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Comparison of tikhur genotype by using GGE BI plot

Vishakha Tiwari, Deo Shankar and DP Singh

Abstract

Tikhur (*Curcuma angustifolia*) is one of the herbs mentioned in ancient scriptures of Ayurveda. It is economically and medicinally important product of India as well as Chhattisgarh. The edible rhizome rich in the starch content is processed to obtain tikhur flour. Tikhur production in Chhattisgarh is fairly high. The experiment carried out in Randomized Block Design on Tikhur genotype in Chhattisgarh state of Bastar district during 2015-16 crop years. The objective of the study is to find which genotype the highest yield and most desirable genotype of Tikhur crop in Bastar region. The GGE bi plot graphically displays G plus GE of a MET in a way that facilitates visual cultivar evaluation and mega-environment identification. This technique can serve as a useful tool for recommendation of Tikhur genotype for specific growing region taking into account the specification of genotype and growing conditions. GGE bi-plot analysis depicted the adaptation pattern of genotypes at varied environments and discrimination ability of environments. The IGDMT-10-1(G5) most stable genotype and E5 most suitable environment all the genotype.

Keywords: Tikhur genotype, GGE BI plot

Introduction

Tikhur is a rhizomatous herb is also known as white turmeric or East Indian arrowroot or Bombay arrowroot. It is economically and medicinally important product of India as well as Chhattisgarh. The edible rhizome rich in the starch content is processed to obtain tikhur flour. Tikhur production in Chhattisgarh is fairly high. Tikhur is cultivated as medicinal crop in many parts of the state under moist deciduous mixed and Sal forest of Chhattisgarh, Madhya Pradesh and Jharkhand. Tikhur is also found in central province, Bihar, Maharashtra and Southern part of India. In Madhya Pradesh, it is widely distributed in Balaghat, Chhindwara and Mandla districts In Chhattisgarh, it is found abundantly in the hilly tracts and forests of Bastar, Dantewada, Bijapur, Narayanpur, Kanker, Rajnandgaon, Kawardha, Dhamtari, Bilaspur, Raipur, Korba, Korea and Sarguja districts Experimental trials are usually carried out in different environments with an aim to evaluate yield stability of different crops under varying environmental conditions (Yan *et al.* 2000). Main environmental effects (E) and genotype environment interaction (GE) have been reported as the most important sources of variation for the measured yield of crops (Dehghani *et al.* 2006)^[1]. Although the measured yield is a combined result of the effects of the genotype (G), E and GE interaction, only G and GE are relevant to cultivar evaluation. There are a number of statistical methods for evaluation of hybrid's performance and their genotypic interactions with the environment. They differ in the parameters used in the assessment, the bio metric procedures employed, and the analysis proposed methodology is known as GGE bi plot for graphical display of GE interaction pattern. It allows visual examination of the relationships among the test environments, genotypes and the GE interactions. It is an effective tool for: (i) mega-environment analysis (e.g. "which won- where" pattern), where specific genotypes can be recommended to specific mega-environments), (ii) genotype evaluation (the mean performance and stability), and (iii) environmental evaluation (the power to discriminate among genotypes in target environments) Different researchers used GGE bi plot for the analysis of GE interactions and evaluation of maize genotypes. The study aims was to i) investigate the stability of grain yield in Tikhur hybrid in the GGE bi plot, ii) graphically summarize the effects of G and GE interaction and to identify, "which won where" iii) To recommend Tikhur hybrids for the specific growing region taking into account the specification of hybrids and growing condition.

Material and Methods

Six genotype collected from five sampling sites of Chhattisgarh were analyzed Tikhur (*Curcuma angustifolia*) genotype for GGE Bi plot model analysis, graphical representation of

data. This study was carried out to determine the yield performances of Tikhur genotypes. Among six genotype of tikhur selected were in five environments for the year 2015-2016. Yield data was collected according to the practices of the respective farmer at each site. Tikhur were collected from five sites as mentioned namely Jagdalpur (E1), Kanker (E2), Dantewada (E3), Bijapur (E4) and Narayanpur (E5).

Statistical Analysis

GGE bi plot was used to generate graphs which are showing (i) “which-won where” pattern, (ii) ranking of hybrids Based on yield and stability, (iii) environment vectors, and (iv) Comparison of environment to ideal environment (Yan and Kang, 2003). The GGE bi plot represents the first two principal components (PC1 and PC2, referred as primary and secondary effects, respectively) derived from subjecting environment centered yield data (yield variation due to GGE), to singular value decomposition (Yan *et al.* 2000).

Result and Discussion

Best Hybrid in each Environment

GGE bi plot method can be used to identify superior maize genotypes for target sites (Dehghani *et al.* 2009) [2]. The bi

plot (Figure 1) represents a polygon, where some hybrids are positioned on the vertexes, while the rest are inside the polygon. As the hybrids positioned on the vertexes have the longest distance from the bi plot origin, they are supposed to be the most responsive. Responsive hybrids are either best or the poorest at one or every environment (Yan and Rajcan, 2002) [6]. The bi plot (Figure 1) represents a polygon, where some hybrids are positioned on the vertexes, while the rest are inside the polygon. As the genotype positioned on the vertexes have the longest distance from the bi plot origin, they are supposed to be the most responsive. Considering this, the genotype IGBT-10-4(G4), and IGDMT-10-1(G5) had the highest seed yield. The three environments were positioned in the same sector on the graph, which indicates that those environments did not differ significantly between themselves. Genotype IGBT-10-4(G4) and IGDMT-10-1(G5) were the highest yielding in E2, IGBLT-10-1(G3) and IGSJT-10-2(G2) in E1 E3 and E4. None of the environments fell in the sectors with IGSJT-10-1(G1) and IGSJT-10-3(G6), indicating that these genotypes are not suitable for growing at this specific location.

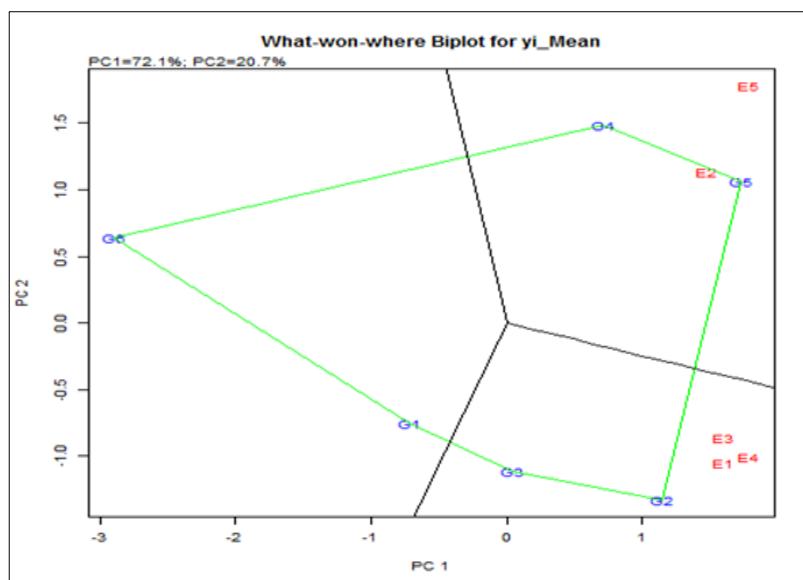


Fig 1: A genotype + genotype × environment interaction bi-plot showing hybrids performance in each environment

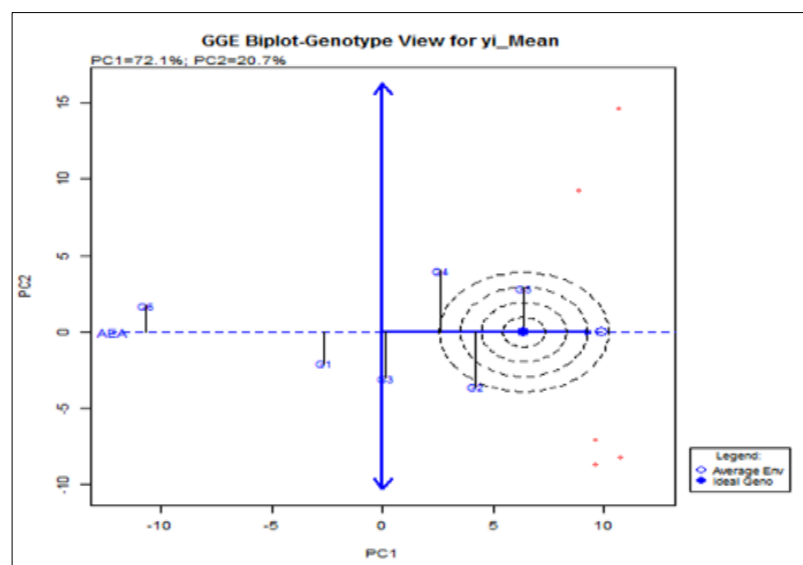


Fig 2: Average tester coordination (ATC) view of the GGE bi plot.

Yan *et al.* (2000) stated that ideal genotypes could be considered those that have a large PC1 score (high yielding ability) and small or absolute PC2 score (high stability). Similarly, the ideal test environment should have a large PC1 score which means that it is more discriminating of the genotypes concerning the genotypic main effect and small or absolute PC2 score (more representative of the overall environment). According to Yan and Kang (2003), an ideal genotype could be defined as one which is the highest yielding across test environments and is absolutely stable in its performance. The average grain yield of the genotype vs. their stability is presented in (Figure 2). The performance line

(average tester coordination, ATC) passes through the bi plot origin with an arrow indicating the circle for the “ideal” genotype. The genotypes positioned the closest to the circle are the highest yielding, those on the upper side of the line are stable, and those in the lower part of the bi plot are not stable. Considering this, the IGDMT-10-1(G5) has the highest average grain yield (as having the highest projection on the performance line, followed by IGSJT-10-2(G2) and IGBT-10-4(G4) (which are located very close to the genotype IGDMT-10-1(G5). The genotype IGSJT-10-3(G6) had the lowest seed yield.

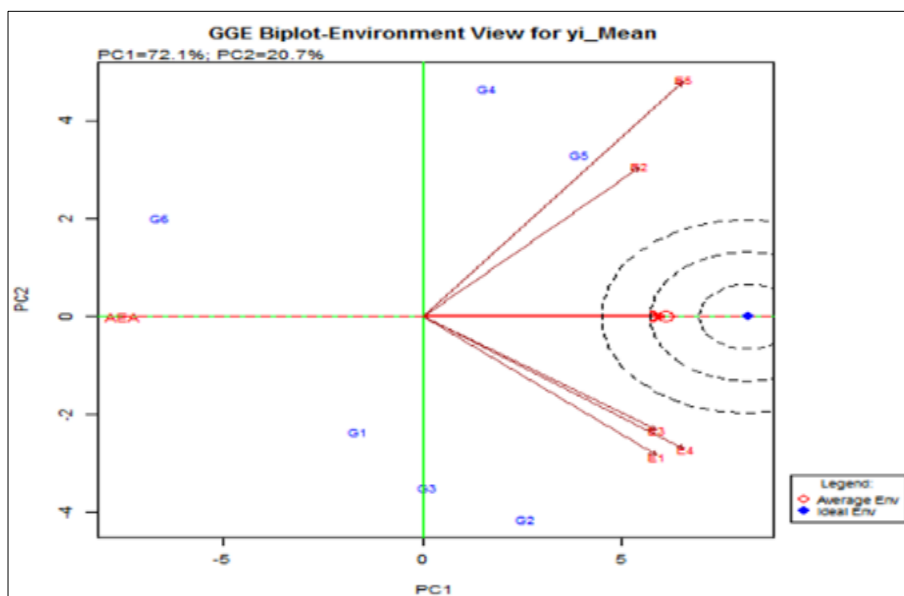


Fig 3: Comparison of hybrids with the ideal hybrid

In figure three the center of the concentric circles is where an ideal genotype should be; its projection on the ATC X-axis was designed to be equal to the longest vector of all genotype, and its projection on the ATC Y-axis was obviously zero, indicating that it is absolutely stable. Therefore, the smaller the distance from a genotype such that the genotype is most

ideal. Thus, genotype IGDMT-10-1(G5) was the closest to the concentric center Genotype IGSJT-10-3(G6) did not seem to be meaningfully different from genotype IGBLT-10-1(G3), while the IGSJT-10-2(G2) was the least stable across the environments.

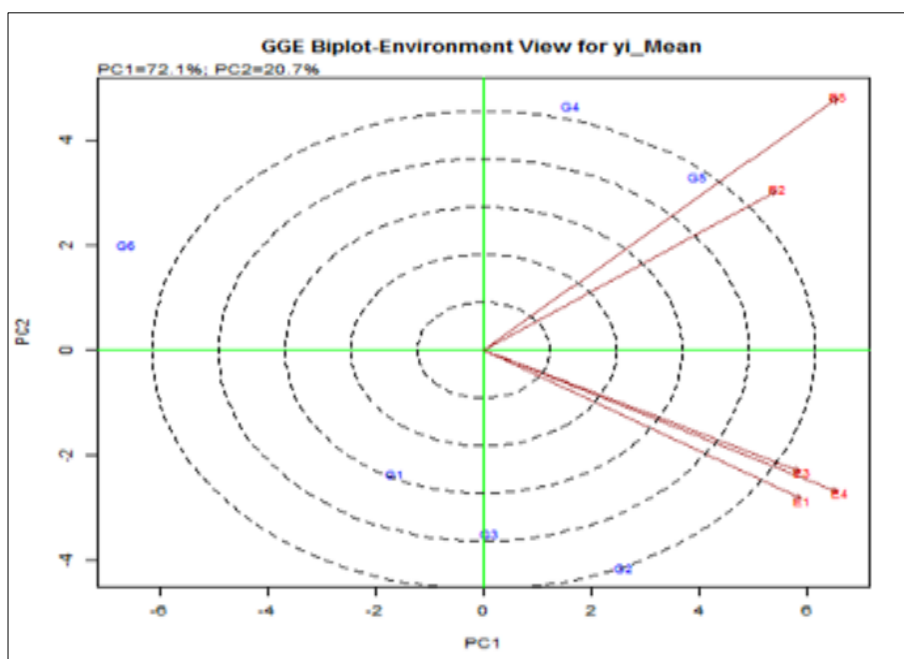


Fig 4: Comparison of environments with an ideal environment

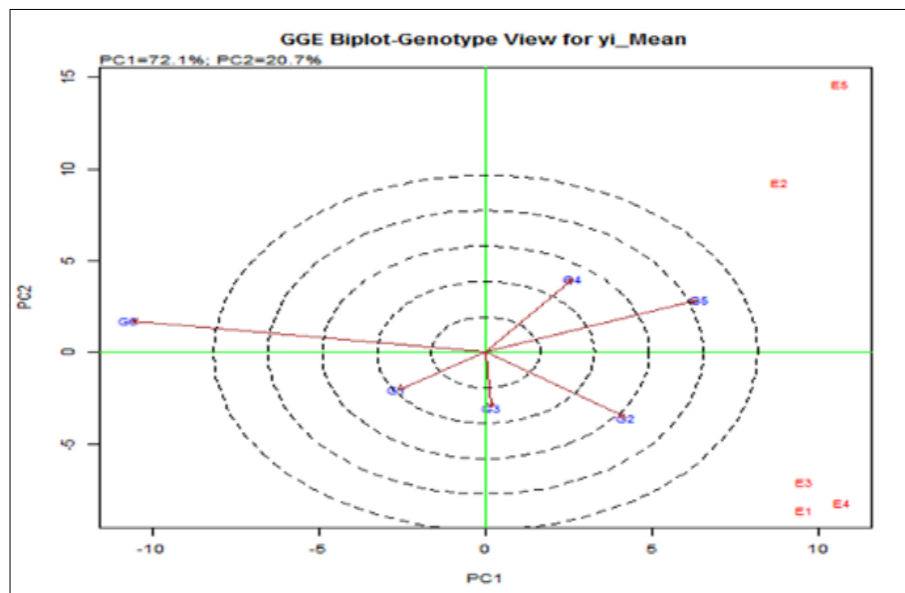


Fig 5: A genotype + genotype \times environment interaction biplot showing relationships among six environments

Environment Ranking Based on both Discriminating Ability and Representativeness

Discriminating ability and representatives of the environments is presented in Figure 4. An ideal environment is the one that is most discriminating for genotypes (the longest distance between the markers of the environment to the plot origin, is a measure of its discriminating ability) and is representative (the shortest projection from the marker of location onto the ATC Y-axis is the measurement of its representative-Considering this, E3 was the most discriminating as well as most representative, as it is far away from the plot origin and had the shortest projection onto ATC Y-axis, respectively. The other environments where irrigation was applied (E1 and E5) were positioned close to E3, which indicates that stable production of maize in this region is possible only with irrigation. On the other hand, the environments where irrigation was not applied didn't have the discriminating ability (were not far away from the origin) and were not representative, as they had large projection onto the ATCY-axis (Figure 4). Relation among environment Relationship among the tested environments is indicated in Figure 5. Both E5 and E4 had the longer vectors, thus they were the best for genetic differentiation of genotype. E3 was the least representative environment in this study. The smallest angles between the vectors of E3 and E4 indicated that they had a strong relationship. Finally, the IGDMT-10-1(G5) most stable genotype and E5 most suitable environment all the genotype.

Reference

1. Dehghani *et al.* BI plot analysis of genotype by environment interaction for barley yield in Iran. *Agron. J.* 2006; 98:388-393.
2. Dehghani *et al.* Interpretation of Genotype-by-Environment Interaction for Late Maize Hybrids' Grain Yield Using a Bi plot Method. *Turkish Journal of Agriculture and Forestry.* 2009; 33:139-148.
3. Ding *et al.* Application of GGE bi plot analysis to evaluate Genotype (G), Environment (E) and G \times E interaction on *P. radiata*: a case study. *Australasian Forest Genetics Conference Breeding for Wood Quality*, 11-14 April 2007, Hobart, Tasmania, Australia, 2007.
4. Ilker *et al.* Assessment of genotype \times environment interactions for grain yield in maize hybrids using AMMI

and GGE bi plot analyses. *Turkish Ja of Field Crops.* 2009; 14(2):123-135.

5. Mitrovic *et al.* Evaluation of experimental maize hybrids tested in multi-location trials using AMMI and GGE bi plot analyses. *Turkish Journal of Field Crops.* 2012; 17(1):35-40.
6. Yan W, Rajcan I. Biplot analysis of test sites and trait relations of soybean in Ontario. *Crop Sci.* 2002; 42:11-20.
7. Yan W. GGE bi plot- A windows application for graphical analysis of multi environment trial data and other types of two way data. *Agron. J.* 2001; 93:1111-1118.
8. Yan *et al.* GGE bi plot vs. AMMI analysis of genotype-by-environment data. *Crop Sci.* 2007; 47:643-655.