

GWAS and Co-expression Network Reveal Ionomeric Variation in Peanut

H. ZHANG*, T. JIANG, and C.Y. CHEN, Crop Soil & Environmental Sciences, Auburn University, Auburn, AL, 36849; M.L. WANG, USDA-ARS, Plant Germplasm Resource Conservation Unit, Griffin, GA 30223; P.M. DANG, USDA-ARS National Peanut Research Lab, Dawson, GA 39842.

Peanut is an important legume providing products with nutrient dense including mineral nutrition. However, the genetic basis underlying the variations in the mineral composition in peanut is still unknown. A genome-wide association studies (GWAS) of the concentrations of 13 mineral elements combine with co-expression network were performed using a diverse panel of 120 U.S. peanut mini core collections cultivated in two years to study genetic variation in peanut ionome. A total of 36 significant quantitative trait loci (QTLs) associated with 5 elemental concentrations were identified with phenotypic variation explained (PVE) from 18.35% to 27.56%, in which 24 QTLs for boron (B), 2 QTLs for copper (Cu), 6 QTLs for sodium (Na), 3 QTLs for sulfur (S), and 1 QTL for zinc (Zn). Of the 36 major QTLs, 21 were located on the B sub-genome and 15 were on the A sub-genome, which suggested that the B sub-genome has more ionome related genomic regions than the A sub-genome. A total of 114 non-redundant candidate causal genes were identified significantly associated with elements accumulation, which include one high-priority overlap (HPO) candidate gene *arahy.KQD4NT* and it is an important elemental/metal transporter gene located on LGB04 with position 5,413,913-5,417,353. The QTLs and candidate genes obtained from this study provide insight into the genetic basis of peanut seed elemental accumulation and will be useful in breeding peanut with mineral nutrition.