

Domestication of microalgal photosynthesis for improved biofuel production

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Because of a high photosynthetic efficiency, microalgae are considered as a promising renewable feedstock for the production of next-generation biofuels. However, if microalgae are nowadays cultivated at an industrial scale for the production of high value compounds, their productivity needs to be improved in order to develop sustainable biofuel production. A great challenge for biotechnology is to increase the productivity of reserve compounds (oil and starch) by domesticating algal photosynthesis. A major limitation is due to the requirement for stress conditions, such as nutrient deprivation, to trigger accumulation of reserve compounds, thus strongly decreasing the biomass productivity. Deciphering signaling networks linking nutrient and energy status to CO₂ fixation, biomass production and reserve accumulation is a major challenge to improve microalgal productivity. In order to identify new regulatory genes and pathways, forward genetic screens have been developed in our laboratory in the model algal *Chlamydomonas reinhardtii*. Insertion mutant libraries have been screened for phenotypes of interest, such as photosynthetic efficiency based on chlorophyll fluorescence imaging, starch or oil accumulation and degradation kinetics based on specific staining. Based on the characterization of such mutant strains, we will discuss how regulatory mechanisms needed for optimal growth and survival in natural environments may limit microalgal productivity in controlled conditions. Biotechnological implications of these data will be discussed.