



# Genotype x environments interactions for grain yield and its components in urdbean (*Vigna mungo* L Wilczek) under rainfed conditions of Jammu region

Sanjeev Kumar\*, J. P. Sharma, Anil Kumar, H. K. Choudhary<sup>1</sup>, A. P. Singh, Rubby Sandghu, Rucku Gupta, Manmohan Singh and Anjani Kumar Singh<sup>2</sup>

Advanced Centre for Rainfed Agriculture, Rakhdhiansar, Shere Kashmir University of Agriculture Sciences & Technology, Jammu; <sup>1</sup>Deptt. of Crop Improvement, CSKHPKV Palampur; <sup>2</sup>Mega Seed Project, Chatha SKUAST Jammu

(Received: November 2019; Revised: March 2020; Accepted: April 2020)

## Abstract

In the present study, AMMI approaches were used to analyse the genotype x environment interactions and stability under targeted environments. The analysis of stability parameters of seed yield/plant in 25 genotypes of urdbean (*Vigna mungo* L.) indicated that six genotypes namely, Mash 479, PLU 499-52, PU19, PLU-4158, Pant 31 and IPU2-43 showed regression coefficient greater than unity (b-1) with non-significant  $S^2_{di}$  values and higher mean values than population mean which exhibited their stability and adaptation to specific favorable environment only. Three genotypes, PU99, No. 13/11 and No.40 indicated that regression coefficient less than unity with higher mean values than population mean with non-significant deviation from the regression coefficient ( $S^2_{di}$ ) and recommended for unfavorable environments. Mash 338 and IPU 96-1 are the most stable genotypes across the environments for seed yield/plant and 1000 seed weight, respectively. Environmental indices indicated that environment ( $E_1$ ) and environment ( $E_2$ ) were the most favorable for number of primary branches/plants, days to 50% flowering, plant height and seed yield/plant, whereas environment ( $E_3$ ) was favorable for pod length and number of seeds/pod. AMMI 1 model exhibited that  $E_1$  and  $E_2$  were the clustered in the same group and exhibited similar type of interaction for seed yield/plant. Genotypes, PLU4158, IPU96-1, Mash479, PLU499-52 and IPU2-43 exhibited high IPCA 1 scores along with high population mean. Based on AMMI 2 model, PLU4158, IPU96-1 and IPU96-6 exhibited high IPCA scores. The selected genotypes may be utilized in *Vigna mungo* improvement programme in targeted location with true type of breeding lines.

**Key words:** AMMI, GEI, principle components, stability, *Vigna mungo*, yield contributing traits

## Introduction

Urdbean (*Vigna mungo* L.Wilczek) is one of the major *Kharif* pulse crop grown in India. This is major pulse crop in Jammu region after Rajamash. The major constraints to develop high yielding varieties of urdbean in India are low inherited yield potential, lack of genetic variability, narrow genetic base and susceptibility to many biotic and abiotic stresses (Subramanian and Gopalakrishnan 2006). This may be due to the utilization of only selected elite lines of urdbean varietal development programme (Gupta 2004). Thus, there is an urgent need to construct the suitable ideotype and to identify the elite donors. Yield, which is an ultimate objective of any crop improvement programme is a complex trait influenced by many traits as well as environment. Hence, there is a great need to identify the suitable genotypes/lines for their yield and yield components prior to practicing breeding.

The genotype x environment interaction is an important parameter for plant breeding programme to identify the stable genotypes that are widely adapted to unique environment (Verma et al. 2008). Additive main effects and multiplicative interaction (AMMI) analysis is one of the most popular multivariate methods to predict adaptation and stability of cultivars over multiple environments. G x E interaction also affects the genetic gains, recommendation and selection of cultivars with wider adaptability (Deitos et al. 2006; Lal et al. 2019). On the other hand, different

\*Corresponding author's e-mail: ssalgotha@gmail.com

genotypes have different performances in each region that can be capitalized to maximize the productivity (Souza et al. 2008). Stability of genotypes over wide range of environments is desirable and depends upon G x E interaction (Ali and Sawar 2008). To understand the structure and nature of G x E interaction is very important in crop improvement programmes because the significant GEI can seriously impairs the efforts in selecting the superior genotypes (Danyali et al. 2012). Eberhart and Russell (1966) developed a methodology to identifying the cultivars with greater adaptability and stability that has been widely used in the identification of genotypes for this purpose (Grunvald et al. 2008). Yan et al. (2007) compared the GGE biplot analyses and AMMI analysis with three aspects of genotype-by-environment data (GED) analyses, namely mega environment analysis, genotype evaluation and test environment analysis. It is commonly known that both GGE and AMMI analysis combine rather than separate G and GE in mega environment analyses and genotype evaluation. It is well accepted nowadays, that the GGE biplot is superior to AMMI graph in mega environment analyses and genotype evaluation because it better explains G+GE and has the inner product property of the biplot. Moreover, the discriminating power vs representativeness view of the GGE biplot is an effective method in evaluating the test environments, which is not possible with AMMI analyses. Model diagnosis for each data set is useful but the accuracy gained from the model diagnosis should not be overstated. To identify the stable genotypes, the data is based on multiyear and multi locations. But for crop improvement programmes in targeted location, there is an urgent need to identify the genotypes in that particular location/environment is also very important. By keeping in view, the above facts under consideration, the present investigation was carried out to identify the stable genotypes for seed yield and its components in targeted environments for urdbean (blackgram) improvement under rainfed conditions.

## Materials and methods

### Plant material and experimental design

The experimental materials comprised with twenty five genotypes of blackgram namely, Uttara (G<sub>1</sub>), Mash 114(G<sub>2</sub>), T-9 (G<sub>3</sub>), Mash 479(G<sub>4</sub>), NP 16(G<sub>5</sub>), JU468(G<sub>6</sub>), DUS19(G<sub>7</sub>), IPU96-6(G<sub>8</sub>), PU99(G<sub>9</sub>), PLU499-52(G<sub>10</sub>), PL4158(G<sub>11</sub>), UH86-4(G<sub>12</sub>), Mash338(G<sub>13</sub>), PU19(G<sub>14</sub>), NKD4-2(G<sub>15</sub>), Pant31(G<sub>16</sub>),

No. 13/11(G<sub>17</sub>), No. 40(G<sub>18</sub>), IPU96-1(G<sub>19</sub>), PGRU99022(G<sub>20</sub>), SPS38(G<sub>21</sub>), IPU2-43(G<sub>22</sub>), IPU96-16(G<sub>23</sub>), UH82-14(G<sub>24</sub>) and STTZ834(G<sub>25</sub>). These genotypes were received from the ICAR-Indian Institute of Pulses Research, Kanpur, Uttar Pradesh. The experiments were conducted in randomized block design with three replications during *kharif* 2016, 2017 and 2018 under rainfed conditions at the experimental farm of Advanced Centre for Rainfed Agriculture (ACRA), Rakhdhiansar of Shere Kashmir University of Agriculture Sciences and Technology (SKUAST), Jammu which is situated at latitude, 32°38'24.00"N and longitude, 74°55' 48.00". Each genotype was sown in eight rows of 4 meter length with spacing of 30 x 10 cm<sup>2</sup>. All the recommended package and practices and plant protection measures were followed for getting good healthy crop.

### Biometrical analysis

Fifteen random plants were selected from each genotypes in each replication in each year to record the data for seed yield and yield attributing traits *viz.*, days to 50% flowering, number of primary branches/plant, plant height, pod length, number of seeds/pod, 1000 seed weight, days to maturity and seed yield/plant. Pooled mean data of all the traits under studied of each year were subjected to analysis of variance and stability parameters using statistical package Windowstat 9.3 version. The stability of each genotype for each trait was calculated by regression of the mean of individual genotypes in environmental index and deviation from regression coefficient from unity as per methodology of Eberhart and Russel model (1966), *i.e.*,

$$Y_{ij} = \mu_i + \beta_{ij} l_j + \sigma_{ij}$$

where,  $Y_{ij}$  = mean of  $i^{\text{th}}$  genotype of  $j^{\text{th}}$  environment,

$\mu_i$  = mean of  $i^{\text{th}}$  genotype over environments,  $\hat{\alpha}_i$  = regression coefficient of  $i^{\text{th}}$  genotype to the change of environment,  $l_j$  = environmental index,  $\sigma_{ij}(S^2D)$  = deviation from regression coefficient. The regression coefficient ( $\beta_i$ ) was tested against t-test for their significance, whereas significance of deviation from regression ( $S^2d_i$ ) was tested by F-test. To analyze the GEI, additive mean effect and multiplicative interaction effects (AMMI) model was used with software Windowstat 9.3 and this statistical model is a combination of customary analysis of variance and principal component analysis.

## Results and discussion

### Analysis of variance and GEI

Homogeneity of variance were tested against homogenous error for each trait studied using Bartlett's test and allow for pooled analysis of variance for eight traits over three environments. Analysis of variance (ANOVA) indicated significant differences among varieties for all the traits (Table 1). Variance due to

from regression coefficient ( $S^2_{di}$ ) and therefore, recommended for specific environment only (Table 2). Genotypes, Mash 338, Pant 31, No. 40 and STTZ 834 for DTF showed mean values at par while No.40, SPS38, IPU96-16 and STTZ834 displayed lesser mean values with average mean value and regression coefficient less than unity ( $b < 1$ ) with least  $S^2_{di}$  and hence, also recommended for unfavorable environment only. For DTM, genotype No.13/11 exhibited lower

**Table 1.** Analysis of variance for stability for yield and its attributing traits

SV	DF	DTF	PH	PBR	PL	S/Pods	DTM	1000SW	SY/PI
Rep. Within Env	6	0.17	0.22	0.03	0.15	0.12	2.42	2.02	0.04
Genotypes	24	43.67***	195.67***	1.35***	0.17**	1.4***	60.78***	21.83***	3.17***
Env. + (Var.* Env)	50	10.03***	110.48***	0.30***	0.08	0.59***	166.21***	2.14	1.90***
Env.	2	40.24***	894.63***	2.48***	0.34*	4.20***	3167.68***	12.40***	23.90***
Gen. *Env	48	8.77***	77.81***	0.20***	0.07	0.44***	41.15***	1.71	0.99***
Env. (Linear)	1	80.49***	1789.26***	4.96***	0.68**	8.4***	6335.35***	24.81***	47.80***
Gen. *Env (Linear)	24	17.00***	151.38***	0.36***	0.08	0.81***	80.10***	2.03	1.84***
IPCA1	25	97.90***	460.33***	3.22***	0.09	0.78***	77.08***	2.31	1.77***
Pooled Deviation	25	0.53	4.07***	0.05	0.06***	0.07***	2.11	1.34***	0.13
Pooled error	144	0.40	0.17	0.04	0.002	0.03	2.11	0.52	0.11
Total	74	20.92	138.11	0.64	0.11	0.86	132.02	8.52	2.31

environments and environment (linear) showed significant differences for all the traits studied indicated that the environments were linear in this investigation. GEI further subdivided into linear (bi) and non-linear ( $S^2_{di}$ ) components. The significance of linear component of GEI was recorded for all the traits except 1000 seed weight. Significant non-linear components (pooled deviation) was recorded for all the traits under studied except days to 50% flowering, days to maturity and grain yield/plant. AMMI analyses were further done to estimate the GEI for yield and its components.

### Stability parameters

The mean performance ( $\mu$ ), regression coefficient ( $b_i$ ) and deviation from regression ( $S^2_{di}$ ) have been presented in (Tables 2 and 3). The perusal of data revealed that all the genotypes had non-significant deviation from regression coefficient for all the traits under studied. Nine genotypes (T9, Mash 114, Mash 479, IPU96-6, PL4158, PU19, SPS38, IPU96-16 and UH 82-14) for days to 50% flowering (DTF) and only one (PL4158) for days to maturity (DTM) showed lesser mean values than population mean with regression coefficient greater than unity ( $b > 1$ ) and least deviation

mean value than population mean with non-significant regression coefficient less than unity and least  $S^2_{di}$  and hence, recommended for unfavorable environment only. However, the genotype IPU96-6 exhibited lesser mean values than population mean with regression coefficient equal to unity ( $b = 1$ ) with minimum deviation from regression coefficient and therefore, identified as stable genotype across the environment for days to maturity which is earlier in maturity value as compared to average mean value.

The genotypes viz., Utara, Mash 114, T9, Mash 479, STTZ834, IPU 96-16 and PU 19 showed higher mean values for plant height than population mean with regression coefficient greater than unity ( $b > 1$ ) along with least deviation from regression coefficient ( $S^2_{di}$ ) indicated their stability and recommendation to specific environment only whereas, NP16, DUS 19, No. 40, IPU 96-1 and IPU2-43 displayed higher mean values than population mean with regression coefficient less than unity along with least deviation from regression coefficient ( $S^2_{di}$ ) indicated recommendation for unfavorable environment only. For number of primary branches/plants, nine genotypes

**Table 2.** Estimates of mean, regression coefficient (bi) and deviation from regression (S<sup>2</sup>di) for various yield and yield component traits *Vigna mungo* (L) Wilczek

Genotypes	Days to 50% heading			Plant Height (cm)			PBR			Seed yield/plant(g)			
	Mean	bi	S <sup>2</sup> di	Mean	bi	S <sup>2</sup> di	Mean	bi	S <sup>2</sup> di	Mean	bi	S <sup>2</sup> di	
G1	Uttara	57.78	-2.366**	-0.38	63.5	3.48*	1.05**	5.22	1.89*	-0.04	4.26	0.60	-0.09
G2	Mash 114	47.17	6.00	0.75	73.52	3.49*	0.30	3.86	-2.28	0.01	4.21	-0.12*	-0.10
G3	T-9	47.97	4.78	0.19	60.27	1.84	0.23	4.12	0.52	0.03	4.54	-0.26*	-0.09
G4	Mash 479	51.68	2.93	0.01	75.12	3.75*	0.03	4.56	0.48	0.02	6.09	1.79*	-0.10
G5	NP 16	58.73	-2.111*	-0.36	57.31	0.72	-0.10	4.82	1.81	-0.03	4.58	0.21*	-0.11
G6	JU468	59.18	-3.568*	-0.27	49.60	0.59*	-0.15	5.84	2.2	-0.03	4.45	1.20	-0.11
G7	DUS19	56.59	-1.083*	-0.37	59.05	0.06	0.28	4.66	-0.55**	-0.04	4.97	0.05*	-0.11
G8	IPU96-6	48.67	2.53	-0.31	45.55	0.78	0.34	3.65	-0.58*	-0.03	4.27	1.65	-0.00
G9	PU99	59.09	0.38	-0.32	66.77	0.88*	-0.16	4.22	0.42	-0.01	5.42	0.45	-0.09
G10	PLU499-52	58.03	0.661*	-0.38	51.01	-1.23*	0.90*	4.86	1.62	0.12*	5.67	2.08	-0.07
G11	PL4158	48.76	2.94	-0.05	46.57	1.58	0.08	3.4	-0.31	0.16*	5.40	3.51	-0.03
G12	Mash338	54.11	0.89	0.68	44.57	-0.74*	0.53*	5.76	2.47	-0.03	4.5	1.45	0.20
G13	UH86-4	56.11	1.70	0.72	46.77	-0.91*	0.39	5.47	3.13	0.05	3.88	0.79	0.21
G14	PU19	53.83	3.12	0.06	56.25	-0.74	2.73***	4.54	-0.24	-0.01	5.50	1.47	-0.03
G15	NKD4-2	55.66	1.15	-0.38	59.93	-0.17	11.34***	4.63	0.00**	-0.04	3.17	0.29*	-0.11
G16	Pant 31	54.83	0.10	-0.33	54.54	1.44	16.29***	4.37	2.06	-0.00	5.72	1.69	-0.06
G17	No. 13/11	53.86	0.86	1.42	54.51	-0.26	12.53***	3.82	2.26*	-0.03	5.13	-0.05	-0.08
G18	No. 40	54.78	0.13	-0.14	57.73	-0.38	11.75***	4.15	0.43	-0.03	6.73	-0.06	-0.08
G19	IPU96-1	55.00	0.00**	-0.38	60.81	0.34*	-0.12	4.28	0.81	0.01	8.27	2.32**	-0.10
G20	PGRU99022	60.22	-3.133*	-0.35	57.41	0.62*	-0.16	5.58	2.51	0.10	5.57	-0.64*	-0.10
G21	SPS38	51.64	2.06	-0.35	49.69	1.23	1.85***	3.59	-0.59	0.04	4.00	0.91	1.56***
G22	IPU2-43	50.28	2.548*	-0.38	63.45	2.20	0.84*	4.26	0.27	-0.02	5.34	2.00	0.07
G23	IPU96-16	49.17	2.52	4.84	59.74	2.73	21.97***	4.33	2.14	-0.14*	4.82	1.55*	-0.10
G24	UH82-14	54.00	1.36	-0.33	53.02	0.77	14.49***	4.80	2.12	-0.03	4.51	1.40	-0.10
G25	STTZ834	55.09	0.59	0.01	64.88	2.93*	0.28	5.00	2.39	-0.03	4.86	0.72	0.22
	<b>Pop. Mean</b>	54.08	1.00	-	57.25	1.00	-	4.54	1.00	-	5.04	1.00	-
	<b>SE(m)</b>	0.51	-	-	1.42	-	-	0.15	-	-	0.25	-	-
	<b>SE (bi)</b>	0.40	-	-	0.23	-	-	0.48	-	-	0.26	-	-

showed higher mean values with regression coefficient greater than unity and minimum deviation from the regression coefficient (Table 2) indicating their stability and adaptation to specific favorable environment only. These genotypes showed higher sensitivity to environment change and greater specificity of adaptability to high yielding environment whereas, Mash 479, DUS 19 and NKD 4-2 exhibited significant regression coefficient less than unity with higher mean values than population mean and minimum deviation from regression coefficient therefore, recommended for unfavorable environments only.

Three genotypes namely, UH86-14, SPS38 and STTZ 834 showed lower mean grain yield values for seed yield than population mean with regression coefficient approaches to unity and S<sup>2</sup>di non-significant hence, their adaptability was poor in all environments. However, five genotypes (PLU499-52, PL4158, PU19, Pant 31 and IPU2-43) showed regression coefficient greater than unity (b $\bar{A}$ 1), minimum S<sup>2</sup>di and higher mean values (Table 2) than population mean which exhibited their stability and adaptation to specific favorable environment only. These genotypes showed higher sensitivity to environmental changes and greater

**Table 3.** Estimates of mean, regression coefficient (bi) and deviation from regression ( $S^2di$ ) for various yield and yield component traits *Vigna mungo* (L) Wilczek

Genotypes	Pod length(cm)			Seeds/pod			DTM			1000SW(g)			
	Mean	bi	$S^2di$	Mean	bi	$S^2di$	Mean	bi	$S^2di$	Mean	bi	$S^2di$	
G1	Uttara	4.64	0.12*	-0.01	6.66	0.27	-0.02	83.00	1.92*	-1.74	35.89	3.63	-0.14
G2	Mash 114	4.81	-0.42	-0.00	6.81	0.67	-0.02	85.62	1.72*	-1.90	37.64	2.69	2.29*
G3	T-9	4.66	0.66	-0.01	6.38	1.09	0.02	85.57	1.75*	-1.89	37.18	0.90	0.47
G4	Mash 479	4.46	0.59	0.00	6.13	1.4	0.01	93.22	1.21	-2.02	37.77	1.83	1.75*
G5	NP 16	4.62	0.55	0.05*	5.65	0.95	-0.03	98.07	0.87	-1.97	33.74	-0.96	0.28
G6	JU468	4.69	0.62	0.02	6.53	2.05	-0.02	94.50	1.30*	-2.07	35.21	0.88	-0.22
G7	DUS19	4.52	2.36	-0.00	6.28	1.45	0.24**	91.84	1.30*	-2.06	37.51	1.49	-0.20
G8	IPU96-6	5.16	-2.25	0.42***	6.63	0.80	0.05	88.33	1.00	-1.95	36.42	2.22**	-0.57
G9	PU99	4.69	1.87	-0.01	6.15	1.43	-0.03	94.10	1.30	-1.42	37.35	0.33	0.50
G10	PLU499-52	4.55	1.91	0.02	6.27	1.59	-0.02	91.63	1.42	5.25	35.71	1.59	0.02
G11	PL4158	4.99	-2.93	0.19***	6.65	0.81	-0.00	79.10	1.30	-1.00	37.29	-0.28	0.00
G12	Mash338	4.33	1.16	0.14***	6.40	1.11	0.33**	91.40	1.38	-1.52	37.47	0.18	-0.56
G13	UH86-4	4.30	1.92	0.08**	6.32	-1.18**	-0.03	91.88	1.39	0.41	37.38	1.00	0.15
G14	PU19	4.33	2.29	0.13**	6.02	1.56	-0.02	93.71	1.23*	-2.11	38.04	0.65	-0.58
G15	NKD4-2	4.61	2.50	0.00	6.03	1.83	-0.03	93.26	1.21	-1.26	35.09	2.03	-0.57
G16	Pant 31	4.44	-0.79	0.00	9.15	-5.61**	-0.03	90.44	0.89	-1.65	43.99	2.85	7.87**
G17	No. 13/11	4.56	1.60	0.02	5.91	1.59	-0.02	88.00	0.00**	-2.11	40.46	-0.22	-0.57
G18	No. 40	4.44	1.04	0.03	6.64	1.42	0.07	86.33	-0.02	4.64	43.82	0.76	1.99*
G19	IPU96-1	4.5	2.20	-0.00	5.68	0.65	-0.02	85.55	-0.04**	-2.05	39.73	1.06	1.52
G20	PGRU99022	5.16	2.60	-0.01	6.68	1.39	0.08	86.60	-0.042*	-1.25	37.34	-0.69**	-0.58
G21	SPS38	4.52	0.27	0.18***	5.82	2.35	0.46***	85.44	0.71	-1.18	36.70	-2.13	1.13
G22	IPU2-43	4.32	4.41	0.03	5.47	2.28	0.01	86.81	0.86*	-2.10	37.18	0.05	1.51
G23	IPU96-16	4.81	0.91	-0.01	6.63	1.34	-0.03	84.00	0.46	-1.46	36.33	-0.69	0.99
G24	UH82-14	4.84	-1.26	-0.01	5.05	1.92	-0.02	92.55	1.18	25.97***	42.91	2.81	3.01*
G25	STTZ834	4.65	3.06	0.02	6.27	1.73	-0.03	84.55	0.59	-1.69	42.11	3.02**	-0.58
	<b>Pop. Mean</b>	4.62	1.00	-	6.37	1.00	-	89.02	1.00	-	38.01	1.00	-
	<b>SE(m)</b>	0.18	-	-	0.18	-	-	1.02	-	-	0.82	-	-
	<b>SE (bi)</b>	1.53	-	-	0.45	-	-	0.09	-	-	1.16	-	-

specificity of adaptability to high yielding environment. The genotypes, PU99, No. 13/11 and No. 40 indicated regression coefficient less than unity, higher mean values with non-significant deviation from the regression coefficient  $S^2di$  hence, recommended for unfavorable environments only. Kumar and Singh (2017) studied stability of lentil genotypes in mid-hills of Jammu region and reported a similar trend in seed yield/plant. The genotypes, PLU 499-52, PL4158, PU19, Pant 31, and IPU2-43 showed higher mean values than population mean with regression

coefficient greater than unity (b-1) and minimum  $S^2di$  values also followed the trend for seed yield per quintal. These findings indicated their stability and adaptation to specific favorable environment. However, the genotypes, PU99, No. 13/11, No. 40 and PGRU 99022 showed regression coefficient less than unity, higher mean values with non-significant deviation from the regression coefficient  $S^2di$  and therefore, recommended for unfavorable environments only.

Seven genotypes namely, Mash114, T9, NP16, JU96-6, JU468, PL4158 and UH82-14 showed higher

mean values for pod length and three genotypes, PU 19, No. 13/11 and No. 40 for 1000 seed weight than population mean with regression coefficient less than unity ( $b < 1$ ) and minimum  $S^2_{di}$  values i.e. non-significant deviation from the regression coefficient hence, recommended for unfavorable environments only. Three genotypes viz., PU99, PGRU99022 and STTZ 834 and Pant 31 and UH 82-14 showed higher mean values for pod length and 1000 seed weight, respectively than population mean with regression coefficient greater than unity ( $b > 1$ ) and minimum  $S^2_{di}$  values indicating their stability and adaptation to specific favorable environment only. The genotypes, No. 40 and Mash 338 and IPU 96-1 showed at par mean values with population mean and regression coefficient equal to unity ( $b = 1$ ) with minimum and significant deviation from regression coefficient, respectively therefore, identified as stable genotypes for pod length and 1000 seed weight. Genotype IPU96-16 showed high mean value than population mean with non-significant  $S^2_{di}$  and regression coefficient approaching to unity indicated wider adaptability across the environment. Kumar and Singh (2017) studied stability by additive main multiplicative interaction (AMMI) model in micro and macro-sperma lentil (*Lens culinaris* L.) in mid hills of Jammu and Kashmir and found similar trend in urdbean. Similar results were obtained by Kumar et al. (2014) in chickpea (*Cicer arietinum* L.) under same environmental conditions.

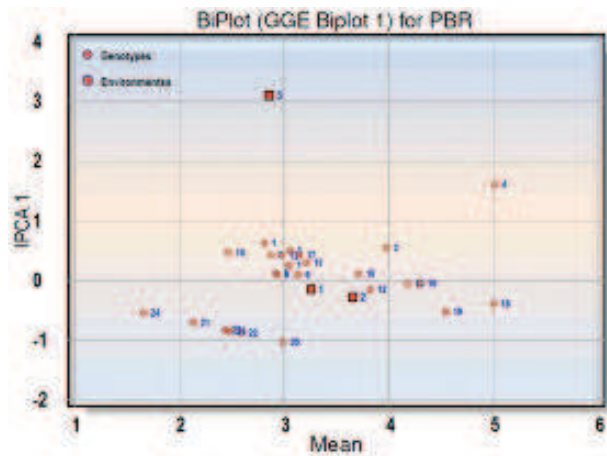
The genotypes, JU468, No.40, PGRU99022 and IPU9616 showed higher mean values for number of seeds/pod than population mean with regression coefficient greater than unity ( $b > 1$ ) and minimum  $S^2_{di}$  values indicated their stability and adaptation to specific favorable environment whereas, five genotypes, namely, Uttara, Mash 114, IPU96-6, PL4158 and Pant 31 showed higher mean values than population mean with regression coefficient less than unity ( $b < 1$ ) and minimum  $S^2_{di}$  values i.e. non-significant deviation from the regression coefficient hence, recommended for unfavorable environments only. Genotypes T9 and Mash338 showed regression coefficient equal to unity ( $b = 1$ ) with higher mean values than the population mean with least deviation from the regression coefficient  $S^2_{di}$  therefore, identified as stable genotypes across the environment for number of seeds/pods. Kannababu et al. (2020) studied stability in sorghum landraces and varieties and reported that high mean and  $b_i = 1$  with non-significant  $\bar{a}^2_{di}$  are suitable for general adaptation across the environments. But the genotypes with high mean,  $b_i$

$> 1$  with non-significant  $\delta^2_{di}$  are considered to be below average in stability. Such genotypes respond favorably to better environments but give poor yield in unfavorable environments. However, genotypes with low mean,  $b_i < 1$  with non-significant  $\delta^2_{di}$  do not respond favorably to good environments and therefore, they are regarded as specifically adapted to poor environments, whereas, Genotypes with any  $b_i$  value with significant  $\delta^2_{di}$  are unstable.

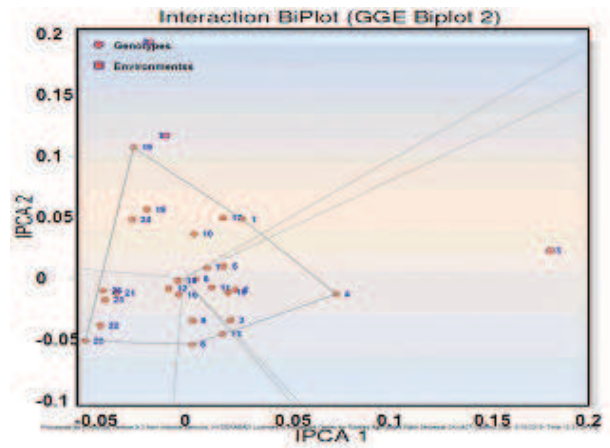
#### **Additive main effects and multiplicative interactions (AMMI)**

The AMMI 1 biplot with main effects plotted against the IPCA1 scores and AMMI 2 biplot plotted against IPCA 1 and IPCA 2 scores. AMMI 1 model indicated that  $E_1$  and  $E_2$  showed similar main effects for days to 50% flowering (DTF). Analysis of genotype main effect showed that 19 genotypes are similar with respect to DTF, however, each had shown different response, i.e., below population mean which is desirable. Based on AMMI 2 model, genotypes viz., G<sub>16</sub>, G<sub>5</sub>, G<sub>1</sub> and G<sub>12</sub> showed lower IPCA1 scores while G<sub>6</sub>, G<sub>13</sub>, G<sub>10</sub> and G<sub>2</sub> also exhibited lower IPCA2 scores in  $E_3$  which is desirable for early days to 50% flowering. AMMI 1 model clustered  $E_1$  and  $E_2$  in the same group (Table 4). G<sub>21</sub>, G<sub>20</sub>, G<sub>24</sub>, G<sub>23</sub> and G<sub>25</sub> are similar and had high IPCA scores with above population mean whereas, G<sub>2</sub>, G<sub>15</sub> and G<sub>18</sub> showed high population mean with negative high IPCA scores. The genotypes G<sub>14</sub> and G<sub>16</sub> were very closed to the point of origin or zero were least affected by the environment.

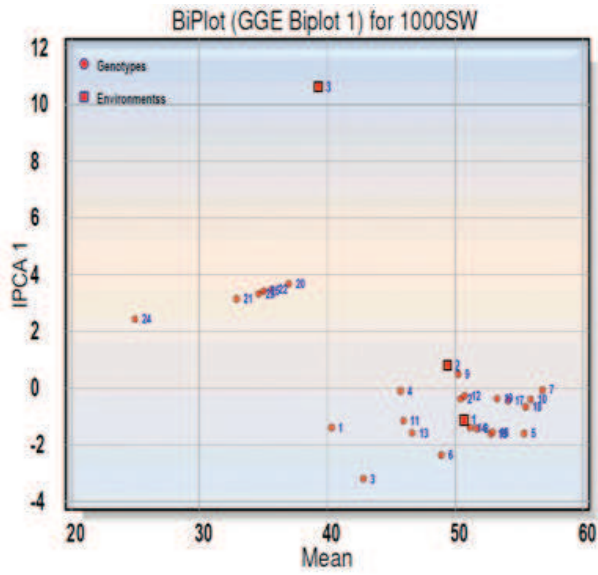
For number of primary branches/plants G<sub>4</sub> had highest positive IPCA scores with high population mean followed by G<sub>1</sub> and G<sub>15</sub>. Environment 1 and 2 showed similar type of main effect (Table 4). Based on AMMI 2 model, G<sub>17</sub>, G<sub>10</sub>, G<sub>19</sub>, G<sub>9</sub>, G<sub>8</sub>, G<sub>18</sub> and G<sub>24</sub> showed high IPCA2 and G<sub>8</sub>, G<sub>7</sub> and G<sub>5</sub> showed high positive IPCA1 positive scores in  $E_1$ . G<sub>12</sub> and G<sub>14</sub> possess a more reliable classification as determined primarily by genotypic effects and the reduced G x E interactions due to very less distance between them or close to the point of origin. As per AMMI 1 model, G<sub>8</sub>, G<sub>11</sub>, G<sub>24</sub>, G<sub>2</sub> and G<sub>3</sub> were isolated for pod length, with high IPCA1 scores (Fig. 1a) with high mean population and clustered with environment ( $E_3$ ). Environment  $E_1$  and  $E_2$  exhibited similar type of main effect (Fig. 2a). On the basis of AMMI 2 model, G<sub>21</sub>, G<sub>16</sub>, G<sub>24</sub>, and G<sub>12</sub> exhibited high IPCA scores. G<sub>3</sub> and G<sub>5</sub> were very close to the point of origin and possess a more reliable classification. In case of number of seeds/pod, G<sub>16</sub>, G<sub>13</sub>, G<sub>1</sub> and G<sub>2</sub> exhibited high IPCA 1 scores along



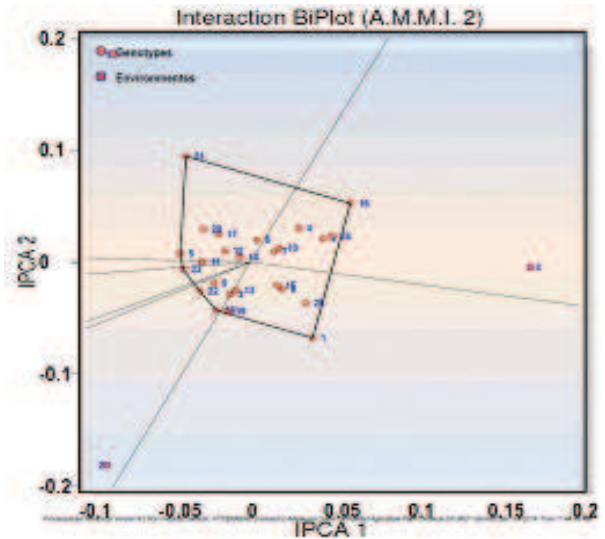
(a) No. of primary branches/plant



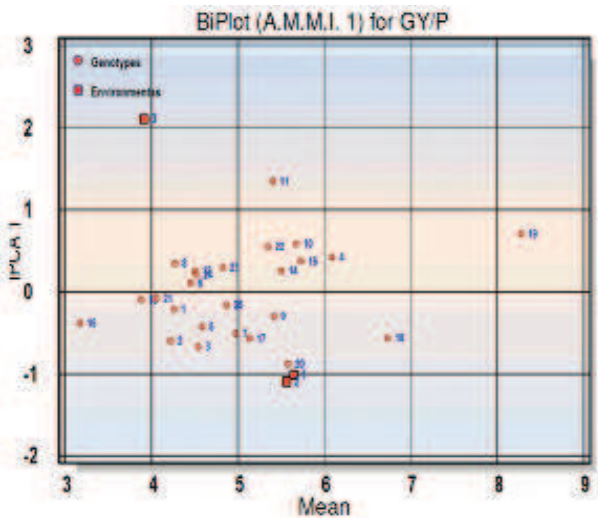
(a) No. of primary branches/plant



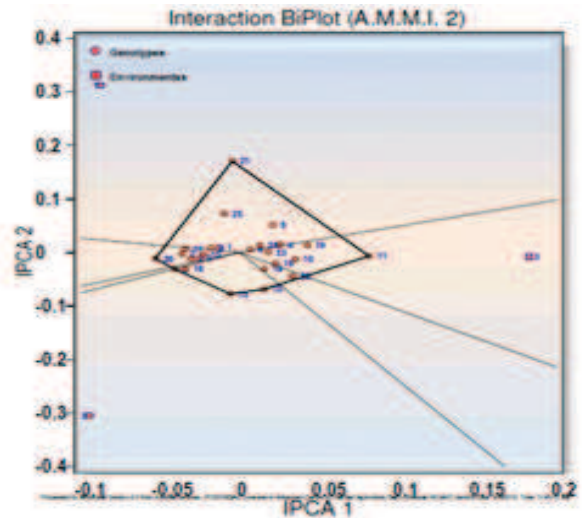
(b) 1000-seed weight



(b) 1000-seed weight



(c) Seed yield/plant



(c) Seed yield/plant

Fig. 1. Interaction biplot for AMMI 1 model on various traits (a-d) in *Vigna mungo* (L.)

Fig. 2. Interaction biplot for AMMI 2 model on various traits (a-h) in *Vigna mungo* (L.)

with high population mean in  $E_3$  whereas  $G_{22}$ ,  $G_{21}$  and  $G_6$  with high negative IPCA 1 scores clustered in  $E_2$ . On the basis of AMMI 2 model,  $G_{21}$ ,  $G_{12}$  and  $G_{20}$  exhibited high IPCA1 score in  $E_2$  and  $G_{13}$  and  $G_{10}$  in  $E_3$  for IPCA2 score.  $G_3$  and  $G_5$  were very close to the origin and possess a more reliable classification. Maximum positive IPCA score was exhibited by  $G_{17}$ ,  $G_{20}$ ,  $G_{18}$  and  $G_{10}$  in  $E_3$  whereas, minimum negative by  $G_1$ ,  $G_3$ , and  $G_{11}$  in  $E_1$ . High IPCA 2 scores were displayed by  $G_{10}$ ,  $G_{18}$ ,  $G_{11}$  and  $G_{12}$  in  $E_3$  which is desirable for days to maturity (DTM).

For 1000 seed weight, the genotypes,  $G_{20}$ ,  $G_{22}$  and  $G_{21}$  exhibited high IPCA1 scores on the basis of AMMI1 model in  $E_2$  whereas  $G_3$ ,  $G_6$  and  $G_1$  showed negative high IPCA1 scores. Environment 2 and Environment 3 exhibited similar type of main interactions (Table 4).  $G_{14}$ ,  $G_{11}$ ,  $G_5$ ,  $G_7$  and  $G_{10}$  in  $E_3$

**Table 4.** Environmental indices of grain yield and yield components traits in *Vigna mungo* L.

S.No. Traits	Environ- ( $E_1$ )	Environ- ( $E_2$ )	Environ- ( $E_3$ )
1 Days to 50% flowering	-0.85	-0.60	1.46
2 Plant height	3.27	3.64	-6.90
3 No. of orimary branches	0.17	0.19	-0.36
4 Pod length	-0.01	-0.11	0.12
5 Number of seeds/pods	-0.26	-0.21	0.47
6 Days to maturity	-6.71	-6.29	13.00
7 1000 seed weight	0.71	-0.01	-0.70
8 Seed yield/plant(g)	0.61	0.52	-1.13

exhibited high IPCA1 scores whereas,  $G_{21}$ ,  $G_{16}$ ,  $G_{20}$ , and  $G_4$  exhibited high IPCA2 scores in  $E_1$  (Figs. 1b and 2b).  $G_{14}$  and  $G_{12}$  were close to the origin and least affected by the  $G \times E$  interaction and therefore showed high stability with respect to 1000 seed weight, a major yield component. For seed yield/plant, AMMI 1 model exhibited that  $E_1$  and  $E_2$  were clustered in the same group and exhibited similar type of interaction (Fig. 1c).  $G_{11}$ ,  $G_{19}$ ,  $G_4$ ,  $G_{10}$  and  $G_{22}$  exhibited high IPCA1 scores in  $E_3$  along with high population mean. As per AMMI 2 model,  $G_{11}$ ,  $G_{19}$ ,  $G_{23}$ ,  $G_1$  and  $G_8$  exhibited high IPCA1 scores in  $E_1$  (Fig. 2c) whereas,  $G_{21}$ ,  $G_{25}$  and  $G_8$  indicated high positive IPCA2 scores (Fig. 2b).  $G_1$  and  $G_{24}$  were close to the point of origin and least affected by the  $G \times E$  interaction and hence these genotypes are more stable.

GEI play an important role in developing the crop varieties. The perusal of pooled analysis of variance (Table 1) indicated that all the traits under study had significant differences among the varieties, environment, environment linear pooled deviation except DTF, DTM &GY/plant. GEI was found significant for all the varieties, environment and environment linear indicated the genetic differences among the genotypes for their regression on environmental index. Significant pooled deviation was recorded for all the traits except DTF, DTM and GY/plant which reflected the presence of sufficient amount of genetic variations in the breeding material. Pooled deviation have practical utility to construct and help in testing the significance of multiple regression models to know the complex mechanism of adaptation (Dar et al. 2009). The trait showed non-significant differences for GEI linear for 1000 seed weight indicating that the performance of the genotypes cannot be predicted over the environments. In such conditions, mean performance and their pooled deviation of genotypes may indicate stability of genotypes. The pattern of stability showed that genotypes No. 40 ( $G_{19}$ ), Mash 338 ( $G_{12}$ ) were found stable for pod length, T9( $G_3$ ) and Mash 338 ( $G_{12}$ ) for number of seeds / pod and IPU96-1( $G_{19}$ ) for 1000 seed weight were stable across the environments.

Due to significance of linear component of GEI, the mean value,  $b_i$  and  $S^2d_i$  were taken under consideration to find out the stable genotypes for DFF, PH, and NPBP. Raturi et al. (2012) studied stability *Vigna radiata* genotypes under arid environment and reported similar findings for some traits. The stable performance of genotypes No.40 ( $G_{18}$ ), Mash 338 ( $G_{12}$ ), T9( $G_3$ ) and IPC96-1( $G_{19}$ ) under all the three environments may be utilized in pulses (blackgram) improvement programmes. The genotypes that gave consistent performance under favorable environment may be utilized for trait manipulations and other breeding programmes under targeted environments. The environmental indices indicated that  $E_1$  and  $E_2$  were desirable for plant height, number of primary branches/plants, 1000 seed weight and grain yield/plant. This indicated that higher plant height promotes the days to fifty percent flowering, no. of primary branches/plants, grain yield/plant and days to maturity whereas, environment  $E_3$  promotes traits viz., pod length and number of seeds/pods. Yimran et al. (2009) reported that tall plant stature is desirable for mechanical harvesting. The AMMI approach revealed that more complex GEI could not facilitates the



graphical visualization of the genotypes in low dimensions. So, AMMI analyses could be used as an alternative procedure to infer the GEI. Namorato et al. (2009) also reported that AMMI approach is more efficient than Eberhart and Russel model (1966) of stability.

To test the main and interaction effects over the environments AMMI1 and AMMI2 biplots were constructed for seed yield and its components. AMMI model indicated the genotypes and environment divided into four groups i.e. right up (high yielder and stable), right down (high yielder and unstable), left down (low yielder unstable) and left up (low yielder stable). In AMMI1, if the main effects have IPCA score near to zero or close to the point of origin indicating the negligible interaction effects and the same sign on IPCA axis for both genotypes and environments indicating the positive interaction effects and vice-versa. The AMMI ANOVA for peanut yield indicated contribution of G, E and GEI to moderate to large variation and identified significant IPCA1 to IPCA3. According to AMMI2 biplot analysis, many genotypes were positioned in the center of the biplot so had the least GxE interaction and showed the most general compatibility (Lal et al. 2019). AMMI2 biplot explains the nature and magnitude of GEI interaction. In AMMI analyses, the IPCA scores give the indication of stability or adaptability of genotypes over environments. The genotypes had greater IPCA scores indicated their specific adoption in given environment and genotypes having IPCA scores close to zero are stable in sampled environment.

For seed yield/plant, AMMI1 model exhibited that  $E_1$  and  $E_2$  were clustered in the same group ( $E_1$  and  $E_2$ ) and exhibited similar type of interaction.  $G_{11}$ ,  $G_{19}$ ,  $G_4$ ,  $G_{10}$  and  $G_{22}$  exhibited high IPCA1 scores in  $E_3$  along with high population mean. Based on AMMI 2 model,  $G_{11}$ ,  $G_{19}$ ,  $G_{23}$  and  $G_1$  and  $G_8$  exhibited high IPCA1 scores in  $E_1$  whereas,  $G_{21}$ ,  $G_{25}$  and  $G_8$  indicated high positive IPCA 2 scores.  $G_1$  and  $G_{24}$  were close to the origin and least affected by the G x E interaction.  $G_{11}$ ,  $G_{19}$  and  $G_{10}$  were outlier as per grain yield is concerned in  $E_3$  and indicated that  $E_3$  better than any other E and these three genotypes were found stable for grain yield/plant. Choudhary et al. (2019) analysed genotype X environment in baby corn following GGE biplot and reported that AMMI2, first (PC1) and second (PC2) principal component were used to account for the variation. For yield and green fodder yield, AMMI2 accounted for explaining genotype and genotype x

environment variation of high order.

These genotypes were more stable as also confirmed by Eberhart and Russel Model (1966). Stable genotypes were identified through this model in different crops under diverse environments earlier by several researchers (Namorato et al. 2009; Sara et al. 2019). From the present study, it was concluded that sufficient amount of genetic variability was present among the genotypes, environment, G x E, environment linear and pooled deviation. The presented results from both the approaches explained the potential of genotypes in terms of seed yield and its components to select the most suitable genotypes and the proper utilization and trait manipulation in *Vigna mungo* L improvement under rainfed conditions of Jammu and Kashmir.

#### Authors' contribution

Conceptualization of research (SK, JPS, AK); Designing of the experiments (SK, JPS, HKC, AK); Contribution of experimental materials (HKC, JPS, SK); Execution of field/lab experiments and data collection (SK, JPS, AK, APS); Analysis of data and interpretation (SK, JPS, RS, RG, MS, AKS); Preparation of manuscript (SK, JPS, AK, HKC).

#### Declaration

The authors declare no conflict of interest.

#### Acknowledgement

The authors are thankful to Director Research of SKUAST Jammu for sanctioning the project and funding under RCM and also thankful to Director Indian Institute of Pulses Research, Kanpur for providing the seed material of urdbean.

#### References

- Ajay B. C., Aravind J., Fiyaz A. R., Kumar N., Lal C., Gangadhar K., Kona P., Dagla M. C. and Bera S. K. 2019. Rectification of modified AMMI stability value (MASV). *Indian J. Genet.*, **79**(4): 726-731. DOI: 10.31742/IJGPB.79.4.11
- Ali Y. and Sawar G. 2008. Genotype x environment interaction in cowpea genotypes. *Indian J., Env. Prot.*, **2**: 125-132.
- Choudhary M., Kumar Bhupender, Kumar P., Guleria S. K., Singh N. K., Khulbe Rajesh, Kamboj M. C., Vyas M., Srivastava R. K., Puttaramanaik, Swain D., Mahajan V. and Rakshit S. 2019. GGE biplot analysis of genotype x environment interaction and identification of mega-environment for baby corn hybrids evaluation in India. *Indian J. Genet.*, **79**(4):

- :658-669). DOI: 10.31742/IJGPB.79.4.3
- Dar S. A., Pir F. A. and Manjar A. 2009. Phenotypic stability in chickpea (*Cicer arietinum* L.) under temperate climate. Trends Biosci., **2**: 4-5.
- Dayali S. F., Razavi F., Segherloo A. E., Dehghani H. and Sabaghpour S. H. 2012. Yield stability in chickpea and study relationship among the univariate and multivariate stability parameters. Res. Pl. Biol., **2**: 46-61.
- Deitos A., Arnhold E. and Miranda G. V. 2006. Yield and combining ability of maize cultivars under different ecogeographic conditions. Crop Br. Appl. Biotech., **6**: 222-227.
- Eberhart S. A. and Russell W. A. 1966. Stability parameters for comparing varieties. Crop Sci., **6**: 36-40.
- Grunvald A. K., Carvalho C. G. P., Oliveira A. C. B. and Andrade C. A. B. 2008. Adaptabilidade e estabilidade de genótipos de girassolno Brasil Central. Pesquisa Agropecuária Brasileira, **43**: 1483-1493.
- Gupta S. S., Kumar S. and Singh B. B. 2004. Relative genetic contributions of ancestral lines to Indian mungbean cultivars based on coefficient of percentage analysis. Indian J. Genet., **64**: 299-302.
- Kannababu N., Madhusudhana, Elangovan M., Avinash S., Das I. K. and Tonapi Vilas A. 2020. Stability analysis for seed longevity in landraces of sorghum [*Sorghum bicolor* (L.) Moench]. Indian J. Genet., **80**(1): 39-49. DOI: 10.31742/IJGPB.80.1.5.
- Kumar S. and Singh P. 2017. Stability by additive main multiplicative interaction (AMMI) model & genetic diversity studies in micro and macro-sperma lentil (*Lens culinaris* L.) in mid hills of Jammu and Kashmir, India. Legume Res., **40**(4): 635-638.
- Kumar S., Sharma M., Khar S. and Singh P. 2014. Stability analysis for seed yield and yield attributing traits in chickpea (*Cicer arietinum* L.) under mid hills of Jammu & Kashmir, India. Legume Res., **37**(5): 552-555.
- Kumar S., Singh P. and Sharma M. 2017. Genetic divergence and stability (AMMI) study in chickpea (*Cicer arietinum* L.) under north western Himalayas of Jammu and Kashmir, India. Legume Res., **40**(5): 842-845.
- Lal Chuni, Ajay B. C., Chikani B. M. and Gor H. K. 2019. AMMI and GGE biplot analysis to evaluate the phenotypic stability of recombinant inbred lines (RILs) of peanut under mid-season water stress conditions. Indian J. Genet., **79**(2): 420-426. DOI: 10.31742/IJGPB.79.2.5.
- Namorto H., Miranda G. V., Souza L. V. D., Oliveira L. R., De-Lima R. O. and Mantovani E. E. 2009. Comparing biplot multivariate analyses with Eberhart and Russell' method for genotype x environment interaction. Crop Breed. Appl. Biotechnol, **9**: 299-307.
- Raturi A., Singh S. K., Sharma V. and Pathak R. 2012. Stability and environmental indices analyses for yield attributing traits in Indian *Vigna radiata* genotypes under arid conditions. Asian J. Agric. Sci., **4**: 126-133.
- Sara M., Abbas R., Reza A. and Alireza Etminan. 2019. Yield stability of rapeseed genotypes under drought stress conditions. Indian J. Genet., **79**(1): 40-47. DOI: <https://doi.org/10.31742/IJGPB.79.1.6>.
- Singh C. M., Mishra S. B., Pandey Anil and Arya Madhuri. 2014. Eberhart – Russell' and AMMI Approaches of Genotype by Environment Interaction (GEI) for Yield and Yield Component Traits in *Vigna radiata* L. Wilczek. IJAEB, **7**(2): 277-292.
- Souframanien J. and Gopalkrishnan T. 2004. A comparative analysis of genetic diversity in black gram genotypes using RAPD and ISSR markers. Theor. Appl. Genet., **109**: 1687-1693.
- Souza L. V., Miranda G. V., Galvao J. C. C., Eckert F. R., Mantovani E. E., Lima R. O. and Guimares L. J. M. 2008. Genetic control of grain yield and nitrogen use efficiency in tropical maize. Pesquisa Agropecuária Brasileira, **43**: 1517-1523.
- Verma S. K., Tuteja O. P. and Monga D. 2008. Evaluation of G x E interaction in relation to stable genetic male sterility based on Asiatic cotton hybrids of north zone. Indian J. agric. Sci., **78**: 375-378.
- Yan W., Kang M. S., Ma B., Woods S. and Cornelius P. L. 2007. GGE Biplot vs AMMI Analysis of genotype-by-environment data. Crop Sci., **47**: 643-655.
- Yimram T., Somta P. and Srinives P. 2009. Genetic variation in cultivated mungbean germplasm and its implication in breeding for high yield. Field Crop Res., **112**: 260-266