

Genetic studies of cowpea [*Vigna unguiculata* (L.) Walp.] for resistance to thrips (*Megalurothrips sjostedti* Trybom) in Cameroon.

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Dr Gonné on his PhD graduation day, 2017.

Background

Thrips are an important cowpea insect pest in Cameroon, and heavy infestation can result in complete loss of harvest. Thrips are usually controlled by the application of insecticides, however this measure is ineffective, represents an additional cost to production and are toxic for humans and the environment. This study was carried out as part of the requirements for a PhD with the following objectives:

1. To identify new source of resistance to flower bud thrips through the screening of germplasm.
2. To determine the inheritance of resistance to thrips in cowpea.
3. To identify QTLs associated with resistance to flower bud thrips in cowpea.

Achievements

1. Two hundred (200) cowpea varieties including 180 landraces were screened for resistance to thrips in two field locations (Guring and Djalingo) and in the screenhouse (IRAD), scoring visual damage to flowers and the number of thrips per flower. Eleven thrip resistant varieties were identified, including Sanzi, from Ghana.
2. Two sets of six generations (P1, P2, F1, F2, BC1P1, BC1P2) developed from crosses between Sanzi (resistant parent) and Vya and Lori (susceptible parents) were evaluated under artificial and natural thrips infestation. The generation mean analysis revealed that both additive and non-additive gene

action were important with dominance x dominance being the most predominant. Broad sense and narrow sense heritability estimated varied from 0.58 to 0.74 and 0.61 to 0.65 for number of thrips per flower and rating of thrips damage, respectively, indicating the influence of the environment on thrips susceptibility. The number of genes controlling thrips resistance was three for number of thrips per flower and between 3 and 4 for score of thrips damage.

3. One hundred and fifty (150) F₂ plants derived from a cross between Sanzi and Vya were used to construct a genetic map with 232 polymorphic SNP markers. Three significant QLTs (Fthp129, Fthp28 and Fthp87) for thrips resistance were detected accounting for 43.2% of the observed phenotypic variation. Further studies are needed to validate these QLTs for their useful exploitation in a molecular breeding programme.



Left to right, (i) thrips on a cowpea flower; (ii) typical symptoms of cowpea flowers attacked by thrips; (iii) collection of flowers infested by thrips, also used to artificially infest plants in the screenhouse to determine the susceptibility or resistance to thrips of tested plants; (iv) the F₂ mapping population derived from Sanzi and Vya grown in the screen house; (v) sampling of leaf tissue from the mapping population for DNA extraction and analysis.