Global transcriptome analysis of Gracilaria changii (Rhodophyta) in response to agarolytic enzyme and bacterium

ABSTRACT

Many bacterial epiphytes of agar-producing seaweeds secrete agarase that degrade algal cell wall matrix into oligoagars which elicit defense-related responses in the hosts. The molecular defense responses of red seaweeds are largely unknown. In this study, we surveyed the defense-related transcripts of an agarophyte, Gracilaria changii, treated with ϐ-agarase through next generation sequencing (NGS). We also compared the defense responses of seaweed elicited by agarase with those elicited by an agarolytic bacterium isolated from seaweed, by profiling the expression of defense-related genes using quantitative reverse transcription real-time PCR (qRT-PCR). NGS detected a total of 391 differentially expressed genes (DEGs) with a higher abundance (>2-fold change with a p value <0.001) in the agarase-treated transcriptome compared to that of the non-treated G. changii. Among these DEGs were genes related to signaling, bromoperoxidation, heme peroxidation, production of aromatic amino acids, chorismate, and jasmonic acid. On the other hand, the genes encoding a superoxide-generating NADPH oxidase and related to photosynthesis were downregulated. The expression of these DEGs was further corroborated by qRT-PCR results which showed more than 90 % accuracy. A comprehensive analysis of their gene expression profiles between 1 and 24 h post treatments (hpt) revealed that most of the genes analyzed were consistently upregulated or downregulated by both agarase and agarolytic bacterial treatments, indicating that the defense responses induced by both treatments are highly similar except for genes encoding vanadium bromoperoxidase and animal heme peroxidase. Our study has provided the first glimpse of the molecular defense responses of G. changii to agarase and agarolytic bacterial treatments.

Keyword: Agarase; Agarolytic bacterium; Defense response; Gene expression; High-throughput sequencing; Quantitative reverse transcription real-time PCR