



Complete Genome Sequence of *Dietzia* sp. Strain WMMA184, a Marine Coral-Associated Bacterium

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ABSTRACT *Dietzia* sp. strain WMMA184 was isolated from the marine coral *Montastraea faveolata* as part of ongoing drug discovery efforts. Analysis of the 4.16-Mb genome provides information regarding interspecies interactions as it pertains to the regulation of secondary metabolism and natural product biosynthesis potential.

Over the last decade, initiatives to identify and develop new chemotypes as tools in the fight against drug resistance have focused, in large part, on devising ways to activate otherwise dormant or “cryptic” biosynthetic gene clusters (BGCs) within microbial organisms (1–3). One means by which this has been accomplished involves the coculturing of two or more microbes within the same vessel; such fermentations often trigger the production of natural products that would otherwise not be produced by virtue of their BGC dormancy (4, 5). It is now clear, as reflected both in the lab and in naturally occurring microbiome systems (6), that microbial cross-communications (both competitive and collaborative in nature) enable the production of small-molecule secondary metabolites that are otherwise unattainable; BGCs for such compounds in the absence of other microbial stimuli remain silent and nonproductive. Coculturing approaches to new chemotypes dictate the importance of genomic data for cocultured organisms; the diversities attainable by such new chemotypes/structures stem, in large part, from the diversity of cocultured organisms (7, 8). In light of these considerations, it is noteworthy that mycolic acid-producing bacteria inclusive of, but not limited to, the genera *Nocardia*, *Mycobacterium*, and *Dietzia* are known to effectively activate actinorhodin and undecylprodigiosin BGCs in *Streptomyces lividans* (9).

To date, there have been only 14 *Dietzia* assemblies deposited in GenBank that are representative of organisms isolated from widely varied environments (10–20); some of these represent significant human pathogens or candidate pathogens (10, 13, 15–18). Marine-derived *Dietzia* representatives are well-known, although only two, *Dietzia alimentaria* 72^T from the Korean seafood *jeotgal* (19), and *Dietzia* sp. strain 111N12-1 from seawater samples from the South China Sea (20), have been rigorously sequenced and deposited to GenBank thus far. This report, as part of our coculture initiatives to identify new antimicrobial chemotypes, signals the GenBank deposition of the third marine-derived *Dietzia* genome sequence.

Dietzia sp. strain WMMA184 was isolated in 2011 from coral mucus of *Montastraea faveolata* collected off the coast of the Florida Keys. WMMA184 was isolated from a plate prepared using M1 medium (21) supplemented with 50% artificial seawater (ASW).

The complete genome of *Dietzia* sp. WMMA184 was sequenced at the Duke Center for Genomic and Computational Biology (GCB) using PacBio RS II (Pacific Biosciences) technology. Reads were assembled using the HGAP assembler (22) into six contigs. Open reading frames were predicted by Prodigal (23) and annotated using the Rapid Annotation using Subsystems Technology (RAST) software (24). The genome was found

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to be 4.16 Mb in length, with a GC content of 69.9%. The biosynthetic potential of the organism was assessed using antiSMASH 4.0 (25) and PRediction Informatics for Secondary Metabolomes (PRISM) (26). Out of 48 putative gene clusters identified, there are 2 terpene clusters, one type I polyketide/saccharide hybrid cluster, and one siderophore BGC housed in the WMMA184 genome.

Accession number(s). The complete genome sequence of *Dietzia* sp. WMMA184 has been deposited at DDBJ/EMBL/GenBank under the project accession number [NXEI00000000](https://ncbi.nlm.nih.gov/nucl/NXEI00000000), which correlates to BioProject PRJNA400578.

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REFERENCES

- Chiang YM, Chang SL, Oakley BR, Wang CC. 2011. Recent advances in awakening silent biosynthetic gene clusters and linking orphan clusters to natural products in microorganisms. *Curr Opin Chem Biol* 15:137–143. <https://doi.org/10.1016/j.cbpa.2010.10.011>.
- Derewacz DK, Covington BC, McLean JA, Bachmann BO. 2015. Mapping microbial response metabolomes for induced natural product discovery. *ACS Chem Biol* 10:1998–2006. <https://doi.org/10.1021/acscchembio.5b00001>.
- Netzker T, Fischer J, Weber J, Mattern DJ, König CC, Valiante V, Schroeckh V, Brakhage AA. 2015. Microbial communication leading to the activation of silent fungal secondary metabolite gene clusters. *Front Microbiol* 6:299. <https://doi.org/10.3389/fmicb.2015.00299>.
- Bertrand S, Bohni N, Schnee S, Schumpp O, Gindro K, Wolfender JL. 2014. Metabolite induction via microorganism co-culture: a potential way to enhance chemical diversity for drug discovery. *Biotechnol Adv* 32:1180–1204. <https://doi.org/10.1016/j.biotechadv.2014.03.001>.
- Marmann A, Aly AH, Lin W, Wang B, Proksch P. 2014. Co-cultivation—a powerful emerging tool for enhancing the chemical diversity of microorganisms. *Mar Drugs* 12:1043–1065. <https://doi.org/10.3390/md12021043>.
- Adu-Oppong B, Gasparrini AJ, Dantas G. 2017. Genomic and functional techniques to mine the microbiome for novel antimicrobials and antimicrobial resistance genes. *Ann N Y Acad Sci* 1388:42–58. <https://doi.org/10.1111/nyas.13257>.
- Bode HB, Bethe B, Höfs R, Zeeck A. 2002. Big effects from small changes: possible ways to explore nature's chemical diversity. *ChemBiochem* 3:619–627. [https://doi.org/10.1002/1439-7633\(20020703\)3:7<619::AID-CBIC619>3.0.CO;2-9](https://doi.org/10.1002/1439-7633(20020703)3:7<619::AID-CBIC619>3.0.CO;2-9).
- Cimermancic P, Medema MH, Claesen J, Kurita K, Wieland Brown LC, Mavrommatis K, Pati A, Godfrey PA, Koehrsen M, Clardy J, Birren BW, Takano E, Sali A, Linington RG, Fischbach MA. 2014. Insights into secondary metabolism from a global analysis of prokaryotic biosynthetic gene clusters. *Cell* 158:412–421.
- Onaka H. 2017. Novel antibiotic screening methods to awaken silent or cryptic secondary metabolic pathways in actinomycetes. *J Antibiot (Tokyo)* 70:865–870. <https://doi.org/10.1038/ja.2017.51>.
- 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>.
- Procópio L, Alvarez VM, Jurelevicius DA, Hansen L, Sørensen SJ, Cardoso JS, Pádula M, Leitão AC, Seldin L, van Elsas JD. 2012. Insight from the draft genome of *Dietzia cinnamea* P4 reveals mechanisms of survival in complex tropical soil habitats and biotechnology potential. *Antonie Leeuwenhoek* 101:289–302. <https://doi.org/10.1007/s10482-011-9633-7>.
- Fang H, Hu B, Nie Y, Tang YQ, Wu XL. 2017. The complete genome of *Dietzia timorensis* ID05-A0528^T revealed the genetic basis for its saline-alkali tolerance. *J Biotechnol* 241:11–13. <https://doi.org/10.1016/j.jbiotec.2016.10.015>.
- Ganguly S, Jimenez-Galisteo G, Pletzer D, Winterhalter M, Benz R, Viñas M. 2016. Draft genome sequence of *Dietzia maris* DSM 43672, a Gram-positive bacterium of the mycolata group. *Genome Announc* 4:e00542-16. <https://doi.org/10.1128/genomeA.00542-16>.
- Diep AL, Lang JM, Darling AE, Eisen JA, Coil DA. 2013. Draft genome sequence of *Dietzia* sp. strain UCD-THP (phylum *Actinobacteria*). *Genome Announc* 1:e00197-13. <https://doi.org/10.1128/genomeA.00197-13>.
- Pilares L, Agüero J, Vázquez-Boland JA, Martínez-Martínez L, Navas J. 2010. Identification of atypical *Rhodococcus*-like clinical isolates as *Dietzia* spp. by 16S rRNA gene sequencing. *J Clin Microbiol* 48:1904–1907. <https://doi.org/10.1128/JCM.01730-09>.
- Niwa H, Lasker BA, Hinrikson HP, Franzen CG, Steigerwalt AG, Whitney AM, Brown JM. 2012. Characterization of human clinical isolates of *Dietzia* species previously misidentified as *Rhodococcus equi*. *Eur J Clin Microbiol Infect Dis* 31:811–820. <https://doi.org/10.1007/s10096-011-1379-7>.
- Hirvonen JJ, Lepistö I, Mero S, Kaukoranta SS. 2012. First isolation of *Dietzia cinnamea* from a dog bite wound in an adult patient. *J Clin Microbiol* 50:4163–4165. <https://doi.org/10.1128/JCM.01939-12>.
- Jones AL, Koerner RJ, Natarajan S, Perry JD, Goodfellow M. 2008. *Dietzia papillomatosis* sp. nov., a novel actinomycete isolated from the skin of an immunocompetent patient with confluent and reticulated papillomatosis. *Int J Syst Evol Microbiol* 58:68–72. <https://doi.org/10.1099/ijs.0.65178-0>.
- Kim J, Roh SW, Bae JW. 2011. Draft genome sequence of *Dietzia alimentaria* 72^T, belonging to the family *Dietziaceae*, isolated from a traditional Korean food. *J Bacteriol* 193:6791. <https://doi.org/10.1128/JB.06229-11>.
- Yang S, Yu M, Chen J. 2017. Draft genome analysis of *Dietzia* sp. 11N12-1, isolated from the South China Sea with bioremediation activity. *Braz J Microbiol* 48:393–394. <https://doi.org/10.1016/j.bjm.2016.10.029>.
- Mincer TJ, Jensen PR, Kauffman CA, Fenical W. 2002. Widespread and persistent populations of a major new marine actinomycete taxon in ocean sediments. *Appl Environ Microbiol* 68:5005–5011. <https://doi.org/10.1128/AEM.68.10.5005-5011.2002>.
- Ge F, Wang LS, Kim J. 2005. The cobweb of life revealed by genome-scale estimates of horizontal gene transfer. *PLoS Biol* 3:e316. <https://doi.org/10.1371/journal.pbio.0030316>.
- Hyatt B, Chen GL, LoCascio PF, Land ML, Larimer FW, Hauser LJ. 2010. Prodigal: prokaryotic gene recognition and translation initiation site identification. *BMC Bioinformatics* 11:119. <https://doi.org/10.1186/1471-2105-11-119>.
- 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. <https://doi.org/10.1093/nar/gkt1226>.
- Blin K, Wolf T, Chevrette MG, Lu X, Schwalen CJ, Kautsar SA, Suarez Duran HG, de Los Santos ELC, Kim HU, Nave M, Dickschat JS, Mitchell DA, Shelest E, Breitling R, Takano E, Lee SY, Weber T, Medema MH. 2017. antiSMASH 4.0—improvements in chemistry prediction and gene cluster boundary identification. *Nucleic Acids Res* 45:W36–W41. <https://doi.org/10.1093/nar/gkx319>.
- Skinnider MA, Dejong CA, Rees PN, Johnston CW, Li H, Webster ALH, Wyatt MA, Magarvey NA. 2015. Genomes to natural products PRediction Informatics for Secondary Metabolomes (PRISM). *Nucleic Acids Res* 43:9645–9662. <https://doi.org/10.1093/nar/gkv1012>.