IN SILICO IDENTIFICATION OF CANDIDATE GENES FOR DEHYDRATION STRESS RESPONSE IN ROBUSTA COFFEE GENOME (COFFEA CANEPHORA L.)

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SUMMARY

Coffea canephora L., which is belonging to the Rubiaceae family, is one of the most popular cultivated coffea worldwide. In this study, we identified and analysed candidate genes that involve in dehydration stresses response in *C. canephora* L. genome. The results showed that genome of *C. canephora* L. consists of 37 protein-coding genes related to drought stress response which are divided into 5 main groups depending on domain and motif such as Dehydration-induced 19 (Di 19); Senescence/dehydration-associated protein-related genes; Dehydration-responsive element-binding protein; Dehydration-responsive protein RD22; Early responsive dehydration (ERD). Determination of subcellular localization indicated that there are 2 protein-coding genes as Cc01_g21190 and Cc08_g08870 localize in chloroplast; 1 protein-coding gene as Cc10_g02270 localize in mitochondria and 1 protein coding gene as Cc05_g03850 localize in peroxisome. The study on candidate protein coding genes relating dehydration stress response is important for elucidating protein functions involved in various cellular processes and stress response.

Keywords: *C. canephora L., genome, ERD, in silico, localization, stress.*

1. INTRODUCTION

C. canephora L. and C. arabica are most coffee bean productions (ICO, 2021) with 30% and 70% in total production worldwide, respectively. ICO (2021) was estimated that an average of 2.25 billion cups of coffee pare are consumed around the world, bringing approximately 12 billion US dollars in income each year. C. canephora L. contents higher caffeine and bitter taste than C. arabica.

In the last two decades, several articles were published about genome sequencing, coffee transcriptomes, and expressed sequence tags (ESTs) for both robusta and arabica coffee plants (Pallavicini et al., 2005) (Esteves Vieira et al., 2006). An oligo-based microarray containing 15,721 coffee genes was constructed to analyze potential genes involved in bean maturation, pathogen resistance, and stress responses (Privat et al., 2011). EST sequences of C. arabica were recently released (Mishra and Slater, 2012). Especially, Denoeud et al., 2014 reported that C. canephora genome contains 25,574 protein-coding genes, 2,573 organellar-to-nuclear genome transfers, 6,812 predicted transposable elements (TEs), and 92 microRNA precursors which were published on Coffee Genome Hub (http://coffee-genome.org).

3-caffeoylquinic acid (chlorogenic acid) and caffeine contents are the most important secondary metabolites of coffee, determining the taste and aroma. It has been reported that there is a strong link between drought conditions and the caffeine as well as chlorogenic acid content of coffee. (Catarino et al., 2021) have mentioned that drought effects increase leaf 5-o-caffeoylquinic acid and caffeine concentrations during the early growth of Coffea arabica plants. The understanding of acclimation strategies to climate changes is decisive to ensure coffee crop sustainability, since these environmental conditions determine the suitability of cultivation areas. Thus, identifying the genes in drought conditions associated with the caffeine biosynthetic pathway in coffee provided the molecular tool help coffee breeding and possibly produce more caffeine contents and caffeine-free coffee for consumers in the future. Some molecular functions of coffee genes related to caffeine biosynthesis were reported. McCarthy et al. (McCarthy et al., 2007) have analyzed XMT and DXMT N-methyltransferases from C. canephora. Denoeud et al. (2014) analyzed information on the convergent evolution of caffeine biosynthesis by some genes such as CcXMT, CcMXMT, CcMTL, CcDXMT, etc. Perrois et al. (2015) demonstrated that differential regulation of caffeine metabolism depends on the transcriptional activity that controls differential

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