





# High-Quality Genome Assembly of *Nannochloris desiccata* 2437 and Its Associated Bacterial Community

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**ABSTRACT** High-quality genome sequences were generated for the nonaxenic marine microalga *Nannochloris desiccata* UTEX 2437 and eight of its associated environmental bacterial species. *N. desiccata* UTEX 2437 is diploid, and its 20.738-Mbp nuclear genome sequence is assembled in 29 contigs.

Microalgae are being widely investigated for the production of biofuels and nutraceuticals. The industry is continuously searching for species with phenotypes that include fast growth and high lipid yields, particularly those grown in brackish or marine waters. A microbial mat was collected from a salt marsh in Laguna Figueroa, Baja California, Mexico, and desiccated. In 1984, a eukaryotic alga from this mat was reconstituted and deposited into the UTEX culture collection as *Chlorella desiccata* 2437, this culture includes a natural microbial community (1). An axenic isolate from UTEX 2437, UTEX 2526, was previously sequenced (NCBI GenBank accession number [JAGTXX000000000](https://www.ncbi.nlm.nih.gov/nuclseq/JAGTXX000000000)). Phylogenetic analysis revealed UTEX 2526 to reside in the genus *Nannochloris* (14).

*Nannochloris desiccata* 2437 was purchased from UTEX, maintained on f/2 agar plates, then grown in liquid silicate-free, modified f/2 medium (Sanders et al., submitted). The culture was illuminated with 300  $\mu\text{moles photons m}^{-2} \text{ s}^{-1}$  with a 16/8-h light/dark cycle and maintained in a 1%  $\text{CO}_2$  atmosphere. Cell pellets were stored at  $-80^\circ\text{C}$ , then thawed, washed, and embedded into 1% low melting point (LMP) agarose plugs. Protoplasting solution was used to remove the cell wall, followed by lysis using proteinase K and digestion using beta-agarase I to release the genomic DNA (gDNA) into the solution. The DNA was subsequently purified using a high salt:phenol:chloroform:isoamyl alcohol protocol and concentrated using AMPure PB beads. gDNA was fragmented using the Megaruptor 2 instrument with a target size of 20 kbp. Libraries were constructed using the PacBio Express low DNA input HiFi template prep protocol, size selected using diluted AMPure PB beads, which removed all DNA fragments of  $<3$  kbp, and sequenced on a PacBio Sequel instrument using chemistry v3.0 and DNA polymerase v3.0. Two single-molecule real-time (SMRT) cells 1M LR were used per library. Twenty-hour movies were recorded, and HiFi reads were extracted using PacBio's ccs v4.2.0 module (<https://github.com/PacificBiosciences/ccs>) (details in the work of Sanders et al., submitted).

Based on the knowledge that this alga species is diploid from the previously assembled UTEX 2526, HiFi reads were assembled using the diploid aware assembler Hifiasm v0.12-r304, with default parameters (2). Bacterial reads were assembled using Flye v2.8.2-b1689 with the  $-\text{meta}$  parameter. The resulting contigs were binned using two different binning tools: METABAT2 v2.12.1 (3) and MaxBin2 v2.2.7 (4). The resulting bins were combined into consensus bins using DASTool v1.1.2 (5). The consensus bins were classified using GTDB-Tk (6), the completeness was assessed using BUSCO (7), and the relative abundance was calculated using the CheckM tools "coverage"

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**TABLE 1** Classification, completeness, and relative abundance information for nine bacterial species identified within UTEX 2437 using GTDB-Tk<sup>a</sup>

GenBank assembly accession no.	Phylum	Class	Order	Family	Genus	Completeness (%)	Abundance (%)
<a href="#">GCA_019739195.1</a>	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Chryseoglobus	97.6	22.3
<a href="#">GCA_019739295.1</a>	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae	Taibaiella	39.5	4.0
<a href="#">GCA_019739315.1</a>	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas	50.0	2.9
<a href="#">GCA_019739235.1</a>	Proteobacteria	Alphaproteobacteria	Hyphomicrobiales	Phyllobacteriaceae	Mesorhizobium	96.8	9.4
<a href="#">GCA_019739205.1</a>	Proteobacteria	Alphaproteobacteria	Hyphomicrobiales	Rhizobiaceae	Rhizobium	82.3	6.3
<a href="#">GCA_019739215.1</a>	Proteobacteria	Alphaproteobacteria	Hyphomicrobiales	Rhizobiaceae	Rhizobium	74.2	5.1
<a href="#">GCA_019739335.1</a>	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Erythrobacteraceae	Erythrobacter	99.2	29.4
<a href="#">GCA_019739225.1</a>	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Aquamicrobium	93.5	17.8

<sup>a</sup>Taxonomy classifications are based on the Genome Taxonomy Database.

and “profile” (8). Eukaryotic and prokaryotic reads in the sample were separated by aligning all of the UTEX 2437 reads (minimap2 v2.17-r941 with the parameter “-ax asm20”) with the axenic assembly of UTEX 2526. The aligned (algal reads) and unaligned (nonalgal) reads were then separated using SAMtools view v1.9 with the parameters -F 4 and -f 4, respectively.

The nuclear genome assembly of *N. desiccata* 2437 is 20.576 Mbp with a GC content of 45.0%. There were 24 contigs with a maximum size of 2.689 Mbp and a contig  $N_{50}$  size of 1.522 Mbp. Organelle genomes were assembled as complete circular contigs, with a 40,238-bp mitochondrial genome and a 93,009-bp chloroplast genome. Genome annotation was performed using BRAKER2 v2.1.5 (9, 10). Functional gene motifs and domains were added using InterProScan v5.26-65.0-intel-2017b (11) against the CDD and TIGRFAM databases. Gene functions were then allocated using the best BLASTP (12) match to the UniProt Swiss-Prot database (13).

Bacterial reads were assembled, resulting in the identification of the presence of eight species with 39.5% to 99.2% completeness, four having benchmarking universal single-copy ortholog (BUSCO) scores of >90%. This includes the complete, 3,220,578-bp, circular genome sequence of *Erythrobacter* sp.

**Data availability.** All genome sequences were deposited at NCBI under BioProject accession number [PRJNA704951](#). The reads for *N. desiccata* UTEX 2437 were deposited in the NCBI SRA under accession number [SRR15813383](#). The bacterial assembly accession numbers are listed in Table 1, and the algal genome assembly can be found under GenBank accession number [GCA\\_019202925](#).

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