

PHYLOGENETICAL APPROACH FOR THE SEARCH OF VALUABLE METABOLIC PRODUCTS IN CYANOBACTERIA

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Cyanobacteria are an important group of microorganism that plays a crucial role in both terrestrial and aquatic ecosystems. Species are beneficial as sources of food, as well as producers of carotenoids, antioxidants and other secondary metabolites. Mass development of cyanobacteria in natural and artificial reservoirs can also cause negative consequences due to the accumulation of toxins. We propose using a phylogenetic approach to detect strains of potential value for the production of various secondary metabolites. Existing phylogenetic methods lack precision and only make use of rDNA or single gene approaches, thus preventing a more detailed understanding of the evolutionary trajectory of cyanobacteria. Advances in molecular and genome studies have revealed the main genes involved in different stages of secondary metabolites production. Several genes have been identified in *de novo* TAG biosynthesis pathway and are known to be involved in lipid synthesis (rbsL, me g6562, accA, accD, dgat g2354, dgat g3280, gat g7063), production of malic enzyme subunits (ACCase and diacylglycerol acyltransferase), and carotenoid synthesis (crtB, crtP, crtQ-1, crtQ-2, crtL, crtL-2, crtO, crtR). The first group of genes is well studied in relation to biofuel production, while the second group has been widely employed in the pharmaceutical, cosmetics, and food industry for natural dyes and antioxidants. This paper will demonstrate how phylogenetic techniques can be used to search for novel strains of carotenoid producing cyanobacteria by elucidating the evolutionary relationship between genes involved in carotenoid synthesis. Many species of carotenoid producing cyanobacteria are already known from the genera *Anabaena*, *Arthrospira*, *Calothrix*, *Lyngbya*, *Microcystis*, *Nostoc*, *Phormidium*, *Scytonema*, *Synechococcus*, *Tolypothrix* and others. *Arthrospira platensis* (*Spirulina*) and *Nostoc commune* are already used in commercial scale production of biomass and metabolites, and several taxa (i.e. *Anabaena cylindrica*, *Calothrix desertica*, *Nostoc sp.*) have sequenced, assembled and annotated genomes. Data are publicly available from the National Center for Biotechnology Information (USA), the National Library of Medicine (NCBI of NLM), Joint Genome Institute of Department of Energy (USA (JGI of DoE) and other research institutions. A phylogenetic analysis revealed which species of cyanobacteria are closely related to known carotenoid producing species. Phylogenetic results were compared with empirical data of secondary metabolite production to compare carotenoid production with total biomass per strain. Our approach also proved useful in detecting producers of dangerous toxins. It was determined that genes mcyA, mcyB, sxtI, cyrA are responsible for toxin production and may be used as early indicators of potential toxicity of biomass or biomass-derived products. A phylogenetic approach is shown to be an indispensable tool in phycobiotechnology that can greatly facilitate identification of novel strains, as well as insure the quality and safety of biological products.