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RESEARCH ARTICLE

Genome-wide identification and expression profiling of chitinase genes in tea (*Camellia sinensis* (L.) O. Kuntze) under biotic stress conditions

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Abstract Chitinases are a diverse group of enzymes having the ability to degrade chitin. Chitin is the second most abundant polysaccharide on earth, predominantly found in insect exoskeletons and fungal cell walls. In this study, we performed a genome-wide search for chitinase genes and identified a total of 49 chitinases in tea. These genes were categorized into 5 classes, where an expansion of class V chitinases has been observed in comparison to other plant species. Extensive loss of introns in 46% of the GH18 chitinases indicates that an evolutionary pressure is acting upon these genes to lose introns for rapid gene expression. The promoter upstream regions in 65% of the predicted chitinases contain methyl-jasmonate, salicylic acid and defense responsive *cis*-acting elements, which may further illustrate the possible role of chitinases in tea plant's defense against various pests and pathogens. Differential expression analysis revealed that transcripts of two GH19 chitinases TEA028279 and TEA019397 got upregulated during three different fungal infections in tea. While GH19 chitinase TEA031377 showed an increase in transcript abundance in the two insect infested tea tissues. Semi-quantitative RT-PCR analysis revealed that five GH19 chitinases viz. TEA018892, TEA031484, TEA28279, TEA033470 and TEA031277 showed significant increase in expression in the tea plants challenged with a biotrophic pathogen *Exobasidium vexans*. The study endeavours in highlighting biotic stress responsive defensive role of chitinase genes in tea.

Keywords Chitinase · *Camellia sinensis* · Differential gene expression · Genome wide identification · Biotic stress

Introduction

Chitin, a derivative of glucose and a natural homopolymer of N-acetylglucosamine, is a major component of fungal and some algal cell walls, exoskeletons of insects, crustaceans and some other invertebrates (Kasprzewska 2003; Li and Roseman 2004). Chitinases catalyze the hydrolytic breakdown of chitin in the β-1-4-glycosidic linkage of N-acetyl glucosamine (GlcNAc) polymers (Xu et al. 2016) and chitosan, the N-deacetylated derivative of chitin (Tanabe et al. 2000). Bacterial peptidoglycan, plant cell wall glycoproteins, arabinogalactan proteins, rhizobial nod factors etc. having GlcNAc in their structures are known to be substrates for chitinases (Grover 2012). Chitin hydrolysis mediated release of oligosaccharides activates pathogen associated molecular patterns (PAMP)-triggered immunity (PTI) in the host plants (Cao et al. 2019).

Chitinases play varied roles in plant growth and development, defense, frost tolerance and symbiotic associations including nodulation and mycorrhiza formation (Kasprzewska 2003; Collinge et al. 1993; Grover 2012). Understanding the role of chitinases in the plant defense mechanisms is important in formulating biotechnological methods of crop protection against pests and pathogens. Pathogenesis-related (PR) proteins are induced in response to different abiotic and biotic stresses in plants

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