

ABSTRACT

Cowpea (*Vigna unguiculata* L.) is an important indigenous legume crop providing dietary proteins, minerals, carbohydrates, fats, vitamins and income to many people in Africa, Asia, and central and South America. However, its production is limited by insect pests, particularly bruchids (*Callosobruchus maculatus*) which is the most destructive and causes storage losses in the quality and quantity of cowpea seeds. To minimize losses due to bruchid infestations, majority of farmers in Sub-Saharan Africa use chemical pesticides which are a health hazard of pesticides to farmers and consumers. The high costs of pesticide and the risk of development resistant bruchids, therefore is need to find safe alternative approach. The use of resistant genotypes is, therefore, a promising alternative control method for the management of *C. maculatus*. However, there is a paucity of information on genetics and sources of cowpea resistance to bruchids. The aim of this study, therefore, was to contribute to the reduction in cowpea storage losses through elucidation of cowpeas genetics of resistance to bruchid.

145 cowpea genotypes were evaluated at Makerere University Agricultural Research Institute, Kabanyolo (MUARIK) for their reaction to *C. maculatus*, in a completely randomized design with three replications. Eighteen genotypes (IT84s-2246, 2419, TVu-2027, WC42, IT97K-499-35, IT95K-207-15, ACC23 × 3B, 182, IT90K-76, NE39×SEC4, WC16, NE4, ALEGI×5T, ACC2×ACC12, WC67, WC48, 3B×2W and SEC1×SEC4) were identified as resistant and could serve as donor parents to introgress resistance to bruchids infestation.

The mechanism of cowpea resistance to bruchid was investigated using four susceptible and three resistant genotypes. Eight biochemical compounds were extracted from seed coat and cotyledon at the Biochemistry laboratory of the National Crops Resources Research Institute (NaCRRI). The results showed that the genotypes presented different amounts of seed coat and cotyledon biochemicals. Correlation analyses of the biochemical compounds with DSI showed that increase in α -amylase inhibitor activity ($r=0.78^{***}$) and carbohydrate content ($r=-0.79^{***}$) in the seed cotyledon contributed to the reduction of bruchid damage suggesting that these biochemical compounds could be used to select for the enhancement of cowpea genotypes resistance to bruchid infestation.

The mode of inheritance and combining abilities of cowpea resistance to bruchid was elucidated by crossing five resistant and four susceptible genotypes in a full diallel mating design, and the F₂ plants and the parents being evaluated at MUARIK. The results indicated that additive gene effects were more important for all of the resistance traits with parents 2419, TVu-2027 and IT84s-2246 showing significant negative GCA effects for number of eggs, insect emergence and holes, and positive effect for median development period suggesting that the parents could be selected for introgressing cowpea resistance to bruchid. Similarly, crosses 2419 × MU9, TVu-2027 × SECOW2W, 2419 × WC69, 2419 × SECOW5T and 2419 × SECOW2W showed negative SCA effects for number of eggs, insect emergence and holes and positive values for median development period indicating resistance that could lead to the selection of resistant varieties.

The genetic basis of resistance to bruchid at molecular level was studied using 217 mini-core accessions previously genotyped at the University of California using 51,128 SNPs. These were phenotyped for their reaction to bruchid at MUARIK. The marker-traits association analysis was performed using the TASSEL version 5.2.15 while identification of candidate genes was done from the cowpea reference genome annotation accessible through Phytozome. The results identified 11 genomic regions associated to bruchid resistance trait. Further analysis of gene prediction using Phytozome, identified six candidate genes associated with the resistance traits which included (i) gene *Vigun08g132300* controlling number of eggs, holes and insect emergence; (ii) *Vigun08g158000* and (iii) *Vigun06g053700* for number of eggs; (iv) *Vigun02g131000*, (v) *Vigun01g234900* and (vi) *Vigun01g201900* for median development period. The identified candidate genes are involved in resistance through carbohydrate and protein biosynthesis, and their regulatory element. The identified candidate genes, therefore, could be incorporated to farmers preferred but susceptible genotypes. The information generated from genome wide association study could be used as a tool for marker assisted breeding.