



Identification of stable genotypes for grain yield and its components in mungbean (*Vigna radiata*)

SANJEEV KUMAR^{1*}, H K CHOUDHARY¹ and ANJANI KUMAR SINGH²

Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Samba,
Jammu & Kashmir 181 133, India

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ABSTRACT

The present study was conducted at the experimental farm of Advanced Centre for Rainfed Agriculture (ACRA) Dhiansar of SKUAST- Jammu during rainy (*kharif*) season 2016, 2017 and 2018 for identification of most stable mungbean (*Vigna radiata* L.) genotypes in diverse environments (E_1 , E_2 and E_3). Genotype Pusa Vishal exhibited regression coefficient equal to unity ($b=0$) with non-significant deviation from regression coefficient and hence showed wider adaptability under poor or good environments. Genotype EC520016 showed earliness in maturity with wider adaptability. Environmental indices indicated that environment E_2 and E_3 were most favourable for yield and majority of yield attributing traits whereas E_3 alone was important for seed yield per plant. Based on AMMI models, G_9 , G_1 , G_3 , G_4 and G_8 exhibited higher IPCA scores coupled with high population mean in E_3 . On the basis of AMMI2, G_{12} and G_{22} exhibited high IPCA1 in E_3 and G_6 , G_{17} and G_9 exhibited high IPCA2 in the same environment. G_3 , G_{18} and G_{19} were present very close to centre point and were least affected by $G \times E$ interactions and their performance was not affected by harsh environments and G_4 , G_{18} and G_{22} were present away from the point of centre and were more affected by $G \times E$ interactions and not stable in performance. Hence, the selected genotypes may be utilized in *Vigna radiata* (L.) improvement programme at targeted environments with true type of breeding lines.

Keywords: AMMI analysis, GEI, Mungo, Stability, Yield

Mungbean (*Vigna radiata* L.) is an important rainy (*kharif*) season pulse crop. India produces 14.76 million tonnes of pulses from an area of 23.63 million ha, making it one of the largest pulses producing countries in the world. However, about 2–3 million tonnes of pulses are imported annually to meet the domestic consumption requirement. Thus, there is a need to increase production and productivity of pulses in the country by more intensive interventions (<http://agropedia.iitk.ac.in>). However, the area under pulses is 26.57 thousand hectares, production remains 84.1 thousand quintals and productivity is 3.17 q/ha in UT of Jammu and Kashmir (Jeelani and Choure 2015). There is a need to identify the high yielding and widely stable varieties for rainfed areas.

Significant achievement in crop production may be possible by breeding varieties for their stability for yield and yield components (Lal *et al.* 2010). The major constraint to develop the high yielding varieties of mungbean are low inherited yield potential, lack of genetic variability,

lack of suitable ideotype and susceptibility to biotic and abiotic factors (Srinives 2006). $G \times E$ interactions have major importance for plant breeders in developing improved varieties. Low levels of interactions are useful for some characters so as to maximize the stable performance over a number of environments. However, for some situation, high interactions are beneficial and can be explored. This regression analysis proposed by Finlay and Wilkinson (1963) was improved upon by Eberhart and Russell (1966). They introduced one more parameter, deviation from regression (S^2Di) which accounts for unpredictable irregularities in the response of genotypes to varying environments. The process of identification of stable genotype is difficult because of $G \times E$ interaction. Although the plant breeders have observed genetic differences for adaptability, they have been unable to fully exploit these differences in breeding stable genotypes. Keeping in view the above-mentioned goals, the study was carried out to evaluate the performance of mungbean genotypes using the GGE biplot technique proposed by Yan and Kang (2003).

MATERIALS AND METHODS

Plant material: The experimental materials comprised 23 genotypes of mungbean, viz. Pusa Vishal (G_1),

¹CSK Himachal Pradesh Krishi Vishvavidyalaya, Palampur, Himachal Pradesh; ²Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Samba, Jammu & Kashmir. *Corresponding author email: ssalgotra@gmail.com

ML1818(G₂), PD139(G₃), IPM2-3(G₄), SML668(G₅), IPM99-125(G₆), Pusa 0672(G₇), IPM2057(G₈), PM2-14(G₉), IPR57(G₁₀), IPM95-31(G₁₁), ML2056(G₁₂), PM5(G₁₃), MH521(G₁₄), Ganga 8(G₁₅), IPM2-3-2(G₁₆), BM63(G₁₇), EC520016(G₁₈), MH9-8-1(G₁₉), V1133(G₂₀), MG331(G₂₁), K851(G₂₂) and LG460(G₂₃). These genotypes were received from the ICAR-Indian Institute of Pulses Research, (IIPR), Kanpur, Uttar Pradesh, India.

Experimental design and growing conditions: The experiments were conducted at the experimental farm of Advanced Centre for Rainfed Agriculture (ACRA), Rakhdhiansar of Sher-e-Kashmir University of Agriculture Sciences and Technology (SKUAST), Jammu. Experiments were conducted in randomized block design with three replications during Rainy season (*kharif*) 2016, 2017 and 2018 under rainfed conditions. Each genotype was sown in eight rows with row length of 4 m and spacing 30 × 10 cm². All the recommended package and practices were followed for getting good healthy crop along with recommended plant protection measures.

Data collection: Fifteen random plants were selected from each genotype in each replication and in each year to record the data for seed yield and its components, viz. days to 50% flowering, number of primary branches/plants, plant height, pod length, number of seeds/pods, 1000 seed weight, days to maturity and seed yield /plant.

Biometrical analysis: Pooled mean data of all the traits studied each year were subjected to analysis of variance and stability parameters using statistical package Indostat 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).

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

where Y_{ij} , mean of i^{th} genotype of j^{th} environment; μ_i , mean of i^{th} genotype over environments; β_i , regression coefficient of i^{th} genotype to the change of environment; I_j , environmental index; σ_{ij} (S²D), deviation from regression coefficient.

The regression coefficient (β_i) was tested against t-test for significance, whereas significance of deviation from regression (S²Di) was tested by F-test. To analyze the GEI, additive mean effect and multiplicative interaction effects (AMMI) model was used. 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 was tested against homogenous error for each trait studied using Bartlett's test and subjected to pooled analysis of variance (Anova) of eight traits including seed yield and its components over the three environments, it indicated significant differences among varieties for all the traits (Table 1). Variance due to environments and environment (linear) showed significant differences for all the traits studied except

Table 1 Analysis of variance of yield and its components for stability and environmental indices in *Vigna radiata*

Source of variation	d.f.	Mean sum of squares					Environmental Indices				
		Days to 50% flowering	Plant height (cm)	No. of primary branches	Pod length (cm)	Seeds/pod	Days to maturity	1000 Seed weight (g)	Seed yield/plant (g)	Traits	E ₁ E ₂ E _{3w}
Rep within Env.	6	1.486 *	0.28	0.09	0.08	0.13 *	0.40	0.17 *	0.13 ***	DFL	1.93 1.65 -3.58
Genotypes	22	13.57 ***	115.66 ***	1.57	0.98***	1.17 ***	2.78***	218.41***	7.89 ***	PH	-2.98 -2.84 5.82
Env. + (Gen. × Env.)	46	11.84***	66.69***	1.10	0.25 ***	0.43***	106.93***	0.13 *	0.07 ***	NPB	-0.22 0.01 0.21
Environments	2	221.48***	584.12***	1.08	1.36***	5.20 ***	2417.48 ***	0.21	0.44 ***	PL	0.18 0.09 -0.28
Gen. × Env.	44	2.32***	43.17***	1.10	0.19***	0.22 ***	1.91 **	0.13	0.05 **	NSP	-0.24 -0.31 0.55
Environments (Lin.)	1	442.97 ***	1168.23***	2.15	2.72 ***	10.40 ***	4834.97***	0.42 *	0.87 ***	DM	5.67 6.17 -11.84
Gen. × Env. (Lin.)	22	4.03 ***	85.62 ***	1.12	0.36 ***	0.39 ***	3.24 ***	0.18 *	0.08 ***	1000 SW	0.01 -0.09 0.09
Pooled Deviation	23	0.57	0.69 *	1.03 ***	0.03 **	0.05	0.55	0.07	0.02	SY (g)	-0.11 -0.05 0.15
Pooled Error	132	0.58	0.41	0.02	0.01	0.04	0.49	0.07	0.02	-	- - -
Total	68	12.40	82.53	1.25	0.49	0.67	73.24	70.75	2.59	-	- - -

Env., Environment; Gen., Genotype; Lin., Linear.

number of primary branches per plant indicated that the environments were linear in this investigation. Genotype environment interaction (GEI) was further subdivided into linear (bi) and non-linear (S^2Di) components. The significance of linear component of GEI was recorded for all the traits except number of primary branches per plant. Significant non-linear components (pooled deviation) were recorded for plant height, number of primary branches/plant and pod length. Additive Main Effects Multiplicative Interaction (AMMI) analyses were further done to estimate the GEI for yield and its components.

Stability parameters

Days to 50% flowering: Genotype G_{18} showed higher mean value than population mean with regression coefficient equal to unity ($b=1$) and thus selected as a stable genotype with wider adaptability.

Plant height: Genotypes G_1 , G_5 , G_7 , G_8 , G_{11} , G_{12} , G_{15} , G_{19} , G_{20} and G_{23} showed lesser mean value than population mean with regression coefficient greater than unity ($b>1$) and least non-significant deviation from regression coefficient (S^2di) and therefore, recommended for unfavourable environment only. G_2 showed regression coefficient approaches to unity and at par with mean value (population) for plant height, hence recommended for wider adaptability. Similar results were also exhibited by Kumar *et al.* (2017b).

Number of primary branches/plants: G_4 showed regression coefficient approaches to unity (0.98) with minimum non-significant deviation from regression coefficient and has above average stability in performance and recommended for wider adaptability.

Pod length: Genotypes G_1 , G_2 , G_7 , G_{12} , G_{14} , G_{19} and G_{23} showed higher mean value than population mean with regression coefficient greater than unity ($b>1$) and minimum non-significant deviation from regression coefficient (S^2Di) indicating their below average stability and adaptation to specific favourable environment only. G_{16} showed minimum

deviation from regression coefficient with regression coefficient approaching unity and well or poorly adapted to all environment hence recommended for general cultivation.

Number of seeds per pod: Genotypes G_7 , G_8 , and G_{18} showed higher mean value than population mean with regression coefficient less than unity ($b<1$) and minimum deviation from regression coefficient (S^2di) and therefore suitable for unfavourable environment. Genotypes G_5 , G_{19} and G_{23} showed higher mean value with regression coefficient equal to unity ($b=1$) and thus selected as genotypes with wider adaptability. These results are in agreement with the findings Kumar *et al.* (2014, 2020a, 2020b).

Days to maturity: Genotypes G_7 , G_{12} , G_{17} , G_{19} and G_{21} showed higher mean value with regression coefficient equal to unity ($b=1$) and thus selected as genotypes with wider adaptability. Genotypes G_8 , G_{13} and G_{23} showed mean value at par with the population mean with regression coefficient equal to unity ($b=1$) and thus selected as genotypes with wider adaptability.

1000 seed weight: Genotype G_{11} and G_{18} showed at par mean value with population mean and regression coefficient equal to unity ($b=1$) and thus selected as genotypes with wider adaptability (Table 2). Genotype G_{18} showed higher mean value than population mean with regression coefficient equal to unity ($b=1$) hence, recommended for general cultivation.

Seed yield per plant: Genotypes G_3 , G_8 and G_9 showed higher mean value than population mean with regression coefficient less than unity ($b<1$) and minimum non-significant deviation from regression coefficient (S^2Di) and therefore, suitable for unfavourable environment. Genotype G_1 showed higher mean value with regression coefficient equal to unity ($b=1$) and thus selected as genotype with wider adaptability in good or poor environment. Similar results were also reported by Kumar *et al.* (2020a, 2020b).

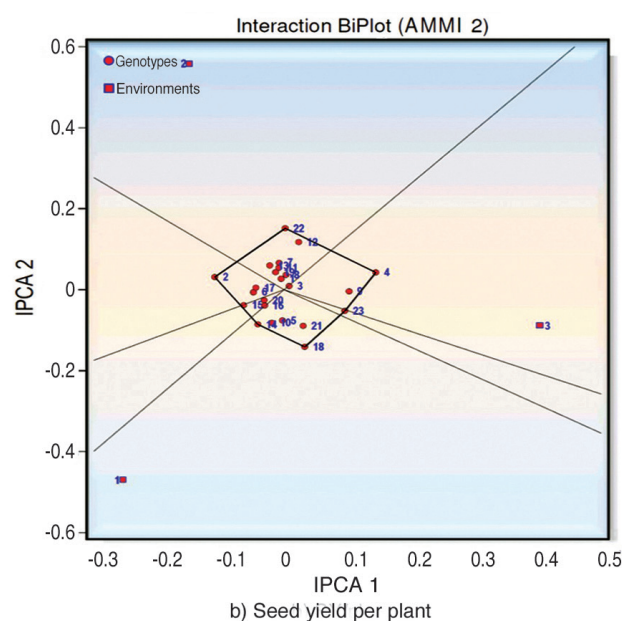
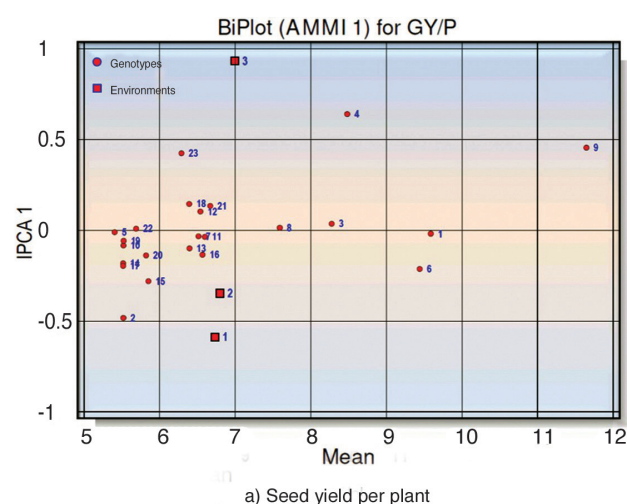


Fig 1 Interaction biplot for AMMI 1 and AMMI 2 models on various traits in *Vigna radiata* L.

Table 2 Estimates of mean (μ), regression coefficient (bi) and deviation from regression (S^2Di) for yield and its components in mungbean genotypes

Genotype	Days to 50% flowering				Plant height (cm)				PBR/PI				Pod length (cm)			
	Mean	bi	R ²	S ² Di	Mean	bi	R ²	S ² Di	Mean	bi	R ²	S ² Di	Mean	bi	R ²	S ² Di
G ₁	45.89	0.99	0.98	-0.18	48.03	2.49**	1.00	-0.40	2.27	5.07	0.74	0.81***	8.23	3.36	0.96	0.04
G ₂	47.44	1.23	0.95	0.78	57.55	1.02	0.99	0.30	3.60	0.53	0.61	0.00	8.12	2.08	0.96	0.01
G ₃	46.33	0.84	1.00	-0.62	53.71	0.64*	1.00	-0.38	3.11	0.91	0.60	0.03	6.71	-0.34	0.71	-0.01
G ₄	47.44	1.60	0.97	0.96	58.62	-0.07*	0.52	-0.19	3.64	0.98	0.72	0.02	8.01	4.66	0.97	0.06*
G ₅	45.56	0.90	0.99	-0.45	55.17	2.59*	1.00	-0.33	2.88	3.86	0.73	0.48***	7.62	-0.23	0.28	0.00
G ₆	50.33	2.05	1.00	-0.46	59.50	2.00	0.98	4.09**	3.89	2.50	0.32	1.23***	7.25	-1.020*	0.98	-0.01
G ₇	46.44	0.87	0.99	-0.53	51.70	2.16	0.99	1.38*	3.10	2.66	0.81	0.14**	8.28	3.35	0.98	0.00
G ₈	46.22	0.99	1.00	-0.58	46.55	2.17*	1.00	-0.32	4.69	12.98	0.71	6.40***	7.21	0.21	0.42	-0.01
G ₉	46.56	0.81	1.00	-0.60	55.36	1.82**	1.00	-0.39	3.34	0.52	0.43	0.01	7.57	-0.01	0.00	0.17**
G ₁₀	46.56	1.54	0.99	-0.02	43.96	-0.15**	1.00	-0.40	3.04	-0.45	0.59	-0.01	7.38	1.61	0.99	-0.02
G ₁₁	45.22	0.43*	1.00	-0.61	55.47	1.13	1.00	-0.39	3.01	0.58	0.25	0.07*	7.61	0.70	0.73	0.00
G ₁₂	49.44	1.33	0.99	-0.38	49.50	1.61	1.00	0.03	3.78	-2.84	0.55	0.61***	8.12	1.18	0.99	-0.02
G ₁₃	44.00	0.56*	1.00	-0.61	60.40	-0.76**	1.00	-0.39	3.00	-0.99	0.84	0.00	8.66	3.41	0.94	0.07*
G ₁₄	48.89	1.55	1.00	-0.53	62.10	-1.09*	0.98	0.57	4.08	-1.43	0.64	0.08*	8.13	1.89	0.95	0.00
G ₁₅	51.56	0.18	0.12	3.74**	52.22	1.60*	1.00	-0.33	2.63	3.18	0.78	0.25***	6.58	-2.37	0.94	0.02
G ₁₆	46.33	0.39	0.62	1.18	61.16	-1.28**	1.00	-0.39	4.07	3.39	0.67	0.51***	7.31	1.04	0.83	0.01
G ₁₇	46.22	0.43*	1.00	-0.61	68.67	-1.38**	1.00	-0.40	2.54	3.40	0.74	0.37***	6.71	-0.96**	1.00	-0.02
G ₁₈	48.78	1.06	0.98	-0.08	65.27	-0.54**	1.00	-0.40	4.29	-2.27	0.75	0.14**	7.53	-0.11	0.06	0.01
G ₁₉	46.56	0.99	1.00	-0.58	54.32	1.49*	1.00	-0.38	3.47	-0.99	0.84	0.00	8.11	2.550*	1.00	-0.02
G ₂₀	53.11	0.68	1.00	-0.60	52.83	2.47	0.99	2.09*	5.06	-2.09	0.10	3.81***	6.79	-1.20	0.63	0.08*
G ₂₁	47.67	1.31	1.00	-0.57	55.95	1.47	1.00	0.05	4.62	2.18	0.05	8.34***	7.50	0.34**	1.00	-0.02
G ₂₂	49.00	0.85	0.93	0.41	56.09	1.75	0.98	3.53**	3.99	-0.66	0.37	0.05	7.09	1.22	0.97	-0.01
G ₂₃	48.11	1.44	0.99	-0.18	45.05	1.86*	1.00	-0.36	3.30	-1.22	0.94	-0.01	7.71	1.64	0.83	0.05
Population mean	47.55	1.00	-	-	55.18	1.00	-	-	3.54	1.00	-	3.54	7.58	1.00	-	-
SE(m)	0.53	-	-	-	0.58	-	-	-	0.72	-	-	0.72	0.13	-	-	-
SE(bi)	0.17	-	-	-	0.12	-	-	-	3.33	-	-	3.33	0.54	-	-	-

Genotype details are given under Materials and Methods section.

Contd.

Table 2 (Concluded)

Genotype	Seeds/pod			Days to maturity			1000-Seed weight			Seed yield/plant		
	Mean	bi	R ²	S ² Di	Mean	bi	R ²	S ² Di	Mean	bi	R ²	S ² Di
G ₁	11.33	0.35	0.82	-0.03	71.33	0.76	1.00	0.23	52.31	2.87	0.55	0.05
G ₂	10.85	1.99	0.99	-0.03	73.89	0.86	1.00	-0.40	53.57	2.13	0.90	0.06
G ₃	11.44	0.35	0.95	-0.04	72.44	0.94	1.00	-0.38	22.52	1.81	0.72	-0.05
G ₄	12.46	-0.13	0.08	0.04	72.44	0.79**	1.00	0.48	51.47	1.80	0.86	-0.06
G ₅	11.97	1.03	1.00	-0.04	72.22	0.89	1.00	-0.33	46.29	2.41	0.88	-0.06
G ₆	11.84	1.87**	1.00	0.04	73.56	0.98	1.00	-0.47	46.22	1.61	0.56	-0.03
G ₇	12.67	-0.26	0.19	0.09	74.11	1.08	1.00	-0.47	59.81	1.27	0.62	-0.05
G ₈	12.36	0.22	0.56	-0.03	73.11	1.00	1.00	-0.37	39.44	2.42	0.96	-0.07
G ₉	11.58	0.73	0.94	-0.03	73.67	0.85*	1.00	-0.46	60.67	-2.21	0.27	0.17
G ₁₀	11.63	-1.16	0.97	-0.03	72.67	1.07	1.00	-0.35	61.20	1.81	0.58	0.03
G ₁₁	11.98	0.77*	1.00	-0.04	73.89	1.146*	1.00	-0.48	49.95	1.06	0.84	-0.07
G ₁₂	12.34	1.42	0.98	-0.02	74.11	1.05	1.00	-0.48	54.40	1.48	0.72	0.05
G ₁₃	11.80	1.61	0.93	0.04	73.22	1.06	1.00	-0.37	39.56	3.65	0.76	0.01
G ₁₄	12.12	1.78	1.00	-0.04	72.11	1.00	1.00	-0.37	52.18	1.81	0.93	-0.07
G ₁₅	10.82	1.84*	1.00	-0.04	72.37	1.04	1.00	-0.37	48.64	2.21	1.00	0.07
G ₁₆	10.72	1.48*	1.00	-0.04	73.99	1.18	1.00	0.98	45.69	1.23	0.52	-0.04
G ₁₇	11.68	0.57	0.54	0.08	73.79	1.03	0.98	4.61**	51.51	2.51	0.93	-0.06
G ₁₈	12.72	0.32	0.92	-0.04	75.56	1.26**	1.00	-0.49	55.62	1.05	0.60	-0.06
G ₁₉	11.81	1.01	1.00	-0.04	73.66	1.07	1.00	0.27	59.95	-12.37	0.90	0.26*
G ₂₀	11.67	1.26	0.98	-0.03	73.78	0.88	1.00	0.28	57.51	0.79	0.27	-0.04
G ₂₁	11.52	1.71	0.76	0.39**	74.83	1.09	1.00	0.73	49.65	1.11	0.29	-0.02
G ₂₂	10.27	3.16*	1.00	-0.04	74.11	0.91	0.99	1.61 *	53.78	-0.55	0.02	0.20
G ₂₃	11.86	1.08	0.91	0.01	73.34	1.07	1.00	-0.47	49.74	3.10	0.49	0.12
Population mean	11.71	1.00	-	-	73.40	1.00	-	-	50.51	1.00	-	-
SE(m)	0.15	-	-	-	0.53	-	-	-	0.18	-	-	-
SE(bi)	0.32	-	-	-	0.05	-	-	-	1.91	-	-	-

Genotype details are given under Materials and Methods.

AMMI model and Biplot Interactions of seed yield/plant(g) and 1000 seed weight(g)

Seed yield per plant: Maximum seed yield per plant was recorded in E_3 followed by E_2 and E_1 (Table 1). Based on AMMI 1 environment E_1 and E_2 showed similar main effects. Genotypes G_9 , G_{11} , G_3 , G_4 and G_8 exhibited higher IPCA scores coupled with high population mean in E_3 . On the basis of AMMI 2, G_{12} and G_{22} exhibited high IPCA1 in E_3 and G_6 and G_{17} and G_9 exhibited high IPCA2 in the same environment. G_3 , G_{18} and G_{19} are presented very close to centre point and are least effected by $G \times E$ interactions whereas G_4 , G_{18} and G_{22} are presented away from the point of centre and are more effected by $G \times E$ interactions and not stable in performance (Fig 1 a & b). Similar results were reported by Kumar *et al.* (2014, 2017a, 2017b, 2020a, 2020b).

It is evident from the environmental indices (Table 1), which type of environment is good or poor for seed yield per plant. The relationship of traits and environments may give a good idea to construct the suitable ideotype for green gram 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. To assess the main and interaction effects over the test environments AMMI 1 and AMMI 2 biplots were constructed for seed yield. AMMI analysis, IPCA score give the identification of stability of the genotypes over environments though adaptation is one of the traits they vary in assortment genotype and selection can thus be made to use the trait to develop cultivars adapted to poor or favourable environment. The stability and wider adaptability are of vital importance in Jammu region of UT of J & K where changes in growing conditions are very high. The main limitation of these genotypes is low yield. From the present study, it was concluded that both the approaches (Eberhart and Russel Model 1966 and AMMI 1 and AMMI 2) revealed the potential of genotypes in terms of yield and indirect traits for selecting the stable genotypes for their proper utilization and trait manipulation in green gram improvement in given environment under rainfed situations.

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