Journal of Oilseed Brassica 1(2) : 66-74, July 2010

GGE biplot analysis for visualization of mean performance and stability for seed yield in taramira at diverse locations in India

K.S. Brar[1*], Pritpal Singh[2], V.P. Mittal[1], Paramjit Singh[1], M.L. Jakhar[3], Yashpal Yadav[4],
M.M. Sharma[6], U .S. Shekhawat[5] and Chakresh Kumar[7]

[1]PAU, Regional Res. Station, Bathinda (Punjab), India.
[2]Department of Genetics & Plant Breeding, PAU, Ludhiana (Punjab)-India.
[3]College of Agri., Rajasthan Agri. Univ., Jobner, (Rajasthan), India
[4]CCSHAU, Regional Res. Station, Bawal (Haryana), India
[5]Rajasthan Agri.Univ., Agri. Res. Station, Sriganganagar, (Rajasthan)-India
[6]Rajasthan Agri. Univ., Bikaner, (Rajasthan)-India
[7]Rajasthan Agri. Univ., Agri. Res. Station, Navgaon, (Rajasthan)-India
**Corresponding author: brar164@hotmail.com*

Abstract

Among different oilseeds, *taramira* or rocket salad (*Eruca sativa L.*) is an important non- edible oilseed crop cultivated in arid and semi-arid parts of India. It is cultivated on marginal areas where sowing gets delayed or cultivation of other crops is not feasible. However, its low yield and varietal instability across environments is not encouraging to make it competitive with other crops. Thus development of genotypes having high seed yield with stable performance is of paramount importance. In the present investigation six genotypes of rocket salad viz., TMB 2006-2, T 27, TMB 2008, RTM 1146, RTM 314 and RTM 1212 were grown at Bawal (Haryana), Bathinda (Punjab), Bikaner (Rajasthan), Jobner (Rajasthan), Sriganganagar (Rajasthan) and Navgaon (Rajasthan) during *rabi* (post-rainy) season of 2008-09. Data recorded on seed yield were subjected to GGE biplot analyses, which revealed that total sums of squares of variation were 78.73% for environments (E), 7.67% for genotypes (G) and 13.60% for genotype by environment interactions (GE). It was demonstrated that seed yield of RTM 1212> T 27> TMB 2006-2>TMB 2008> RTM 314, while RTM 1146 was lowest yielder. However, RTM 1146 was the most stable genotype across the locations followed by TMB 2006-2 and T 27. RTM 314 and TMB 2006-2 were found to be least stable while RTM 1212 was moderately stable for seed yield. Exploitation of G coupled with GE revealed that RTM 1212 was the winner genotype with respect to its performance at Bikaner, Bathinda, Jobner and Sriganganagar locations while T 27 was identified as the winner genotype at Bawal and Navgaon . GGE biplot analyses also elucidated that owing to its high mean performance, RTM 1212 may prove a better donor over RTM 1146 for transferring stability genes.

***Key words**: Eruca sativa, genotype x environment interaction, GGE biplot, seed yield, stability analysis*

Introduction

Among different oilseed crops, *taramira* or rocket salad (*Eruca sativa L.*) is an important crop cultivated in arid and semi-arid parts of India. Being drought hardy and adapted to poor management conditions, it is an important non-edible oilseed crop of the low rainfall areas. It has an efficient root system to extract moisture from lower soil horizons (Singh, 1983). It also grows well in those marginal areas where sowing is delayed or cultivation of other crops is not feasible. However, its yield potential along with varietal stability across environments is not encouraging to make it competitive with other crops. Thus, information on varietal stability to varied environments, along with high yield in this crop may prove helpful in isolating genotype(s) which are responsive to better environments and maintain satisfactory yields under poor management. But genotype x environment interaction (GEI) remains one of the major sources of vexation and opportunity of plant improvement is hampered as GEI effects are directly involved in the determination of adaptability (Robbertse, 1989). Because of its universal presence and consequences, GEI necessitates conduct of multi-environment trials (METs), which has resulted in the development of numerous methods for analyzing multiplicative interactions based on their consistency in response to environments (Pinthus, 1973; Lin and Binns, 1988; Kang and Pham, 1991). One strategy involves factorial regression of the genotype x environment (GE) matrix against environmental factors, genotypic traits, or their combinations (Baril *et al.*, 1995). A second strategy, "Additive Main effects and Multiplicative Interactions" (AMMI) model, involves correlation or regression analysis that relates the genotypic and environmental scores derived from a principal component analysis of the GE interaction matrix to genotypic and environmental covariates (Zobel *et al.*, 1988). A recently released Windows-based software package, GGE Biplot, can be used to perform analyses similar to the popular AMMI model. However, GGE Biplot removes the effect of the environment (E) and focuses on the combined effect of G + GE components relevant to cultivar evaluation (Yan, 2001). The objective of this investigation was to use GGE Biplot to evaluate the performance and stability of seed yield among six strains of *taramira* across six diverse locations in India with higher precision by removing the noise caused by E.

Materials and Methods

The experimental material comprising of six genotypes of taramira viz., TMB 2006-2, T 27, TMB 2008, RTM 1146, RTM 314 and RTM 1212 generated at Jobner (Rajasthan) and Bawal (Haryana) and tested in the All India Coordinated Research Project on Rapeseed & Mustard during *rabi* (post-rainy) season of 2008-09 at Bawal (28°06'N , 76°56'E and 266 msl), Bathinda (30°58N, 74°18'E and 211 msl), Bikaner (28°01'N, 73°18'E and 251 msl), Jobner (26°58'N, 75°23'E and 431 msl), Sriganganagar (29°55'N, 73°33'E and 164 msl) and Navgaon (27°34'N, 76°35E). The genotypes were accommodated in 1.50 x 5.0 m plots with three replications in Randomized Block Design (RBD). The analysis was conducted and biplots generated using the "GGEbiplot" software developed by Yan (2001).

The model for GGE Biplot

A GGE biplot is constructed by subjecting the GGE matrix i.e., the environment-centred data, to singular value decomposition (SVD) as devised by Eckart and Young (1936). The GGE matrix is decomposed into three component matrices, which are the singular value (SV) matrix (Array), the genotype eigenvector matrix, and the environment (or traits) eigenvector matrix. So the model for a GGE biplot (Yan, 2001) based on Singular Value Decomposition (SVD) of first two principal components is

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{1j} + \lambda_2 \xi_{i2} \eta_{2j} + \varepsilon_{ij} \qquad [1]$$

where, Y_{ij} is the measured mean yield of genotype i (=1, 2,…n) in environments j (=1, 2,…m), μ is the grand mean, $\hat{a}_j$ = the main effect of environment j, $(\mu + \beta_j)$ being the mean yield across all genotypes in environment j, $\ddot{e}_1$ and $\ddot{e}_2$ are the singular values (SV) for the first and second principal component (PC 1 and PC 2), respectively, ξ_{i1} and ξ_{i2} are eigenvectors of genotype i for PC 1 and PC 2, respectively, η_{1j} and η_{2j} are eigenvectors of environment j for PC 1 and PC 2, respectively, $\mathring{a}_{ij}$ is the residual associated with genotype i in environment j.

PC 1 and PC 2 eigenvectors cannot be plotted directly to construct a meaningful biplot before the singular values are partitioned into the genotype and environment eigenvectors. Singular value partitioning is implemented by

$$g_{il} = \lambda_l^{fl} \xi_{i1} \text{ and } e_{lj} = \lambda_l^{1-fl} \eta_{lj} \qquad [2]$$

f_ι is the partitioning factor for $PC_{é}$. The f_ι can range between 0 and 1. To visualize the relationship among genotypes the GGE biplot based on genotype metric preserving (row metric preserving) is appropriate (i.e. f=1; S.V.P=1) and to visualize the relationship among environments, GGE biplot must be based on environment-metric preserving (column metric preserving) (i.e., f=0; S.V.P=2) but for symmetrical partitioning (i.e., f=0.5) S.V.P=3 has been used sometimes but not necessarily the most useful singular value partitioning method. So from the equation [1] to generate the GGE biplot we get equation [3]:

$$Y_{ij} - \mu - \beta_j = g_{i1}e_{1j} + g_{i2}e_{2j} + \varepsilon_{ij} \qquad [3]$$

If the data were environment-standardized, the common formulae for GGE biplot are rearranged as:

$$(Y_{ij} - \mu - \beta_j)/ s_j = \sum_{l=1}^{k} g_{il}e_{lj} + \varepsilon_{ij} \qquad [4]$$

where s_j is the standard deviation in environment j, l= 1, 2, …, k, g_{il} and e_{lj} are $PC_é$ scores for genotype and environment *j*, respectively.

In the present study environment standardized model [4] was used to generate biplot of "which-won-where" while for the analysis of relationship between trials, genotype and environment evaluation unstandardized model [3] was used.

Results and Discussion

The results are presented in two sections: section one involves analysis of variance, which represents percentage of the total sums of squares accounted for by G, E, and GE interactions over the location under testing; section two exhibits mean performance and stability of genotypes which includes the interrelationship among genotypes and locations, mean performance of genotypes at different locations, stability of genotypes across the locations, ranking of genotypes based on performance in specific location and across the locations, comparison among the genotypes and "which-won-where" pattern to identify the best genotypes in each environment for six genotypes of taramira.

Analysis of Variance

The percentage of the total sums of squares accounted for by G, E, and GE interactions were used as an indicator of variation attributed to seed yield (table 1).

Variation due to G or GE interactions is a measure of how cultivars respond across environments/ locations. The environmental component (E) represents how the cultivar means were different across the locations in spatial stability in this study. In the previous studies in different crops, it had been shown that for the traits having low heritability, the environment component of variation contributes the large proportion of the total variation, while traits with high heritability are influenced less by environment (Ethridge and Hequet, 2000; Kerby *et al*., 2000; Epinat-Le *et al*., 2001). The total sum of squares were 78.7% for environment, 7.7% for genotype, and 13.6% for the interaction for seed yield per ha, which is a major economic trait. As environment accounted for 78.7% of the total variation for seed yield per ha it was expected to be influenced more by the environmental sites, because of its polygenic control. But relative contribution of GE component variance was very high as compared to the G component of variance indicating that genetic improvement of this trait will be very low. The high contribution of E component to the extent of 80% when trials were conducted across 13 years in wheat and 59% across 10 years

Table 1: Degree of freedom, sums of squares, significance levels and total percentage of total variation of genotype (G), environment (E) and genotype by environment (GE) interaction by traits

Seed yield per ha								
	Source	DF	SS	MS	F	P	SS (%)	Heritability (bs) (%)
Seed yield per ha	Environment (E)	5	10489315.8	2097863.0	38.2	0.00001	78.73	7.18
	Rep (E)	12	2063.7	172.0	0	1.0		
	Genotype (G)	5	1022948.8	204589.8	3.5	0.00001	7.67	
	GEI	25	1812195.6	72487.8	0.8	0.00001	13.60	
	Error	60	911097.0	86415184.9				
	Total	107	14237621.7					

in soybean was also reported by Yan and Kang (2003). Similarly Kerby *et al*. (2000) and Blanche *et al*. (2006) also reported very high estimates for E components in cotton across the locations and years. The heritability estimates were 7.2%, for seed yield. The heritability estimates 40.5 to 84.8% reported by earlier workers (Brar *et al*., 2007; Dash and Pandey, 2009; Singh *et al*., 2009) in rapeseed-mustard are on higher side due to confounding effect of GE and E, which are eliminated in the present investigation.

Interrelationship among genotypes and locations

Summary of the interrelationships among the environments for different traits provides figure 1. The lines connecting the biplot origin with the markers for the environments are called environment vectors. The angle between the vectors of two environments is related to the correlation coefficient between them. The cosine of the angle between the vectors of two environments approximates the correlation coefficient between them (Kempton, 1984; Kroonenberg, 1995; Yan, 2002). Based on the cosine of angles of environment vectors, the six locations for seed yield are grouped into three groups. The presence of wide obtuse angles i.e. strong negative correlations among the locations is indication of strong cross-over genotype by environment interactions (Yan and Tinker, 2006). The distance between two environments (locations) measures their dissimilarity in discriminating the genotypes. Thus, six locations for seed yield per ha fell into three apparent groups. Sriganganagar and Jobner formed one group; group two involved Bikaner and Bathinda; the third group consisted of Navgaon and Bawal. The concentric circles on the biplot help to visualize the length of the environment vectors, which is proportional to the standard deviation within the respective environments and is discriminating ability of the environments (Kroonenberg, 1995). Therefore, among the six locations Bikaner and Navgaon were the most discriminating (informative) while Sriganganagar was the least discriminating for seed yield. Figure 1 represents the "Average-Environment Axis (AEA)" having the small circle at the end of arrow showing the average coordination of all test locations, and AEA is the line that passes through the average environment and biplot origin (Yan, 2001). A test location that has a smaller cosine of angle with AEA is more representative than other test locations. Moreover, the test environments that are both discriminating and representative are good for selecting widely adaptive genotypes. Thus, for seed yield though Bathinda had very close angle with AEA but the environmental conditions at this location were not much discriminating as Bathinda did not have sufficient vector length. Thus Bikaner and Navgaon are suitable locations for selecting high yielding genotypes having wider adaptability in *taramira*.

Mean performance of genotypes at different locations

Both vectors for genotype and environment, as drawn in fig 1, are helpful to visualize the specific interactions between a genotype and a location i.e. the performance of each genotype in each location (Yan and Tinker, 2006). The performance of a genotype at a specific location is better if the angle between its vector and the location vector is <90° ; is poorer than average if the angle is >90° ; and it is near average if the angle is about 90°, which is based on the "inner product property" principle of biplot (Gabriel, 1971). Thus, the potential of seed yield of RTM 1146 is below average at all locations (obtuse

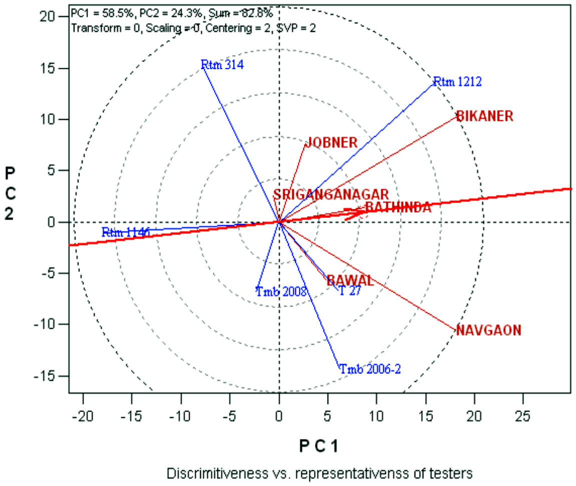

Figure 1: GGE biplot showing the performance of each genotype at each location for seed yield in taramira

angles). Whereas the performance of RTM 1212 is above average at Bikaner, Bathinda, Jobner and Sriganganagar, while it was near average at Navgaon and Bawal. Similarly genotypes T27 and TMB 2006-2 gave better yield than average at Bawal and Navgaon locations. Strain RTM 314 was well adapted to Sriganganagar only for seed yield.

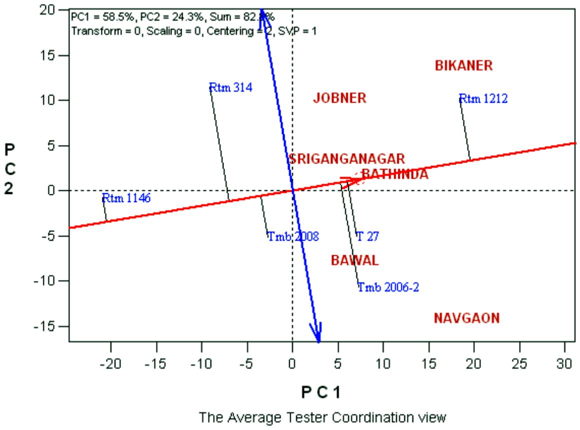

Figure 2: Average- environment coordination (AEC) view to show the mean performance and stability of genotypes seed yield per hectare

Stability of genotypes across the locations

The ideal genotype should have high mean performance coupled with high stability to give wide adaptability in the target region. As depicted in figure 2 the single-arrowed line called average–environment coordination abscissa (or AEA) points to higher mean seed yield across the locations. Thus, RTM 1212 had the highest mean yield, followed by T27 and TMB 2006-2. Genotype TMB 2008 had mean yield similar to grand mean while RTM 1146 and RTM 314 had mean yield less than overall mean yield across all locations. The double-arrow line is the AEC ordinate and it points to greater variability (poor stability) in either direction. The instability index calculated as per Eberhart and Russel (1966) model (table 2) has the same magnitude as depicted by GGE biplot (fig. 2). Thus, RTM 314 and TMB 2006-2 are highly unstable genotypes, whereas TMB 2008 was most stable across the locations for seed yield. The RTM 314 is unstable for seed yield as it has performed better than average at Bikaner, Jobner and Sriganganagar and poor at Bawal and Navgaon locations. The TMB 2006-2 strain is also unstable as its performance was opposite to RTM 314 at different sites.

Table 2: Seed yield performance (kg) at different environment, average over environments and stability statistics

Cultivar	Seed yield at different locations (kg/ ha)						Mean	Stability statistics
	Bathinda	Bikaner	Bawal	Jobner	Navgaon	Sriganga Nagar		
TMB 2006-2	1034	833	1711	1239	1852	860	1255	11.78
T 27	945	927	1467	1289	1852	780	1210	6.15
TMB 2008	1015	688	1430	1342	1704	840	1170	4.58
RTM 1146	833	469	1215	1337	1407	850	1019	-2.72
RTM 314	911	917	1518	1399	1259	920	1154	-12.82
RTM 1212	1177	1229	1326	1548	1852	880	1335	-6.97
Mean	986	846	1445	1359	1654	855	1190	

Ranking of genotypes based on performance in a specific location and across locations

Suppose, we want to see the yield potential of different genotypes at Bawal location, the line will be drawn that passes through the biplot origin and Bawal location. The genotypes T27 and TMB 2006-2 gave highest yield, RTM 314 provided the lowest, while TMB 2008 and RTM 1212 gave average yield. At Jobner location the ranking of genotypes was just opposite to that of Bawal indicating the clear-cut presence of cross-over interaction (COI), which necessitates exploitation of GEI. It is pertinent to mention that these are the only locations conducting breeding work on *taramira* in India. Figures 3 and 4 showed opposite adaptability of genotypes to these locations indicating the role of natural selection in restructuring genetic make-up for adaptation for its native place. This means that specific adaptability of genotypes at these locations is entirely different and GEI can be exploited for selecting genotypes rather than ignoring it. We can also visualize biplot for best adaptability of genotypes in a specific location as well. The yield of RTM 1212 was highest at Bikaner followed by Bathinda, Jobner and least at Bawal (fig. 5). Similarly, TMB 2006-2 gave extreme response to seed yield at Bawal and Navgaon (fig. 6). When we rank genotypes across locations/ environments it should be done with respect to an ideal genotype that lies on AEA (absolutely stable) in the positive direction and has a vector length equal to the longest vector of the genotypes on the positive side of AEA i.e., highest mean performance. Therefore, genotypes which are

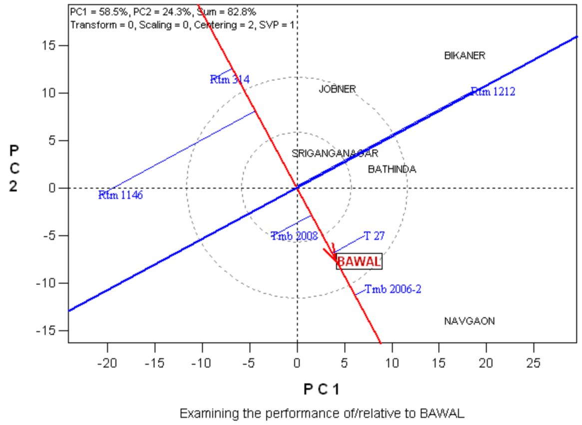

Figure 3: Ranking of genotypes based on performance of *Bawal* location

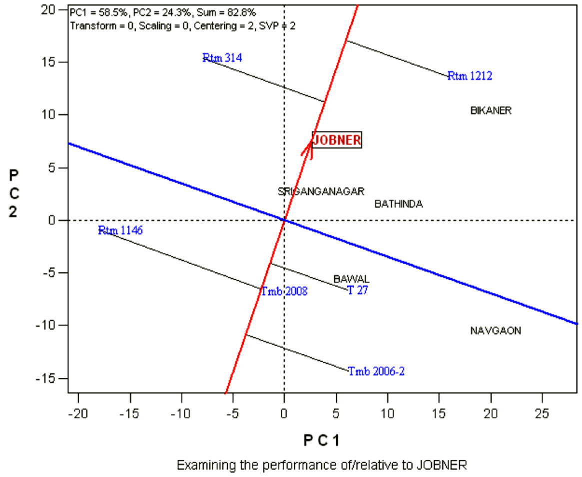

Figure 4: Ranking of genotypes based on performance of *Jobner* location

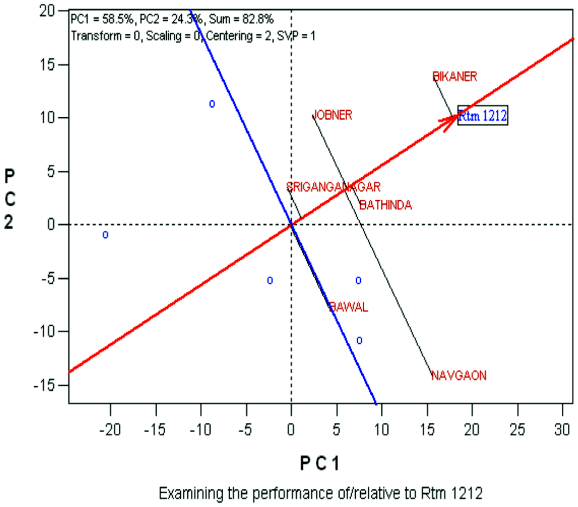

Figure 5: Ranking of locations in terms of the relative performance of genotype RTM 1212

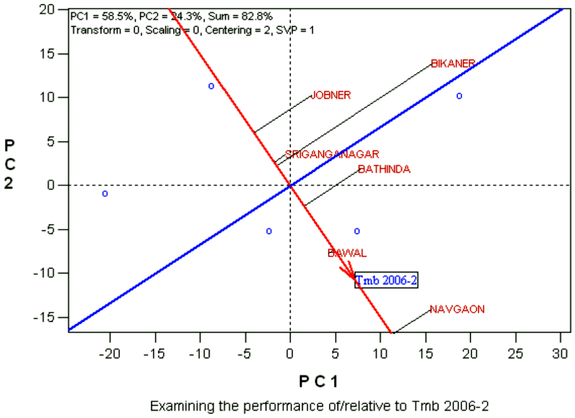

Figure 6: Ranking of locations in terms of the relative performance of genotype TMB 2006-2

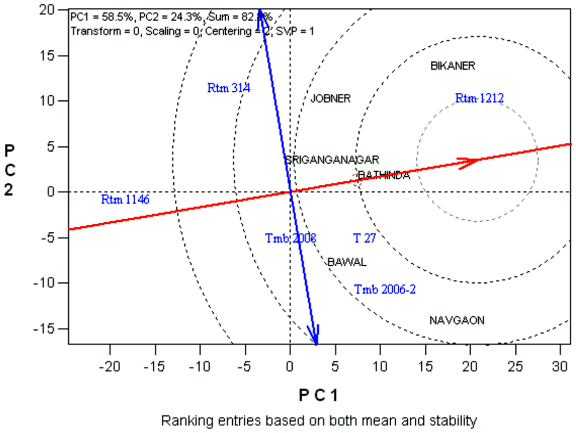

Figure 7: The average-environment coordination (AEC) view to rank genotypes relative to an ideal genotype for seed yield per hectare in taramira

closer to “ideal genotype” are more desirable than others (Yan and Tinker, 2006) and thus, RTM 1212 was high yielding with consistent performance across the locations (fig. 7). The genotype RTM 1146 though low yielder, showed highest stability among all genotypes. Yan and Tinker (2006) are of the view that when we are interested to transfer “stability gene” to other genotypes it should be desirable to use a donor having high mean performances along with stability. Thus, RTM 1212 can prove to be a better donor than RTM 1146 as far “stability genes” are concerned.

Comparison among the genotypes

The distance between two genotypes approximates the Euclidean distance between them and hence, is a measure of dissimilarity among the genotypes (Kroonenberg, 1995). Therefore, RTM 1212 and RTM 1146 are quite different in their genetic make-up with respect seed yield whereas, TMB 2008, T 27 and TMB 2006-2 are very close to each other (fig 8). The biplot origin also represents a “virtual” genotype with grand mean value and zero contribution of additive effect of genotype (G) as well as multiplicative interactions (GE). The vector length of a genotype of the origin of biplot is due to the contribution of G and/or GE. Genotypes located near to the biplot origin have little contribution to G or GE (TMB 2008) while genotypes having longer vectors indicate the contribution of G and/or GE. Therefore, genotypes with the longest vectors are either the best (RTM 1212) or the poorest (RTM 1146) or most unstable (RTM 314, T 27 and TMB 2006-2). RTM 1212 can be considered as the best genotype as its angle is very close to the ideal genotype coupled with longer vector length. Further, the angle between vector of a genotype and the AEA partitions the vector length into components of G and GE.

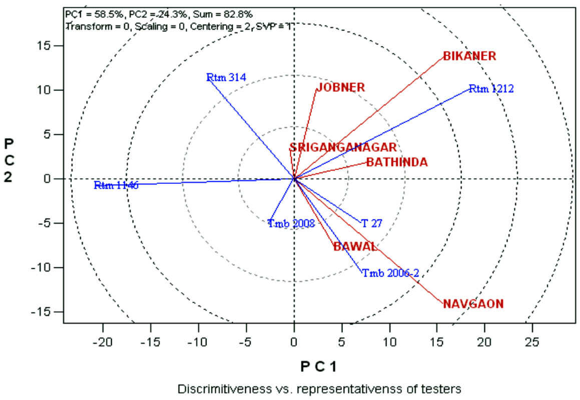

Figure 8: the genotypes-vector viewto show similarities in their performance in individual location for seed yield per hectare

Right angle with AEA means that the contribution is only due to GE; an obtuse angle depicts the contribution of G, which leads to less than average mean performance; and an acute angle again means the contribution of G but on higher side. To visualize the genetic make-up of different genotypes it is desirable to use SVP1 i.e., genotype centring (fig. 8). Thus, there is major contribution of G for RTM 1212 and RTM 1146 for seed yield but in opposite direction and these two can perform consistently across the locations than other genotypes. RTM 314, TMB 2008 and TMB 2006-2 are unstable as the genotypes are located almost at right angle to AEA and there is a major contribution of the GE component of variance.

The “which-won-where” pattern of genotypes

One of the most attractive features of GGE biplot is its ability to show the “which-won-where” pattern of a genotype by environment dataset as it graphically addresses important concepts such as cross-over GE, mega-environment differentiation, specific adaptation, etc (Yan and Tinker, 2006). The polygon view of the GGE biplot (fig. 9) indicates the

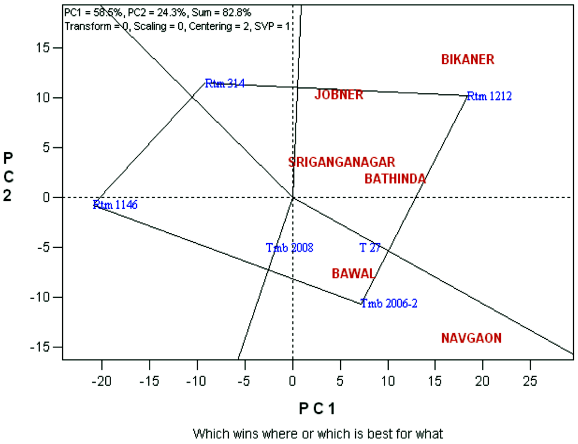

Figure 9: The which-won-where view of the GGE biplot to show which genotypes performed better in which location for seed yield

best genotype(s) in each environment and groups of environments (Yan *et al*., 2000; Yan and Hunt, 2001). The polygon is formed by connecting the markers of the genotypes that are farthest away from the biplot origin such that all other genotypes are contained in the polygon. The rays are lines that are perpendicular to the sides of the polygon or their extension (Yan and Kang, 2003). In figure 9, ray 1 is perpendicular to the side that connects genotype TMB 2006-2 with RTM 1212, ray 2 is perpendicular to the side that connects genotype RTM 1212 with RTM 1146 and so on. These four rays divide the biplot into four sectors. Six locations fall in the two sectors. Genotypes located on the vertices of the polygon reveal the best or the poorest in one or other environment. The RTM 1212 gave high yield at Sriganganagar, Jobner, Bikaner and Bathinda locations, while TMB 2006-2 at Bawal and Navgaon. The other genotypes RTM 314 and RTM 1146 lying on the vertices did not respond at any of the locations.

The large environmental main effect in the expression of a phenotype is not relevant to cultivar evaluation. Also G and GE must be considered together to make meaningful selection decisions rather than G alone, especially when cross-over GE interactions dominating (Kerby *et al*., 2000). During breeding phase, the natural selection plays important role in restructuring the genetic make-up of crop plants. During the evaluation phase we have to identify the real worth of a genotype for high mean performance along with its stability along with to wide range of environments as well as site specific adaptability to harvest the maximum genetic gain for a trait. A higher order epistatic interaction seems to be influencing specific adaptability for particular location or geographical region. In Spain, Molecular marker Assisted Selection (MAS) studies involving 14 loci in *Avena barbata* populations, being adapted to extreme abiotic stress have shown that progressively larger changes were accompanied by consistently greater restructuring of genetic make-up involving higher order epistatic interactions in the diverging populations (Yan and Tinker, 2006). In the present investigation it is also clear that germplasm generated at *Jobner* was much adapted to its native location than *Bawal* and *vice versa*. Only these locations have responsibility to generate the elite germplasm of *taramira* and AICRP (R&M) Trials of *taramira* are conducted to realize the worth of elite genotypes for temporal as well as spatial stability. It was also realized in a Joint European Spring Barley Trial (Yan *et al*., 2000) that METs play crucial role to know the genetic worth of the genotype rather than single location testing (years only) for refinement of variance components of GE for the selection of cultivars. Further Talbot (Zobel *et al*., 1988) also agreed that broadening the range of environments may dilute the effect of the years but enhance somewhat contribution of the locations and can often provide as extreme genotype response to geographical niches for specific adaptability. In the present investigation genotypes have shown larger contribution of GE than G component of variance (Table 1.) indicating that some genotypes extremely responded to specific locations. Thus selection based on G only i.e. averaging genotypes across the locations will ignore the GE. For seed yield the environment of *Jobner* is totally different from *Navgaon* and *Bawal* showing the change of raking in genotypes for yield potential. Thus selection based on G only will not be justified for full utilization of yield potential of some genotypes due to their extreme response to specific adaptations due to the involvement of cross-over GE interaction. However, to characterize the cross-over GE Interaction, pattern should be confirmed for two to three years having same genotypes and locations.

References

Allard, R. W. 1999. *Principles of Plant Breeding* (Second Edition). John Wiley & Sons, Inc. New York, 1-254 p.

Baril, C. P., Denis, J. B., Wustman, R. and van Eeuwijk, F. A. 1995. Analyzing genotype-by-environments for selection and recommendation of common wheat genotypes in Italy. *Plant Breed*., **113:** 197-205.

Blanche. A., Sterling, B., Gerald, O. M., Zumba, J. Z., Caldwell, D., and Hayes, J. 2006. Stability comparisons between conventional and near-isogenic transgenic cotton cultivars**.** *J. Cotton Sci*., **10**: 17–28.

Brar, K.S., Mittal V. P., and Singh, P. 2007. Estimation of genetic parameters, character association and path analysis for seed yield and its components in Indian mustard (*Brassica juncea* Coss & Czern). ISOR National Seminar, DOR, Hyderabad India.

Dash, S. S. and Pandey, A. 2009. Genetic variability and association of yield and its components in toria, *Brassica rapa* L. var *toria* germplasm. *J. Oilseeds Res. (Special issue)* **26**: 53-55.

Eberhart, S. A. and Russel, W. A. 1966. Stability parameters for comparing varieties. *Crop Sci.*, **6**: 36-40.

Eckart, C. and Young, G. 1936. The approximation of one matrix by another of lower rank. *Psychometrika* **1**: 211-218.

Epinat-Le, Signor., Dousse, C. S., Lorgeou, J., Denis, J. B., Bonhomme, R., Carolo, P., Charcosset, A. 2001. Interpretation of genotype x environment interactions for early maize hybrids over 12 years. *Crop Sci.*, **41**: 663-669.

Ethridge, M. D. and Hequet, E. F. 2000. Fiber properties and textile performance of transgenic cotton versus parent varieties. In: *Proc. Beltwide Cotton Conf.*, San Antonio, TX. 4-8 Jan 2000, Natl. Cotton Counc. Am., Memphis, TN, USA. pp. 488-494.

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

Kang, M. S. and Pham, H. N. 1991. Simultaneous selection for high yielding and stable crop genotypes. *Agron. J.*, **83**: 161-165.

Kempton, R. A. 1984. The use of biplots in interpreting variety by environment interactions. *J. Agric. Sci.*, **103**: 123-135.

Kerby, T., Burgess, J., Bates, M., Albers, D., Lege, K. 2000. Partitioning variety and environment contribution to variation in yield, plant growth, and fiber quality. In: *Proc. Beltwide Cotton Conf.*, New Orleans, LA. 7-10 Jan 2000. Natl. Cotton Counc. Am., Memphis, TN, USA. pp. 528- 532.

Kroonenberg, P. M. 1995. Introduction to biplots for G x E tables. Department of Mathematics, Research Report 51, University of Queensland, Australia.

Lin, C.S. and Binns, M.R. 1988. A superiority measure of cultivar performance for cultivar x location data. *Can. J. Plant Sci.*, **68**: 193-198.

Pinthus, M. J. 1973. Estimate of genotypic value: A proposed method. *Euphytica*, **22**: 121-123.

Riggs, T. J. 1986. Collaborative spring barley trials in Europe 1980-82. Analysis of grain yield. *Zeitschrift fur Pflanzenuchtung* **96**: 289-303.

Robbertse, P. J. 1989. The role of genotype-environment interaction in adaptability, *S. African For. J.*, **109**: 183-91.

Singh, B. P. 1983. Response of *taramira* to sulphur application. *Indian J. Agric. Sci.*, **53**: 676-680.

Singh, M., Rao M., Shekhar, R., Dixit, R. K. 2009. Genetic variability and character association in Indian mustard, (*Brassica juncea*) .*J. Oilseeds Res* **26**: 56-57.

Tallbot, M. 1984. Yield variability of crop varieties in the United Kingdom. *J. Agric Sci.*, Cambridge **124**: 335-342.

Yan, W. 2001. GGE Biplot- A Windows application for graphical analysis of multi-environment trial data and other types of two-way data. *Agron. J.*, **93**: 1111-1118.

Yan, W. 2002. Singular value partition for biplot analysis of multi-environment trial data. *Agron. J.*, **94**: 990-996.

Yan, W. and Hunt, L. A. 2001. Interpretation of genotype x environment interaction for winter wheat yield in Ontario. *Crop Sci.*, **41**: 19-25.

Yan, W. and Kang, M. S. 2003. GGE biplot analysis: A graphical tool for breeders, geneticists and agronomists. CRC Press, Boca Raton, FL, USA. 1-271 p.

Yan, W. and Tinker, N.A. 2006. Biplot analysis of multi-environment trial data: principles and applications. *Can. J. Plant Sci.*, **86**: 623-645.

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

Zobel, R. W., Wright, M. J., and Gauch Jr, H. G. 1988. Statistical analysis of a yield trial. *Agron. J.*, **80**: 388-393.

●