Advances in editing microalgal genomes

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With 2 figures

Abstract: There have been significant advances in microalgal genomics over the last decade. Nevertheless, there are still insufficient tools for the manipulation of microalgal genomes and the development of microalgae as industrial biofactories. Several research groups have recently contributed to progress by demonstrating that particular nucleases can be used for targeted and stable modifications of the genomes of some microalgal species. The nucleases include Meganucleases, Zinc Finger nucleases, TALE nucleases and, as shown most recently, the CRISPR/Cas9 system. These molecular editing tools allow gene knock-out and gene knock-in manipulations and the introduction of enzyme variants; they will facilitate the study of microalgae and in particular gene function and, thereby favoring exploitation of the metabolic potential of microalgae.

Keywords: Microalgae, biotechnology, targeted genome modifications, engineered nucleases, TALENs, CRISPR/CAS9 system

Microalgae, the rough diamond of biotechnology

Microalgae have enormous potential as cell factories: like plants properties, they can produce complex molecules using CO₂ as a substrate; like microorganisms, they grow rapidly; and they produce a wide variety of bioproducts (proteins, carbohydrates, lipids and pigments). Consequently, they are the rough diamonds of biotechnology (Barra et al. 2014). Microalgae also have potential as expression systems for medically useful proteins and as edible vaccines (Specht et al. 2010). Against the background of the exhaustion of fossil fuels and efforts to decrease greenhouse gas emissions, microalgae have emerged as promising biocatalysts for the sustainable production of chemicals and biofuels, because they can accumulate and store energy-rich compounds, such as triacylglycerol and carbohydrates (Alonso et al. 2000). Nevertheless, a number of barriers need to be overcome before profitable commercialisation of microalgae in the chemical and biofuel markets.

Traditional techniques to improve performance and yield

For several years, there have been efforts to develop the metabolic potential of microalgae. Various techniques are available for enhancing cell growth and/or the accumulation of bioproducts. Oceanographic campaigns have been conducted to explore biodiversity and discover new species with particular properties. In parallel, there has been work to optimise cultivation conditions to enrich microalgae in specific compounds. Nutrient deprivation has been successfully used to boost lipid content, although generally at the expense of biomass productivity (Hu et al. 2008, Breuer et al. 2012). Physical and chemical mutagens have been used to modify the genetic heritage, and efficient, rapid and robust high-throughput screening- methodologies have been employed with the aims of circumventing dependence on stress and to decrease cultivation-related costs (Huesemann et al. 2009, Beacham et al. 2015). This strategy is attractive, but the control of genome modifications is still limited impeding research into microalgal metabolism, a prerequisite for metabolic engineering.

From classical genetic tools to targeted genome editing

The development of new and affordable methods for whole-genome sequencing, and the availability of techniques allowing transformation of more than 50 microalgal species facilitate analysis of gene function. Techniques now used are based on random insertional mutagenesis followed by phenotypic selection (Galván et al. 2007) or on modulation of gene expression by overexpression or silencing targeted genes using RNA interference (Schroda et al. 1999, Schroda 2006, Doron et al. 2016) or microRNA (Molnár et al. 2007, Zhao et al. 2009, Cerutti et al. 2011, Doron et al. 2016).