Indian J. Genet., 70(3): 271-276 (2010)

Inheritance of fusarium wilt resistance in pigeonpea [C*ajanus cajan* (L.) Millspaugh]

R. Karimi, James O. Owuoche[1]* and S. N. Silim[2]

Kenya Agricultural Research Institute (KARI), P.O. Box 340, Machakos, Kenya
[1]Department of Crops, Horticulture and Soil Science, Egerton University, P.O. Box 536, Egerton, Kenya
[2]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), P.O. Box 39063, Nairobi, Kenya

(Received: April 2010; Revised: August 2010; Accepted:August 2010)

Abstract

Fusarium wilt caused by *Fusarium udum* Butler is the most important disease of pigeonpea worldwide. Objectives of this study were to determine the mode of genetic inheritance of Fusarium wilt resistance in different pigeonpea accessions and to determine different genes governing resistance that exists in pigeonpea accessions. F_1, F_2 and backcross populations were developed by crossing resistant accessions (ICEAP 00554, ICEAP 00557) with susceptible accessions (KAT 60/8, ICP 7035). The Parents, F_1, F_2, backcrosses (BC_1F_1 and BC_2F_1) populations were evaluated for Fusarium wilt resistance. F_2 populations derived from ICEAP 00554 × KAT 60/8, ICEAP 00557 × KAT 60/8, ICEAP 00554 × ICP 7035, ICEAP 00557 × ICP 7035 crosses exhibited a 3:1 ratio which indicated that resistance to Fusarium wilt was under the control of major gene, however, a recessive gene was detected from ICP 7035 × KAT 60/8 cross. The genes detected could be valuable for wilt resistance breeding.

Key words: Pigeon pea, *Fusarium udum*, isolate

Introduction

Fusarium wilt (*Fusarium udum* Butler) is an important soil borne disease of pigeonpea [*Cajanus cajan* (L.) Millsp], which causes significant yield losses in susceptible cultivars throughout the pigeonpea growing areas [1, 2]. In the last two decades, ICRISAT has been conducting research in India to overcome the pigeon pea production constraints associated with Fusarium wilt [3]. Several Fusarium wilt resistant lines have been identified and developed, nonetheless, these germplasm are not adapted to Kenyan environment due to photoperiod and temperature sensitivity [4]. Among some resistant pigeon pea varieties, segregation for resistance to Fusarium wilt does occur in subsequent generations because of variation in isolates [5, 6]. Consequently, development of durable and adaptable pigeonpea varieties is one of the most efficient and economical method to control Fusarium wilt.

The knowledge of genetic inheritance is essential for formulation of strategy on how to transfer the genes into adapted susceptible varieties. In pigeonpea, resistance to fusarium wilt has been reported to be under the control of two complementary genes [7], single dominant gene [8], 2 genes [9], major genes [7, 10], duplicate genes and even multiple factors [11] and a single recessive gene [12]. Apart from dominant, recessive and complementary gene action on the control of Fusarium wilt [5, 13] has been reported. Dominant epistatic gene interaction and a single dominant gene play a significant role in controlling resistance to wilt [7]. Digenic and quantitative genes that are resistant to Fusarium wilt have been observed although quantitative inheritance is often influenced by environment; the resistance depends on the source of the gene [14].

Information on allelic relationship for Fusarium wilt resistance in pigeonpea is inadequate. In a cross between two resistance lines, there is independence in the genes controlling resistance to Fusarium wilt [9]. Therefore, objectives of this study were to determine the inheritance of Fusarium wilt resistance in different pigeonpea backgrounds and to determine different resistant genes that exist in pigeonpea genotypes

Materials and methods

The study was conducted at Kenya Agricultural Research Institute (KARI)-Kiboko and KARI-Katumani

*Corresponding author's e-mail: owouche@yahoo.com
Published by Indian Society of Genetics & Plant Breeding, F2, First Floor, NASC Complex, PB#11312, IARI, New Delhi 110 012
Online management by indianjournals.com

Research Centre in Eastern Kenya (Table 1).

Seedling test

Fifty-one pigeonpea accessions/varieties of medium and long duration that originated from Kenya, Tanzania, Uganda, Mozambique and ICRISAT (India) were screened for resistance. The activity was carried out in a green house at KARI-Katumani research station. Varieties ICEAP 00040 from ICRISAT is resistant to Fusarium wilt. However, KAT 60/8 that is medium (but early) maturing is susceptible to Fusarium wilt. Three different isolates of the *Fusarium wilt* fungus from *KM* (Machakos), *EM* (Makueni) and *KB* (Makueni) pigeonpea growing areas in Kenya were used. The *KM* and *EM* isolates were collected from farmers' fields while the *KB* isolate was collected from the wilt-sick plot at Kiboko research station. In this study *KB* isolate which is the most virulent among the *F. udum* pathotypes was included to help identify accessions with resistance to more than one strain. Inoculum was prepared using diseased stems according to the modification of the protocol described by Laslie and Summerell [15]. The seedlings were inoculated using root-dip inoculation technique described by Okiror [16]. Observations were made and scoring done using a disease rating scale described by Nene *et al.* [17]

Screening of F_1, F_2 and Backcross populations

Development of F_1, F_2 and Backcrosses populations : Four medium duration genotypes were used as parents (Table 2). ICEAP 00554 and ICEAP 00557 were used as the resistant parents while KAT 60/8 and ICP 7035 as susceptible varieties (Table 3). ICEAP 00554 and ICEAP 00557 are selections from Tanzanian landraces; KAT 60/8 is a selection from local germplasm and a popular pigeonpea commercial variety in Kenya. ICP 7035 is an introduction from India. The first crossing was done in Feb.-April, 2008 using Griffin's mating design I, model I to generate F_1 populations. Resistant × resistant and susceptible × susceptible crosses were made to obtain information on the allelic relationship on the resistant and susceptible parents, respectively (Table 1). F_2, BC_1F_1 and BC_2F_1 populations were derived from F_1 seeds. F_1 and F_2 populations derived from resistant × resistant (ICEAP 00554 × ICEAP 00557) and susceptible × susceptible (KAT 60/8 and ICP 7035) crosses were developed for allelic study.

Screening of Accessions, F_1, Backcrosses and

Table 1. Description of experimental site

Site	Location		Average Temp. (^oC)	
		Altitude (meter asl)	Feb.	Oct.
KARI-Katumani	37^{o}14'E; 1^{o}35'S	1600	27.9	26.4
KARI-Kiboko	2^{o}10'S ;37^o 40'E	975	26.3	24.9

Source: KMD, 2008

Table 2. Mating scheme of the four pigeonpea (*Cajanus cajan*) cultivars used to develop F_1, F_2 populations for genetic analysis

	KAT 60/8	ICP 7035	ICEAP 00554	ICEAP 00557
KAT 60/8		×	×	×
ICP 7035	×		×	×
ICEAP 00554	×	×		×
ICEAP 00557	×	×	×	

KAT= Katumani 60/8; ICEAP= ICRISAT East African Pigeonpea

Table 3. Differential reaction of 13 pigeonpea (*Cajanus cajan*) accessions and 7 genotypes to three Fusarium wilt isolates *KM*, *EM* and *KB*.

		Isolate		
Genotype	Country of origin	KM	EM	KB
Accession 111	Tanzania	+	+	-
Accession 112	Tanzania	+	+	-
Accession 5	Tanzania	+	+	-
Accession 32	Tanzania	+	+	-
Accession 29	Tanzania	+	+	-
Accession 103	Tanzania	+	-	-
Accession 120	Tanzania	+	-	-
Accession 19	Tanzania	+	-	-
Accession 107	Tanzania	+	+	-
Accession 24	Tanzania	+	-	-
Accession 38	Tanzania	+	+	-
Accession 45	Tanzania	+	-	-
Accession 82	Tanzania	+	-	-
ICEAP 00040	Kenya	+	+	+
ICEAP 00020	Kenya	+	+	+
ICEAP 00554	Tanzania	+	+	+
ICEAP 00557	Tanzania	+	+	+
ICEAP 00576-1	Kenya	+	+	+
KAT 60/8	Kenya	-	-	-
ICP 7035	India	-	-	-

KM=Kimutwa, *EM*= Emali, *KB*=Kiboko; + = resistant (= 36.6% wilt incidence), - = susceptible (= 36.6% wilt incidence); KAT= Katumani 60/8; ICEAP= ICRISAT East African Pigeonpea

Segregating Populations

Preparation of Inoculum and plant inoculation : A Kiboko (KB) isolate of the Fusarium wilt fungus was obtained from a highly susceptible *var*. KAT 60/8. Stems from diseased plants of this *var*. were used and the inoculum was prepared according to the modification of the protocol described by Laslie and Summerell [15]. Soil was mixed with sand at a ratio of 3:1 and the damp mixture was sterilized using soil sterilizer (THERMOFORCE LTD) for 1.5 hours at 82 ^{o}C**.** It was then placed in polythene bags (16cm × 16cm × 8cm) in the greenhouse. A total of 60 seeds each for F_1, BC_1F_1, BC_2F_1 and parents while 200 seeds for F_2 were evaluated. Four seeds were sown in each bag. The seeds were surface sterilized in 1% sodium hypochlorite for one minute and rinsed three times in sterile dH_2O. Seven days after germination, the seedlings were inoculated using root-dip inoculation technique described by Okiror [16]. For controls of both the susceptible and resistant lines, the distal end of the root system was cut, and the seedlings dipped in sterile dH_2O. Immediately after transplanting, watering was done at an interval of two days. The polythene bags were then placed in a greenhouse and maintained at about 22-32^{o}C. The seedlings were sprayed with insecticide [Duduthrin (Lambda-cyhalothrin)] at the rate of 17.5g ha^{-1} to control insect pests. Control of weed was done by hand weeding. The number of resistant and susceptible seedlings to Fusarium wilt was observed.

Data analysis

Chi-square analysis was performed using SAS software, SAS Institute [18] to test the goodness of fit between the theoretical models and observed ratios of resistant to susceptible plants .

Results and discussion

Inheritance studies

Among the pigeon pea parents used in this study, *KB* isolate of Fusarium wilt was virulent to *var.* KAT 60/8 and ICP 7035 but no susceptible reaction was noted on the resistant *var*. ICEAP 00554 and ICEAP 00557 (Table 3). All the F_1 progenies that were derived from ICEAP 00554 (resistant) × KAT 60/8 (susceptible), ICEAP 00557 (resistant) × KAT 60/8 (susceptible) and their reciprocal crosses were resistant to Fusarium wilt isolate *KB* at seedling stage (Table 4). Similar results were observed on the ICEAP 00557 (resistant) × ICP 7035 (susceptible), ICEAP 00554 (resistant) × ICP 7035 (susceptible) and their reciprocal crosses. Lack of difference in disease reaction from crosses between resistant × susceptible and their reciprocals indicated that cytoplasmic effects did not play any role in the expression of resistance to Fusarium wilt isolate KB. The resistance conferred was located in the genome. No difference in disease reaction was observed in the resistant × susceptible and their reciprocal crosses.

The number of resistant and susceptible observed in F_2 populations derived from resistant × susceptible and their reciprocal crosses demonstrated a good fit to one gene model with a ratio of 3:1 (resistant: susceptible) (Table 4). Evidently, frequencies of their respective F_2 genotypes derived from reciprocal crosses did not differ significantly from the expected frequencies (Tables 4) and this suggests that resistance to Fusarium wilt is conferred by single gene [13]. When KAT 60/8 was used as a recurrent parent in a backcross program, BC_2F_1s segregated into a ratio of 1: 1. However, some of the BC_1F_1 populations where ICP7035 was used as a recurrent parent did not fit the expected segregation ratio. The disease reactions observed in the BC_1F_1 and BC_2F_1 populations with the KAT 60/8 as a recurrent parent confirmed the one gene model detected in the F_2 pigeonpea populations. In some of the BC_2F_1 populations with ICP7035 as a recurrent parent, the data deviated from the expected segregation ratio of 1: 1 (resistant: susceptible) and this may be due to variable penetrance of the spores during the inoculation. As positive control, fusarium wilt KB was virulent to the susceptible parents but avirulent to resistant parents.

Allelic Relationship of Genes in the Resistant and Susceptible Parents

The F_1 genotypes from resistant × resistant and susceptible × susceptible crosses of pigeon pea genotypes were resistant and susceptible to Fusarium wilt, respectively (Table 5). As expected, no F_2 genotypes from resistant × resistant crosses were susceptible to Fusarium wilt. Nevertheless, segregation was observed on F_2 genotypes derived from reciprocal crosses between susceptible (KAT 60/8) × susceptible (ICP7035) parents. The number of resistant and susceptible plants observed in the F_2 populations [KAT 60/8 and ICP7035 ($\chi^2_{0.05}$ = 0.166, P≥0.733)] and its reciprocal ($\chi^2_{0.05}$ = 0.153, P≥0.696)] was conformed to a ratio of 1:3 (resistant: susceptible) phenotypic ratio one gene action (Table 5).

At seedling stage the resistance to *Fusarium* wilt is controlled by digenic [5, 9] and polygenes [14]. Contrary to the findings in this study major gene effect were detected in KAT 60/8 × ICEAP 00554, 00554 ×

Table 4. Genetic analysis of resistance to *Fusarium* wilt in pigeonpea populations derived from resistant × susceptible crosses

Pedigree	Observed frequencies					
	Generations	R	S	Ratio R:S	χ^2	P
Crosses using KAT 60/8 × ICEAP 00554 as parents						
KAT 60/8	P1		40			
ICEAP 00554	P2	40				
KAT 60/8 × ICEAP 00554	F_1	60				
KAT 60/8 × ICEAP 00554	F_2	159	51	3.1	0.057	0.811
ICEAP 00554 × KAT 60/8	F_1	60				
ICEAP 00554 × KAT 60/8	F_2	167	53	3.1	0.097	0.755
KAT 60/8 × ICEAP 00554*[1]	BC_2F_1	22	25	1:1	0.191	0.662
ICEAP 00554 × KAT 60/8*[1]	BC_2F_1	20	24	1:1	0.364	0.546
Crosses using KAT 60/8 × ICEAP 00557 as parents						
KAT 60/8	P1		40			
ICEAP 00557	P2	40				
KAT 60/8 × ICEAP 00557	F_1	60				
KAT 60/8 × ICEAP 00557	F2	159	57	3:1	0.222	0.637
ICEAP 00557 × KAT 60/8	F_1	60				
ICEAP 00557 × KAT 60/8	F_2	153	56	3:1	0.359	0.549
KAT 60/8 × ICEAP 00557*[1]	BC_2F_1	26	29	1:1	0.164	0.686
ICEAP 00557 × KAT 60/8*[1]	BC_2F_1	21	26	1:1	0.532	0.466
Crosses using ICP 7035 and ICEAP 00554 as parents						
ICP 7035	P1		40			
ICEAP 00554	P2	40				
ICP 7035 × ICEAP 00554	F_1	60				
ICP 7035 × ICEAP 00554	F_2	156	47	1:1	0.369	0.543
ICEAP 00554 × ICP 7035	F_1	60				
ICEAP 00554 × ICP 7035	F_2	157	49	3:1	0.167	0.687
ICP 7035 × ICEAP 00554*[1]	BC_2F_1	33	20	1:1	3.189	0.074
ICEAP 00554 × ICP 7035*[1]	BC_2F_1	27	21	1:1	0.750	0.386
Crosses using ICP 7035 × ICEAP 00557 as parents						
ICP 7035	P1		40			
ICEAP 00557	P2	40				
ICP 7035 × ICEAP 00557	F_1	60				
ICP 7035 × ICEAP 00557	F_2	162	49	3:1	0.355	0.551
ICEAP 00557 × ICP 7035	F_1	60				
ICEAP 00557 × ICP 7035	F_2	167	51	3:1	0.300	0.584
ICP 7035 × ICEAP 00557*[1]	BC_2F_1	26	18	1:1	1.455	0.228
ICEAP 00557 × ICP 7035*[1]	BC_2F_1	35	19	1:1	4.741	0.029

KAT 60/8, KAT 60/8 × ICEAP 00557, ICEAP 00557 × KAT 60/8 (Table 4), ICP 7035 × ICEAP 00554, ICEAP 00554 × ICP 7035 , ICP 7035 × ICEAP 00557 and ICEAP 00557 × ICP 7035 (Table 4). Single recessive gene action has also been shown to confer resistance to Fusarium wilt of pigeonpea [12]. In this study, it is hypothesized that a recessive resistant gene was present in accession ICP7035 and expressed when placed in KAT60/8 background. Several factors may have contributed to these differences. First, the sources and genetic background of the resistant materials used in this study were different from those in earlier studies and this could have contributed to the differences. Resistant genes for fusarium wilt in pigeon pea are expressed differently depending on the source and the background in which the gene is placed [14].

Secondly, some of the studies were carried out in the wilt boxes [5, 9] and others under field conditions [12]. In the field, the environmental and edaphic factors may influence both the disease severity and the expression of the resistance. As a result, methods of assessing this disease resistance often affect the conclusions of the genetic studies. *Fusarium udum* isolates from the same sites (country) and diverse geographical origin has been shown to exhibit high variability in pathogenecity on pigeonpea genotypes [16, 18, 19].

In the allelic test, the resistant reaction in F_1 plants and lack of susceptible segregates among the F_2 populations from crosses between resistant × resistant parents suggests that the wilt resistant genes in the two genotypes ICEAP 00554 and ICEAP 00557 were allelic. Because F_1 population were resistant to Fusarium wilt this was evidence that resistance is controlled by dominant. This evidence is supported by the segregation pattern of 3:1 of F_2 populations. As expected all F_1 progenies from crosses between susceptible and susceptible parents were susceptible indicating that each of the two genotypes carried a gene for susceptibility and there was no novel genes from recombination. Segregation for resistant was observed in the F_2 populations derived from the crosses between susceptible and susceptible parents (Table 5). However, no complementary gene action reaction was observed. The susceptibility of F_1 to Fusarium isolate KB and segregation of F_2 genotypes derived from KAT 60/8 (susceptible) × ICP 7035 (susceptible) crosses gave a ratio of 48 : 136 (resistant : susceptible) while F_2 genotypes from its reciprocal cross exhibited a ratio of 57: 161 (resistant: susceptible) both of them giving a fit of 1: 3 (resistant : susceptible). This clearly indicates the presence of a recessive gene that result from recombination between the two accessions (Table 5). It is therefore suggested that a novel recessive gene was detected from the crosses between the two susceptible accessions. Introgression of recessive resistance genes from ICP7035 with those from ICEAP 00554, ICEAP 00557 could be valuable source of resistant for pigeonpea breeders.

Screening pigeonpea seedlings by artificial inoculation in the greenhouse permits examination of a large number of populations for resistance under uniform disease pressure. Although this was the best approach for identifying major genes in genetic studies there could be differences in seedling and adult reaction to Fusarium wilt. It is therefore advisable to screen pigeon pea at seedling and adult stages. This study confirms that resistant to Fusarium wilt is controlled by a single dominant and a recessive gene. Breeding programs can therefore easily incorporate these genes for resistance into cultivars where Fusarium wilt is a problem after ascertaining isolate resistant. The recessive gene detected suggest that ICP7035 could be one of the sources of resistance.

Table 5. Genetic analysis of resistance to Fusarium wilt in pigeonpea (*Cajanus cajan*) populations derived from resistant × resistant and susceptible × susceptible crosses

Pedigree	Generations	Observed frequencies R	S	Ratio R:S	χ^2	P
Populations derived from crosses between ICEAP 00554 and ICEAP 00557						
ICEAP 00554	P1					
ICEAP 00557	P2					
ICEAP 00554 × ICEAP 00557	F_1	60				
ICEAP 00554 × ICEAP 00557	F_2	174				
ICEAP 00557 × ICEAP 00554	F_1	60				
ICEAP 00557 × ICEAP 00554	F_2	162				
Populations derived from crosses between KAT 60/8 and ICP 7035						
KAT 60/8	P1		40			
ICP 7035	P2		40			
KAT 60/8 × ICP 7035	F_1		48			
KAT 60/8 × ICP 7035	F_2	48	136	1:3	0.116	0.733
ICP 7035 × KAT 60/8	F_1		51			
ICP 7035 × KAT 60/8	F_2	57	161	1:3	0.153	0.696

Acknowledgement

This study was supported by Alliance for Green Revolution in Africa (AGRA), Moi University, Kenya Agricultural Research Institute (KARI) and International Crops Research Institute for the Semi-Arid Tropics (ICRISAT). These institutions are highly acknowledged.

References

1. **Kannaiyan J., Nene Y. L., Reddy M. V., Ryan J. G. and Raju T. N.** 1984. Prevalence of pigeonpea diseases and associated crop losses in Asia, Africa and the Americas. Tropical Pest Management. **30**: 62-71.
2. **Reddy M. V., Sharma S. B. and Nene Y. L.** 1990. Pigeonpea: Disease Management. Pp. 303-348. *In*: Nene, Y.L., S.D. Hall and V. K. Sheila (eds.). The Pigeonpea. C.A.B. International.
3. **Reddy M. V., Raju T. N., Sharma S. B., Nene Y. L. and McDonald D.** 1993. Handbook of pigeobpea diseases, *In*: En. Summaries in En. Fr.. Information Bulletin. 14. Patancheru, A.P. 502 324, India: International Crops Research Institute for the Semi-Arid Tropics. 64. pp.
4. **Silim S. N., Coe R., Omanga P. A. and Gwata E. T.** 2006. The response of pigeonpea genotypes of different duration types to variation in temperature and photoperiod under field conditions in Kenya. Journal of Food, Agriculture and Environment, **4**: 209–214.
5. **Kimani P. M.** 1991. Pigeonpea improvement research in Kenya: An Overview. *In*: Singh, Laxman, Silim, S.N., Ariyanagam, R.P., and Reddy, M.V. (eds). Proceedings of the First Eastern and Southern Africa Regional Legumes (Pigeonpea) workshop, 25-27 Jun 1990, Nairobi, Kenya. Eastern Africa Regional Cereals and Legumes (EARCAL) Program, International Crops Research Institute for the Semi-Arid Tropics. Pp. 108-117.
6. **Hillocks R. J., Minja E., Silim S. N. and Subrahmanyam P.** 2000. Diseases and pests of pigeonpea in eastern Africa. International Journal of Pest Management, **46**: 7–18.
7. **Parmita P., Rajini R. and Singh R. M.** 2005. Inheritance of resistance to *Fusarium* wilt in pigeonpea [*Cajanus Cajan* (L.) Millsp.]. Journal of Arid Legumes, **2:** 2005.
8. **Pawar N. B. and Mayee C. D.** 1986. Reaction of pigeonpea genotypes and their crosses to *Fusarium* wilt. Indian Phytopathology, **39**: 70-74.
9. **Okiror M. A.** 2002. Genetics of resistance to *Fusarium udum* in pigeonpea [*Cajanus cajan* (L.) Millsp.]. Indian Journal of Genetics and Plant breeding, **62**: 218-220.
10. **Singh I. P., Vishwa Dhar, Chaudhary R. C. and Pandey D. K.** 1998. Genetic of *Fusarium* wilt resistance in pigeonpea. *In*: National Symposium on Management of Biotic and Abiotic Stresses in Pulse Crops, 26–28th June 1998, IIPR, Kanpur, pp. 15.
11. **Mehrotra R. S. and Ashok A.** 2007. Plantphytopathology, http://books.google.co.ke/book.
12. **Jain K. C. and Reddy M. V.** 1995. Inheritance of resistance to *Fusarium* wilt in pigeonpea (*Cajanus cajan* L.). Indian J Genet., **55**: 434–437.
13. **Kotresh H., Fakrudin B., Punnuri S. M., Rajkumar B. K., Thudi M., Paramesh H., Lohithaswa H. and Kuruvinashetti M. S**. 2006. Identification of two RAPD markers genetically linked to a recessive allele of a *Fusarium* wilt resistance gene in pigeonpea (*Cajanus cajan* L. Millsp). Euphytica, **149**: 113-120.
14. **Odeny D. A.** 2001. Inheritance of resistance to *Fusarium* Wilt in Pigeonpea. *In*: Silim, S.N., Mergeai, G. and Kimani P.M. (eds). Status and potential of pigeonpea in Eastern and Southern Africa: Proceedings of a regional workshop, 12-15 Sep, 2000, Nairobi, Kenya. B-5030 Gembloux, Belgium: Gambloux Agricultural University; and Patancheru 502 324, Andra Pradesh India: International Crops Research Institute for the Semi-Arid Tropics. 232 pp.
15. **Laslie J. F. and Summerell B. A.** 2006. *Fusarium* Laboratory Manual. 2-14. Blackwell Publishing.
16. **Okiror M. A.** 1986. Breeding for Resistance to *Fusarium* wilt of pigeonpea [*Cajanus cajan* (L.) Millsp.] in Kenya. PhD. Thesis, Department of Crop Science, University of Nairobi, Kenya.
17. **Nene Y. L., Kannaiyan J. and Reddy M. V. 1981.** Pigeonpea diseases: resistance screening techniques. Information Bulletin No. 9. ICRISAT, India.
18. **SAS Institute.** 2001. SAS procedure for personal Computers Computers. Version 8 SAS Inst., Cary, NC, USA.
19. **Gaur V. K. and Sharma L. C.** 1989. Variability in single spore isolate of *Fusarium udum* Butler. Mycopathologia, **107**: 9-15.
20. **Kiprop E. K., Baudoin J. P., Mwang'mbe A. W., Kimani P. M., Mergeaia G. and Maquets A.** 2002. Characterization of Kenyan isolates of *Fusarium udum* from pigeonpea [*Cajanus cajan* (L.) Millsp.] by cultural characteristics, Aggressiveness and AFLP Analysis. Journal of Phytopathology, **150**: 517-525.