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GGE BIPLOT & AMMI ANALYSIS OF YIELD STABILITY IN MULTI-ENVIRONMENT TRIAL OF SOYBEAN [*Glycine max* (L.) Merrill] GENOTYPES UNDER RAINFED CONDITION OF NORTH WESTERN HIMALAYAN HILLS

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ABSTRACT

Soybean [*Glycine max* (L.) Merrill] is major oilseed crop globally. It is grown in diverse agro-ecological conditions and the performance of quantitative traits often varies due to significant genotype × environment interaction (GEI) therefore, the integration of yield and stability is one of the common objective of soybean breeding. The present investigation was carried out to study genotype × environment interaction (GEI) through GGE biplot and AMMI analysis over four environments (Majhera, Palampur, Bajaura and Almora) with 32 genetically diverse genotypes for four traits *viz*., grain yield, days to 50% flowering, days to maturity and 100 seed weight under rainfed condition of North Western Himalayan hills using randomised complete block design. The analysis of variance revealed that environments (E), genotypes (G) and genotype × environment interactions (GEI) accounted about 19.61%, 26.18% and 40.71% of the total variation, respectively. GGE biplot graphically displayed interrelationships between test locations as well as genotypes and facilitated visual comparisons through two-dimensional biplot between the first two principal components (PCI and PCII) which explained 74.40% variation for grain yield, 91.98% for days to 50% flowering, 83.27% for days to maturity and 84.68% for 100 seed weight. The GGE biplot suggested suitability of all the four test locations to be used for multi-location trials on the basis of discrimination ability and representativeness. Genotypes, 'C 17' ('PS 1556') was found the best performing genotypes in terms of grain yield followed by 'C 11' ('VLS 89'), 'C 4' ('PS 1550') and 'C 10' ('DS 3102') whereas, in terms of high grain yield and stability both 'C 11' ('VLS 89') was found as the ideal genotype. In the test locations Majhera, Palampur and Almora, winning genotypes for grain yield were 'C 17' ('PS 1556') and 'C 11' ('VLS 89') while, 'C 34' ('VLS 59') was the winning genotype at Bajaura.

Keywords: AMMI, GGE biplot, GEI, MET and soybean [*Glycine max* (L.) Merrill].

INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is one of the most important crop in the world because of its versatile end uses and presently, largest source of edible oil among the oilseed crops (Bhartiya *et al.,* 2014). It is grown worldwide in a diverse range of environments in tropical, subtropical and temperate climates. It was introduced in India during 1960's for exploring its potential as a commercial crop (Bisaliah, 1986) and presently, it occupies 10.02 million ha area with the production and productivity of 11.64 million tonnes and 1162 kg/ha, respectively (Anonymous, 2014-15). The phenomenal gain in area and production of soybean in the country was owing to the concerted efforts for developing high yielding cultivars and their wide cultivation. In the development and identification of suitable genotypes for target environment, multi-environment testing is an important activity but generally, grain yield superiority is considered and the interaction of the cultivar with target environment *i.e.* genotype × environment interaction (GEI) is given little or no attention in this process (Rakshit *et al*., 2012). Besides, multi-environment trial (MET) data are not sufficiently exploited to their full potential and the genotypic evaluation is limited only to genotype main effects (G) whereas, genotype and environment interaction are ignored as noise (Yan and Tinker, 2006). Grain yield of each cultivar is a measure of genotype main effect (G), environment main effect (E) and the genotype × environment interaction (GEI) in each test environment (Yan and Tinker, 2005) but the genotype × environment interaction (GEI) reduces the correlation between phenotype and genotype as well as influence selection progress (Rao *et al*., 2011). Genotype evaluation trials leading to variety identification generally faces two major difficulties, first existence of a strong genotype × environment interaction (GEI) for key trait like yield and secondly an undesirable association between the key trait and some trait of significant importance like days to flowering, days to maturity and 100 grain weight *etc*. Data analysis of key trait address the genotype × environment interaction (GEI) for key trait whereas, joint analysis along with the traits of significant importance accommodates the associations among them (Yan, 2014). Ideally, the variety assessment should be done through multi-year data, however, such data of coordinated trials are usually unbalanced due to change (dropping) of genotypes in different years making interpretations of data difficult. An alternative could be inclusion of all check genotypes to get sufficient number of test genotypes however, this also runs a risk of major influence of regional check. Under such condition, analysis of single year multi-location data can be an option. Although, this may not be the best choice as the estimated heritability would be low, data from single year multi-location evaluation are sufficient enough for identifying location specific superior genotypes deserving promotion. In addition, the extent to which heritability is lowered depends on the magnitude of the genotype–year variance/ genotypic variance and genotype–year–location variance/genotypic variance (Yan, 2014).

In India, soybean is grown in diverse agro ecological zones ranging from Northern hill and plain, North Eastern, Central and Southern Zone. Among all soybean growing zones, in hills agro-climatic conditions are most challenging and are highly variable in terms of soil characteristics, rainfall, temperature *etc.* and differences in altitude and sunshine hours renders significant impact on genotype × environment interaction (GEI) in determining crop yield (Shukla *et al.,* 2006). In North Western Himalayan region, soybean is grown as major *Kharif* crop mainly at altitudinal range 700-1700 masl (Dangwal *et al*., 2007). Genotype × environment interactions (GEI) remained a challenge in selecting genotypes across diverse agro-climatic conditions and make the identification of the best genotypes with high yield and stability difficult (Kumar *et al*., 2014). Genotype × environment interactions (GEI) has great influence on the performance of cultivar especially, in marginal fragile environments of hills and also one of the main reasons for the failure of cultivars to attain predicted yield levels. In this situation, multi-environment trials (MET) can be used effectively to accurately evaluate the performance of cultivars across locations, predict the yield level as well as examine the stability of genotypes for target location for the selection of the best genotypes for target environments (Mustapha *et al*., 2014).

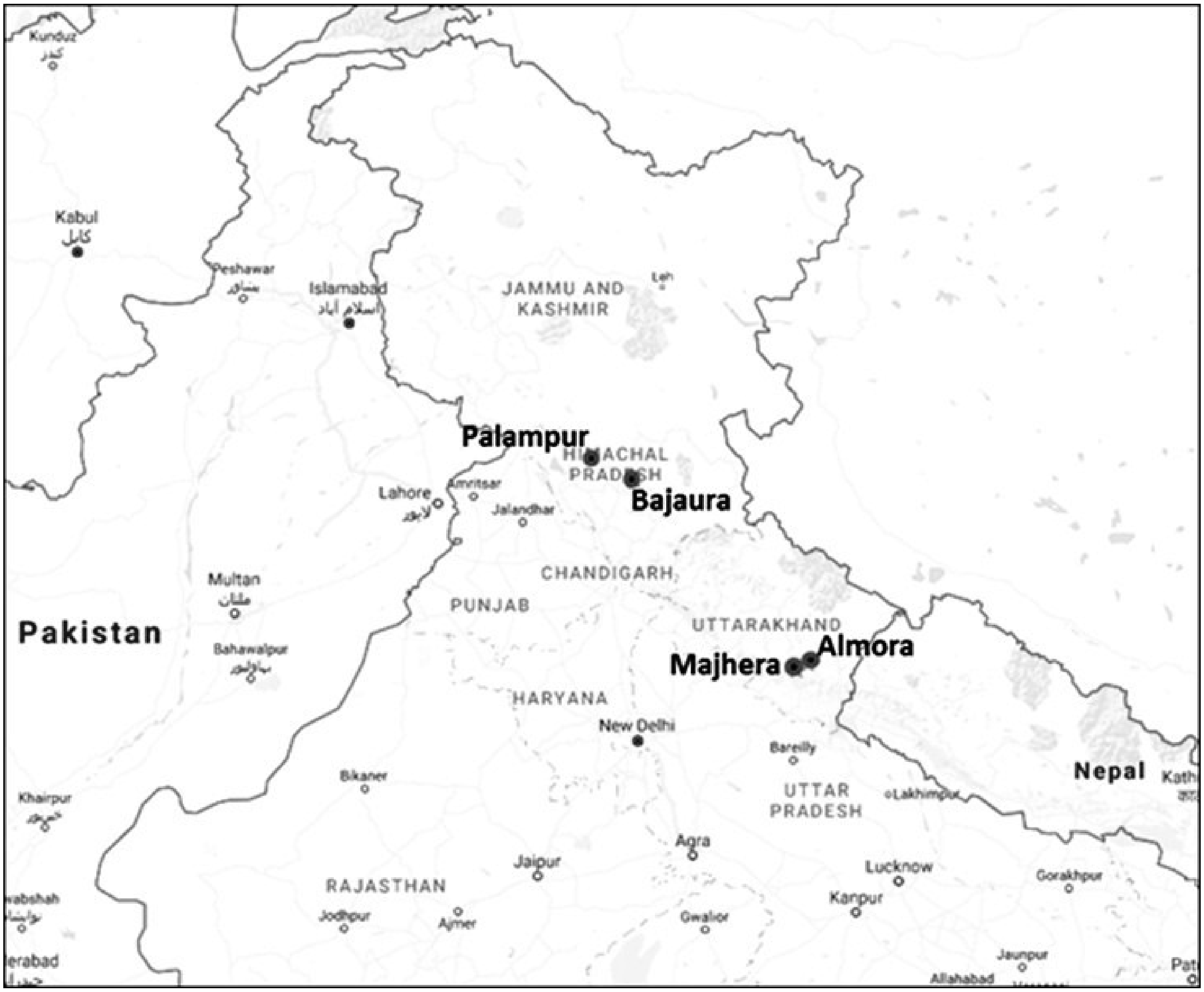
In general, genotype × environment interactions (GEI) are usually small in genotypic variation whereas, genotype (G) and environment (E) explains most of the variation (80% or higher) (Yan and Kang, 2003). It is, therefore, essential that genotypes are identified based on detailed understanding of their genotype × environment interactions (GEI), so that environment specific recommendations could be made. A wide array of statistical techniques have been developed to study and reveal the nature of this complex genotype × environment interactions (GEI), among them additive main effects and multiplicative interaction (AMMI) can effectively assess the stability and adaptability of genotypes (Pacheco and Vencovsky, 2005) whereas, GGE biplot enables the simplistic graphical visualization of complex genotype × environment interactions (GEI) (Yan *et al.,* 2000).

The present investigation was done with the objective to study genotype × environment interaction (GEI) through GGE biplot and AMMI analysis over four environments in 32 genetically diverse soybean genotypes for traits *viz*., grain yield, days to flowering, days to maturity and 100 seed weight in rainfed condition of North Western Himalayan hills.

MATERIALS AND METHODS

The genetic materials of the present investigation comprised 32 new soybean genotypes along with 3 commercial checks *viz*., 'PS1092', 'VL Soya 59' and 'VL Soya 63'. The genotypes in this study were from the Initial Varietal Trial conducted under AICRP on soybean during rainy season of 2014. Multi-environment testing (MET) conducted at 4 locations namely, Almora, Palampur, Bajaura and Majhera which represented rain-fed agro-ecology at different altitudes of North Western Himalayan hills. General information on soybean genotypes used in the study are presented in Table 1 and the detailed features of the testing locations and sowing time at particular location are given in Table 2.

The experiment was conducted in randomized complete block design at each location, with plots accommodating standard plant population (90-95 plants) in 3 rows each of 3 m length with 45 × 10 cm^2 crop geometry in three replications and standard crop management practices were adopted across all the locations. Crop was harvested plot wise at physiological maturity to record the grain yield data (kg/ha), 100 seed weight (g) of each treatment and observations on phenological stages were collected using standard methods (IBPGR, 1984). Plot yield data were converted to kg/ha using the plot size as factor. The grain yield (kg/ha), 100 seed weight(g), days to 50% flowering and days to maturity data were subjected to AMMI analysis of variance using JMP genomics (6.0 version) for the interpretation G×E interaction and for the graphical representation of MET data, GGE biplot analysis was executed using R software (version 3.1.3) and GGE Biplot GUI package. The MET data was analysed without scaling (Scaling=0) to generate a tester centred (Centering=2) GGE biplot, genotype focused singular value partitioning (SVP=1) for visualising mean versus stability of genotypes, environment-focused single value partitioning (SVP=2) was employed for location evaluation and which won where option was used to identify which genotype was winner in given set of environment (Yan and Tinker, 2006).



Locations of multi-environment testing (MET) in NW Himalayan hills

RESULTS AND DISCUSSION

Analysis of variance: The analysis of variance over environments revealed the relative magnitude of genotypes (G), environments (E), Genotype × environment interactions (GEI) which clearly exhibited that G, E and GEI effects are significant for all of the traits under study (Table 3). ANOVA is an additive model that effectively describes the main effects and determines if genotype × environment interaction (GEI) is a significant source of variation (Samonte *et al*., 2005).The ANOVA for grain yield using the AMMI method explained that the soybean grain yield was significantly ($p<0.01$) affected by environments (E), genotype (G) and genotype × environment interactions (GEI). As per AMMI analysis, environments (E), genotypes (G) and genotype × environment interactions (GEI) accounted about 19.61%, 26.18% and 40.71% of the total variation, respectively and genotype × environment interactions (GEI) is more than the genotypic and environment effects. However, the first principal component (PCI), second principal component (PCII) and third principal component (PCIII) explained 24.88%, 11.37% and 6.61% respectively, of the total G×E variation (40.71%). The genotype × environment interactions (GEI) refers to differential ranking of genotypes across environments and only genotype (G) and genotype × environment interactions (GEI) are relevant to cultivar evaluation particularly, when genotype × environment interaction (GEI) is determined as repeatable (Hammer and Cooper, 1996). The genotype × environment interactions (GEI) may complicate the process of selecting superior genotypes, recommendation of a genotype for a target environment and reduces the selection efficiency in different breeding programs (Ebdon and Gauch, 2002; Gauch, 2006). The large G×E effects depicted genotypic differences in the performance, different wining genotypes at different locations as well as possibility of different mega environments in testing locations (Mohahamadi *et al*., 2009; Rakshit *et al*., 2012). However, multiyear data is required for the confirmation of the observed pattern of mega environments (Yan and Tinker, 2006).

Mean performance and stability of genotypes: In the GGE biplot technique developed by Gabriel (1971), the complex genotype × environment interactions (GEI) are simplified in different PCs and the data are presented graphically against various PCs where, PCI approximates the G (mean performance), PC II approximates the G×E (a measure of instability) for each genotype (Yan and Tinker 2006). Genotypic performance and stability were graphically visualized through GGE biplot (Fig.1a-d) using environment centered (centering=2) and genotype metric preserving (SVP=1) model for traits *viz*., grain yield, days to 50% flowering, days to maturity and 100 seed weight. The first two PCs explained 74.40% variation for grain yield, 91.98% for days to 50% flowering, 83.27% for days to maturity and 84.68% for 100 seed weight. Thus, the biplots may safely be interpreted as effective graphical representation of the variability in MET data. If the first two PCs explain more than 60% of the variability in the data and the combined effect account for more than 10% of the total variability that implies the biplot adequately approximates the variability in genotype × environment data (Yang *et al*., 2009; Rakshit *et al*., 2012).

In biplot, mean performance of genotype is measured by the average environment coordination (AEC) abscissa which represents average environment and points towards higher mean values (Farshadfar *et al*., 2012).Whereas, stability is represented by AEC ordinate which points towards greater genotype × environment interactions (GEI) effect *i.e.* poor stability in either direction of genotypes *i.e*. greater the absolute length of the projection in either direction shows greater variability or less stability (Yan *et al*., 2000). Accordingly, C17 (PS 1556) was the best performing genotypes in terms of grain yield of 2556kg/ha followed by C11 (VLS 89) and C4 (PS 1550) with 2403kg/ha and 2305kg/ha, respectively whereas, C15 (MACS 1460) and C12 (RVS 2008-24) were poor yielders. It may be observed that the genotype C1 (AMS 1002), C31 (NRC 100), C23 (DSb 24) and C34 (VLS 59) are least stable for grain yield contrary to genotype C30 (KDS 780) with high stability though not high grain yielder. Among all genotypes C11 (VLS 89) and C13 (MAUS 706) exhibited considerable stability with high mean performance for grain yield. For flowering duration genotype C22 (RSC 10-15 took maximum days for maturity (65 days) among all the entries whereas, C30 (KDS 780) was the earliest (52 days). Interestingly, though C11 (VLS 89) was among the best yielders and as in C17 (PS 1556) and C10 (DS 3102) but it was relatively early (111 days) in maturity than ‘C10’ (‘DS 3102’) and ‘C17’ (‘PS 1556’) which was having high mean values 116 days and 118 days, respectively *i.e.* long reproductive phase. Among all the genotypes under study ‘C11’ (‘VLS 89’) was found most stable for days to maturity as well as early than the best performing soybean genotypes. For 100 seed weight, ‘C9’ (‘NRC 116’) was highest (18.42 g), whereas, ‘C18’ (‘JS 20-87’) was lowest (9.03g) among other high yielding genotypes. Although, C11 (VLS 89) ranked second for mean grain yield after C17 (PS 1556) but found promising for 100 seed weight.

Since the main attention was to get high yielding genotypes across the environment therefore, for further analysis more weight was given on grain yield. Graphical representation of GEI through GGE biplot offers benefit of identification of genotypes which are closest to ideal genotype and ideal environment as well. Ideal genotype situated at the centre of the concentric circles in GGE biplot, having greatest vector length of highest yielding genotype with zero GEI and selection of superior genotypes provided that the genotypic PCI scores have a near-perfect correlation with the genotype main effects, ideal genotypes should have a large PC1 score (high yielding ability) and a small (absolute) PC2 score (high stability). Genotypes located closer to the ‘ideal genotype’ are more desirable than others (Rakshit *et al*., 2012; Yan and Tinker 2006). The ranking of the genotypes for the grain yield in terms of ideal genotype which is high performer with high stability across the environments is depicted in Fig.2. Thus, it may be stated that ‘C11’ (‘VLS 89’) could be considered as ideal genotype which had high grain yield among all genotypes and most stable across the test environments, therefore, ‘C 4’ (‘PS 1550’) and ‘C 10’ (‘DS 3102’) were closest to ideal genotype followed by ‘C 17’ (‘PS 1556’) and more desirable than the rest of soybean genotypes for North Western Himalayan hills. The most ideal genotype, ‘C 11’ (‘VLS 89), performed best at Bajaura (2543kg/ha), while almost similar yield levels at rest three locations viz., Almora (2337kg/ha), Palampur (2387 kg/ha) and Majhera (2346kg/ha) (Table 4). The above result suggests slight crossover GE interaction (order of genotypes based on their performance varied depending on the testing environment) for the most ideal genotype ‘C 11’ (‘VLS 89). Whereas, ‘C22’ (‘RSC 10-15’) and ‘C15’ (‘MACS 1460’) were unfavourable as situated very far from the ideal genotype

Environment evaluation: GGE biplots are useful to understand the relationship between the testing environments and identify the test environment that effectively identifies superior genotypes for mega environments and representative of mega environments (Yan *et al*., 2007). The relationship among test environments were studied based on environment-centered (centering=2) and environment-metric preserving (SVP=2) without scaling. In the environmental vector view of GGE biplot (Fig.3e-h), the lines that connects test environment to the biplot origin are called environment vectors and the cosine of the angle between the vectors of two environments approximates the correlation between them *i.e.* acute angle represents positive, obtuse angle depicts negative correlation, large G×E and strong crossovers and right angle represents no correlation between environments (Yan and Tinker, 2006). However, the test environments with longer vectors are more discriminating of the genotypes whereas, a test environment marker with a very short vector provided little or no information about the genotype differences (Yan *et al*., 2007). Representativeness of test environments can be measured by angle between test environment with Average Environment Axis (AEA) and environment with smaller angles with AEA are most representative of the average test environments (Yan and Tinker, 2006). Accordingly, for days to 50% flowering, Palampur was found most discriminating and representative therefore, suitable environment for selecting generally adapted genotypes. Palampur was found most discriminating and Almora was found representative for days to maturity whereas, for grain yield, Bajaura was most discriminating whereas, Almora was most representative location. All the test locations are discriminating and representative for one or more traits and show its suitability to be used as test environment for multi environment trials (MET). Almora was the most closest to average environment followed by Palampur. Whereas, ranking the genotypes in most near to average environment *i.e.* most representative (Almora) showed that 'C17' ('PS 1556') yielded maximum followed by 'C11' ('VLS 89'), 'C34' ('VLS 59'), 'C4' ('PS 1550') and 'C10' ('DS 3102'). For selecting generally adapted genotypes for grain yield, Palampur was found suitable based on both discrimination and representativeness.

Which–won–where and mega environment identification: Most attractive feature of GGE biplot is 'Which-won-where' analysis, in which crossover genotype × environment interactions (GEI), mega-environment differentiation, specific adaptation of genotypes etc. are graphically addressed (Rakshit *et al*., 2014). Visualization of the which-won-where pattern of multi environment trial data is important for studying the possible existence of different mega-environments (ME) in a region (Kaya *et al*., 2006). Which–won–where graph is constructed first by joining the farthest genotypes from the biplot origin so that, all other genotypes are contained within polygon and subsequently, perpendicular lines/equality lines drawn from biplot origin on each side of the polygon, separating the biplot into several sectors with one genotype at the vertex of the polygon. The polygon view of a GGE biplot explicitly displays the which-won-where pattern, and hence is a laconic summary of the G×E interaction pattern (GEI) of a MET data set. All the genotypes in biplot were arranged in such a way that some of them were on the vertices whereas, the rest were inside the polygon. These vertex genotypes were the most responsive since, they have the longest distance from the biplot origin. Responsive genotypes were those having either the best or poorest performance in one or all environments (Yan and Rajcan, 2002) falling within the sectors. In the 'Which–won–where biplot', the environments distributed by equality lines into different sectors for grain yield (7), days to 50% flowering (6), days to maturity (7) and 100 seed weight (7) (Fig.4i-l). For grain yield, the polygon had seven genotypes, *viz*., C17 (PS 1556), C34 (VLS 59), C1 (AMS 1002), C15 (MACS 1460), C22 (RSC 10-15), C31 (NRC 100) and C23 (DSb 24) at the vertices. All the environments were retained into two sectors and may be due to latitudinal and longitudinal differences the testing locations may be partitioned into two mega environments one with Majhera (29°30' N and 79°28' E), Palampur (32°6'N and 76°23'E) and Almora (29°36' N and 79° 40' E) and second mega environment encompassed Bajaura (31°8'N and 77°E). In first mega environment (Majhera, Palampur and Almora) C17 (PS 1556) and C11 (VLS 89) and in Bajaura with C34 (VLS 59) were the winning genotypes.

Table 1. Soybean genotypes used for multi-environment trial (MET) at different locations in North Western Himalayan hills.

Code	Genotype	Pedigree	Source
C1	AMS 1002	Mutant of JS 93-05	PDKV, Amravati
C2	RVS 2007-6	JS 20-10/MAUS 162	RVSKV, Sehore
C3	MACS 1442	MACS 1037/JS 335	ARI, Pune
C4	PS 1550	PS 1029 /PS 1241	GBPUA&T, Pantnagar
C5	JS 20-98	JS 98-52 /SL 710	JNKVV, Jabalpur
C6	KDS 869	JS 335/EC 538800	K. Digraj, Maharashtra
C7	RSC 10-46	Bragg/JS 335	IGAU, Raipur
C8	DSb 28-3	JS 93-05/EC 241780	UAS, Dharwad
C9	NRC 116	-	DSR, Indore
C10	DS 3102	-	IARI, Delhi

C11	VLS 89	VLS 47/EC 361364	VPKAS, Almora
C12	RVS 2008-24	JS 335/PK 1042	RVSKV, Sehore
C13	MAUS 706	-	MAU, Parbhani
C14	AMS1004	Mutant of JS 93-05	PDKV, Amravati
C15	MACS 1460	RKS 24/ JS 95-60	ARI, Pune
C16	KDS 753	JS 93-05/EC 241780	K. Digraj, Maharashtra
C17	PS 1556	(PS1042/ MACS 450)/(PS1024/PS 1241)	GBPUA&T, Pantnagar
C18	JS 20-87	JS 97-52/JS(15)90-5-12-1	JNKVV, Jabalpur
C19	NRC99	EC546882/PS 1024	DSR, Indore
C20	SL 1028	PK 1223/SL(E)4	PAU, Ludhiana
C21	VLS 88	VLS 47/EC 361363	VPKAS, Almora
C22	RSC 10-15	RSC 4/Indian soya 9	IGAU, Raipur
C23	DSb 24	MACS 450/Local black soybean	UAS, Dharwad
C24	DS 3101	-	IARI, Delhi
C25	RVS 2008-8	JS93-05/RKS24	RVSKV, Sehore
C26	MACS 1454	PS 1347/TS 99-76	ARI, Pune
C27	PS 1552	PS 1214/Hardee	GBPUA&T, Pantnagar
C28	JS 20-96	JS 97-52/JSM 286	JNKVV, Jabalpur
C29	AMS 1003	Mutant of JS 93-05	PDKV, Amravati
C30	KDS 780	JS 93-05/ AMS 51	K. Digraj, Maharashtra
C31	NRC 100	G 841/NRC 7	DSR, Indore
C32	KBS 23-2014	JS 335/KHSb-2	UAS, Bengaluru
C33	PS 1092	(Check)	GBPUA&T, Pantnagar
C34	VL Soya 59	(Check)	VPKAS, Almora
C35	VL Soya 63	(Check)	VPKAS, Almora

Table 2. Locations used for evaluation of soybean genotypes in North-Western Himalayan hills.

Parameters	Almora	Bajaura	Palampur	Majhera
Altitude (m)	1250	1090	1290	905
Latitude	29°36′ N	31°8′N	32°6′N	29°30′N
Longitude	79°40′E	77°E	76°23′E	79°28′E
Total Rainfall (mm)	630.8	338.3	1010.4	634.0
Average Temp ^{0}C (max)	29.44	30.43	27.3	30.35
Average Temp ^{0}C (min)	17.14	17.37	17.5	21.72
Date of sowing	30.06.2014	08.07.2014	24.06.2014	07.07.2014

Note: Weather data for soybean crop season (June-Oct, *Kharif* 2014)

Table 3. Additive Main Effects and Multiplicative Interaction (AMMI) Analysis of variance of soybean genotypes

Source	DF	Mean Square Values of Different Traits				% SS	G×E (%)
		Days to 50% flowering			Grain yield	(GY)	(GY)
Env	3	1561.56**	8746.67**	118.04**	10477608**	19.61	-
Rep(Env)	8	7.02**	3.51	3.15**	79358.32	0.40	-
Genotypes	34	151.01**	143.48**	49.95**	1234084**	26.18	-
Env×Genotypes	102	15.96**	69.70**	6.14**	639711**	40.71	-
IPCA I	36	26.43**	140.39**	6.82**	1107874.4**	-	24.88
IPCA II	34	13.07**	35.09**	6.72**	536096.6**	-	11.37
IPCA III	32	8.46**	25.55**	4.70**	330999.9**	-	6.61
Error	272	1.41	2.23	0.58	73232.5	-	12.43

**Significant at the 1% probability level

Table 4. Mean values for days to 50% flowering, days to maturity, 100 seed weight (g) and grain yield (kg/ha) of soybean genotypes (C1 to C35) tested at four locations (Majhera, Palampur, Bajaura and Almora) of NW Himalayan hills.

Code	Days to 50% flowering					Days to maturity					100 seed weight (g)					Grain yield (kg/ha)				
	E1	E2	E3	E4	Mean	E1	E2	E3	E4	Mean	E1	E2	E3	E4	Mean	E1	E2	E3	E4	Mean
C1	59	63	67	56	62	112	111	128	98	112	8.97	10.93	9.70	9.80	9.85	1144	2988	1391	1556	1770
C2	54	63	60	52	57	114	114	125	98	113	10.65	12.38	12.45	13.83	12.33	1654	2074	1679	2716	2031
C3	55	56	60	49	55	111	111	133	100	114	11.89	14.67	16.19	13.74	14.12	1802	2650	1580	1975	2002
C4	56	62	63	56	59	120	114	131	103	117	13.52	11.09	13.42	15.19	13.30	1778	2148	2502	2790	2305
C5	54	56	60	51	55	105	106	123	95	107	9.93	12.52	14.07	10.88	11.85	1407	2173	1992	1901	1868
C6	57	67	62	54	60	112	107	124	95	110	11.28	12.42	11.59	10.07	11.34	1770	2938	1449	2049	2052
C7	57	58	66	57	59	113	114	124	107	115	9.03	11.61	11.48	11.70	10.95	1465	2675	1506	2642	2072
C8	63	58	63	51	59	112	105	123	96	109	11.92	14.26	13.90	12.12	13.05	2091	2008	1827	1975	1975
C9	51	52	55	51	52	114	109	123	108	113	15.39	19.57	19.28	19.43	18.42	971	1202	2058	2049	1570
C10	55	57	62	50	56	117	112	129	106	116	8.90	12.66	10.72	10.21	10.62	1621	2198	2461	2840	2280
C11	55	56	62	50	56	114	105	123	102	111	12.85	15.76	14.91	14.41	14.48	2337	2543	2387	2346	2403
C12	56	57	63	52	57	114	107	127	106	114	11.96	13.03	14.43	13.51	13.23	1202	1984	1128	2025	1585
C13	54	52	60	50	54	107	101	123	96	107	10.39	14.87	13.70	13.41	13.09	1778	2609	2016	2148	2138
C14	56	57	61	52	57	112	99	127	97	109	9.16	9.84	10.64	10.65	10.07	897	1638	1498	1901	1484
C15	55	56	62	49	56	106	102	123	97	107	8.39	12.44	13.65	11.87	11.59	444	2115	1185	790	1134
C16	63	57	64	53	59	115	114	126	111	117	11.52	15.56	11.06	13.84	12.99	1152	2420	1679	2790	2010
C17	56	56	62	51	56	119	113	129	111	118	9.57	14.13	12.31	13.52	12.38	1465	2527	3342	2889	2556
C18	63	63	68	58	63	115	113	126	106	115	8.36	10.07	9.90	7.80	9.03	1556	1712	1761	1926	1739
C19	52	57	59	51	55	117	108	127	100	113	12.27	13.94	14.10	12.52	13.21	2362	1844	2074	1284	1891
C20	57	63	66	57	61	117	111	126	108	115	9.22	15.58	11.90	11.38	12.02	1111	1737	1877	2148	1718
C21	54	56	61	52	56	114	109	124	105	113	10.83	16.58	14.92	16.69	14.75	1572	2691	2477	1432	2043
C22	64	65	70	60	65	120	117	129	112	120	10.28	10.57	11.28	14.23	11.59	872	872	1556	1556	1214
C23	63	63	68	56	63	115	114	127	107	116	11.25	12.36	11.97	13.20	12.20	1317	1416	2634	2716	2021
C24	58	64	67	56	61	114	119	124	106	116	11.13	15.83	10.05	15.73	13.19	1613	2156	1926	1975	1918
C25	55	52	56	49	53	110	102	126	96	108	10.18	11.83	12.76	12.35	11.78	872	1556	1029	2790	1562
C26	60	63	68	56	62	116	117	104	110	112	10.33	12.21	12.07	16.14	12.69	1078	1045	1827	1901	1463
C27	62	63	70	58	63	122	119	105	112	114	13.44	12.36	15.03	17.15	14.49	1045	1457	2189	2049	1685
C28	62	56	67	56	60	111	109	127	98	111	9.26	11.33	12.14	10.16	10.72	1267	1333	1704	2642	1737
C29	57	58	64	52	58	111	107	123	96	109	11.03	12.17	11.33	10.10	11.16	1103	1909	1309	1975	1574
C30	54	51	51	50	52	111	109	123	97	110	8.81	14.08	15.22	12.26	12.59	881	1885	1276	2049	1523
C31	51	56	59	52	55	95	108	123	94	105	12.43	9.74	11.57	9.57	10.83	1243	889	1399	2840	1593
C32	54	56	60	52	56	112	111	124	96	111	15.97	14.62	12.81	12.55	13.99	1597	1695	1399	2346	1759
C33	48	59	50	51	52	107	109	133	98	111	13.66	18.18	16.67	16.80	16.33	1366	2765	1144	1930	1801
C34	51	52	58	50	53	106	112	125	97	110	14.49	19.08	17.67	16.34	16.90	2148	3169	1613	2148	2270
C35	51	49	60	48	52	111	104	126	107	112	13.90	17.67	17.17	15.09	15.96	2000	2864	1572	1901	2084
Mean	56	58	62	53	-	113	110	125	102	-	11.2	13.59	13.2	13.10	-	1428	2054	1784	2142	-
CD	1.85	0.85	2.2	1.36	-	2.95	0.69	2.29	1.83	-	0.84	1.20	0.85	1.75	-	389.69	142.43	423.95	580.61	-
CV (5%)	2.01	0.9	2.18	1.59	-	1.61	0.38	1.12	1.10	-	4.65	5.42	3.96	8.24	-	16.74	4.25	14.58	16.63	-

E1=Almora, E2=Bajaura, E3=Palampur & E4= Majhera

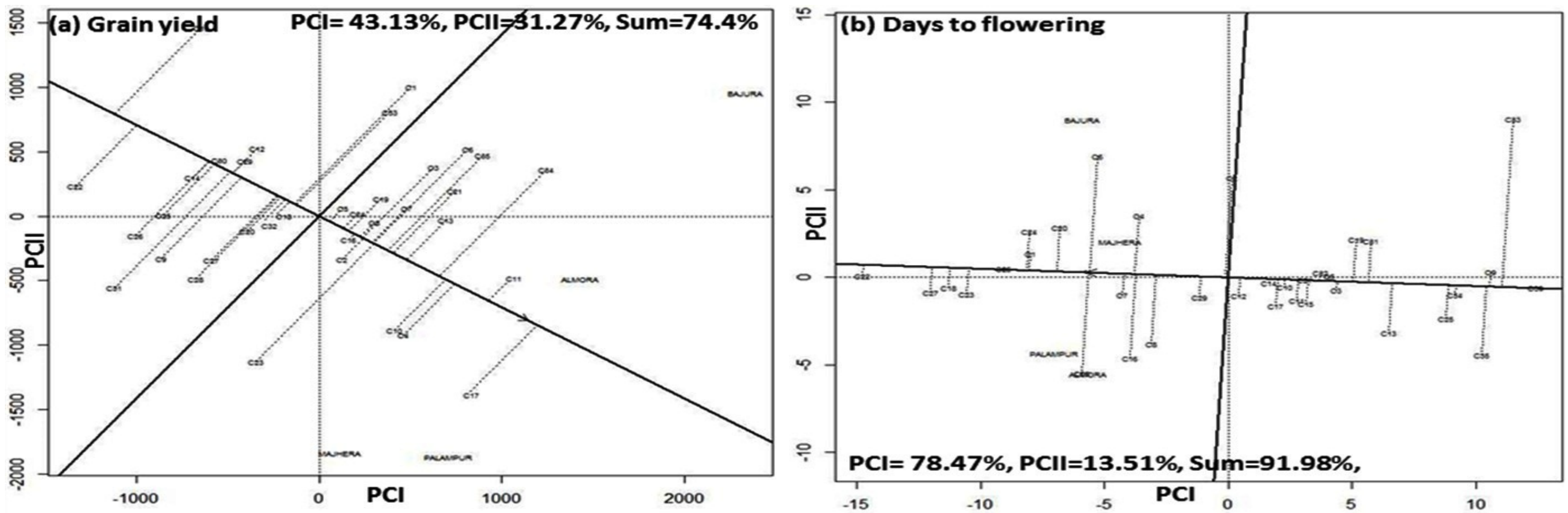


Fig. 1 (a & b). GGE biplots for ranking of genotypes based on mean performance for grain yield and days to flowering

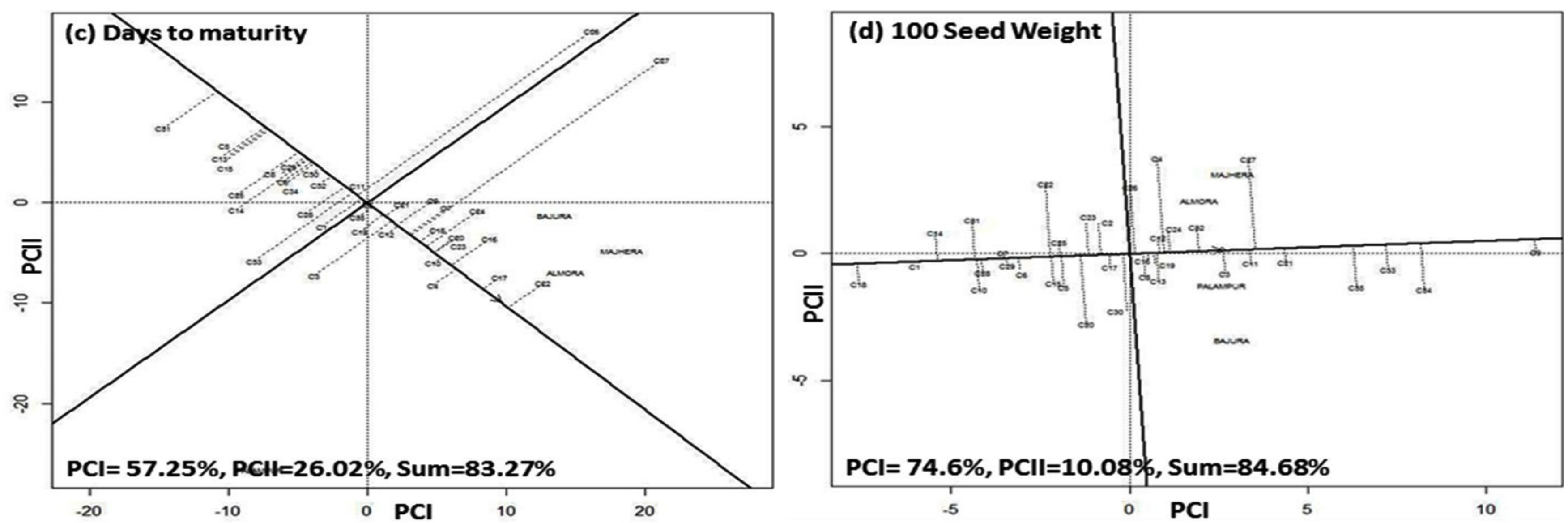


Fig.1(c & d).GGE biplots for ranking of genotypes based on mean performance for days to maturity and 100 seed weight

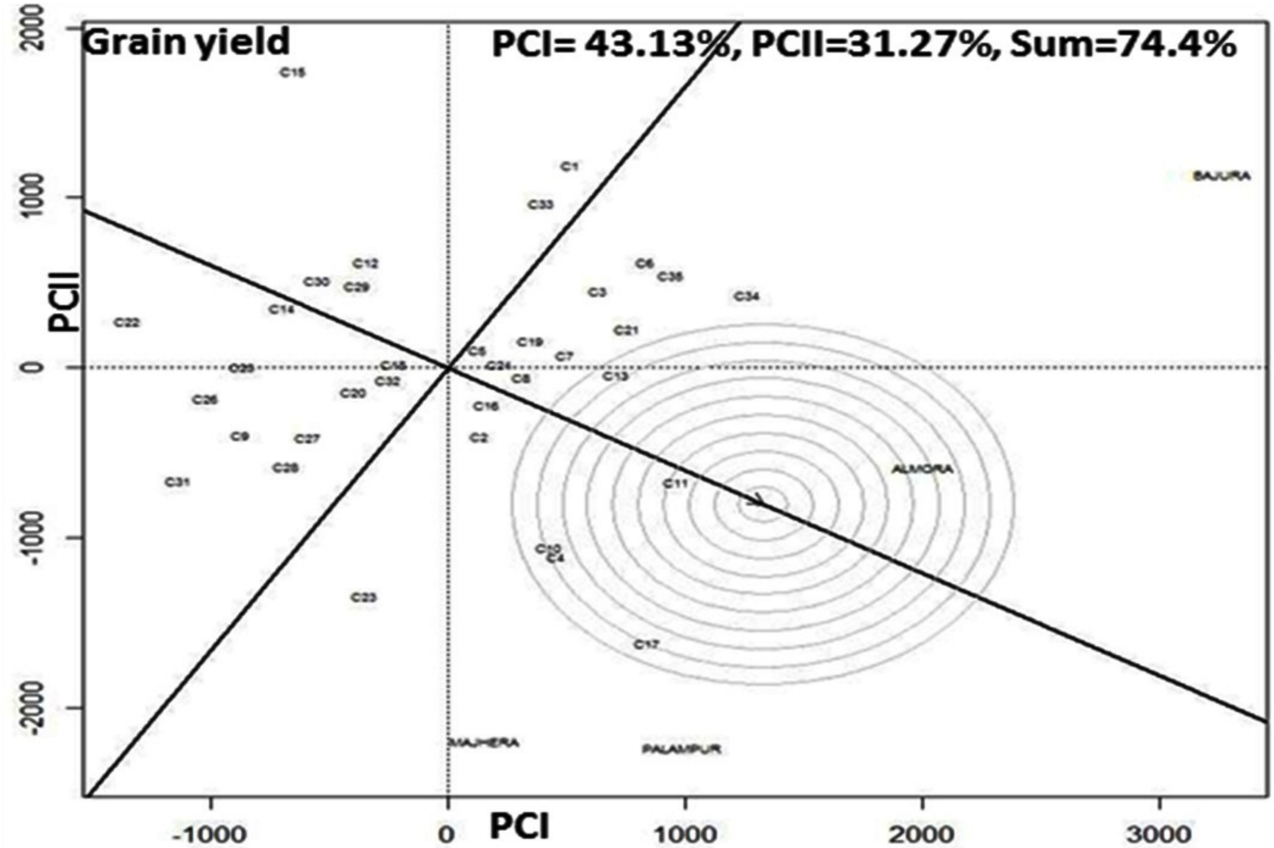


Fig.2. Average- environment coordination view to rank soybean genotypes relative to an ideal genotype

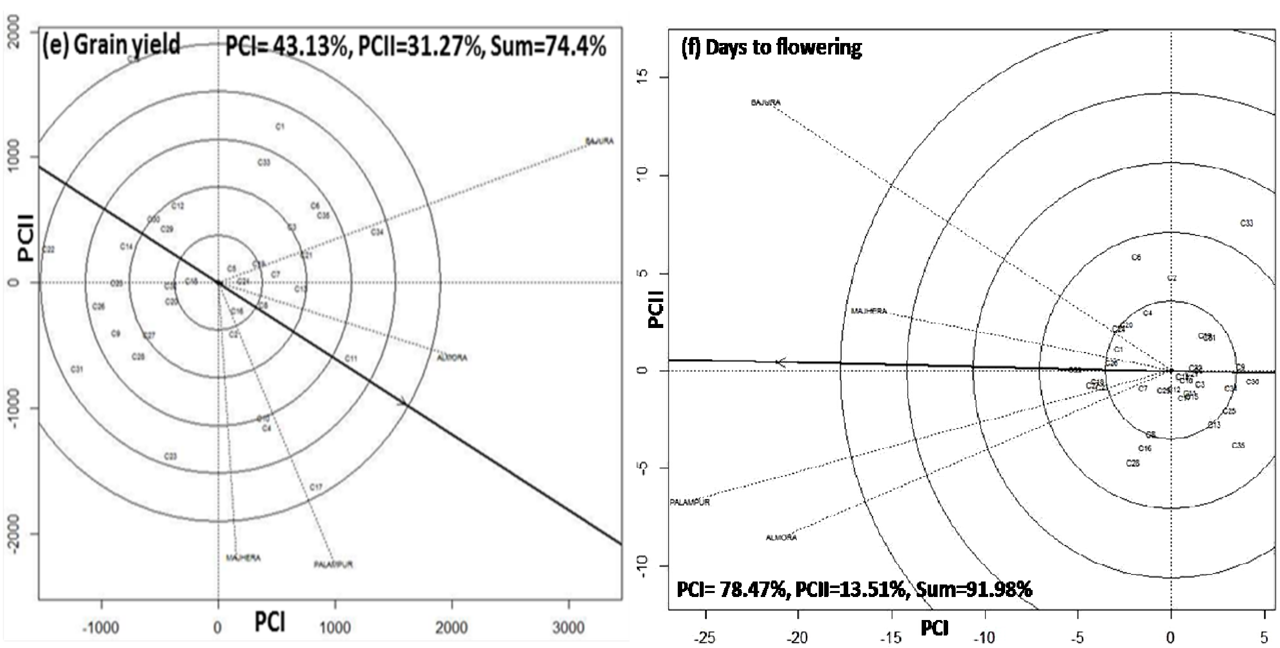


Fig. 3 (e & f). Discriminating versus representativeness view for grain yield and days to flowering

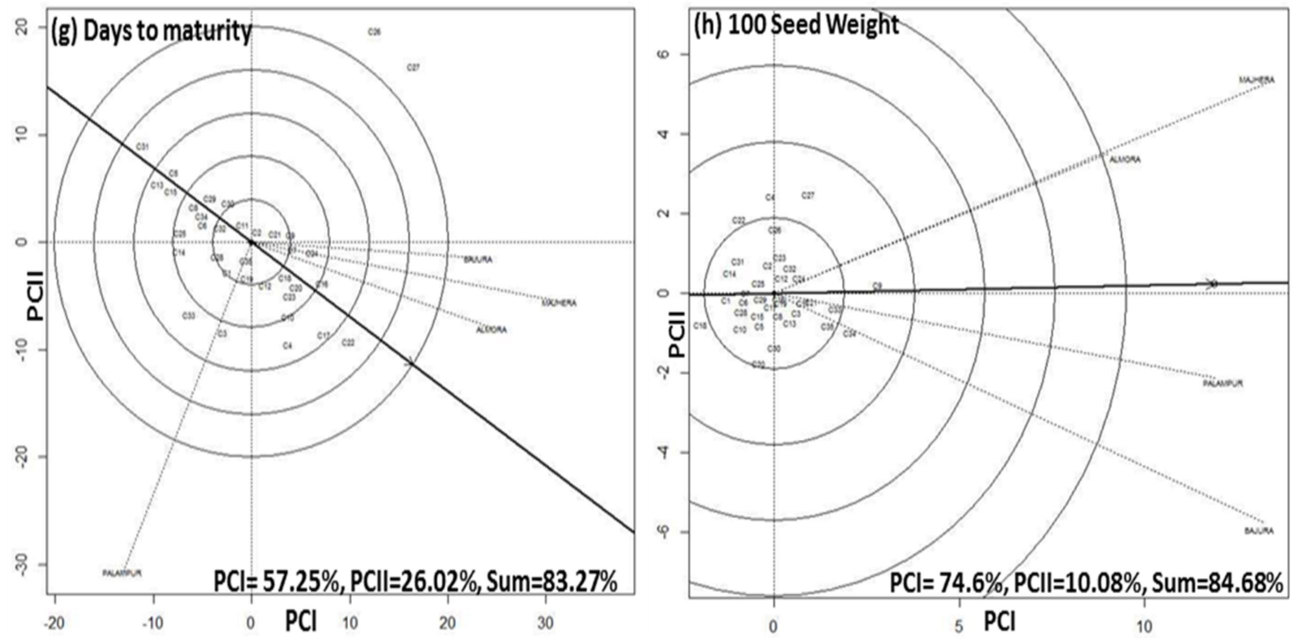


Fig.3 (g & h). Discriminating versus representativeness view for days to maturity and 100 seed weight

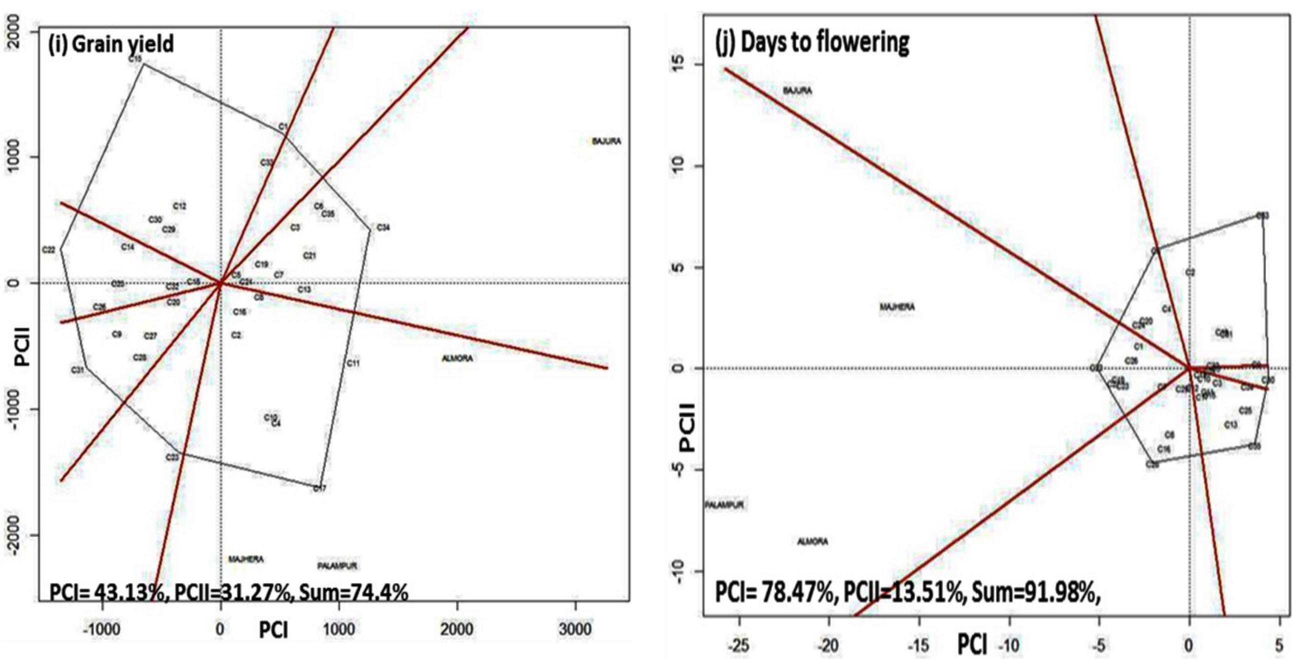


Fig.4 (i & j). Which -Won-where analysis of soybean genotypes for grain yield and days to flowering

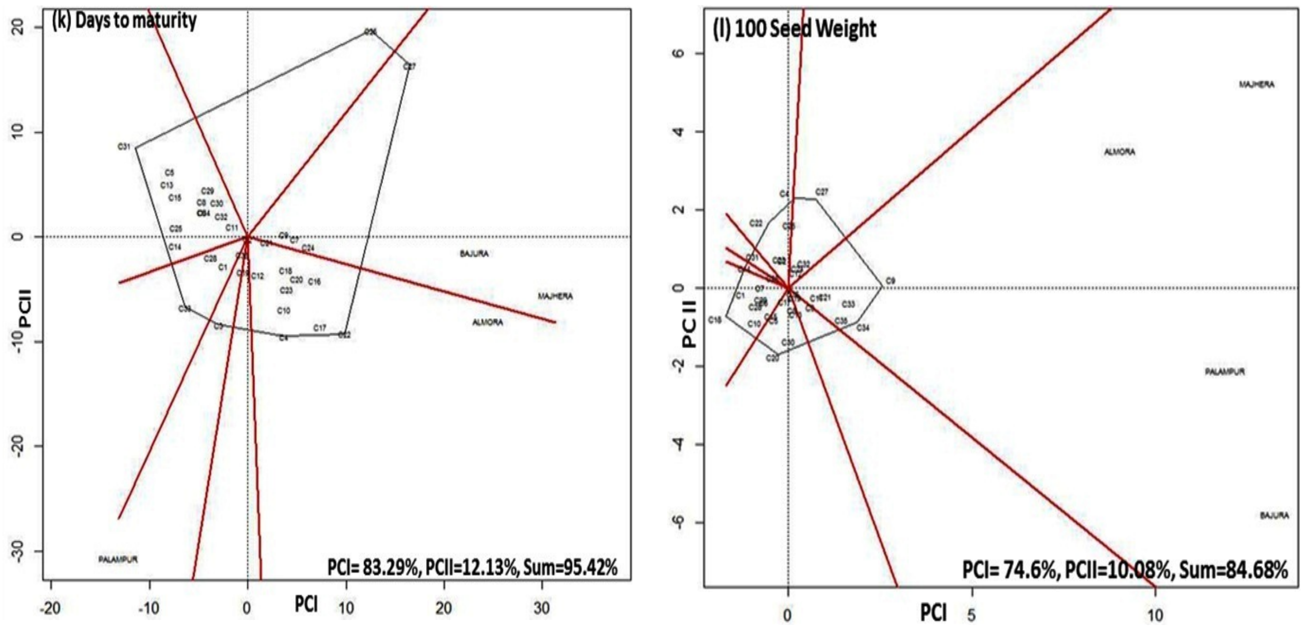


Fig.4 (k & l). Which -Won-where analysis of soybean genotypes for days to maturity and 100 seed weight

Conclusion: Genotype × environment interaction (GEI) plays a crucial role in the performance of genotypes in an environment but its importance generally ignored and stability of the genotypes is not given any consideration. Development of cultivars is a time consuming, resource and labour intensive task and in the existing procedure of varietal release, mean performance of a genotype over years and locations, and its superiority over the checks is only considered and multi-environment trial (MET) data is not utilized to its full potential. In the present investigation, effort was made to identify high yield and stable genotypes by analysing multi environment data to take the stability of the genotypes into consideration and graphical visualization has expediently aided in identification of stable and superior soybean genotypes across testing environments. Although, all the testing environments exhibited their suitability to be used for multi-location trials on the basis of their discriminative ability and representativeness but their ability to discriminate differ trait wise. It was also found that genotype showing stability for one trait not necessarily stable for other trait as well as differing with test locations. Thus, during soybean breeding programme the trait of interest need to be prioritized as per the need of particular geographical and agro-climatic regions.

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REFERENCES

Anonymous 2014-15. Director's Report and Summary Tables of Experiments, All India Coordinated Research Project on Soybean, Directorate of Soybean Research, Indore, Madhya Pradesh.

Bhartiya, A., K. Singh, J.P. Aditya, Puspendra and M. Gupta (2014). Residual relative heterosis and heterobeltiosis for different agro morphological traits as selection index in early segregating generation of soybean [*Glycine max* (L.) Merrill] crosses. Soybean Res., 12(1):28-35.

Bisaliah, S. (1986). Soybean development in India. CGPRT No. 5, ESCAP/CGPRT Centre.

Dangwal, D., R.K. Maikhuri, L.S. Rawat and V.S. Negi (2007). Spatio-temporal dynamics of diversity of traditional grain legumes of Central Himalaya. CSM-BGBD internal project report, CSM-BGBD, India.

Ebdon, J.S. and H.G. Gauch (2002). Additive main effect and multiplicative interaction analysis of national turfgrass performance trials: I. Interpretation of genotype × environment interaction. Crop Sci., 42: 489-496.

Farshadfar, E., R. Mohammadi, M. Aghaee and Z. Vaisi (2012). GGE Biplot analysis of genotype × environment interaction in wheat-barley disomic addition lines. Aust. J. Crop Sci., 6: 1074-1079.

Gabriel, K. R. (1971). The biplot graphic display of matrices with application to principal component analysis.Biometrika,58: 453-467.

Gauch, H. G. (2006). Statistical analysis of yield trials by AMMI and GGE. Crop Sci.,46:1488-1500.

Hammer G. L. and Cooper M. (1996). Plant adaptation and crop improvement. CABI, Wallingford.

International Board for Plant Genetic Resources (IBPGR) (1984). Descriptors of soybean. IBPGR Secretariat, Rome, IBPGR/84/183.

Kaya, Y., M. Akcura and S. Taner (2006). GGE biplot analysis of multi-environment yield trials in bread wheat. Turk. J. Agric. For., 30: 325-337.

Kumar, A., S. Kumar, C. Kapoor, R. Bhagawati, A. Pandey and A. Pattanayak (2014). GGE biplot analysis of genotype × environment interaction in soybean grown in NEH regions of India. Environ. Eco., 32 (3A): 1047-1050.

Mohammadi, R., M. Aghaee, R. Haghparast, S.S. Pourdad, M. Rostaii, Y. Ansari, A. Abdolahi and A. Amri (2009). Association among non-parametric measures of phenotypic stability in four annual crops. J. Plant Sci. Biot., 3: 20-24.

Mustapha, M. and H.R. Bakari (2014). Statistical evaluation of genotype by environment interactions for grain yield in millet (*Pennisetum glaucum* (L) R. Br). The Int. J. of Eng. Sci., 3(9): 7-16.

Pacheco, R.M. and D. J.B. Vencovsky (2005). Use of supplementary genotypes in AMMI Analysis.Theor. Appli. Genet., 110: 812-818.

R Development Core Team (2012).R: A language and environment for statistical computing. R foundation for statistical computing, Vienna, Austria. ISBN 3-900051-07-0, URL http://www.r-project.org/.

Rakshit, S., K.N. Ganapathy, S.S. Gomashe, A. Rathore, R.B. Ghorade, M.V. Nagesh Kumar, K. Ganesmurthy, S.K. Jain, M.Y. Kamtar, J.S. Sachan, S.S. Ambekar, B.R. Ranwa, D.G. Kanawade, M. Balusamy, D. Kadam, A. Sarkar, V.A.Tonapi and J.V. Patil (2012). GGE biplot analysis to evaluate genotype, environment and their interactions in sorghum multi-location data. Euphytica, 185:465–479.

Rakshit, S., K.N. Ganapathy, S.S. Gomashe, M. Swapna, A. More, S. R. Gadakh, R. B. Ghorade, S. T. Kajjidoni, B.G. Solanki, B.D. Biradarand Prabhakar (2014). GGE biplot analysis of genotype × environment interaction in *Rabi* grain sorghum [*Sorghum bicolor* (L.) Moench]. Indian J. Genet., 74(4): 558-563.

Rao, P.S., P.S. Reddy, A. Rathore, B.V. Reddy and S. Panwar (2011). Application GGE biplot and AMMI model to evaluate sweet sorghum (*Sorghum bicolor*) hybrids for genotype × environment interaction and seasonal adaptation. Indian J. Agri. Sci., 81 (5): 438-44.

Samonte, S. O. P. B., L.T. Wilson, A. McClung and J. C. Medley (2005). Targeting cultivars onto rice growing environments using AMMI and SREG GGE biplot analysis. Crop Sci., 45: 2414-2424.

Shukla, S.K., V. Mahajan and H.S. Gupta (2006). Horsegram in Uttaranchal: status, constraints and prospects. Horsegram research: An introduction. In: Kumar D.(ed), Horsegram in India. p144.

Yan, W. and N.A. Tinker (2006). Biplot analysis of multi-environment trial data: Principles and applications. Canadian J. Plant Sci., 86: 623–645.

Yan, W. and I. Rajcan (2002). Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Sci., 42: 11-20.

Yan, W. and N.A. Tinker (2005). An integrated biplot analysis system for displaying, interpreting and exploring Genotype × environment interaction. Crop Sci., 45: 1004–16.

Yan, W., L.A. Hunt, W.Q. Sheng and Z. Szlavnics (2000). Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Sci., 40: 597–605.

Yan, W., M.S. Kang, S. Wood and P.L. Cornelius (2007). GGE biplot *vs.* AMMI analysis of genotype by environment data. Crop Sci., 47: 643-655.

Yan, W. (2014). Crop Variety Trials: Data Management and Analysis. Wiley Blackwell. 360 p.

Yan, W. and M.S. Kang (2003). GGE-biplot analysis: A graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton, FL, USA.

Yang, R.C., J. Crossa, P.L. Cornelius, J. Burgueno (2009). Biplot analysis of genotype x environment interaction: proceed with caution. Crop Sci., 49:1564-1576.