

Research Application Summary

Developing cowpea and bean genotypes with tolerance to bruchid beetle

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Abstract

Cowpea and beans are important grain legume pulses in sub-Saharan Africa, but yields have been characteristically low as a result of both abiotic and biotic stresses. Among the biotic stresses infestation by the bruchid beetles *Callosobruchus maculatus* and *Acanthoscelides obtectus* are major problems which cause yield losses of up to 100% in cowpea and bean, respectively. To address this problem a collaborative research is being undertaken between University of Zambia (Zambia) and the Department of Agricultural Research Services (DARS) in Malawi whose objectives are to develop cowpea genotypes with tolerance to *Callosobruchus maculatus* and to improve efficiency of selection through identification of molecular markers linked to *Acanthoscelides obtectus* in beans. In Zambia eight cowpea genotypes (mutants and their parents) and two other popular susceptible genotypes (Musandile and Namuseba) are being evaluated. These were planted in January 2015 in three locations (University of Zambia (UNZA), Golden Agriculture Research Trust (GART) and Msekera in Zambia using a randomised complete block design (RCBD) with three replications. Storage evaluations were done in the Laboratory at the University of Zambia. In Malawi, similar trials were conducted in January 2016 and evaluations are yet to be done. For molecular mapping, a cross involving a susceptible and resistant bean genotype [Lyambai x Carioca] is now being advanced to F₄. The results obtained so far showed that there were significant differences (p< 0.05) among genotypes with regards to mean bruchid adults' emergence across locations in Zambia. The interaction between genotype x location was not significant. The locational mean genotypic performance was significant (p< 0.05) at UNZA and GART. From the experiment the mutant LT 11-5-2-2 and BB 14-16-22 were identified to be tolerant to bruchid attack in and across both locations and they outperformed their parental genotypes. For Malawi field characterization has been done and lab storage evaluations are yet to be done

Key words: Beans, bruchid beetles, cowpeas, Malawi, Zambia

Résumé

Le niébé et le haricot sont d'importantes légumineuses à graines en Afrique sub-saharienne, mais elles sont caractérisées par de faibles rendements en raison des stress biotiques et abiotiques. Parmi les stress biotiques, l'infestation par les bruches *Callosobruchus maculatus* et *Acanthoscelides obtectus* sont des problèmes majeurs qui entraînent des pertes de rendement allant jusqu'à 100% au niveau du niébé et du haricot. Pour pallier ce problème, une recherche collaborative a été initiée entre l'Université de Zambie (Zambie) et le Département des services de recherche agricole (SMCD) au Malawi dont les objectifs sont de développer des génotypes de niébé tolérants aux *Callosobruchus maculatus* et d'améliorer l'efficacité de la sélection par l'identification des marqueurs moléculaires liés à *Acanthoscelides obtectus* au niveau du haricot. En Zambie, huit génotypes de niébé (mutants et leurs parents) et deux autres génotypes sensibles populaires (Musandile et Namuseba) sont en cours d'évaluation. Ces génotypes ont été semés en janvier 2015 dans trois zones (Université de Zambie (UNZA), Golden Trust Agriculture Research (GART) et Msekera) en Zambie en utilisant un dispositif de Bloc Aléatoires Complets (BAC) avec trois répétitions. Les évaluations au cours du stockage ont été effectuées au laboratoire à l'Université de Zambie. Au Malawi, des essais similaires ont été menés en janvier 2016 et les évaluations sont encore à faire. Pour la cartographie moléculaire au niveau du haricot, un croisement entre un génotype sensible et un génotype résistant [Lyambai x Carioca] est maintenant avancé en F4. Les résultats obtenus jusqu'à présent ont révélé des différences significatives ($p < 0,05$) entre les génotypes en ce qui concerne l'émergence des adultes de bruches en Zambie. L'interaction entre génotype x environnement n'a pas été significative. La performance génotypique moyenne est significative ($p < 0,05$) à UNZA et GART. Les mutants LT 11-5-2-2 et BB 14-16-22 ont été identifiés pour comme tolérants à l'attaque des bruches au niveau des deux sites et ils ont été plus performants que leurs parents. Pour le site du Malawi, la caractérisation a été faite et les évaluations en stockage au laboratoire sont encore à faire.

Mots clés: Haricots, bruches, haricots, Malawi, Zambie

Background

Biotic challenges reducing grain yields of beans and cowpea are pests and diseases. Bruchids are responsible for the largest post-harvest losses to stored seeds. Resistance to these beetles is thus important. Bruchid attack on dry beans in Zambia and Malawi is a serious problem as most beans are not stored for longer periods (more than 3 months). The bruchid beetle *Callosobruchus maculatus* and *Acanthoscelides obtectus* causes severe losses in storage, distorts the taste and reduces the market value and acceptance to the consumers in cowpea and bean respectively. It is against this background that the collaborative research project between University of Zambia (Zambia) and the Department of Agricultural Research Services (DARS) (Malawi) is being undertaken whose objectives are to develop cowpea genotypes with tolerance to *Callosobruchus maculatus* and to improve efficiency of selection through identification of molecular markers linked to *Acanthoscelides obtectus* in beans.

Literature application

Bruchids (*Callosobruchus maculatus*) cause yield losses in bean and cowpea primarily in their larva stage where they perforate the grains, feed on the contents, create holes and ultimately contaminate the grains (Swella and Mushobozy, 2007). Preservation of cowpea and beans by using chemicals can be used to control bruchids but disastrous effects resulting from grain poisoning and environmental contamination have led to the limited use of this approach (Ali *et al.*, 2004). The use of resistance varieties is therefore appropriate, environmentally friendly and a cheaper approach for small scale farmers. Apart from introgression of a resistant trait from a donor parental genotype, one way of creating variation to aid in identifying resistant genotypes is by the use of mutagens in mutation breeding. Identification of desirable traits particularly quantitatively inherited ones pose a challenge due to its dependence on environmental influence (Bertland *et al.*, 2007). Even though the genome for cowpea and bean have been mapped (Yu *et al.*, 2000; Muchero *et al.*, 2009) information of molecular markers linked for resistance to bruchid tolerance is scanty. This research seeks to identify molecular markers linked for tolerance to bruchid infestation in bean. It has been reported that there is an association between seed size and yield to *C. maculatus* resistance in cowpea (Kananji 2007; Mei *et al.* 2009; Ponnusammy *et al.* 2014). This implies that utilisation of cowpea agronomic traits such as yield and its components may cluster tolerant genotypes to *C. maculatus* together.

Study description

The project is being implemented in Zambia and Malawi. In Zambia, the project commenced in January 2015 eight genotypes (mutants and their respective parents) and two other popular susceptible genotypes (Musandile and Namuseba) were planted in three sites namely; Chipata, Chibombo and Lusaka [University of Zambia (UNZA)]. For molecular mapping studies in beans, a cross involving a susceptible and resistant genotype [Lyambai x Carioca] is now being advanced to F₄. The cowpea mutants were harvested and evaluated for tolerance to *Callosobruchus maculatus* in the laboratory at the University of Zambia.

The activities in Malawi were implemented in January 2016. The experiments were planted in all the three sites, i.e., Chitedze, Chitala and Baka Research Stations using a randomized complete block design with three replications. Some mutants (including Musandile, a Zambian popular but susceptible genotype to bruchid attack) and other Malawian popular genotypes were characterized. Mean parameters measured were number of pods per plant, number of seeds per pod, 100 seed weight, height, number of days to 50% flowering, and Yield ha⁻¹. Laboratory evaluations are yet to be undertaken.

Research application

The results obtained so far showed that there were significant differences ($p < 0.05$) among genotypes with regards to mean adults' emergence across locations in Zambia. The mean genotypic locational performance was significant ($p < 0.05$) at UNZA and GART. The mutant LT 11-5-2-2, BB-14-16-22 were identified to be tolerant to bruchid in and across both locations and they outperformed their parental genotypes (Table 1). Cluster analysis (Fig. 1) on

Table 1. Mean adult emergence of bruchid 33 days after oviposition at UNZA Laboratory

Genotypes	Across locations	UNZA	GART
BB 14-16-2-2	3.34	2.16	4.43
BB 7-9-7-5	3.12	3.82	2.7
BB PRT	4.24	3.11	5.31
LT 4-2-4-1	4.18	3.41	4.74
LT 11-5-2-2	3.25	3.02	3.16
LT 3-8-4-1	3.72	3.35	4.12
LT 3-8-4-6	3.64	3.49	4.85
LT PRT	4.34	4.07	4.14
Musandile	4.39	4.76	4.17
Namuseba	4.26	4.47	3.4
LSD	0.84	1.41	1.36

BB PRT (Bubebe) and LT PRT (Lutembwe)- Parental genotypes; BB 14-16-2-2 and BB 7-9-7-5 are mutants created from BB PRT; LT 11-5-2-2, LT 4-2-4-1, LT 3-8-4-6 and LT 3-8-4-1 are mutants created from LT PRT. LSD; F- protected least significant difference at $\alpha = 0.05$

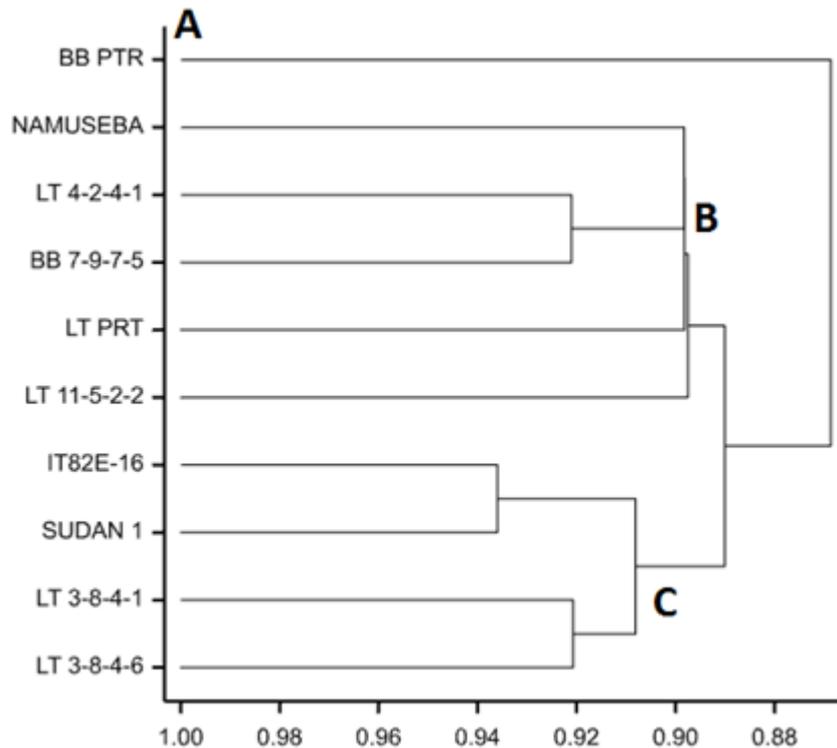


Figure 1. A dendrogram depicting similarity relationships among cowpea genotypes, with cluster groups A, B and C at 89.5 % similarity level based on evaluated agronomic traits

characterized genotypes using agronomic traits in Malawi revealed three distinct groups A, B and C.

The next steps will involve genotypic storage evaluation in Malawi to identify tolerant genotypes to *C. maculatus* and to crisscross for any association in the clustering pattern. Furthermore on station and on farm evaluation on identified cowpea genotypes will be done in Zambia and advancement of [Lyambai x Carioca] cross to F₅ to create a mapping population will be undertaken

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