

Research Application Summary

Enhancing genetic resistance to soybean rust disease

Maphosa, M.^{*1}, Talwana, H.¹, Mukankusi, C.², Bandyopadhyay, R.³ & Tukamuhabwa, P.¹

^{*}University of Zimbabwe, Department of Crop Science, Box MP167, Mount Pleasant, Harare, Zimbabwe

¹Makerere University, Department of Crop Science, P. O. Box 7062, Kampala, Uganda

²CIAT Bean Program, Kawanda Agricultural Research Institute, P.O Box 6247, Kampala, Uganda

³International Institute of Tropical Agriculture, PMB 5320, Ibadan, Nigeria

Corresponding author: mcebisimaphosa@yahoo.co.uk

Abstract

Soybean is an important crop worldwide with unrivalled protein quality and content. Sustenance of soybean productivity is, however, compromised by the devastating soybean rust disease caused by the fungus *Phakopsora pachyrhizi*. Some resistant genotypes have been identified in exotic germplasm that can be utilised in enhancing genetic resistance of the locally adapted varieties. Thus this study seeks to utilise exotic and farmer preferred varieties to formulate breeding programme for resistance to soybean rust. The study is also using marker assisted selection to introgress selected specific resistance genes into one genetic background. Preliminary results show characteristic resistance phenotypic responses for the crosses involving exotic parents with single gene resistance. Field evaluation of F₂ and F₃ progenies respectively will give conclusive results on the resistance breeding values of the selected parental materials during the forthcoming two seasons (September - December 2010) and (March - June 2011). Preliminary results on gene pyramiding have identified makers *Satt620 (Rpp2)*, *Sat460 (Rpp3)* & *Satt288 (Rpp4)* as being polymorphic and usable for marker assisted selection. Selection using these polymorphic markers on the F₂ progenies will begin shortly.

Key words: Gene pyramiding, *Glycine max*, marker assisted selection, *Phakopsora pachyrhizi*

Résumé

Le soja est une plante importante dans le monde entier avec une qualité et un contenu de protéine incomparables. Cependant, la subsistance de la productivité de soja est menacée par la maladie dévastatrice de la rouille causée par le champignon *Phakopsora pachyrhizi*. Quelques génotypes résistants ont été identifiés dans le germoplasme exotique qui peut être utilisé pour augmenter la résistance génétique des variétés localement adaptées. Ainsi, cette étude cherche à utiliser les variétés exotiques et préférées par les fermiers pour formuler le

programme propice à la résistance face à la rouille de soja. L'étude emploie également la sélection assistée par le marqueur pour incorporer les gènes sélectionnés de résistance spécifique dans un contexte génétique. Les résultats préliminaires montrent des réponses phénotypiques à résistance caractéristique pour les hybrides faisant participer les parents exotiques avec une résistance particulière de gène. L'évaluation sur terrain respectivement des progénitures F_2 et F_3 donnera des résultats concluants sur les valeurs de reproduction de résistance des matériaux parentaux choisis pendant les deux saisons prochaines (Septembre - Décembre 2010) et (Mars - Juin 2011). Les résultats préliminaires sur l'aspect pyramidal de gène ont identifié les marqueurs *Satt620* (*Rpp2*), *Sat460* (*Rpp3*) & *Satt288* (*Rpp4*) comme étant polymorphiques et utilisables pour la sélection assistée par marqueur. Le choix employant ces marqueurs polymorphes sur les progénitures F_2 commencera dans un bref délai.

Mots clés: Pyramidation des genes, *Glycine max*, Selection par marqueur, *Phakopsora pachyrhizi*

Background

Soybean, *Glycine max*, is one of the most important and versatile crops worldwide. Despite its importance yield losses of up to 80% are incurred due to the virulent and highly variable soybean rust, *Phakopsora pachyrhizi* (Yorinori *et al.*, 2005). Such a threat jeopardises the livelihood and nutritional well-being of millions of people. Genetic resistance is a strategically important means of managing soybean rust. Exotic germplasm from the Orient, where the disease has been endemic for a long time, have higher levels of resistance despite their narrow adaptability. Thus the present study seeks to utilise exotic and farmer preferred varieties to formulate breeding programme for resistance.

Literature Summary

Soybean improvement is largely dependent on the generation of bi-parental crosses and advancement of segregating progenies to homozygosis. In this context, combining ability studies provide a guide for selecting elite parents and desirable combinations to be used in the formulation of a systematic breeding project. Diallel analysis used in combining ability studies allows for the evaluation and identification of more promising crosses with superior segregating lines (Lopes *et al.*, 2001; Awan *et al.*, 2005). High potential parents can be identified and used in breeding programmes to aid the development of soybean cultivars with resistance to soybean rust. The rapid change in

soybean rust pathogen populations raises a continuous threat to the effectiveness of available varieties with specific resistance. Hence, there is need to develop effective durable resistance against soybean rust. One way of sustaining the effectiveness of existing major genes is through gene pyramiding. However, this task has been challenging due to the difficulty in selecting plants with multiple resistance genes based on phenotype (Mohler and Singrun, 2004). Thus, MAS using tightly linked gene specific markers is of importance in improving selection efficiency during gene pyramiding to enhance the effectiveness of resistance to ASR.

Study Description

Nine genotypes comprising *Rpp2*, *Rpp3*, *Rpp4*, Maksoy 2N, Namsoy 4M, UG 5, Wondersoy and Nam2 (Table 1) were selected for use in this study. These accessions and varieties represent different levels and modes of resistance to soybean rust. Hybridisation was done using Griffing's diallel Method II /Model I in a screen house. Method II/Model I uses n parents, $[n(n-1)/2]$ crosses in the F_2 - F_3 generation without reciprocals (Shattuck *et al.*, 1993). Bi-parental crosses were done to generate the F_1 progeny prior to evaluating F_2 and F_3 progeny. A randomised complete block design with two replicates in 2 X 2m rows will be used to evaluate the segregating progeny in a soybean rust hotspot. Data analysis on disease severity, defoliation percentage, RAUDPC and response to rust will be done using a general ANOVA in GENSTAT (Payne *et al.*, 2007) with parents and crosses as fixed factors and replicates as random factors. Molecular markers *Satt620* (*Rpp2*), *Sat460* (*Rpp3*) & *Satt288* (*Rpp4*) will be used to identify F_2 progenies with two gene combinations evaluate their field performance.

Research Application

Preliminary results show that resistance genes in exotic genotypes are different from those in the local varieties. This is evidenced by the different sized PCR amplicons (Table 2). Furthermore, this enables utilisation of simple sequence repeat markers *Satt620*, *Sat460* and *Satt288* in screening segregating populations for resistance genes *Rpp2*, *Rpp3* & *Rpp4* respectively. This will expedite the introgression of these resistance genes into susceptible backgrounds through early stage assay.

Recommendation

Marker assisted gene pyramiding is feasible for the three soybean rust resistance genes despite the absence of differentiating races necessary in conventional gene pyramiding.

Table 1. Genotype and description of selected soybean lines for diallel analysis.

Type	Genotype	Pedigree	Stem Termination	Maturity ^a	Response to rust	Remark	Source ^b
Accession	G8586	-	Determinate	Early	Resistant to isolate Australia 72-1 India 73-1 Philippines 77-1 Taiwan 72-1	has <i>Rpp2</i> rust resistance gene	AVRDC-Taiwan
Accession	G7955	-	Determinate	Early	Resistant to isolate India 73-1	has <i>Rpp3</i> rust resistance gene	AVRDC-Taiwan
Accession	UG5	-	Semi-determinate	Late	Resistant	Resistant but gene unknown	NARO-MAK Uganda
Commercial Variety	-	Nam2 x GC00138-29	Semi-determinate	Late	Moderately resistant	Variety with a single resistance	NARO-MAK Uganda
Commercial Variety	-	Duiker X TGx1835-10E	Semi-determinate	Late	Tolerant	Variety name Maksoy 2N resistance gene?	NARO-MAK Uganda
Breeding line	-	Duiker X TGx1835-10E	Semi-determinate	Medium	Tolerant	Breeding line under evaluation	NARO-MAK Uganda
Commercial variety	-	-	Determinate	Late	Susceptible	Wondersoya Obsolete variety	IITA Nigeria
Commercial variety	87D-668	-	Semi-determinate	Late	Susceptible	Nansoy 2 Obsolete variety	IITA Nigeria

^aEarly maturity <90 days; Medium 91-100 days, Late Maturity >100 days.^bAVRDC Asian Vegetable Research Development Centre, NARO-MAK collaboration between National Agricultural Research Organisation and Makerere University.

Table 2. Polymorphism screen between the exotic and local resistant parents for the three resistance loci *Rpp2*, 3 & 4.

Gene	Marker	Linkage group	Parent	Base pairs
<i>Rpp2</i>	<i>Satt620</i>	J	G8586(<i>Rpp2</i>)	320
			G7955(<i>Rpp3</i>)	327
			G10428(<i>Rpp4</i>)	330
			Nam4	300
			UG5	290
<i>Rpp3</i>	<i>Sat460</i>	C2	G8586(<i>Rpp2</i>)	250
			G7955(<i>Rpp3</i>)	160
			G10428(<i>Rpp4</i>)	260
			Nam4	180
			UG5	155
<i>Rpp4</i>	<i>Satt288</i>	G	G8586(<i>Rpp2</i>)	280
			G7955(<i>Rpp3</i>)	220
			G10428(<i>Rpp4</i>)	230

Acknowledgement

This research is financed by RUFORUM. We further thank the National Crops Resources Research Institute, Makerere University and AVRDC for providing the germplasm.

References

- Awan, S.I., Malik, M.F.A. and Siddique, M. 2005. Combining ability analysis in intervarietal crosses for component traits in hexaploid wheat. *Journal of Agriculture and Social Sciences* 1:316-17.
- Lopes, Â.C.A., Vello, N.A. and Pandini, F. 2001. Seed yield combining ability among soybean genotypes in two locations. *Crop Breeding and Applied Biotechnology* 1:221-228.
- Mohler, V. and Singrun, C. 2004. General considerations: marker assisted selection. In: Lörz, H. and Wenzel, G. (Eds.). *Molecular marker systems in plant breeding and crop improvement (biotechnology in agriculture and forestry)*, vol 55. Springer, Berlin, Germany. pp. 305-317.
- Payne, R.W., Murray, D.W., Harding, S.A., Baird, D.B and Soutar, D.M. 2007. *Genstat for Windows* (10th Ed.) Introduction. VSN International, Hemel.
- Shattuck, V.I., Christie, B and Corso, C. 1993. Principles for Griffing's combining ability analysis. *Genetica* 90:73-77.
- Yorinori, J.T., Morel, P.W., Frederick, R.D., Costamilan, L.M., Bertagnolli, P.F., Hartman, G.E., Godoy, C.V. and Nunes Junior, J. 2005. Epidemics of soybean rust (*Phakopsora pachyrhizi*) in Brazil and Paraguay from 2001 to 2003. *Plant Disease* 89:675-677.