Phenotypic Stability Analysis in Blackgram [*Vigna mungo* (L.) Hepper] Using Eberhart and Russell and AMMI Models

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ABSTRACT

Twelve blackgram genotypes were evaluated for several characters over six environments (3 sowing dates with 2 fertility levels). The analysis of variance of Eberhart and Russell (1966) indicated that GXE (linear) was significant for characters *viz.,* days to maturity, pod length, number of seeds per pod and seed yield per plant under study and that genotypes differed significantly. AMMI is a useful tool for interpreting genotype x environment interaction in multi-environment trials. Among the AMMI components first four IPCA axes were explained most of the portion of G X E interaction than other IPCA axis for the five characters under study. According to AMMI analysis the genotypes like the genotypes 1 and 6 (plant height); 5, 11, 12 and 8 (number of pods per plant); 5, 9 and 10 (number of seeds per pod); 2, 5 and 3 (for 1000 seed weight); 1, 3 and 7 (seed yield per plant); 12,5 and 3 (protein content) are more stable because they are having IPCA score near zero i.e. they show less interaction with environments. According to Eberhart and Russell the genotypes like 6 and 7 (plant height); 2, 4 and 10 (number of pods per plant); 6 and 7 (number of seeds per pod); 4, 5,11 and 12 (1000 seed weight); 6 and 10 (seed yield per plant); 4,5,9 and 10 (protein content) showed desirable performance.

Key words : AMMI, Blackgram, Stability

Blackgram is an important pulse crop cultivated round the year in almost all parts of India. In Andhra Pradesh, it is grown in 4.21 lakh hectares, with a productivity of 695 kg/ha. The analysis of variance (ANOVA) is useful for identifying and testing sources of variability, it provides no insight into the particular pattern of the underlying interaction. The ANOVA model is additive and effectively describes the main (additive) effects, while the interaction (residual from the additive model) is non-additive and requires other techniques, such as principal component analysis (PCA) to identify interaction patterns. Thus ANOVA and PCA models combined to constitute the Additive Main effects and Multiplicative Interaction (AMMI) model (Zobel *et al.,* 1988).

MATERIAL AND METHODS

Twelve black gram genotypes namely, AKU-7, LBG-752, T-9, LBG-20, LBG-17, PBG-1, PBG-107, MBG-162, MBG-207, LBG-648, LBG-623 and LBG-645 were sown during *rabi,* 2006 (six environments) three sowing dates i.e., 15-09-2006, 30-09-2006 and 15-10-2006; with two fertility levels i.e 20kg N: 50kg P ha^{-1} (only basal) and 20kg N: 50kg P ha^{-1} (basal) + 20kg N ha^{-1} (top dressing) in each date of sowing, thus providing six environments at Agricultural Research Station (ARS) Madhira, Khammam district in Andhra Pradesh. Material was grown in randomized block design with three replications with 4 rows of 4m length per genotype per replication. An inter-and intra-row spacing of 30 cm and 10 cm was practiced. The observations recorded on 11 characters were given in Table 2. Stability parameters were analyzed using regression model (Eberhart and Russell, 1966) and AMMI model (Gauch and Zobel, 1988). According to Eberhart and Russell the genotype with high mean, unit regression coefficient and non-significant deviation from regression was considered to be stable over environments. According to AMMI model, when one interaction PCA axis accounts for most of G x E, a feature of AMMI model is the biplot procedure in which genotypes and environments taking mean values on abscissa and IPCA 1 scores on ordinate are plotted on the same diagram, facilitating inference about specific interactions as magnitude of IPCA 1 values of individual genotypes and environments (Sharma *et al.*, 1998).The biplot of the first two IPCA axis demonstrates the relative magnitude of the GE interaction effect is determined by the product of the correct PCA scores, cultivars or environments with a small GE interaction will have small scores and be close to the centre of the axis *i.e.*, they are stable across environments (Bahman Shafi *et al.,*1992)

RESULTS AND DISCUSSION

The pooled analysis of variance (Table 1) revealed that mean sum of squares due to genotypes

was highly significant for all characters indicating, presence of substantial variability among the genotypes. The mean sum of squares due to environment was also highly significant for all characters except for days to 50% of flowering and days to maturity, indicating variability among environments.

The genotype x environment was non-significant for all the characters except for number of seeds per pod, seed yield per plant and yield kg/plot when tested against both pooled error and pooled deviation. indicating non-differential response of the genotypes in different environments. While genotype - environment (linear) component of interaction was significant for all characters except for days to 50% flowering, plant height, number of primary branches per plant, number of pods per plant and yield kg/plot, indicating linear response of genotypes to changing environment. The pooled deviation was highly significant for all the characters except days to maturity, pod length, number of seeds per pod, seed yield per plant and 1000 seed weight indicating that non-linear component of genotype-environment interaction was also predominant for all the characters studied except for days to maturity, pod length, number of seeds per pod, seed yield per plant and 1000 seed weight.

The stability parameters mean, regression coefficient and deviation from regression of each genotype were calculated and presented (Table 2). The linear regression was regarded as measure of responsiveness and S^2di as measure of stability. A genotype with non-significant S^2di was considered as stable.

As revealed from Table 6, incase of seed yield per plant five genotypes (AKU-7, T-9, PBG-1, PBG-107 and LBG-648) did not interact with environments as indicated by both bi and S^2di, being non-significant. Therefore, prediction of performance was perfect in case of these genotypes. Out of these genotypes, PBG-1 had highest mean value. LBG-645 genotype possessed higher mean value and exhibited significant higher bi value leading to the inference that it showed below average stability and is suitable for high yielding environments.

Based on stability parameters, AKU-7 and T-9 were found to be stable for days to 50% flowering and days to maturity with lower mean values. Among the twelve genotypes PBG-1 and PBG-107 were identified as stable genotypes for plant height, while for number of primary branches per plant the stable genotypes are LBG-645 and MBG-207. Among twelve genotypes, LBG-20, PBG-1 and PBG-107 were found to be stable for seeds per pod. While,

LBG-20, LBG-17, LBG-623 and LBG-645 were found to be stable for 1000 seed weight.

MBG-207 had higher number of pods per plant along with regression coefficient (bi) approaching unity and non-significant deviation from regression (S^2 di), thus turned out stable for this trait. This indicated that the stability of various components traits might be responsible for observed stability of seed yield per plant. Manikannan *et al.* (2002) also arrived at similar conclusion regarding stability of seed yield.

For plant height, the GXE interaction was significant and was further partitioned into AMMI components with the contribution of 56.49, 28.83, 9.04 and 4.72% to the total GXE interaction variance. The first AMMI component representing interaction pattern were significant and contributed 56.49% of the interaction component with 27.27% of the degrees of freedom for GXE interaction. By AMMI1 (Fig. 1) the genotypes 6 and 8 are specifically adapted to certain environments. Genotype 8 showed interaction with environment IV and the genotypes 3, 5, 6 and 10 are stable genotypes because their IPCA1 score is near to zero. By AMMI 2 interaction biplot (Fig. 2) the genotypes 1 and 6 were identified as most stable ones because they are situated close to the center of IPCA axis. The environments I, V and VI were more discriminating ones as indicated by the longest distance between their marker and origin.

For number of pods per plant, AMMI analysis of variance indicated that the genotype main effect, environmental additive effect and GXE (non-additive effect) were significant and have effects accounted 88.02, 2.43 and 9.54% of the total variance respectively. In the Table 3 among the 4 IPCA axes, the first 3 IPCA axes declared significant by an F-test with contribution of 55.48, 24.58, 14.12 and 5.82% to the total GXE interaction variance. According to AMMI1 (Fig. 3) biplot genotypes 1,2,10 and 11 generally adaptable to all environments and more stable. Genotypes like 7, 9, 6 and 3 had high mean and large value of $IPCA_1$ score hence specifically adapted to certain environments. By AMMI 2 (Fig 4) the genotypes 5, 11,12 and 8 are more stable over environments as they are close to the center of IPCA axis.

For number of seeds per pod, AMMI analysis of variance showed that the genotype main effect, environmental additive effect and GXE non-additive effect were significant with the contribution of 51.15%, 19.12% and 29.71% of the total variance, respectively. In this model, $IPCA_1$ explained 67.62% of the interaction SS (Table 3). The remaining $IPCA_2$,

$IPCA_3$ and $IPCA_4$ explained 16.42%, 10.61% and 3.26% of the interaction sum of squares, respectively. The model captured 91.23% of the treatment SS, using 71 degrees of freedom (df) 11 for genotypes, 5 for environments and 48 for $IPCA_1$ to $IPCA_4$. According to AMMI 1 (Fig 5) genotypes 5, 11, 3, 10 and 2 were suitable to specific environments. In AMMI 2 (Fig 6) biplot genotypes 5, 9 and 10 are stable across environments but $IPCA_2$ axis is non-significant for this trait.

For 1000-seed weight, AMMI analysis of variance showed that the genotype main effect, environmental additive effect and GXE non- additive effect were significant with the contribution of 69.92%, 11.79% and 18.28% of the total variance, respectively. In this model $IPCA_1$ explained 80.48% of the interaction SS (Table 3). The remaining $IPCA_2$, $IPCA_3$ and $IPCA_4$ explained 12.53%, 3.88% and 2.26% of the interaction SS, respectively. The model captured 84.54% of the treatment SS, using 71 degrees of freedom (df) 11 for genotypes, 5 for environments and 48 for $IPCA_1$ to $IPCA_4$. According to AMMI1 (Fig 7) genotypes 9, 2 and 11 are suitable to specific environments. In AMMI 2 (Fig 8) biplot genotypes 2, 5 and 3 are stable across environments.

For seed yield per plant, AMMI analysis of variance partitioned the treatment sum of squares into additive genotype and environment effects and non- additive GE interaction effects. These sources were all significant at the 0.01 probability level and accounted for 84.06, 2.99 and 12.93% of the treatment combinations SS respectively (Table 3). In its first interaction IPCA axis, this model captures more than half of the GE interaction SS (83.4%) in only 27.77% of the interaction degrees of freedom. The remaining two IPCA axis $IPCA_3$ and $IPCA_4$ are also significant but contributing less to the G X E interaction sum of squares. According to AMMI1 (Fig 9), genotypes 1, 4 and 5 are more stable because their IPCA scores are near to zero and genotypes 8, 9 and 10 are specially adapted to a particular environment. By AMMI 2 (Fig 10) stable genotypes are 1, 3 and 7.

For protein content, AMMI analysis of variance indicated that all the three sources *i.e.,* genotype main effect, environmental additive effect and GXE (non-additive) effects have significant effects and accounted for 63.46, 6.81 and 29.91% of the total variance, respectively indicating there by differential response of genotypes. In Table 3 showed that the $IPCA_1$ and $IPCA_2$ were significant and accounted for 54.55%, 25.77%, of the genotype x environment interaction sum of squares with 15 and 13 degrees of freedom. Whereas as, $IPCA_3$ and $IPCA_4$ explained 11.98% and 5.42% of the total GXE interaction sum of squares with 11 and 9 df respectively, but they are not significant. By AMMI1 (Fig 11) the genotypes 1,9,10 and 5 were stable over environments. Genotypes 7, 8and 6 had high mean and high IPCA score hence specifically adopted to certain environments. By AMMI 2 (Fig 12) genotypes like 12, 5 and 3 are more stable. Environments II, VI, and IV are discriminating ones. Crossa *et al.* (1991) in wheat conducted AMMI analysis and predicted the stability of genotypes on the basis of mean performance and the magnitude of $IPCA_1$ scores.

The results discussed here confirm that AMMI analysis with its biplot is a very useful tool in analyzing data. It explains comprehensively both the effects due to genotypes and environments and also their interaction patterns. ANOVA could explain only the genotypes and environments but not their interaction. AMMI partition the non-linear interaction component of genotype with environment interaction and also helps in having deeper insight into study of environmental contribution to GXE interaction as also pointed out by Zobel *et al.*, (1988).

By comparing these two models for five characters like plant height, number of pods per plant, number of seeds per pod, 1000 seed weight, seed yield per plant and protein content the results have shown that according to AMMI analyses the genotypes 1 and 6 (plant height); 5, 11,12 and 8 (number of pods per plant); 5, 9 and 10 (number of seeds per pod); 2, 5 and 3 (for 1000 seed weight); 1, 3 and 7 (seed yield per plant); 12, 5 and 3 (protein content) are more stable because they are having IPCA score near zero *i.e,* they show less interaction with environments. According to Eberhart and Russell the genotypes like 6 and 7 (plant height); 2, 4 and 10 (number of pods per plant); 6 and 7 (number of seeds per pod); 4, 5,11 and 12 (1000 seed weight); 6 and 10 (seed yield per plant); 4,5,9 and 10 (protein content) showed desirable performance.

In the pooled analysis of variance the genotype-environment interaction component was non-significant for plant height, number of pods per plant and protein content. Where as genotype - environment interaction (linear) component as per Eberhart and Russell (1966) was non- significant for plant height and number of pods per plant. But significant for number of seeds per pod, 1000 seed weight, seed yield per plant and protein content.

While in AMMI model IPCA 1 component significantly explained the genotype-environment interactions, in case of plant height (56.49%), number of pods per plant (55.48%), number of seeds

Table 1. Analysis of variance for stability (Eberhart and Russell, 1966) for 11 quantitative characters in blackgram [*Vigna mungo* (L.) Hepper] during *rabi*, 2006.

Source	df	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches / plant	No. of pods / plant	Pod length	No. of seeds / pod	Seed yield / plant	1000 seed weight	Yield kg / plot	Protein content
Genotype	11	103.2**++	186.7**++	150.0**++	0.65**++	79.3**++	0.7**++	0.8**	6.2**++	167.0**++	0.03**++	12.2**++
Environment	5	0.773	0.269	12.032*+	0.312**++	4.83*++	0.11**++	0.7**	0.49**++	61.9**++	0.01**++	2.89*++
Genotype x Environment	55	1.970	0.622	4.503	0.074	1.721	0.01	0.1**++	0.19**++	8.7**++	0.002+	1.1
Environment + (Genotype x Environment)	60	1.870	0.593	5.130	0.093*+	1.980	0.021**	0.1**++	0.21**++	13.1**++	0.003**++	1.2*+
Environment (Linear)	1	3.866	1.345	60.162**++	1.561**++	24.158**	0.557**	0.36**++	2.46**++	309.8**++	0.097**++	14.4**++
Genotype x Environment (Linear)	11	2.383	1.310**++	6.373	0.114	1.496	0.020*	0.2**++	0.59**++	30.7**++	0.002+	2.3*++
Pooled deviation	48	1.711**	0.413	3.699**	0.058**	1.629*	0.010	0.050	0.08	2.954	0.001*	0.7*
Pooled error	132	0.902	0.658	2.074	0.034	1.104	0.019	0.053	0.09	4.523	0.001	0.5

** = Significant at 1% probability level against pooled error   + = Significant at 5% probability level against pooled deviation

* = Significant at 5% probability level against pooled error   ++ = Significant at 1% probability level against pooled deviation

Table 2 . Estimates of stability parameters in blackgram [*Vigna mungo* (L.) Hepper]

S.No.	Genotype	Days to 50% flowering Mean	bi	S²di	Days to maturity Mean	bi	S²di	Plant height Mean	bi	S²di	No. of primary branches /plant Mean	bi	S²di	No. of pods / plant Mean	bi	S²di	Pod length Mean	bi	S²di
1	AKU-7	36.44	2.30	-0.62	74.61	2.00	-0.58	21.77	0.97	-0.22	1.95	0.69	-0.01	16.20	0.70	-0.71	4.31	1.71	-0.008
2	LBG-752	45.83	-2.74	0.12	79.55	1.67	-0.53	25.58	-0.58*	-0.82	2.69	-0.16	-0.005	17.43	1.01	-0.30	4.42	1.50	-0.012
3	T-9	35.27	1.00	-0.84	75.00	0.67	-0.50	19.08	0.24	-0.86	1.98	0.65	-0.02	8.20	1.66	7.48**	4.49	-0.21	0.048**
4	LBG-20	38.00	1.94	-0.31	72.83	-5.49*	-0.34	24.99	-0.18*	-1.59	2.41	-0.17*	-0.02	17.25	0.79	0.09	4.62	0.57	-0.018
5	LBG-17	47.83	1.12	-0.73	81.38	1.34	-0.24	25.71	0.29*	-1.78	2.75	0.03*	-0.02	16.84	1.09	-0.95	4.62	0.93	-0.014
6	PBG-1	42.94	2.58	-0.46	73.05	1.67	1.12*	36.27	1.38	-1.96	2.97	1.00	0.13**	20.39	1.49	2.54*	5.57	0.21	-0.018
7	PBG-107	43.77	3.56	0.22	81.61	-1.15	-0.34	33.63	1.07	1.73	2.38	1.41	-0.01	12.98	0.62	0.51	4.59	1.05	-0.011
8	MBG-162	39.83	-2.19	1.81*	79.27	1.17	-0.50	27.79	1.34	22.22*	2.17	1.79	-0.01	16.67	1.15	-0.18	4.49	1.41	-0.018
9	MBG-207	38.66	-2.89	7.87**	81.11	1.34	-0.22	23.39	-0.03*	-1.82	2.73	1.55	-0.01	21.37	-0.06*	-0.89	4.29	0.60	-0.017
10	LBG-648	47.44	-1.41	-0.46	92.11	9.51*	-0.19	26.03	1.76	-1.58	2.83	0.33	0.24**	20.43	3.16	0.11	4.18	0.73	-0.019
11	LBG-623	40.94	3.35	2.99**	78.50	-1.82	-0.26	24.46	3.11	1.07	2.62	2.65	0.06*	19.85	0.23*	-1.03	4.22	1.35	-0.015
12	LBG-645	41.05	5.32	0.45	85.94	1.17	-0.34	32.24	2.60	4.76*	2.56	2.30*	-0.02	16.31	0.10	-0.83	4.33	2.11	-0.012
	Population mean	41.50			79.58			26.74			2.50			16.99			4.51		

S.No.	Genotype Mean	No. of seeds/pod bi	S²di	Seed yield / plant Mean	bi	S²di	1000 seed weight Mean	bi	S²di	Yield kg/ plot Mean	bi	S²di	Protein content Mean	bi	S²di
1	AKU-7 4.66	0.34*	-0.050	3.62	0.21	-0.07	44.43	1.24	-0.41	0.24	0.57*	-0.001	23.84	0.18	0.93*
2	LBG-752 4.25	1.42	-0.004	5.35	1.78*	-0.08	54.47	1.55*	-4.15	0.27	0.80	-0.001	21.16	0.10	0.54
3	T-9 4.52	1.37	-0.013	4.64	1.76	-0.06	45.34	1.46	-2.23	0.24	0.78	-0.001	21.36	1.20	-0.14
4	LBG-20 4.81	3.15	0.214**	4.89	0.12*	-0.07	54.25	1.39	-1.80	0.29	0.85	-0.001	25.85	0.82	-0.17
5	LBG-17 4.47	1.06	-0.039	5.13	-0.29*	-0.07	54.54	1.40	-2.40	0.31	0.80	-0.001	24.80	1.19	-0.39
6	PBG-1 5.73	0.21*	-0.043	7.85	1.75	-0.05	55.93	-1.47*	4.92	0.49	2.41*	0.001*	23.53	4.42*	-0.47
7	PBG-107 4.97	-0.79*	0.000	5.34	1.72	-0.06	57.16	0.20*	-3.99	0.28	1.20	0.001	24.10	-0.94	2.61**
8	MBG-162 4.63	0.03*	-0.048	4.70	2.79*	-0.05	44.87	-0.59*	-1.68	0.27	0.95	0.002**	23.07	1.05	0.85*
9	MBG-207 4.37	0.96	0.027	5.53	-3.41*	0.18*	44.09	1.29	-3.23	0.42	0.50	0.008**	24.52	0.12	-0.24
10	LBG-648 4.46	1.36	-0.046	5.96	2.57	0.05	57.47	2.53*	-0.29	0.40	1.06	-0.001	24.53	0.15	-0.39
11	LBG-623 4.56	1.20	-0.013	6.06	0.77	0.28**	52.23	1.55	-1.11	0.35	0.85	-0.001	21.98	2.57*	-0.18
12	LBG-645 4.63	1.66	-0.008	5.80	2.19*	-0.07	53.89	1.41	-1.99	0.37	1.18	-0.001	23.19	1.13	-0.11
	Population mean 4.67			5.41			51.568			0.332			23.498		

Table 3. ANOVA of AMMI model for different characters in blackgram [*Vigna mungo* (L.) Hepper]

Source	Plant height			No. of pods per plant			No. of seeds per pod			1000 seed weight			Seed yield per plant			Protein content		
	DF	MSS	% explained	DF	MSS	% explained	DF	MSS	% explained	DF	MSS	% explained	DF	MSS	% explained	DF	MSS	% explained
Trials	71	27.58**	-	71	13.96**	-	71	0.26**	-	71	37.00**	-	71	1.15**	-	71	2.98**	-
Genotypes	11	150.09**	84.28	11	79.36**	88.02	11	0.88**	51.15	11	167.00**	69.92	11	6.27**	84.06	11	12.22**	63.46
Environments	5	12.03*	3.07	5	4.83*	2.43	5	0.72**	19.12	5	61.97**	11.79	5	0.49*	2.99	5	2.88*	6.81
Gx E interaction	55	4.50	12.64	55	1.72	9.54	55	0.10	29.71	55	8.73	18.28	55	0.19	12.93	55	1.14	29.91
PCA I	15	9.32*	56.49	15	3.50**	55.48	15	0.25**	67.62	15	25.77**	80.48	15	0.59**	83.45	15	2.28**	54.55
PCA II	13	5.49	28.83	13	1.79**	24.58	13	0.07	16.42	13	4.63	12.53	13	0.11	13.76	13	1.24*	25.77
PCA III	11	2.03	9.04	11	1.21*	14.12	11	0.054	10.61	11	1.69	3.88	11	0.02	2.21	11	0.68	11.98
PAC IV	9	1.29	4.72	9	0.61	5.82	9	0.02	3.26	9	1.20	2.26	9	0.004	0.42	9	0.37	5.42
Residual	7	0.32	0.92	7	0.00	0.00	7	0.016	2.10	7	0.58	0.85	7	0.002	0.16	7	0.20	2.27
Pooled residual	55	4.50		16	0.34		40	0.04		55	8.73		55	0.19		27	0.45	

** = Significant at 1% probability level   * = Significant at 5% probability level

DF = Degrees of freedom   MSS = Mean sum of squares

Fig 1. Biplot (AMMI 1) for plant height (cm) in blackgram [*Vigna mungo* (L.) Hepper]
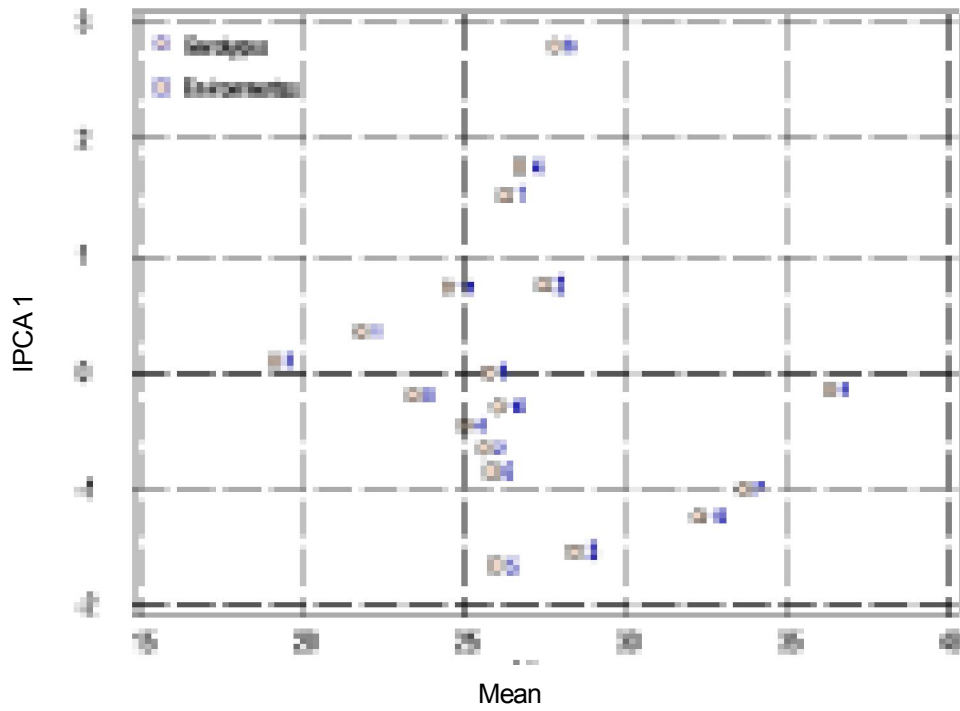
Fig 2. Interaction biplot (AMMI 2) for plant height in blackgram [*Vigna mungo* (L.) Hepper]
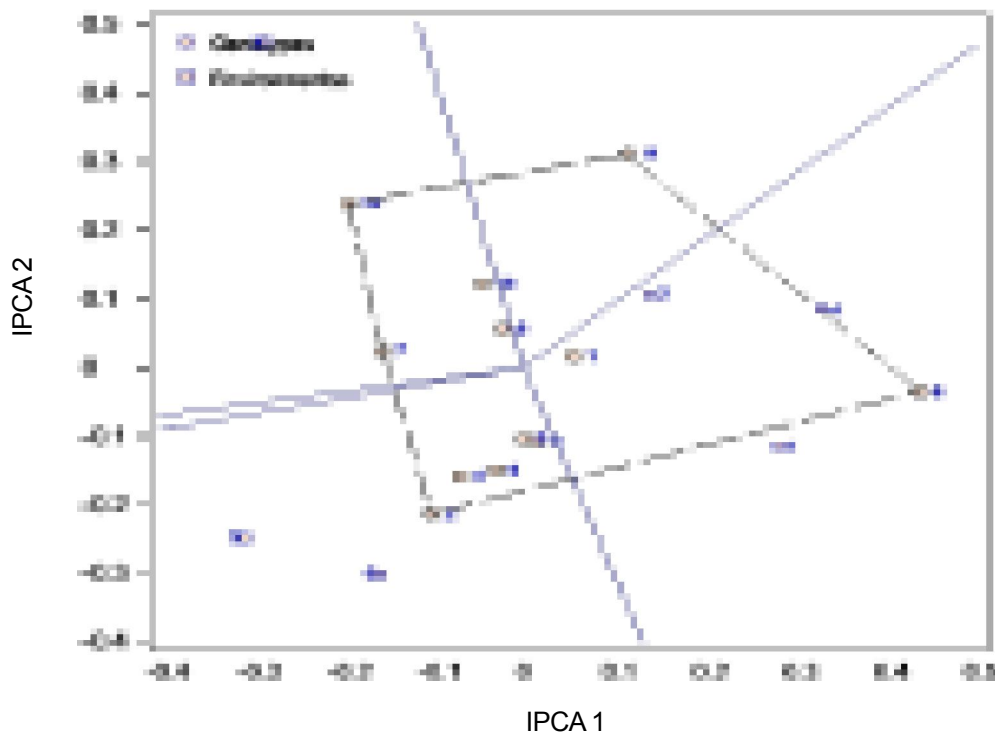
Genotypes of blackgram

1. AKU 7,   2.LBG-752,   3.T-9,   4.LBG-20,   5.LBG-17,   6.PBG-1,
7. PBG-107,   8.MBG-162,   9.MBG-207,   10.LBG-648,   11.LBG-623,   12.LBG-645.

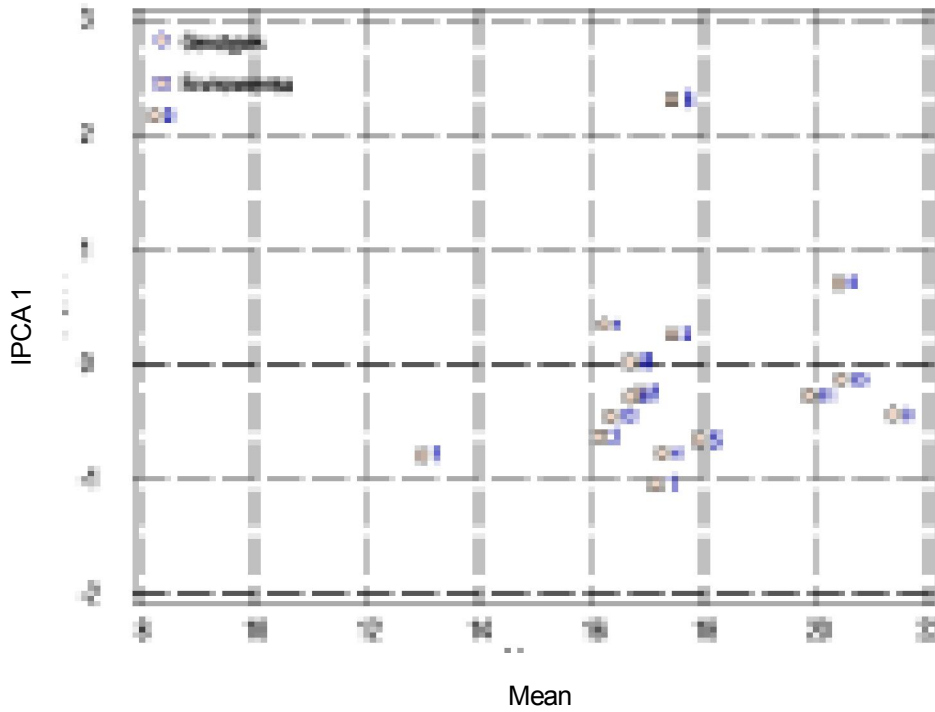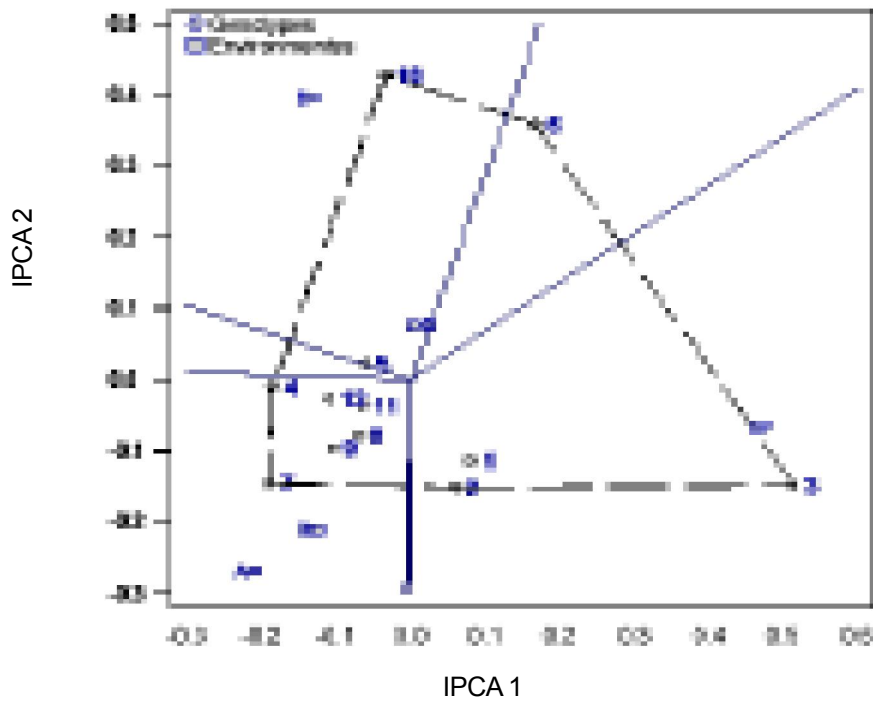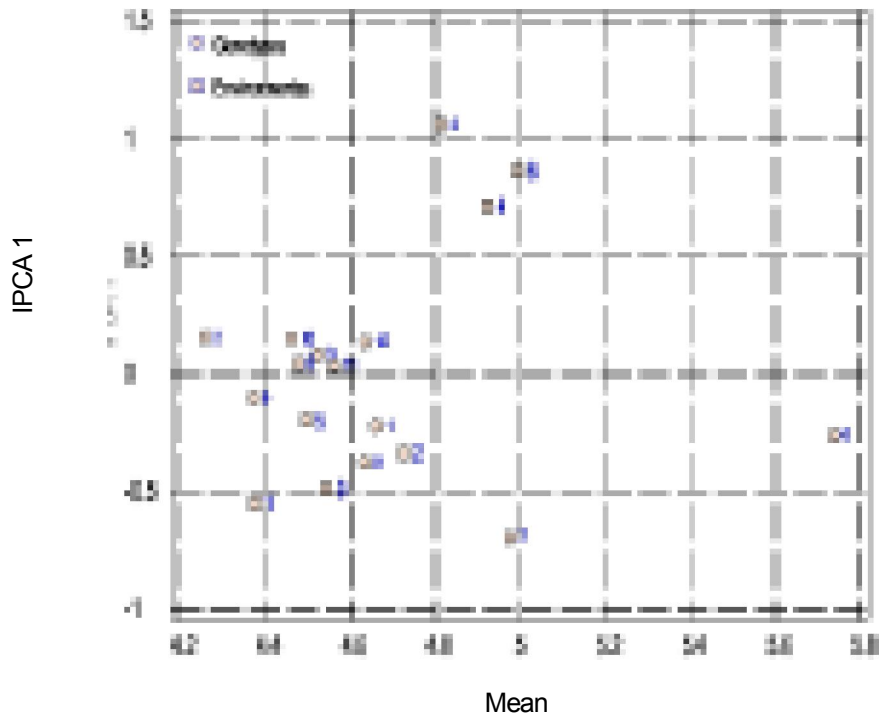Fig 3. Biplot (AMMI 1) for number of pods plant⁻¹ in blackgram [*Vigna mungo* (L.) Hepper]
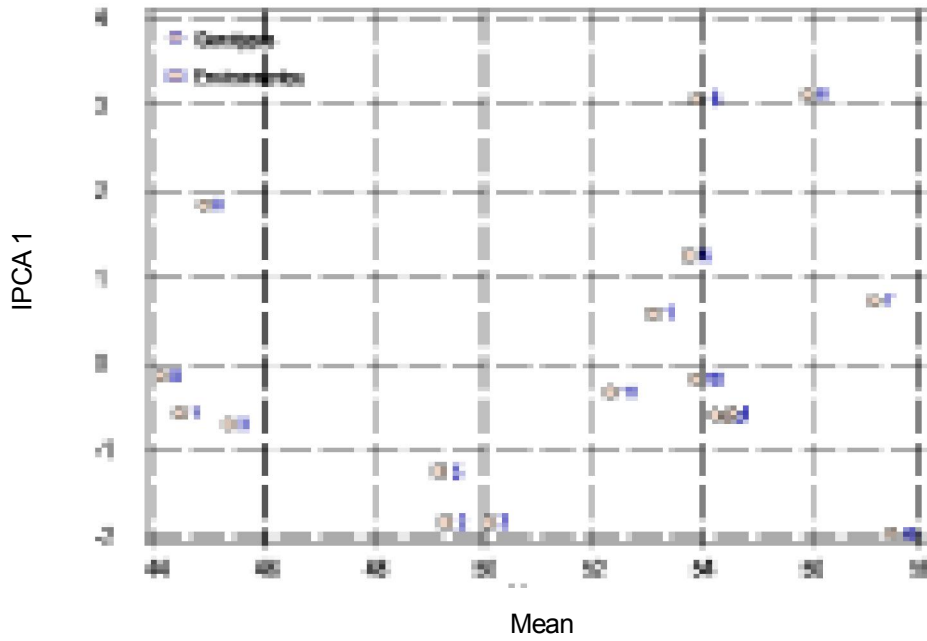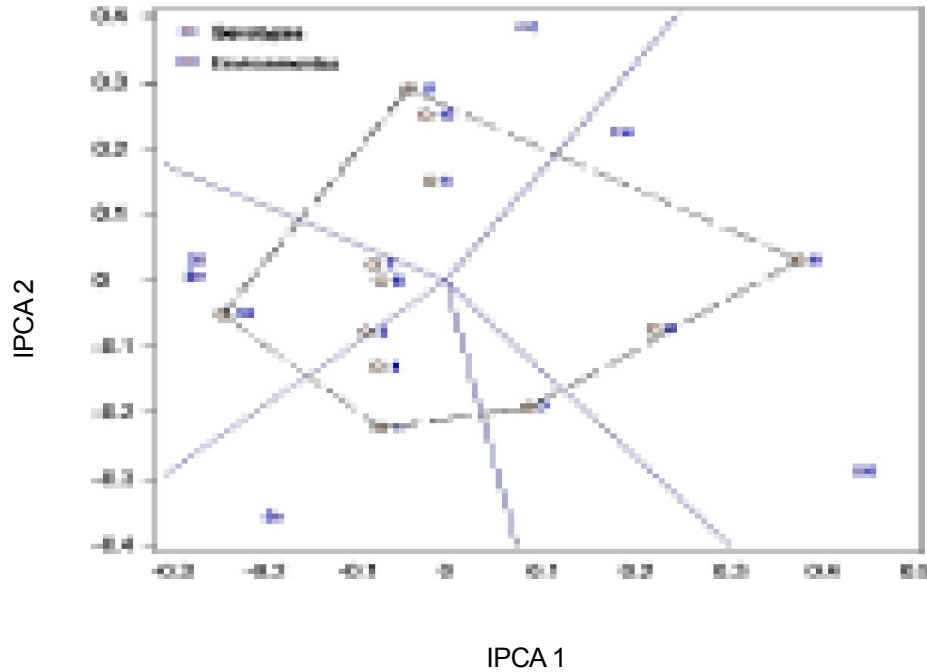

Mean

Fig 4. Interaction biplot (AMMI 2) for number of pods plant⁻¹ in blackgram [*Vigna mungo* (L.) Hepper]

IPCA 1

Genotypes of blackgram

1. AKU 7,	2.LBG-752,	3.T-9,	4.LBG-20,	5.LBG-17,	6.PBG-1,
7. PBG-107,	8.MBG-162,	9.MBG-207,	10.LBG-648,	11.LBG-623,	12.LBG-645.

Fig 5. Biplot (AMMI 1) for number of seeds per pod in blackgram [*Vigna mungo* (L.) Hepper]


Mean

Fig 6. Interaction biplot (AMMI 2) IPCA 2 (not significant) for number of seeds per pod in blackgram [*Vigna mungo* (L.) Hepper]
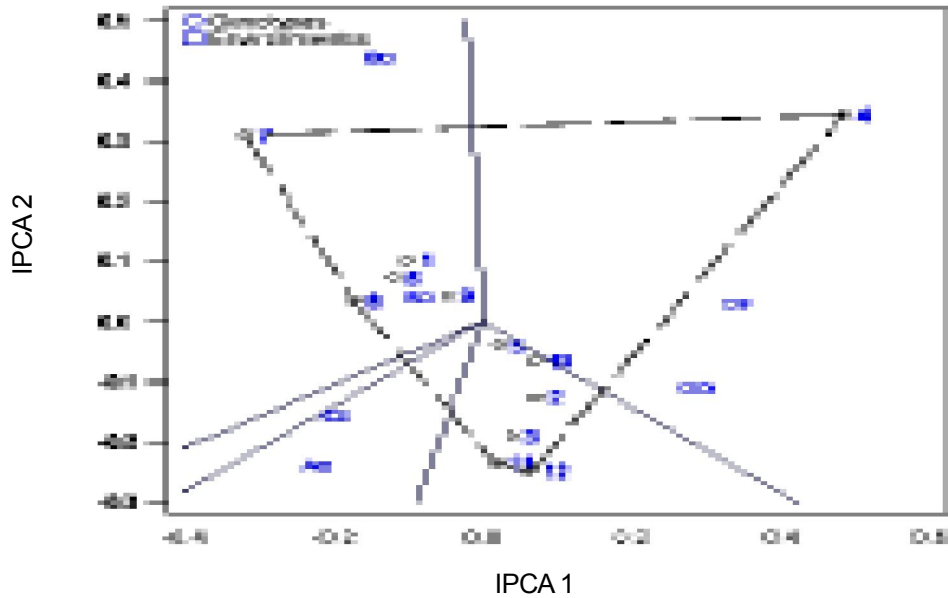
IPCA 1

Genotypes of blackgram

1. AKU 7,	2.LBG-752,	3.T-9,	4.LBG-20,	5.LBG-17,	6.PBG-1,
7. PBG-107,	8.MBG-162,	9.MBG-207,	10.LBG-648,	11.LBG-623,	12.LBG-645.

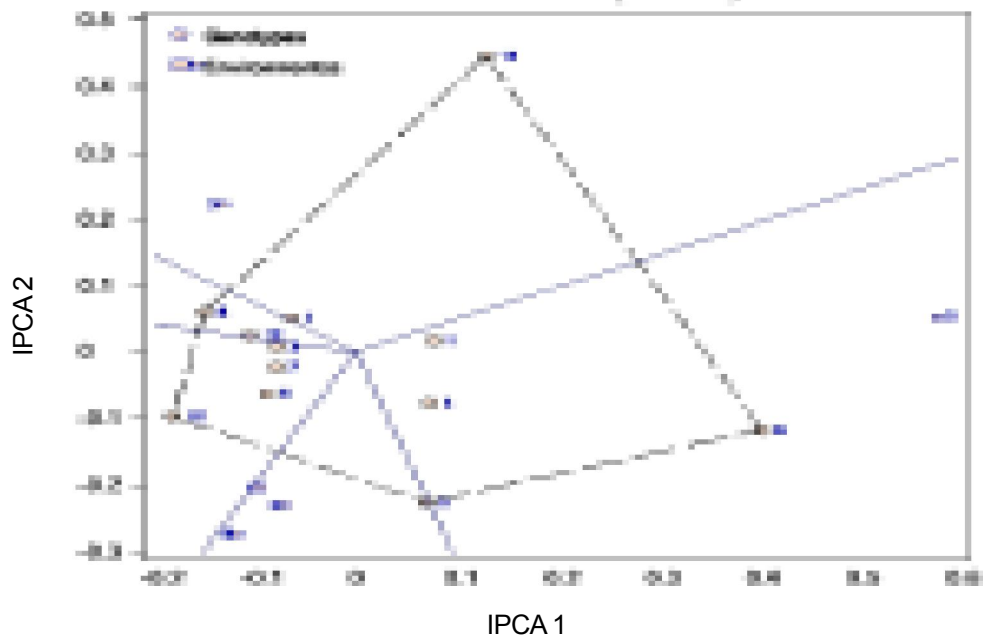Fig 7. Biplot (AMMI 1) for 1000 seed weight in blackgram [*Vigna mungo* (L.) Hepper]

Fig 8. Interaction biplot (AMMI 2) for 1000 seed weight in blackgram [*Vigna mungo* (L.) Hepper]

Genotypes of blackgram
1. AKU 7,   2.LBG-752,   3.T-9,   4.LBG-20,   5.LBG-17,   6.PBG-1,
7. PBG-107,   8.MBG-162,   9.MBG-207,   10.LBG-648,   11.LBG-623,   12.LBG-645.

Fig 9. Biplot (AMMI 1) for seed yield per plant in blackgram [*Vigna mungo* (L.) Hepper]
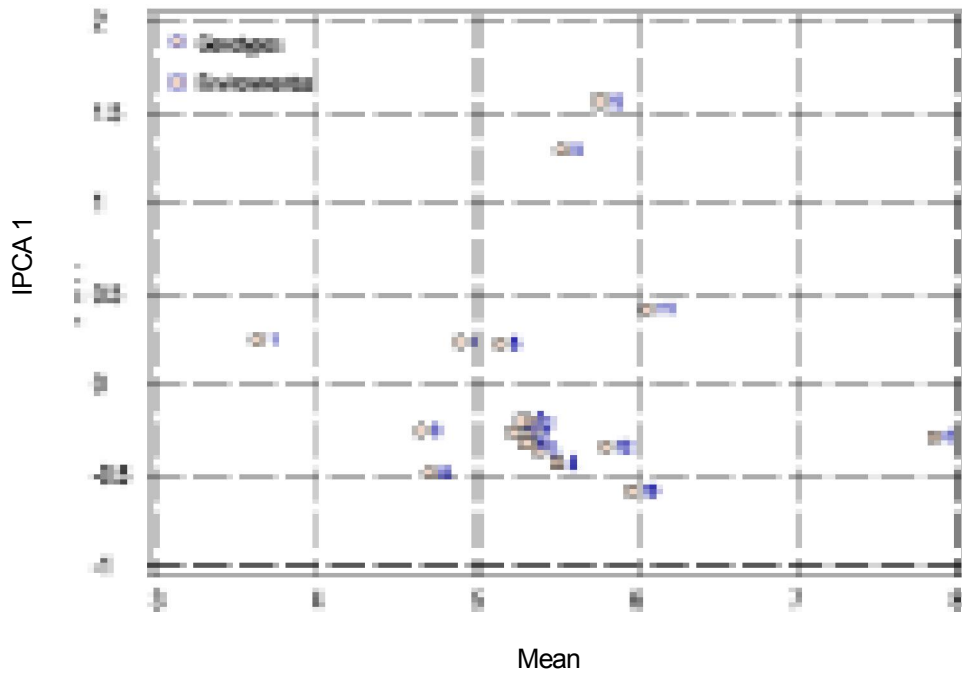
Fig 10. Interaction biplot (AMMI 2) for seed yield per plant in blackgram [*Vigna mungo* (L.) Hepper]

Genotypes of blackgram
1. AKU 7,   2.LBG-752,   3.T-9,   4.LBG-20,   5.LBG-17,   6.PBG-1,
7. PBG-107,   8.MBG-162,   9.MBG-207,   10.LBG-648,   11.LBG-623,   12.LBG-645.

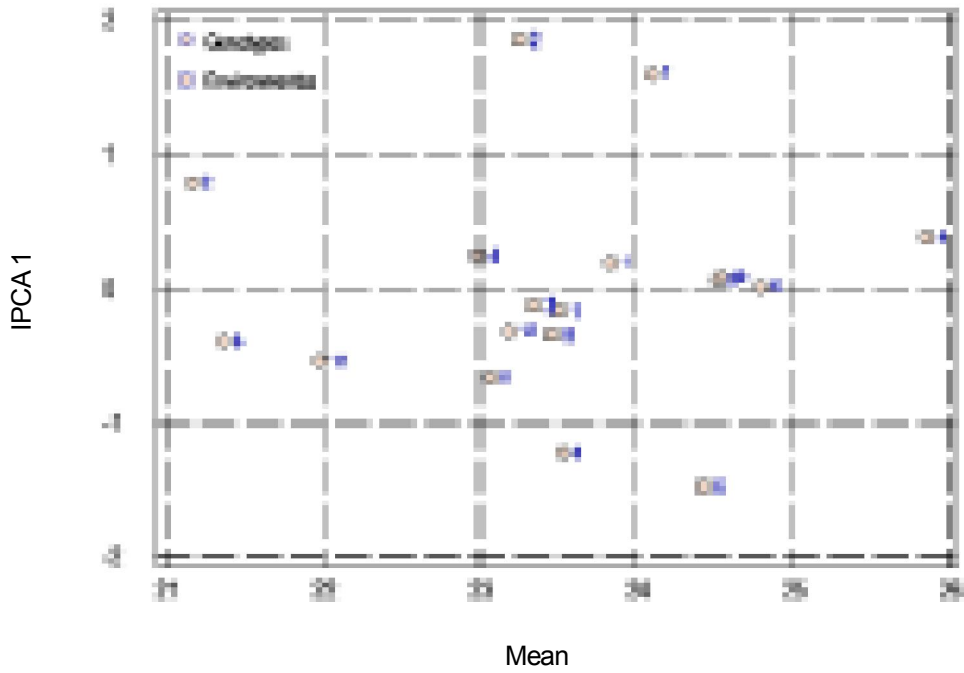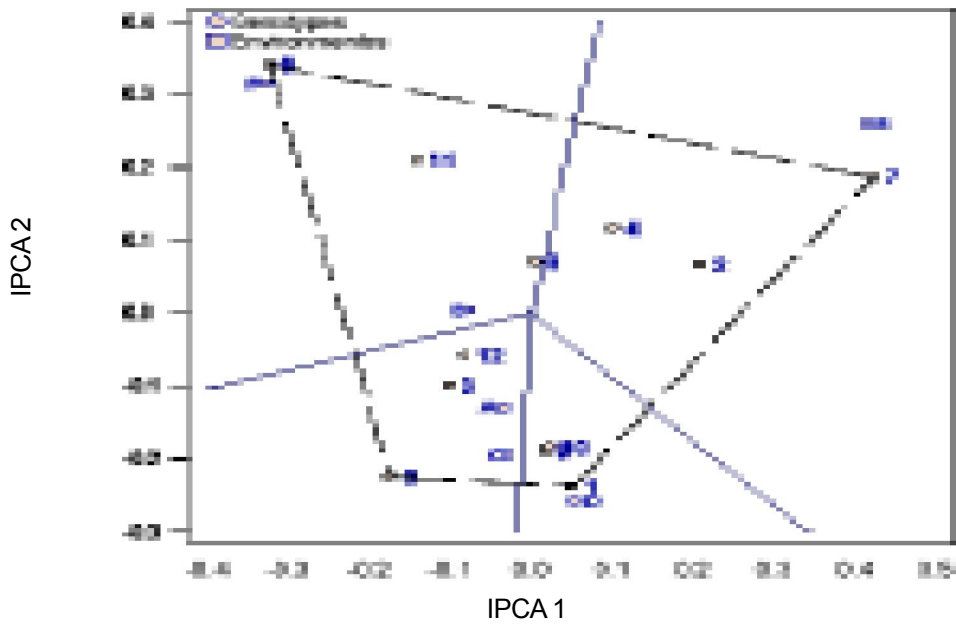Fig 11. Biplot (AMMI 1) for protein content (%) in blackgram [*Vigna mungo* (L.) Hepper]

Fig 12. Interaction biplot (AMMI 2) for protein content (%) in blackgram [*Vigna mungo* (L.) Hepper]

Genotypes of blackgram

1. AKU 7,	2.LBG-752,	3.T-9,	4.LBG-20,	5.LBG-17,	6.PBG-1,
7. PBG-107,	8.MBG-162,	9.MBG-207,	10.LBG-648,	11.LBG-623,	12.LBG-645.

per pod (67.62%), 1000 seed weight (80.48%), seed yield per plant (83.45%) and protein content (54.55%) bringing out the specific use of AMMI in assisting the breeder to pinpoint the stable genotypes for the above characters, which is not possible in case of linear regression model.

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