaca* strain Ech703 (accession no. NC\_012880), *D. zeae* strain Ech586 (accession no. NC\_013592), *D. chrysanthemi* strain Ech1591 (accession no. NC\_012912), and *D. dadantii* strain Ech3937 (accession no. NC\_014500), along with a draft *D. zeae* strain sequence, have been deposited in GenBank.

We announce draft genome sequences of 17 isolates of *Dickeya*, including isolates of *D. dadantii*, *D. chrysanthemi*, *D. zeae*, and *D.*

*paradisiaca* and five isolates currently unassigned to a species (Table 1). The 12 isolates assigned to species are *D. dadantii* type strain NCPPB 898, isolated from pelargonium (Comoro Islands); former *D. dadantii* subspecies *dieffenbachiae* type strain NCPPB 2976, isolated from dieffenbachia (United States); *D. dadantii* NCPPB 3537, isolated from potato (Peru); *D. chrysanthemi* type strain NCPPB 402, isolated from chrysanthemum (United States); *D. chrysanthemi* biovar *parthenii* NCPPB 516, from *Parthenium argentatum* (Denmark); *D. chrysanthemi* NCPPB 3533, isolated from potato (United States); *D. zeae* CSL RW192, isolated from river water (England); *D. zeae* MK19, isolated from river water (Scotland); the *D. zeae* phylotype II type strain NCPPB 2538, isolated from maize (United States); *D. zeae* NCPPB 3531 and NCPPB 3532, both isolated from potato (Australia); and *D. paradisiaca* type strain NCPPB 2511, isolated from plantain (Colom-

TABLE 1 Statistics for the 17 draft *Dickeya* genome sequences

Species	Strain	Accession no.	No. of contigs	No. of assembled bases	N <sub>50</sub>	No. of predicted coding sequences
<i>D. chrysanthemi</i>	NCPPB 402 <sup>T</sup>	AOA00000000	12	4,797,070	2,467,266	4,447
<i>D. chrysanthemi</i>	NCPPB 516	AOOC00000000	35	4,614,776	443,362	4,444
<i>D. chrysanthemi</i>	NCPPB 3533	AOOJ00000000	91	4,723,912	102,359	4,467
<i>D. dadantii</i>	NCPPB 898 <sup>T</sup>	AOOE00000000	52	4,933,637	191,282	4,591
<i>D. dadantii</i>	NCPPB 2976 <sup>T</sup>	AOOG00000000	84	4,810,532	114,781	4,552
<i>D. dadantii</i>	NCPPB 3537	AOOL00000000	47	4,805,222	222,170	4,430
<i>D. zeae</i>	NCPPB 2538 <sup>T</sup>	AOOF00000000	46	4,559,915	237,408	4,225
<i>D. zeae</i>	NCPPB 3531	AOOI00000000	29	4,623,158	385,197	4,256
<i>D. zeae</i>	NCPPB 3532	AONW00000000	19	4,555,162	330,312	4,261
<i>D. zeae</i>	CSL RW192	AONY00000000	56	4,696,643	240,868	4,402
<i>D. zeae</i>	MK19	AOOR00000000	35	4,669,100	417,168	4,346
<i>D. paradisiaca</i>	NCPPB 2511 <sup>T</sup>	AONV00000000	43	4,627,470	160,099	4,376
Unassigned	NCPPB 569	AOOD00000000	66	4,215,441	142,291	4,060
Unassigned	NCPPB 3274	AOOH00000000	62	5,110,316	166,211	4,729
Unassigned	CSL RW240/1	AONZ00000000	82	4,380,918	159,782	4,107
Unassigned	DW0440	AOON00000000	234	4,330,262	68,778	4,132
Unassigned	MK7	AOOO00000000	66	4,926,896	190,720	4,513

bia). The five isolates with unassigned species are CSL RW240/1 from river water (England), DW0440 from river water (Finland), MK7 from river water (Scotland), NCPPB 569 from sugarcane (Australia), and NCPPB 3274 from *Aglaonema* (St. Lucia).

All strains were sequenced using 454 pyrosequencing (Roche, Branford, CT). Isolates NCPPB 402<sup>T</sup> and NCPPB 2511<sup>T</sup> were sequenced using paired-end libraries, and the remaining isolates were sequenced using single-end libraries. Sequences of nine strains (CSL RW192, CSLRW 240/1, DW0440, MK7, MK19, NCPPB 402<sup>T</sup>, NCPPB 2538<sup>T</sup>, NCPPB 2976<sup>T</sup>, and NCPPB 3531) were assembled *de novo* using 454 Life Sciences NEWBLER v2.5.3; meta-assemblies of NEWBLER *de novo* and reference-guided assemblies to the above-named sequences from GenBank were used for NCPPB 516 and NCPPB 3533 (to accession no. NC\_012912); NCPPB 2511<sup>T</sup> (to accession no. NC\_012880); NCPPB 569, NCPPB 898<sup>T</sup>, NCPPB 3274, and NCPPB 3537 (to accession no. NC\_014500); and NCPPB 3532 (to accession no. NC\_013592).

Coding sequences for each isolate were annotated using Prodigal and RAST gene callers and BLAST using query sequences known to be missed by those packages. tRNAScan-SE was used to identify tRNA sequences. A detailed comparative genomic analysis of these and previously published draft *Dickeya* sequences (5) will follow in a future publication.

**Nucleotide sequence accession numbers.** The draft sequences of these *Dickeya* strains are available in GenBank under the following accession numbers: [AONV000000000](#) (NCPPB 2511<sup>T</sup>), [AONW000000000](#) (NCPPB 3532), [AONY000000000](#) (CSL RW192), [AONZ000000000](#) (CSL RW240), [AOOA000000000](#) (NCPPB 402<sup>T</sup>), [AIOC000000000](#) (NCPPB 516), [AOD000000000](#) (NCPPB 569), [AOOE000000000](#) (NCPPB 898<sup>T</sup>), [AOF000000000](#) (NCPPB 2538<sup>T</sup>), [AOG000000000](#) (NCPPB 2976<sup>T</sup>), [AOOH000000000](#) (NCPPB 3274), [AOOI000000000](#) (NCPPB 3531), [AOOJ000000000](#) (NCPPB 3533), [AOOL000000000](#) (NCPPB 3537), [AON000000000](#) (DW0440), [AOK000000000](#) (MK7), and [AOKR000000000](#) (MK19).

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## REFERENCES

- Toth IK, van der Wolf JM, Saddler G, Lojkowska E, Helias V, Pirhonen M, Tsror L, Elphinstone JG. 2011. *Dickeya* species: an emerging problem for potato production in Europe. *Plant Pathol.* **60**:385–399.
- 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 zaeae* sp. nov. *Int. J. Syst. Evol. Microbiol.* **55**:1415–1427.
- Brady C, Cleenwerck I, Denman S, Venter S, Rodríguez-Palenzuela P, Coutinho TA, de Vos P. 2012. Proposal to reclassify *Brenneria quercina* (Hildebrand & Schroth 1967) Hauben et al. 1999 into a new genus, *Lonsdalea* gen. nov., as *Lonsdalea quercina* comb. nov., descriptions of *Lonsdalea quercina* subsp. *quercina* comb. nov., *Lonsdalea quercina* subsp. *iberica* subsp. nov. and *Lonsdalea quercina* subsp. *britannica* subsp. nov., emendation of the description of the genus *Brenneria*, reclassification of *Dickeya dieffenbachiae* as *Dickeya dadantii* subsp. *dieffenbachiae* comb. nov., and emendation of the description of *Dickeya dadantii*. *Int. J. Syst. Evol. Microbiol.* **62**: 1592–1602.
- 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, Garlant L, Hélias V, Pothier JF, Pflüger V, Duffy B, Tsror L, Manulis S. 2013. *Dickeya solani* sp. nov., a pectinolytic plant pathogenic bacterium isolated from potato (*Solanum tuberosum*). *Int. J. Syst. Evol. Microbiol.*, in press.
- Pritchard L, Humphris S, Baeyen S, Maes M, Van Vaerenbergh J, Elphinstone J, Saddler G, Toth I. 2013. Draft genome sequences of four *Dickeya dianthicola* and four *Dickeya solani* strains. *Genome Announc.* **1**(4):e00087-12. doi:[10.1128/genomeA.00087-12](#).