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MULTI-ENVIRONMENT RESPONSE IN SEED YIELD OF SOYBEAN [*GLYCINE MAX* (L.) MERRILL], GENOTYPES THROUGH GGE BIPLOT TECHNIQUE

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Abstract

Multi-environment data of 7 different locations for seed yield of 182 soybean diverse genotypes were analyzed. The objectives were to find out the 1) homogenous groups of similar genotypes and similar environments through cluster analysis 2) genotypic main effects and genotype environment interaction (GGE) in graphic display which make able visual evaluation of both genotypes and environments and 3) performance of genotypic groups across environments and environmental groups over genotypes through biplot. Analysis of variance of seed yield revealed 13.12% genotypic and 47.93% environmental effect. While, partitioning into groups of each genotype, environment and their interaction effects were observed 80.84%, 95.8% and 60.86% respectively. Maximum (means) seed yield 15.94 $\pm$ 0.18g plant^{-1} was observed for Grp-8 followed by Grp-9 with the value of 14.90 $\pm$ 0.97g plant^{-1} while, minimum seed yield 7.53 $\pm$ 0.48g was observed for Grp-10. The fusion level of 7 environments revealed 3 location (Islamabad, Mingora and Mansehra) in main group A and 4 locations (Faisalabad, Quetta, Gilgit and Tandojam) were in main group B. Fifteen genotypic groups derived from 182 genotypes have 3 main groups A, B and C. Genotypic group having large distance from origin has a large genotype plus interaction as Grp-9 and Grp-3. Coordination of three dimensions biplot for any one G or E showed small angle for similar type and large for dissimilar to each other, while larger projection of a genotypic group on an environment vector has more and this genotypic group deviates from the average in the environment.

Introduction

Soybean [*Glycine max* (L.) Merrill] is highly sensitive crop to photoperiod, temperature and altitude. For strong breeding program of any crop such as soybean testing over diverse environment is very important to ensure that the selected genotypes have acceptable performance in variable environments within the target region. Effective interpretation and utilization of data in making selection decisions, however, remain a major challenge to researchers. There are two major tasks for researcher to determine whether the target region is homogeneous or should be divided into different mega-environments; the second is to select superior cultivars for a given mega-environment on the basis of end product i.e. yields. It is often difficult to determine the pattern of genetic response of different genotypes across the environments without the help of graphical display of the data (Yan *et al*., 2001). It is possible for huge number of accessions to portray the relationship between the genotypes and environments for each attribute graphically. Gabriel (1971, Kroonenberg (1995), Yan *et al*., (2000) and Yan & Hunt

(2001) proposed a GGE biplot that allows visual examination of the GE interaction pattern of the data. GGE biplot refers to the genotype main effect (G) and the genotype x environment interaction (GE), which has two sources of variation that are relevant to cultivar evaluation. In these GGE biplots, genotypes are depicted by numbers and environments by vectors from the origin. It can be used to identify superior cultivars and test environments that facilitate identification of such cultivars (Gwanama *et al.,* 2000).

The GGE biplot can effectively identify the GE interaction pattern of the data. It shows which cultivar won in which environments, and thus facilitates mega-environment identification. Therefore, multilocation trials are essential for addressing the mega-environment issue. Ideal cultivars should have a large PC1 score (high yielding ability) and a small (absolute) PC2 score (high stability). Similarly, ideal test environments should have a large PC1 score (more discriminating of the genotypes in terms of the genotypic main effect) and small (absolute) PC2 score (more representative of the overall environment) (Yan *et al*., 2000; Yan & Hunt, 2001).

The objective of this study was to graphically summarize the effects of genotypes (G) and genotype environment (GE) interaction and to answer the question of "which won where" in soybean and to examine the possible existence of different environments. It also illustrates the genotypic group performance in a series of environment groups through performance plots.

Materials and Methods

A set of 182 soybean genotypes was evaluated in 7 environments of Pakistan during 2005-06, to identify the patterns of G x E interaction. One hundred and eighty two soybean genotypes were sown with single row 45cm apart, 5m long in augmented design at 7 locations viz., Quetta, Islamabad, Mingora, Gilgit, Mansehra, Faisalabad and Tandojam. The data for grain yield plant^{-1} was recorded. Analysis of variance of mean data of five plants of each genotype over seven environments used for seed yield was conducted to examine the partitioning of sums of squares to G, E and G x E interaction. For classification, a hierarchical agglomerative clustering method (Williams, 1976) with incremental sum of squares (Ward, 1963) as the fusion criterion was applied to the matrices of all the studied attributes. Dendograms for each attribute were constructed on the basis of fusion level to investigate similarities in pattern of performance among genotypes (in response to environments) and environments (in discriminating among genotypes). The biplot technique developed by Gabriel (1971) was used to make possible the display in a single graph of the performance of each genotype at each environment. In biplot, each genotype is represented by a point, called a marker, defined by the genotype's scores on all principal components (PCs), and each environment is represented by a vector defined by environment's scores on all PCs. Biplot can be multidimensional, but two-dimensional biplots, using only the first and the second PCs are most common, both for biological reasons as well as for easy comprehension (Kroonenberg, 1976).

Results and Discussion

Analysis of variance of seed yield revealed 13.12% genotypic and 47.93% environmental effect. While partitioning into groups of each genotype, environment and their interaction

effects were observed 80.84%, 95.8% and 60.86% respectively (Table 1). The results are supported with the findings of Arshad *et al*., (2006) and Malik *et al*., (2007) who obtained considerable variability for seed yield in soybean. Maximum average seed yield 15.94 $\pm$ 0.18g plant^{-1} was observed for grp-8 with frequency of 8 genotypic membership followed by grp-9 with the value of 14.90 $\pm$ 0.97g plant^{-1} but low (3) in frequency of genotypic membership, while minimum seed yield 7.53 $\pm$ 0.48g was observed for Grp-10. Maximum number of genotypes 27 was observed in grp-5 with the average seed yield 13.15 $\pm$ 0.25g plant^{-1}. Grp-4 and grp-9 both groups showed same frequency of genotypic membership viz. Chippewa-64, Elgin and Pk-3794 for grp-4 and Carlin, Centur and Ware for grp-9.

The environmental dendrogram for seed yield plant^{-1} is presented in Fig. 1 constituted two main groups A and B. At 50% of the fusion level 4 subgroups were observed. Subgroup II and IV each one consisted of one location Mansehra and Tandojam respectively; subgroup I had two locations viz., Islamabad and Mingora. While three locations Faisalabad, Quetta and Gilgit were found in subgroup III. The genotypic denrogram presented in Fig. 2 revealed 15 clusters comprising of varying frequencies of each (Table 2) had three main groups A, B and C. Whereas at 50% fusion level, 8 genotypic subgroups were observed. Main group A comprised of two subgroups; subgroup I had grp-1and grp-2 and subgroup II had also two members; grp-3 and grp-4. The high yielding groups viz., grp-5, grp-6, grp-7 grp-8 and grp-9 were found in main group B. In main group C consists of low yielding members i.e., grp-10, grp-11, grp-12, grp-13, grp-14 and grp-15.

The results of the coordination analysis are presented in 3 dimension biplot of the 1st and 2nd principal components (Fig. 3). The GGE biplot is constructed by plotting the primary effect scores of each genotype (as x-axis) and each environment against their respective secondary effect scores (as y-axis). In these biplots, genotypes are represented by numbers and environments by vectors generating from the origin. Biplots can be used to evaluate cultivars for their yield potential and stability and to evaluate trial sites for their discriminating ability and representiveness. Entries that are close together are similar in performance across environments, while adjacent environments are similar in the way they discriminate among genotypes. Low yielding with poor environment tends to be on the bottom left quadrant of the joint plot as interpretative of a biplot by Kroonenberg (1995). As Fig. 3 shows, Gilgit (E-6) is in fourth quarter and more distance from origin reveal unstable and low yielding environment. Islamabad, Mingora and Tandojam are showed unstable with average yield potential areas, whereas, Mansehra, Faisalabad and Quetta showed average stability with average to good potential areas.

The grp-9 fall far away from origin and in positive side showed unstable with good yield group. While grp-8 fall near to origin than grp-9 which reveal good in yield potential with average stability. Genotypic groups grp-13 and grp-14, being in the upper left quadrant, but closer to the origin gave the low average yields (small primary scores) and were defined as widely adapted over the sites (small secondary scores). Grp-11 and grp-12 are closely related in their yield potential as well as their response to varying environments as indicated by acute angle formed between grp-11, origin and grp-12. Similarly, grp-1 is closely associated with grp-2 in its behavior regarding yielding ability and across sites performance is unstable. Ihsan *et al*., (2007) also indicated same pattern of finding for seed yield in 10 sunflower hybrids over seven locations. Entry grp-5 can also be termed as good yielding and stable because of its large primary affect scores and almost near zero secondary scores. Grp-3, and grp-4 had the yields which were above the average (primary scores < 0) and were highly unstable (large absolute secondary value). Genotypic groups grp-10 lying closer to the origin (small primary score) had lowest in yield with average stability.

Table 1. Analysis of variance for the G x E model with partition of the sum of squares for G x E model for two-way grouping model of 182 accessions of soybean for grain yield planted at seven environments during 2005-06.

Source of variation	DF	SSQ	MSQ	(%)
Genotypes	**181**	**4418.05**	**24.41***	**13.12**
Between groups (Genotypes)	14	3571.67	255.12**	80.84
Within groups (Genotypes)	167	846.28	5.068	19.16
Environments	**6**	**16139.27**	**2689.88**	**47.93**
Between groups (Environment)	3	15461.13	5153.71**	95.80
Within groups (Environment)	3	678.14	226.05	4.20
G x E interaction	**1086**	**13118.36**	**12.08****	**38.96**
Between G. grp x between E.grp	42	529.41	7.563**	60.86
Within G. grp x within E. grp	501	2500.87	4.99	19.06
Remainder of interaction	543	4900.24	9.02	37.35
Total sum of squares		33675.67		
Total sum of squares between groups		24750.05		
Percentage of total sum of squares retained between groups		73.50		

G. = Genotpe, **E.** = Environment, **grp**. = Group

** Significant at 1% probability level

* Significant at 5 % probability level

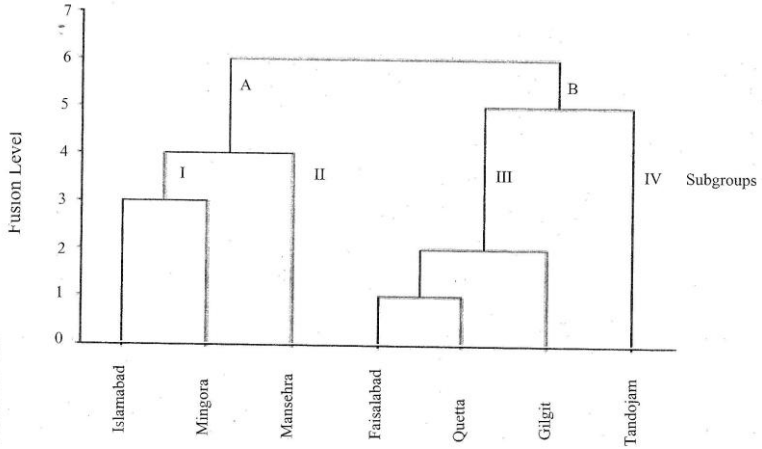

Fig. 1. Dendrogram presented clustering of seven environments on basis of grain yield (g) plant^{-1} of 182 genotypes of soybean.

Larger projection of a genotypic group on an environment vector (the point given by drooping a perpendicular line, onto the environment vector, from the genotypic group), the more this genotypic group deviate from the average in the environment (Kroonenberg, 1995). The angle between vectors (environments) and grp members is observed far greater than 90° which revealed greater deviation. Among all 15 member groups, grp-12 found small angle value and could be performed better in seed yield for Gilgit (E-6). The performance of member groups grp-15, grp-1, grp-2, grp-10, grp-4 and grp-3 for seed yield is not promising for all the 7 environments while, other group members could be average in performance for this trait over all 7 environments. Therefore, on the basis of these results new genotypes could be introduced or these genotypes could be tested other than these environments.

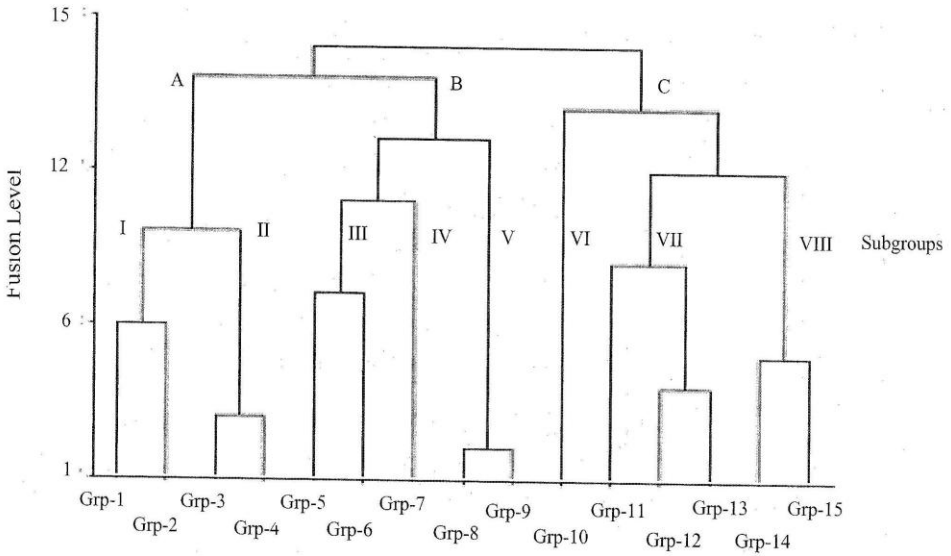

Fig. 2. Dendrogram presented clustering of 15 groups of 182 genotypes of soybean over seven environments on basis of grain yield (g) plant^{-1}.

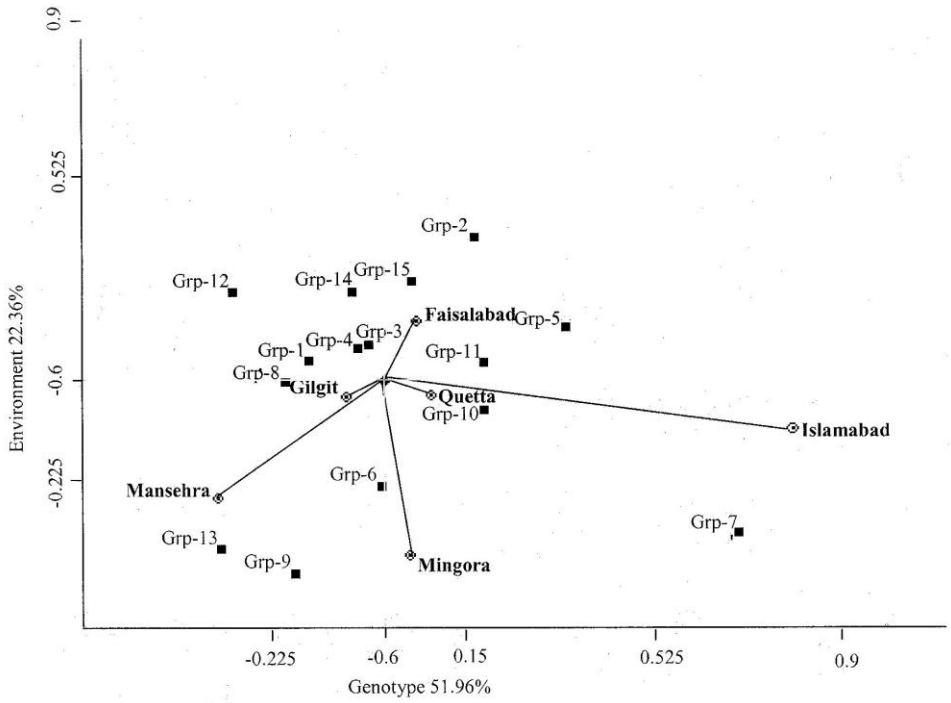

Fig. 3. Genotype environment Interaction got grain yield (g) plant^{-1} of 182 soybean genotypes over six locations.

Table 2. Frequency distribution and subgroup consisting of 182 soybean accession for grain yield plant^{-1} (g).

Groups	Means ± SE	*f*	Sub groups	Genotypic membership
Grp.1	11.70 ± 0.25	17	I	95012, 95-4, Ags-66, Amcor, Calland, Chusei, Corsoy-79, Egsy-91-7, GC-84058-8-4, GC-8405-1-9-1, Hay Wood, Hm 8468, NARC I, S.B.L, Ss-39-99, Virgina and Z.Z
Grp.2	12.39 ± 0.227	20	I	95083, 95091, Aust-94-1, Black Hack, C-686, Ca-96, Century-84, Cumberland, Flint, Flow-350, Interpide, Maf-0211, NARC-V, No-10, No-37, No-5484, No-58, Pixie, Pkn-140-3-1and Swat-84
Grp.3	13.24 ± 0.30	6	II	AGS 19, Ags-194, GC 90013-23-6-1, IAC 100, Linuolin and NARC-I
Grp.4	13.62 ± 0.54	3	II	Chippewa-64, Elgin and Pk-3794
Grp.5	13.15 ± 0.25	27	III	95014, 95085, AGS 314, AGS 93, AGS-194, Foster, Gail, GC 86018-427-3, H.M-1, Hardin, Harlin, Harper, Icai-124, Kanrich, Manta, Nautilus, No-57, No-6, Pc-82, Platte, Provar, PSC-62, SH-1274, SSN-129, Walter, Wels and Zane
Grp.6	14.16 ± 0.51	12	III	Aksarbean, Alamo, Bonus, Decada, Ed-73-37, Ertou No-2, Hack, Hawkeye, Hong Kong, Loppa, PC-82 and Ufv-1
Grp.7	11.33 ± 0.41	12	IV	95037, 95038, 95049, 95024-A, AGS 5, Gc 9004, Poland Yellow, S-39-40, Sof-II, Swat-84, Valder and Williams
Grp 8	15.94 ± 0.18	8	V	95023-B, Ajmeri, Aust-94-2, Calquit, Calquit, Ddtp-329, HS-17 and Washington
Grp.9	14.90 ± 0.97	3	V	Carlin, Centur and Ware
Grp.10	7.53 ± 0.48	9	VI	95020, 95029, 95029, 95029, 95030, 95035, 95039, R X(5-2-1) and V-BSS
Grp.11	11.57 ± 0.28	14	VII	95022, 95025, A-3127, Clark, Clay, Crawford, F-8827, Fabulin, Kura, No-13, Okland, Rawal-1, S-72-60 and Williams-82
Grp.12	10.78 ± 0.32	15	VII	95031, 80b4007, 95-3, Beeson, Db-1601, Duiker, Exp-15, Hamption-266, Mld-96, NARC-II, NARC-VII, No-54, NS-82-5250, Rampage and Steele
Grp.13	9.87 ± 0.49	11	VII	95093, Amsoy, Cns-210, Ed-73-112, GC 84058-8-4, NARC-IV, No-2, PR 16, Semmes, Sooty and Tn-81-142
Grp.14	11.16 ± 0.41	11	VIII	Ak(Kames), Davis, Hm-8437, Hs-16, NARC-II, NARC-III, PSC-56, Rahim 98, Togyukong, V-1 and Wilson-6
Grp.15	10.05 ± 0.20	14	VIII	Bragg, GC 86018-427-3, Henery, Hs-18, Mitchel, Monkey Hair, No-4, Ottawa, Perry, Spritto, Suehsine, Triton, V-Spardy and Wels-2

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