

***Phakopsora pachyrhizi* diversity and rust resistance in soybean genotypes in Uganda**

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Abstract

The objectives of this study were twofold: (i) to validate use of SSR markers in assessing *Phakopsora pachyrhizi* diversity in Uganda and (ii) to assess elite soybean lines for resistance to rust in diverse locations in Uganda. A dendrogram constructed from the similarity data of the isolates from the five locations grouped the isolates into two clusters. The first cluster consisted of isolates from MUARIK, Iki Iki and Mubuku and the other cluster consisted of isolates from NaCRRI and Nakabango. Maksoy 3N had the lowest rust score of 2.9 while Duiker had the highest mean score of 4.0.

Key words: *Phakopsora pachyrhizi*, soybean lines, yield stability

Résumé

Les objectifs de cette étude étaient de deux ordres: (i) valider l'utilisation des marqueurs SSR dans l'évaluation de la diversité de *Phakopsora pachyrhizi* en Ouganda et (ii) évaluer les lignées élités du soja pour la résistance à la rouille dans des endroits divers en Ouganda. Un dendrogramme construit à partir des données de similitude des isolats provenant des cinq sites a rassemblé les isolats en deux groupes. Le premier groupe se composait des isolats provenant de MUARIK, IkiIki et Mubuku et l'autre groupe se composait d'isolats provenant de NaCRRI et Nakabango. Maksoy 3N a obtenu le score le plus bas de la rouille de 2,9 tandis que Duiker a obtenu le plus haut score moyen de 4,0.

Mots clés: *Phakopsora pachyrhizi*, lignées de soja, stabilité du rendement

Background

Management options recommended for soybean rust disease include chemical sprays, cultural practices and deployment of resistant varieties. Deployment of resistant cultivars still remains the cheapest and most viable strategy to manage soybean rust in Africa and other countries in the developing world (Twizeyimana *et al.*, 2008). However, breeding for resistance

to soybean rust disease remains a great challenge due to lack of resistant parental lines in most breeding programmes. Use of specific rust resistance genes for development of rust-resistant soybean varieties has been complicated by the high variability within *Phakopsora pachyrhizi* species. After deployment, single resistance genes succumb to certain isolates of the pathogen (Hartman *et al.*, 2005). To ensure longevity of any form of resistance, it is important to know the pathogen diversity in the major production areas of any region, so that each pathogen population is catered for. SSR markers were employed in this study to assess genetic diversity in selected elite soybean lines in Uganda. The study also sought to establish the level of rust resistance among the 24 elite soybean lines.

Literature Summary

Soybean varieties Maksoy 1N and Namsoy 4M were released in 2004 and are widely grown in Uganda. These were initially resistant to soybean rust but later succumbed to the disease (Tukamuhabwa *et al.*, 2009). Soybean rust resistance inheritance studies showed that these two varieties contain specific resistance genes to soybean rust (Kiryowa *et al.*, 2005). Knowledge of pathogen diversity allows development of varieties with resistance to match prevailing *P. pachyrhizi* pathotypes in the different geographical zones (Twizeyimana *et al.*, 2009). Diversity in *P. pachyrhizi* can be easily and accurately determined using molecular markers. The only diversity study of *P. pachyrhizi* in Uganda was done by Lamo (2004) using Random Amplified Polymorphic DNA. Freire *et al.* (2008), undertook a diversity study based on sequence differences of the internal transcribed spacer regions of Brazilian and South African isolates. Anderson *et al.* (2008) on the other hand, determined soybean rust pathogen diversity using SSR markers.

Study Description

Rust isolates from five Ugandan sites (Namulonge, Nakabango, Iki-Iki, Ngetta and Mubuku) were collected using handheld Liliput® vacuum pumps and bulked in separate vials according to location. To characterise the *P. pachyrhizi* isolates, their genomic DNA was extracted and assayed using a set of 9 SSR primers. The banding pattern of each isolate was visually assessed and the bands were scored as present (1) or absent (0) to create a binary matrix. The 24 elite lines were planted in a randomised complete block design (RCBD) with three replications in all the five sites; using a spacing of 60cm between rows and 5cm within rows. Each plot had three rows per genotype.

Research Application

No comprehensive study had been done in Uganda to assess *P. pachyrhizi* diversity using molecular markers. Preliminary results in this study have shown that SSR markers can be used to effectively determine genetic diversity of *P. pachyrhizi* thus providing valuable information for future work on genetic diversity and population structure of the soybean rust fungus in Uganda (Fig. 1). A dendrogram constructed from the similarity data of the isolates from the five locations grouped the isolates into two clusters. The first cluster consisted of isolates from Makerere University Agricultural Reserach Institute, Kabanyolo (central Uganda), Iki Iki (eastern Uganda) and Mubuku (western Uganda) and the other cluster consisted of isolates

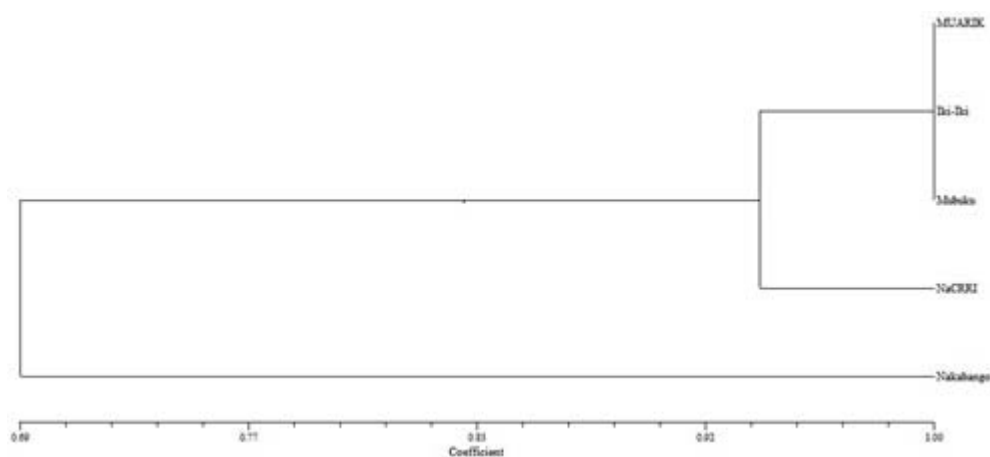


Figure 1. Dendrogram of isolates from five locations in Uganda.

Table 1. Soybean Rust disease scores of selected soybean genotypes tested at five locations for four seasons in Uganda.

Genotypes	Locations					Mean
	Iki-Iki	Mubuku	NaCRRRI	Nakabango	Ngetta	
DXT 3.11	3.6	4.6	2.9	3.2	3.3	3.4
DXT 5.16	3.7	4.3	3.0	3.2	3.3	3.4
DXT 10.9	3.7	4.7	3.3	3.7	3.3	3.7
DUIKER	3.8	4.9	3.6	4.2	3.3	4.0
NAM 1	4.1	4.3	3.3	3.9	3.2	3.7
Maksoy 3N	3.3	3.4	2.3	2.8	3.2	2.9
CV %	8	11.3	16.8	12.9	2.2	
L.s.d	0.094	0.168	0.1716	0.1459	0.0236	

*Rust scores range from 1-5, where 1 is the most susceptible and 5 most resistant.

from NaCRRRI (central Uganda) and Nakabango (eastern Uganda).

Table 1 shows the performance of a selection of genotypes across locations for rust resistance. Genotype Maksoy 3N (the resistant local check) had a mean rust score of 2.9. This genotype could still be the basis for introducing resistance to rust in other high yielding genotypes. DXT 3.11 and DXT 5.16, the next best genotypes had a mean score of 3.4, showing that genotypes with potential of being used as sources of rust resistance are still lacking, calling for more screening work.

Acknowledgement

We are grateful for the financial support from the Regional Universities Forum for Capacity Building in Agriculture (RUFORUM) and Makerere University for providing the germplasm and research facilities.

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