

ABSTRACT

Soybean [*Glycine max* (L.) Merrill], an annual legume that belongs to the family Fabaceae is grown in every continent for its high protein (40%) and oil (20%) content. Soybean was introduced to Uganda in the 1900s. However, for the first time in Uganda, soybean is threatened by a storage pest *Callosobruchus chinensis*. *C. chinensis* causes tremendous losses because of its high fertility, ability to re-infest, short generation times and irreversible damage which is direct on the grain. *C. chinensis* causes overall seed weight loss, loss of seed viability and altered nutritional quality. Utilization of resistant varieties is the most effective, economical and environmentally sustainable method but it is obstructed by lack of sources of resistance and information on genetics of inheritance.

Consequently, studies were undertaken to establish sources, basis, and inheritance of resistance to *Callosobruchus chinensis* in soybean. The specific objectives of the study were to:- (i) Determine sources of resistance to bruchids in the available germplasm in Uganda, (ii) determine the biochemicals associated with bruchid resistance in soybean and (iii) determine the mode of inheritance of resistance to bruchids in soybean. The studies were carried out at Makerere University Agricultural Research Institute–Kabanyolo (MUARIK) and National Crops Resources Research Institute (NaCCRI)- Namulonge between 2015 and 2018. Four hundred and ninety eight genotypes from Uganda, Zimbabwe, USA and Taiwan were infested with 1-3 day old unsexed bruchids under a no choice test in a randomized complete block design with three replicates. Genotypes showed variations in response to *C. chinensis* indicating differences in resistance levels implying that they contain different amounts of intrinsic and extrinsic factors responsible for resistance. The highest resistance was observed in genotypes AVRDC G8527 and PI G89 while AVRDC G 2043 was the most susceptible. Therefore AVRDC G8527 and PI G89 were the identified sources of resistance.

Based on the results of the no choice test, eight genotypes with varying resistance levels were assessed for biochemical concentrations. The biochemical concentrations of soybean indicated that high tannins, total antioxidants, peroxidase activity and low flavonoids were associated with resistance to *C. chinensis*. The study established that

secondary and not primary metabolites were associated with resistance to *C. chinensis* in soybean. The study also identified that in some genotypes *C. chinensis* was probably detoxifying the biochemicals associated with resistance possibly through sequestering, increased secretions or and altered biochemical composition.

To comprehend the mode of gene action and inheritance patterns of resistance of *C. chinensis*, nine soybean genotypes were crossed under full diallel mating design. Subsequently genetic analysis was conducted on the F₂ progenies and parents to generate the general and specific combining abilities, maternal effects and heritability values. Significant differences in the GCAs and SCA amongst genotypes indicated the presence of both additive and non-additive gene action. The study identified SREB-15C, S-Line 9.2 and S-Line 13.2A as useful parents in breeding for resistance to *C. chinensis* based on general combining abilities. The presence of maternal effects signified the importance of direction of the cross during hybridization. The Baker's ratio of seed weight loss was unity indicating greater predictability of progeny performance based on the GCA alone and better transmission of trait to the progenies. Crosses with significant negative SCA effects such as SREB-15C x S-Line 13.2A, SREB-15C x Maksoy 3N would be very beneficial in the development of *C. chinensis* resistant varieties and therefore were recommended as start up material for the bruchids breeding programme.