Research Application Summary

Genetics of resistance to groundnut rosette virus disease among groundnut landraces in Uganda

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Abstract

Groundnut rosette virus disease (GRVD) is caused by a trio of viral components and is a major disease that can cause 100% crop losses in an epidemic situation. Thus, continued effort to develop resistant groundnut cultivars is critical in sub-Saharan Africa (SSA), the only region in which the disease exists. In this study, the mode of inheritance of GRVD resistance will be determined for three resistant introduced lines (Serenut 2, 3 and 8). These lines, together with one aphid resistant line, were crossed with four susceptible land races in a line-by-tester mating scheme. F_2 segregants arising from 16 F_1 crosses, along with parental lines, were planted in the field in an alpha lattice design with 3 replications. Inoculation is being done using the infector row technique, which is known to maintain a high disease inoculum pressure in the field. Genotypic differences will be evaluated using GCA and SCA effects estimated from the data for disease incidence. The narrow and broad sense coefficients of genetic determination, type of gene action, heritability and the number of genes conditioning resistance to GRVD will also be determined.

Key words: Chlorotic and green rosette, groundnut, heritability, infector row technique, inheritance

Résumé

La maladie du virus des rosettes d'arachides (GRVD) est causée par un trio de composants viraux et constitue une maladie grave qui peut causer des pertes de récolte de 100% dans une situation d'épidémie. Ainsi, un effort soutenu pour développer des cultivars résistants des arachides est essentiel en Afrique sub-saharienne (ASS), la seule région où cette maladie existe. Dans cette étude, le mode de transmission de la résistance à GRVD sera déterminé pour trois lignées résistantes introduites (Serenut 2, 3 et 8). Ces lignées, ensemble avec une lignée

résistante contre les pucerons, ont été croisées avec quatre races agraires sensibles dans un système d'accouplement lignée-testeur. Les séparateurs F_2 provenant de 16 croix F_1, ainsi que des lignées parentales, ont été plantés dans le champ dans une conception en treillis alpha avec 3 répétitions. L'inoculation se fait en utilisant la technique des rangées infectieuses, qui est connu pour maintenir une pression élevée de l'inoculum de la maladie dans le champ. Les différences génotypiques seront évaluées en fonction des effets de GCA et SCA estimés à partir des données sur l'incidence de la maladie. Les coefficients au sens étroit et large de détermination génétique, le type d'action des gènes, l'héritabilité et le nombre de gènes conditionnant la résistance à GRVD seront également déterminés.

Mots clés: Rosette chlorotique et verte, arachide, héritabilité, technique des rangées infectieuses, héritage

Background

Groundnut (*Arachis hypogaea* L.) is an important crop in both subsistence and commercial agricultural systems in many African communities and world-over. Groundnut rosette is an economically important disease that occurs across sub-Saharan Africa (SSA) in a recurring and persistent manner. It results from the synergistic interaction of three viral components; groundnut rosette virus (GRV), its satellite RNA (Sat-RNA), and groundnut rosette assistor virus (GRAV). The disease is spread by an aphid vector, *Aphis craccivora* Koch (Waliyar *et al*., 2007). Two contrasting symptoms of the disease have been noted: chlorotic rosette and green rosette, which are attributed to variants of the Sat-RNA (Taliansky *et al*., 2000). A milder type with mosaic symptoms has also been reported. The cost of annual yield losses due to GRVD have been estimated as high as US $156 million across SSA (Naidu *et al*., 1999). Okello *et al.* (2010) asserts that the disease is severe in various hotspot areas of Uganda among locally adapted land races that lack genetic resistance. Genetic studies on GRVD suggest that resistance to this viral disease is complex, polygenic and governed partly by a pair of independent complementary recessive genes (Nigam and Bock, 1990). Misari *et al.* (1988) reported that described resistance to GRVD is not simply inherited.

Literature Summary

Efforts in breeding resistance to GRVD since 1954 have resulted in the release of an aphid-resistant line (ICG 12991) and several pathogen resistant lines such as ICGV-SM93530 (Naidu *et al*., 1999). These resistant lines could be very good sources for improvement of local commercial and farmer-preferred

varieties, which are highly susceptible (Misari *et al*., 1988). Potential gains due to adequate control of GRVD has been calculated at US$121 million annually, considering mainly improved genetic resistance to the disease (Waliyar *et al*., 2007). Resistance is reportedly due to the production by the resistant host plants of an antivirus substance (Wynne and Beute, 1991). Recent reports have shown that this resistance is directed towards GRV and Sat-RNA, but not GRAV (Waliyar *et al*., 2007). Hence, the current study sought to provide insight into the mode of inheritance of GRVD resistance to the three components of the disease among selected accessions.

Study Description

Three resistant lines and one aphid-resistant line were crossed with four susceptible land race genotypes in a line-by-tester mating design in 2011 at National Semi Arid Resources Research Institute (NaSARRI) Serere, and at Makerere University Agricultural Research Institute at Kabanyolo (MUARIK). These lines were selected based on the varying levels of resistance and susceptibility to GRVD. Sixteen F_1 progeny and their eight parents were evaluated in an alpha lattice design with 3 replications in the 2012A season (March - June) at NaSARRI. High disease pressure was maintained across the entire field using the infector row technique adapted from ICRISAT (Bock and Nigam, 1988).

Disease incidence was recorded at 20, 40, 60 and 80 days after planting, while severity data were recorded for four consecutive weeks from 8 days after inoculation, as described by Olurunju *et al.* (2001). Plants were scored for incidence (PDI) and for severity using a 1-5 disease rating scale recommended by ICRISAT (Waliyar *et al*., 2007).

Existence of disease causal agents in the field was verified by reverse transcription (RT) PCR techniques at the College of Agricultural and Environmental Sciences Biotechnology laboratory, Makerere University.

Data analysis based on disease incidence, severity, and AUDPC will be carried out using GENSTAT in order to and to understand the inheritance and to indentify the best families for use in future GRVD breeding programmes. Hybridization experiments resulted in an average success rate of 65% in both sites, with decapitation of the pistil serving as an indicator for successful pollination, as illustrated by Lim and Gumpil (1984). The 2012A field experiment is ongoing.

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