bioRxiv preprint doi: https://doi.org/10.1101/2020.05.24.113969; this version posted May 25, 2020. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

Draft Genome Sequences of Seven Strains of *Dickeya dadantii*, a Quick Decline-causing Pathogen in Fruit Trees, Isolated from Japan

Takashi Fujikawa [a,#], Hiroe Hatomi [a], Nobuyoshi Ota [a]

[a]Institute of Fruit Tree and Tea Science, National Agriculture and Food Research Organization (NARO), Tsukuba, Ibaraki, Japan

Running title: Genome sequences of 7 *D. dadantii* strains in Japan

#Corresponding author: ftakashi@affrc.go.jp

bioRxiv preprint doi: https://doi.org/10.1101/2020.05.24.113969; this version posted May 25, 2020. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

Abstract

Plant pathogenic bacterium *Dickeya dadantii* causes quick decline in fruit trees (apple, Japanese pear, and peach). In this study, we report on the draft genome sequences of seven strains of *D. dadantii* isolated from fruit trees with typical quick decline symptoms in Japan.

Dickeya dadantii is a plant pathogenic bacterium that causes soft rot disease in various plants (1). In addition to being a soft-rot pathogen, it causes quick decline (QD) in fruit trees, such as apple, peach, and Japanese pear trees (2, 3). The symptoms of QD include red-brown sap leakage from the trunk and/or branches, softening bark, defoliation, leaf and shoot necrosis, and dieback. However, the lifecycle of *D. dadantii* is not yet well understood. The genetic characteristics of this bacterium will need to be defined to develop effective measures for the control of QD. To this end, we performed whole-genome sequencing (WGS) of seven *D. dadantii* strains isolated from fruit trees with symptoms of QD.

The strains sequenced in this study were obtained from the Institute of Fruit Tree and Tea Science (NARO) (Table 1), isolated from apple, peach, and Japanese pear trees, and identified as *D. dadantii* according to our previous studies (2, 3). The strains were cultivated in YP broth (2) at 27°C for 1 day with agitation at 140 rpm. Then, 1-ml

bioRxiv preprint doi: https://doi.org/10.1101/2020.05.24.113969; this version posted May 25, 2020. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

aliquots of each culture were used for DNA extraction with a DNeasy mini kit (Qiagen, Hilden, Germany). Their genome sequences were determined using WGS, as previously reported (4, 5, 6, 7). Briefly, the genomic DNA was sequenced using an Ion PGM sequencer with an Ion PGM Hi-Q View OT2 kit, an Ion PGM Hi-Q View Sequencing kit, and a 318 Chip kit v2 (Thermo Fisher Scientific, Waltham, MA, USA), according to the manufacturer's instructions. Default parameters were used unless specified otherwise. The sequence reads were quality controlled (quality score <20) and the adapter sequences were removed using the CLC Genomics Workbench (version 10, except for Kunimi3-1 (ver. 12), and BI1-1 (ver. 20)). Using the resulting reads, contigs (filtered with a size >500 bp) were assembled *de novo* using the CLC Genomics Workbench. The draft genomes were annotated using the NCBI Prokaryote Genome Annotation Pipeline (PGAP).

The WGS analysis indicated that the genome size of the seven strains was 4.7-4.9 Mbp with a G+C content of 56.1-56.4% (Table 1). The genome information of this species was previously published in NCBI as 4.7-5.0 Mbp with a G+C content of 56.3-56.5% (e.g. strains 3937 and DSM 18020; GenBank accession no. CP002038 and CP023467, respectively), which supports the results of our WGS analysis. Moreover, PGAP identified 4,311-4,488 genes and multiple rRNA and tRNA genes in these genomes (Table 1). This information can be used to compare the genomes and gene

bioRxiv preprint doi: https://doi.org/10.1101/2020.05.24.113969; this version posted May 25, 2020. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

expression patterns of different strains or species. Therefore, the results of our WGS analysis may help to elucidate the characteristics of *D. dadantii*, a bacterium related to the virulence of QD.

Data availability

All WGS projects in this study have been deposited at DDBJ/ENA/GenBank. The corresponding read data are available from the Sequence Read Archive (SRA) with the accession numbers provided in Table 1.

Acknowledgments

We would like to express our gratitude to Ms. M. Taguchi and Ms. A. Sasaki for supporting this work and to the members of IFTS-NARO for their helpful discussions. We would also like to thank Editage (www.editage.jp) for English language editing. This work received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

References

1. Reverchon S, Nasser W. 2013. *Dickeya* ecology, environment sensing and regulation of virulence programme. Environ Microbiol Rep 5:622□636.

bioRxiv preprint doi: https://doi.org/10.1101/2020.05.24.113969; this version posted May 25, 2020. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

2. Ota N, Fujikawa T. 2020. Reproduction of bacterial quick decline of fruit trees after soil inoculation with *Dickeya dadantii*. J Gen Plant Pathol 86:199□204.

3. Fujikawa T, Ota N, Sasaki M, Nakamura T, Iwanami T. 2019. Emergence of apple bacterial quick decline caused by *Dickeya dadantii* in Japan. J Gen Plant Pathol 85:314□319.

4. Fujikawa T, Sawada H. 2016. Genome analysis of the kiwifruit canker pathogen *Pseudomonas syringae* pv. *actinidiae* biovar 5. Sci Rep 6:21399.

5. Fujikawa T, Sawada H. 2019. Genome analysis of *Pseudomonas syringae* pv. *actinidiae* biovar 6, which produces the phytotoxins, phaseolotoxin and coronatine. Sci Rep 9:3836.

6. Nakazono-Nagaoka E, Fujikawa T, Shikata A, Tachaapaikoon C, Waeonukul R, Pason P, Ratanakhanokchai K, Kosugi A. 2019. Draft genome sequence data of *Clostridium thermocellum* PAL5 possesing high cellulose-degradation ability. Data in Brief 25:104274.

7. Sawada H, Fujikawa T, Nishiwaki Y, Horita H. 2020. *Pseudomonas kitaguniensis* sp. Nov., a pathogen causing bacterial rot of Welsh onion in Japan. Int J Sys Evol Microbiol. https://doi.org/10.1099/ijsem.0.004123

Table 1. Genome data and accession numbers of seven *Dickeya dadantii*.

	Strain information		Genome information					PGAP[a] annotation			Reads information			
Strain	**Isolation host**	**Isolation area**	**GenBank accession no.**	**Genome size (bp)**	**G+C content (mol%)**	**No. of contigs**	**N_{50}**	**Total no. of genes**	**rRNAs (5S, 16S, 23S)**	**tRNAs**	**SRA[b] accession no.**	**No. of reads**	**Average length (bp)**	**Genome coverage (×)**
BI1-1	Apple	Japan: Iwate	JABEOZ000000000	4,663,807	56.2	271	39,637	4,311	1, 2, 1	46	SRR11696188	673,373	229.2	33.1
BI3-1	Apple	Japan: Iwate	PHRA00000000	4,771,676	56.3	92	151,183	4,331	4, 1, 1	61	SRR11692751	5,046,907	298.9	316.1
Aka1-1	Peach	Japan: Fukushima	JABEPA000000000	4,714,768	56.4	268	43,532	4,429	5, 1, 1	57	SRR11696187	592,688	258.8	32.5
Yana2-2	Peach	Japan: Fukushima	JABEPB000000000	4,825,596	56.4	204	61,681	4,432	3, 2, 1	48	SRR11696186	1,510,292	255.4	79.9
Kunimi-3	Peach	Japan: Fukushima	SMHE00000000	4,869,298	56.5	141	96,135	4,446	2, 1, 2	62	SRR11730645	1,941,545	287.6	114.7
Kousui1-1	Japanese pear	Japan: Saga	JABEPC000000000	4,881,710	56.1	193	68,290	4,488	5, 1, 3	53	SRR11696185	1,308,248	263.2	70.5
Housui2-1	Japanese pear	Japan: Saga	JABEPD000000000	4,882,493	56.2	197	56,134	4,481	4, 1, 6	49	SRR11696184	1,746,612	258.4	92.4

[a]NCBI Pipeline Genome Annotation Pipeline

[b]short read archive

bioRxiv preprint doi: https://doi.org/10.1101/2020.05.24.113969; this version posted May 25, 2020. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.