

## GGE BIPLLOT ANALYSIS VISUALIZATION OF MEAN PERFORMANCE AND STABILITY FOR SEED YIELD IN SAFFLOWER (*CARTHAMUS TINCTORIUS*) AT DIVERSE LOCATIONS IN INDIA

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### ABSTRACT

Twenty three genotypes of safflower were grown at 14 diverse locations ranging from 13°56'N to 30°26'N latitude and 74° 25'E to 88° 15'E longitude covering vast area of India. The total sums of squares were 75.58% for environment, 6.53% for genotype, and 17.89% for the interaction for seed yield per hectare. Genotypes like NARI 63, NARI 62, SSF 708, SSF 773, SSF 98, SSF 99, SSF 104, SSF 710, AKA 98-3, NARI 63, A-1 and PBNS 83 exhibited consistency for yield over all sites while genotypes like SSF 773, JSI 120, JSI 117, AKS 311, PBNS 88 and JSI 132 were most unstable performer across the locations because of their extreme adaptability to some specific locations. The SSF 773 gave highest yield at *Bathinda Tandur*, *Raichur* and *Achalpur* while NARI 63 at *Berhampore* and *Akola* locations. However, NARI 62 and SSF 708 were best adaptive to *Dharwad* and *Parbhani*. At *Annigeri* site PBNS 90 was the winner genotype. Biplot analysis showed genotypic like NARI 63, NARI 62 and SSF 708 had additive gene(s) for increasing yield potentials and can prove better donor for developing genotypes having wider adaptability for high yield in safflower.

**KEY WORDS:** Safflower, *Carthamus Tinctorius*, Stability Analysis, Ggebiplot, Genotype by Environment Interaction

### INTRODUCTION

Safflower is one of the oldest oilseed crop cultivated in 60 countries (Gyalai, 1996). Crop is rich in poly unsaturated fatty acids (linoleic acid 78%), plays an important role in reducing blood cholesterol level and considered as a healthy cooking medium (Shivani *et al.* 2009). It is cultivated in peninsular India under irrigated as well as rainfed conditions. Being low yielder, the need of identification of high yielding stable performing germplasm / cultivars is utmost important (Shinde *et al.* 2009). Thus, information on varietal stability with high yield to varied environments in safflower may helpful in isolating genotype(s). A recently released window based software package “GGE Biplot” was used to evaluate the performance and stability of seed yield among 23 strains of safflower across 14 diverse locations in India. 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).

### Materials and Methods

The experimental material comprising of twenty three genotypes of safflower viz., 98/99/104, A-1, AKA 98-3, AKS 311, AS 96-2, JSI 117, JSI 120, JSI 132, NARI 62, NARI 63, NARI 64, NARI 65, PBNS 40, PBNS 83, PBNS 84, PBNS 88, PBNS 90, PBNS 91, S 11-105-3-1(O), SSF 708, SSF 710, SSF 741 and SSF 773 and tested in the “ All India Coordinated Research Project” on Safflower during *rabi* 2008-09 at *Achalpur* (21°15'N, 77° 31'E and 369 msl), *Akola* (20°27'N, 75° 44'E and 282 msl), *Annigeri* (15°26'N, 75° 26'E and 625 msl), *Badnapur* (19°52'N, 75° 26'E and 325 msl),

*Bathinda* (30°26'N, 74° 26'E and 211 msl), *Berhampore* (24°06'N, 88° 15'E and 19 msl), *Dharwad* (15°28'N, 75° 26'E and 701 msl), *Hiriyur* (13°56'N, 76° 33'E and 630 msl), *Indore*(22°43'N, 75° 50'E and 560 msl), *Parbhani* (19°16'N, 76° 54'E and 409 msl), *Phaltan* (17°55'N, 74° 25'E and 600 msl), *Solapur* (17°40'N, 75° 54'E and 476 msl) and *Tandur* (17°14'N, 77° 35'E and 450 msl). Thus, latitude (13°56'N to 30°26'N) and longitude (74° 25'E to 88° 15'E) covering vast area of Indian. The Experiment were conducted IN RDB with three replications The genotypes were grown in 2.25 x 5.0 metres plots. The analyses were conducted and biplot generated using the “GGEbiplot” software (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- 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 SVD of first two principal components is:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{1j} + \lambda_2 \xi_{i2} \eta_{2j} + \varepsilon_{ij} \quad (1)$$

Where  $Y_{ij}$  is the measured mean yield of genotype  $i$  ( $=1, 2, \dots, n$ ) in environments  $j$  ( $=1, 2, \dots, m$ ),  $\mu$  is the grand mean,  $\beta_j$  = the main effect of environment  $j$ ,  $(\mu + \beta_j)$  being the mean yield across all genotypes in environment  $j$ ,  $\lambda_1$  and  $\lambda_2$  are the singular values (SV) for the first and second principal component (PC 1 and PC 2), respectively,  $\xi_{i1}$  and  $\xi_{i2}$  are eigenvectors of genotype  $i$  for PC 1 and PC 2 respectively,  $\eta_{1j}$  and  $\eta_{2j}$  are eigenvectors of environment  $j$  for PC 1 and PC 2, respectively,  $\varepsilon_{ij}$  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;

$$g_{il} = \lambda_l^{f_l} \xi_{il} \text{ and } e_{lj} = \lambda_l^{1-f_l} \eta_{lj} \quad (2)$$

Where  $f_l$  is the partitioning factor for PC <sub>$l$</sub> . The  $f_l$  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)

$$Y_{ij} - \mu - \beta_j = g_{i1} e_{1j} + g_{i2} e_{2j} + \varepsilon_{ij} \quad (3)$$

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

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

Where  $s_j$  is the standard deviation in environment  $j$ ,  $l= 1, 2, \dots, k$ ,  $g_{il}$  and  $e_{lj}$  are PC <sub>$l$</sub>  scores for genotype  $I$  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 DISCUSSIONS

### Analysis of Variance

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 in spatial stability across the locations. Total sums of squares were 75.58% for environment, 6.53% for genotype, and 17.89% for GE interaction for seed yield.

Environment accounted for 75.58% of total variation for seed yield of different varieties and expected to be more influenced by environment across the locations because of polygenic control in nature. Relative contribution of GE component to total variance for seed yield was high as compared to G component indicating that genetic improvement of this trait will be very low. The contribution of E component was as high as 80% when trials were conducted across 13 years in wheat and 59% across 10 years in soybean (Yan and Kang 2003). Similarly Kerby *et al.* (2000) and Blanche *et al.* (2006) also reported very high estimates E components in cotton across the different location and years. The heritability estimates was 6.53%, for seed yield. Shivani *et al.* 2009 and Wakode *et al.* 2009 reported that heritability estimates in safflower were on higher side. This may be due to confounding effect of GE and E, which is eliminated in the present investigation.

## MEAN PERFORMANCE AND STABILITY OF THE GENOTYPES ACROSS THE LOCATIONS

### Interrelationship Among Genotypes and Locations

The lines marked for the environments connect the biplot origin and are called environment vectors (Fig 1)). The angle between the vectors of two environments is related to the correlation coefficient between them. The cosine angle between two environments vectors approximates the correlation coefficient between them (Kempton 1984; Kroonenberg 1995; Yan, 2002). The fourteen locations for seed yield broadly be grouped into three groups based on cosine angle between environment vectors. The presence of wide obtuse angles represent strong negative correlations among the locations and indication of strong cross-over genotype by environment interactions (Yan and Tinker 2006).

Fourteen locations for seed yield revealed that environmental conditions of *Annigeri*, *Hiriyur*, *Phaltan*, *Dharwad* were entirely different from *Raichur*, *Bathinda*, *Tandure* and *Achalpur* thus forming different groups. Obtuse angles between these groups indicates that genotypes will show cross-over interactions at these sites. Climatic conditions of *Indore*, *Solapur*, *Badnapur*, *Akola* and *Berhampore* were intermediate to both these groups of environment. 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 discriminating ability of the environments (Krooneberg 1995). The locations *Bathinda*, *Annigeri* and *Phaltan* were most discriminating (informative) while *Solapur* and *Hiriyur* least discriminating for seed yield.

Average-Environment Axis (AEA) having the small circle at the end of arrow shows the average coordination of all locations, and is the line that passes through the average environment and biplot origin (Yan 2001). A location that has a smaller cosine of angle with AEA was more representative than other test locations. Moreover, the test environments that are both discriminating and representative are good for selecting wide adaptive genotypes. Thus for seed yield, *Berhampore* is ideal site for selecting high yielding genotypes having wider adaptability in safflower than *Bathinda*, *Annigeri* and *Phaltan* due to bigger cosine of angle with AEA.

### Mean Performance Genotypes at Different Locations

The performance of a genotype at a specific location is better if the angle between its vector and the location's vector is  $<90^\circ$ ; is poorer if the angle is  $>90^\circ$ ; and it is near average if the angle is about  $90^\circ$  which is based on the "inner product property" principle of biplot (Gabriel 1971). Seed yield potential of PBNS 83, S-II-105-3-1(0), AS 96-2-5, PBNS 88, PBNS 40, PBNS 91 and NARI 60 are below average at all locations (owing to obtuse angles) while the performance of NARI 63, NARI 62, SSF 708, SSF 98 SSF 99 SSF 105, SSF 741, SSF 710, SSF 773 A 1, and AKA 98-3 above average at all the locations.

### Stability of Genotypes Across the Locations

The ideal genotype should have both high mean performance coupled with high stability to give wide adaptability. The single-arrowed line called average–environment coordination abscissa (or AEA) points to higher mean seed yield across the locations (fig 2). The double-arrow line is the AEC ordinate and it points to greater variability (poor stability) in either direction. NARI 63 had the highest mean yield, followed by NARI 62, SSF 708, SSF 773, SSF 98 SSF 99 SSF 104, SSF 710, AKA 98-3, NARI 63 and A-1 were yielder at all the locations. The instability index calculated as per Eberhart and Russel model (1966) (table 2.) has the same trend of magnitude as depicted by GGE biplot (Fig. 2). NARI 63, NARI 62, SSF 708, SSF 773, 98/99/104, SSF 710, AKA 98-3, NARI 63, A-1 and PBNS 83 exhibited consistency for yield over all sites while genotypes like SSF 773, JSI 120, JSI 117, AKS 311, PBNS 88 and JSI 132 were most unstable performer across the locations because of their extreme adaptability to some specific locations.

### Ranking of Genotypes Based on Performance in Specific Location and Across the Locations

The line has drawn which passes through the biplot origin and particular location represent the yield potential of different genotypes at that location. The genotypes AKS 311, PBNS 90 and PBNS 88 gave maximum seed yield whereas JSI 117 had lowest yield, while SSF 741, 98/99/104 and SSF 710 had average yield potentials at *Annigeri* location. At *Bathinda* location the ranking of genotypes were just reverse of *Annigeri* indicating the clear-cut presence of cross-over interactions (COI), which necessitates exploitation of GEI (Fig-4). This means that specific adaptability of genotypes for these locations is entirely different and GEI can be exploited while selecting genotypes for cultivation rather than ignoring. The yield potential of NARI 63 was above general mean at all locations, while PBNS 83 was poorest yielder genotypes at all sites (Fig. 5& 6). Similarly, the adaptability of genotypes to different locations is depicted in table 3.

The ranking of genotypes across locations it should be done with respect to ideal genotype which point on AEA (absolutely stable) in the positive direction and has a vector length equal to the longest vectors of the genotypes on the positive side of AEA i.e. highest mean performance. Genotypes which are closer to “ideal genotype” are more desirable than others (Yan and Tinker 2006). NARI 63, NARI 62 and SSF 708 were high yielding having consistence performance across the locations (fig. 7). The genotype PBNS 83 though low yielder but showed highest stability among all the genotypes. Yan and Tinker (2006) reported that to transfer “stability gene” to other genotypes it would have high mean performances to act as desirable donor. Thus genotype NARI 63, NARI 62, SSF 708, SSF 741, SSF 710, 98/99/104, AKS 98-5 and A 1 can prove better donor to transfer “stability genes”.

### Comparison Among the Genotypes

The distance between two genotypes approximates the Euclidean distance between them, thus is a measure of dissimilarity among the genotypes (Kroonenberg 1995). Genotype NARI 63 and PBNS 83 were quite different in their genetic make-up, while NARI 63, NARI 62, SSF 708, SSF 741, SSF 710, 98/99/104, AKS 98-5 and A 1 very close to each other (fig. 8). The biplot origin also represent a “virtual” genotype that assumes the grand mean values and zero contribution additive effect of genotype (G) and multiplicative interactions (GE). The vector length of a genotype from the origin of biplot is due the contribution of G or GE or both. Genotypes those are located near to the biplot origin have little contribution viz., S-96-2, PBNS 40, PBNS 91, PBNS 84 and NARI 65 of G or GE or both. Genotypes having longest vectors were either best (NARI 63) or poorest (PBNS 83) or most unstable (JSI 117, PBNS 88 and SSF 773). The NARI 63 could be considered as best genotype as its angle very close to ideal genotype coupled with longer vector length. Angle between vector of a genotype and the AEA partitions the vector length into components of G and GE. A right angle with AEA means that the contribution is due to GE only; an obtuse angle depicts the contribution of G, which leads to lower

than average mean performance; and an acute angle again mean the contribution of G but in higher side. There was major contribution of G for NARI 63, NARI 62 and SSF 708 and had additive gene(s) for increasing yield potentials while PBNS 83 also possessed additive gene(s) but in recessive form and these genotype (s) can perform consistently across the locations than other genotypes. Genotypes like JSI 120, JSI 117, JSI 132, PBNS 90 and AKS 311 were unstable as the genotypes located almost right angle with respect to AEA and there was major contribution of GE component of variance.

#### The “Which-Won-Where” Patterns of the Genotypes

Ray one is perpendicular to the side that connects genotype JSI 117 and genotype SSF 773, ray two is perpendicular to the side that connects genotype SSF 773 and NARI 63 and so on (Fig. 9). These eight rays divide the biplot into eight sections, and fourteen locations fall into five of them. Genotypes located on the vertices of the polygon reveals the best or the poorest in one or more environment. The SSF 773 gave highest yield at Bathinda, Tandur, Raichur and Achalpur locations while at Berhampore and Akola showed congenial conditions for NARI 63. NARI 62 and SSF 708 were best adaptive to Dharwad and Parbhani. At Annigeri site PBNS 90 was best adoptive.

#### CONCLUSIONS

In the present investigation genotypes have shown larger contribution GE than G component of variance (Table 1.) indicating that some genotypes extremely responded to some locations specifically viz., SSF 773 extremely responded at *Bathinda* while NARI 63 at *Berhampore* though these strains were developed somewhere else.

#### REFERENCES

1. Allard R W (1999) Principles of Plant Breeding. 2<sup>nd</sup> edn. Wiley, New York.
2. 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.
3. Blanche, Sterling B., Gerald O. Myers, Jimmy Z. Zumba, David Caldwell, and James Hayes. 2006. Stability comparisons between conventional and near-isogenic transgenic cotton cultivars. *J Cotton Science* 10:17–28
4. Cullis B R, Thomson FM, Fisher J A, Gilmour A R and Thomson R (1996) The analysis of the NSW wheat variety database. I. Modeling of error variance. *Theor Appl Genet.* 92 : 21-27
5. Eckart C and Young G (1936) The approximation of one matrix by another of lower rank. *Psychometrika* 1 : 211-218
6. Eberhart S A and Russel W A (1966) Stability parameters for comparing varieties. *Crop Sci.*, 6 : 36-40.
7. Epinat-Le Signor, Dousse C S, Lorgeou J, Denis J B, Bonhomme R, Carolo P and Charcosset A (2001) Interpretation of genotype x environment interactions for early maize hybrids over 12 years. *Crop Sci.* 41 :663-669
8. 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. p 488-494*
9. Gabriel K R (1971) The biplot graphic display of matrices with application to principal component analysis. *Biometrika* 58: 453-467

10. Gyalai J (1996) Market outlook for safflower. In Proceedings of North American Safflower Conference, great falls, Montana, January, 17-18 (lethbridge, AB ) Canada, p: 15.
11. Kang M S and H N Pham (1991) Simultaneous selection for high yielding and stable crop genotypes. *Agron J.* 83 :161-165
12. 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
13. Kempton R A (1984) The use of biplots in interpreting variety by environment interactions. *J Agric Sci.* 103 : 123-135
14. Kroonenberg P M (1995) Introduction to biplots for G x E tables. Department of Mathematics, Research Report 51, University of Queensland, Australia.
15. Kerby T, Burgess J, Bates M, Albers D and 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. p 528- 532
16. Pinthus M J (1973) Estimate of genotypic value: A proposed method. *Euphytica.* 22 :121-123
17. Riggs T J (1986) Collaborative spring barley trials in Europe 1980-82. Analysis of grain yield. *Zeitschrift fur Pflanzenuchtung.* 96 :289-303
18. Robbertse P J (1989) The role of genotype-environment interaction in adaptability, *So African For J.* 109:183-191
19. Shivani D, Bhadru D, Sreelakshmi C and Kumar P A (2009) Variability and character association analysis in wilt resistant lines of safflower, *Carthamus tinctorius* L. *J Oilseeds Res.* 26(S) :33-36
20. Shinde S K, Kale S D and Kadam J R (2009). SSF 658, a new non-spiny safflower variety. *J Oilseeds Res.* 26(S) :113-115
21. Tallbot M (1984) Yield variability of crop varieties in the United Kingdom. *J Agric Sci. Cambridge,* 124 : 335-342
22. Wakode M M, Patil H E and Deshmukh S N (2009) Genetic evaluation of safflower , *Carthamus tinctorius* L. genotypes. *J Oilseeds Res.* 26(S) :117-119
23. 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
24. Yan W (2002) Singular value partition for biplot analysis of multi-environment trial data. *Agron J.* 94: 990-996
25. Yan W and Hunt L A (2001) Interpretation of genotype x environment interaction for winter wheat yield in Ontario. *Crop Sci.* 41:19-25
26. Yan W and Kang M S (2003) GGE biplot analysis: A graphical tool for breeders, geneticists and agronomists. CRC Press, Boca Raton, FL. p. 271
27. Yan W and Nicholas A Tinker (2006) Biplot analysis of multi-environment trial data: Principles and applications. *Can J Plant Sci.* 86 : 623-645

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

APPENDICES

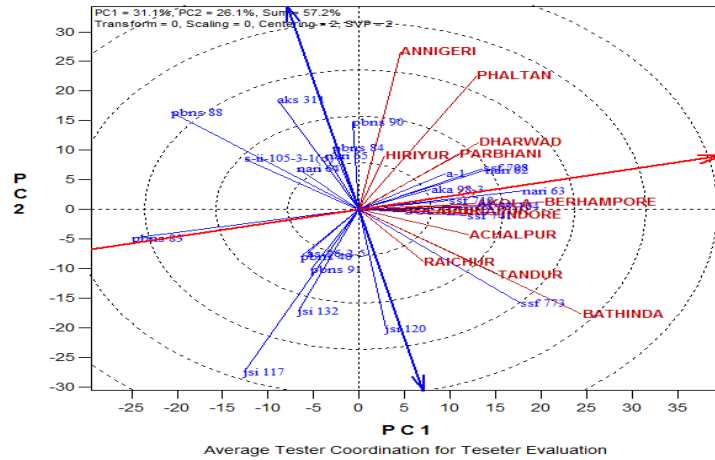


Fig.1: The GGE Biplot Showing the Performance of Each Genotype at Each Location for Seed Yield in Safflower

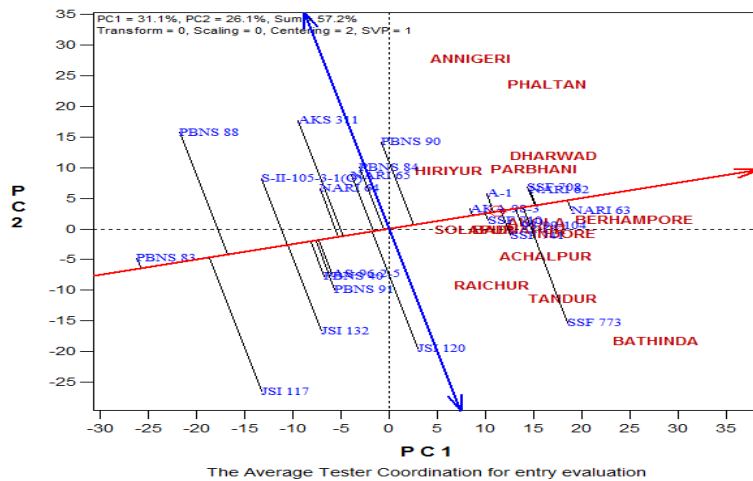
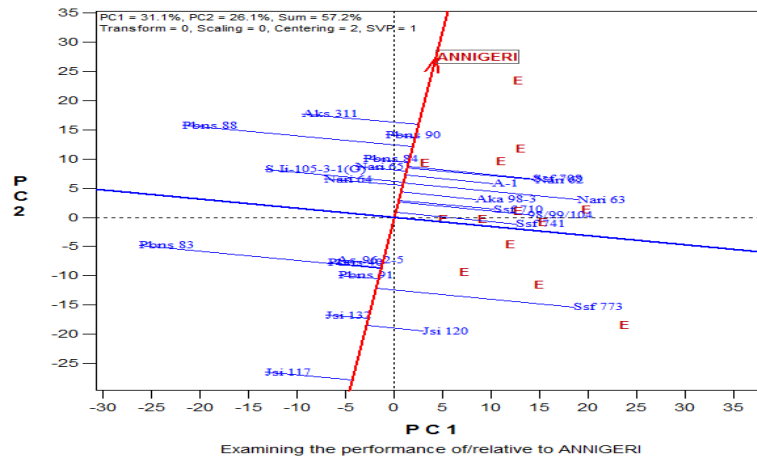
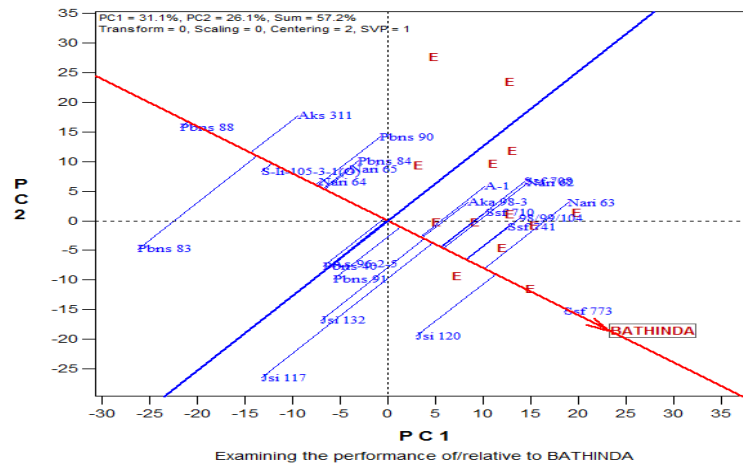


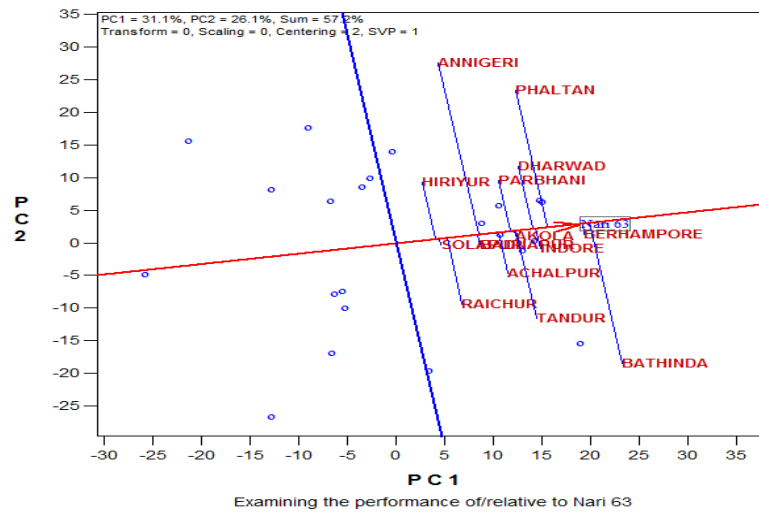
Fig. 2: The Average- Environment Coordination (AEC) View to Show the Mean Performance and Stability of Genotypes Seed Yield Per Hectare



**Fig.3: Ranking of Genotypes Based on Performance of Annigeri Location**



**Fig.4: Ranking of Genotypes Based on Performance of Bathinda Location**



**Fig 5: Performance A1 Genotype at Different Locations**

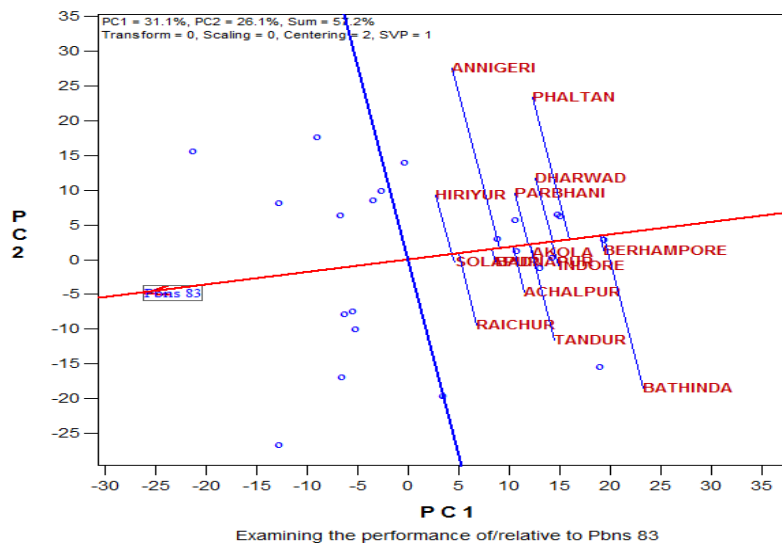




Fig. 6: Performance PBNS 83 Genotype at Different Locations

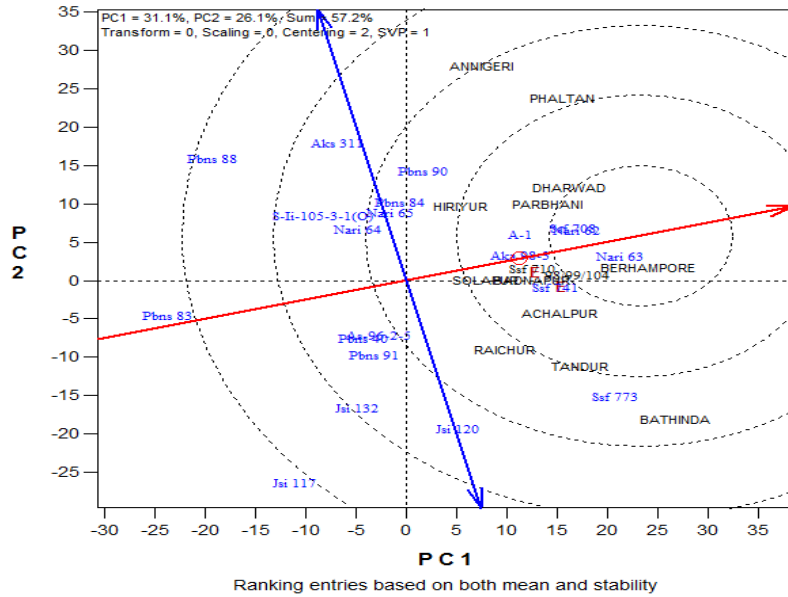


Fig. 7: The Average-Environment Coordination (AEC) View to Rank Genotypes Relative to an Ideal Genotype for Seed Yield per Hectare in Safflower

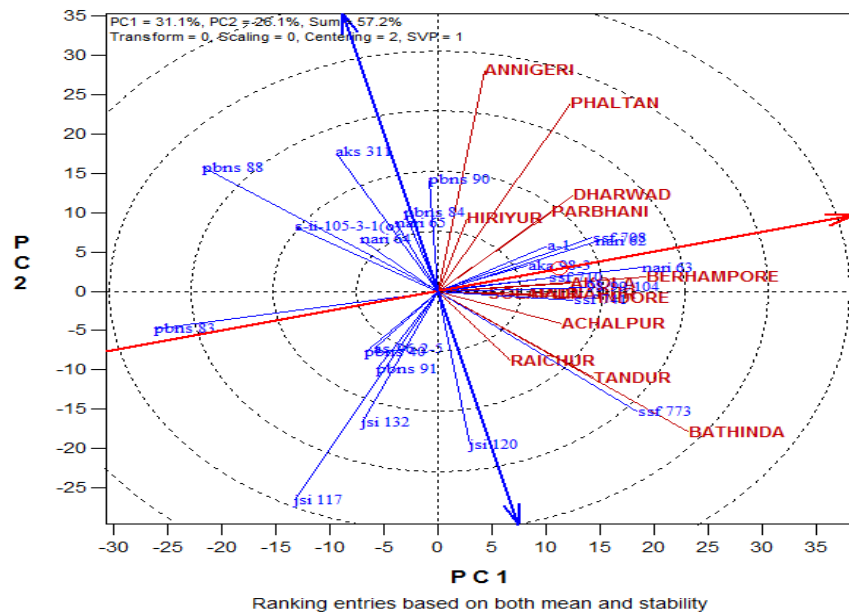


Fig. 8: The Genotypes-Vector View to Show Similarities in Their Performance in Individual Location for Seed Yield per Hectare.

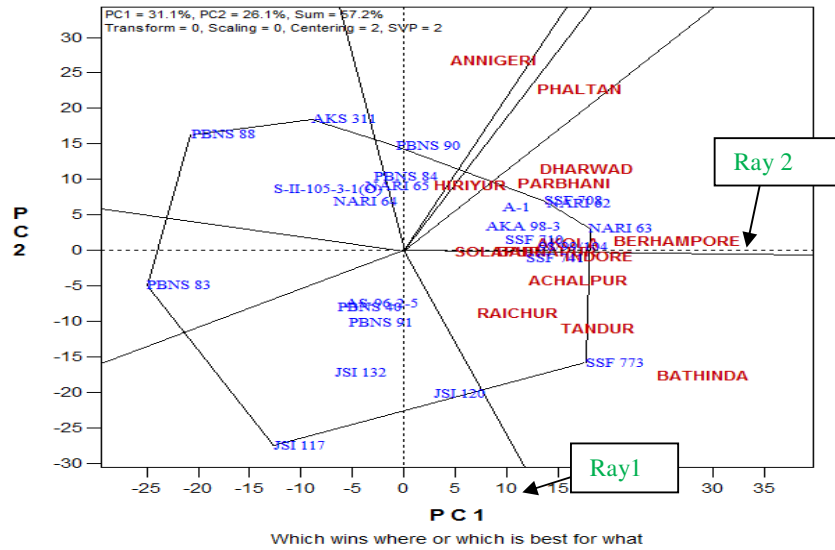


Figure 9: The Which-Won-Where View of the GGE Biplot to Show which Genotypes Performed Best in Which Location for Seed Yield

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 hectare								
	Source	DF	SS	MS	F	P	SS (%)	Heritability (%) (in narrow sense) across environments
Seed yield per hectare	Environment (E)	13	237341750.7	1825706	623.9	0.00001	75.58	6.11
	Rep(E)	28	3593693.62	128346.2	4.4	0.00001		
	Genotype (G)	22	20498395.58	931745.3	31.8	0.00001	6.53	
	GEI	286	56183840.28	196447	6.7	0.00001	17.89	
	Error	616	18026500.64	29263.8				
	Total	965	335644180.9					

**Table 2: Seed Yield Per Hectare (Kg) in Each Environment, Averaged Over Environments and Stability Statistics for Each Cultivar**

Cultivar	Locations (kg/ha)													Stability statistics		
	Akola	Annigeri	Badnapur	Darwad	Indore	Raichur	Solapur	Tandure	Achalpura	Bathinda	Berhampur	Hiriyur	Parbhani		Phaltan	Maen
NARI 65	1009	1812	1047	1017	2711	1025	998	1218.4	2335	1962	1227	980	875	1842	1433	-0.2114
PBNS 90	687	1971	805	1301	2657	1028	827	1283.4	1986	2066.7	1578	1319	1245	1769	1466	0.083
SSF 710	1299	1576	939	1375	3221	1271	1106	1401.5	2281	2256.8	1766	1168	736	1609	1572	0.1955
PBNS 88	757	1670	682	1388	1906	1181	762	961.3	1583	1548	1071	1661	870	1661	1264	0.8992
AS-96-2-5	982	1543	923	1141	2684	1204	921	1401.5	1959	2256.8	1245	1149	1277	671	1383	0.5076
S-II-105-3-1(o)	757	1871	692	1251	2415	1256	1106	1159.4	1557	1866.9	1229	1035	1142	1313	1332	-0.6315
NARI 63	1074	1700	966	1689	2496	1546	1009	1696.6	2201	2732	1922	902	1320	1906	1654	-0.3054
AKS 311	1186	1764	644	1606	2657	827	719	939.3	1959	1512.6	1353	1181	1346	1519	1372	-0.7097
JSI 132	794	1033	870	1120	2174	1279	800	1589.5	2013	2559.6	1304	800	777	1092	1300	-0.0812
SSF 773	1229	1129	1020	1354	3543	1700	955	1755.6	2045	2827.1	1492	1012	1870	945	1634	0.9841
SSF 708	1100	1594	1235	1302	2764	1192	961	1433.5	2415	2308.3	1895	1229	1704	1742	1634	-0.1846
PBNS 83	776	1367	843	347	2469	1149	789	998.3	2040	1607.6	794	916	1206	955	1161	-0.1575
PBNS 91	939	1097	1020	1080	2362	1272	993	1503.5	1906	2421.1	1235	1052	606	1484	1355	-0.3306

Cultivar	Locations (kg/ha)											Stability statistics				
	Akola	Annigeri	Badnapur	Darwad	Indore	Raichur	Solapur	Tandure	Achalpure	Bathinda	Berhampure		Hiriyur	Parbhani	Phaltan	Maen
A1	NARI 64	NARI 62	JSI 117	SSF 741	PBNS 84	JSI 120	AKA 98-3	98/99/104	PBNS 40							
1189	784	1159	765	1406	778	913	1240	1186	977							
1497	1404	1936	582	1714	1997	1027	1239	1530	1059							
853	923	1020	585	1031	789	913	1074	1100	859							
1791	1465	1110	569	1131	1375	1200	1517	1623	1799							
2550	2496	2952	2603	2469	2630	2281	2442	2711	2254							
894	1305	1157	1223	1535	1075	1469	1205	1430	1214							
966	955	848	816	1079	870	988	1090	934	864							
1471.5	1165.4	1680.5	1455.5	1632.6	1358.5	1761.6	1460.5	1541.5	1347.4							
2335	2013	2147	2308	2389	2067	2254	2523	2308	2174							
2369.6	1876.7	2706.2	2343.8	2628.9	2187.5	2836.6	2351.8	2482.3	2169.8							
1804	1208	1516	1286	1640	1100	1530	1310	1809	1299							
1712	1302	1370	850	1575	989	1149	1256	1009	1208							
1260	1136	1325	694	1107	1220	601	1193	1018	752							
1440	1617	1891	805	1530	1644	1137	2009	1696	988							
1581	1404	1630	1206	1633	1434	1433	1565	1598	1355							
0.1089	-0.076	0.2635	-0.0184	0.0578	0.5191	0.1895	-0.3551	-0.1448	-0.3844							

**Table 3: Ranking of Genotypes at Different Locations**

Location	Ranking of genotypes to specific location in descending order of yield potential
Achalpur	SSF 773 > NAR I63 > 98/99/104 > SSF 741 > NARI 62 > SSF 708 > JSI 120 > SSF 710 > A 1 > AKA 98-3 > JSI 132 > PBNS 91 > JSI 117 > AS 96-2-5 > PBNS 40 > PBNS 90 > NARI 65 > PBNS 84 > NAR I64 > S-II-105-3-1(O) > AKS 311 > PBNS 83 and PBNS 88.
Akola	NARI 63 > SSF 773 > NARI 62 > SSF 708 > SSF 741 > 98/99/104 > A 1 > SSF 710 > AKS 93 > JSI 120 > PBNS 90 > PBNS 84 > NARI 65 > AS 96-2 > PBNS 91 > NARI 64 > PBNS 40 > AKS 311 > JSI 132 > S-II-105-3-1-(o) > JSI 117 > PBNS 88 and PBNS 83.
Annigeri	AKS 331 > PBNS 90 > PBNS 88 > PBNS 84 > SSF 708 > NARI 62 > NARI 65 > A 1 > S-II-105-3-1-(O) > NARI 63 > NARI 64 > AKA 98-3 > SSF 710 > 98/99/104 > SSF 741 > AS 96-2-5 > PBNS 40 > PBNS 83 > PBNS 91 > SSF 773 > JSI 132 > JSI 120 and JSI 117.
Badnapur	SSF 773 > NARI 63 > NARI 62 > SSF 708 > 98/99/104 > SSF 741 > SSF 710 > A 1 > AKA 98-3 > JSI 120 > PBNS 90 > PBNS 84 > NARI 65 > AS 96-2-5 > PBNS 91 > PBNS 40 > JSI 312 > NARI 64 > AKA 311 > JSI 117 > S-II-105-3-1-(o) > PBNS 88 and PBNS 83.
Bathinda	SSF 773 > JSI 120 > NARI 63 > 98/99/104 > SSF 741 > SSF 710 > NARI 62 > SSF 708 > JSI 117 > JSI 132 > AKA 98-3 > A 1 > PBNS 91 > AS 96-2-5 > PBNS 40 > NARI 65 > PBNS 84 > PBNS 90 > NARI 64 > S-II-105-3-1-(O) > PBNS 83 > AKA 311 and PBNS 88.
Berhampore	NARI 63 > SSF 773 > NARI 62 > SSF 708 > 99/99/104 > SSF 741 > SSF 710 > A 1 > AKA 98-3 > JSI 120 > PBNS 90 > PBNS 84 > NARI 65 > PBNS 91 > AS 92-2-5 > NARI 64 > PBNS 40 > JSI 132 > AKS 311 > s-II-105-1-(O) > JSI 117 > PBNS 88 and PBNS 83
Dharwad	NARI 63 > SSF 708 > NARI 62 > A 1 > 99/99/104 > PBNS 90 > SSF 741 > SSF 710 > AKA 98-3 > AKS 311 > PBNS 84 > NARI 65 > SSF 773 > NARI 64 > S-II-105-3-1 (O) > PBNS 88 . AS 96-2-5 > PBNS 91 > PBNS 40 > JSI 120 > JSI 132 > PBNS 83 AND JSI 117
Hiriyur	AKS 311 > PBNS 90 > SSF 708 > NARI 62 > PBNS 88 > PBNS 84 > A 1 > NARI 63 > NARI 65 > AKA 98-3 > NARI 64 > S-II-105-3-1(O) > SSF 710 > 98/99/104 > SSF 741 > AS 96-2-5 > PBNS 40 > SSF 773 > PBNS 91 > PBNS 83 > JSI 132 > JSI 120 AND JSI 117
Indore	SSF 773 > NARI 63 > NARI 62 > SSF 708 > 98/99/104 > SSF 741 > SSF 710 > A 1 > AKA 98-2 > JSI 120 > PBNS 90 > PBNS 84 > NARI 65 > AS 96-2-5 > PBNS 91 > PBNS 40 > JSI 132 > NARI 64 > AKS 331 > JSI 117 > S-II-105-3-1(O) > PBNS 88 AND PNBS 83
Parbhani	NARI 63 > SSF 708 > NARI 62 > A 1 > 98/99/104 > PBNS 90 > SSF 710 > SSF 741 > AKA 98-3 > AKS 311 > PBNS 84 > NARI 65 > SSF 773 > NARI 64 > S-II-105-3-1(O) > PBNS 88 > AS 96-2-5 > PBNS 40 > PBNS 91 > JSI 120 > JSI 132 > PBNS 83 AND JSI 117.
Phaltan	SSF 708 > NARI 62 > PBNS 90 > NARI 63 > AKS 311 > A 1 > PBNS 84 > AKA 98-3 > 98/99/104 > SSF 710 > NARI 65 > SSF 741 > PBNS 88 > NARI 64 > S-II-105-3-1(O) > SSF 773 > AS 96-2-5 > PBNS 40 > PBNS 91 > JSI 120 > PBNS 83 > JSI 132 AND JSI 117.
Raichur	SSF 773 > JSI 120 > JSI 117 > JSI 132 > NARI 63 > SSF 741 > 98/99/104 > SSF 710 > PBNS 91 > NARI 62 > SSF 708 > AKA 98-3 > AS 96-2-5 > PBNS 40 > A 1 > NARI 64 > NARI 65. PBNS 84 > PBNS 83 > PBNS 90 .> S-II-105-3-1(O) > AKS 311 AND PBNS 88
Solapur	SSF773 > NARI 63 > 98/99/105 > SSF 741 > NARI 62 > SSF 708 > SSF 710 > A 1 > AKA 98-3 > JSI 120 > PBNS 90 > PBNS 84 > NARI 65 > PBNS 91 > AS 96-2-5 > JSI 132 > PBNS 40 > NARI 64 > AKS 311 > JSI 117 > S-II-105-3-1(O) > PBNS 88 AND PBNS 83
Tandur	SSF733 > JSI 120 > NARI 63 > SSF 741 > 89/99/104 > SSF 710 > NARI 62 > SSF 708 > JSI 117 > JSI 132 > AKA 98-3 > A 1 > PBNS 91 > AS 96-2-5 > PBNS 40 > NARI 65 > PBNS 84 > NARI 64 > PBNS 90 > S-II-105-3-1(O) > PBNS 83 > AKS 311 AND PBNS 88.

