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Research Article

Stability analysis for yield and yield components over seasons in cowpea [*Vigna unguiculata* L. (Walp.)]

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Abstract:
Twenty diverse genotypes including one local check (C-152) of cowpea were evaluated over three seasons to study the stability parameters *viz*., regression coefficient (bi) and mean square deviations (s^2di) from linear regression along with *per se* performance for five yield related traits. Variances due to genotype, environment, genotype x environment, environment + (genotype x environment), environment (linear) were significant for pods per plant and seed yield per plant. Based on the stability analysis, the genotype IL3 was found stable across the seasons for test weight. Genotypes such as M17, Goa local and Bailhongal local were stable and superior across all the environments for seed yield.

Key Words: Cowpea, regression coefficient, genotype, stability etc.

Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) is a valuable warm season pulse crop grown for its grain, vegetable and also for fodder purpose in both tropical and subtropical zones of Africa, Asia and U.S.A. Although it is considered as a multi-season crop, its productivity is comparatively high in *kharif* season compared to other seasons as the crop will suffer from water deficit at the physiological maturity in summer. Phenotypically stable genotypes are of great importance because the environmental condition vary from season to season and year to year. Wide adaptation to a particular environment and consistent performance of recommended varieties/ hybrids are very important for successful cultivation of cowpea. Although many varieties are recommended for the cultivation, the information on the stability is lacking. In the present study, some important genotypes of cowpea have been evaluated for G x E interactions for identifying the high yielding stable genotypes for cultivation and for their utilization in breeding programme.

Materials and methods

The study consisted of twenty genotypes of cowpea *viz,*. eight mutants (M-3, M-8, M-12, M-14, M-17, M-19, M-22, M-23), two local landraces (Bailhongal local and Goa local), two released varieties (V-118 and C-152), three backcross derivatives (IL-2, IL-3 and IL-4), one tropical *vigna* variety (TVX-944E), one IPS (Individual Plant selection in F_2) progeny (DC-14), one germplasm collection (C-70), and one recombinant line (T4) were sown in a randomized complete design with three replications during late *kharif* 2003, summer and *kharif* seasons of 2004 at the Botany garden located at University of Agricultural Sciences Dharwad.. Each plot comprised 4 lines of 4 m length. The spacing adopted between rows and plants within a row was 45 cm and 20 cm respectively. Data were recorded on five characters *viz.,* pods per plant, pod length, seeds per pod, test weight and seed yield per plant from five random normal and healthy plants and the mean values were computed and were subjected to genotype x environment interaction as per the procedure suggested by Eberhart and Russel (1966).

Results and discussion

The pooled analysis of variance (Table 1) revealed that mean sum of squares due to genotypes and environments were significant for the traits *viz*., pods per plant, pod length, test weight and seed yield per plant indicating the presence of variability among the genotype and environments for these traits. Thiyagarajan and Rajasekaran (1989) also had the same opinion on these traits. The G x E interaction was significant for pods per plant and seed yield per plant indicating the differential response of the genotypes in different seasons for these characters. The mean sum of squares for pooled deviations was significant against pooled error for all the characters except clusters per plant. It indicates the greater role of unpredictable component towards the differences in stability of the genotypes. Krishna Prasad *et al.* (1994), Manivannan et al. (1999) and Pan *et al.* (2001) also reported such preponderance of non-linear components of genotype x environment interaction in early pea and garden pea respectively.

According to Eberhart and Russel (1966) an ideally adopted genotype would be the one having higher mean value, regression coefficient, bi=1 near unity with least deviation from regression $s^2d_{i=}0$. In the present study, the genotypes M3, V-118, M17, M19, M22 and Bailhongal local and T4 recorded higher mean value, regression coefficient nearer to unity with non-significant deviation from regression coefficient indicated that these genotypes are stable across all the environments (Table 2). A high degree of predictability for pods per plant, pod length, 100-grain weight and harvest index was reported by Birari *et al*. (1993) in their study involving seven promising genotypes.

The genotypes IL4, Goa local and IL2 had higher mean pod length with bi value more than unity and non-significant deviation from bi values indicated that they are specially adapted to favorable environments. Although the genotypes M3 and DC14 had higher mean value and regression coefficient lesser than unity but significant S^2di values indicate that these two genotypes are sensitive to all the environments with unpredictable performance. Eight genotypes (IL3, Goa local, C-70, IL4, C-152, IL2, M14 and Bailhongal local) recorded higher mean values compared to population mean, bi value more than unity and non-significant deviation from regression values indicating their suitability for favorable environments. The genotype M8 had bi value lesser than unity, non-significant S^2di value indicating its suitability for poor environments.

Out of twenty, five genotypes (TVX-944E, M3, Goa local, M8 and DC14) were identified as unpredictable in nature as indicated by their significant S^2di value. Only one genotype (IL3) was considered to be superior and stable in its expression over all the three environments as indicated by its higher mean value, bi value lesser than unity and non-significant deviation from regression coefficients.

With respect to seed yield, three genotypes (M17, Bailhongal local, Goa local) were considered to be more superior and stable across all the environments as indicated by their higher mean values, bi value lesser than unity and non-significant S^2di. However, the genotypes, M23, M22, M14, IL4 and M12 had higher mean seed yield and non-significant S^2di but bi value more than unity which indicate that these genotypes are suitable only for favorable environments.

The present study revealed that, M-17, Goa local and Bailhongal local were found stable with high mean yield and had average responses to the changes in environmental conditions. The genotypes M3, M23, M12 and IL3 were out yielder compared to the yield levels of check variety C-152. The genotype IL3 was stable with respect to test weight across all the season. Hence these genotypes should be further confirmed over locations and used in the future breeding programme for increased yield.

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Table 1. Pooled analysis of variance for six parameters under varied environments (over different seasons)

Traits	df.	Pods per plant	Pod length (cm)	Seeds per pod	Test weight (g)	Seed yield per plant (g)
Genotypes	19	24.36**	5.74**	2.02	85.35**	24.51*
Environment	2	117.05**	6.78**	8.99**	4.73**	221.87**
Genotypes x environment	38	6.15*	1.24	1.23	0.47	11.11*
Environment + (Genotypes x environment)	40	11.69**	1.52	1.62	0.69	21.64**
Environment (Linear)	1	234.10**	13.56**	17.98**	9.46**	443.73**
Genotype x Environment (Linear)	19	6.84	1.17	1.52	0.34	12.28
Pooled Deviation	20	5.19*	1.25**	0.90**	0.58**	9.44**
Pooled Error	114	8.18	1.08	1.22	0.65	4.07

*Significance at 5 % probability level, ** Significance at 1 % probability level

Table 2. Stability analysis for Pods per plant and Pod length of genotypes over three seasons

Genotypes	Pods per plant			Pod length (cm)			Seeds per pod			Test Weight (g)			Seed yield per plant (g)		
	Mean	bi	S^2d	Mean	bi	S^2d	Mean	bi	S^2d	Mean	bi	S^2d	Mean	bi	S^2d
TVX-944E	11.94	-0.12	5.17	13.49	-0.15	-0.34	10.73	0.60	-0.40	8.81	0.84	0.77*	9.97	-0.18	2.58
IL4	11.62	1.51	10.78*	15.58	2.22	-0.34	12.52	2.75	0.76	8.77	2.37	-0.11	16.51	1.26	0.09
M3	12.20	1.10	-2.68	16.49	-0.28	9.20*	12.85	-0.30	1.79*	12.27	2.10	0.83*	17.82	1.11	13.98**
V-118	17.23	1.14	0.74	13.53	0.70	-0.34	11.57	1.39	-0.35	9.94	1.18	-0.20	14.18	0.29	0.27
M17	13.02	1.11	-2.70	14.56	-0.28	-0.26	11.43	0.50	-0.40	11.55	1.55	0.88	14.97	0.83	-1.04
M19	14.13	1.28	-0.28	14.21	1.48	0.07	11.76	-0.15	-0.17	9.58	1.26	0.19	13.50	1.18	-1.31
M23	16.58	0.41	-1.35	13.25	1.31	-0.31	11.99	-0.40	-0.41	9.59	0.36	-0.10	18.90	1.44	-1.14
GL	8.18	0.42	0.33	17.38	2.17	-0.19	12.24	2.20	0.69	27.08	2.16	2.24**	15.12	0.87	-1.23
IL3	10.52	0.22	5.19	16.98	3.87	1.06*	12.93	3.33	-0.39	20.46	-0.47	0.16	16.51	0.45	8.18**
C-152#	10.67	0.92	10.60*	14.72	2.81	2.37**	13.07	1.72	4.21	9.58	0.69	-0.04	15.59	0.89	90.53**
IL2	11.27	1.37	5.79	15.98	1.67	-0.20	13.32	2.11	0.53	9.54	0.71	-0.14	12.82	0.91	21.38**
M8	10.64	1.65	3.11	13.58	0.57	1.05*	12.93	-0.36	-0.08	9.67	0.31	1.26*	11.66	1.30	4.53*
T4	12.19	0.90	-2.53	13.54	-0.11	-0.23	11.70	0.19	0.52	10.33	-0.14	0.59	14.97	0.88	6.99*
M12	15.71	1.58	16.21**	14.66	0.47	0.27	11.36	-0.40	-0.32	11.90	1.58	0.47	15.86	1.50	3.53
M22	14.08	1.08	3.02	12.66	0.95	-0.31	10.18	-0.34	-0.19	9.65	0.52	-0.05	15.23	1.66	-1.27
KM-5	6.22	-1.04*	-2.43	14.14	0.52	3.34**	12.10	-0.77	2.32**	11.38	0.60	-0.06	7.36	-0.62*	-1.29
M14	13.62	1.74	-1.35	14.38	0.04	0.02	12.30	1.28	-0.38	10.25	0.75	-0.16	15.06	1.46	1.81
Bailhongal local	12.71	1.25	-2.51	13.94	2.89	0.58	12.63	3.00	-0.17	9.35	0.42	-0.02	14.49	0.94	-0.61
C-70	7.51	0.91	6.66	15.35	0.71	0.90	12.97	2.09	-0.21	11.49	2.72	-0.20	9.92	0.76	5.69*
DC14	9.90	2.57	-2.56	16.94	-1.55	1.49*	12.18	1.56	2.44**	25.06	0.49	0.90*	17.31	3.06	9.92**
Population mean	12.10			14.77			12.14			12.32			14.39		
CV	23.33			7.06			9.32			5.83			18.39		
SEm	2.18			0.86			0.93			0.58			2.44		

#- Local check, *Significance at 5 % probability level, ** Significance at 1 % probability level