

Research Application Summary

Inheritance of resistance to *Fusarium* root rot (*Fusarium redolens*) in selected genotypes of cowpea in Uganda

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Abstract

Cowpea production in Uganda is constrained by *Fusarium* root rot disease caused by *Fusarium redolens*. The use of resistant cultivars is the most economical long-term strategy to manage the disease and knowledge of the inheritance of resistance to the disease is important for cultivar development. Ten parents were crossed using a North Carolina mating Design II. Four of the parents were used as males and the other six of them as female parents. Of the female parents, four had intermediate resistance while two were susceptible. The resistant male parents were Asontem, Danila, IT89KD-288 and NE 70. The four female parents with intermediate resistance were SECOW 2W, SECOW 3B, NE 50 and NE 6 while the susceptible female parents were KVU 27-1 and WC 66. The F₂ progeny alongside the parents were planted in wooden boxes containing soil inoculated with *F. redolens* in the greenhouse. Severity of *Fusarium* root rot was scored using the CIAT 1 to 9 scale at 28 days after planting. Data were subjected to Analysis of Variance. General combining ability (GCA) was significant ($P < 0.05$) suggesting that resistance was due to additive genetic effects. This suggests that selection for resistance to *Fusarium* root rot in later generations should be effective. The specific combining (SCA) was not significant ($P > 0.05$) indicating that non additive genetic effects were not important. The chi square test suggested the action of single gene with dominance for some parents used in the crosses and at least two gene pairs with epistasis for other parents.

Key words: Cowpea genotypes, disease resistance, *Fusarium redolens*, General combining ability, segregation patterns, specific combining ability, Uganda

Résumé

La production de niébé en Ouganda est limitée par la maladie de la pourriture des racines due à *Fusarium redolens*. L'utilisation de cultivars résistants est la stratégie à long terme la plus économique pour gérer la maladie et la connaissance du mode de transmission de la résistance à la maladie est importante pour le développement des cultivars. Dix parents ont été croisés en utilisant un modèle de croisement de la Caroline du Nord II. Quatre des parents étaient considérés comme mâles et les six autres comme des femelles. Parmi

les femelles, quatre avaient une résistance intermédiaire tandis que deux étaient sensibles. Les parents mâles résistants étaient Asontem, Danila, IT89KD-288 et NE 70. Les quatre femelles à résistance intermédiaire étaient SECOW 2W, SECOW 3B, NE 50 et NE 6 tandis que les femelles sensibles étaient KVU 27-1 et WC 66. La descendance F2 ensemble avec leurs parents ont été plantés dans des caisses en bois contenant de la terre inoculée avec *F. redolens* sous la serre. La sévérité de la pourriture des racines due à la fusariose a été notée à partir du 28 jours après la plantation à l'aide de l'échelle de CIAT qui varie de 1 à 9. Les données ont été soumises à une analyse de variance. L'aptitude générale à la combinaison (GCA) était significative ($P < 0,05$) suggérant que la résistance était due à des effets additifs des gènes. Cela suggère que la sélection pour la résistance à la pourriture des racines due au *Fusarium* dans les générations ultérieures devrait être efficace. La combinaison spécifique (SCA) n'était pas significative ($P > 0,05$) indiquant que les effets génétiques non additifs n'étaient pas importants. Le test du chi carré a suggéré l'action d'un seul gène avec dominance pour certains parents utilisés dans les croisements et d'au moins deux paires de gènes avec épistasie pour d'autres parents.

Mots clés: Génotypes du niébé, résistance à la maladie, *Fusarium redolens*, aptitude générale à la combinaison, modèles de ségrégation, aptitude spécifique à la combinaison, Ouganda

Introduction

Cowpea (*Vigna unguiculata* (L.) Walp) belongs to the family Leguminosae, tribe Phaseoleae, and belongs to the genus *Vigna*, in the section *Catiang*. The presence of a wide genetic diversity suggests the centre of origin of cowpeas to be the Southern Africa (Boukar *et al.*, 2013). Cowpea is a true diploid with $2n = 2x = 22$ and a genome size of about 620 million base pairs (Timko *et al.*, 2007).

Cowpea is an important food legume crop with both the leaves and the seed used in the preparation of various nutritious food types. It is high in protein (23-30%) (Boukar *et al.*, 2011) and is an important supplement to the protein deficient staple diets in Uganda that are based principally on millet, sorghum, maize and sweet potatoes among others. It fixes nitrogen and this makes it an important rotation crop for the management of soil fertility. The crop is drought tolerant and produces yields in areas where other annual legume crops fail to produce seed (Bisikwa, 2013). Some cultivars of cowpeas are known to suppress weeds through causing suicidal germination of seeds of parasitic weed *Striga hermonthica* (Traore, 2011). Yields of cowpea however are low due to a variety of causes like pests and diseases (Edema *et al.*, 1997) among them *Fusarium* root rot. This disease can reduce yields by up to 84% in common bean (Mukankusi *et al.*, 2011). When conditions are favorable there is considerable levels of infection and reduced or complete loss of yield for susceptible genotypes (Namasaka *et al.*, 2017). It is difficult to control *Fusarium* root rot because of the ubiquitous soil borne nature of the disease.

Development and use of resistant varieties is the most feasible and cost effective method to control *F. redolens* in cowpea as the greatest percentage of cowpea farmers are resource poor farmers (Adipala, 1999). Breeding for resistance to the pathogen requires knowledge of the inheritance of resistance and the type of gene action. This informs the selection of breeding methods for efficient introgression of resistance into the adapted cultivars.

Information on inheritance of resistance to other root rot pathogens like *Fusarium solani* has been reported to be complex and strongly influenced by the environment (Mukankusi *et al.*, 2011). It has also been reported that resistance is due to two to three genes that display partial dominance and epistasis (Ongom and Nkalubo, 2012). Furthermore information on inheritance of resistance to *F. redolens* is equally important in breeding for resistant varieties but this information is still lacking which limits the breeders' understanding of the pattern of inheritance of resistance to *F. redolens*. Wanjala *et al.* (2017) reported additive gene action for resistance to *F. redolens* but the number of genes involved in this inheritance was not determined. The objective of this study was to determine the number of genes and the mode of gene action that controls resistance to *F. redolens* at later generations.

Materials and methods

This study was conducted in a screen house at Makerere University Agricultural Research Institute (MUARIK) in Kabanyolo located at 0°28'N 32°37'E 1200m above sea level with an average temperature of 21.5°C, and an annual rainfall of 1150mm with mainly sandy clay loam soils. Twenty four F2 populations were generated from crosses involving ten parents using North Carolina Design II. Among the ten parents used were four resistant males (Asontem, Danila, IT89KD-288 and NE 70) and six females, four of which were intermediate in resistance and two susceptible (SECOW 2W, SECOW 3B, NE 50, NE 6 and KVVU 27-1, WC66 respectively). The F2 populations were evaluated for resistance to Fusarium root rot. The pedigrees of the parents and the F2 progeny evaluated are presented in Table 1).

Table 1. Pedigrees of the parents and F2 populations evaluated for resistance to Fusarium root rot in the Screen house at Kabanyolo, Kampala, Uganda during the November 2017-July 2018 season

F3 populations	F3 populations	Parents
KVVU 27-1 X Asontem	KVVU 27-1 X IT89KD-288	KVVU 27-1
NE 50 X Asontem	NE 50 X IT89KD-288	NE 50
NE 6 X Asontem	NE 6 X IT89KD-288	NE 6
SECOW 2w X Asontem	SECOW 2w X IT89KD-288	SECOW 2w
SECOW 3B X Asontem	SECOW 3B X IT89KD-288	SECOW 3B
WC 66X Asontem	WC 66 X IT89KD-288	WC 66
KVVU 27-1 X Danila	KVVU 27-1 x NE 70	Asontem
NE 50 X Danila	NE 50 x NE 70	Danila
NE 6 X Danila	NE 6 x NE70	IT89KD-288
SECOW 2w X Danila	SECOW 2w x NE 70	NE 70
SECOW 3B X Danila	SECOW 3B x NE 70	
WC 66 X Danila	WC 66 x NE 70	

The parents and the crosses were planted in boxes containing soil inoculated with an isolate of *Fusarium redolens* (Paidha 19) from infected seeds collected from a community market in Paidha, Zombo district. This was in a screen house in a chamber modified with a transparent polyethene to increase humidity. The multiplication of inoculum in the soil

was done according to Mukankusi *et al.* (2011). The trial design was a modified 8 x 12 alpha lattice with three replications. The wooden boxes measured 150 cm× 100 cm× 13 cm) The seeds of genotypes were surface sterilized by soaking them in 70% ethanol then allowed to dry before planting. Seed was planted in soil in boxes that were inoculated with *Fusarium redolens*. Each plot consisted of a single row of 15 plants representing an F2 cross or parent. At twenty eight days after inoculation the plants were uprooted washed and scored for root rot severity using the CIAT 1 – 9 scale where 1 = no visible symptoms and 9 = approximately 75% or more of the hypocotyls and root tissues affected with advanced stages of rotting, combined with severe reduction in the root system. The data collected was subjected to Restricted Maximum Likelihood (ReML) analysis using GENSTAT 18th edition to estimate General and Specific combining ability and chi-square tests were used to elucidate the genetic models for resistance to *F. redolens*.

Results and Discussion

Genotypes

There were significant differences ($P < 0.05$) among genotypes for resistance to *Fusarium redolens*. This was expected given that there were resistant and susceptible parents and the crosses were expected to exhibit different levels of resistance due to segregation.

GCA

There were significant differences in GCA for the male parents ($P < 0.05$). This indicates the presence of additive gene action in the mode of inheritance for resistance to *F. redolens*. There were no significant differences ($P < 0.05$) for GCA and SCA for the female parents. The GCA effects for male parents Asontem and Danila had negative values but only Danila was significant at $P < 0.05$ (Table 2). This suggested that this parent has a good breeding value for use as a parent to transmit resistance to *F. redolens*. The other two male parents had positive effects that were not significant ($P > 0.05$). This suggests that these parents were of limited value for transmitting resistance to *F. redolens*. The GCA effects of the female parents were not significantly different from zero ($P > 0.05$) (Table 2). However, the parent NE 6 had a negative GCA effect of -0.38 suggesting that it had some value as a parent in the development of progenies with resistance.

Table 2. General combining ability (GCA) effects for the male and female parents for transmission of resistance to *F. redolens*

Males		Females	
ASONTEM	-0.14 ^{ns}	KVU 27-1	0.02 ^{ns}
DANILA	-0.46 [*]	NE 50	0.07 ^{ns}
IT89KD-288	0.33 ^{ns}	NE 6	-0.38 ^{ns}
NE 70	0.28 ^{ns}	SECOW 2W	0.19 ^{ns}
		SECOW 3B	-0.06 ^{ns}
		WC 66	0.17 ^{ns}

*denotes significant at $p < 0.05$ and ns denotes non-significant

Table 3. Chi square goodness of fit for observed ratios of resistant and susceptible progeny in F2 populations based on the hypothesis of a single gene locus

CROSS	Number of Plants	Observed		χ^2 under single gene model ratio (DF=1) 3 : 1
		Resistant	Susceptible	
KVU 27-1 X	22	6	16	0.06 ^{ns}
ASONTEM				
NE 50 X ASONTEM	104	15	89	6.21*
NE 6 X DANILA	95	35	60	7.11**
SECOW 2W X NE 70	37	7	30	0.73 ^{ns}
SECOW 2W X NE 70	28	9	19	0.76 ^{ns}
SECOW 3B X NE 70	65	12	53	1.48 ^{ns}
WC 66 X NE 70	91	13	78	5.57*

*, **, *** significant deviation from model ratios at $\alpha = 0.05, 0.01, 0.001$, respectively and ns no significant deviation from model ratios

Chi square goodness of fit

The results for the goodness of fit of the observed data based on the hypothesis of a single gene locus with simple dominance are presented in Table 3. For three of the crosses, NE 50 X ASONTEM, NE 6 X DANILA, WC 66 X NE 70 the observed ratios of resistant to susceptible F2 progeny significantly deviated from the 3:1 ratio ($P < 0.05$) (Table 3). This suggests that there is more than one gene locus involved in the inheritance of resistance. This result corroborates the finding that there was more than one gene locus and that there is additive gene action. The other three crosses did not deviate from the 3:1 ratio suggesting that one gene locus was involved in controlling resistance.

Conclusion

It can be concluded that for some genotypes there is a single gene with simple dominance that controls resistance. In some parents however there is evidence that there is more than one gene pair involved in the inheritance of resistance and that there is additive gene action. One parent Danila was observed to have a good GCA for resistance and that it is a desirable parent for use in developing progeny with resistance to fusarium root rot.

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