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Eberhart – Russell' and AMMI Approaches of Genotype by Environment Interaction (GEI) for Yield and Yield Component Traits in *Vigna radiata* L. Wilczek

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Abstract

Evaluation of genotype by environment interaction (GEI) is very important for development of crop varieties with good potential. In this study, Eberhart - Russell' and AMMI approaches were used to analyse the pattern of stability under targeted environment. The pattern of stability parameters of seed yield indicated that two genotype *viz.,* G2 and G36 exhibited high mean seed yield with non-significant s^2di, whereas G33 showed average seed yield (mean) and non-significant s^2di. Environmental indices indicated that environment A and environment B were most favourable for most of the yield component traits, whereas environment C was unfavourable for almost all the yield and yield component traits. Based on AMMI 1; G1, G2, G18, G4, G3, G24, G22 and G25 were found stable for seed yield. For seed yield; genotypes and environments were grouped into nine sectors (AMMI 2). The first sector consist of with environment B with high IPCA score for some outlier genotypes *i.e.* G25, G14 and G22, indicated that the environment B was better than other environments and three genotypes were found stable for SYP. The selected genotypes may be utilized in *Vigna radiata* improvement programme at targeted location with true type of breeding lines.

Highlights

- Based on Eberhart – Russell approach, G2 and G36 were found stable for seed yield; whereas G1, G2, G18, G4, G3, G24, G22 and G25 were found stable based on AMMI 1.

- Genotypes and environments were grouped into nine sectors based on AMMI 2 and G25, G14 & G22 were found stable for seed yield.

- Environment B (timely sown) was found ideal for seed yield followed by environment A (early sown) and C (late sown).

The major constraint to develop the high yielding varieties of *Vigna radiata* (L.) Wilczek are low inherited yield potential, lack of genetic variability, lack of suitable ideotype, poor harvest index and susceptibility to biotic and abiotic factors (Souframanien and Gopalkrishnan 2004; Srinives, 2006). This may be due to utilization of only some

selected genotypes of *Vigna radiata* (L.) Wilczek in varietal development programme (Gupta, 2004). Thus, there is need to construct the suitable ideotype and identify the suitable and stable donors. Yield is ultimate objective of any crop improvement programme and depends upon its yield component traits. The yield component traits are highly influenced by the environment. Thus, first we need to identify the stable genotypes for their yield and yield component traits. The genotype × environment interaction (GEI) have immense importance in breeding programme to identify the stable genotypes that are widely adapted to unique environment (Verma *et al.*, 2008). Stability of genotypes over wide range of environments is desirable and depends upon GEI (Ali and Sawar, 2008). To understand the structure and nature of GEI is very important in crop improvement programmes because the significant GEI can seriously impair efforts in selecting the superior genotypes (Danyali *et al.*, 2012).

To identify the stable genotypes, the data is based on multi-year, multi-location and/ or multi-season. But for crop improvement programmes in targeted location, there is need to isolate some lines/ genotypes in that particular targeted location for proper utilization of those lines. Thus, evaluation of genotypes at targeted location is also very important. Stability analysis in targeted location required multi-year data but it is time taken. Thus, creation of environments can be done by adjusting the sowing dates to manage this problem and identify the stable genotypes in single season under targeted location. The isolated genotypes can be used for general cultivation and / or trait manipulation in greengram improvement. Keeping the above facts under consideration, the present experiment was conducted to identify the stable genotypes for yield and yield component traits in targeted location for greengram improvement.

Materials and Methods

Plant material

The experimental material comprised thirty-six genotypes of *Vigna radiata* (L.) Wilczek *viz.,* HUM 12 (G1), IPM 02-14 (G2), NDM 9-18 (G3), ML 1666 (G4), DM 05-12-1-42-3 (G5), DMS 01-34-2 (G6), DMS 03-17-2 (G7), DM 99-11-5 (G8), SML 668 (G9), Samrat (G10), DMC 17 G11), Meha (G12), Sona selection (G13), IPM 2K-14-9 (G14), DM 05-74-11 (G15), IPM 99-01-10 (G16), PM 2 (G17), P 1131 (G18), DMS 02-11-4 (G19), IPM 99-1-6 (G20), P 1232 (G21), P. Vishal (G22), P 1131 (G23), IPM 2K-15-4 (G24), P 9531 (G25), PM 08-2 (G26), NDM 12-

308 (G27), DMS 02-11-13 (G28), IPM 99-394 (G29), SML 1186 (G30), PM 5 (G31), SML 1151 (G32), P Baishakhi (G33), AKM 8803 (G34), HUM 16 (G35) and TMB 37 (G36). These genotypes were numbered serially G1 to G36. The entries were received from Pulse Breeding Section, Department of Plant Breeding and Genetics, Tirhut College of Agriculture, Dholi, Muzaffarpur, Bihar, India.

Experimental design and growing condition

The experiment was conducted at Crop Research Farm of TCA, Dholi (RAU, Pusa), which is situated (25.5^0N, 35.4^0E, 52.12 m MSL) in district Muzaffarpur of North Bihar, India. The experiment was conducted in Randomized Block Design (RBD) with three replications under three environments by adjusting the sowing dates at 15 days interval *viz.,* 10 July 2012 (early sown as E_1), 25 July 2012(timely sown as E_2) and 11 August 2012 (late sown as E_3). Each genotype was sown in six rows in plot of four m length with 30 cm inter-row and 10 cm intra-row (inter-plant) spacing.

Data collection

Five random plants were selected from each genotype in each replication to record the data for all the yield and yield component traits (except days to 50% flowering) *viz.,* plant height (PH), number of primary branches per plant (NPBP), number of secondary branches per plant (NSBP), number of clusters per plant (NCP), number of pods per cluster (NPC), pod length (PL), number of seeds per pod (NSP), selling percentage (SP), seed index (SI), biological yield per plant (BYP), harvest index (HI) and seed yield per plant (SYP). Days to 50% flowering (DFF) was recorded on plot basis. Pod mass (PM) and seed mass (SM) were recorded by weighing the 10 pods and seeds from these 10 pods from five randomly selected plants and averaged. Pod wall mass (PWM) obtained by subtracting the seed mass from pod mass. Pod wall proportion (PWP) is an index obtained by dividing the weight of pod wall by weight of whole pod.

Biometrical analysis

The data for all the traits were subjected to analysis of variance and stability parameters using statistical package Windostat 8.6 version. The stability of the genotypes for each trait was calculated by regression of the mean of individual genotypes in environmental index and deviation from the regression coefficient from unity as per methodology of Eberhart and Russell model (1966). The model is:

$$Y_{ij} = \mu_i + \beta_i I_j + \sigma_{ij}$$

Where, Y_{ij} = mean of the ith genotype at j^{th} environment, μ_i = mean of the ith genotype over environments, β_i = regression coefficient of the ith genotype to the change of environments, I_j = environmental index, σ_{ij} (S^2D) = deviation from regression coefficient.

The regression coefficient (β_i) was tested against t-test for their significance, whereas significance of deviation from regression (SSd_i^2) was tested by F test. To analyze the GEI, the additive mean effect and multiplicative interaction effects (AMMI) model was used 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 homogeneous error for each trait study using Bartlett's test and allow for pooled analysis of variance (ANOVA) on 17 yield and yield component traits over three environments, indicated the significant differences among genotypes for all the traits studied except PM, PWM, PWP, SM, SP and HI; have been presented in Table 1. Variance due to environments and environment (linier) showed significant differences for all the traits studied except PM, indicated the environments are variable in this investigation. GEI further subdivided into linear (bi) and non linear (s^2di) components. The significance of linear component of GEI was recorded for DFF, PH and NSBP. Significant non linear component (pooled deviation) was recorded for all the traits studied except DFF. AMMI analysis was further done to estimate the GEI for various yield and yield component traits. IPCA 1 was found significant for all the traits studied, whereas IPCA 2 was found significant for six traits *viz.,* DFF, PH, NSBP, NSP, PM and SI.

Stability parameters

The mean performance (μ), regression coefficient (bi) and deviation from regression (S^2di) have been presented in Table 2. The perusal of data revealed that all the genotypes hadn't non-significant deviation from regression coefficient for all the traits studied. The pattern of stability parameters for various the yield component traits indicated that out of 36 genotypes, two genotype *viz.,* G2 and G36 exhibited high mean seed yield with non-significant $s^2di = 0$, whereas G33 showed average seed yield (mean) and non-significant

$s^2di = 0$. Similarly G15, G16, G20, G35 (NPBP), G3, G6, G15, G18, G29, G33 (NCP); G32 (NPC); G31, G32 (PL); G7, G18, G23, G26, G35 (NSP); G26, G29 (PM); G18, G26 (PWM), G9, G17, G18, G29 (PWP), G1, G12, G30 (SM); G1, G2, G8, G14, G21, G27, G35 (SP); G4, G11, G26 (SI); G12, G15 (BYP); G6, G15, G36 (HI); G36 (SYP) G11, G33 (NPC); (PL); G4 (NSP); G28 (PWP) and G3, G5, G14, G16, G17 (SI) were exhibited high mean with non-significant $s^2di = 0$ for various yield component traits given in parenthesis. Whereas, G34 (NCP); G11, G12 (NPC); G26 (PL); G17, G36 (NSP); G32 (PWM) and G3, G6, G7, G10, G12, G18, G19, G28 (SI) were exhibited low to average mean with non-significant $s^2di = 0$ for various yield component traits given in parenthesis. The mean value, bi and s^2di were taken under consideration to find out the stable genotype(s) for DFF, PH and NSBP. None of the genotypes exhibited high mean with unity of bi and minimum deviation from regression coefficient (s^2d) for DFF, PH and NSBP. G4, G5, G9, G28, G29 (DFF); G9, G11, G16, G17, G18, G19, G26, G27, G29, G31 (PH) and G15, G32 (NSBP) were exhibited high mean with bi>1 and non significant $s^2d = 0$, whereas G11, G30, G34, G35 (DFF); G24 (PH); G11, G17, G30 (NSBP); G34 (NCP); G11, G12 (NPC); G26 (PL); G17, G36 (NSP); G32 (PWM) and G3, G6, G7, G10, G12, G18, G19, G28 (SI) were exhibited low to average mean with bi = 1 and non significant $s^2d = 0$ for various yield component traits given in parenthesis.

Environmental indices

Environmental index was calculated from mean of all the genotypes in each environment by subtracting the grand mean. The environmental indices for various yield component traits have been presented in Table 3. Environmental indices indicated that environment A (E1) was most favourable for DFF, PH, NPBP, NSBP, NPC, PL, PM, SM and SI and unfavourable for NCP, NSP, SP, HI and SYP, whereas for NCP, NSP, SP, HI and SYP. Environment B (E2) was found most favourable environment. Moreover, E2 also found good for rest of the yield component traits. Environment C (E3) was unfavourable for almost all the yield and yield component traits.

Additive main effect and multiplicative interaction (AMMI)

AMMI biplot for various yield and yield component traits have been presented in Figure 1(A-J) and 2 (A-J). The

Table 1: Analysis of variance (ANOVA) for stability parameters on various yield and yield component traits in *Vigna radiata* (L.) Wilczek.

SV	DF	DFF	PH	NPBP	NSBP	NCP	NPC	PL	NSP	PM	PWM
					Traits						
Replication within E	6	6.97**	10.63	0.21	0.84*	3.67	1.06	0.29	4.34*	0.001	0.001
G	35	19.18**	131.47**	1.98**	3.59**	5.01*	1.07*	0.57	3.45**	0.001	0.001
E + (G x E)	72	11.09**	68.61**	0.67**	1.26**	12.75**	1.22*	0.77**	7.72**	0.004	0.002 *
E	2	298.80**	886.18**	9.88**	21.61**	344.06**	21.31**	19.45**	241.70**	0.008	0.031 **
G x E	70	2.87	45.25	0.40	0.68*	3.28	0.64	0.23	1.04	0.004	0.001
E (Linier)	1	597.60**	1772.36**	19.76**	43.21**	688.11**	42.62**	38.90**	483.41**	0.017	0.062 **
G x E (Linier)	35	3.86*	61.25*	0.49	1.02**	3.78	0.66	0.13	0.58	0.003	0.001
Pooled Deviation	36	1.83	28.44**	0.31**	0.34**	2.71**	0.61**	0.32**	1.45**	0.004 **	0.001 **
Pooled Error	210	1.38	1.26	0.07	0.07	0.55	0.12	0.05	0.39	0.001	0.001
Total	107	13.74	89.17	1.10	2.02	10.22	1.17	0.70	6.33	0.005	0.002

SV	DF	PWP	SM	SP	SI	BYP	HI	SYP
				Traits				
Replication within E	6	8.38	0.001	6.55	0.37**	3.38	28.45	0.877
G	35	48.52	0.004	44.53	0.28**	50.08**	98.61	4.628 **
E + (G x E)	72	133.58**	0.004	139.63**	0.39**	35.78*	149.24*	2.768
E	2	2964.14**	0.067**	3089.63**	12.95**	331.14**	2873.07**	49.95**
G x E	70	52.71	0.002	55.34	0.029	27.34	71.41	1.42
E (Linier)	1	5928.27**	0.134**	6179.26**	25.90**	662.27**	5746.15**	99.91**
G x E (Linier)	35	50.261	0.002	48.69	0.023	33.65	52.16	0.87
Pooled Deviation	36	53.63**	0.003**	60.28**	0.03**	20.44**	88.15**	1.92**
Pooled Error	210	13.634	0.001	14.655	0.012	0.802	8.28	0.166
Total	107	105.759	0.004	108.522	0.353	40.453	132.67	3.376

SV = Source of variation, G = Genotypes, E = Environments, DFF= Days to 50% flowering (Days), PH= Plant height (cm), NPBP= Number of primary branches per plant, NSBP= Number of secondary branches per plant, NCP= Number of clusters per plant, NPC= Number of pods per cluster, PL= Pod length (cm), PM= Pod mass (g), PWM= Pod wall mass (g), PWP= Pod wall proportion (%), SM= Seed mass (g), SP= Selling percentage, SI= Seed index (%), BYP= Biological yield per plant (g), HI= Harvest index (%), SYP= Seed yield per plant (g).

Table 2: Estimates of mean (μ), regression coefficient (bi) and deviation from regression (S²di) for various yield and yield component traits in *Vigna radiata* (L.) Wilczek

Genotypes   Traits

	DFF			PH			NPBP		
	Mean	bi	S²Di	Mean	bi	S²Di	Mean	bi	S²Di
G1	28.33	0.89	-1.15	42.32	1.74	49.28	2.7	0.33	0.47 **
G2	32.89	1.59	-1.43	41.73	0.98	1.06	3.16	1.14	-0.03
G3	32.89	0.73	-0.63	45.75	0.88	20.55	3.144	1.77	0.11
G4	35.44	1.82	-1.09	51.17	0.67	39.37	3.40	0.81	0.16
G5	34.11	1.16	1.87	54.79	-0.59	68.27	2.82	-0.01	0.29*
G6	33.44	0.97	1.22	44.84	-0.59	36.11	2.61	1.26	-0.08
G7	31.78	0.53	3.31	44.49	0.76	-1.20	3.04	0.33	0.05
G8	35.00	0.70	-1.35	47.93	2.31	3.82	2.40	0.47	-0.07
G9	35.89	1.37	-1.18	52.29	1.90	67.84	3.23	1.62	0.86**
G10	30.11	-0.23	-0.55	44.79	1.94	36.59	3.07	0.08	0.43*
G11	31.33	1.06	-1.34	52.04	1.42	32.23	2.94	0.51	0.13
G12	31.67	0.20	2.03	40.64	1.95	55.34	3.26	-0.05	-0.07
G13	44.11	1.12	18.66**	33.15	1.41	0.08	7.48	0.19	0.84**
G14	32.11	0.80	-1.06	33.63	0.05	8.93	3.05	1.50	0.38*
G15	31.33	1.22	0.69	54.33	0.39	13.77	3.30	1.24	-0.03
G16	31.22	1.17	0.14	52.78	1.40	55.62	3.79	2.74	0.12
G17	31.78	1.63	-0.82	55.27	1.55	46.34	2.94	1.28	-0.03
G18	32.89	2.15*	-1.41	57.55	1.12	-1.47	2.71	1.74	0.15
G19	32.11	0.55*	-1.53	57.81	1.47	14.56	2.59	1.14	-0.03
G20	32.33	0.78	0.63	38.24	-2.26	12.33	3.29	2.11	0.08
G21	31.33	1.25	-1.47	48.86	1.56	67.49	2.81	1.04	0.24*
G22	32.11	0.77	-1.48	48.49	2.04	1.62	3.00	-0.32	1.37**
G23	31.56	0.49	1.28	55.77	1.05	-1.30	2.73	0.76	-0.02
G24	31.44	0.33	-1.44	46.39	1.15	6.30	2.81	1.45	0.14
G25	32.33	0.78	-0.97	52.55	-0.259	22.92	2.67	1.39	-0.08
G26	32.33	0.97	-0.95	54.99	1.144	-1.35	2.79	1.53	0.07
G27	33.44	0.94	-1.36	56.22	2.864	5.67	3.02	1.27	0.22
G28	33.78	1.15	0.88	48.06	1.495	4.05	2.79	1.65	0.67**
G29	34.11	1.49	-1.46	58.23	2.089	113.41	3.18	1.59	0.90**
G30	33.00	1.06	-1.34	45.98	0.932	119.24	3.56	2.49	0.59**
G31	31.00	1.25	-1.47	53.11	1.241	4.59	2.46	1.13	-0.06
G32	30.89	1.93*	-1.53	44.63	-1.896	44.19	2.54	-0.02	0.24*
G33	31.44	0.62	7.67*	47.12	0.968	8.54	3.04	-0.89	-0.01
G34	31.78	1.02	-0.61	38.41	0.088	2.96	3.22	-0.08	0.06
G35	28.78	1.02	-0.99	52.64	0.34	0.91	3.59	3.41	0.10
G36	32.44	0.75	2.18	47.82	2.7	10.30	2.94	-0.61	0.13
Mean	32.57+95.67			48.47+3.77			3.12+0.39		

Traits

	NSBP			NCP			NPC		
	Mean	bi	S²Di	Mean	bi	S²Di	Mean	bi	S²Di
G1	3.29	-0.52	-0.07	11.77	1.63	13.94**	5.49	0.44	0.61*
G2	3.12	-0.11*	-0.09	12.72	1.69*	-0.62	4.38	-0.21	-0.08
G3	2.90	0.81	0.30*	12.70	1.41	-0.60	4.59	0.65	0.07
G4	3.11	-1.20	0.60**	10.35	-0.08	3.20*	4.70	1.38	0.60*
G5	2.90	-0.60	0.78**	9.61	0.52*	-0.63	4.16	-0.05	-0.05
G6	3.36	0.32	0.41*	11.70	1.36	-0.50	3.71	0.38	1.26**
G7	3.01	0.88	0.27*	10.59	1.16	7.65**	4.93	1.11	1.19**

Contd.......

	Mean	bi	S²Di	Mean	bi	S²Di	Mean	bi	S²Di
G8	3.07	1.16	-0.09	10.13	1.06	4.32**	6.32	3.50	7.33**
G9	3.03	1.76	1.62**	9.91	0.62	-0.51	4.74	0.35	0.12
G10	2.83	0.77	0.17	8.87	0.91	1.58	3.18	1.06	0.38
G11	2.62	1.08	0.20	9.21	0.02	-0.06	4.46	1.08	0.07
G12	2.76	0.73	0.15	10.67	0.31	13.94**	3.81	0.99	0.81*
G13	9.30	4.50*	-0.02	11.20	0.43	-0.28	4.28	0.44	-0.13
G14	2.70	1.02	1.71**	9.29	1.32	0.10	4.96	2.11	1.27**
G15	3.20	1.71	0.16	10.67	1.21	-0.63	3.64	0.18	-0.11
G16	2.58	1.70	-0.03	8.79	0.95	0.91	4.40	1.73	0.01
G17	2.64	1.06	0.02	9.31	1.46	1.88*	4.00	1.98	-0.04
G18	3.12	1.27	-0.015	10.58	1.77	-0.35	4.20	1.82	-0.11
G19	3.41	1.33	0.70**	9.39	1.57	5.12**	4.16	1.11	-0.05
G20	3.47	1.41	0.43*	8.90	1.08	-0.56	3.47	1.13	-0.05
G21	3.07	0.96	-0.07	9.19	0.88	0.46	4.39	-0.16	0.05
G22	2.50	0.50	-0.07	8.06	0.86	-0.45	3.96	0.54	0.41
G23	2.82	1.10	0.22	9.37	0.76	0.36	3.76	0.37*	-0.15
G24	3.14	1.70	1.13**	7.63	0.82	0.18	3.89	0.38	-0.02
G25	2.90	0.58	0.51*	8.20	0.89	7.29**	3.76	1.22	0.79*
G26	2.83	0.98	-0.06	10.94	1.21	2.99*	4.43	0.49	0.54*
G27	2.76	0.42	-0.09	9.82	0.68	0.04	3.89	0.70	0.01
G28	2.80	1.59	0.14	10.44	1.45	7.13**	3.88	1.37	-0.12
G29	3.08	1.54	-0.04	11.39	1.33	-0.62	3.88	0.65	-0.08
G30	2.53	1.07	-0.02	9.73	1.44	3.77**	3.47	1.20	0.74*
G31	2.50	1.29	0.01	8.19	0.87	-0.58	4.06	1.27*	-0.15
G32	3.20	1.65	-0.04	10.07	0.76	0.17	4.43	1.26	-0.09
G33	3.34	0.79	-0.08	12.30	1.15	-0.60	4.34	1.06	0.08
G34	2.42	0.13	0.04	9.91	1.06	0.01	4.94	2.08	1.12**
G35	3.01	1.30	-0.05	8.63	0.95	2.45*	4.21	1.61	0.05
G36	3.12	1.38	-0.07	8.88	0.52	3.95**	4.03	0.76	0.36
Mean	3.12+0.41			9.98+1.16			4.25+0.55		

Genotypes

	NCP			NPC			PL		
	Mean	bi	S²Di	Mean	bi	S²Di	Mean	bi	S²Di
G1	11.77	1.63	13.94**	5.49	0.44	0.61*	6.74	0.83	0.26*
G2	12.72	1.69*	-0.62	4.38	-0.21	-0.08	6.50	1.07	0.54**
G3	12.70	1.41	-0.60	4.59	0.65	0.07	6.97	1.64	0.51**
G4	10.35	-0.08	3.20*	4.70	1.38	0.60*	6.22	1.02	0.57**
G5	9.61	0.52*	-0.63	4.16	-0.05	-0.05	6.32	0.93	0.01
G6	11.70	1.36	-0.50	3.71	0.38	1.26**	6.22	1.54	0.41**
G7	10.59	1.16	7.65**	4.93	1.11	1.19**	6.11	0.59	0.01
G8	10.13	1.06	4.32**	6.32	3.50	7.33**	6.04	1.19	0.40**
G9	9.91	0.62	-0.51	4.74	0.35	0.12	6.20	1.18	0.14
G10	8.87	0.91	1.58	3.18	1.06	0.38	6.82	0.84	0.16
G11	9.21	0.02	-0.06	4.46	1.08	0.07	6.05	0.95	0.97**
G12	10.67	0.31	13.94**	3.81	0.99	0.81*	7.00	1.11	0.21*
G13	11.20	0.43	-0.28	4.28	0.44	-0.13	5.13	0.79	2.01**
G14	9.29	1.32	0.10	4.96	2.11	1.27**	6.35	0.72	0.01
G15	10.67	1.21	-0.63	3.64	0.18	-0.11	6.18	0.55	0.14
G16	8.79	0.95	0.91	4.40	1.73	0.01	6.40	1.22	0.42**
G17	9.31	1.46	1.88*	4.00	1.98	-0.04	6.26	0.90	-0.06
G18	10.58	1.77	-0.35	4.20	1.82	-0.11	6.12	0.95	-0.06

Contd.......

G19	9.39	1.57	5.12**	4.16	1.11	-0.05	5.52	1.13	0.09
G20	8.90	1.08	-0.56	3.47	1.13	-0.05	6.01	0.95	-0.02
G21	9.19	0.88	0.46	4.39	-0.16	0.05	5.66	1.08	0.25*
G22	8.06	0.86	-0.45	3.96	0.54	0.41	6.81	1.12	0.24*
G23	9.37	0.76	0.36	3.76	0.37*	-0.15	6.49	1.45	0.32*
G24	7.63	0.82	0.18	3.89	0.38	-0.02	6.26	1.50	0.12
G25	8.20	0.89	7.29**	3.76	1.22	0.79*	6.06	0.96	-0.05
G26	10.94	1.21	2.99*	4.43	0.49	0.54*	5.89	1.00	-0.03
G27	9.82	0.68	0.04	3.89	0.70	0.01	5.68	1.00	0.48**
G28	10.44	1.45	7.13**	3.88	1.37	-0.12	6.08	0.79	0.11
G29	11.39	1.33	-0.62	3.88	0.65	-0.08	6.33	1.18	0.04
G30	9.73	1.44	3.77**	3.47	1.20	0.74*	6.48	0.87	0.30*
G31	8.19	0.87	-0.58	4.06	1.27*	-0.15	7.15	1.44	0.10
G32	10.07	0.76	0.17	4.43	1.26	-0.09	6.63	1.35	0.15
G33	12.30	1.15	-0.60	4.34	1.06	0.08	5.86	0.49	0.25*
G34	9.91	1.06	0.01	4.94	2.08	1.12**	6.60	-0.26	-0.02
G35	8.63	0.95	2.45*	4.21	1.61	0.05	6.23	0.93	0.05
G36	8.88	0.52	3.95**	4.03	0.76	0.36	6.89	1.03	0.56**
Mean	9.98+1.16			4.25+0.55			6.29+0.40		

Genotypes					Traits				
		NSP			PM			PWM	
	Mean	bi	S²Di	Mean	bi	S²Di	Mean	bi	S²Di
G1	8.80	1.00	0.69	0.43	1.66	0.01**	0.16	1.10	0.01*
G2	9.01	0.83	-0.44	0.42	3.26	0.01**	0.16	0.59	0.01*
G3	9.11	0.93	-0.49	0.45	3.36	0.03**	0.15	0.25	0.01*
G4	10.13	1.01	0.08	0.43	0.96	0.01*	0.16	0.03*	-0.01
G5	7.37	1.04	3.49**	0.43	1.39	0.01**	0.16	-0.40	0.01
G6	10.03	1.08	8.53**	0.40	-0.89	0.01*	0.16	1.34	-0.01
G7	10.88	1.26	0.64	0.39	-1.09	0.01**	0.14	1.31	0.01
G8	8.86	1.38	0.91	0.39	1.26	0.01**	0.14	1.62	0.01
G9	9.21	1.18	-0.41	0.44	-1.88	0.01*	0.20	2.41	0.01
G10	9.73	0.95	-0.32	0.37	0.10	0.01*	0.17	0.40	-0.01
G11	10.06	0.89	8.04**	0.39	5.88	0.01**	0.17	-0.01	0.01
G12	10.48	1.22	1.46*	0.47	1.50	0.01**	0.19	0.83	0.01
G13	4.79	0.339*	-0.48	0.36	1.50	0.01**	0.14	0.73	0.01
G14	8.64	0.91	-0.47	0.38	-3.15	0.01**	0.14	2.10	0.01*
G15	9.00	1.23	-0.17	0.41	0.87	0.02**	0.16	-0.59	0.01**
G16	8.55	0.87	-0.38	0.38	-0.76	0.01**	0.18	0.99	0.01*
G17	9.19	1.08	0.15	0.38	2.14	0.01**	0.17	1.47	0.01
G18	9.97	1.14	-0.49	0.35	-3.37*	-0.01	0.19	2.27	-0.01
G19	9.07	0.78	0.84	0.34	0.17	0.01**	0.14	2.53	0.01**
G20	10.20	0.82	1.52*	0.34	-0.29	0.01**	0.14	2.81	0.01**
G21	10.01	0.97	0.20	0.37	1.16	0.01	0.14	1.15	-0.01
G22	9.61	1.33	4.36**	0.49	-4.41	0.01	0.19	1.96	-0.01
G23	10.68	1.24	0.02	0.45	5.26	0.01**	0.17	0.53	0.01
G24	10.06	0.83	2.02*	0.42	4.73	0.01**	0.15	0.23	-0.01
G25	9.80	0.81	1.07	0.35	3.31	0.01	0.13	0.41	0.01
G26	9.79	1.15	-0.08	0.45	1.81	0.0002	0.18	1.54	0.01
G27	9.31	0.79	2.14*	0.33	7.02	0.01**	0.13	0.16	0.01**
G28	10.40	0.83	-0.42	0.34	2.57	0.01	0.15	0.37	-0.01
G29	9.18	0.99	-0.31	0.41	4.01	-0.01	0.17	0.624*	-0.01

Contd.......

G30	10.26	0.89	0.75	0.41	1.45	0.01**	0.13	1.59	0.01**
G31	10.33	0.81	0.04	0.50	-0.54	0.01*	0.19	0.65	-0.01
G32	9.72	1.00	-0.16	0.33	-1.34	0.01	0.15	1.04	-0.01
G33	9.64	1.36	2.29*	0.38	-3.80	0.01**	0.16	1.57	0.01
G34	8.87	0.93	0.11	0.42	2.61	0.01**	0.19	-0.05	0.01*
G35	10.29	1.15	0.04	0.38	0.79	0.01**	0.15	1.72	0.01
G36	9.40	1.00	-0.36	0.44	-1.26	0.01**	0.19	0.75	0.01
Mean	9.46+0.85			0.40+0.05			0.16+0.03		

Genotypes   Traits

	PWP			SM			SP		
	Mean	bi	S²Di	Mean	bi	S²Di	Mean	bi	S²Di
G1	38.28	1.25	40.92*	0.27	1.62	-0.01	61.56	1.27	35.08
G2	38.44	1.35	28.30	0.26	2.14	0.01*	61.22	1.40	22.91
G3	33.75	-0.16	27.45	0.30	0.21	0.02**	65.59	-0.03	27.73
G4	37.73	0.296*	-13.49	0.27	0.49	0.01	62.39	0.27*	-14.43
G5	37.84	-0.36	125.07**	0.27	0.05	0.01**	61.70	-0.25	127.29**
G6	40.42	0.99	21.34	0.24	0.73	0.01**	59.44	0.99	23.61
G7	36.78	0.55	-10.65	0.24	-0.12	0.01**	63.16	0.54	-11.07
G8	37.09	1.31	-11.74	0.25	1.00	0.01**	63.34	1.20	-13.58
G9	44.56	1.48	2.17	0.25	0.70	0.01	56.47	1.25	5.38
G10	44.77	0.498*	-13.31	0.20	0.51	0.01	55.06	0.52*	-14.34
G11	43.18	0.79	-5.35	0.23	1.63	0.01**	56.47	0.84	-7.36
G12	41.31	0.97	-6.95	0.28	1.45	0.01	58.43	1.00	-9.12
G13	38.73	0.78	7.50	0.22	0.67	0.01	61.42	0.73	8.70
G14	37.94	1.32	416.18**	0.24	0.64	0.01**	61.92	1.28	429.93**
G15	38.87	0.32	101.89**	0.25	0.88	0.01 *	61.27	0.31	98.75**
G16	47.06	0.90	24.95	0.20	0.73	-0.01	55.80	1.19	141.51**
G17	43.56	1.52	-12.29	0.22	1.31	0.01*	57.01	1.39	-11.97
G18	53.26	1.25	-6.03	0.16	0.47	0.01 **	46.56	1.26	-5.03
G19	37.48	1.93	243.57**	0.20	0.90	0.01	61.87	1.98	258.43**
G20	38.88	2.31	152.32**	0.20	1.33	0.01 *	60.95	2.28	168.4**
G21	39.73	1.425*	-13.45	0.23	1.28	0.01	60.83	1.29	-14.01
G22	38.91	0.71	14.98	0.29	-0.25	0.01**	61.18	0.67	16.26
G23	37.31	0.85	-12.86	0.28	1.68	0.01**	62.33	0.90	-14.09
G24	37.32	1.317*	-13.42	0.27	2.39	0.01**	62.50	1.324*	-14.42
G25	38.64	0.88	-13.15	0.21	1.20	0.01	61.19	0.89	-13.76
G26	40.64	1.42	20.20	0.27	1.67	0.01**	59.04	1.44	23.70
G27	38.43	1.19	18.75	0.21	1.73	0.01**	61.74	1.13	21.86
G28	45.89	1.02	3.52	0.18	1.25	0.01	53.90	1.05	0.42
G29	41.56	1.12	4.66	0.24	1.71	0.01**	58.11	1.16	1.34
G30	32.67	2.00	194.46**	0.28	2.41	0.01	67.33	1.98	177.60**
G31	37.32	0.24	-10.80	0.31	0.10	0.01	62.43	0.28	-11.90
G32	44.07	0.88	36.81	0.19	0.36	0.01**	56.32	0.78	39.83
G33	41.74	0.95	-4.28	0.22	0.07	0.01**	58.86	0.81	-3.2274
G34	46.43	0.73	14.82	0.22	1.30	-0.01	53.57	0.73	11.73
G35	39.70	1.25	106.08**	0.23	1.16	0.01**	61.41	1.47	182.41**
G36	43.11	0.73	-13.1549	0.25	0.63	0.01**	57.02	0.69	-13.80
Mean	40.37+5.18			0.24+0.04			59.71+5.49		

Contd.......

Genotypes				Traits				
	SI			BYP			HI		
	Mean	bi	S²Di	Mean	bi	S²Di	Mean	bi	S²Di
G1	3.04	1.11	-0.02	25.31	-1.45	3.74*	33.55	0.49	39.90*
G2	3.25	1.00	-0.02	22.96	-0.21	47.22**	33.25	0.66	-3.5
G3	3.28	1.02	-0.01	26.09	0.16	18.35**	19.47	0.59	10.89
G4	3.39	1.13	-0.02	33.58	3.95	23.35**	19.20	1.18	11.25
G5	3.27	1.08	-0.01	24.73	0.26	22.36**	15.36	0.57	59.60**
G6	2.89	1.00	-0.02	15.19	1.58	-0.83	29.49	1.60	11.04
G7	2.81	1.02	-0.01	19.49	3.22	4.19*	23.41	1.58	2.28
G8	2.98	1.45	-0.01	23.45	2.66	60.71**	16.49	0.96	5.21
G9	2.86	0.51	-0.02	23.68	2.46	38.09**	18.69	1.19	50.56*
G10	2.81	1.07	-0.02	14.46	0.64	3.10*	20.64	0.90	-3.61
G11	3.27	1.16	-0.02	19.51	0.74	22.35**	15.92	0.80	68.29**
G12	3.05	1.05	-0.02	20.28	2.76	2.36	23.55	1.39	-8.46
G13	2.77	0.398*	-0.02	21.66	-0.86	-0.18	17.12	0.18	8.4214
G14	3.14	1.04	-0.02	21.83	1.74	4.25*	26.77	2.15	157.15**
G15	3.03	0.96	-0.01	20.66	2.12	1.31	24.30	1.14	-3.70
G16	3.25	1.02	0.03	22.36	-1.08	48.35**	17.58	0.67	90.68**
G17	3.14	1.01	-0.02	15.84	0.84	18.50**	24.40	0.97	182.54**
G18	2.77	1.06	-0.02	21.83	1.39	6.94**	23.50	1.04	51.30**
G19	2.65	1.07	-0.015	24.31	-0.04	31.27**	16.73	0.17	16.92
G20	2.67	0.79	-0.02	16.64	-0.07	0.05	23.76	0.33	9.77
G21	3.23	1.05	0.08 *	17.49	0.71	38.72**	27.24	0.83	43.30*
G22	3.22	0.86	-0.01	16.78	1.62	-0.19	34.04	2.52	616.63**
G23	3.27	1.10	0.17**	17.79	0.48	19.038**	24.04	0.64	29.43*
G24	3.25	1.04	0.07*	21.94	1.21	76.82**	26.34	0.96	417.18**
G25	3.25	1.08	0.07*	18.41	-0.92	6.3035 **	31.71	1.63	136.78**
G26	3.57	1.25	0.04	19.51	-0.04	2.12	16.38	0.63	-7.12
G27	2.39	0.88	0.10*	19.69	2.51	23.69**	19.94	1.38	0.92
G28	2.77	1.02	-0.01	17.27	1.56	52.96**	23.91	1.28	102.08**
G29	3.11	0.99	-0.02	16.75	-0.27	34.51**	20.89	0.52	258.49**
G30	3.29	1.06	-0.02	18.26	2.43	49.84**	21.01	1.33	34.97*
G31	3.81	0.95	0.01	19.96	2.00	13.64**	16.27	0.93	-4.54
G32	2.96	0.92	0.01	12.81	-0.19	4.01*	32.05	-0.18	154.65**
G33	2.65	0.86	0.01	18.14	3.01	15.21**	24.07	1.62	32.01*
G34	2.77	1.10	-0.02	21.37	-0.70	7.65**	20.93	0.27	46.41*
G35	2.78	0.96	0.08*	14.32	0.96	4.30*	32.20	1.63	233.20**
G36	3.65	0.96	0.14**	15.24	0.82	-0.70	31.26	1.47	4.23
Mean	3.06+0.13			19.99+3.20			23.48+6.64		

Contd.......

| Genotypes | | Traits | |
| | SYP | | |
	Mean	bi	S²Di
G1	8.62	2.21	3.42**
G2	7.70	1.58	6.66**
G3	4.98	1.08	-0.18
G4	5.61	1.32	2.035**
G5	3.63	1.03	0.60*
G6	4.00	0.79	-0.17
G7	3.61	1.00	0.56*
G8	3.30	0.66	1.26**
G9	3.74	0.89	-0.16
G10	2.88	0.69	-0.17
G11	2.85	0.71	0.53
G12	4.07	0.83	1.27**
G13	3.74	0.73	0.52
G14	5.18	2.39	8.06**
G15	4.55	0.66	0.0598
G16	3.83	1.38	2.70**
G17	3.51	0.81	0.34
G18	4.96	1.27	6.45**
G19	4.17	0.60	4.59**
G20	3.93	0.36	0.89*
G21	4.46	0.60	0.47
G22	4.78	1.50	7.49**
G23	4.13	0.554*	-0.19
G24	4.89	0.23	3.45**
G25	6.03	2.71	5.85**
G26	3.21	0.91	0.38
G27	3.30	1.05	1.01*
G28	3.48	0.99	0.01
G29	3.16	0.66	0.63*
G30	2.99	0.92	0.03
G31	2.85	0.79	-0.17
G32	3.94	-0.08	0.38
G33	3.37	1.02	0.26
G34	4.41	0.69	1.50**
G35	4.16	1.28	1.51**
G36	4.49	1.21	0.46
Mean	4.24+0.98		

Serial number of genotypes are according to materials and methods, G = Genotypes, DFF= Days to 50% flowering (Days), PH= Plant height (cm), NPBP= Number of primary branches per plant, NSBP= Number of secondary branches per plant, NCP= Number of clusters per plant, NPC= Number of pods per cluster, PL= Pod length (cm), PM= Pod mass (g), PWM= Pod wall mass (g), PWP= Pod wall proportion (%), SM= Seed mass (g), SP= Selling percentage, SI= Seed index (%), BYP= Biological yield per plant (g), HI= Harvest index (%), SYP= Seed yield per plant (g)

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Table 3: Environmental indices of various yield and yield component traits in *Vigna radiata* (L.) Wilczek

Traits	E1	E2	E3
Days to 50% flowering	2.28	0.96	-3.24
Plant height	5.72	-2.55	-3.16
Number of primary branches per plant	0.56	-0.09	-0.47
Number of secondary branches per plant	0.71	0.11	-0.82
Number of clusters per plant	1.54	2.01	-3.56
Number of pods per cluster	0.63	0.23	-0.86
Pod length	0.65	0.14	-0.80
Number of seeds per pod	1.18	1.79	-2.97
Pod mass	0.02	0.01	-0.02
Pod wall mass	-0.01	-0.02	0.03
Pod wall proportion	-4.75	-5.71	10.46
Seed mass	0.03	0.02	-0.05
Shelling percentage	5.06	5.64	-10.69
Seed index	0.44	0.24	-0.68
Biological yield per plant	-0.54	-2.73	3.27
Harvest index	2.70	7.27	-9.97
Seed yield per plant	0.52	0.83	-1.35

AMMI 1 biplot with main effects plotted against the IPCA 1 score and AMMI 2 biplot plotted against IPCA 1 and IPCA 2. AMMI 1 indicated that E2 and E3 showed similar main effect for NPBP among all environments A, B, C (E1, E2, E3). Analysis of genotype main effect showed that G2, G3, G6, G7, G9, G11, G13, G14, G15, G16, G18, G19, G20, G21, G24, G25, G26, G27, G28, G29, G30 and G35 are similar for NPBP but they showed different response for this trait *i.e.* above grand mean. Based on AMMI 2 model G16, G28 and G35 showed similar pattern *i.e.* high IPCA 1 and IPCA 2 score but G35 had maximum score.

For NCP, AMMI 1 model indicated that E1 and E2 are clustered in same group. G32, G27, G9, G4, G12 and G13 are similar and showed high IPCA 1 scores with above population mean, whereas G7, G8, G15, G28, G18, G29, G6, G33, G1, G2 and G3 showed high population mean but negative IPCA1 score. Based on AMMI 2, G28, G1 and G4 exhibited high IPCA 1 and IPCA 2 scores. Based on AMMI 1 model E2 and E3 (B and C) were clustered in same group and showed similar type of main effect interaction for NPC. G8 had highest IPCA 1 score with high population mean followed by G1, G14, G34, G2, G3, G4, G8, G12 and G17 and G18 for this trait. Based on AMMI 2 model G8, G1 and G6 were isolated with high IPCA scores for environments A, B and C, respectively for this trait. Based on AMMI 1, G3 G31 and G34 exhibited high IPCA 1 score coupled with high population mean in environments A, B and C, respectively for PL. However,

G3 had pattern was recorded in AMMI 2 for this trait. G20, G26, G1, G2, G30 and G16 also found high IPCA scores and clustered with environment B.

Based on AMMI 1; G12, G16, G24, G31 and G36 were found with high IPCA score and above mean, whereas on the basis of AMMI 2; G20, G15 and G27 had highest IPCA score for PWM. The minimum IPCA (AMMI 1) score with low mean was recorded for G19, G20, G14, G27, G7, G8, G13, G32, G6, G33, G23 and G17 and clustered with environment A. For SM, G12, G22 and G30 were isolated for high IPCA 1 score, high mean value and clustered with environment A by AMMI 1, where as G14 was found good IPCA 1 score for environment B. G3, G5 and G7 were secured negative IPCA sores for environment A (based on AMMI 2). Environment B exhibited positive IPCA 1 but negative IPCA 2 score. Environment C showed positive value for both IPCA.

Based on AMMI 1; G14, G19, G20, G8, G27 and G21 were isolated with high IPCA score and high mean (SP) and clustered with environment B (1E). In this model, environment A and B exhibited similar main effect. On the basis of AMMI 2; G19 and G20 (A), G14 (B), G4, G3 and G5 (C) were isolated for SP in respective environments given in parenthesis. Maximum BYP was recorded in environment C followed by B and A. Environment A and B, both are clustered into single group had average mean and negative IPCA score. Whereas G1, G16, G24 and G4 had good score for IPCA 1 and IPCA 2. Maximum HI was
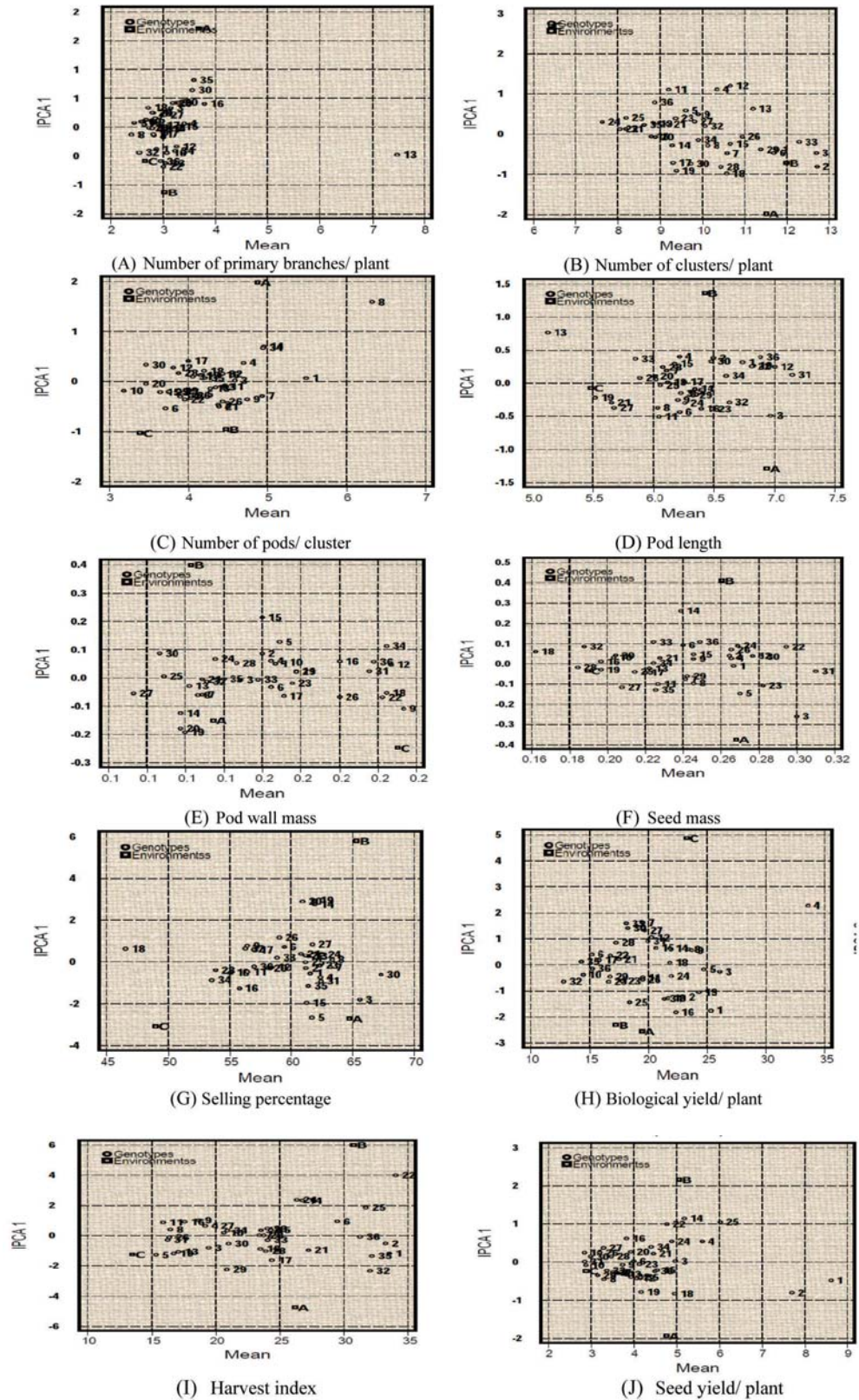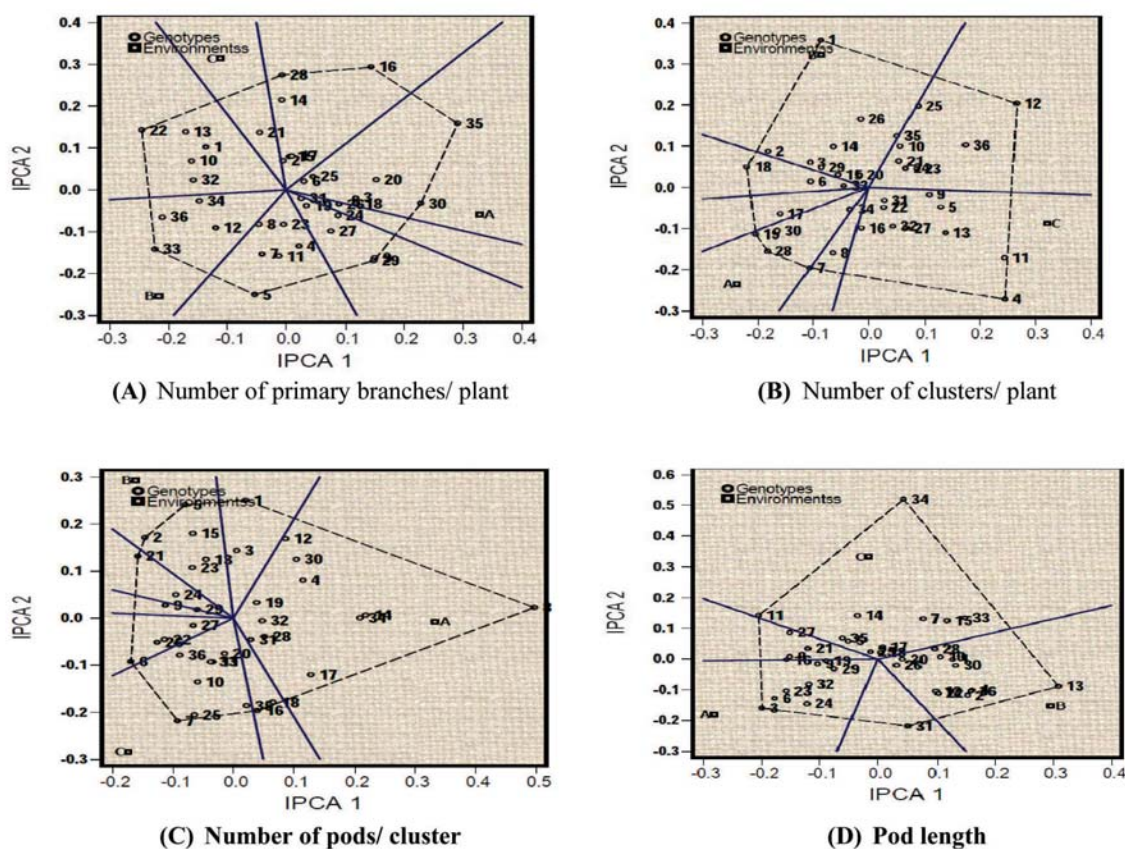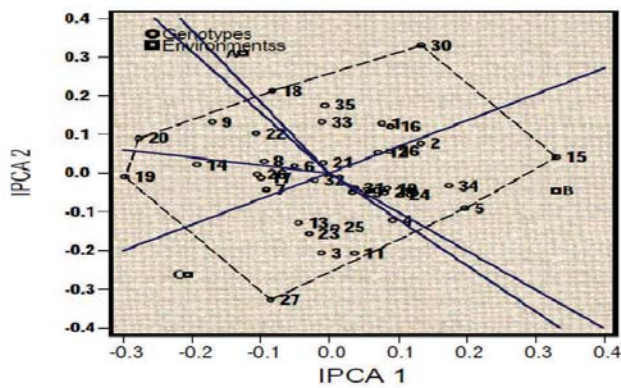
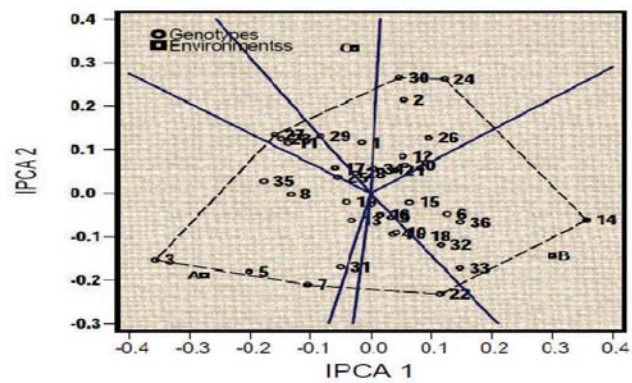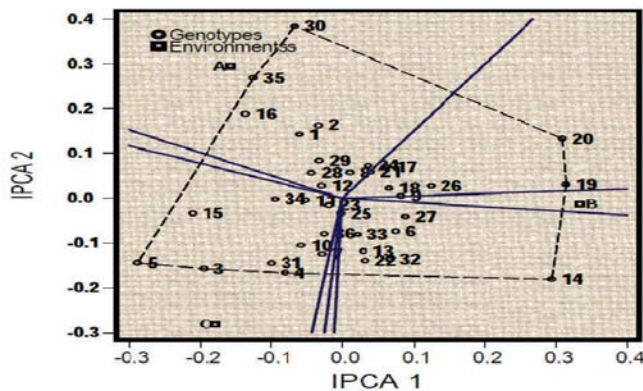**Fig 1:** Interaction biplot for AMMI 1 model on various traits (A-J) in *Vigna radiata* (L.) Wilczek

recorded in environment B followed by environment A and C. G22, G24, G1, G25 and G6 had high IPCA score (Fig 1I) with high population mean (AMMI 1), whereas G24 had highest score (AMMI 2) in environment B. G14, G12, G6, G27, G4, G15, G9, G10, G8, G23, G11, G6 and G24 had also good IPCA score and clustered with environment B.

Maximum SYP was recorded in environment B followed by environment A and C. Based on AMMI 1; environment A and B showed similar main effects. G1, G2, G18, G4, G3, G24, G22 and G25 had good IPCA score and mean value. On the basis of AMMI 2; G19 and G32 had good IPCA score and clustered with environment A, whereas G25, G14, G22 and G24 had high IPCA scores and clustered with environment B. G1, G2 and G18 had good IPCA scores for environment C.

GEI play important role in developing the crop varieties by comparing them over a series of environments. Therefore, before going to stability analysis we must need to assess the significance of GEI. Eberhart and Russell model is used for this purpose in present study. The perusal of pooled analysis of variance (ANOVA) indicated that almost all the traits studied had significant differences among the genotype (PM, PWP, PWM, SM, SP and HI), environment (PM), environment (linier) [PM] and their pooled deviation (DFF) except some traits given parenthesis. GEI was found significant only for NSBP, whereas significance of linear component of GEI was recorded for DFF, PH and NSBP, indicated the genetic differences among the genotypes for their regression on environmental index. The traits showed non-significant differences for GEI (linear) indicated that the performance of the genotypes cannot be predicted over

(A) Number of primary branches/ plant

(B) Number of clusters/ plant

(C) Number of pods/ cluster

(D) Pod length

Fig 2: Interaction biplot for AMMI 2 model on various traits (A-D) in *Vigna radiata* (L.) Wilczek

(E) Pod wall mass

(F) Seed mass

(G) Selling percentage
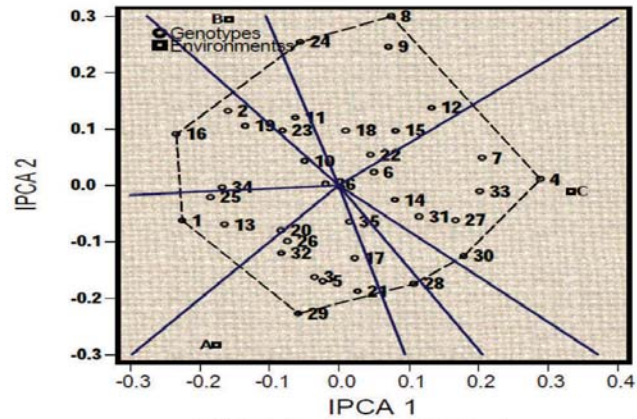
(H) Biological yield/ plant
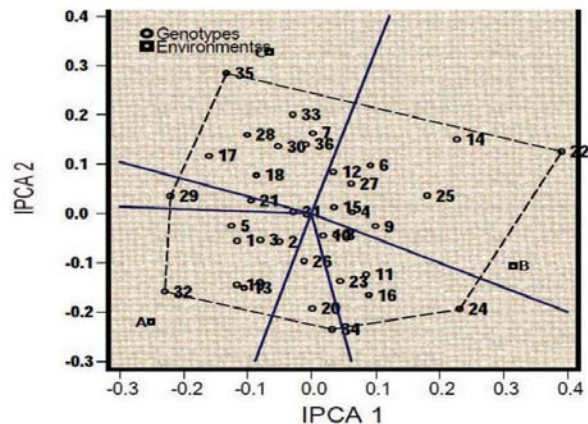
(I) Harvest index
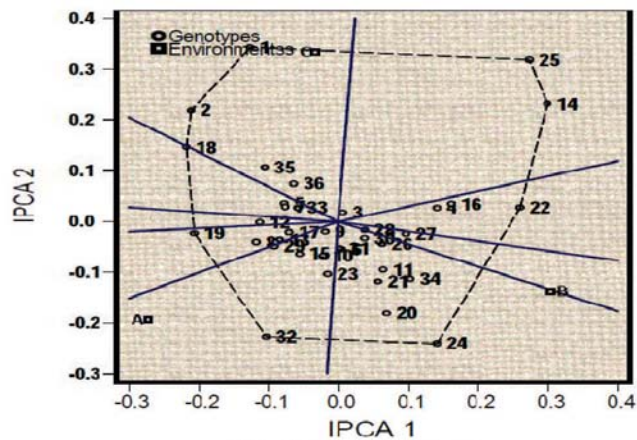
(J) Seed yield/ plant

Fig 2: Interaction biplot for AMMI 2 model on various traits (E-J) in *Vigna radiata* (L.) Wilczek

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the environments. In such situation, mean performance and their pooled deviation of genotypes are important selection criteria for stability of the genotypes. Significant pooled deviation was recorded for all the traits studied except DFF reflected the presence of sufficient genetic variation in breeding material. Such pooled deviation may also be practical value to construct and test the utility of multiple regression models to know more critically the complex mechanism of adaptation (Dar *et al*., 2009).

The pattern of stability showed two genotypes (G2, G36) were found stable across the environments, whereas only one genotype (G33) was found with consistent performance under better environment for SYP. Similarly four genotypes (NPBP), six genotypes (NCP); one genotype (NPC); two genotypes (PL); five genotypes (NSP); two genotypes (PM); two genotypes (PWM), four genotypes (PWP), three genotypes (SM); seven genotypes (SP); three genotypes (SI); two genotypes (BYP); three genotypes (HI); were found stable across the environments, whereas G34 (NCP); G11, G12 (NPC); G26 (PL); G17, G36 (NSP); G32 (PWM); G3, G6, G7, G10, G12, G18, G19, G28 (SI) were found suitable for better environments in relation to yield component traits given in parenthesis.

Due to significance of linear component of GEI, the mean value, bi and s²di were taken under consideration to find out the stable genotype(s) for DFF, PH and NSBP. Similar finding for DFF (Raturi *et al*., 2012) have earlier been reported by several researchers given in parenthesis. None of the genotype was found stable for these traits. The genotypes G4, G5, G9, G28, G29 (DFF); G9, G11, G16, G17, G18, G19, G26, G27, G29, G31 (PH); G15, G32 (NSBP) were isolated as better genotypes which give good performance under better environments. The stable performance of genotypes *viz.,* G2, G11, G33, G4, G28, G3, G5, G14, G16 and G17 under all three tested environments may be utilize in future breeding programme for greengram improvement in relation to yield and yield component traits. The genotypes that gives consistent performance under better environments may be utilize for trait manipulation and other breeding programme under targeted environment.

The environmental indices indicated that environment A (early sown) was desirable for enhancement of some yield component traits *viz.,* DFF, PH, NPBP, NSBP, NPC, PL, PM, SM and SI; have been presented in Table 3. This result indicated that early sowing promote the PH, branching capacity, podding, length of pod, PM, SM and SI. However

several researchers supported the importance of tall plant stature in greengram. Yimram *et al.,* (2009) reported that tall plant stature is desirable for mechanical harvesting. Thangavel *et al.,* (2011) observed that most of the high yielding genotypes were tall plant type and vice-versa; may be due to differences in capturing the sunlight. Branching Pattern also helps to make the canopy and capture more sunlight and accumulate the photosynthate, resulting enhance the yield *via* yield component traits. But in present study early sowing give benefit for some of the yield component traits but low yield performance as compare to timely sowing. It may be due to long vegetative phase retaining more biomass but due to unfavourable environmental conditions it gives poor HI and SYP. Greengram is very sensitive to environmental fluctuations, which causes indeterminate growth, tall plant stature and several flower flashing. Several flower flashes in greengram divert their energy towards the production of flowers but not contributed much more for high yield. It may be due to non-availability of enough assimilates due to inadequate phloem tissue development in distal part of raceme (Begum *et al.,* 2007; Mondal *et al*., 2001a). The environment B *i.e.* timely sown exhibited higher value for almost all the yield and yield component traits studied, whereas environment C was found unfavourable for all the traits studied. It may also due to weather fluctuation. Thus, it is evident from environmental indices, which type of environment is good and/ or poor for yield and yield component traits. The relationship of traits and environments may give a good idea to construct the suitable ideotype for greengram improvement.

The AMMI approach revealed that more complex GEI could not facilitate graphical visualization of the genotypes in low dimensions. So, AMMI analysis can be used as alternative procedure to interpret the GEI. Namorato *et al.,* (2009) also reported the AMMI approach is more efficient than the Eberhart and Russell model of stability. To assess the main and interaction effects over the test environments; AMMI 1 and AMMI 2 biplots were constructed for various yield and yield component traits. AMMI model stratify the genotypes and environments into four groups *i.e.* right up (high yielder and stable), right down (high yielder unstable), left right (low yielder unstable) and left up (low yielder stable). In AMMI 1 model, if the main effects have IPCA score near to zero, 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. AMMI 2 biplot explain the nature and

magnitude of GEI interaction. In AMMI analysis, the IPCA scores give indication of stability or adaptability of the genotypes over environments (Rasidi *et al.*, 2013). The genotypes had greater IPCA score indicated their specific adoption in given environment and genotypes having IPCA scores close to zero are stable in sampled environment.

For SYP; the eight genotypes (G1, G2, G18, G4, G3, G24, G22 and G25) were found stable based on AMMI 1, whereas on the basis of AMMI 2; G19 and G32 were found with stable performance as shown in Fig 1J and Fig 2J, respectively. For this trait the genotypes and environments were grouped into nine sectors. The first sector consist of with environment B with high IPCA score for some outlier genotypes *i.e.* G25, G14 and G22, indicated that the environment B was better than other environments and three genotypes were found stable for SYP. The sectors grouped without environments had delimiting genotypes close to each other and they did not delineate environments due to their similar performances. This report is agreed with similar report of Namorato *et al.*, (2009).

The presented results through both approaches demonstrated the potential of genotypes in terms of yield and their component traits to select the suitable genotypes for proper utilization and trait manipulation in *vigna sadiata* L. Wilczek improvement under targeted environment.

Acknowledgement

References

Ali, Y. and Sawar, G. 2008. Genotype x environment interaction in cowpea genotypes. *Indian Journal of Environmental Protection* **2**: 125-132.

Begum, S., Islam, M.A. and Prodhan, A.K.M.A. 2007. Anatomy of rachis of the inflorescence in pigeon pea. *International Journal of Bot*any **3**: 85–90

Dar, S.A., Pir, F.A. and Manjar, A. 2009. Phenotypic stability in chickpea (*Cicer arietinum* L.) under temperate climate. *Trends in Biosci*ences **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. *Research in Plant Biol*ogy **2**: 46-61.

Eberhart, S.A. and Russell, W.A. 1966. Stability parameters for comparing varieties. *Crop Sciences* **6**:36-40.

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 Journal Genetics and Plant Breeding* **64**: 299-302.

Mondal, M.M.A., Fakir, M.S.A., Juraimi, A.S., Hakim, M.A., Islam, M.M. and Shamsuddoha, A.T.M. 2011a. Effects of flowering behavior and pod maturity synchrony on yield of mungbean [*Vigna radiata* (L.) Wilczek]. *Australian Journal of Crop Sci*ence **5**:945-953.

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 Breeding and Applied Biotech*nology **9**: 299-307.

Rashidi, M., Farshadfar, E. and Jowkar, M.M. 2013. AMMI analysis of phenotypic stability in chickpea genotypes over stress and non-stress environments. *International Journal of Agricultural and Crop Sciences* **5**: 253-260.

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 Journal of Agricultural Sciences* **4**: 126-133.

Souframanien, J. and Gopalkrishanan, T. 2004. A comparative analysis of genetic diversity in black gram genotypes using RAPD and ISSR markers. *Theoretical and Applied Genet*ics **109**: 1687-1693.

Srinives, P. 2006. Research direction and legume crop development. In Proceeding of National Legume Crop Res Conference held at Rimkok Resort Hotel, Chian Rai, Thailand. pp 389.

Thangavel, P., Anandan, A. and Eswaran, R. 2011. AMMI analysis to comprehend genotype by-environment (G × E) interactions in rainfed grown mungbean (*Vigna radiata* L.). *Australian Journal of Crop Sciences* **5**: 1767-1775.

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 Journal of Agricultural Sci*ences **78**: 375-378.

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*earch **112**: 260-266.