Research Note

GGE Bi-plot analysis in castor (*Riccinus communis* L.) for vidarbha region of Maharashtra state

S. B. Sakhare*, M. B. Nagdeve and D. T. Deshmukh
Department of Agricultural Botany, Dr. Panjabrao Deshmukh Agricultural University, Akola-444 104 (MS)
E-mail : sanjaysakhare@rediffmail.com

Abstract
The present study was undertaken to explore the effect of genotype (G) and genotype × environment interaction (GEI) on yield of 10 castor varieties evaluated during three growing seasons (2010-2013). Yield data were analyzed using GGE biplot method. According to the results of combined analysis of variance, genotype × environment interaction was highly significant at 1% probability level, where G and GEI captured 68% of total variability. The first two principal components (PC1 and PC2) explained 98% of the total GGE variation, with PC1 and PC2 explaining 94.9% and 3.1% respectively. The first mega environment comprised of environments E1 and E3 with the hybrid DCH 519 being the winner; the second mega environment consisted of environment E2 with the hybrid GCH 7 being the winner. Mean performance and stability of genotypes indicated that the hybrid GCH 7 was highly stable with high yield.

Castor (*Ricinus communis* Linn.) is an important oilseed crop and is widely grown in tropical, sub-tropical and temperate parts of the world. Castor seed contains 42 to 58 per cent oil. Castor oil and its derivatives have wide range of uses in the manufacture of lubricants, plastics, adhesives, waxes, polishes, coating applications, inks, paints, varnishes, cosmetics, perfumes, flavours, fragrances, textile dyes and medicinal uses. India is the world leader in castor seed as well as oil production and dominates the international castor oil trade.

The *Vidarbha* region of Maharashtra state is mostly rainfed and the castor crop may find a suitable place in a predominantly mono-cropping system of soybean and cotton which will help in diversification of the prevailing system. Therefore, it is necessary to identify potential stable varieties of castor suitable for the region.

GE interaction is a major problem in the stability of varieties because it reduces the association between genotypic and phenotypic values as well as complicates the process of selecting genotypes with superior performance (Delacy *et al.,* 1996; Yan, 2002). Therefore, the first goal of plant breeders in a crop breeding program is the development and identification of genotypes which are stable or adapted to a wide range of diversified environments (Farshadfar, 2011). The exact prediction of weather for the ensuing season is still not possible and there is wide variability from season to season and hence the performance of genotypes changes because of GE

interaction. Therefore, the assessment of GE interaction is necessary.

Numerous methods have been developed to reveal patterns of GE interaction such as joint regression (Finlay and Wilkinson, 1963; Eberhart and Russel, 1966; Perkins and Jinks, 1968), additive main effects and multiplicative interaction (AMMI) (Gauch, 1992) and type B genetic correlation (Burdon, 1977; Yamada, 1962). Yan *et al*., (2000) proposed another methodology known as GGE-biplot for graphical display of GE interaction pattern of multi environment trial data with many advantages. In total phenotypic variation, E explains most of the variation whereas G and GE are usually small (Yan, 2002). However, only G and GE interaction are relevant to genotype evaluation particularly when GE interaction is identified as repeatable (Hammer *et al.,* 1996). Hence, Yan *et al*., (2000) deliberately put the two together and referred to the mixture as GGE. GGE biplot analysis is an effective method which is based on principal component analysis (PCA) to fully explore METs. Therefore, the present study was carried out with the objectives of assessment of effect of genotype (G) and genotype × environment interaction (GEI) on yield and identification of potential stable variety over years.

The experimental material comprising of 10 varieties/hybrids of castor (Table 1) were evaluated in complete randomized block design

using three replications at AICRP for Dryland Agriculture, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (M.S.) during *kharif* seasons of 2011-12 (E1), 2012-13 (E2) and 2013-14 (E3). The yield data were subjected to combined analysis of variance. The data were graphically analyzed for interpreting GE interaction using GGE biplot software (Yan, 2001). GGE biplot methodology, composed of two concepts, the biplot concept (Gabriel, 1971) and the GGE concept (Yan *et al.,* 2000), was used to visually analyze the MET data. This methodology uses a biplot to show the factors (G and GE) that are important in genotype evaluation and that are also the sources of variation in GE interaction analysis of MET data (Yan, 2001). The graphs were generated based on (i) "which-won-where" pattern and (ii) ranking of genotypes on the basis of yield and stability.

The results of combined ANOVA for yield data indicated that the differences among all sources of variation were highly significant (Table 2). The results revealed that there was a differential yield performance among ten varieties/hybrids across testing environments due to the presence of GxE interaction. The presence of GxE interaction complicates the selection process as GxE interaction reduces the usefulness of genotypes by confounding their yield performance through minimizing the association between genotypic and phenotypic values (Comstock and Moll, 1963).

A GGE biplot is a data visualisation tool, which graphically displays a G×E interaction in a two-way table (Yan *et al*. 2000). The polygon view of a biplot is the best way to visualize the interaction pattern between genotypes and environments (Yan and Kang, 2003); to show the presence or absence of crossover GxE interaction which is helpful in estimating the possible existence of different mega environments. Visualization of the "which won where" pattern of MET data is necessary for studying the possible existence of different mega environments in the target environment. Fig. 1 represents a polygon view of ten varieties/hybrids MET data obtained from this investigation. In this biplot, a polygon was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes were placed within the polygon. The partitioning of GE interaction through GGE biplot analysis showed that PC1 and PC2 accounted for 94.9% and 3.1% of GGE sum of squares, respectively, explaining a total of 98% variation. The vertex genotypes in this study were DCH519, GCH 7, Aruna, 48-1, AKC 1, DCH 177 and DCS 9. These genotypes were the best or the poorest genotypes in some or all of the environments because they were farthest from the origin of the

biplot. From the polygon view of biplot analysis of MET data in three years, the genotypes fell in five sections and the test environments fell in two sections. The first section contained the test seasons 2010-11 (E1) and 2011-12 (E2) which had the genotype DCH 519 as the winner; the second section comprised of the season 2012-13 (E3) with GCH 7 as the best yielder. The vertex genotypes Aruna, 48-1, AKC 1, DCH 177 and DCS 9 were not the top-yielding genotypes in any seasons.

The ranking of ten varieties/hybrids of castor based on their mean yield and stability performance is shown in Fig. 2. The line passing through the biplot origin is called the average tester coordinate (ATC), which is defined by the average PC1 and PC2 scores of all environments. Genotypes more close to concentric circle represented higher mean yield. The line which passes through the origin and is perpendicular to the ATC with double arrows represents the stability of genotypes. Either direction away from the biplot origin on this axis indicates greater GE interaction and reduced stability. For selection, the ideal genotypes are those with both high mean yield and high stability. In the biplot, they are close to the origin and have the shortest vector from the ATC. The hybrid, GCH 7 can be considered as stable genotype with high yield. The other genotypes on the right side of the line with double arrows have yield performance greater than mean yield and the genotypes on the left side of this line had yield less than mean yield. Another hybrid with higher yielding performance but low stability was DCH 519, whereas the genotypes with low yield and low stability were Aruna, DCS 9, DCH 177, AKC 1 and 48-1.

From the present study, it can be concluded that genotype × environment interactions were highly significant. The first two principal components (PC1 and PC2) explained 98% of the total GGE variation, with PC1 and PC2 explaining 94.9 and 3.1, respectively. The first mega environment contains seasons 2010-11 and 2011-12 (E1 and E2) with the hybrid DCH 519 being the winner; the second mega environment contains season 2012-13 (E3) with the hybrid GCH 7 being the winner. Mean performance and stability of genotypes indicated that the hybrid GCH 7 was highly stable with high yield.

References

Gauch H.G. 1992. Statistical analysis of regional yield trials: AMMI analysis of factorial designs. Elsevier, Amsterdam, Netherlans Golestani

Burdon R.D. 1977. Genetic correlation as a concept for studying genotype-environment interaction in forest tree breeding. *Silvae Genet*. **26**: 168–175.

Comstock R.E. and Moll R.H.1963. Genotype x Environment Interactions. Symposium on Statistical Genetics and Plant Breeding. National Academy Science National Research Council, Washington, D.C., pp: 164-196

Delacy I.H., Basford K.E., Cooper M. and Bull J.K. 1996. Analysis of multi-environment trials an historical perspective. Plant Adaptation and Crop Improvement. Eds. M. Cooper and G. L. Hammer. CAB international, UK

Eberhart S.A. and Russell W.A. 1966. Stability parameters for comparing varieties. *Crop Sc*i. **6**: 36–40.

Farshadfar E. 2011. Chromosomal localization of the genes controlling adaptation in Agropyron elongatum using a new AMMI–based simultaneous selection index of yield and yield stability. *Int J Plant Breed*. **5**(2): 80–83.

Finlay K.W. and Wilkinson G.N. 1963. The analysis of adaptation in a plant breeding programme. *Aust J Agric Res*. **14**: 742-754.

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

Hammer G.L. and Cooper M.1996. Plant adaptation and crop improvement. CAB International, Wallingford, UK, pp 636.

Perkins J.M. and Jinks J.L. 1968. Environmental and genotype-environmental interactions and physical measures of the environment. *Heredity*.**25**: 29–40.

Yamada Y. 1962. Genotype × environment interaction and genetic correlation of the same trait under different environments. *Jap J Genet*. **37**: 498-509. Yan

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 partitioning in biplot analysis of multi-environment trial data. *Agron J.* **94**: 990-9

Yan W. and Kang M.S. 2003. GGE Biplot Analysis: A Graphical Tool for Breeders, geneticists and Agronomists. 1st Edn., CRC Press LLC., Boca Roton, Florida, pp: 271

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.

Table 1. List of varieties/ hybrids of castor

Sr. No.	Name	Sr. No.	Name
1	AKC-1	6	GCH-4
2	DCS-9	7	GCH-5
3	48-1	8	GCH-6
4	DCH-177	9	ARUNA
5	DCH-519	10	GCH -7

Table 2. Combined analysis of variance for yield across three environments.

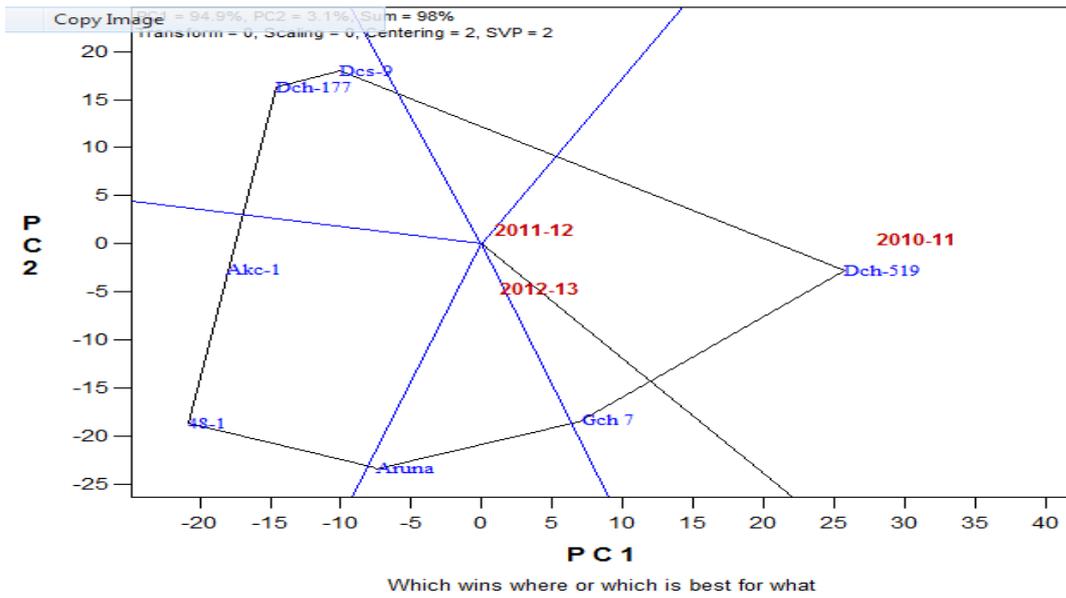| Source	Degrees of freedom	Mean sum of squares
Varieties (G)	9	302664.24**
Environment (E)	2	1549897.00**
GE interaction	18	299199.09**
Error	60	44023.27

771

Fig. 1 Polygon view of genotype- environment interaction for ten varieties/hybrids over three test environments.
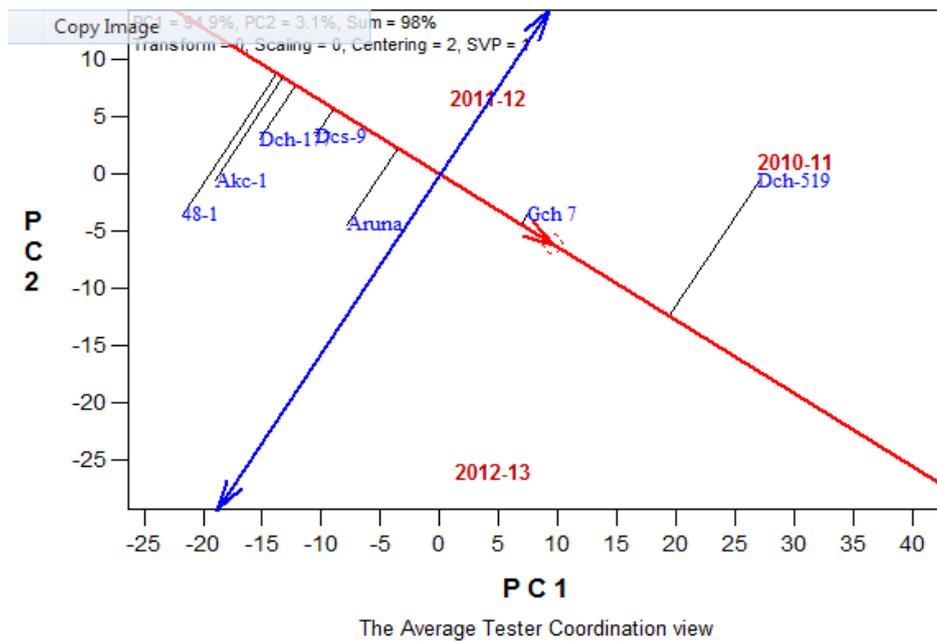

Fig. 2.GGE biplot showing the ranking of genotypes for both yield and stability   performance over environments.