



Draft Genome Sequence of the Biofuel-Relevant Microalga *Desmodesmus armatus*

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ABSTRACT A draft genome of 906 scaffolds of 115.8 Mb was assembled for *Desmodesmus armatus*, a diploid, lipid- and storage carbohydrate-accumulating microalga proven relevant for large-scale, outdoor cultivation, and serves as a model alga platform for improving photosynthetic efficiency and carbon assimilation for next-generation bioenergy production.

Microalgae, having higher annual biomass production relative to terrestrial crops and potential for cultivation in salt water on nonarable lands, are critical future feedstocks for renewable liquid fuels (1–4). *Desmodesmus*, taxonomically divergent from the genus *Scenedesmus* (5, 6), has been shown to exhibit phenotypic plasticity and resilience, allowing survival in harsh and variable environments, including brackish and salt water (7–12), and to possess other beneficial traits for outdoor, large-scale, biofuel-relevant cultivation, as follows: it thrives in temperatures of 35 to 45°C (13–15), resists toxins (12) and grazers (16), accumulates microcrystalline guanine and polyphosphate (17) and lutein as an important coproduct for aquaculture (15), settles rapidly (13), and has diverse, sporopollenin-containing cell walls (18–20). *Desmodesmus* achieved areal harvest yield productivities of 9 to 20 g/m² day (annual average of 11.4 g/m² day) over the course of 2 years in outdoor, large-scale saltwater cultivation (2, 11, 21, 22) and can accumulate >55% dry cell weight (dcw) lipids (14, 23) or carbohydrates (13), both important cellular components for biofuels, making it amenable to a fractionation-based conversion pathway (24–26). Here, we report the draft nuclear and chloroplast genomes, ploidy, and potential bioenergy-relevant engineering targets of *D. armatus*.

D. armatus (Fig. 1), originally isolated from Las Cruces, NM, wastewater treatment ponds in 2012, was grown photoautotrophically in flat-sided bottles in modified artificial seawater medium (MASM) under constant illumination (4000K LED flat panels, 180 μmol photons/m²), supplemented with 2% CO₂. MASM contains the following (g/liter): NaCl (8), MgSO₄·7H₂O (2.5), KCl (0.6), NaNO₃ (0.85), CaCl₂·2H₂O (0.3), Tris (1), KH₂PO₄ (0.05), NH₄Cl (0.03), thiamine-HCl (3.5 mM stock; 1 ml/liter), cyanocobalamin (10 μg/L stock; 1 ml), and trace element stock (6 ml/liter). Trace element stock was made up of the following (g/liter): Na₂-EDTA (1.0), FeCl₃·6H₂O (0.2), MnCl₂·4H₂O (0.072), ZnCl₂ (0.02), Na₂MoO₄·2H₂O (0.013), and CoCl₂·6H₂O (0.004). Genomic DNA was extracted from midexponential cells as described (27). PacBio sequence data consisted of average polymerase reads of 741,936 ± 76,024 bp, having a mean insert length of 6,026 ± 784 bp and generating a total assembly size of 116.31 Mb in 906 contigs with an N₅₀ value of 341,806 bp and a GC content of 56.6%, and was determined to be diploid (28). This compares with the genomes of *Tetradasmus obliquus* (108.72 Mb; 29) and *Scenedesmus obliquus* (207.97 Mb; 30). Sixteen scaffolds (totaling 112,885 bp) contain chloroplast sequences identified using BLASTN against published chloroplast genomes for *Chlorella vulgaris* C-27 (31) and *Monoraphidium neglectum* (32). Proteins that may be beneficial for a robust, outdoor, bioenergy-relevant alga were identified.

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FIG 1 Typical cenobium with terminal spines and intracellular changes in morphology of *D. armatus* under nitrogen-replete and -deplete (inset) conditions. Nitrogen-deplete conditions occur in late-stage cultures once nitrogen is depleted from the medium.

The presence of homologs of *Chlamydomonas reinhardtii* STT7 and LHCSR1/3 and the dioxygen reductases Flv3 and PTOX confirms the ability for state transition and nonphotochemical quenching processes involved in energy dissipation essential for maintaining photosynthetic electron transport chain integrity in high or fluctuating irradiances (33) and may be useful targets for the improvement of photosynthetic efficiency and harvest yields in open ponds. Polyphosphate kinase was also identified, suggesting polyphosphate production as an energy or phosphate reserve. In conclusion, the innate robustness and proven reliability of *D. armatus* in outdoor mass culture provides a robust yet flexible chassis for genetic engineering efforts, potentially leading to the commercial use of *D. armatus* as a bioenergy-relevant alga.

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [VIIQ00000000](https://www.ncbi.nlm.nih.gov/nuclink/VIIQ00000000).

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