

Genome-wide Identification and Expression Analysis under High Temperature Stress of *HSP70* Gene Family in Passion fruit

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Abstract

Passion fruit has been as an emerging tropical fruit tree and plays a very important role in tropical agriculture in Guangxi. However abiotic stresses such as high temperature seriously affect the yield and quality of fruit. In this study, in order to study the resistant mechanism of Passion fruit response to high temperature stress, the heat shock protein 70 (*HSP70*) gene families were identified using bioinformatics methods, the expression profiles of *HSP70* genes under high (42°C) temperature and natural hot weather were assayed by quantitative real time PCR (qRT-PCR) method. The results showed that 17 *HSP70* genes were identified from Passion fruit, which encode 562 to 922 amino acids, the molecular weight was between 62.04 to 102.86 kD, and the theoretical isoelectric point ranged from 5.08 to 5.57. phylogenetic tree analysis showed that the *HSP70* proteins were divided into four subgroups: A, B, C, D1 and D2. Structural analysis showed that the number of introns in *HSP70* genes varied from 1 to 17. The relative expression of *PeHSP702* and *PeHSP703* was up-regulated obviously after high temperature of 42°C treating for 3 hours and at 3:00 pm in hot weather, and then we can speculate that these genes play key roles in response to heat stress.

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