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Research Application Summary

Agronomic performance of cowpea populations with resistance to *Fusarium redolens* in three agro-ecological zones in Uganda

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Abstract

Breeding populations of cowpea with resistance to Fusarium root rot caused by *Fusarium redolens* were developed at Makerere Regional Center for Crop Improvement (MaRCCI). These were evaluated for agronomic performance at three sites in Uganda. A total of 23 populations were created using the North Carolina mating Design II. The parents consisted of four males (Asontem, Danila, IT89KD-288 and NE 70) that are resistant to Fusarium root rot. The females consisted of two released varieties SECOW 2W and SECOW 3B and four landrace cultivars, two with intermediate resistance NE 6, NE 50 and two that are susceptible namely KVU 27-1 and WC 66. These were evaluated at Kabanyolo, Arua and Serere research stations in Uganda during the 2017B season. Plots were 3m wide and 2.5m long with an inter row spacing of 75cm and 20cm between plants giving four rows with eight plants each and the design was 5 x 8 alpha lattice replicated three times. The variables measured were days to 50% flowering, number of pods per plant, seed yield per plot and scab disease severity scored on a 1 to 5 scale where 1 = 0% infected plants and 5 = 50% or greater infection. There was a significant genotype x location interaction ($P<0.001$) for all variables measured. At each of the three sites there were significant differences ($P<0.01$) among genotypes for days to 50% flowering, seed yield and scab score. There were no significant differences ($P>0.05$) among genotypes for number of pods per plant. The results indicate that superior lines can be selected within these populations.

Key words: Breeding populations, cowpea, Fusarium root rot, genotype, genotype x site interaction, *Sphaceloma* sp.

Résumé

Des populations reproductrices de niébé résistantes à la pourriture des racines due à *Fusarium redolens* ont été développées au Centre Régional de Makerere pour l'Amélioration des Cultures (MaRCCI). Ceux-ci ont été évalués pour leurs performances agronomiques sur trois sites en Ouganda. Au total, 23 populations ont été créées en utilisant le dispositif de croisement de la Caroline du Nord II. Les parents étaient composés de quatre mâles

(Asontem, Danila, IT89KD-288 et NE 70) résistants à la pourriture des racines due à la fusariose. Les femelles se composaient de deux variétés livrrées SECOW 2W et SECOW 3B et de quatre cultivars, deux avec une résistance intermédiaire NE 6, NE 50 et deux qui sont sensibles à savoir KVU 27-1 et WC 66. Ceux-ci ont été évalués à Kabanyolo, Arua et Serere Research stations en Ouganda pendant la saison 2017B. Les parcelles mesuraient 3 m de large et 2,5 m de long avec un espacement l de 75 cm entre les lignes et 20 cm entre les plantes, ce qui donnait quatre lignes de huit plantes chacune et le dispositif expérimental était un alpha plan de 5 x 8 répliqué trois fois. Les variables mesurées étaient le nombre de jours à50% de floraison, le nombre de gousses par plante, le rendement en graines par parcelle et la gravité de la maladie de la gale notée sur une échelle de 1 à 5 où 1 = 0% de plantes infectées et 5 = 50% ou plus d'infection. Il y avait une interaction génotype x localité significative (P <0,001) pour toutes les variables mesurées. À chacun des trois sites, il y avait des différences significatives (P <0,01) entre les génotypes pendant des jours jusqu'à 50% de floraison, de rendement en graines et de score de gale. Il n'y avait pas de différences significatives (P> 0,05) entre les génotypes pour le nombre de gousses par plante. Les résultats indiquent que des lignées supérieures peuvent être sélectionnées au sein de ces populations.

Mots clés: populations reproductrices, niébé, pourriture fusarienne des racines, génotype, interaction génotype x site, *Sphaceloma* sp.

Introduction

Cowpea (*Vigna unguiculata* (L.) Walp) is believed to have originated in the southern parts of Africa (Singh, 2014). Cowpea is mainly grown in the Eastern and Northern parts of Uganda and is a major legume food crop in semi-arid tropics (Timko and Singh, 2008). Among the food legume crops, in Uganda cowpea is ranked fourth after beans, groundnuts and soybean (Ronner *et al.,* 2013). Cowpea contains 23-30% protein (Boukar *et al.,* 2011). This makes it an important protein supplement to the protein deficient staple diets based principally on finger millet, sorghum, sweet potato, maize, among others. It also contains 176-387µg/g iron (Okonya and Maass, 2014). Cowpea fixes nitrogen and improves soil fertility and makes a good rotation crop (Omae *et al.,* 2014). The crop is drought resistant and produces yields where other legume crops would fail (Bisikwa, 2013). Household income from selling cowpea improves the livelihoods of the small holder farmers.

Small holder farmers achieve low mean yields for cowpeas, in the range of 500kg/ha yet potentially cowpea yield is estimated at 1500 to 3000kg/ha (Bisikwa, 2013). This has been attributed to many factors including diseases, pests, farmers preference of early but low yielding landrace cultivars (Peter, 2013) and other constraints associated with agronomic management of the crop. The most important diseases are Fusarium root rot caused by *Fusarium redolens* and scab caused by *Sphaceloma* sp. The use of disease resistant cultivars is the most economical long term strategy (Adipala *et al.,* 2001). Existing short duration cultivars however are low yielding giving yields in the range of 500kg/ha. Material with resistance to Fusarium root rot was developed at the Makerere Regional Centre for Crop Improvement. However, the materials have not been tested for their yield and agronomic performance. The objective of this research was to determine the yield and agronomic characteristics of populations with known resistance to Fusarium root rot.

Materials and methods

A trial was conducted to evaluate the agronomic characteristics of 40 genotypes across three agro-ecological zones in Uganda during the 2017B (August to December) season. The genotypes included twenty-three F_3 populations derived from crosses with parents that are resistant to Fusarium root rot, ten parents and a total of seven advanced lines from MaRCCI which were also used as checks alongside the parents. The pedigrees of the forty lines are shown in Table1.

Table 1. Pedigrees of the of the genotypes evaluated for yield and agronomic characteristics at Kabanyolo, Serere and Arua Research Stations in Uganda during the 2017B season (August to December)

F3 populations	Parents	Advanced lines (checks)
KVU 27-1 X Asontem	KVU 27-1	SECOW 5T (check 1)
NE 50 X Asontem	NE 50	SECOW 4W (check 2)
NE 6 X Asontem	NE 6	ACC 2 X SECOW 2W (check 3)
SECOW 2w X Asontem	SECOW 2w	ACC 12 X SECOW 2W (check 4)
SECOW 3B X Asontem	SECOW 3B	SECOW 1T (check 5)
WC 66X Asontem	WC 66	Alegi X ACC 12 (check 6)
KVU 27-1 X Danila	Asontem	SECOW 5T X SECOW 4W (check 7)
NE 50 X Danila	Danila	
NE 6 X Danila	IT89KD-288	
SECOW 2w X Danila	NE 70	
SECOW 3B X Danila		
WC 66 X Danila		
KVU 27-1 X IT89KD-288		
NE 50 X IT89KD-288		
NE 6 X IT89KD-288		
SECOW 2w X IT89KD-288		
SECOW 3B X IT89KD-288		
WC 66 X IT89KD-288		
KVU 27-1 x NE 70		
NE 50 x NE 70		
NE 6 x NE70		
SECOW 2w x NE 70		
WC 66 x NE 70		

This trial was carried out at three sites, one was at Makerere University Agricultural Research Institute at Kabanyolo, (MUARIK). Kabanyolo is located at 0°28'N 32°37'E 1200m above sea level with an average temperature of 21.5 ^{0}C, and an annual rainfall of 1150mm. The soil is characterized by sandy clay loam soils. The second site based at Abi-ZARDI Research Station in Arua is located 34°58'N 30°56'E, 1206m above sea level with average temperature of 24^{0}C, annual rainfall of 1250mm and Sandy clay loams. The National Agricultural Semi-Arid Resource Research Institute (NaSARRI) in Serere serve as the third site and is located 1°35'N 33o35'E at an altitude of 1140m above sea level, has a black soil type with average temperature of 26.05^0 C and annual rainfall of 1419mm. The trial was laid out as a 5 x 8 alpha lattice with three replications. Plots were 3m wide and 2.5m long with an inter row spacing of 75cm between rows and 20cm between plants with four rows having 8 plants each. The variables measured were days from planting to 50% flowering, scab disease score at onset of pods, number of pods per plant at harvest and seed yield per plot in kg/plot. The days to 50% flowering were recorded on the date when 50% of the plants in each plot had at least one open flower. Scab disease severity was scored on a random sample of five plants per net plot using a 1 to 5 rating scale where 1 = 0% infected plants and 5 = 50% or greater infection (foliage severely damaged or pods transformed into mummies containing virtually no seeds) (Nakawuka *et al.,* 1997). The scoring was done at 82 days after planting. The number of pods per plant was derived from a pod count on all the plants in the net plot and the plant count per plot at harvest. Data collected were analysed using Restricted Maximum Likelihood (ReML) analysis using software GENSTAT 18th edition and mean separation of genotypes using Fisher's protected Least Significant Difference (LSD) at $p<0.05$.

Results and Discussion

Mean squares from the analysis of variance are presented in Table 2. There was a significant genotype x location interaction ($P<0.001$) for all variables except for days to 50% flowering where ($P<0.05$). This means that the ranking of genotypes at different sites was different. This implies that several sites are required for testing advanced lines before release. There were significant differences among genotypes across sites ($P<0.05$) for yield and at ($P<0.001$) for scab disease score indicating the presence of genetic variability for resistance to this disease. Selection for resistance to scab among the populations should be possible. There were no significant differences among genotypes across sites for days to 50% flower and for number of pods per plant suggesting that these two variables were stable across environments. There were highly significant differences in the mean days to 50% flower from one site to another ($P<0.001$). This suggests that the genotypes tend to reach flowering earlier at some sites and later at other sites. However there were no significant differences in the mean seed yield of the genotypes averaged within site from one location to the next. There were significant differences ($P<0.05$) in the mean disease score among sites. This suggests that the disease severity is different from site to site such that some sites had a lower disease severity than others.

Table 2. Mean squares for days to 50% flowering (FLOW50), number of pods per plant (POD.NO), Sphaceloma scab disease severity at 82 Days after planting (SCAB), seed yield in kg/ha for genotypes evaluated at Kabanyolo, Serere and Arua research stations in Uganda during the 2017B season (August to December, 2017)

Source of variation	DF	Significance of mean squares			
		FLOW50	POD.NO	SCAB	Yield
Location	2	12820***	394^{ns}	17424*	887276^{ns}
Genotype	39	5^{ns}	15^{ns}	294***	51519.26*
Genotype x Location	78	3*	21***	259***	29111.9***
Pooled error	133.4-202.6	2.10	7.04	112	14181.46
SED	0.23	0.42	2.49	18.71	
CV	2.01	14.49	16.42	19.64	

*, **, *** denotes significant at P= 0.05, 0.01, 0.001 levels respectively; ns denotes not significant

Table 3. Means days to 50% flowering (FLOW50), number of pods per plant (POD. NO), Grain yield in kg/ha, Sphaceloma scab disease severity (SCAB) score at the 82 Days after planting at Kabanyolo during the 2017B season (August to December)

Genotype	FLOW50	POD.NO	Yield (kg/ha)	SCAB
Asontem	78^{ab}	15^{klm}	430^{ijklm}	2.2^{cdefghi}
KVU 27-1 X Asontem	72^{cdefgh}	14^{lm}	758^{bcdefghij}	1.3^{ghi}
NE 50 X Asontem	75^{abcde}	20^{efghijklm}	734^{bcdefghijk}	2.3^{bcdefgh}
NE 6 X Asontem	74^{abcdef}	21^{defghijklm}	1076^{abc}	2.3^{bcdefgh}
SECOW 3B X Asontem	70^{efgh}	19^{hijklm}	1055^{abcd}	1.7^{efghi}
WC 66 X Asontem	71^{defgh}	21^{defghijklm}	1163^{ab}	2.7^{abcdef}
SECOW 2w X Asontem	73^{bcdefg}	18^{ijklm}	956^{abcde}	2.3^{bcdefgh}
check 1	73^{bcdefg}	24^{bcdefghijk}	895^{abcdefg}	2.3^{bcdefgh}
check 2	72^{cdefgh}	25^{abcdefghi}	727^{bcdefghijk}	1^{i}
check 3	68^{fgh}	30^{abc}	622^{defghijklm}	1.2^{hi}
check 4	73^{bcdefg}	21^{defghijklm}	283^{lm}	1.7^{efghi}
check 5	70^{efgh}	30^{abc}	934^{abcdef}	2.5^{bcdefg}
check 6	73^{bcdefgh}	22^{bcdefghijklm}	727^{bcdefghijk}	1.5^{fghi}
check 7	71^{defgh}	15^{klm}	736^{bcdefghijk}	1.8^{defghi}
Danila	72^{cdefgh}	30^{abc}	772^{bcdefghij}	2^{cdefghi}
SECOW 2w X Danila	76^{abcd}	24^{bcdefghijk}	488^{ghijklm}	2^{cdefghi}
KVU 27-1 X Danila	73^{bcdefgh}	21^{defghijklm}	513^{fghijklm}	2.7^{abcdef}
NE 50 X Danila	79^{a}	15^{klm}	483^{ghijklm}	2.7^{abcdef}
NE 6 X Danila	71^{defgh}	19^{hijklm}	842^{abcdefghi}	3^{abcd}
SECOW 3B X Danila	74^{abcdef}	20^{efghijklm}	719^{cdefghijkl}	2.3^{bcdefgh}
WC 66 X Danila	74^{abcdef}	22^{bcdefghijklm}	660^{cdefghijklm}	3.5^{ab}
SECOW 2W X IT89KD-288	74^{abcdef}	29^{abcde}	763^{bcdefghij}	2.7^{abcdef}
WC 66 X IT89KD-288	78^{ab}	20^{efghijklm}	448^{hijklm}	3^{abcd}
KVU 27-1 X IT89KD-288	75^{abcde}	23^{bcdefghijkl}	424^{ijklm}	2cd^{efghi}
NE 50 X IT89KD-288	77^{abc}	17^{ijklm}	640^{cdefghijklm}	3.2^{abc}

NE 6 X IT89KD-288	76^{abcd}	16^{jklm}	570^{efghijklm}	3.8^{a}
SECOW 3B X IT89KD-288	74^{abcdef}	23^{bcdefghijkl}	882^{abcdefgh}	2.3^{bcdefgh}
IT89KD-288	72^{cdefgh}	17^{ijklm}	393^{jklm}	2.3^{bcdefgh}
KVU 27-1	68^{fgh}	25^{abcdefghij}	1236^{a}	1.5^{fghi}
NE 50	72^{cdefgh}	29^{abcdef}	520^{efghijklm}	1.7^{efghi}
NE 6	77^{abc}	20^{efghijklm}	560^{efghijklm}	1.8^{defghi}
NE 70	72^{cdefgh}	33^{a}	725^{bcdefghijk}	1.3^{ghi}
SECOW 2W X NE 70	77^{abc}	14l^{m}	284l^{m}	1.2^{hi}
WC 66 X NE 70	70^{efgh}	27^{abcdefgh}	483^{ghijklm}	2.2^{cdefghi}
KVU 27-1 X NE 70	79^{a}	14l^{m}	301^{klm}	1^{i}
NE 50 X NE 70	71^{defgh}	15^{klm}	524^{efghijklm}	1.7efghi
NE 6 X NE 70	68^{fgh}	21^{fghijklm}	794^{bcdefghij}	2.5^{bcdefg}
SECOW 2W	72^{cdefgh}	17^{jklm}	271^{m}	1.3^{ghi}
SECOW 3B	74^{abcde}	29^{abcdefg}	396^{jklm}	1.7^{efghi}
WC 66	77^{abc}	30^{ab}	558^{efghijklm}	2.8^{abcde}
F-test	**	***	***	**
Mean	73.3	21.7	658.7	2.1
S.E.	2.8	4.5	220.6	0.7
CV	4.7	25.2	41.0	38.3
LSD 0.05	5.6	8.9	440.4	1.3

Means followed by the same letter along the column for different genotypes are not significantly different at p<0.05. *, **, *** denotes significance at p=0.05, 0.01, 0.001 respectively, ns = not significant.

Grain yield. There were significant differences (P<0.001) among genotypes for grain yield at Kabanyolo. The grain Yield ranged from a low of 271 kg/ha for the genotype SECOW 2W to a high of 1236 kg/ha for genotype KVU 27-1 which is one of the parents used in the crosses. This however was not significantly different from the genotypes, SECOW 3B X IT89KD-288, NE 6 X Danila, SECOW 1T, NE 6 x Asontem, SECOW 3B x Asontem, WC 66 x Asontem, SECOW 2w x Asontem. A total of six F3 populations were not significantly different from the highest yielding check cultivar. The potential segregation among these to produce transgressive segregants exists making it possible for selection of superior types.

Days to 50% flowering. Genotypes were also significantly different in terms of days to 50% flowering (P<0.01) at Kabanyolo where ACC 2 x SECOW 2W and KVU 27-1 as earliest maturing checks were not significantly different from NE 6 x NE 70 which all reached 50% flowering at 68 days. Eight of the populations were not significantly different from the checks (NE 50 x NE 70, NE 6 x NE 70, WC 66 x NE 70, NE 6 x Danila, KVU 27-1 x Danila, WC 66 x Asontem, SECOW 3B x Asontem, KVU 27-1 x Asontem) and this indicates that early maturing genotypes exist within these populations adding the extra value of *F. redolens* resistant early maturing genotypes.

Number of pods per plant. For number of pods per plant at Kabanyolo, genotypes exhibited significant differences (P<0.001) and genotypes WC 66 x NE 70, SECOW 2W x IT89KD-288 were not significantly different from NE 70 which had the highest number of pods per plant.

Scab disease severity. Genotypes responded significantly differently in terms of Scab disease severity ($P<0.01$). The lowest severity scores were observed for NE 70 and SECOW 4w the check cultivars but the response of KVU 27-1 x NE 70, SECOW 2W x NE 70, KVU 27-1 x Asontem, SECOW 3B x Asontem, SECOW 2W x DANILA, WC 66 x NE 70, NE 50 x NE 70 and KVU 27-1 x IT89KD-288 were not significantly different from the check cultivars ($P<0.05$) suggesting genetic variability for Scab resistance among the F3 populations studied. Hence, the test materials should be subjected to multi-location evaluation to advance and select suitable parents for breeding for Scab resistant genotypes.

Conclusion

There were genotypes that were superior to the best check varieties. Some of these had a combination of Scab disease resistance (KVU 27-1 x NE 70, SECOW 2W x NE 70, KVU 27-1 x Asontem, SECOW 3B x Asontem, SECOW 2W x DANILA, WC 66 x NE 70, NE 50 x NE 70 and KVU 27-1 x IT89KD-288) and others good agronomic traits like earliness (NE 50 x NE 70, NE 6 x NE 70, WC 66 x NE 70, NE 6 x Danila, KVU 27-1 x Danila, WC 66 x Asontem, SECOW 3B x Asontem, KVU 27-1 x Asontem), high yielding ability (SECOW 3B X IT89KD-288, NE 6 X Danila, SECOW 1T, NE 6 x Asontem, SECOW 3B x Asontem, WC 66 x Asontem, SECOW 2w x Asontem) compared to the check cultivars. These lines can be used as parental lines to improve the other breeding populations or the local germplasm.

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References

Adipala, E., Nampala, P., Karungi, J. and Isubikalu, P. 2001. A review on options for management of cowpea pests: Experiences from Uganda. *Integrated Pest Management Reviews* 5 (3): 185-196.

Bisikwa, J. 2013. McKnight Foundation Collaborative Crops Research Project No: 09-480. Improving food security through participatory development of high yielding and pest resistant cowpea varieties in uganda annual progress report — narrative.

Boukar, O., Massawe, F., Muranaka, S., Franco, J., Maziya-Dixon, B., Singh, B. and Fatokun, C. 2011. Evaluation of cowpea germplasm lines for protein and mineral concentrations in grains. Plant Genet. Resour. *FirstView* 1–8. doi:10.1017/S1479262111000815

Nakawuka, C.K. and Adipala, E. 1997. Identification of sources and inheritance of resistance to Sphaceloma scab in cowpea. *Plant Disease* 81 (12): 1395-1399.

Okonya, J.S. and Maass, B.L. 2014. Protein and iron composition of cowpea leaves: an evaluation of six cowpea varieties grown in eastern Africa. *African Journal of Food, Agriculture, Nutrition and Development* 14 (5): 2129-2140.

Omae, H., Saidou, A.K. and Tobita, S. 2014. Improving millet-cowpea productivity and

soil fertility with crop rotation, row arrangement and cowpea density in the Sahel, West Africa. *J. Agric. and Environ. Sci.* 14: 110-115.

Peter, D.S., 2013. Farmer preferences and market integration of cowpea in Uganda. Doctoral dissertation, Makerere University, Uganda.

Ronner, E. and Giller, K.E. 2013. Background information on agronomy, farming systems and ongoing projects on grain legumes in Tanzania. N2Africa Milestones. *Accessed* 17: 9-13.

Singh, B.B. 2014. Cowpea: The food legume of the 21st century. Madison, WI: Crop Science Society of America.11pp.

Timko, M.P. and Singh, B.B. 2008. Cowpea, a multifunctional legume. pp. 227-258. In: Genomics of tropical crop plants. Springer, New York, NY.