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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

A. Bhartiya[1*], J. P. Aditya[1], V. Kumari[2], N. Kishore[3], J. P. Purwar[4], A. Agrawal[4] and L. Kant[1]

[1]ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan, Almora-263601, Uttarakhand, India, [2]CSKHPKV, Palampur-176062, Himachal Pradesh, India, [3]CSKHPKV, Hill Agricultural Research and Extension Centre, Bajaura-175125, Kullu, Himachal Pradesh, India & [4]GBPUA&T, Agriculture Research Station, Majhera, Nainital-263135, Uttarakhand, India
[*]Corresponding author's e-mail:anuradhagpb@gmail.com

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).

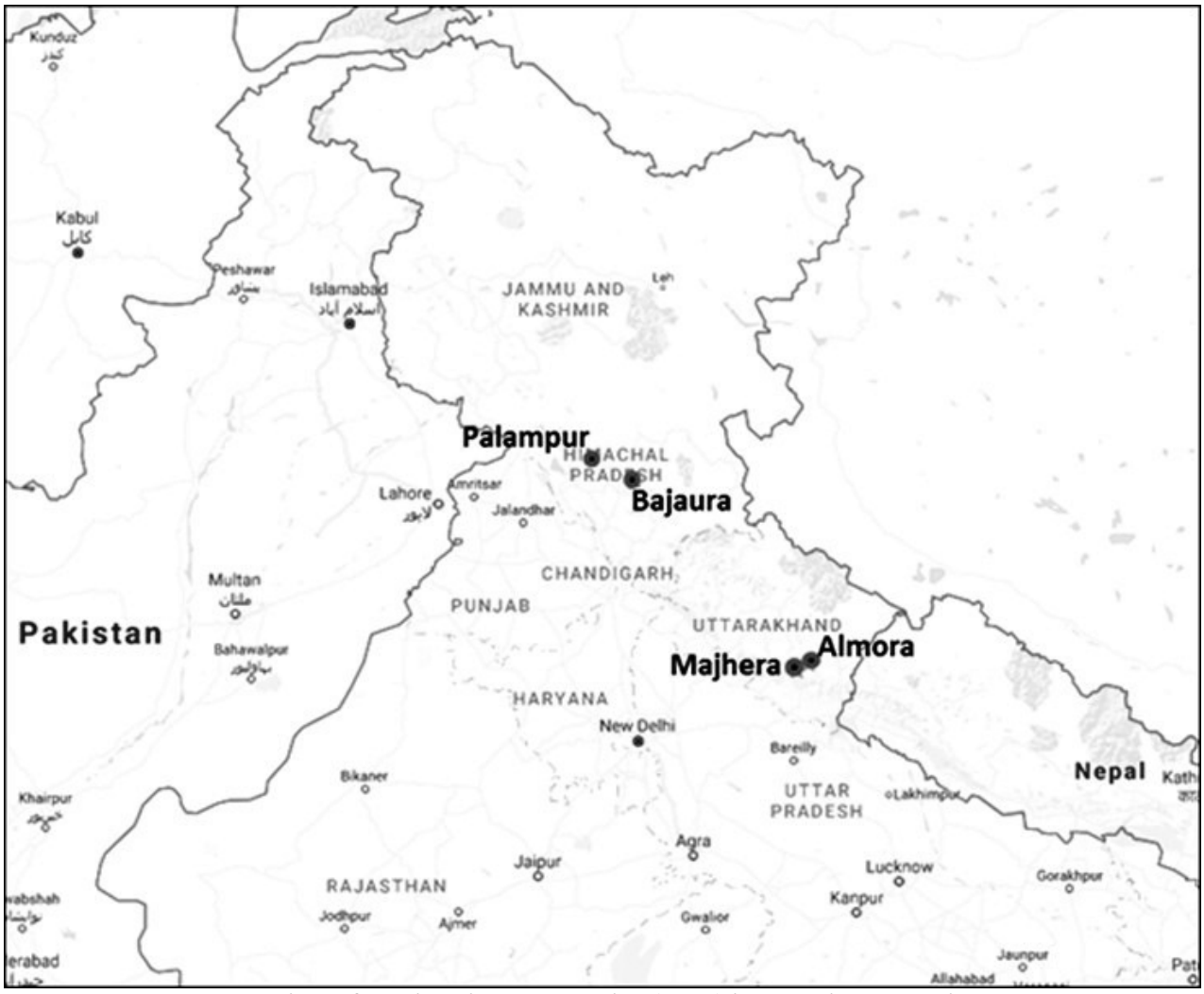
In general, genotype × environment interactions (GEI) are usually small in genotypic variation whereas, genotype (G) and environment (E) explains most of the variation (80% or higher) (Yan and Kang, 2003). It is, therefore, essential that genotypes are identified based on detailed understanding of their 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 (29º30' N and 79º28' E), Palampur (32º6'N and 76º23'E) and Almora (29º36' N and 79º 40' E) and second mega environment encompassed Bajaura (31º8'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

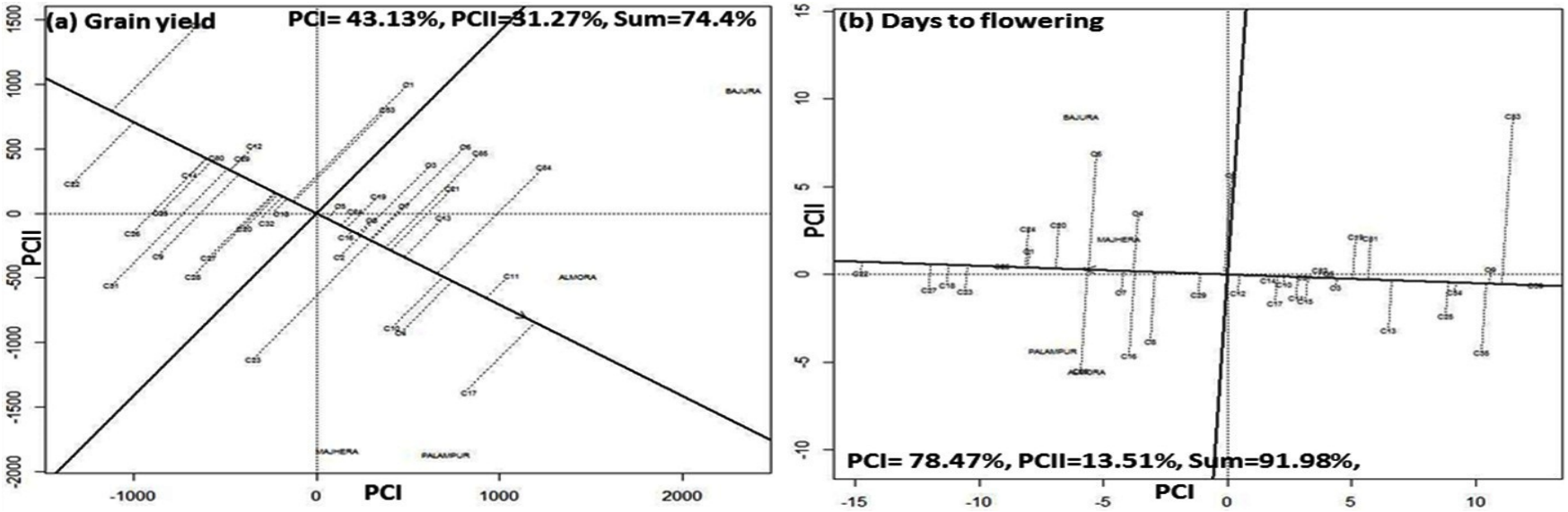


Fig. 1 (a & b). GGE biplots for ranking of genotypes based on mean performance for grain yield and days to flowering

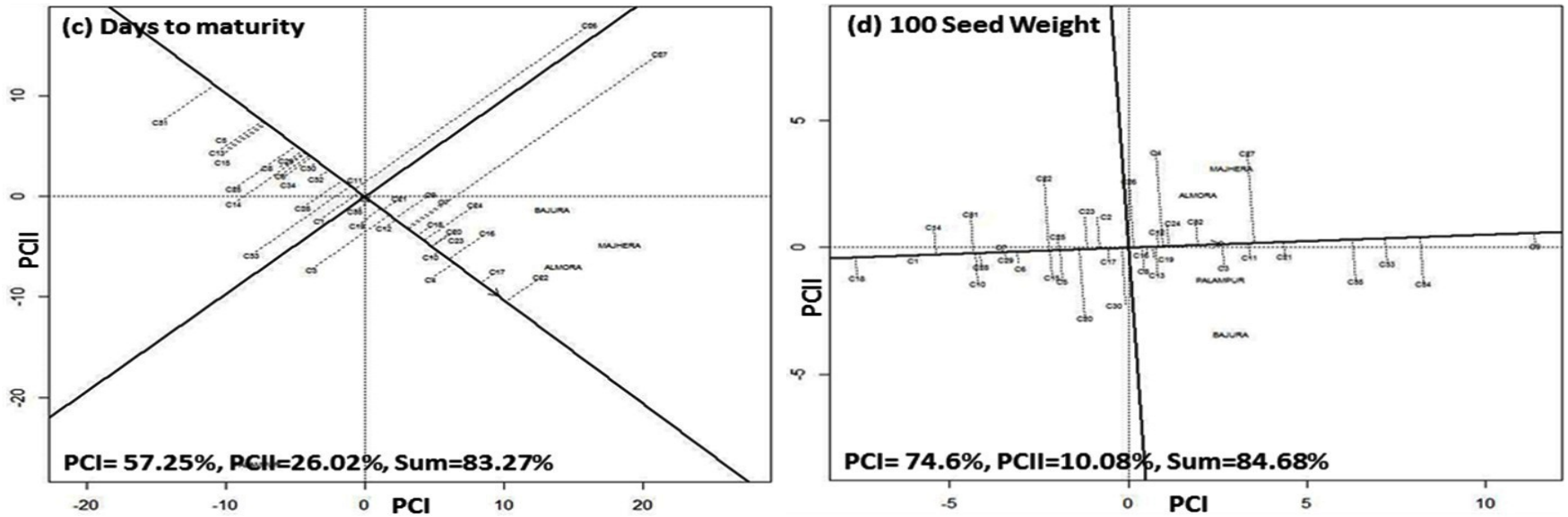


Fig.1(c & d).GGE biplots for ranking of genotypes based on mean performance for days to maturity and 100 seed weight

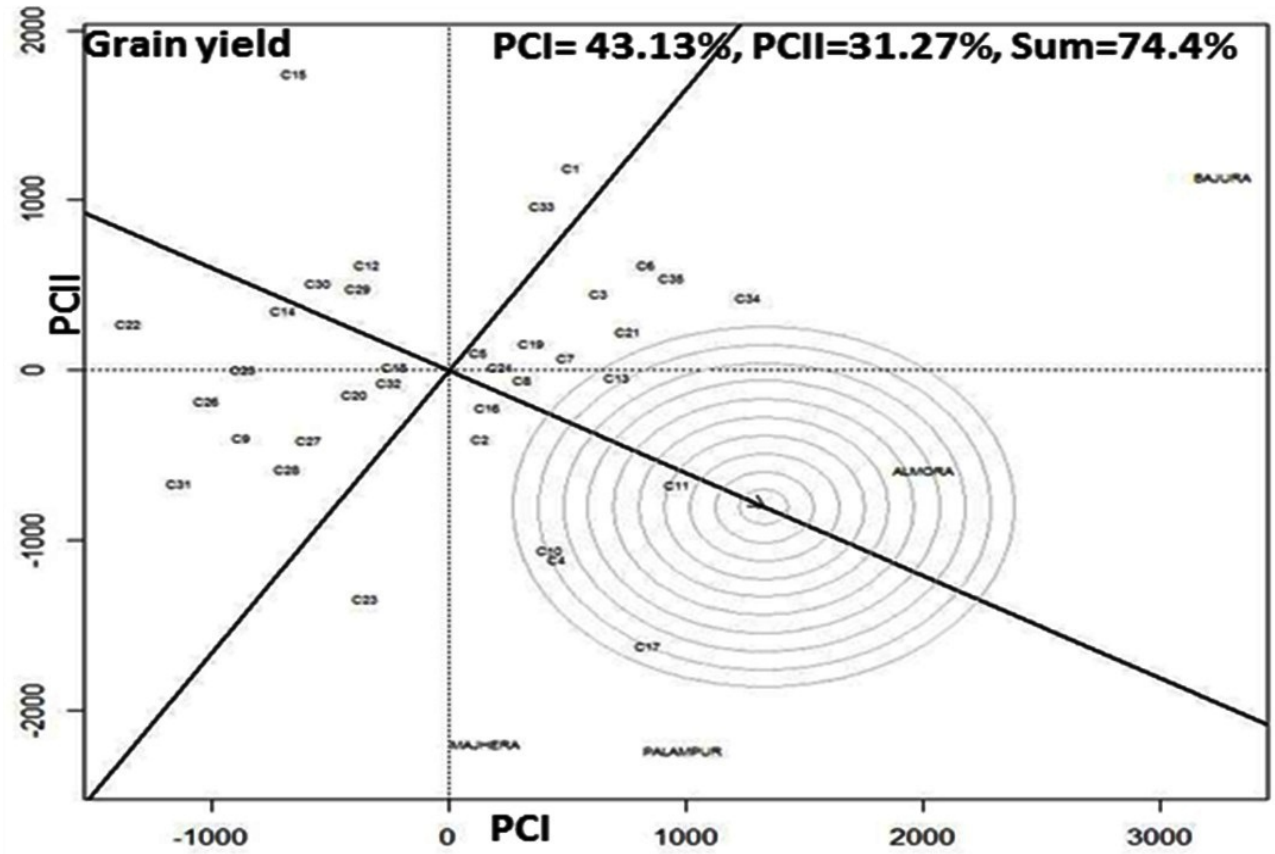


Fig.2. Average- environment coordination view to rank soybean genotypes relative to an ideal genotype

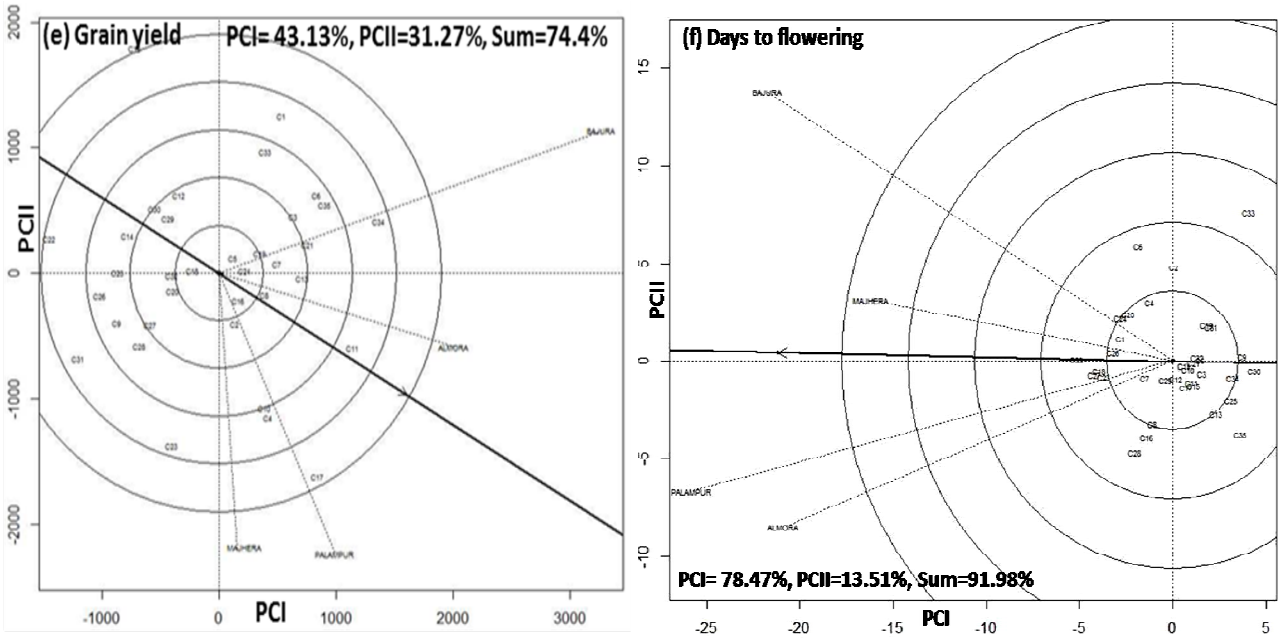


Fig. 3 (e & f). Discriminating versus representativeness view for grain yield and days to flowering

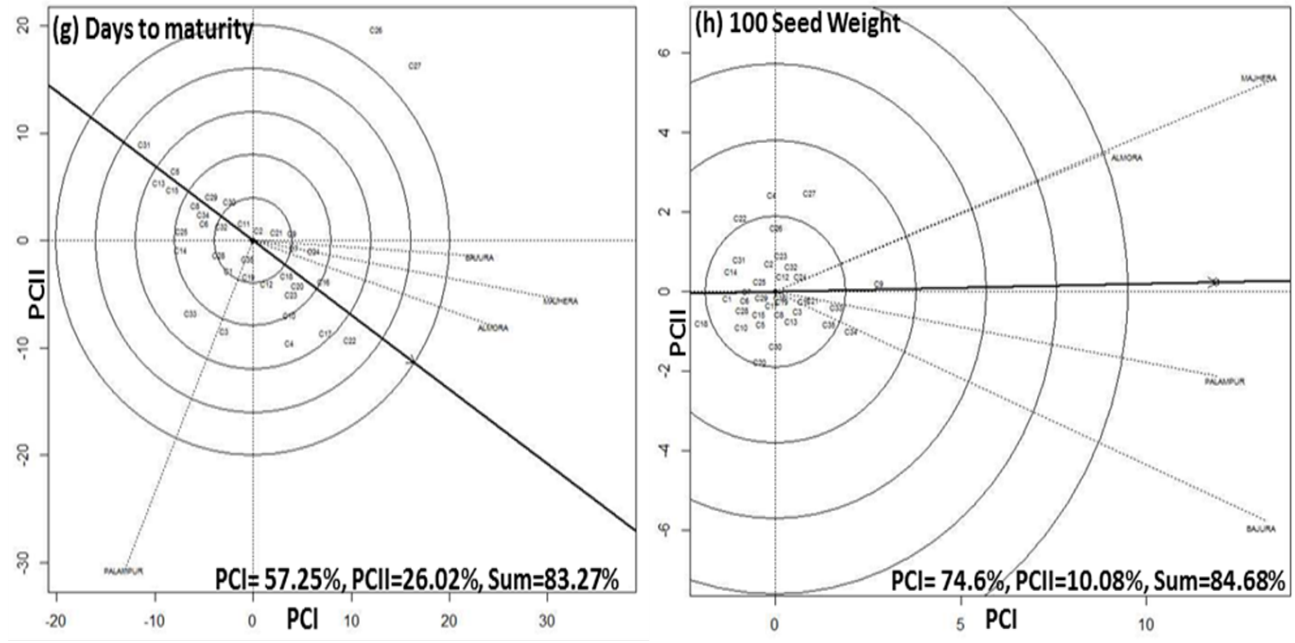


Fig.3 (g & h). Discriminating versus representativeness view for days to maturity and 100 seed weight

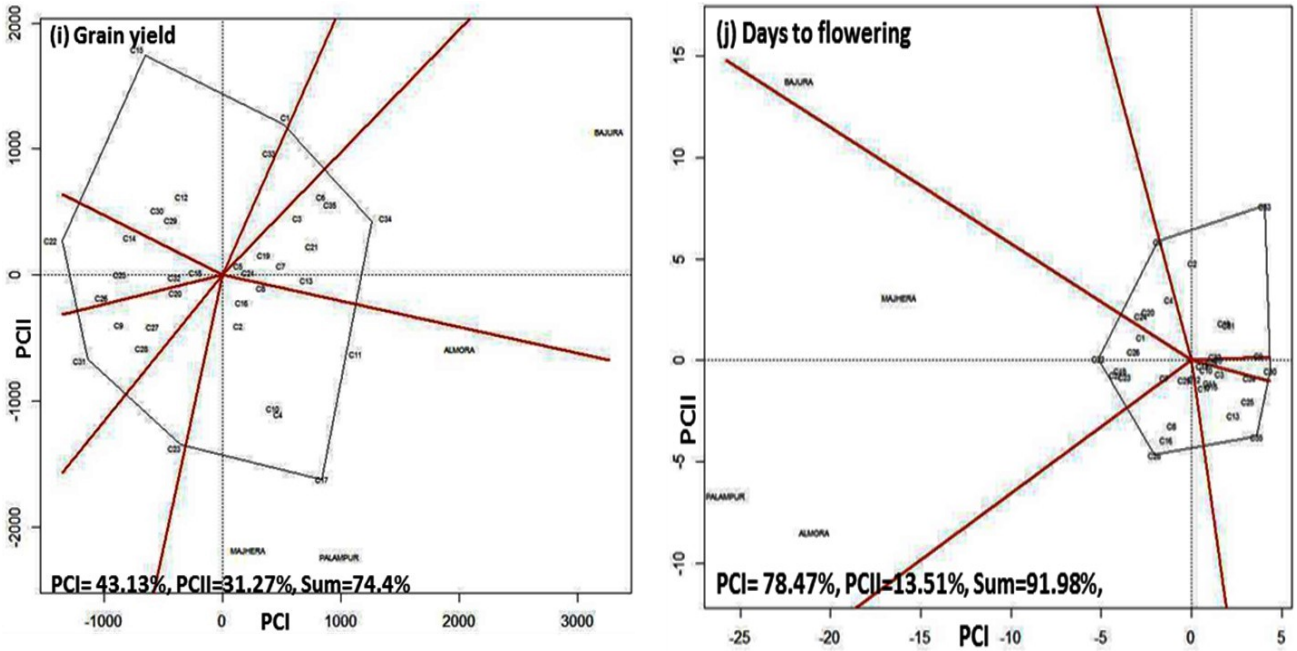


Fig.4 (i & j). Which -Won-where analysis of soybean genotypes for grain yield and days to flowering

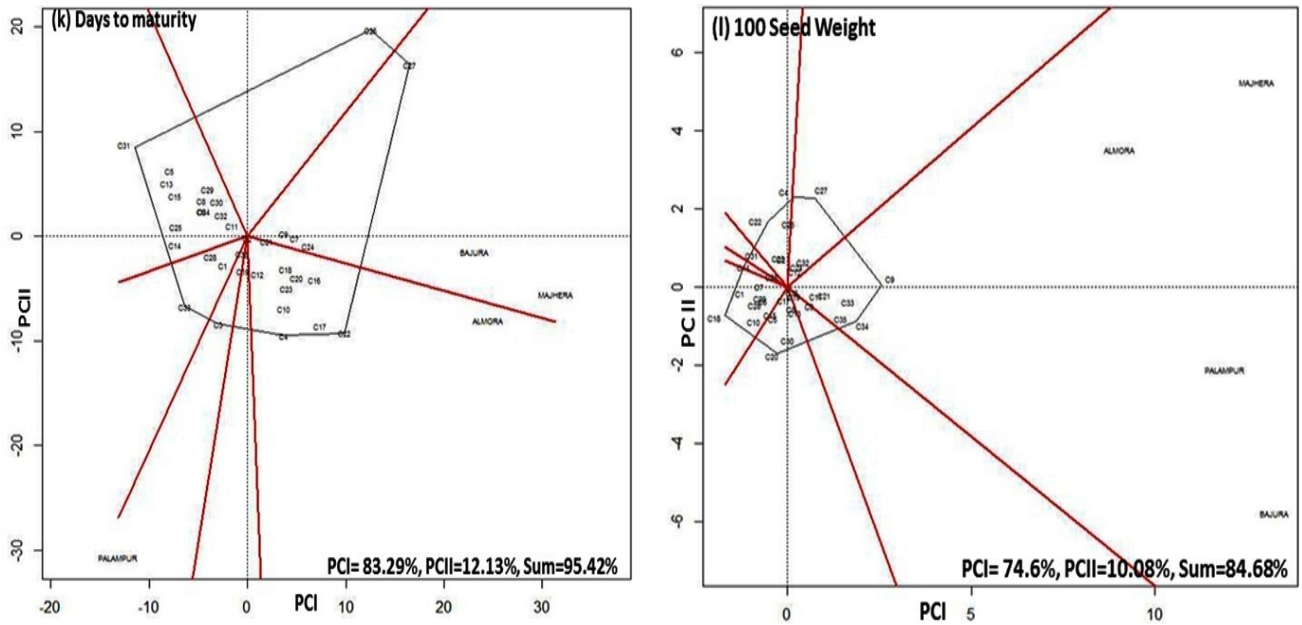


Fig.4 (k & l). Which -Won-where analysis of soybean genotypes for days to maturity and 100 seed weight

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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