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Stability analysis of soybean [*Glycine max* (L.) Merrill] genotypes under multi-environments rainfed condition of North Western Himalayan hills

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Abstract

In the present study, performance of five promising soybean genotypes over 4 locations during *kharif* 2013, 2014 and 2015 were investigated using GGE biplot analysis. Location attributed the highest proportion of the variation for all the traits except 100 seed weight ranging from 26.97-86.81% whereas, genotype contributed only 3.01-60.51% and genotype x location interaction contributed 6.01-31.42% of total variation. For 100 seed weight genotype has contributed major proportion of variation (66.26%) than location (31.08%) and genotype x location interaction (2.65%). Superior genotypes for key traits *viz*., grain yield (VLS 86) and 100 seed weight (Himso 1685) were effectively identified using GGE biplot graphical approach. It may be stated from present study that, VLS 86 was the closest to ideal genotype with stability for high grain yield as well as earliness. 'Which-won-where' study partitioned the testing locations into two mega-environments: first with three locations with VLS 86 as the winning genotype; second mega environment encompassed only one location with Himso 1685 as the winning genotype. Existence mega environments was found correlated with the rainfall pattern and clearly suggested that different entries need to be selected and deployed for realising maximum grain yield in hill zone.

Keywords: Genotype × Environment Interaction (GEI), GGE biplot, soybean, stability

Introduction

Soybean [*Glycine max* (L.) Merrill] is the foremost oilseed crop in the world (Mikic and Peric 2013). Among major agricultural commodities, it has a prominent place contributing 26.7% to the global vegetable oil production and about two thirds of the world's protein concentrate for livestock feeding (Agarwal et al. 2013). The richness in oil (20%) and protein (40%) makes it a potential crop to alleviate protein malnutrition in developing world. India is the fifth largest producer of soybean in the world and it has occupied 10.91 mha acreage with the production and productivity of 10.37 mt and 951 kg/ha, respectively (DES, 2014-15). Across all soybean growing regions in India, genotype × environment interactions (GEI) remained a challenge in selection and identification of the best genotype(s) with high yield and stability (Kumar et al. 2014). Among all the soybean growing zones, hills represent most challenging agro-climatic conditions and differences in altitude and sunshine hours render significant impact on genotype × environment interaction in determining crop yields. Genotype × environment interaction is one of the main causes impacting yield in marginal fragile environments as well as impose difficulty in drawing valid conclusions from varietal trials (Cheelo et al. 2017). It is, therefore, imperative that genotypes should be identified based on detailed understanding of their genotype × environment interaction and multi-environment trials data can serve as guide for the selection of the best genotypes for target environments (Mustapha et al. 2014). The GGE-Biplot method is efficient in detecting the genotype by environment interaction and identifying the most stable genotypes and best environment (Heidari et al. 2016; Sousa et al. 2018). Keeping this in view, the present

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investigation was carried out with the objective to examine the stability of upcoming soybean varieties developed for NW Himalayan hills of India.

Materials and methods

The present investigation comprised soybean genotypes namely, VLS 86 and Himso 1685 along with three checks *viz*., PS 1092, VL Soya 59 and VL Soya 63. The genotypes in this study were found promising under AICRP on soybean multi-environment trial conducted for three consecutive years (2013, 2014 and 2015) at four locations having diverse ecological conditions namely, Majhera, Almora, Palampur and Bajaura of N-W Himalayan states. The experiment was conducted in Randomized Complete Block Design (RCBD) with 45×10 cm^2 crop geometry in three replications during *kharif* 2013 and four replications during *kharif* 2014 and 2015 with recommended dose practices *viz*., basal dose of 20:80: 20: $N:P_2O_5:K_2O$ kg/ha, seed rate 75kg/ha, two hand weeding at 20 and 40 DAS and maintained plant population of 0.4 million/ ha across all the locations. Observations on the grain yield (kg/ha), 100 seed weight (g), days to 50% flowering and days to maturity of each treatment were recorded using standard methods (IBPGR 1984). To get the overall insight into the Genotype (G), Location (L) and Genotype (G) x Location (L) interaction the data for days to 50% flowering, days to maturity, 100 seed weight and grain yield was subjected to analysis of variance for each year in 2013, 2014 and 2015 separately as well as combined analysis. After detecting the significant genotype (G) x location (L) interaction by combined analysis of variance, the MET data was subjected to further analysis for genotype and location evaluation through GGE biplot analysis using software "GGE Biplot version 7.0" (Yan et al. 2000).

Results and discussion

Analysis of variance

Analysis of variance precisely depicted that genotype (G), location (L) and genotype and location interaction (GL) were highly significant ($p<0.01$) for the traits *viz*., days to 50% flowering, days to maturity, 100 seed weight and grain yield in all the three seasons separately as well as in the combined analysis (Table 1). Among various traits, location contributed maximum variation for days to maturity (73.17%) followed by grain yield (61.68%) and days to flowering (57.34%) as per combined analysis of all the testing years. In multi-environment trials, E accounts for 80% of the

Table 1. ANOVA and proportion of variation (G+L+GL) explained by Genotype (G), Location (L) and GL interaction for different quantitative traits

Trait	Year	Proportion of G+L+GL (%)			MS		
		G	L	GL	G	L	GL
Grain yield (Kg/ha)	2013	13.15	76.72	10.13	1.2E x 10^6**	1.0E x 10^7**	3.3E x 10^5**
	2014	41.61	26.97	31.42	9.2E x 10^5**	7.9E x 10^5**	2.3E x 10^5**
	2015	3.01	86.81	10.18	2.6E x 10^5**	1.0E x 10^7**	3.0E x 10^5**
	Combined	23.92	61.68	14.40	1.8E x 10^6**	6.4E x 10^6**	3.7E x 10^5**
Days to 50% flowering	2013	20.39	59.65	19.96	31.3**	122**	10.2**
	2014	31.93	57.64	10.44	143.2**	344.7**	15.6**
	2015	29.21	64.20	6.59	80.8**	236.8**	6.1**
	Combined	34.57	57.34	8.08	237**	524.1**	18.5**
Days to maturity	2013	10.82	64.09	25.09	60.1**	474.2**	46.4**
	2014	9.53	76.33	14.14	311.4**	3324**	154**
	2015	19.31	73.44	7.26	597.6**	3031**	74.9**
	Combined	14.44	73.17	12.38	751.6**	5077**	214.8**
100 Seed weight (g)	2013	57.72	26.08	16.2	77.2**	46.5**	7.2**
	2014	60.51	30.58	8.913	106**	71.5**	5.2**
	2015	43.22	50.78	6.01	76.3**	119.5**	3.5**
	Combined	66.26	31.08	2.65	1003.43**	470.66**	40.18**

total yield variation, whereas G and GE interaction each account for around 10% variation (Gauch and Zobel 1997). Location was the most important source of variation (relative to G) for all the traits except for 100 seed weight in which, genotype main effect (66.26%) was more over location main effect (31.08%) may be because seed traits are quantitatively inherited traits controlled and influenced not only by the seed genome but also by the maternal plant genome (Zhang et al. 2009).

Mean and stability of the genotypes across locations

Year-wise character means of soybean genotypes and locations under testing over 3 years in North Western Himalayan hills are presented in Table 2. Results of average environment coordination (AEC) view of GGE biplot for traits *viz*., days to 50% flowering, days to maturity, 100 seed weight and grain yield were generated by combined analysis of 3 years (Fig. 1). The first two PC (PC1 & PC II) jointly explained 98.8%, 98.5%, 99.8% and 97.2% of total variation for traits days to flowering, days to maturity, 100 seed weight and grain yield, respectively. Mean performance was exhibited in average-environment coordination (AEC) view in which VLS 86 followed by Himso 1685 were the best performing genotypes for grain yield followed by VL Soya 63 and VL Soya 59. Himso 1685 and PS 1092 were least stable for grain yield and VLS 86 was found relatively stable among all soybean genotypes. VL Soya 59 was found stable for days to 50% flowering and PS1092 was earliest among all the soybean genotypes, whereas VLS 86 took maximum duration to flower but found early in maturity than other soybean genotypes. For 100 seed weight, all the genotypes exhibited stability with Himso 1685 as the highest grain weight genotype and VLS 86 for lowest grain weight among all the soybean genotypes. Interestingly, VLS 86 took longest duration for flowering with early in maturity and low 100 seed weight than other genotypes *i.e.* lesser grain filling duration. It could be due to the positive genetic correlation of 100 seed weight with grain filling period *i.e.*, genotypes with lesser seed size take shorter period to fill grain or *vice-versa* (Bekele and Alemahu 2011).

Table 2. Year-wise character means of soybean genotypes and locations under testing over 3 years in North Western Himalayan hills

Genotype/location	Days to 50% flowering				Days to maturity				Grain yield (kg/ha)				Seed weight (g)			
	2013	2014	2015	Combined	2013	2014	2015	Combined	2013	2014	2015	Combined	2013	2014	2015	Combined
Genotype[a]																
VLS 86	59	57	55	57	117	113	110	113	2855	2393	1531	2260	14.84	13.67	11.96	13.49
Himso1685	57	56	55	56	120	122	123	121	2819	2351	1430	2200	21.30	20.80	17.22	19.77
PS 1092	54	50	50	51	117	119	111	115	2054	1809	1256	1706	15.67	16.17	12.92	14.92
VLS 59	56	52	52	53	114	112	106	111	2421	2326	1434	2060	16.22	16.25	12.40	14.96
VLS 63	56	54	54	55	119	113	110	114	2477	2155	1615	2082	16.46	16.35	12.32	15.04
Location[b]																
Almora	53	51	54	53	110	113	111	111	2016	1926	1854	1932	15.28	14.09	12.01	13.79
Majhera	57	50	49	52	120	102	96	106	2626	2275	387	1763	17.51	16.45	10.63	14.86
Bajaura	57	53	55	55	116	115	115	115	3639	2231	1901	2590	19.11	18.42	15.04	17.52
Palampur	59	60	57	59	123	133	126	127	1819	2395	1671	1962	15.70	17.63	15.77	16.37
Grand mean	57	54	53	54	117	116	112	115	2525	2207	1453	2062	16.90	16.65	13.36	15.52
CV%	2.78	0.96	2.03	1.98	1.24	0.99	0.84	1.01	7.35	8.89	7.66	8.24	5.7	6.2	4.78	5.71
CD%	2.67	0.75	1.58	1.60	2.47	0.67	1.37	1.73	316.02	287.20	162.98	248.26	1.64	1.51	0.93	1.32
h^2_{bs}	0.67	0.89	0.92	0.91	0.23	0.51	0.87	0.61	0.74	0.75	-	0.77	0.91	0.95	0.95	0.98

[a]Genotype means are based on 4 locations data over 3 years; [b]Location means are based on five soybean genotypes data over 3 years

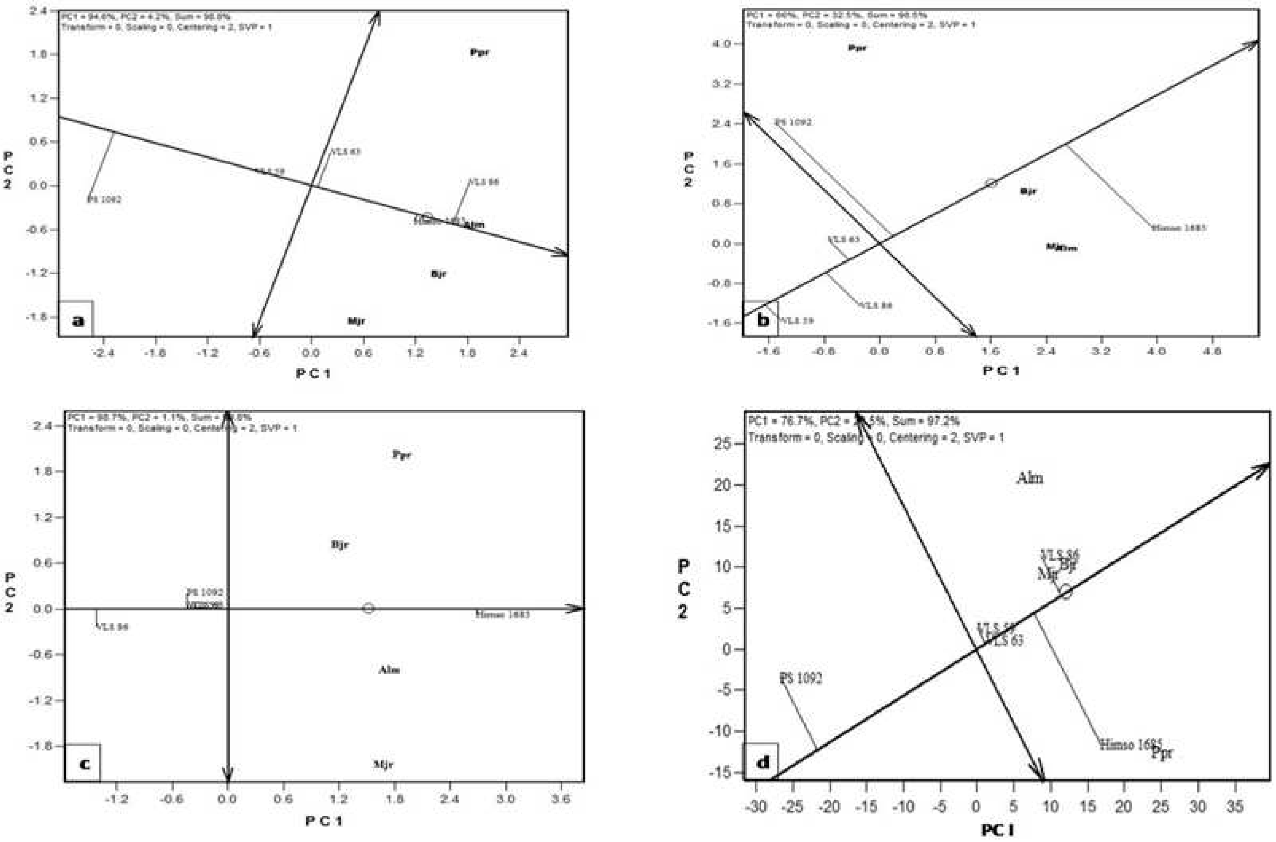

Fig. 1. Mean versus stability GGE biplots for (a) Days to 50% flowering (b) Days to maturity (c) 100 seed weight and (d) Grain yield

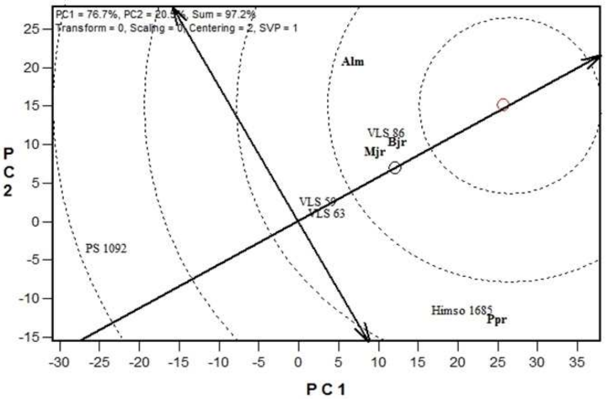

Fig. 2. Ranking of genotypes relative to an ideal genotype (the small circle on average environment coordinate, AEC)

Since, grain yield is a key trait of economic importance therefore, for further analysis focus was made on this particular trait. The GGE biplot also has a usage in selecting superior cultivars and test location provided that PC1 scores have a near-perfect correlation with the genotype main effects and ideal genotype should have a large PC1 score (high yielding ability) and small PC2 score (high stability) similarly, ideal test environments should have a large PC1 score *i.e.*, more discrimination of the genotypes in terms of the genotypic main effect and small (absolute) PC2 score *i.e.*, more representative of the overall environment (Farshadfar and Sadeghi 2014). Therefore, it may be stated that VLS 86 was close to ideal genotype which had highest grain yield among all genotypes (Fig. 2) with highest yielding at Almora followed by Bajuara, Majhera and Palampur.

Environmental evaluation based on GGE biplots

In the environment vector view of GGE biplot, results revealed that majority of the angles between their vectors are acute thus all of the locations were highly correlated for days to 50% flowering and for 100 seed weight. Similarly, for grain yield all the locations were found highly correlated (acute angle) with an exception between Almora and Palampur which exhibited no correlation with each other in combined analysis (Fig. 3). Distance between two environments was visualised through the length of environmental vectors which

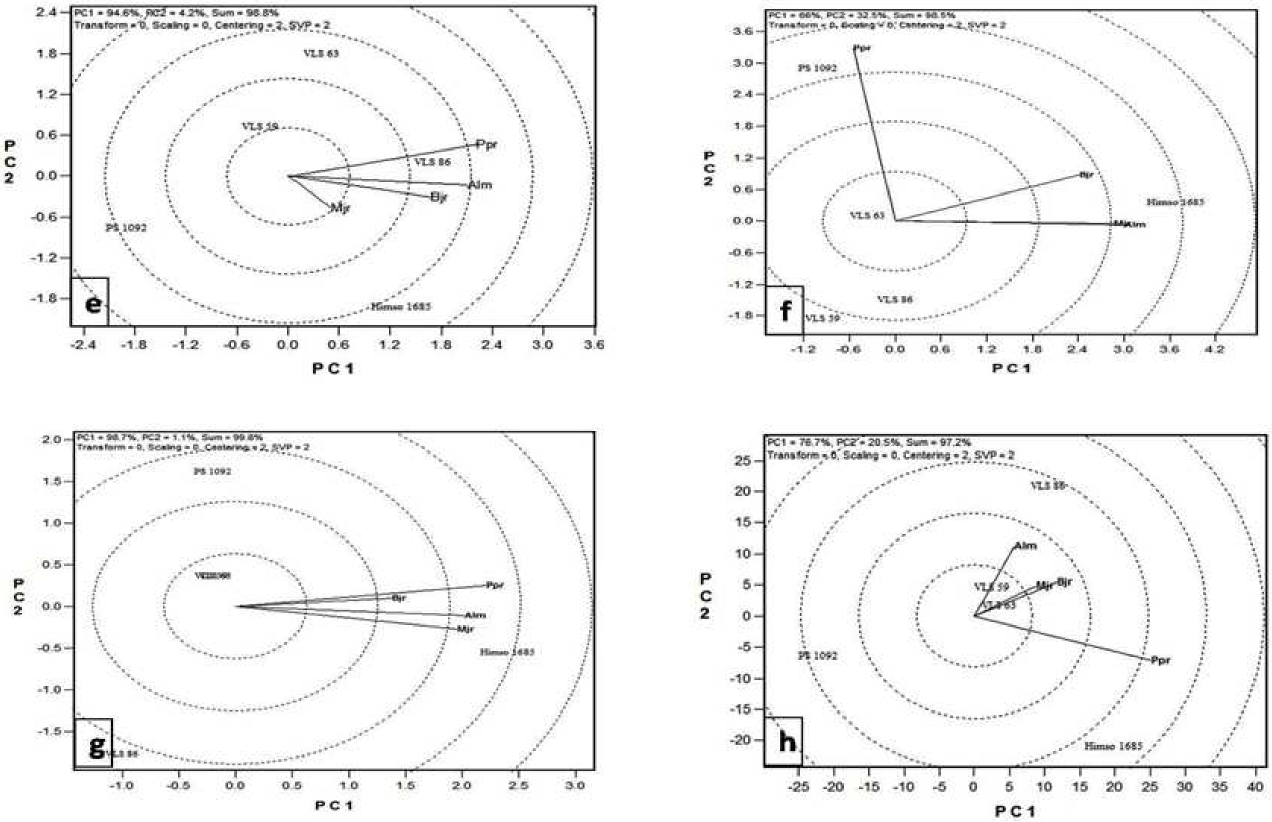

Fig. 3. **Environmental vector view for (e) Days to 50% flowering (f) Days to maturity (g) 100 Seed weight (h) Grain yield**

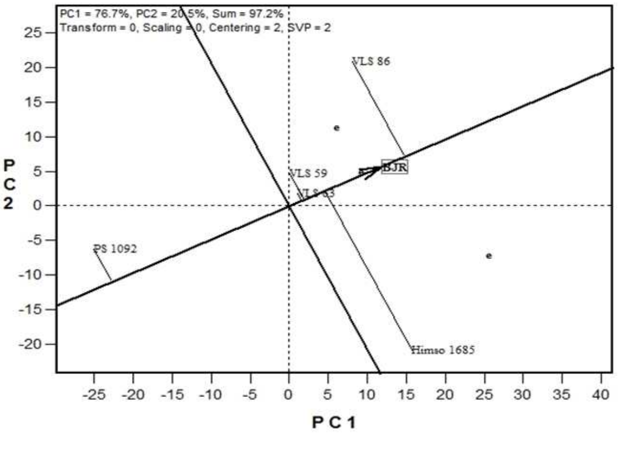

Fig. 4. **Ranking of genotypes based on their performance in near ideal location, Bajaura**

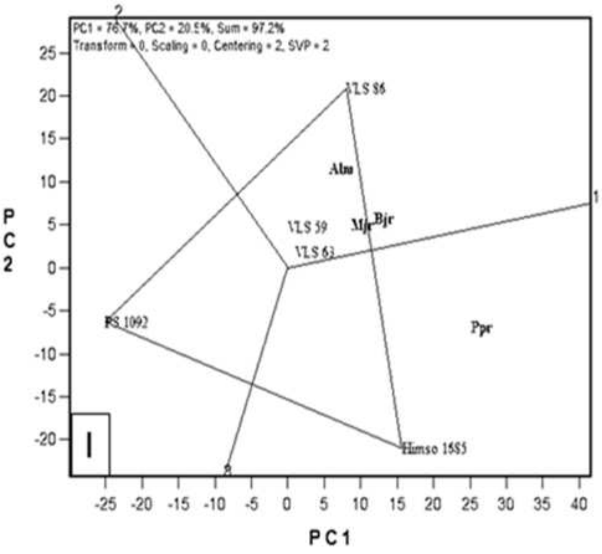

Fig. 5. **Which-won-where GGE biplots for (l) Grain yield**

Graphical visualization through GGE Biplot analysis has expediently aided in identification of stable and superior soybean genotypes across testing environments of North Western Himalayan hills of India. It has been recommended by several scholars that GGE-biplot analysis is the best method for the analysis of the relationships among the test environments, genotypes and the GEI (Kannababu et al. 2017; Yihunie and Gesesse, 2018). As per the discriminative ability and representativeness, all the testing environments were found apt to be used for multi-location trials but their ability to discriminate differed trait wise. It was also found that stability of soybean genotypes differed trait wise as well as for test locations. Existence of mega environments emphasised the need of different type of soybean cultivars in each mega environment to realise the maximum yield potential. Thus, during soybean breeding programme, the trait of interest needs to be prioritized as per the need of particular geographical and agro-climatic regions.

Authors' contribution

Conceptualization of research (AB, LK, AP); Designing of the experiments (AB, VK, AA, JPP, NK); Contribution of experimental materials (AB, VK, AA, JPP, NK); Execution of field/lab experiments and data collection (AB, VK, AA, JPP, NK); Analysis of data and interpretation (JPA, LK, AP); Preparation of manuscript (AB, JPA, LK, AP).

Declaration

The authors declare no conflict of interest.

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