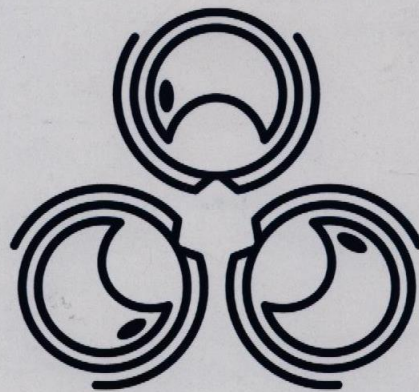


69th Yamada Conference

17th International Conference on the
Cell & Molecular Biology of
Chlamydomonas

Program and Abstracts



Chlamydomonas 2016

June 26-July 1, 2016

Kyoto International Conference Center, Kyoto, Japan

P-29

Identification of genes encoding enzymes involved in wax ester metabolism in *Euglena gracilis*

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A unicellular phytoflagellated protozoan, *Euglena gracilis*, has an ability to produce and accumulate wax esters, which have a great potential as an alternative biofuel, instead of triacylglycerol under oxygen-limited conditions. The metabolic pathway of anaerobically wax ester synthesis in *E. gracilis* has identified and designated as 'wax ester fermentation' due to a concomitant generation of ATP without any energy loss during the wax ester production. When anaerobically treated *Euglena* cells are transferred into aerobic conditions, wax esters are then promptly degraded. The aim of this study is to identify the key metabolic enzymes involved in wax ester synthesis and degradation for improving wax ester accumulation more effectively.

We have performed a comprehensive gene expression analysis in *E. gracilis* for the first time, and identified some genes related to wax ester metabolism (Yoshida et al., 2016). According to wax ester synthesis, in addition to components for known fatty acyl-CoA reductase and wax ester synthase, we identified another six components, annotated as wax ester synthase/acyl-CoA:diacylglycerol acyltransferase (WSD). Gene silencing experiment for WSD and yeast recombinant WSD expression system showed that WSD functions as a dominant enzyme for wax ester synthesis in *E. gracilis*. In addition, we obtained possible lipid esterases which are related to wax degradation by differentially expressed gene analysis and functional phospho-proteomic analysis. We will discuss the mechanism of wax ester synthesis and degradation in response to anaerobic and aerobic conditions, respectively. Yoshida, et al., (2016) *De novo* assembly and comparative transcriptome analysis of *Euglena gracilis* in response to anaerobic conditions. *BMC Genomics*, 17:182.

P-30

Isolation of new cyanobacteria strains –fatty acids producers as prospective source for biodiesel production from different ecosystems of Kazakhstan

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Nowadays, because of waste pollution of the planet by its using led to the attractiveness of biodiesel production - an environmentally friendly fuel based on renewable bio-resources. The usage of cyanobacteria could become a suitable alternative because they are more effective biological producers of fatty acids and universal renewable source of biomass. That is why the aim of this study is to isolate new cyanobacteria strains – fatty acid producers, prospective for biodiesel production. Objects of this work were newly isolated cyanobacteria strains from extreme nature sources. The molecular and genetic identification was based on analysis of 16S rRNA gene. Quantitative analysis of lipids carried out according to the Folch's method. In water samples from extreme habitats (cold lake Issyk, hot spring Turgen, bay Kurty with high salt concentration from lake Balkhash, hot springs of Karlovy Vary(Czech Republic)) 19 representatives of cyanobacteria were detected. Eight of them were isolated as algologically and bacteriologically pure culture. Their biochemical properties were studied, fatty acid composition was determined. For the first time the high amount of C14 and C16 fatty acids in cyanobacteria was detected. The isolated Cyanobacterium sp. IPPAS B-1200 strain synthesize up to 30% of myristic (14: 0) and 10% myristoleic (14: 1Δ9) acids. The total amount of palmitic acid (16: 0) and palmitoleic (16: 1Δ9) reaches 60%. Cyanobacterium sp. IPPAS B-1200-2 strain was obtained by auto selection method. It differs from initial Cyanobacterium sp. IPPAS B-1200 strain by higher productivity of biomass and lipids accumulation suitable for biotechnological biodiesel production. The strain Cyanobacterium sp. IPPAS B-1200-2 can be used as potential source for biodiesel production. Sarsekeyeva F., Zayadan B.K., Ussebaeva A., Bedbenov V.S., Sinetova M.A., Los D.A. Cyanofuels – biofuels from cyanobacteria: reality and perspectives // *Photosynth. Res.* -2015. –Vol. 125.- P. 329-340. Zayadan B.K. Ecological biotechnology of phototrophic microorganisms. – Almaty. 2011. – 368 p.

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