

RNA-Seq-mediated transcriptomic analysis of heat stress response in a polar *Chlorella* sp. (Trebouxiophyceae, Chlorophyta)

Sze-Wan Poong¹ · Kok-Keong Lee^{1,2} · Phaik-Eem Lim¹ · Tun-Wen Pai³ · Chiew-Yen Wong^{4,5} · Siew-Moi Phang^{1,6} · Chien-Ming Chen³ · Cing-Han Yang³ · Chun-Cheng Liu³

Received: 11 December 2017 / Revised and accepted: 14 March 2018
 © Springer Science+Business Media B.V., part of Springer Nature 2018

Abstract

The current outlook on mitigation of global warming does not appear promising, with figures in the reduction of anthropogenic greenhouse gas emissions lagging far behind climate goals. A recent environmental report even postulated a high possibility of temperature increase of at least 3 °C by 2100. Despite the low number of human inhabitants in Antarctica, the Antarctic Peninsula was reported as one of the most rapidly warming locations on earth. Many studies have shown that heat stress modulates physiological performance in many species of microalgae; however, studies to elucidate the molecular mechanisms of high-temperature thermotolerance are generally focused on the model species, i.e. *Chlamydomonas reinhardtii*. Furthermore, previous transcriptomic work in this aspect generally employed the microarray technique and/or involved the tropical or temperate strains, and few were conducted on the polar strains. In this study, RNA-Seq-mediated transcriptomic analysis was undertaken to compare the whole transcriptome profile of an Antarctic *Chlorella* sp. grown at ambient (4 °C) versus stress-inducing high (33 °C) temperatures and harvested at the 120-h time point. The findings of this study indicated a coordinated response to fine tune balance between energy production and utilisation for biosynthesis by redirecting carbon provision, and the arrest of cell division as a coping mechanism for an intense and relatively long period of stress. The strategies undertaken by this alga in acclimation to heat stress are somewhat similar to the heat stress response of the model species.

Keywords Antarctic · Energy metabolism · Gene expression · Global warming · Temperature

Electronic supplementary material The online version of this article (<https://doi.org/10.1007/s10811-018-1455-9>) contains supplementary material, which is available to authorized users.

✉ Phaik-Eem Lim
 phaikkeem@um.edu.my

✉ Tun-Wen Pai
 twp@mail.ntou.edu.tw

¹ Institute of Ocean and Earth Sciences, University of Malaya, 50603 Kuala Lumpur, Malaysia

² Institute of Graduate Studies, University of Malaya, 50603 Kuala Lumpur, Malaysia

³ Department of Computer Science and Engineering, National Taiwan Ocean University, Keelung, Taiwan, Republic of China

⁴ School of Health Sciences, International Medical University, 57000 Kuala Lumpur, Malaysia

⁵ National Antarctic Research Centre, University of Malaya, 50603 Kuala Lumpur, Malaysia

⁶ Institute of Biological Sciences, Faculty of Science, University of Malaya, 50603 Kuala Lumpur, Malaysia

Introduction

The recently released UN Environment Emissions Gap Report 2017 (UNEP 2017) noted that current national pledges on mitigation efforts to reduce global anthropogenic greenhouse gas emissions contribute to only a third of the reduction in emissions required by 2030 to meet climate goals. The same report highlighted a high possibility of temperature increase of at least 3 °C by 2100. Despite their much lower number of human populations, the polar regions are not spared from the ongoing threats of global warming. In fact, the Antarctic Peninsula is reportedly one of the most rapidly warming locations on earth. According to a combined analysis of weather station and satellite data from 1957 to 2006 by Steig et al. (2009), Antarctica has warmed at a rate of about 0.12 ± 0.07 °C per decade with West Antarctica experiencing the most warming at 0.17 ± 0.06 °C per decade. The highest temperature recorded thus far for the Antarctic Continent was 17.5 °C on March 2015 at the Argentine Research Base Esperanza located near the northern tip of the Antarctic