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Seasonal variations in soybean (*Glycine max* L. Merrill) genotypes under different environments

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Abstract

Stability analysis was carried out in eight soybean genotypes including checks over eight environments (four locations for two years) to identify phenotypically stable genotypes that could perform more or less uniformly under different environmental conditions for various economic traits. Pooled analysis of variance for stability in the performance of different genotypes of soybean was significant for number of branches per plant, number of pods per plant, 100 seed weight (g), days to maturity, number of seed per pod, seed yield (q/ha), protein content (%) and oil content (%) indicating that the materials selected possessed significant variation for all the characters under study. Significant mean square due to environment confirming that the environments selected were variable and random and influenced the expression of most of the traits selected for stability studies. Mean squares arising due to GxE interaction were significant for most of the traits except plant height (cm) and days to 50 % flowering revealing that most of the characters under study were having differential response to the changing environments and the characters showing non-significant mean square revealed, by and large, less effect of the changing environments. In the present study, the genotypes BS-1, BAUS-31 and RAUS-5 having higher mean could be recommended for cultivation across environments on the basis of stability performance for various economic traits.

Keywords: Stability, Genotype – environment interaction, Soybean

Introduction

In India, *Glycine max* has emerged as one of the major oilseed crop and revolutionized rural economy and lifted the socio-economic status of the soybean farmers. It belongs to family Leguminosae and subfamily Papilionaceae. It is commercially grown in northern India, hilly area of Uttar Pradesh, Punjab, Himanchal Pradesh, Madhya Pradesh and Maharashtra. Genotype – environment interaction (GxE) is of major importance to a breeder in the process of developing new varieties. In plant breeding programme, many potential genotypes are usually evaluated in different environments (locations) before selecting the certain genotypes. GxE interaction has masking effect on the performance of a genotype and hence the relative ranking of the genotypes do not remain the same over number of environments. For quantitative traits such as seed yield (q/ha), the relative performance of the different genotypes often varies from one environment to another i.e., genotype- environment interaction (GxE) exist. Change in ranking make it difficult to the plant breeder to decide which genotypes should be selected. A number of statistics have been proposed to measure the phenotypic stability of different genotypes over the fluctuating environments. In soybean breeding programme it is, therefore, important to screen and identify the phenotypically stable genotypes which could perform more or less uniformly under different environmental conditions. In view of scanty information with respect to adaptability to newly developed soybean genotypes, the present investigation was carried out to determine genotype x environmental interaction and stability parameters for various economic traits and to identify stable genotype(s).

Materials and methods

The experimental materials for the present investigation comprised of eight soybean genotypes including two commercial checks (JS-335 as national check and BS-1 as local check). These genotypes were grown over eight environments [(four locations i.e., Birsa Agricultural University(BAU) Farm(E1), ZRS, Darisai(E2), ZRS, Dumka(E3) and ZRS, Chianki (E4) for two years) during 2013 and 2014] in a randomized block design with three replication in all the location of Jharkhand. The entire environments were diverse in nature with respect to the temperature, humidity and rainfall. (Table 1). All the environments had low status of nitrogen and organic carbon (Table 2). Soil of Darisai (E2) and Chianki (E4) is acidic while that of Dumka (E3) and BAU, Farm (E1) is moderately acidic. The experiment site were different in nutrient status

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Table 1: Mean of environmental parameters during experiment in different location.

Environment/Year			Temp.(⁰ C)		Relative Humidity		Total rainfall
			Max.	Min.	At 7 AM	At 2 PM	(mm)
E1	BAU, Farm	2013	27.44	21.15	75.89	53.11	47.14
		2014	28.31	20.48	79.45	52.54	39.72
E2	Darisai	2013	30.71	16.45	83.50	62.07	6.78
		2014	31.89	18.76	80.49	60.45	18.54
E3	Dumka	2013	30.43	20.48	92.17	74.95	52.38
		2014	32.58	21.59	89.48	65.45	45.78
E4	Chianki	2013	33.36	22.58	79.70	58.39	42.37
		2014	33.16	21.16	77.19	52.48	34.15

Table 2: Soil health status of all the location under study.

Environments	BAU, Farm (E1)	Darisai (E2)	Dumka (E3)	Chianki (E4)
Soil health status				
pH	Moderately acidic	Acidic	Moderately acidic	Acidic
Nitrogen (Kg/ha)	Low	Low	Low	Low
Phosphorous (Kg/ha)	High	High	Medium	Medium
Potassium (Kg/ha)	Medium	Medium	Medium	Medium
Sulphur (mg/Kg)	Low	Low	Low	Low
Organic carbon (%)	Low	Low	Low	Low

There were eight rows of each genotype in a plot with a row spacing of 45cm. Observation were recorded on five competitive plants for seven characters namely plant height (cm), number of branches per plant, number of pod per plant, 100 seed weight(g), number of seed per pod, protein content (%) and oil content(%). Days to 50% flowering, days to maturity and seed yield (kg/plot) were recorded on plot basis. The analysis of variance pooled over locations was carried out to detect the differences among the genotypes, environments and GxE interaction. If GxE interaction is not significant then further stability analysis for that trait will be biased. The stability parameters were estimated using Eberhart and Russell (1966) ^[1] model. Higher mean is desirable by the breeders for any traits (Xi). They used two parameters for stable genotype, (i) Linear regression or regression coefficient (bi) should be unit and (ii) Mean square deviation from the regression (S^2_{di}) should be equal to zero or non-significant. Mean provides a measure of comparing the different genotypes. While the coefficient of regression and deviation from regression provides an estimate of GxE interaction.

Result and discussion

Pooled analysis of variance for stability performance of different genotypes showed highly significant difference for all the traits thus, indicating that the material selected possessed significant variation for all the characters studies. Significant mean square due to environment confirming random and variable nature of environments selected, which influenced the expression of most of the traits studied. (Table 3) Mean square arising due to genotype x environment (G x E interaction) revealed that significant differential response to the changing environments except for the traits plant height (cm) and days to 50 % flowering. Therefore, their further stability analysis for these two traits were not done.

Component analysis of environment+ (genotype x environment) partitioned in to linear and non-linear components revealed that the mean square due to environments (linear) were significant for all the characters. It confirmed that the environments were random and different and they exercised influence on the expression of the traits and this variation could have arisen due to the linear response of the regression of the cultivar to the environments. The mean squares due to GxE (Linear) were significant for most of the traits viz. number of primary branches per plant, number of pods per plant, 100 seed weight(g), days to maturity, number of seeds per pod, seed yield (q/ha), protein content(%) and oil content(%) revealed that the behavior of the genotypes could be predicted over the environments more precisely and accurately as the G x E interaction was the outcome of the linear function of the environmental components (Sudaric *et al.* 2006, Ramana and Satyanarayana 2005) ^[2]. However, mean squares due to GxE (linear) were non-significant for plant height (cm) and days to 50% flowering indicating possible absence of genetic differences among the genotypes for their regression on the environmental index making difficult the prediction for the performance of these traits (Khan *et al* 2008) ^[7].

The non-linear component arising due to the heterogeneity measured as mean square due to pooled deviation was significant for number of days to 50% flowering, plant height (cm), pods per plant, 100 seed weight (g), days to maturity, number of seeds per pod, seed yield (q/ha), protein content (%) and oil content (%) revealing presence of non-linear response of the genotypes to the changing environments (Joshi *et al.* 2005) ^[4]. The significant pooled deviation for above characters confirms contribution of the non-linear component to the total GxE interaction.

Table 3: Analysis of Variance for genotype-environment interaction for different characters of soybean pooled over eight environments

Sources	Df	Days to 50 % flowering	Plant height (cm)	Branches /plant	No. of pods/ plant	100 seeds wt. (g)	Days to maturity	No. of seeds / pod	Seed yield (q/ha)	Protein content (%)	Oil content (%)
Genotype (G)	7	10.15*	45.82**	13.73**	90.22**	7.24**	515.26**	2.85**	3.15**	93.29**	45.29**
Environment (E)	7	573.30**	34.24**	15.92**	68.23**	6.46**	1622.91**	6.83**	17.23**	1476.83**	207.50**
G x E	49	4.44	1.15	0.25**	1.21**	1.72**	19.19*	0.18**	0.88**	9.21**	7.28**
E+ (GxE)	56	75.55	5.28	2.21**	9.59**	2.31	219.66**	1.01**	2.92*	192.66**	32.31**
Environment (Linear)	1	4013.10**	239.67**	111.43**	477.61**	45.24**	11360.37**	47.78*	120.61**	10337.81**	1452.50**
G x E (Linear)	7	16.79	1.99	1.76**	8.28**	11.24*	25.26**	1.16*	5.91**	61.99**	14.59**
Pooled deviation	48	100.03**	42.27**	0.11**	1.50**	5.48**	2.87	0.48**	1.79**	17.39**	2.87**
Pooled error	112	8.21	1.12	0.08	0.32	0.57	6.95	0.07	0.33	3.13**	1.00

*and **, significant at 5 and 1% of probability level, respectively.

The genotype differed with respect to stability of these traits making its prediction more difficult. However, the magnitude of linear component i.e., environment(Linear) and genotype x environment (Linear) was many times higher than the non-linear components (pooled deviation) for most of the characters revealing that the prediction of the stability could be reliable though it may get affected to some extent (Singh *et al.* 2001 and Mondal *et al.* 2005) [5, 6].

Comparing the GxE interaction with non-linear component, it was significant for most of the traits except plant height (cm) and days to 50% flowering. In the traits where non-linear component was non-significant, the GxE interaction for these traits were greatly influenced by environmental factors and there exist either no relationship or complex relationship between genotype and environmental effect making its prediction more difficult for the traits.

In the present study (Table 4a) the genotypes showing average

stability and high to moderate mean performance than the population mean were BAUS-96, BS-1, JS-97-52 and RAUS-5 for number of branches per plant; BAUS-31, BAUS-40 and JS-97-52 for number of pods per plant; BSUS-96, BS-1, BAUS-31, and JS-80-21 for 100 seed weight (g); BAUS-96, BAUS-31, BAUS-40, RAUS-5 and JS-335 for days to maturity (should be minimum); BAUS-96, BS-1, JS-80-21 and JS-335 for number of seeds per pod (Table 4b) BS-1 and BAUS-31 for seed yield (q/ha) ; BAUS-96, BS-1, BAUS-31, JS-80-21 for protein content (%) and RAUS-5 for oil content (%).

Genotypes showing below average stability (bi significant and >1) and specially adapted to favourable environments were JS-335 for plant height (cm) ; BAUS-96, BS-1 for number of pods per plant; BAUS-40 for 100 seed weight(g); JS-97-52 and RAUS-5 for number of seeds per

Table 4(a): Stability parameters (regression coefficient bi and deviation from regression S²di)

Genotype	No. of branches /plant			No. of pods/plant			100 seed weight			Days to maturity		
	Mean	bi	S ² di	Mean	bi	S ² di	Mean	Bi	S ² di	Mean	bi	S ² di
BAUS-96	2.85	0.735	-0.006	39.90	1.361*	3.934	12.59	-0.259	0.55	105.46	0.989	6.8
BS-1	3.00	1.299	0.0572	40.99	1.065	2.647	13.32	0.941	0.116	110.45	0.839	3.89
BAUS-31	2.96	0.738	0.0874**	38.29	1.023	0.256	12.65	1.501	0.49	105.68	0.179	-2.24
BAUS-40	2.75	1.047	0.0064	33.81	1.091	3.089	13.45	2.992*	0.363	106.53	1.089	-0.67
JS 97-52	2.98	1.637	-0.011	38.34	0.981	-0.089	9.76	-0.579	1.435*	112.34	1.859*	3.45
JS 80-21	2.69	0.617	0.063*	36.12	0.878	1.894	13.03	1.735	0.191	110.38	1.377	-1.56
RAUS-5	2.79	0.513	0.058	34.11	0.572	2.064	12.17	3.906*	-0.176	107.37	1.067	-2.78
JS-335	3.01	1.411*	0.0037	39.87	1.033	9.563*	12.03	-2.237	0.525	104.39	0.598	0.03
Population mean	2.88	1.000	-	37.68	1.001	-	12.375	1.000	-	107.825	1.000	-
S.Em (±)	0.11	0.848	-	1.43	0.152	-	0.28	1.98	-	1.07	0.76	-

*and **, significant at 5 and 1% of probability level, respectively.

Table 4(b): Stability parameters (regression coefficient bi and deviation from regression S²di)

Genotype	No. of seeds/ pod			Seed yield			Protein content			Oil content		
	Mean	bi	S ² di	Mean	bi	S ² di	Mean	Bi	S ² di	Mean	bi	S ² di
BAUS-96	2.53	1.81	0.275	17.167	2.670*	0.103	41.62	-0.259	-0.059	18.56	1.362	-0.012
BS-1	2.75	0.975	0.463	18.607	1.330	-0.163	41.27	0.941	0.318	20.41	1.771*	0.002
BAUS-31	2.26	0.827	-0.024	17.721	0.130	0.687	41.52	1.501	0.412	18.43	0.932	0.000
BAUS-40	2.13	1.321	0.064	18.692	-1.534*	-0.168	42.23	2.992*	0.220	18.12	0.938	0.011
JS 97-52	2.47	2.31*	0.0527	15.233	1.620	-0.283	40.67	-0.579	1.063	18.15	1.746	0.012
JS 80-21	2.69	1.201	0.007	15.107	1.280	-0.151*	40.78	1.735	0.117	17.86	-0.582*	0.004
RAUS-5	2.61	-1.387*	0.263	18.440	0.820	-0.089*	41.28	3.906*	-0.113	19.33	1.073	0.021
JS-335	2.73	0.951	0.278	15.833	1.690*	-0.200	41.34	-2.237*	0.415	18.67	0.761	0.001
Population mean	2.52	1.001	-	17.100	1.001	-	41.34	1	-	18.69	1.000	-
S.Em (±)	0.234	0.193	-	0.520	0.670	-	0.316	0.743	-	0.071	0.701	-

pod; BAUS-40 for seed yield (q/ha); BAUS-40, RAUS-5 and JS-335 for protein quality (%); BS-1 for oil content (%). None of the genotypes was found to stable under poor environment with average or higher mean than the population mean.

Considering the stability parameters, it has been found that three genotypes i.e., BS-1, BAUS-31 and RAUS-5 were having higher mean and stable for maximum number of characters including seed yield (q/ha). But with respect to oil

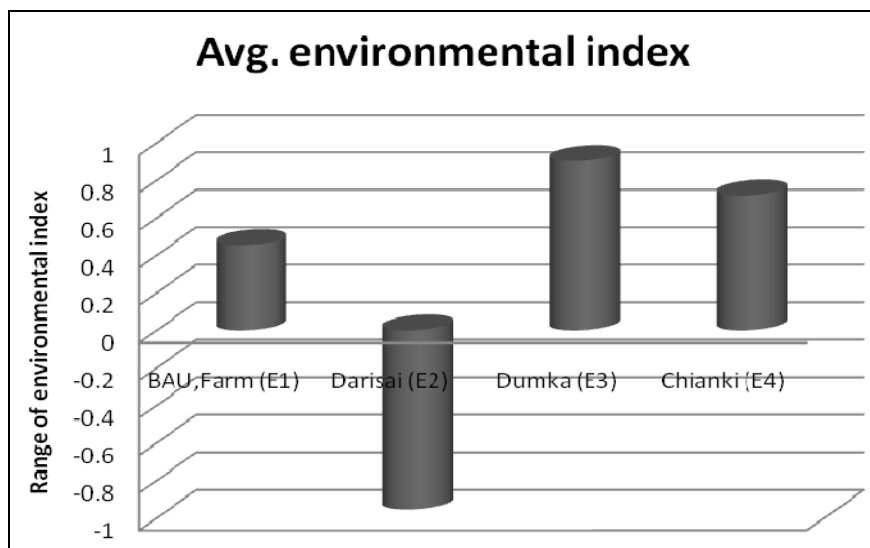
yield along with higher seed yield (q/ha) only two genotypes, namely BS-1 and RAUS-5 were found to be superior and stable. Further, the compensating mechanism of component characters in imparting homeostasis being important, these genotypes would be useful in future breeding programme, as in a homeostasis genotype, the component characters may shift in a compensatory manner in changing environment to give consistent performance of the economic characters (Khan *et al.* 2008) [7].

The adaptability and performance of the genotype depends upon the nature of environment influencing the expression of

the traits. The environmental index for all the characters is presented (Table 5). The positive value of environmental index indicates the positive effect of environment on the expression of the trait where as negative value of environmental index has negative effect on the expression of the trait. The means of environmental index for all the characters revealed that Dumka (E3) and Chianki (E4) were favourable environment where as BAU, Farm (E1) was average and Darisai (E2) was poor environments for the expression of the traits (Graph 1).

Table 5: Environmental index for different characters under different environments

Characters	BAU, Farm (E1)	Darisai (E2)	Dumka (E3)	Chianki (E4)
Number of branch per plant	0.06	0.15	-0.09	-0.12
Number of pod per plant	4.36	-5.3	7.57	4.39
100 seed weight	-0.07	0.06	-0.17	0.18
Days to maturity	-0.46	-3.53	0.32	1.65
Number of seed per pod	-0.208	0.25	0.083	-0.125
Grain yield (q/ha)	0.39	0.12	0.08	-0.6
Protein content (%)	-0.37	0.57	-0.47	0.28
Oil content (%)	-0.06	0.05	-0.1	0.1
Mean	0.455	-0.954	0.903	0.719
Type of environments	Average	Poor	Favourable	Favourable



Graph 1: Graph showing the environmental index

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