

Identification and Expression Analysis of *WRKY* Gene Family under Drought Stress in Peanut (*Arachis hypogaea* L.)

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WRKY transcription factors play crucial roles in the regulation mechanism adapting to the complex environment in plant. In this study, *AhWRKY* family were comprehensively analyzed using bioinformatics approaches combing with the transcriptome sequencing data of the drought-tolerant peanut variety 'L422'. A total of 158 *AhWRKY* genes were identified and renamed according to their distribution on the chromosomes. Based on the structural features and phylogenetic analysis of *AhWRKY* proteins, the peanut *WRKY* family members were classified into three groups, of which group II included five subgroups. Subsequently, the results of the gene structure and conserved motifs of the *AhWRKY* genes further proved the accuracy of the clustering analysis. In addition, 12 tandem and 136 segmental duplication genes were identified. And the analysis result indicated that segmental duplication events were the main driving force in the evolution of *AhWRKY* family. The collinearity analysis found 32 collinear gene pairs between *Arachis hypogaea* and two diploid wild ancestors (*A. duranensis* and *A. ipaënsis*), which provided valuable clues for phylogenetic characteristics of peanut *WRKY* gene family. Furthermore, 19 stress-related *cis*-acting elements were found in the promoter regions. The gene expression level of *WRKY* gene family members in response to drought stress was also studied. And 138 *AhWRKY* genes were induced by drought stress, which showed essential function in response to drought stress. These results could provide fundamental insights for further studying *WRKY* genes in drought-tolerant peanut improvement.