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The Genome of the Cyanobacterium *Microcoleus vaginatus FGP-2,* a Photosynthetic Ecosystem Engineer of Arid Land Soil Biocrusts Worldwide

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Abstract

Microcoleus vaginatus is a filamentous *cyanobacterium* (Order *Oscillatoriales)* that is abundant in surface soils in arid lands worldwide. The genome of *M. vaginatus* strain FGP-2 was sequenced to explore the genomic basis for photosynthesis, dessication tolerance, ability to produce novel alkanes, and other features which contribute to this organism's ability to pioneer colonization of bare aridosols and function as a major component of biological soil crusts.

Introduction

Arid lands comprise about 40% of the total Earth land mass, and much of the undisturbed soil surface in arid lands worldwide is colonized by biological soil crusts (biocrusts) (1). Cyanobacteria in the genus *Microcoleus*, particularly strains of *M. vaginatus* are the most abundant in biocrusts worldwide, where they help stabilize the soil surface and contribute significantly to soil carbon inputs (1).

The 'improved high quality draft' (4) genome of *M. vaginatus* strain FGP-2, an isolate from a dark pinnacled crust near Moab, UT, assembled into 6,698,929 bp distributed across 40 contigs with an average GC content of 46%. Automated gene modeling produced 5478 genes, of which 64% could be assigned a predicted function. Comparison of *M. vaginatus* FGP-2 to the marine isolate, *Microcoleus chthonoplastes* PCC 7420 (8) via a modified version of Ortholuge (7) identified only 2044 orthologs, suggesting considerable divergence, and confirming that these two organisms are not closely related (9).

The *M. vaginatus* draft genome encodes three nearly identical (98% protein identity) copies of D1, a major target protein in photodamage, which presumably enable *M. vaginatus* to quickly express and replace photoinactivated D1. Each of the three paralogs encode a glutamate (Glu) at position 130, instead of glutamine (Gln). In *Synechocystis PCC6803*, the Glu containing D1 form has been shown to increase phototolerance under high light conditions (3) and site-directed mutagenesis of D1-Q130E at position 130 (Gln to Glu conversion) ultimately reduces oxidative damage caused by back electron flow in PSII (5, 11).

Arid land soil microorganisms are subjected to extremes in temperature, salinity, and moisture availability, and may accumulate organic compounds as osmoregulatory solutes in response to salt stress and dessication (10, 12, 13). A gene cluster encoding homologs of malto-oligosyltrehalose synthase and malto-oligosyltrehalose trehalohydrolase (TreYZ) was identified. These genes may enable *M. vaginatus* to synthesize trehalose from glycogen (15), which is typical of moderately osmotolerant cyanobacteria (12), and agrees with early physiological studies (2). The genome also houses a trehalose synthase homolog, which could be important for either the synthesis or degradation of trehalose from maltose (15).

Directly downstream of TreYZ are homologs of an acyl-acp reductase and an aldehyde decarbonylase, the products of which have been experimentally verified to synthesize heptadecane and pentadecane alkanes in multiple cyanobacterial genera (14). The is consistent with a previous report indicating that an isolate of *M. vaginatus* produces an unusual variety of branched alkanes and apolar carbon compounds, the most dominant being heptadecane (6).

The genome of *M. vaginatus* FGP-2 constitutes an invaluable tool to understand the unique adaptations that enable microbial colonization of arid environments as well as the potential for generation of alternative biofuels.

Nucleotide sequence accession number. The sequence and annotation of the draft genome of *M. vaginatus* FGP-2 is available at GenBank/EMBL/DDBJ under accession number XXXXXXXX.

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