

PB-16

Genome Wide Association Studies for Protein Content in Cowpea (*Vigna unguiculata* L. Walp)

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Cowpea (*Vigna unguiculata* L. Walp., $2n=2x=22$) is one of the most important legume crops which has dietary protein and essential nutrients for the people in sub-Saharan Africa, East-Asia, and other developing countries. Among them, cowpea protein is a high-quality source of vegetable protein in legumes, with relatively low fat content and higher essential amino acid content than other grains. The development of varieties with high protein content for protein supply is one of the main goals of genetic improvement of legumes. In this study, a total of 384 cowpea germplasm were genotyped with 51K Cowpea iselect consortium array. After seeds were harvested in 2018, their crude protein concentration were determined using the Kjeldahl method. Genome-wide association analysis was conducted with Compressed Mixed Linear Model (CMLM) using GAPIT (Genomic Association and Prediction Integrated Tool). We discovered 13 SNPs located on two different chromosomes (chr. 6 and chr. 4) that might be significantly associated with protein content. However, most of candidate genes were found on chromosome 6 including protein kinase activity and CAP (Cysteine-rich secretory protein family) and aminopeptidase activity. As a result, this study provides the sources that could be helpful to research genetic and breeding program of cowpea.

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