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Genome of *Dietzia cinnamea* 55, a desert-isolated microbe with plant growth-promoting properties for grain crops

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ABSTRACT Here, we report the genome sequence of *Dietzia cinnamea* 55, isolated from the Negev Desert, Israel. *D. cinnamea* 55 was found to promote the growth of several cereal crops (corn, wheat, and pearl millet) in greenhouse and field studies.

KEYWORDS whole genome sequencing, *Dietzia cinnamea*, plant growth promotion, PGPR

The genus *Dietzia* is composed of Gram-positive, aerobic, non-sporulating, non-acid-alcohol fast, catalase-positive actinobacteria (1). Members of the genus *Dietzia* have been isolated from a variety of habitats, including clinical samples (1–3) and environmental sources, such as soil (4, 5) and plant tissue (6). Studies have shown that *Dietzia* spp. can promote plant growth, especially under conditions of environmental stress (7–9). *Dietzia cinnamea* 55 was isolated from the rhizosphere of the shrub *Zygophyllum dumosum* in the Negev Desert, Israel (10). Biosafety testing against the model organisms *Caenorhabditis elegans* and *Galleria mellonella* supports lack of pathogenicity, whereas inoculation studies of the economically significant cereal crops corn, wheat, and pearl millet (Fig. 1) have shown that *D. cinnamea* 55 is an efficient plant growth-promoting bacterium (9).

D. cinnamea 55 was obtained from the laboratory collection of AMH and cultivated in LB medium aerobically at 30°C (9). DNA was extracted using a Quick-DNA HMW Magbead Kit (Zymo Research) per the manufacturer's instructions and fragmented using Covaris gTubes following instructions from the manufacturer (4 passes at 7,000 rpm through the gTube orifice). The average size of the sheared gDNA was checked at the TapeStation 4200 (Agilent). Multiplexed microbial libraries were prepared using the PacBio SMRTbell prep kit 3.0 together with the SMRTbell barcoded adapters 3.0 according to the PacBio protocol. Final whole genome libraries were not size-selected but simply purified via a standard procedure using 1× SMRTbell cleanup beads. DNA sequencing was performed using the PacBio Sequel IIe platform. Demultiplexing and adapter trimming were done using Lima v2.9.0 (https://github.com/pacificbiosciences/barcoding). All reads were then targeted for assembly by Canu v2.2 (11). Assembled genomes were further refined by Circlator v1.5.5 (12) to identify circular contigs, remove redundant non-circular contigs, and rotate circular contigs to start with *dnaA*, which resulted in a non-circular genome and circular plasmid (Table 1). A completeness check was performed by CheckM v1.0.18 (13), and the N50 value was determined by Assembly stats v1.01 (https://github.com/sanger-pathogens/assembly-stats). Genome ORF calling and annotation were performed by NCBI's PGAP v6.6 (14) and the IMG Annotation Pipeline v.5.1.17 (15). The high-quality reads, completeness, and N50 quality values for *D. cinnamea* 55 strain were 31,790, 99.41%, and 3,621,220 bp, respectively, with an average nucleotide identity (ANI) value of 96.2% against *D. cinnamea* IMMIB RIV-399^T. ANI was

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FIG 1 Response of food crop plants *to D. cinnamea* 55 inoculation. Corn (A), wheat (B), and pearl millet (C) plants inoculated with *D. cinnamea* 55 (right side of each panel) result in significantly increased grain production compared with uninoculated controls (left) as measured by mass and seed number.

TABLE 1 Properties of the finished *D. cinnamea* 55 genome

Contig	Topology	Size (bp)	GC%	Coverage	Protein coding	# 16S	# tRNA
#1	Non-circular	3,621,320	71	66.0X	3,247	4	50
#2	Circular	73,967	65.5	66.0X	74	0	0
Total		3,695,287	71	66.0X	3,321	4	50

calculated using contigs and the Ezbiocloud ANI calculator (16). All software tools used default parameters that were stated in each tool's manual.

Properties of the finished genome of *D. cinnamea* 55 are summarized in Table 1. All 16S sequences had greater than 99.65% similarity to the published 16S sequence of *D. cinnamea* IMMIB RIV-399^T, confirming it was correctly assigned (17, 18).

The finished genome of *D. cinnamea* 55 includes genes related to abiotic stress tolerance, including oxidative stress (catalase, peroxidase, and superoxide dismutase), osmotic stress (L-ectoine synthase and trehalose synthase), and heavy metal tolerance (multicopper oxidase, copper-exporting ATPase, Cd2+/Zn2+-exporting ATPase, and arsenate reductase). Additionally, potential plant growth-promoting functions, such as siderophore biosynthesis (siderophore synthetase, L-2,4-diaminobutyrate decarboxylase, and lysine N6-hydroxylase) and acetoin biosynthesis (acetolactate synthase and zinc-type alcohol dehydrogenase), are also present. Finally, the genome encodes genes for carotenoid biosynthesis (phytoene synthase, phytoene dehydrogenase, and phytoene desaturase), which has been implicated in both oxidative stress tolerance and rhizosphere colonization (19).

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DATA AVAILABILITY

The raw sequencing reads have been deposited under the SRA accession number SRR27400239, and the assembled genome is listed under the GenBank accession numbers CP143053 and CP143054. The genome sequence has also been deposited in IMG/M under the taxon ID 8076078741.

REFERENCES

1. Koerner RJ, Goodfellow M, Jones AL. 2009. The genus *Dietzia*: a new home for some known and emerging opportunist pathogens. FEMS Immunol Med Microbiol 55:296–305. https://doi.org/10.1111/j.1574-695X.2008.00513.x
2. Brown WD, Feinberg N, Stedman E, Dejace J, Hale AJ. 2022. *Dietzia cinnamea*: an increasingly recognized human pathogen. IDCases 29:e01539. https://doi.org/10.1016/j.idcr.2022.e01539
3. Rammer P, Calum H, Moser C, Björnsdóttir MK, Smedegaard H, Høiby N, Bjarnsholt T. 2013. *Dietzia papillomatosis* bacteremia. J Clin Microbiol 51:1977–1978. https://doi.org/10.1128/JCM.03313-12
4. Yamamura H, Lisdiyanti P, Ridwan R, Ratnakomala S, Sarawati R, Lestari Y, Triana E, Kartina G, Widyastuti Y, Ando K. 2010. *Dietzia timorensis* sp. nov., isolated from soil. Int J Syst Evol Microbiol 60:451–454. https://doi.org/10.1099/ijs.0.012229-0
5. Li J, Chen C, Zhao GZ, Klenk HP, Pukall R, Zhang YQ, Tang SK, Li WJ. 2009. Description of *Dietzia lutea* sp. nov., isolated from a desert soil in Egypt. Syst Appl Microbiol 32:118–123. https://doi.org/10.1016/j.syapm.2008.11.007
6. Li J, Zhao G-Z, Zhang Y-Q, Klenk H-P, Pukall R, Qin S, Xu L-H, Li W-J. 2008. *Dietzia schimae* sp. nov. and *Dietzia cercidiphylli* sp. nov., from surface-sterilized plant tissues. Int J Syst Evol Microbiol 58:2549–2554. https://doi.org/10.1099/ijs.0.2008/000919-0
7. Bharti N, Pandey SS, Barnawal D, Patel VK, Kalra A. 2016. Plant growth promoting rhizobacteria *Dietzia natronolimnaea* modulates the expression of stress responsive genes providing protection of wheat from salinity stress. Sci Rep 6:34768. https://doi.org/10.1038/srep34768
8. Barnawal D, Bharti N, Pandey SS, Pandey A, Chanotiya CS, Kalra A. 2017. Plant growth-promoting rhizobacteria enhance wheat salt and drought stress tolerance by altering endogenous phytohormone levels and TaCTR1/TaDREB2 expression. Physiol Plant 161:502–514. https://doi.org/10.1111/ppl.12614
9. Khan N, Martínez-Hidalgo P, Humm EA, Maymon M, Kaplan D, Hirsch AM. 2020. Inoculation with a microbe isolated from the negev desert enhances corn growth. Front Microbiol 11:1149. https://doi.org/10.3389/fmicb.2020.01149
10. Kaplan D, Maymon M, Agapakis CM, Lee A, Wang A, Prigge BA, Volkogon M, Hirsch AM. 2013. A survey of the microbial community in the rhizosphere of two dominant shrubs of the Negev Desert highlands, *Zygophyllum dumosum* (Zygophyllaceae) and *Atriplex halimus* (Amaranthaceae), using cultivation-dependent and cultivation-independent methods. Am J Bot 100:1713–1725. https://doi.org/10.3732/ajb.1200615
11. Koren S, Walenz BP, Berlin K, Miller JR, Bergman NH, Phillippy AM. 2017. Canu: scalable and accurate long-read assembly via adaptive*k*-mer weighting and repeat separation. Genome Res 27:722–736. https://doi.org/10.1101/gr.215087.116
12. Hunt M, Silva ND, Otto TD, Parkhill J, Keane JA, Harris SR. 2015. Circlator: automated circularization of genome assemblies using long sequencing reads. Genome Biol 16:294. https://doi.org/10.1186/s13059-015-0849-0
13. Parks DH, Imelfort M, Skennerton CT, Hugenholtz P, Tyson GW. 2015. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. Genome Res 25:1043–1055. https://doi.org/10.1101/gr.186072.114
14. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI prokaryotic genome annotation pipeline. Nucleic Acids Res 44:6614–6624. https://doi.org/10.1093/nar/gkw569
15. Chen I-M, Chu K, Palaniappan K, Ratner A, Huang J, Huntemann M, Hajek P, Ritter SJ, Webb C, Wu D, Varghese NJ, Reddy TBK, Mukherjee S, Ovchinnikova G, Nolan M, Seshadri R, Roux S, Visel A, Woyke T, Eloe-Fadrosh EA, Kyrpides NC, Ivanova NN. 2023. The IMG/M data management and analysis system v.7: content updates and new features. Nucleic Acids Res 51:D723–D732. https://doi.org/10.1093/nar/gkac976
16. Yoon SH, Ha SM, Lim JM, Kwon SJ, Chun J. 2017. A large-scale evaluation of algorithms to calculate average nucleotide identity. Antonie Van Leeuwenhoek 110:1281–1286. https://doi.org/10.1007/s10482-017-0844-4
17. Lee I, Chalita M, Ha SM, Na SI, Yoon SH, Chun J. 2017. ContEst16S: an algorithm that identifies contaminated prokaryotic genomes using 16S RNA gene sequences. Int J Syst Evol Microbiol 67:2053–2057. https://doi.org/10.1099/ijsem.0.001872
18. Yoon SH, Ha SM, Kwon S, Lim J, Kim Y, Seo H, Chun J. 2017. Introducing EzBioCloud: a taxonomically united database of 16S rRNA gene sequences and whole-genome assemblies. Int J Syst Evol Microbiol 67:1613–1617. https://doi.org/10.1099/ijsem.0.001755
19. Bible AN, Fletcher SJ, Pelletier DA, Schadt CW, Jawdy SS, Weston DJ, Engle NL, Tschaplinski T, Masyuko R, Polisetti S, Bohn PW, Coutinho TA, Doktycz MJ, Morrell-Falvey JL. 2016. A carotenoid-deficient mutant in *Pantoea* sp. YR343, a bacteria isolated from the rhizosphere of *Populus deltoides*, is defective in root colonization. Front Microbiol 7:491. https://doi.org/10.3389/fmicb.2016.00491