Deciphering the molecular functions of defense signaling molecules between brown algal host and endophyte with a focus on the oxylipin pathway.

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Abstract

The oxylipin pathways are known to be involved in defense signaling in plants and animals. In brown algae, an evolutionary independent eukaryotic lineage, oxylipins deriving from both C18- and C20- Polyunsaturated Free Fatty Acids are produced during stress defense responses. Their biosynthetic pathways and roles as signals molecules during biotic interactions are still unknown. Genomic approaches have identified several CYP5164 genes, homologous to the plant CYP74 gene family, which may play an important part in defense signaling between brown algal host and endophyte. To decipher the biological functions of these genes in the model brown algal, *Ectocarpus sp.7,* and the endophytic Ectocarpales *Laminarionema elsbetiae*, targeted and un-targeted metabolomic analyses were performed to compare the global metabolome of control and stressed algal cultures. LC-MS analysis was used to mine for differences in the overall metabolic profiles and to investigate the occurrence or absence of specific oxylipins of CRISPR knock-out mutants for the CYP5164B1 and wild-type strains. In addition, recombinant CYP5164B1 proteins were produced to characterize *in vitro* biochemical activities by GC-MS and to identify brown algal-specific substrates. These approaches will indicate whether the profiles of mutant oxylipins are consistent with the previously determined catalytic activity of the recombinant enzyme. The combination of *in vivo* metabolomic approaches and targeted biochemical characterization will enable CYP5164 activity to be integrated into a more global metabolic context in a brown algal model and contribute to a better understanding of CYP-based defense and chemical signaling in brown algae during biotic interactions.

Keywords: Algal endophyte, Brown algae, Ectocarpales, Oxylipin pathway, Oxidative stress, Metabolomics

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