Algal Research 41 (2019) 101532

Contents lists available at ScienceDirect

Algal Research

journal homepage: www.elsevier.com/locate/algal

Expression analysis of potential transcript and protein markers that are related to agar yield and gel strength in *Gracilaria changii* (Rhodophyta)

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ARTICLE INFO

Keywords:
Agar yield
Gel strength
Gracilaria
Transcript marker
Protein marker

ABSTRACT

The supply of agar as an important gelling and thickening agent in various industrial applications depends heavily on harvesting of natural seaweed resources and seaweed farming. To facilitate the selection of good seaweed source with higher agar yield and stronger gel strength, accurate and rapid screening method using molecular markers is necessary to replace the tedious, laborious and time-consuming conventional method which involves agar extraction and gel analysis. In this study, we characterized the expression of a number of algal transcripts and proteins from an agar producing seaweed, *Gracilaria changii* with the aim to identify potential markers for agar yield and gel strength. In total, 15 candidate transcripts that are directly or indirectly related to putative agar biosynthetic pathway were identified based on literature search. The transcript abundance of 4 and 11 of these candidates were found to be significantly ($P < 0.05$) correlated to the agar yield and gel strength of six *G. changii* samples, respectively. Among these marker genes, the transcript levels of GcFBPA and GcGALE have the highest linear correlation to both agar yield and gel strength. The protein abundance of GcFBPA and GcGALE was further examined on 13 *G. changii* samples and was found to have highly significant ($P < 0.01$) correlation to agar gel strength and agar yield, respectively. GcFBPA and GcGALE may have good potential to be used for molecular screening of yield traits and gel quality of *G. changii* at both RNA and protein levels.

1. Introduction

Agar is an important gelling and thickening agent used in processed foods, cosmetics, pharmaceutical, medical and biotechnological products [1]. The global demand for agar has increased between 2009 and 2015, at an annual average growth rate of 7% for its sales volume, outperforming other commercial hydrocolloids such as carrageenans and alginates [2]. In order to meet the high demand for agar and to overcome shortage of raw materials due to uncontrolled harvesting at natural beds [3], seaweed domestication and farming, and resource management are gaining attention from both academia and industry [4–6].

Seaweeds from the genus *Gracilaria* account for 91% of the total commercial agar production in 2015 [2]. The agar yield is an economically important factor for the selection of the right agarophyte population for agar production while the gel strength serves as the main indicator for agar quality [7]. Although seaweed species with better agar yield and gel quality have been identified for agar production previously [8,9], agar properties are also highly variable depending on environmental and physiological factors [7]. Thus, mass harvesting and processing of agarophytes without prior knowledge of their agar properties have caused poor agar yield and gel quality [5]. Failure to maximize the agar yield and gel quality from limited natural seaweed resources is not only an economic loss but also a threat to sustainable supply of agar.

In the past decades, seaweed farmers and traders evaluated the quality of their raw materials based on the following procedures: seaweed harvesting and drying, agar extraction and processing, and multiple tests to determine the agar properties [10]. However, this traditional procedure is time consuming, expensive, laborious, and requires a huge amount of sample for accurate evaluation of agar yield and gel quality. In recent years, the relationship between the expression of putative agar biosynthesis genes and agar yield in *Gracilaria* and *Gracilariopsis* species have been analyzed. Li et al. (2010) found that the

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https://doi.org/10.1016/j.algal.2019.101532
Received 2 January 2019; Received in revised form 22 April 2019; Accepted 2 May 2019