REVIEW



Genome editing in diatoms: achievements and goals

Peter G. Kroth¹ · Atle M. Bones² · Fayza Daboussi³ · Maria I. Ferrante⁴ · Marianne Jaubert⁷ · Misha Kolot^{5,6} · Marianne Nymark² · Carolina Río Bártulos¹ · Andrés Ritter⁷ · Monia T. Russo⁴ · Manuel Serif³ · Per Winge² · Angela Falciatore⁷

Received: 28 March 2018 / Accepted: 7 August 2018 © Springer-Verlag GmbH Germany, part of Springer Nature 2018

Abstract

Diatoms are major components of phytoplankton and play a key role in the ecology of aquatic ecosystems. These algae are of great scientific importance for a wide variety of research areas, ranging from marine ecology and oceanography to bio-technology. During the last 20 years, the availability of genomic information on selected diatom species and a substantial progress in genetic manipulation, strongly contributed to establishing diatoms as molecular model organisms for marine biology research. Recently, tailored TALEN endonucleases and the CRISPR/Cas9 system were utilized in diatoms, allowing targeted genetic modifications and the generation of knockout strains. These approaches are extremely valuable for diatom research because breeding, forward genetic screens by random insertion, and chemical mutagenesis are not applicable to the available model species *Phaeodactylum tricornutum* and *Thalassiosira pseudonana*, which do not cross sexually in the lab. Here, we provide an overview of the genetic toolbox that is currently available for performing stable genetic modifications in diatoms. We also discuss novel challenges that need to be addressed to fully exploit the potential of these technologies for the characterization of diatom biology and for metabolic engineering.

Keywords Diatom · Genome editing · TALEN · CRISPR · Conjugation · Promoter · Mutant screening

Communicated by Neal Stewart.

Peter G. Kroth Peter.Kroth@uni-konstanz.de

- Angela Falciatore angela.falciatore@upmc.fr
- ¹ Fachbereich Biologie, Universität Konstanz, 78457 Konstanz, Germany
- ² Cell, Molecular Biology and Genomics Group, Department of Biology, Norwegian University of Science and Technology, 7491 Trondheim, Norway
- ³ LISBP, Université de Toulouse, CNRS, INSA, 135 Avenue de Rangueil, 31077 Toulouse, France
- ⁴ Integrative Marine Ecology, Stazione Zoologica Anton Dohrn, Villa Comunale 1, Naples 80121, Italy
- ⁵ Institute of Plant Sciences and Genetics in Agriculture, Robert H. Smith Faculty of Agriculture, Food and Environment, The Hebrew University of Jerusalem, 76100 Rehovot, Israel
- ⁶ Department of Biochemistry and Molecular Biology, Tel-Aviv University, Tel-Aviv 69978, Israel
- ⁷ Laboratoire de Biologie Computationnelle et Quantitative, Institut de Biologie Paris-Seine, Sorbonne Université, CNRS, 75005 Paris, France

Published online: 23 August 2018

Introduction

Diatoms are unicellular algae which represent an essential part of the planktonic and benthic communities (Malviya et al. 2016) and contribute significantly to global primary production (Armbrust 2009). They also have peculiar cellular and metabolic features, which likely are a result of their evolution by multiple secondary endosymbiotic events (Archibald 2015). During the last two decades, significant efforts have been devoted to develop molecular tools to foster studies of diatom biology and ecology, but also to establish these algae as a significant, renewable and sustainable resource of biomass for feed, food, energy, and other value-added products. After the first reports on successful biolistic transformation of diatoms such as Cyclotella cryptica (Dunahay et al. 1995) and Phaeodactylum tricornutum (Apt et al. 1996; Falciatore et al. 1999) had been published, this transformation method quickly became the standard for genetic diatom modification (Fischer et al. 1999, Apt et al. 2002; Buhmann et al. 2014; Ifuku et al. 2015). More recently, highly efficient protocols for introducing transgenes into diatoms via electroporation (Niu et al. 2012; Miyahara