

TITLE: PLASTICITY OF HYDROCARBON BIOSYNTHETIC PATHWAYS IN CYANOBACTERIA

AUTHORS: APAZA-CASTILLO, G. A.¹; SOUZA, B. C. E. ¹; RIANO-PACHON D. M.²; FIORE M. F. ¹

INSTITUTION: 1. CELLULAR AND MOLECULAR BIOLOGY LABORATORY, CENTER FOR NUCLEAR ENERGY IN AGRICULTURE, UNIVERSITY OF SÃO PAULO, , PIRACICABA- SP- BRAZIL. 2. COMPUTATIONAL, EVOLUTIONARY AND SYSTEMS BIOLOGY LABORATORY, CENTER FOR NUCLEAR ENERGY IN AGRICULTURE, UNIVERSITY OF SÃO PAULO, PIRACICABA- SP- BRAZIL.

ABSTRACT:

Cyanobacteria are photosynthetic oxygenic bacteria that belong to a restricted group capable of synthesizing long-chain hydrocarbons from fatty acids. This feature has been associated to flexibility and curvature of the membrane due to the accumulation of hydrocarbons in the cytoplasmic membranes and thylakoids. Currently, cyanobacteria biomass is being applied for biotechnological purposes as biofuels and the biosynthetic mechanism of this natural process is a model for genetic engineering. These microorganisms can synthesize hydrocarbons through two pathways: synthesis of terminal alkane by acyl-ACP reductase (Aar) plus aldehyde deformylating oxygenase (Ado) enzymes and production of terminal alkene by olefin synthase (Ols). Cyanobacterial genomes encoding Aar/Ado or Ols pathways have been reported, but never both together in the same taxon. However, a recent study based on GC-MS analyses showed that the strain *Oxynema* sp. CENA135 synthesizes both types of hydrocarbons. Here, we sequenced the genome of strain CENA135 in order to identify the genes coding for the enzymes involved in hydrocarbon synthesis. Total genomic DNA was extracted from unicyanobacterial culture using the AllPrep DNA/RNA Kit and then subjected to construct an 8-kb mate-pair library and sequencing on the Illumina HiSeq 2500 platform. The reads were analyzed and pre-processed with FastQC, PEAR and PRINSEQ, high quality reads were then assembled with SPAdes. Functional annotation was performed with RAST server, and the search for hydrocarbon biosynthetic pathways was submitted to antiSMASH, NAPDOS and BLAST analyses. The results of the hydrocarbons biosynthetic pathways found in the *Oxynema* sp. CENA135 genome are discussed in comparison to those identified in the cyanobacterial genomes available in GenBank.

Keywords: alkane, alkene, genome, biofuel

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