The Direct Photobiological Conversion of CO_2 into C(1) Compounds

Claudia Durall de la Fuente

High demand of new and renewable energies is needed since it is known that petroleum reserves will be exhausted in not many decades.

Some scientists are trying to obtain energy from water, wind or solar power. Others are trying to generate genetically modified organisms which can produce substances of human interest. Different organisms such as plants, yeast and bacteria have been modified to produce alcohols, biofuels and sugars whose combustion leads to obtain energy.

Interestingly, cyanobacteria are organisms which perform photosynthesis and, as its name indicates, they are bacteria. Cyanobacteria grow under light condition, with water, taking CO_2 and some inorganic substances. Since these microorganisms are easy to modify genetically, different producing biofuel pathways have been introduced. Nowadays, it is possible to obtain biofuels by growing these modified microorganisms. However, the amount of product of interest is still low.

Despite that, if we consider that pathways work as production chains, more final product could be obtained if more amount of substrate is incorporated. Thus, incorporating more CO_2 into the cells can increase the generation of product of interest.

Bar-even and partners (2010) designed different non-existing native pathways (MOG pathways) which theoretically improve the incorporation of CO_2 into photosynthetic organisms. After a comparison among the MOG pathways was done, we conclude that C4 Glyoxylate Cycle/Lactate option was the best candidate to introduce into the cyanobacterium *Synechocystis* PCC 6803.

The aim of my study was to introduce, individually, two of the eleven genes (Phoshoenolpyruvate carboxylase (PEPc) and Malate dehydrogenase (MDH) present in the Lactate option-MOG pathway into the cyanobacterium *Syenchocystis* PCC 6803. Both genes are present in this cyanobacterium so an additional copy of the native gene was inserted. The expression of the inserted genes was compared between the natural strain and the modified ones. Also, in PEPc modified cyanobacterium the protein level was examined compared to natural strain. It has been demonstrated that the introduction of both genes have led to an increase of the gene expression and the amount of protein in the modified PEPc cyanobaterium is higher than wild type *Syenchocystis* PCC 6803. Further experiments are required in order to verify if the increased amount of proteins are active and therefore are catalysing their reaction more efficiently.

Degree project in Applied Biotechnology, Master of Science (2 years), 2013
45 hp till masterexamen, 2013 Biology Education Centre and Department of Photochemistry and Molecular Science, Ångstrom, Uppsala University. Supervisor: Peter Lindblad and Elias Englund