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GENOTYPIC-ENVIRONMENT INTERACTION AND DISEASES SCREENING STUDIES IN PIGEONPEA [*CAJANUS CAJAN* (L.) MILLSP.]

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ABSTRACT

A study was conducted to examine the Genotypic x environment interaction of the fifteen advanced genotypes of pigeonpea including four checks (TS-3R, GRG-811, GRG-152 and GC-11-39) at five locations viz., Kalaburagi (E₁), Bheemaranagudi (E₂), Malnoor (E₃), Bidar (E₄) and Hagari (E₅), during *kharif* 2022-23. The experiment for screening *Fusarium* wilt and SMD was laid out at Zonal Agricultural Research Station, Kalaburagi and Agricultural Research Station, Bidar respectively during *kharif* 2022-23, using respective resistant and susceptible checks for wilt and SMD. Pooled ANOVA for stability revealed that the mean sum of squares due to varieties, G x E interaction, environments and environment linear were significant for grain yield (q/ha). The genotypes viz., GRG-152(Ch), KRG-33, GRG-811(Ch), TS-3R(Ch), NAM-314, NAM-2151, NAM-2435, NAM-2150 and NAM-2545 had higher mean performance, non significant regression coefficient and deviation from regression, indicating their adaptation to all the environments. The genotypes viz., GRG-152(Ch), KRG-33, GRG-811(Ch), TS-3R(Ch), NAM-314, NAM-2151, NAM-2435 and NAM-2545 showed moderate resistant to both FW and SMD coupled with higher mean value than population mean as indicated by its *per se* performance and stable across the locations under rain fed situations.

Keywords: Pigeonpea, stability, Genotype x Environment (G x E) *Fusarium* wilt (FW) and sterility mosaic diseases (SMD).

Introduction

Pigeonpea [*Cajanus cajan* (L.) Mill sp.] 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). India is considered as the native of pigeonpea (Van der Maesen, 1980) because of its natural genetic variability available in the local germplasm and the presence of its wild relatives in the country.

It is cultivated in varied agro climatic conditions ranging from moisture stress and input starved conditions to irrigated conditions. Pigeonpea breeders look forward for widely adapted genotypes responsive to input intensive as well as input deficient agriculture in order to enhance production and productivity of the crop. 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. Among the biotic stresses, *Fusarium* wilt (FW) and sterility mosaic diseases (SMD) are considered to be the most important diseases of pigeonpea in India. SMD and FW cause substantial losses to pigeonpea production and have been identified as the “must-have” traits for pigeonpea in India. As the diseases are endemic in the subcontinent and continue to be responsible for greater losses (Reddy *et al.*, 1998). Breeding resistant varieties is considered to be one of the most effective and economic methods of reducing crop losses and has received top priority. With this back ground the present study was undertaken under rainfed situation in five different locations to identify stable genotypes of pigeonpea for seed yield and disease resistant.

Materials and Methods

The experiments were conducted at five locations *viz.*, Kalaburagi (E₁), Bheemaranagudi (E₂), Malnoor (E₃), Bidar (E₄) and Hagari (E₅), belong to three Agro Climate Zones (AEZ) of Karnataka (Table 1). Fifteen genotypes subjected for stability analysis consisted of 11 advanced lines *viz.*, KRG-33, NAM-2085, NAM-2088, NAM-2150, NAM-2151, NAM-2545, NAM-2435, NAM-314, CORG-9701, ICPL-19063, ICPL-19064 and four checks (TS-3R, GRG-811, GRG-152 and GC-11-39). The experiments were carried out during *khariif* 2022-23 in a randomized complete block design (RCBD) with three replications. Each entry was sown in 6 rows of 4 meters length with a spacing of 90 cm between the rows and 30 cm between plants. Standard agronomic practices were followed and plant protection measures were taken as and when required by following the recommended package of practices (Anon., 2017). Grain yield per plot was recorded and scaled to q/ha at 10 per cent moisture. The grain yield data of 15 genotypes at five locations were subjected to Eberhart and Russell (1969) using statistical analysis package software Windostat 9.2 (Table 2, 3 and 4).

The experiment for screening *Fusarium* wilt and SMD was laid out at Zonal Agricultural Research Station, Kalaburagi and Agricultural Research Station, Bidar respectively using respective resistant and susceptible checks for wilt and SMD (Table 5). All the genotypes were sown in two row of 5 m length with two replications and susceptible check was sown after every 5th row. A spacing of 60 cm and 20 cm between the rows and plants respectively was followed for wilt and 75x30cm for SMD. The 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

Many stability models have been developed to identify the stable genotype. Eberhart and Russell (1969) model is the one which has been used in pigeonpea and in other crops by several workers. According to Eberhart and Russell (1969), a variety is said to be stable when regression coefficient (*bi*) is equal to one, deviation from regression (*S²di*) as close to zero as possible with high mean performance. Allard and Bradshaw (1964) suggested selection of stable genotype depends upon genotype having less interaction with environments.

The above three measures of assessing the stability of genotype *viz.*, mean, regression coefficient (*bi*) and the mean square deviation (*S²di*) were employed in assessing the stability of genotypes included in the present study. The linear regression (*bi*) could simply be regarded as the measure of response of a particular genotype and it is of greater than one then the genotypes is said to be sensitive to environment changes but adapted to favorable environments. If it is less than one it indicates above average stability. If this is accompanied by the high mean value then, the genotype is said to be better adapted to widely differing situations for unfavorable environment and if the mean value is low, greater *G × E* interaction indicated (Finlay and Wilkinson, 1963). On the other hand, deviation around the regression line is considered as a better measure of stability. With respect to the non-linear component of the *G × E* interaction, the genotype with the lowest standard deviation will be the most stable and vice-versa. The results of present study on stability parameters are discussed below.

Pooled ANOVA for stability revealed that the mean sum of squares due to varieties, *G × E* interaction, environments and environment linear were significant for grain yield (q/ha) (Table 2). This demonstrated that genotypes respond differently to variation in environmental condition, indicated that the deviation from linear regression also contributed substantially toward the differences in stability of genotypes. The results are in accordance with Balakrishna and Natarajratnam (1989); Sawargaokar *et al.* (2011); Pawar *et al.* (2013); Patel and Tikka (2014);

Kumara *et al.* (2015); Singh *et al.* (2015); Meena *et al.* (2017); Ramesh *et al.* (2017), Deepak Pal *et al.* (2020) and Muniswamy. S *et al.* (2022).

The environmental index (Fig 1) ranging from -5.679 to 6.745 indicates significant variations over five different locations (Table 3). The genotypes *viz.*, GRG-152 (Ch) and KRG-33 showed the highest (25.64 q/ha and 21.87 q/ha) mean value respectively, while, ICPL-19063 showed the lowest (11.21 q/ha) mean value for grain yield quintal per ha. The average grain yield (q/ha) over five different locations was 18.28 q/ha (Table 4). In Bheemarayanagudi and Bidar location plants exhibit maximum grain yield per hectare as indicated by highest environmental index of 6.745 and 4.083 respectively and Malnoor and Hagri location offered restriction to have more grain yield per hectare as it had minimum environmental index of -5.679 and 14.417 respectively (Table 3).

All varieties showed non-significant regression coefficient and deviation from regression (Table 4). The genotypes *viz.*, GRG-152 (Ch), KRG-33, GRG-811 (Ch), TS-3R (Ch), NAM-314, NAM-2151, NAM-2435, NAM-2150 and NAM-2545 were found to have higher mean value than population mean with bi and S2di values (Fig 2) not significantly different from 1 and 0, respectively.

Considering stability parameters of 15 genotypes tested over five different locations (Fig 2), the genotypes NAM-2150, ICPL-19063, ICPL-19064, CORG-9701, GC-11-39 (Ch), NAM-2088, NAM-2435 and TS-3R (Ch) which had regression value less than unity are found suitable for poor environment whereas, the varieties GRG-152 (Ch), NAM-2151, NAM-2545, NAM-2085, KRG-33, NAM-314 and GRG-811 (Ch) with regression value more than unity were found suitable for favorable environment (Fig 3).

The genotypes *viz.*, GRG-152 (Ch), KRG-33, GRG-811 (Ch), TS-3R (Ch), NAM-314, NAM-2151, NAM-2435, NAM-2150 and NAM-2545 had higher mean performance, non significant regression coefficient and deviation from regression, indicating their adaptation to all the environments. These findings are in accordance with 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), Niranjana Kumar (2013), Ramesh *et al.* (2017), Manish Sharma *et al.*

(2020) and Muniswamy. S *et al.* (2022).

The results of *Fusarium* wilt disease reaction study indicated that out of 15 genotypes, 11 showed moderately resistant reaction ranging from 12.82 to 26.89 for (Table 5) with resistant check (ICP 8863) showing wilting of 8.62 per cent and susceptible check (ICP 2376) 85.61 per cent.

The genotypes *viz.*, GRG-152 (Ch), KRG-33, GRG-811 (Ch), TS-3R (Ch), NAM-314, NAM-2151, NAM-2435, NAM-2150 and NAM-2545 were moderately resistant to wilt as well as in the track of high yield as indicated by their *per se* performance. Sharma *et al.*, (2013), evaluated the pigeonpea to identify the resistance to FW under artificial field epiphytotic conditions. Prashanti *et al.* (2009) screened 88 lines of pigeonpea and identified 14 resistant lines for *Fusarium* wilt and Muniswamy. *et al.* (2021) screened 19 genotypes of pigeonpea identified 14 genotypes showed resistant reaction for *Fusarium* wilt.

Resistant disease reaction for SMD was observed in 2 out of 19 genotypes with PDI range of 3.7 (ICPL - 19064) to 4.69 per cent (ICPL - 19063). Moderate resistant disease reaction for SMD was observed in 13 genotypes (including three check varieties) with PDI range of 10.13 (NAM 2085) to 20.46 per cent (NAM 2150) (Table 5). Sharma *et al.*, (2013) identified combined resistance to FW and SMD in 54 lines, out of 3000 germplasm evaluated for three consecutive years. Muniswamy *et al.* (2017) screened 23 pigeonpea genotypes and identified combined resistant lines for wilt and SMD. Muniswamy *et al.* (2021) screened 19 genotypes of pigeonpea identified 4 genotypes and 5 genotypes showed resistant reaction and moderate resistant disease reaction for sterility mosaic disease respectively.

From the present study, it can be concluded that the genotypes GRG-152 (Ch), KRG-33, GRG-811 (Ch), TS-3R (Ch), NAM-314, NAM-2151, NAM-2435 and NAM-2545 showed moderate resistant to both FW and SMD coupled with higher mean value than population mean as indicated by its *per se* performance and stable across the locations. Hence, these genotypes can be further validated and can be used directly as a variety or can also be used as a donor parent for generating new breeding material for development of variety.

Table 1: Agro-climatic characteristics of testing environments

Location/ Environment	Agroclimatic zones of karnataka	Longitude and Latitude	Altitude (>MSL)	Soil type
Bidar	1	17 ⁰ 55'N 77 ⁰ 39'E	710	Medium Black and Laterite
Bheemarayana gudi	2	16 ⁰ 7'N 76 ⁰ 79'E	411	Deep Black
Kalaburagi	2	17 ⁰ 20'N 76 ⁰ 49'E	443	Medium Black
Malnoor	2	16 ⁰ 28' N 76 ⁰ 28' E	383	Medium Black
Hagari	3	15 ⁰ 9'N 77 ⁰ 30'E	508	Medium Black

Table 2: Pooled analysis of variance for stability analysis (Eberhart and Russell, 1966) for grain yield (q/ha) in pigeonpea over five locations under rain fed situations

Sources of variation	df	Grain yield (q/ha)
Rep within Env	10	4.265
Varieties	14	76.072***
Env. + (Var. * Env.)	60	39.057***
Environments	4	429.239***
Var. * Env.	56	11.187
Environments (Lin.)	1	1716.955***
Var. * Env. (Lin.)	14	10.958
Pooled Deviation	45	10.513***
Pooled Error	140	2.858
Total	74	46.06

* & ** - Significant at 0.05 and 0.01 level of probability, respectively

Table 3: Environmental indices for grain yield (q/ha) in pigeonpea over five locations under rain fed situations

Characters	Environmental index				
	Env. 1	Env. 2	Env. 3	Env. 4	Env. 5
Grain yield q/ha	-0.732	6.745	-5.679	4.083	-4.417

Table 4: Stability parameters of 15 genotypes of pigeon pea for grain yield (q/ha) over five locations under rain fed situations.

Sl.No	Genotypes / Varieties	Grain yield (q/ha)		
		Mean	bi	s ² di
1	KRG-33	21.87	1.29	1.11
2	NAM-2085	17.44	1.28	9.95
3	NAM-2088	17.92	0.80	2.39
4	NAM-2150	18.96	0.59	1.06
5	NAM-2151	19.83	1.14	2.45
6	NAM-2545	18.42	1.15	4.76
7	NAM-2435	19.46	0.90	-0.66
8	NAM-314	20.40	1.51	13.35
9	CORG-9701	16.08	0.69	2.48
10	ICPL-19063	11.21	0.61	21.02
11	ICPL-19064	12.01	0.69	33.05
12	TS-3R (Ch)	20.82	0.98	6.95
13	GRG-811 (Ch)	21.15	1.51	2.94
14	GRG-152 (Ch)	25.64	1.08	11.67
15	GC-11-39 (Ch)	13.03	0.78	0.89
	Population Mean		18.28	

*- Significant at 5% probability level

** - Significant at 1% probability level
Deviation from regression

bi – Regression coefficient S²di –

Table 5: Disease reaction of pigeon pea genotypes for *Fusarium* wilt and sterility mosaic disease under rain field condition for Kharif 2022-23.

Sl.No	Genotypes	<i>Fusarium</i> Wilt		Sterility Mosaic Disease	
		PDI %	Reaction	PDI %	Reaction
1	KRG - 33	19.46	MR	14.14	MR
2	NAM 2085	26.89	MR	10.13	MR
3	NAM 2088	18.26	MR	18.71	MR
4	NAM 2150	18.08	MR	20.46	S
5	NAM 2151	19.07	MR	18.50	MR
6	NAM 2545	16.29	MR	17.91	MR
7	NAM 2435	20.36	MR	17.22	MR
8	NAM 314	18.86	MR	10.44	MR
9	CORG - 9701	26.65	MR	15.46	MR
10	ICPL - 19063	71.36	S	4.69	R
11	ICPL - 19064	61.24	S	3.70	R
12	TS3R (Ch)	45.92	S	25.27	S
13	GRG - 811 (Ch)	12.82	MR	14.94	MR
14	GRG - 152 (Ch)	16.06	MR	13.03	MR
15	GC- 11 - 39	35.81	S	11.87	MR
16	ICP 8863 (RC for FW and SC for SMD)	8.62	R	38.82	S
17	BSMR 736 (RC for SMD)	-	-	13.52	MR
18	ICP-2376 (SC for FW)	85.61	S		

Where,

MR=Moderately resistant

R = Resistant , PDI = per cent disease incidence S=Susceptible,

SC= Susceptible check

RC= Resistant check, FW= *Fusarium* wilt , SMD= Sterility mosaic disease

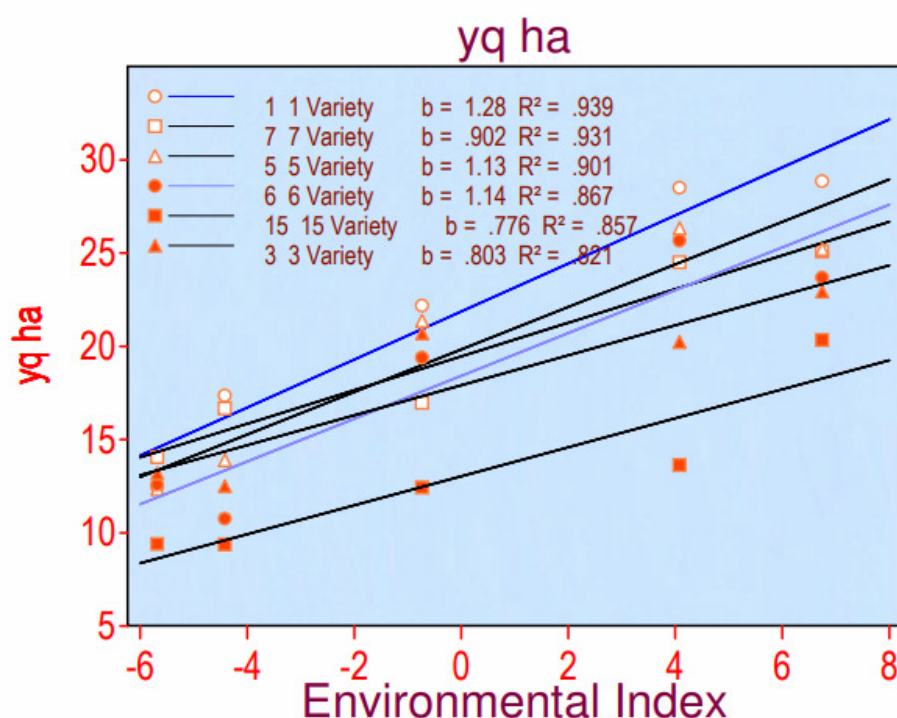


Fig. 1: Stability analysis for grain yield (q/ha) of 15 pigeonpea genotypes (G) and five environments (E) based on environmental index.

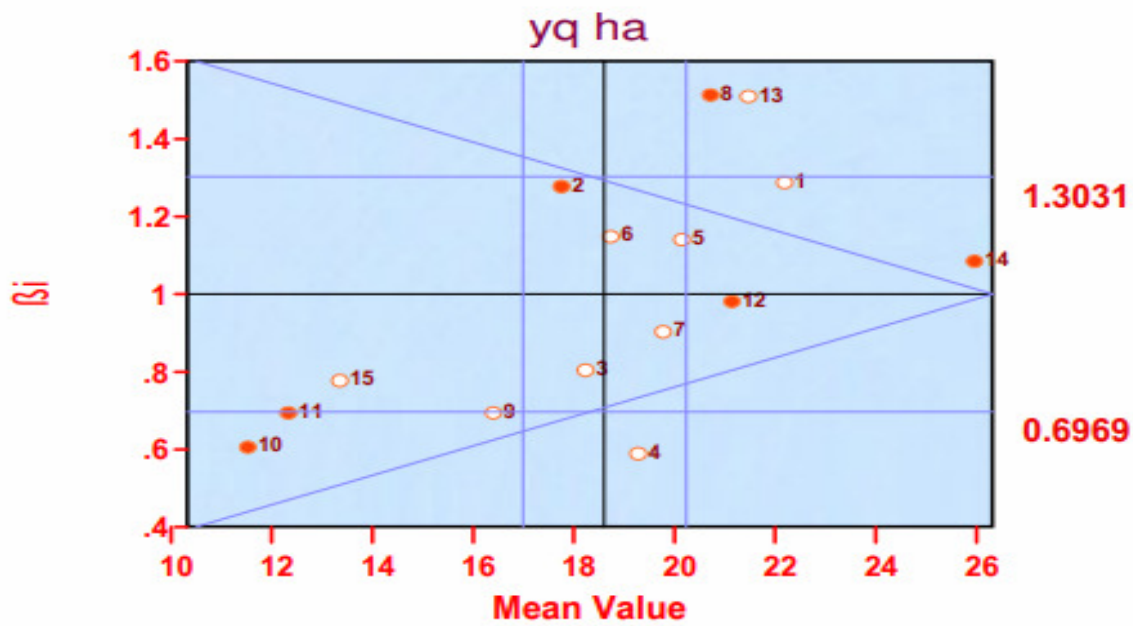


Fig. 2: Stability analysis for grain yield (q/ha) of 15 pigeonpea genotypes (G) and five environments (E) based on Mean value and Regression coefficient (bi).

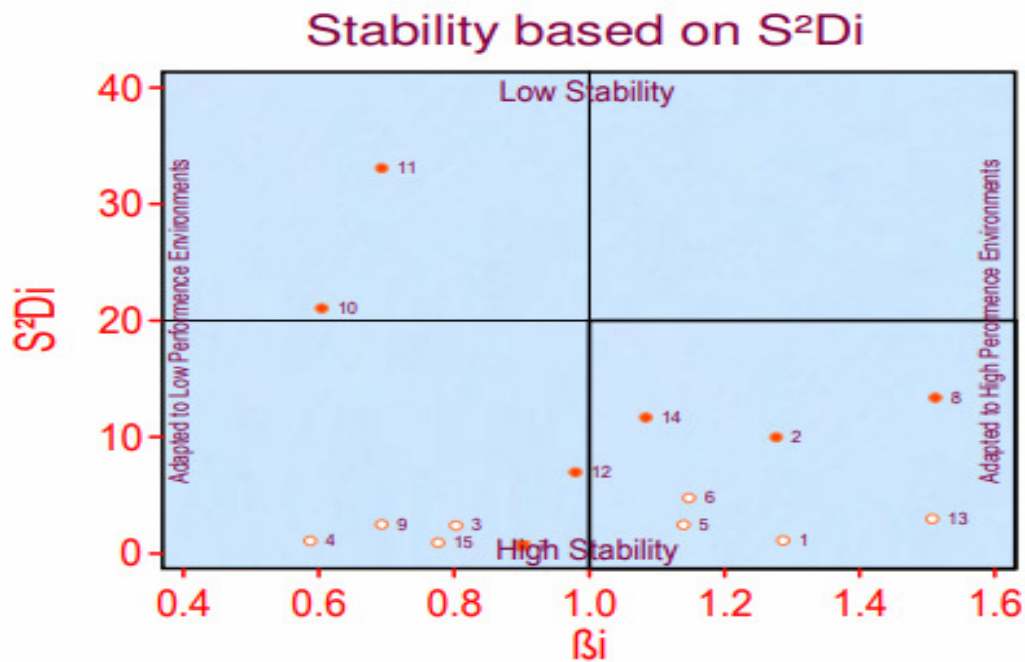


Fig. 3: Stability analysis for grain yield (q/ha) of 15 pigeonpea genotypes (G) and five environments (E) based on Deviation from regression (S²di) and Regression coefficient (bi).

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