

Genome-wide Identification and Expression Analysis of bZIP Gene Family under Drought Stress in Peanut

B. GAO, J-J CHEN, S-L CUI, M-Y HOU, G-J MU, H-Y CHEN, X-L YANG*, L-F LIU*,
North China Key Laboratory for Crop Germplasm Resources of Education Ministry,
Laboratory for Crop Germplasm Resources of Hebei, College of Agronomy, Hebei
Agricultural University, Baoding, Hebei 071001, China

In this study, the bZIP transcription factors of 112 from the genome of peanut diploid ancestors were identified through bioinformatics, including 55 family members in A genome and 57 in B genome. They were named *AradubZIP1-AradubZIP55* and *AraipbZIP1-AraipbZIP57*, respectively. Their gene structure, conservative motif, phylogenetic, physiochemical properties and subcellular localization were also analyzed. Besides, the gene expression pattern of 32 homologous sequences of tetraploid peanut of L422 response to drought stress in late growth stage in the inverted three leaves were also studied. The results showed that 55 members in the A genome and 57 members in B were divided into four subgroups spreading in 20 chromosomes according to phylogenetic tree. However, the 32 members in L422 were located on 18 chromosomes except A04 and B04, all of which were unstable proteins, and most of them were located in nuclear. It was found that *AhybZIP15* and *AhybZIP31* in L422 peanut had a high homology with AT5G06950 and AT5G06960 in *Arabidopsis thaliana*, respectively. According to the role of AT5G06950 and AT5G06960 in *Arabidopsis thaliana*, we speculated that they played an important role in improving the drought tolerance of peanut leaves in later growth stage. These results provide a reference for studying the regulation of bZIP gene family in drought-tolerant growth process of peanut in later growth stage.