Stability for disease, genotype x environment interaction for yield and its components in pigeonpea [*Cajanus cajan* (L.) Millsp.]

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ABSTRACT

The material for study of genotype x environment (G x E) interaction comprised of 23 genotypes, which were tested in four environments, during *kharif*-2012 and 2013 at two locations in Agricultural Research Station, Kalaburagi and Raddevadgi located in north eastern dry zone (Zone 2) of Karnataka. The experiment was laid out in lattice design with two replications. Highly significant differences among genotypes were observed for all the characters except number of pods per plant and yield per plant. Environmental +(Genotype x Environment) interaction was significant for days to 50 per cent flowering, day to maturity, plant height, pod bearing length, number of pods per plant and seed yield per plant. The variance due to pooled deviation was highly significant for all the characters which reflect the presence of sufficient genetic variability in the material. Stability parameters for seed yield per plant indicated that ASHA(ch) was stable and desirable, followed by RVK-275 and GRG-811 which were specifically adopted for favourable and poor environments respectively. Two years of field screening for *Fusarium* wilt (FW) and Sterility Mosaic Disease (SMD) yielded three genotypes *viz.*, GRG-811, GRG-2009 and ASHA for resistance to *Fusarium* wilt and moderate resistance to SMD. Hence, these genotypes can be used directly as a variety or choice of parent for hybridization programme.

Key words: *Fusarium* wilt (FW), Genotype x Environment (G x E), , Pigeonpea, Stability.

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is an important grain legume which occupies a major place in dietary requirement. It belongs to sub-tribe *Cajaninae* and has diploid genome with 11 pairs of chromosomes (2n = 2x = 22) comprising a genome of 833.1 Mbp (Varshney *et al.,* 2012). It is cultivated in varied agro climatic conditions ranging from moisture stress and input starved conditions to irrigated conditions. Selection and yield testing are the two major phases of varietal development and the later one is highly influenced by the locations and years of testing. The magnitude of G x E interaction and its components has a direct bearing on the environmental domain of the varieties to be recommended for commercial cultivation. Performance of genotypes in terms of productivity without stability serves no purpose. It is important that the genotypes must not only be productive but also be responsive to increasing fertility status and varied levels of intensities of management of the crop. Realizing the significance of this, 23 genotypes were evaluated in four environments. This helped in determining the stability for performance with respect to seed yield and yield attributes.

Lower productivity of pigeonpea in India is attributed to factors such as biotic and abiotic stresses. Among the biotic stresses, *Fusarium* wilt and sterility mosaic diseases are considered to be the most important diseases of pigeonpea in India. Control of Sterility Mosaic Disease (SMD) and *Fusarium* wilt (FW) by chemical methods though effective, is not feasible economically and non eco- friendly (Nene and Reddy, 1977). Breeding resistant varieties is considered to be one of the most effective and economic methods of reducing crop losses and has received top priority.

MATERIALS AND METHODS

The material for study of GxE interaction comprised of 23 genotypes, which were tested in four environments *viz., Kharif*-2012, ARS Gulbarga (Environment-1), *Kharif*-2013, ARS Gulbarga (Environment-2), *Kharif*-2012, ARS Raddevadgi (Environment-3) and *Kharif*-2013, ARS Raddevadgi (Environment-4). The trials were laidout in a lattice design with two replications. Each genotype was sown in two rows of 4m length was followed with spacing of 90 cm between rows and 20 cm between the plants. Observations were recorded on five randomly selected plants in each replication in each environment in respect of nine different metric characters *viz.*, days to 50 % flowering, plant height (cm), number of branches per plant, number of pods per plant, pod bearing length (cm), number of seeds per pod, days to maturity, seed yield per plant (g) and hundred seed weight (g). Stability analysis was carried out by using the stability model proposed by Eberhart and Russell (1966).

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Experimental layout for screening *Fusarium* wilt and SMD was laid out at Agricultural Research Station, Kalaburagi and Bidar respectively. All the genotypes were sown in single row with two replications and susceptible check was sown after every 10th row and screened for two years (*Kharif* 2012 and *kharif* 2013). A row length of 4 meters each was maintained with spacing of 75 cm and 30 cm between the rows and plants respectively. The observations on per cent wilt was recorded at flowering and at physiological maturity by counting number of dead plants (due to *Fusarium* wilt) among the total number of plants present per genotype and per cent disease incidence (PDI)was estimated. Similarly, observations on SMD were recorded by counting number of plants infected with sterility mosaic virus among total number of plants present per genotype and PDI was calculated. The categorization of PDI value was carried out according to the scale given by (Singh *et al.,* 2003) *viz.,* 0-10%=Resistant, 10.1-30%=Moderately Resistant, 30.1-100% Susceptible.

RESULTS AND DISCUSSION

Pooled analysis of variance (Table 1) as per Eberhart and Russell's (1966) model indicated that the Mean Sum of Squares (MSS) due to genotype was significant for all the characters except for number of pods per plant and yield per plant. Whereas, MSS due to environment was significant for all the characters. The genotype x environmental interaction was non significant for all the characters under study. However, further partitioning of genotype x environmental interaction indicated that, Environmental +(Genotype x Environment) interaction was significant for days to 50 per cent flowering, day to maturity, plant height, pod bearing length, number of pods per plant and seed yield per plant. While G x E (linear) was significant only for days to maturity indicating the absence of genetic differences among varieties for regression on environmental indices and thus the further prediction of genotypes would be difficult for these traits. The mean sum of squares (MSS) due to environments and environment (linear) was highly significant for all the characters under study except for 100 seed weight. It indicates the influence of environment on the genotypes. The characters having significant Environmental + (Genotype x Environmental) were considered for stability analysis. Therefore, a total of six characters *viz.,* days to 50 per cent flowering, day to maturity, plant height, pod bearing length, number of pods per plant and seed yield per plant were studied for G x E interaction. The results are in accordance with Shoran *et al.*, (1981), Balakrishna and Natarajratnam (1989) and Sawargaokar *et al.,* (2011). In contrast, significant G x E (linear) for number of seeds per pod and 100 seed weight was observed by Muthiah and Kalaimagal (2005). Ghodke *et al.,(1992)* obtained non significant G x E for majority of the traits. The variance due to pooled deviation was highly significant for all the characters which reflect the presence of sufficient genetic variability in the material

Table 1: ANOVA for stability of different quantitative traits over four environments

Source of Variation	d.f	DFF	DM	PH	Br/plant	PBL	NPPP	NSPP	Yd/ pnt	100 SW
Rep within Env.	4	7.61	10.36	50.7	9.65	56.5	220.0	0.03	40.29	0.29
Varieties	22	382.715 **	483.62**	846.9**	48.06**	173.6**	738.5	0.16**	121.30	2.19**
Env.+ (Gen.x Env.)	69	56.44*	130.06*	458.28**	20.11	105.8**	1705.1**	0.07	128.72*	0.91
Environments	3	359.555 **	576.07**	7649.6**	77.94**	1374.4**	18995.8**	0.56**	911.16**	0.41
Genotype X Environment	66	42.66	109.78	131.3	17.48	48.1	919.2	0.05	93.15	0.93
Environments (Lin.)	1	1078.66**	1728.20**	22948.7**	233.82**	4123.1**	56987.3**	1.67**	2733.48**	1.24
Genotype X Env.(Lin.)	22	57.74	162.46*	117.4	14.95	50.8	1231.5	0.04	102.04	1.07
Pooled Deviation	46	33.59**	79.82**	132.3**	17.93**	44.8**	729.8**	0.05*	84.85**	0.83**
Pooled Error	88	1.62	1.67	24.2	4.45	11.2	97.8	0.03	9.62	0.04
Total	91	135.32	215.53	552.2	26.87	122.2	1471.4	0.09	126.93	1.22

**=>Significant at P=0.01   *=>Significant at P=0.05

DFF: Days to fifty per cent flowering   NPPP: Number of pods per plant
DM: Days to maturity   NSPP: Number of seeds per pod
PH: Plant height   Yd/pnt: Seed yield per plant
Br/plant: Branches per plant   SW: Seed weight
PBL: Pod bearing length

Once the G x E interaction was found significant, the next task was to identify the stable genotypes which interact less with the environments giving a near consistent performance across environments. The term stable genotype has been used for the average performance in all environments. Hence, such a stable variety has a high mean, unit regression and a minimum deviation from regression. Table 2 shows that the stability parameters for seed yield components. Yield being the economic product, naturally, the genotypes with highest seed yield per plant are preferred. Based on overall performance across environments, the genotype ASHA (51.8 gms) recorded highest seed yield per plant, followed by RVK-275, GRG-811, BDN-2008-1 *etc.* Among all genotypes ASHA (ch) exhibited stable and desirable performance as indicated by high mean and non significant bi and S^2d_i values. RVK-275 had high mean with significant regression value of more than one hence, it is suitable for favorable environments. In contrast to this GRG-811 was suitable for poor environments as regression value of less than unity. Shoran *et al.* (1981); Muthiah and Kalaimagal (2005); Vannirajan *et al.* (2007); Patel *et al.* (2009); Sreelakshmi *et al.*(2010); Thanki *et al.* (2010); Sawargaonkar *et al.* (2011) and Niranjan Kumar (2013)

identified genotypes with average responsiveness and also genotypes with higher environmental sensitivity.

ICP-14832 was the earliest to flower (71 days), followed by ICP 16309, TJT-501. Early flowering up to 105 days (medium duration) coupled with early maturity is desirable in pigeonpea. The deviation from regression (S^2d_i) was non significant for the genotypes AKT-9913, RKV-284, GRG-811 and ICP-995. Further, regression co-efficient (bi) of these four genotypes did not differ significantly from one. The genotype RVK -284 was found to have average stability as it had bi value near to unity. The genotypes AKT-9913, GRG-811 and ICP-995 were suitable for high input environments as they have bi value more than unity. The result was in conformity with Shoran *et al.* (1981), Sreelakshmi *et al.* (2010), Patel *et al.* (2009), Vannirajan (2007) who identified genotypes with average responsiveness and also genotypes with higher environmental sensitivity.

The genotypes ICP-14832, ICP 16309, ICP-7366, TJT 501 *etc.,* were early maturing lines. The deviation from regression (S^2d_i) was significant for all the entries except for BDN-2008-1, RKV-284, and ICP-995. The genotypes BDN-2008-1 and RKV-284 were suitable for low input environments as they have bi values significantly deviated

Table 2: Mean and stability parameters in 23 genotypes of pigeonpea

Traits	Days to 50% flowering			Days to Maturity			Plant height (cm)		
Genotypes	Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di
AKT 9913	98	-1.2	1.4	146.5	14.9**	0.27	159	26.54	1.19
BDN-2008-1	104.1	5.7*	0.1	151.3	-0.8	-0.76$	161.2	-22.1	0.82
BDN-2008-12	91.3	9.2**	0.04	138.9	126.3**	0.99	150.6	32.3	0.93
Bennur local	90.8	19.2**	0.75	139.3	45.4**	0.99	144.7	-12.46	1.37
GRG- 2009	104.4	23.2**	2.3	156	67.9**	2.06	159.6	87.23*	0.73
JKM-189	106.3	8.2**	0.93	153.1	19.1**	0.11	176.4	1.38	1.05
JKM-7	110.3	32.0**	1.77	159.5	17.3**	1.06	182.5	116.35**	1.22
RVK-275	101.9	9.8**	0.97	152.1	9.5**	1.43	161.5	25.89	1.09
RVK-284	102.4	-1.1	0.96	156	-1.7	2.17$	166.8	80.03*	1.61
RVK-285	100	206.7**	0.91	150.1	197.5**	0.83	180.2	8.34	1.22
TJT-501	88.4	96.3**	-0.19	137.9	148.6**	0.73	151.9	242.61**	1.03
TTB-7	105.8	28.4**	1.16	156.1	30.1**	0.55	172	383.06**	1.31
ICP 12654	103.5	26.9**	0.42	155.4	17.1**	1.54	148.9	-6.22	1.33
ICP 13673	114.4	68.8**	3.99	175.5	553.7**	3.73	160.9	369.84**	1.06
ICP 16309	82	57.5**	1.65	132.3	61.6**	1.98	136.4	28.2	0.53
GRG 811	99.6	2.5	1.59	148.1	5.6*	1.4	159.3	14.77	1.22
ICP 14832	70.8	82.8**	1.45	124.5	110.8**	4.75	127.1	71.35*	0.87
ICP 4715	102.8	10.3**	1.96	155.9	186.6**	0.8	151.2	295.04**	0.3
ICP 6971	98.6	13.6**	-0.21	147.8	43.0**	0.28	156.1	47.31	1.09
ICP 7366	92.4	13.0**	-1.85$	134.5	101.3**	-2.81	132.3	380.27**	0.65
ICP 995	105.6	2.4	1.42	153	1.2	0.86	160.7	168.48	1.35
ASHA (ch)	108.6	10.7**	0.91	158.5	21.2**	0.001	177.2	36.1	0.78
TS-3R (ch)	94.1	4.4*	0.58	141.9	12.8**	0.027	150.4	85.48*	0.27
Population mean	98.9			148.9			157.7		

Where,

**=>Significantly deviating from zero at P=0.01   bi= regression co-efficient

* => Significantly deviating from zero at P=0.05 S^2di= deviation from regression co-efficient

(Contd…)

Table 2: Mean and stability parameters in 23 genotypes of pigeonpea.

Traits	Pod bearing length (cm)			Number of pods/plant			Seed yield per plant(g)		
Genotypes	Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di
AKT 9913	42.2	-9.2	1.45	146.8	668.4**	0.93	42.2	64.23**	0.06
BDN-2008-1	36	133.4**	0.42	147.1	952.8**	1.3	45.3	303.73**	0.14
BDN-2008-12	48.7	40.2*	1.3	144.9	-38.1	1.4	44.2	73.13**	1.01
Bennur local	39.9	43.2*	1.32	129.6	770.7**	0.34	40.4	49.11**	-0.12
GRG- 2009	29.8	26.7	0.49	132.6	375.8*	0.71	42.4	123.22**	-0.32
JKM-189	36	37.6*	2.01	121.9	165.4	0.69	34.2	38.23*	1.07
JKM-7	34.1	11.8	1.68	145.7	-60.5	1.97$	40.6	53.37**	2.93
RVK-275	27.3	38.1*	1.35	169.8	-92.6	1.77$	48.9	-6.32	2.30$
RVK-284	30.9	7.1	0.83	121.3	433.5**	0.36	34.5	17.25	0.51
RVK-285	41.4	-2.4	0.38	140.3	839.0**	0.76	41.4	60.15**	0.27
TJT-501	40.3	62.5**	1.32	146.4	3414.7**	2.46	42.5	379.93**	2.17
TTB-7	30.1	7	0.91	131.7	-28.9	1.75$	35.3	20.52	1.14
ICP 12654	20	12.4	0.69	148.8	114.7	2	39.7	8.95	2.06
ICP 13673	27.5	-10.3	0.58	154.3	646.9**	0.73	45.1	34.04*	0.12
ICP 16309	36.1	-1.1	1.18	151.5	1002.0**	1.28	37.7	4.88	1.65
GRG 811	40.5	43.3*	0.84	146.2	663.6	0.34	45.4	19.4	0.24
ICP 14832	26.6	3.9	-0.38$	131.3	61	-0.06	32.1	98.28**	1.96
ICP 4715	25.5	70.2**	1.3	143.1	107.8	0.36	43.1	36.56*	1.16
ICP 6971	28.8	65.8**	0.75	160.9	1228.8**	0.85	40.4	3.71	1.22
ICP 7366	34.6	96.6**	0.92	129.9	1349.6**	0.63	28.9	189.66**	2.18
ICP 995	36.3	46.7*	1.44	155.3	-93.9	-0.18	33.8	26.09*	0.63
ASHA (ch)	33.1	-1.8	0.54	173.6	1999.6**	0.76	51.9	-0.17	0.7
TS-3R (ch)	35.1	5.7	1.58	148.6	-65.8	1.75	43.1	101.75**	-0.08
Population mean	33.9			144.4			40.5		

where
**=>Significantly deviating from zero at P=0.01   bi= regression co-efficient
* => Significantly deviating from zero at P=0.05   S²di= deviation from regression co-efficient

from unity. The results are in accordance with Singh (1984) and Thanki *et al.* (2010) identified genotypes having average and above average stability for this trait. Sreelakshmi *et al.* (2010) obtained three stable genotypes (ICPL 98008, ICPHL 4979-2 and ICP 77303) for maturity.

The genotypes BDN-2008-1, BDN-2008-12, RVK-275 and ICP6971 had desirable plant height. TTB-7 and ICP-16309 were stable and had desirable pod bearing length. Stability parameters for seed yield per plant indicated that ASHA(ch) was stable and desirable, followed by RVK-275 and GRG-811 which were specifically adopted favorable and poor environments respectively.

In the present study a total of 4 out of 23 genotypes showed resistant reaction for *Fusarium* wilt (FW)(Table 3), with PDI range of 6.17 (TS-3R) to 8.47 (GRG-2009). Out of 4 resistant genotypes, ASHA and GRG-811 produced narrow range of PDI, indicating its consistency over the years. Moderately resistant reaction for FW was observed in 10 out of 23 genotypes with frequency 43.4 per cent. The genotypes GRG-2009 and GRG 811 were wilt resistant as well as in the track of high yield as indicated by their *per se* performance. Hence, these genotypes can be used as variety or choice of parent for hybridization programme. The results are in agreement with Sharma *et al.,* (2012), they evaluated

the pigeonpea to identify the resistance to FW under artificial field epiphytotic conditions. Sharma *et al.,* (2013) identified combined resistance to FW and SMD in 54 lines, out of 3000 germplasm evaluated for three consecutive years during. Prashanti *et al.* (2009) screened 88 lines of pigeonpea and identified 14 resistant lines, further they identified OPG 08, RAPD primer linked to *Fusarium* wilt resistance at 920bp.

Moderate resistant disease reaction for SMD was observed in 3 genotypes (including one check variety) out of 23 genotypes with PDI range of 18.9 (GRG-811) to 29.1 per cent. Three genotypes *viz.,* GRG-811, GRG-2009 and ASHA showed resistance to FW and moderate resistance to SMD.

From the present study it can be concluded that the genotypes *viz.,* ASHA(ch), RVK-275 and GRG-811 was stable and desirable, which were specifically adopted favorable and poor environments respectively. Two years of field screening for *Fusarium* wilt and SMD yielded three genotypes *viz.,* GRG-811, GRG-2009 and ASHA showed resistance to FW and moderate resistance to SMD and high yielding as indicated by their *per se* performance. Hence, these genotypes can be used directly as a variety or choice of parent for hybridization programme.

Table 3: Disease reaction of pigeonpea genotypes for *Fusarium* wilt and sterility mosaic disease under   field condition for two seasons.

Traits	Wilt incidence (%)		PDI	Reaction	Wilt incidence (%)		PDI	Reaction
Genotypes	2012-13	2013-14	Mean		2012-13	2013-14	Mean	
AKT 9913	38.84	23.5	31.2	S	93.8	76.7	85.2	s
BDN-2008-1	28	24.6	26.3	MR	90.6	96	93.3	S
BDN-2008-12	26.08	29.1	27.6	MR	100	17.6	58.8	S
Bennur local	24.05	18.4	21.2	MR	96.9	88.9	92.9	S
GRG- 2009	7.24	9.7	8.47	R	29.3	20	24.6	MR
JKM-189	26.09	27.3	26.7	MR	96	72.7	84.4	S
JKM-7	24.65	28	26.3	MR	100	71.4	85.7	S
RVK-275	47.5	45.2	46.4	S	100	76.9	88.5	S
RVK-284	34.09	25.6	29.8	MR	76.9	70.6	73.8	S
RVK-285	31.8	28.1	30	MR	88.9	28	58.4	S
TJT-501	59.38	32.7	46	S	94.1	87.5	90.8	S
TTB-7	67.61	20	43.8	S	90	90	90	S
ICP 12654	32.35	34	33.2	S	92.6	64.3	78.4	S
ICP 13673	7.69	17.5	12.6	MR	82.4	73.3	77.8	S
ICP 16309	20	42.2	31.1	S	75	20	47.5	S
GRG 811	4.84	9.8	7.3	R	25.8	12	18.9	MR
ICP 14832	1.82	26.9	14.4	MR	96.3	80	88.2	S
ICP 4715	93.44	50	71.7	S	69.7	62.5	66.1	S
ICP 6971	92.06	35.3	63.7	S	96	84	90	S
ICP 7366	95.71	34.3	65	S	90	70	80	S
ICP 995	19.04	6.9	13	MR	71.4	64.3	67.9	S
ASHA (ch)	5.63	8.7	7.2	R	29.9	28.4	29.1	MR
TS-3R (ch)	7.14	5.2	6.17	R	100	88.5	94.2	S

Where,

MR=Moderately resistant

R = Resistant ,   PDI = per cent disease incidenceS=Susceptible

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