Research Application Summary

Combining ability for resistance to soybean rust in F_2 and F_3 soybean populations

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Abstract

Combining ability for soybean rust resistance was estimated from a half diallel cross of eight soybean lines using disease severity and sporulation rates as indices for resistance. A consistent contribution of additive gene action was observed at MUARIK in Uganda across F_2 and F_3 despite high environment contribution to both severity and sporulation rate. The simultaneous evaluation of F_3 populations in five diverse locations produced similar results with significant GCA effects for both traits. There were, however, greater genotypic effects to soybean rust severity and sporulation across the five test environments, although severity and sporulation rate genetic systems acted independently. Additive and additive x additive epistatic gene effects were the most common form of GCA controlling resistance. Specific combining ability did not always contribute to soybean rust resistance. Parental line UG 5 was the most outstanding producing the greatest number of resistant populations. This study underscores the importance of additive gene effects in the control of soybean rust severity and sporulation rate.

Key words: Additive gene effects, *Glycine max*, *Phakopsora pachyrhizi*, soybean rust resistance

Résumé

La capacité de combinaison pour la résistance à la rouille du soja a été estimée à partir d'une croix à moitié des diallèlesde huit lignées de soja en utilisant la sévérité de la maladie et les taux de sporulation comme indices de résistance. Une contribution cohérente de l'action additive des gènes a été observée à MUARIK en Ouganda à travers F_2 et F_3, malgré la contribution environnementale élevée à la sévérité et au taux de sporulation. L'évaluation simultanée des populations F3 dans cinq endroits différents a produit des résultats similaires avec des effets de GCA importants pour les deux traits. Il y avait, cependant, de plus grands effets génotypiques à la sévérité de la rouille du soja et à la sporulation dans les cinq environnements de test, bien que la sévérité et les systèmes génétiques de taux de sporulation ont agi indépendamment. Les effets des gènes épistatiquesadditifs et additif x additif étaient la forme la plus commune de la résistance déterminante du GCA. L'aptitude spécifique à la combinaison n'a pastoujours contribué à la résistanceà larouille du soja. La lignée parentale UG 5 a été la plus remarquable produisant le plus grand nombre de populations résistantes. Cette étude souligne l'importance des effets génétiques additifs dans le contrôle de la sévérité de la rouille du soja et le taux de sporulation.

Mots clés: Effets génétiques additifs, *Glycine max*, *Phakopsora pachyrhizi*, résistance à la rouille du soja

Background

Soybean rust (*Phakopsora pachyrhizi* Syd) is a very important disease in many soybean growing areas causing losses of up to 75% in unprotected fields under heavy infestation (Yorinori *et al*., 2005). Most of the resistant germplasm sources maybe un-adapted to the environment for which the disease resistance trait is sought. Thus prior to incorporating germplasm with any form of resistance into a soybean rust breeding programme it is important to evaluate their breeding potential with locally adapted, farmer preferred varieties. Selection of parents for hybridisation requires critical consideration given that phenotypic performance alone does not always provide adequate information for breeding purposes. Combining ability studies provide a guide for selecting elite parents and desirable cross combinations for systematic breeding. More so, the expression of soybean rust resistance genes is influenced by the genetic backgrounds in which they are introgressed making it worthwhile to test the effectiveness of these resistance genes in different backgrounds (DeLucia *et al*., 2008; Yamanaka *et al*., 2010; Lemos *et al*., 2011). In diallel analysis for combining ability of a self pollinated crop like soybean F_2 and F_3 generations give better predictions on the performance of lines due to the decreased level of dominance gene effects (Bhullar *et al*., 1979) and availability of ample seed. Therefore, this study was aimed at i) determining soybean rust resistance combining ability parameter estimates across the F_2 and F_3 generations in one environment during different seasons, ii) assessing the role of genotype x environment in combining ability for soybean rust severity and sporulation rate in five geographically diverse environments in the F_3 generation using Griffing's diallel analysis Method 2/Model 1, and iii) identifying parents and crosses with good combining ability for soybean rust resistance through estimates of general and specific combining abilities.

Literature Summary

Genetic resistance is the most economic and strategically important means of reducing yield losses due to soybean rust compared to chemical control. Several specific and partially resistant sources of soybean rust resistance have been identified in various germplasm collections. Genes R*pp1*, R*pp2*, R*pp3*, R*pp4*, R*pp5* and R*pp?(Hyuuga)* with resistance to specific rust races have been identified and mapped to different linkage groups (Hyten *et al*., 2007; Monteros *et al*., 2007; Garcia *et al*., 2008). The effectiveness of these resistance genes depends on the prevalent rust races in a particular location. For example, R*pp2* and R*pp4* were effective in Brazil (Kato and Yorinori, 2008); R*pp2*, R*pp3* and R*pp4* in South Africa (Pretorius *et al*., 2007); R*pp2* and R*pp3* in Uganda (Oloka *et al*., 2008) and R*pp1* and R*pp4* in Nigeria (Twizeyimana *et al*., 2009). This therefore implies that there is no universally acceptable resistant genotype.

Several other unnamed sources of specific gene resistance exist such as UG5, FT2, GC00138-29 which are effective in various parts of the world (Kawuki *et al*., 2003; Laperuta *et al*., 2008). In addition other sources of germplasm utilise partial resistance characterised by a semi-compatible reaction with a range of red brown phenotypic manifestations with reduced sporulation and lesion density (Bonde *et al*., 2006; Jarvie, 2009; Walker *et al*., 2011). However, most of the resistant sources maybe un-adapted to the environment for which the disease resistance trait is sought. Thus prior to incorporating germplasm with any form of resistance into a soybean rust breeding programme it is important to evaluate their breeding potential with locally adapted, farmer preferred varieties.

Study Description

The experiments were carried out at five sites; Makerere University Agricultural Research Institute-Kabanyolo (MUARIK), National Crops Resources Research Institute (NaCRRI), Nakabango (NAK), Iki-Iki (IKI) and Kasese (KAS). Three SBR resistant lines G8586 (R*pp2*), G7955 (R*pp3*), UG 5; three moderately resistant cultivars Namsoy 4M, MNG 11.2, Maksoy 2N and two susceptible cultivars Wondersoya and Nam 2 (Table 8) were crossed in a 8 x 8 diallel mating scheme with no reciprocals to generate 28 F_1 hybrids during 2008 and 2009. Data on disease severity and sporulation were collected from the parents, F_2 and F_3 families separately at different times based on the final severity and sporulation measure. Reaction responses were assessed and grouped into three; red brown (RB), tan (T) and mixed reactions (MX).

Research Application

Our study observed that red brown lesions were consistently associated with low sporulation which corroborates observations made by Bonde *et al*. (2006). Sporulation is an important attribute in breeding for soybean rust resistance as it ensures low secondary infection during the growing season. Each location, however, had a unique pathogen profile as evidenced by the distinct responses of the parental genotypes. Future evaluations for resistance will require assessment of genotypes in these areas since each seems to have a different pathogen profile. Based on severity and sporulation scores MUARIK and KAS maybe having mixed or aggressive pathogen races. This is due to predominance of mixed and tan lesions with

Table 1. Mean soybean rust severity and sporulation, general and specific combining ability of eight parental soybean lines evaluated at MUARIK in F2 and F3 during the 2010 and 2011 seasons respectively.

Parents	Severity				Sporulation rate			
	Mean score	GCA	Mean score	GCA	Mean score	GCA	Mean score	GCA
	F_2		F_3		F_2		F_3	
1.G8586(R*pp2*)	3.0	-0.38***	3.5	-0.51*	2.0	-0.48**	3.3	-0.68***
2.G7955(R*pp3*)	2.0	-0.52***	2.5	-0.27	1.5	-0.90***	4.5	-0.54***
3.UG 5	2.5	-0.71***	4.0	-0.95**	1.5	-0.81***	4.5	-0.78***
4.Namsoy 4M	4.0	0.10	4.5	-0.16	3.5	0.11	5.0	0.41*
5.Maksoy 2N	2.5	-0.29**	4.5	-0.04	3.0	0.22***	5.0	0.17
6.MNG 11.2	3.0	-0.11	4.0	0.20	2.0	0.19	4.5	0.04
7.Nam 2	7.0	0.99***	7.0	0.66**	5.0	0.85***	5.0	0.42*
8.Wondersoya	5.5	0.93***	4.5	1.08***	5.0	0.83***	5.0	0.96***
Mean	3.7		4.3		2.9		4.6	
r	0.86**		0.53^{ns}		0.91**		0.72*	

	Severity mean squares		Sporulation mean square	
	F_2	F_3	F_2	F_3
GCA	4.1285***	4.141*	4.5508***	3.799***
SCA	0.4653	3.664*	0.3688	1.6484
Error	0.595	1.875	0.6025	1.054
CV%	14.5	20.7	12.7	20.8
GCA/SCA	8.872	1.13	12.33	2.25
Baker's ratio	0.95	0.69	0.96	0.82

GCA, general combining ability; SCA specific combining ability, r-correlation.
***significant at *P*d"0.001, *significant at P≤0.05.

profuse sporulation. Mixed responses are generally associated with a mixture of races and complex virulence patterns (Bonde *et al*., 2006; Miles *et al*., 2008). However, studies on the race composition of each location need to be undertaken for more accurate deductions to be made about predominant races. In our study we observed no consistent association between high severity and sporulation rating combining ability estimates. This concurs with observations made by Walker *et al*. (2011) that high severity is not always associated with heavy sporulation. This suggests that selection for the two traits has to be done independently to improve soybean rust resistance.

Recommendation

This study has demonstrated the importance of additive gene action in controlling soybean rust severity and sporulation across F_2 and F_3, and locations. However, the two genetic systems of severity and sporulation seem to act independently of each other. Based on the positive correlation between sporulation GCA estimates and parental means at MUARIK in the F_2 and F_3, and severity in F_3 selection of parents for good GCA for soybean rust resistance can be based on performance. Follow up studies need to be done to identify the resistance gene in UG 5 and undertake mapping studies on the gene as it has proved to be very valuable. Further, selection of F_3 progenies across environments for soybean rust severity and sporulation can reliably result in promising genotypes.

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References

Bhullar, G.S., Gill, K.S. and Khehra, A.S. 1979. Combining ability analysis over F1-F5 generations in diallel crosses of bread wheat. *Theoretical Applied Genetics* 55:77-80.

Bonde, M.R., Nester, S.E., Austin, C.N.S., Frederick, R.D. and Miles, M.R. 2006. Evaluation of virulence of *Phakopsora pachyrhizi* and *P. meibomiae* isolates. *Plant Disease* 90:708-716.

De Lucia, A., Gilli, J., Soldini, D., Salines, L., Blaszchik, J. and Fariza, S. 2008. Current situation of breeding for resistance to soybean Asian rust (*Phakopsora pachyrhizi*) in Argentina: Assessment of the official germplasm bank. pp. 1-5. In: Kudo, H., Suenaga, K., Soares, R.M., Toledo, A. (Eds.), Facing the challenges of soybean rust in South

America. Japan International Research Center for Agricultural Sciences (JIRCAS), Tsukuba, Ibaraki, Japan.

Garcia, A., Calvo, É.S., Kiihl, R.A.S., Harada, A., Hiromoto, D.M. and Vieira, L.G.E. 2008. Molecular mapping of soybean rust (*Phakopsora pachyrhizi*) resistance genes: discovery of a novel locus and alleles. *Theoretical Applied Genetics* 117:545-553.

Hyten, D.L., Hartman, G.L., Nelson, R.L., Frederick, R.D., Narvel, J.M.and Cregan, P.B. 2007. Map location of *Rpp1* locus that confers resistance to soybean rust in soybean. *Crop Science* 47:837-841.

Jarvie, J.A. 2009. A review of soybean rust from a South African perspective. *South African J. of Science* 105:105-108.

Kato, M., Yorinori, J.T., 2008. A study on a race composition of *Phakopsora pachyrhizi* in Brazil: a difficulty of race identification. pp. 94-98. In: Kudo, H., Suenaga, K., Soares, R.M., Toledo, A. (Eds.). Facing the challenge of soybean rust in South America. Japan International Research Centre for Agricultural Science (JIRCAS), Tsukuba, Ibaraki, Japan.

Kawuki, R.S., Adipala, E. and Tukamuhabwa, P., 2003. Yield loss associated with soybean rust (*Phakopsora pachyrhizi* Syd.) in Uganda. *Phytopathology* 151:7-12.

Laperuta, L., Arias, C., Ribeiro, A., Rachid, B., Pierozzi, P., Toledo, J., Pipolo, A. and Carneiro, G. 2008. New genes conferring resistance to Asian rust: allelic testing for the *Rpp2* and *Rpp4* loci. *Pesq agro* 43:1741-1747.

Lemos, N.G., Braccini, A., Abdelnoor, R.V., Oliveira, M.C.N., Suenanga, K. and Yamanaka, N. 2011. Characterisation of R*pp*2, R*pp*4 and R*pp*5 for resistance to soybean rust. *Euphytica* 182:53-64.

Miles, M.R., Morel, W., Ray, J.D., Smith, J.R., Frederick, R.D. and Hartman, G.L. 2008. Adult plant evaluation of soybean accessions for resistance to *Phakopsora pachyrhizi* in the field and green house in Paraguay. *Plant Disease* 92:96-105.

Monteros, M.J., Missaoui, A., Phillips, D., Walker, D.R. and Boerma, H.R. 2007. Mapping and confirmation of the 'Hyuuga' red-brown lesion resistance gene for Asian soybean rust. *Crop Science* 47:829-836.

Oloka, H.K., Tukamuhabwa, P., Sengooba, T. and Shanmugasundram, S. 2008. Reaction of exotic germplasm to *Phakopsora pachyrhizi* in Uganda. *Plant Disease* 92: 1493-1496.

Pretorius, Z.A., Visser, B. and du Preez, P.J. 2007. First report of Asian soybean rust caused by *Phakopsora pachyrhizi* on kudzu in South Africa. *Plant Disease* 91:1364-1366.

Twizeyimana, M., Ojiambo, P.S., Sonder, K., Ikotun, T., Hartman, G.L. and Bandyopadhyay, R. 2009. Pathogenic variation of *Phakopsora pachyrhizi* infecting soybean in Nigeria. *Phytopathology* 99:353-361.

Yamanaka, N., Yamaoka, Y., Kato, M., Lemos, N.G., Passianotto, A.L.L., Santos, J.V.M., Benitez, E.R., Abdelnoor, R.V., Soares, R.M. and Suenaga, K. 2010. Development of classification criteria for resistance to soybean rust and differences in virulence among Japanese and Brazilian rust populations. *Trop. Plant Path*. 35:153-162.

Yorinori, J.T., Paiva, W.M., Frederick, R.D., Costamilan, L.M., Bertagnolli, P.F., Hartman, G.L., Godoy, C.V. and Nunes, J.J. 2005. Epidemics of soybean rust (*Phakopsora pachyrhizi*) in Brazil and Paraguay from 2001 to 2003. *Plant Disease* 89:675-677.