



G × E Interaction and path analysis for yield and its attributing traits in advanced genotypes of pigeonpea [*Cajanus cajan* (L.) Millsp.]

Ramesh¹, S. Muniswamy^{1*}, Yamanura² and Bharathi¹

¹Agricultural Research Station, Aland Road, Kalaburagi-585101 (Karnataka), INDIA

²University of Agriculture Sciences, Krishi nagar, Dharwad - 580005 (Karnataka), INDIA

*Corresponding author. E-mail: muniswamygp@gmail.com

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Abstract: The present investigation was carried out during *kharif*-2012, 2013 and 2014 under rain fed condition at the Agricultural Research Station, Kalaburagi located in north eastern dry zone (Zone 2) of Karnataka, to know the stability and path analysis of the twenty genotypes of pigeonpea including check WRP-1. Highly significant differences among genotypes were observed for all the characters except primary branches. Environmental + (Genotype × Environment) interaction was significant for days to maturity, primary branch, pod bearing length, and seed yield per plant. The variance due to pooled deviation was highly significant for all the characters except for primary branches, pod length and number of seeds per pod which reflect the presence of sufficient genetic variability in the material. Out of 20 genotypes studied, RVK-275 (\bar{X} =38.713, b_i =1.7 and S^2_{di} = -9.67) and AKT-9913 (\bar{X} =43.397, b_i =2.86 and S^2_{di} = -7.42) were found to be a stable for seed yield and test weight, across the environments with good stability under rain fed conditions compared to local check. Path analysis revealed that days to flower initiation (3.942 and 1.123), days to maturity (1.493 and 0.960), primary branches (0.667 and 0.045), pod bearing length (1.153 and 0.394), number of pods per plant (0.661 and 0.463) and 100 seed weight (0.352 and 0.426) had the highest positive direct effect on grain yield both at genotypic and phenotypic level. For maximizing the grain yield per plant emphasis should be given in selection of such characters for further improvement in pigeonpea.

Keywords: Genotype × Environment (G × E), Path coefficient analysis, Pigeonpea, Stability

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is one of the grain legume crop of rainfed agriculture in the semi-arid tropics belongs to member of family *Fabaceae* and it is invariably cultivated as annual crop, it is an often cross pollinated crop reported to have 20% – 70% cross pollination (Saxena and Kumar, 2010). 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 a short-lived perennial shrub in which plants may grow for about five years and turn into small trees. India is considered as the native of pigeonpea (Vander and Messen, 1980) because of its natural genetic variability available in the local germplasm and the presence of its wild relatives in the country. Pigeonpea is the important grain legume which occupies a major place in dietary requirement. 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 × 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, 20 genotypes were evaluated in four environments. This helped in determining the stability for performance with respect to seed yield and yield attributes.

Path coefficient analysis is an important tool for plant breeder in partitioning the correlation coefficients into direct and indirect effects of independent variables on dependent variable *i.e.* seed yield. 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. With this back ground the present study was undertaken under rain fed situation in three Environment to identify stable genotypes and direct and indirect effects of Pigeonpea for seed yield and its component traits.

MATERIALS AND METHODS

The present experiment material comprised of 20 genotypes of pigeonpea received from Indian Institute

Table 1. Pooled MSS values for different quantitative traits over three environments.

Traits	Varieties	Env + (Var x Env)	Environments	Varieties x Environment	Varieties x En- vironment.(Lin)	pooled deviation
Days to flower initiation	344.16**	156.48**	1431.67**	89.36*	143.71**	33.26**
Days to 50 % flowering	363.85**	137.06**	1122.05**	85.23**	141.344**	27.65 **
Days to 80% pod maturity	315.34**	96.625	21.8	100.56	136.23*	61.64 **
Plant height (cm)	621.11**	1237.91**	21613.70**	165.51	207.16	117.65**
Primary branches	4.33	5.826	21.56*	4.99	6.02	3.773
Secondary branches	8.35*	10.242**	115.38**	4.71	6.15	3.103 **
Pod bearing length (cm)	139.79*	61.918	249.97*	55.18	55.97	51.66 **
Number of seeds per pod	0.36**	0.440**	7.49**	0.068*	0.11 **	0.025
Pod length (cm)	0.36**	0.839**	14.74**	0.108	0.13	0.081
Number of pods per plant	1705.61**	894.67**	2479.30**	811.27*	1301.92**	304.58**
Yield per plant (gm)	200.28**	96.49	499.57**	75.29	999.14**	62.80 **
100 seed weight (gm)	7.84**	0.997**	0.025	1.048**	0.05	0.235 **

*, ** significant at 5% and 1% level respectively

of Pulses Research, Kanpur. The trials were conducted in a randomized block design with two replications in three seasons *viz.*, *kharif*-2012, 2013 and 2014 grown under rain fed condition. The plot size of between plants two rows each with 4m length was followed with spacing of 75 cm between rows and 25 cm between the plants. Observations were recorded on five randomly selected plants in each replication in each environment in respect of 12 different metric characters *viz.*, days to flower initiation, days to 50 per cent flowering, days to 80 per cent pod maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, pod bearing length (cm), number of pods per plant, number of seeds per pod, pod length (cm), 100- seed weight (g) and seed yield per plant (g). Stability analysis was carried out by using the stability model proposed by Eberhart and Russell (1966), path coefficient analysis was carried out as per principle given by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Variance due to Genotype × Environment found significant for days to flower initiation, days to 50% flowering, number of seeds per pod, number of pods per plant and 100 seed weight. Significant Genotype × Environment interaction for seed yield and other traits has also been reported earlier (Manivel *et al.*, 1999). Analysis of variance for stability showed significant differences among the genotypes under study (Table 1). Mean sums of squares due to varieties found highly significant for all characters studied except primary branches. Mean sums of square due to environments found significant for all characters studied except days to 80% maturity and 100 seed weight. The variance due to Genotype × Environment (Linear) showed non significant differences for all most all the traits except days to flower initiation, days to 50 % flowering, days to 80 % pod maturity, number of seeds per pod, number of pods per plant and yield per plant indicating the absence of genetic differences among varieties for re-

gression on environmental indices and thus the further predication of genotypes would be difficult for these traits. Environmental + (Genotype × Environment) interaction was significant for days to maturity, primary branch, pod bearing length, and seed yield per plant. The characters having significant environmental + (Genotype × Environmental) were considered for stability analysis. Hence, a total of four out of twelve characters were subjected for stability analysis. The magnitude of Genotype × Environment component was greater than non-linear component for 100 seed weight indicating its major role in the expression of the trait and the performance of the genotypes for seed yield may be predicted across the environment with great precision (Kuchanur *et al.*, 2008). The variance due to pooled deviation was highly significant for all the characters except for primary branches, pod length and number of seeds per pod which reflect considerable genetic diversity in the material. In the present study the stability was assessed by the parameters suggested by Eberhart and Russel (1966).

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. The genotypes, RVK-275 (\bar{X} =38.713, b_i =1.7 and S^2_{di} = -9.67) and AKT-9913 (\bar{X} =43.397, b_i =2.86 and S^2_{di} = -7.42) had high mean, regression value around unity and minimum deviation from regression for the character seed yield per plant and test weight. Therefore these genotypes had not only better yield but also stable performance across the environments, while primary branches and plant height of the genotypes BDN-2008-1 JKM-7 and WRP-1 had shown the more mean value but had b_i around 1 with non significant S^2_{di} value this reveals that this genotype can perform well under the unfavorable condition. BDN-2008-1, ICP-4575 and ICP-8840 had high mean, regression value around unity and minimum deviation from regression. Therefore these genotypes had stable for

Table 2. Mean and stability parameters in 20 genotypes of pigeonpea.

Traits	Days to flower initiation			Days to 50% flowering			Days to maturity			Plant height (cm)		
	Mean	bi	S ² di	Mean	bi	S ² di	Mean	bi	S ² di	Mean	bi	S ² di
PUSA2001	73.00	1.20	7.49	79.00	1.09	-1.38	135.67	1.40	214.67	116.33	1.05	12.58
JKM189	95.83	1.46	4.25	106.50	1.87	69.82	151.33	-2.36	-3.23	141.22	1.41	46.73
BDN-2008-1	96.33	1.89	-2.89	100.83	1.92	25.21	151.83	-1.24	114.09	132.11	1.40	181.26
JKM-7	107.50	0.94	41.39	114.67	1.17	7.39	165.17	-2.34	0.00	159.58	0.63	213.26
ICP 11477	82.00	-0.76	0.21	85.83	-0.84	-2.78	132.83	23.74	13.47	133.11	0.67	53.70
ICP 13579	114.17	1.29	104.03	120.00	1.53	61.25	168.17	-4.95	9.43	129.50	0.88	84.30
ICP 995	96.00	1.63	8.87	102.67	1.86	2.92	154.00	-3.58	10.86	131.17	0.95	-2.43
ICP 4575	93.00	1.61	-3.18	101.17	1.37	-2.43	151.17	-6.12	2.18	118.00	1.52	21.32
ICP 14471	77.83	2.02	79.87	84.83	2.29	236.31	138.17	-1.03	137.61	110.72	1.55	202.22
AKT 9913	92.83	0.77	3.88	100.83	0.54	0.51	153.00	3.97	7.95	132.56	1.01	-14.55
ICP 348	96.67	1.28	17.82	102.67	1.20	25.37	153.50	3.90	72.13	117.28	1.19	25.56
ICP 7366	83.00	-0.16	12.52	87.17	-0.30	1.97	132.50	13.00	196.59	104.08	0.68	-15.16
ICP 8840	102.17	1.40	-2.84	107.83	1.40	-1.82	158.00	-2.45	47.14	137.22	0.93	219.71
RVK 275	102.00	-0.22	29.28	107.67	-0.34	-2.73	158.00	1.44	92.72	144.00	0.66	219.94
BENNUR LOCAL	89.00	0.08	41.12	93.00	-0.02	33.39	142.67	5.32	143.71	123.47	0.99	228.24
RVK 285	101.50	0.50	35.35	106.17	0.42	12.98	158.00	-0.87	-2.89	150.00	1.29	-1.60
BDN 2008-12	92.33	-1.14	37.31	97.50	-1.51	-2.33	147.83	12.34	117.50	127.92	0.50	89.92
JSA 59	109.75	1.91	57.44	115.83	2.20	13.27	163.58	-10.42	-2.33	151.83	0.90	260.68
BDN 711	90.83	2.79	128.30	97.08	2.69	18.10	151.75	-6.85	-3.04	124.08	0.77	149.50
WRP-1 (Ch)	82.67	1.50	-2.13	89.00	1.45	-2.88	145.83	-2.89	-0.27	117.06	1.02	71.15
Population mean	93.921			100.013			150.65			130.062		

Contd.

Table 2. Mean and stability parameters in 20 genotypes of pigeonpea.

Traits	Primary branches			Secondary Branches			Pod bearing length (cm)			Number of seeds /pod		
	Mean	bi	S ² di	Mean	bi	S ² di	Mean	bi	S ² di	Mean	bi	S ² di
PUSA2001	10.06	0.00	-2.08	2.945	-0.08	2.31	29.417	-1.31	34.81	4.557	0.63	-0.04
JKM189	11.39	-0.09	9.27	3.443	0.3	1.49	38.75	2.88	21.46	4.112	1.26	0.01
BDN-2008-1	10.28	2.19	-0.38	5.417	1.12	5.14	40.055	0.08	93.61	4.723	0.63	-0.04
JKM-7	11.56	1.33	-3.43	3.662	-0.27	2.6	35.833	2.99	72.45	4.333	0.94	-0.04
ICP 11477	9.67	0.87	-1.39	3.055	1.73	9.37	37.082	0.4	13.71	4.612	1.73	-0.04
ICP 13579	10.89	1.33	-1.15	6.057	1.97	-0.08	34.495	3.25	-5.01	4.805	0.86	0.19
ICP 995	9.67	1.42	-3.43	4.702	1.62	3.01	31.945	2.78	-13.8	4.0	0.71	-0.03
ICP 4575	13.50	5.52	34.70	4.945	1.34	0.23	22.972	1	-10.07	3.332	0.7	-0.03
ICP 14471	8.61	1.91	-0.42	2.643	0.86	3.08	26.555	1.69	100.55	4.083	0.94	-0.02
AKT 9913	10.61	-1.23	-2.75	4.777	0.94	-0.63	40.445	1.36	19.19	4.36	0.79	-0.03
ICP 348	11.50	3.06	-3.41	6.833	1.15	11.79	29.612	-0.17	74.79	3.972	0.63	-0.03
ICP 7366	9.72	-1.62	-3.46	1.115	-0.36	0.19	24.888	-1.31	2.21	3.805	1.34	0.01
ICP 8840	11.06	2.24	-3.24	7.233	2.2	-0.63	35.943	1.34	27.14	4.057	1.1	-0.04
RVK 275	12.40	2.09	3.19	7.002	1.3	0.09	27.193	3.11	-9.98	4.557	1.1	0.02
BENNUR LOCAL	10.28	-0.81	-2.83	4.835	1.49	8.75	44.388	0.13	-13.97	4.333	0.94	-0.04
RVK 285	8.95	0.55	-1.84	5.608	1.51	-0.63	43.112	0.03	-14	4.417	0.95	-0.03
BDN 2008-12	9.78	-0.64	-3.25	6.057	1.46	-0.51	42.973	0.55	-7.36	4.333	1.18	-0.03
JSA 59	9.17	0.39	-3.31	4.363	0.83	1.59	24.638	1.43	189.45	4.11	1.85	-0.04
BDN 711	9.64	-0.30	-3.49	3.667	0.25	-0.3	28.25	1.26	120.17	4.5	1.41	-0.04
WRP-1 (Ch)	10.11	1.81	-1.60	2.388	0.64	2.56	38.998	-1.51	56.88	4.028	0.31	-0.03
Population mean	10.441			4.54			33.88			4.25		

Contd.

Contd.

Traits	Pod length (cm)			Number of pods/plant			Seed yield per plant(g)			100 seed weight (g)		
	Mean	bi	S ² di	Mean	bi	S ² di	Mean	bi	S ² di	Mean	bi	S ² di
Genotypes												
PUSA2001	4.893	1.22	0.03	109.722	-1.73	-65.25	24.435	-0.18	-2.79	9.605	-20.63	0.31
JKM189	4.243	0.9	0	123.668	0.95	160.92	26.9	1.07	84.07	10.48	17.16	0.6
BDN-2008-1	4.862	1.56	-0.05	139.5	3.35	1361.49	41.342	3	445.17	8.89	-1.02	0.24
JKM-7	4.465	1.05	0.19	146.722	0.2	-84.64	28.372	0.51	2.77	8.453	-10.99	0.18
ICP 11477	4.65	0.64	-0.01	136.943	1.73	-45.23	25.552	0.44	-9.7	8.46	-47.09	0.09
ICP 13579	5.005	1.03	-0.05	150.943	1.66	-104.67	33.025	1.06	38.47	8.353	-7.13	-0.12
ICP 995	4.238	1.29	-0.01	138.833	3.73	-135.51	31.188	-0.11	1.51	7.41	4.46	0.11
ICP 4575	3.783	0.58	0.08	111.833	2.22	148.41	20.65	0.52	13.7	7.878	4.23	-0.07
ICP 14471	4.297	1.38	0.13	94.445	4.6	290.62	18.792	1.13	-9.71	8.58	-17.99	0.37
AKT 9913	4.277	1.02	0.12	167.167	0	289.36	43.397	2.86	-7.42	9.83	24.29	-0.1
ICP 348	4.048	0.84	0.2	120.667	2.87	362.4	30.8	1.8	37.41	8.343	-8.19	-0.13
ICP 7366	3.943	0.63	-0.05	90.833	0.01	-55.69	16.06	-0.83	-2.37	7.667	-31.93	0.03
ICP 8840	4.105	0.79	-0.05	169.943	2.1	-28.18	38.812	2.22	27.75	8.905	12.04	0.37
RVK 275	4.567	0.94	0.03	153.61	2.28	-145.22	38.713	1.7	-9.67	9.9	5.64	-0.13
BENNUR LOCAL	4.282	1.01	0.02	138.61	0.28	131.22	43.35	-0.09	74.34	9.202	3.92	-0.12
RVK 285	4.578	1.13	0	140.167	2.23	1010.89	36.947	2.56	49.95	11.323	27.85	0.32
BDN 2008-12	4.472	0.51	-0.01	161.833	0.06	482.5	37.518	2.41	253.26	8.722	19.56	-0.13
JSA 59	5.028	1.52	0.07	94.667	-5.43	-144.87	24.943	0.8	-10.18	14.817	81.52	0.43
BDN 711	4.553	0.86	0.06	121.472	-2.25	-143.2	32.722	1.21	-7.31	9.418	-27.99	-0.09
WRP-1 (Ch)	4.288	1.13	-0.04	116.112	1.16	-129.76	37.585	-2.09	-8.56	9.822	-7.77	-0.13
Population mean	4.43			131.39			31.555			9.303		

days to flower initiation RVK-275 and AKT-9913 were found to be a stable for seed yield per plant and test weight, across the environments with good stability under rainfed conditions.

The path coefficient analysis also measures the comparative significance of causal factors involved. This is simply a standardized partial regression analysis, wherein total correlation value is sub divided into causal scheme. The results of genotypic and phenotypic path coefficient analysis for twelve quantitative characters are presented in (Table 3).

High rate (between 0.30 to 0.99) of positive direct effects were observed at genotypic and phenotypic level by means of the traits *viz.* days to flower initiation (3.942 and 1.123), days to maturity (1.493 and 0.960), primary branches (0.667 and 0.045), pod bearing length (1.153 and 0.394), number of pods per plant (0.661 and 0.463) and 100 seed weight (0.352 and 0.426) both at genotypic and phenotypic level. It indicates that, emphasis can be laid on these six characters during selection of genotypes for improvement of yield. Thanki *et al.* (2010), Chandirakala and Subbaraman (2010) and Bhadru (2011) reported positive direct effect on grain yield with days to maturity, number of pods per plant, number of seeds per pod and 100 seed weight. While days to maturity (-5.203 and -1.907) and plant height (-0.746 and -0.285) had negative direct effect on seed yield both at genotypic and phenotypic levels while secondary branches (-0.383) and number of seeds per pod (-1.164) at genotypic level and pod length at phenotypic level had negative direct effect on seed yield registered negative direct effects on yield both at genotypic and phenotypic level, indicating this trait is not the criteria for yield improvement. Bhadru (2011) observed negative direct effect of days maturity. The highest indirect effects of days to flower initiation *via* days to 50% flowering, days to maturity, plant height and 100 seed weight, similarly days to maturity *via* plant height both at genotypic and phenotypic level. Indirect contribution of days to flower initiation through days to 50% flowering, days to maturity, plant height and 100 seed weight. In plant breeding, it is very difficult to have complete knowledge of all component traits of yield. The residual effect permits precise explanation about the pattern of interaction of other possible components of yield. In other words, residual effect measures the role of other possible independent variables was not included in the study on the dependant variable. Relatively low residual values of was observed at genotypic and phenotypic level respectively. It indicates the low unexplained variation and characters included in the present study accounted for most of the variation.

Conclusion

From the present study it can be concluded that genotypes 'RVK-275 and AKT-9913' were found to be a

Table 3. Direct and indirect effects of quantitative characters on seed yield per plant at genotypic and phenotypic level.

Characters	Genotypic	Phenotypic	Days to flower initiation	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches	Secondary branches	Pod bearing length (cm)	Number of seeds /pod	Pod length (cm)	Number of pods/plant	100 seed weight (g)
Days to flower initiation	3.942	1.123	1.411	-5.152	1.411	-0.545	0.285	-0.251	0.073	-0.193	0.343	0.299	0.106
Days to 50% flowering	3.903	1.110	1.434	-5.203	1.434	-0.546	0.327	-0.237	0.048	-0.119	0.283	0.280	0.108
Days to maturity	3.726	1.056	1.493	-4.995	1.493	-0.533	0.300	-0.250	0.056	-0.180	0.348	0.300	0.113
Plant height (cm)	2.883	0.794	1.067	-3.809	1.067	-0.746	0.120	-0.146	0.343	-0.416	0.533	0.311	0.186
Primary branches	1.687	0.286	0.671	-2.555	0.671	-0.135	0.667	-0.215	-0.177	0.560	-0.543	0.277	-0.128
Secondary Branches	2.579	0.684	0.973	-3.215	0.973	-0.285	0.374	-0.383	0.240	-0.155	0.039	0.456	0.012
Pod bearing length (cm)	0.248	0.093	0.073	-0.216	0.073	-0.222	-0.102	-0.080	1.153	-0.543	0.056	0.447	-0.005
Number of seeds / pod	0.654	0.154	0.231	-0.530	0.231	-0.266	-0.321	-0.051	0.538	-1.164	1.037	0.332	0.051
Pod length (cm)	1.116	0.273	0.429	-1.215	0.429	-0.328	-0.299	-0.012	0.053	-0.996	1.211	0.061	0.188
Number of pods/ plant	1.781	0.467	0.677	-2.201	0.677	-0.351	0.279	-0.265	0.781	-0.586	0.111	0.661	-0.072
100 seed weight (g)	1.173	0.330	0.474	-1.582	0.474	-0.388	-0.240	-0.013	-0.016	-0.166	0.638	-0.134	0.357
			0.304	-0.570	0.304	-0.144	-0.010	0.004	0.009	0.052	-0.211	-0.076	0.426

Genotypic Residual = 0.120; Phenotypic Residual = 0.181

stable for seed yield and test weight with under rainfed conditions. These genotypes can be recommended for general cultivation and could be used in breeding programme to develop high yielding genotypes. Path analysis revealed that days to flower initiation, days to maturity, pod bearing length, primary branches, number of pods per plant and 100 seed weight were emerged as most important characters for the improvement of seed yield. Hence, emphasis should be placed on these characters while breeding for high yield of pigeonpea.

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