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Genome-wide identification and characterization of the *CsSnRK2* family in *Camellia sinensis*

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Abstract: The sucrose nonfermenting 1 (SNF1)-related protein kinase 2 (*SnRK2*) genes play central roles in plant stress signal transduction. In this study, 8 *SnRK2* genes were identified from the tea plant genome database and named *CsSnRK2.1-8*. Phylogenetic analysis showed that the *CsSnRK2* genes were classifiable into three groups, similar to those of *Arabidopsis thaliana*, *Oryza sativa* and maize. The coding sequences (CDSs) of all *CsSnRK2s* were separated by eight introns, and their exon-intron organizations exhibited high similarity to those of other plants. The fluorescence of GFP fused with *CsSnRK2.3* was detected in only the cytoplasm, while the rest of the proteins showed GFP signal in both the nucleus and the cytoplasm. The results of the expression patterns of the *CsSnRK2* genes showed that *CsSnRK2s* were differentially induced by salt, polyethylene glycol (PEG) and abscisic acid (ABA) stress. Interestingly, The expression of *CsSnRK2.3* was inhibited by ABA, suggesting the complicated roles of *CsSnRK2s* in the ABA signal transduction pathway. Some *CsSnRK2* gene pairs showed significant expression change correlations under stresses, indicating that *CsSnRK2s* might exhibit synergistic effects of signal regulation in response to various stresses. In summary, this comprehensive analysis will facilitate further studies of the *SnRK2* family of *Camellia sinensis* and provide useful information for the functional validation of *CsSnRK2s*.

Keywords: *Camellia sinensis*; *SnRK2* genes; abiotic stress; expression pattern

1. Introduction

In nature, plants are frequently exposed to multiple adverse environmental conditions, such as high salinity, drought and extreme temperatures, which seriously affect their growth, development and productivity (Kulik et al., 2011). To cope with these stresses while completing their life cycles, plants have evolved sophisticated signal transduction pathways for stress response (Fujita et al., 2006; Liu et al., 2016). In all these different signal transduction pathways, protein phosphorylation and dephosphorylation significantly influence the regulation of both physiological morphology and the gene expression associated with basic cellular activities (Fujita et al., 2006). In particular, the sucrose nonfermenting-1-related protein kinase (*SnRK*) family has been widely reported to play vital roles in growth, development and stress signal transduction in plants (Dong et al., 2012; Kobayashi et al., 2004; Kobayashi et al., 2005; Zhang et al., 2016).

Plant *SnRKs* can be classified into *SnRK1*, *SnRK2* and *SnRK3* subfamilies based on sequence similarity and domain structure (Hrabak et al., 2003). Among these subfamilies, *SnRK2* has been well studied in many plants due to its essential roles in stress response and ABA signal transduction (Fujii et al., 2009; Fujita et al., 2013; Yoshida et al., 2014; Zhu, 2016). In the past decades, the *SnRK2* gene family has been identified in many plant genomes, including 10 *SnRK2* genes in *Arabidopsis thaliana* (Boudsocq et al., 2004), 10 in *Oryza sativa* (Kobayashi et al., 2004), 11 in *Zea mays* (Huai et al., 2008), 8 in grapevine (Liu et al., 2016) and 10 in wheat (Zhang et al., 2016).

Increasing evidence supports the involvement of *SnRK2* genes in responses to a variety of abiotic stresses in plants. In *Arabidopsis thaliana*, *SnRK2.2/SnRK2.3/SnRK2.6* were confirmed to participate in the ABA signalling network and act as major regulators in response to water stress (Yoshida et al., 2006;

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