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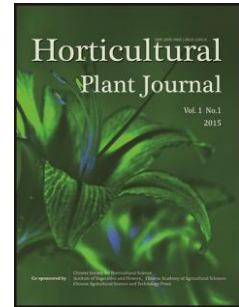
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Genome-wide Identification and Expression of *ARF* Gene Family During Adventitious Root Development in Hot Pepper (*Capsicum annuum*)

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Abstract

Auxin response factors (ARFs) are transcription factors that activate or repress the expression of primary/early auxin response genes by binding to auxin-responsive elements (AuxREs) in their promoter regions. The ARFs play important roles in diverse developmental processes. To explore the *ARF* gene family in hot pepper (*Capsicum annuum* L.), we performed a genome-wide identification and expression analysis. In this study, 19 pepper *ARF* genes (*CaARFs*) clustered into three phylogenetic groups (I, II, and III) were comprehensively analyzed. Conserved domain analysis showed that all *CaARFs* contained a B3 DNA-binding domain and a middle domain, but two members lacked the carboxy-terminal dimerization (CTD) domain. The number of introns in *CaARF* genes ranged from 1 to 13 and the gene structure was similar among genes in the same phylogenetic group. Additionally, prediction of *CaARFs* promoter elements and putative targets for microRNAs suggested that the regulation of *CaARFs* may occur at both transcriptional and posttranscriptional levels. Most *CaARFs* were expressed in more than one tested tissue, and most *CaARFs* were identified as being responsive to exogenous auxin. Moreover, time-course transcription profiles of *CaARFs* revealed their roles in adventitious rooting of hypocotyl cuttings from pepper seedlings. Therefore, our results will provide a foundation for better understanding the regulatory mechanisms and molecular functions of *CaARFs* in hot pepper.

Keywords: hot pepper; auxin response factor; phylogenetic analysis; gene structure; promoter element; adventitious root

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