

Draft genome sequence of a novel species of *Winogradskyella* (strain PC D3.3) isolated from a Red Antarctic macroalgae

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ABSTRACT We report the draft genome sequence of *Winogradskyella* sp. nov. PC D3.3, a Flavobacteriia isolated from the surface of the red macroalgae *Plocamium cartilagineum* collected in King George Island, Antarctica. The genome assembly comprised 4,212,977 bp, with 33.32% G + C content and 3,748 coding sequences.

KEYWORDS Antarctica, *Winogradskyella*, macroalgae, *Plocamium cartilagineum*, draft genome, Flavobacteriia

During a survey of culturable bacteria from Antarctic macroalgae, a strain of *Winogradskyella*, designated PC D3.3, was isolated from the red alga *Plocamium cartilagineum*. Members of *Winogradskyella* (Flavobacteriaceae) are gram-negative, rod-shaped, and produce non-diffusible, yellow to orange pigments (1). They are widespread in marine environments (1) and are commonly associated with macroalgae (2–4), but reports from Antarctic macroalgae remain scarce (5, 6), underscoring the value of sequencing strain PC D3.3.

PC D3.3 was isolated from the surface of a healthy *P. cartilagineum* thallus collected in the subtidal zone of Shoa Island (62°12'12"S, 58°56'37"W), King George Island, Antarctica, on marine agar 2216 (BD) at 20°C. Microbiological processing of macroalgal samples followed Sánchez Hinojosa et al. (6). Colonies were purified by repeated streaking, and purity was verified by Gram staining and colony morphology. Genomic DNA was extracted from 72 h marine broth cultures using the GeneJET Genomic DNA Purification Kit and quantified with a Qubit fluorometer. Whole-genome sequencing was performed at AUSTRAL-omics (Valdivia, Chile). Libraries were prepared from 400 ng DNA with the ONT Native Barcoding Kit 24 V14 and sequenced on a MinION using a Flongle (R10.4.1) flow cell. Bead-based cleanups were performed according to the ONT protocol, without additional size selection. Reads were basecalled with Dorado v0.5.1 (high-accuracy model; <https://github.com/nanoporetech/dorado>), assessed for quality with NanoPlot v1.42.0 (7), and reads with $Q < 7$ were discarded. *De novo* assembly was performed with Flye v2.9.1 (8), and genome annotation was performed with Prokka v1.14.6 (9) and DRAM (10). Carbohydrate-active enzymes were identified in DRAM using dbCAN HMM profiles (E -value $< 1 \times 10^{-15}$; coverage > 0.35). Average nucleotide identity (ANI) and average amino acid identity were calculated with FastANI (11) and CompareM (<https://github.com/donovan-h-parks/CompareM>), and digital DNA-DNA hybridization values were estimated with the GGDC server (12). Default parameters were used unless otherwise specified.

The complete 16S rRNA gene was retrieved from the assembled genome and compared against EzBioCloud version 2025.04.21 (<https://www.ezbiocloud.net/>) (13). PC D3.3 showed 98.14% sequence similarity to *Winogradskyella ludwigii* HL116^T (accession no. JABFDF000000000) and 97.85% to *Winogradskyella sediminis* S5-23-3^T (accession no. KF312887). At the whole-genome level, PC D3.3 was closest to *Winogradskyella psychrotolerans* D3R19 (GCF_018860565.1; 85.8% ANI), followed by *Winogradskyella*

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thalassocola DSM 15363 ([GCF_900099995.1](https://doi.org/10.1093/g3journal/gkz095); 85.4% ANI). Digital DNA-DNA hybridization (formula 2) yielded a maximum value of 29.0% with *W. psychrotolerans* D3R19, far below the 70% species threshold. These results suggest that PC D3.3 is likely a novel species within the genus *Winogradskyella*.

Oxford Nanopore sequencing produced 91,978 reads (719.4 Mb total) with a raw read N50 of 12,793 bp, and the genome of strain PC D3.3 was assembled into a single 4.21 Mb circular contig (assembly N50 = 4.21 Mb). The genome size is 4,212,977 bp, with 33.32% G + C content. The draft genome contains 3,748 coding sequences and 61 RNA genes (12 rRNA, 48 tRNA, and 1 transfer-messenger RNA). The genome encodes diverse polysaccharide-degrading enzymes for starch, hemicellulose (GH13 and GH43), alginate, and pectin (PL1, PL6, PL7, PL14, and PL17), suggesting that *Winogradskyella* sp. PC D3.3 contributes to the marine carbon cycle by utilizing polysaccharides from its algal host.

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Jojoy John, Conceptualization, Data curation, Formal analysis, Methodology, Validation, Writing – original draft, Writing – review and editing | Amit Kumar, Conceptualization, Formal analysis, Writing – original draft, Writing – review and editing | Jenifer Alvarez, Investigation | Radhakrishnan Mannikam, Conceptualization, Writing – review and editing | Luis Vargas-Chacoff, Conceptualization, Funding acquisition, Writing – review and editing | Sergio Leiva Poveda, Conceptualization, Data curation, Funding acquisition, Investigation, Methodology, Project administration, Supervision, Writing – original draft, Writing – review and editing

DATA AVAILABILITY

All data are available under BioProject [PRJNA1381634](https://doi.org/10.6084/m9.figshare.31259503). Raw reads are deposited as accession [SRS27497605](https://doi.org/10.6084/m9.figshare.31259503), the genome assembly under GenBank accession [JBSYWG000000000](https://doi.org/10.6084/m9.figshare.31259503), and DRAM annotations at <https://doi.org/10.6084/m9.figshare.31259503>. This is the first version of the genome.

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