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GGE BIPLLOT ANALYSIS FOR YIELD PERFORMANCE OF GRAIN AMARANTH GENOTYPES ACROSS DIFFERENT ENVIRONMENTS IN WESTERN INDIA

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ABSTRACT

Stable performance of grain amaranths genotypes at specific environment is critical for obtaining high and consistent yield. This study was conducted to assess grain yield stability of thirteen genotypes in varied environments in three successive growing seasons and effects of genotype (G) and genotype×environment (GE) interaction were illustrate graphically based on “what-won-where” to advocate genotypes for a specific environment, using GGE biplot. Result of study revealed that GGE biplot was effective to recognize stable and highest yield (1648.92 kg/ha) genotype as G₅ followed by G₆ (1457.24 kg/ha) and G₃ (1268.62 kg/ha) genotypes while the genotype G₇ had the lowest grain yield and was the least stable across varying environments. This study could be aid tool for endorsement of amaranths genotypes for specific environment, taking into elucidation the peculiarities of genotypes and growing stipulation.

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1 Introduction

Grain amaranth belong to the genus *Amaranthus* is one of the astounding underutilized pseudocereal with rich nutritional diet profile and seldom utilized as used as food grain, leafy vegetables, forage and ornamentals for long. It includes approximately 60 species (Sauer, 1967), of them five major species considered for grain production of grain type Amaranth viz., *A. hypochondriacus* L. (2n=32), *A. cruentus* (2n=34), *A. caudatus* L. (2n=32 and occasionally 2n=34 also), *A. adulis* Spegazzini (2n=32) and *A. tricolor* (2n=34) (Patel et al., 2014). Grain amaranths is rich in "Protein complements" with higher lysine content than other cereal grains which offers remarkable opportunity to exploit grain amaranth (Bressani, 1989). It has been well reported that amaranth leaves are excellent sources of protein, with its maximum accumulation in the blossoming phase (Kadoshnikov et al., 2005). Therefore, it is a good diet supplement to pulses for sulphur rich amino acid. Crop is widely spread over Asia with astounding genetic and morphological diversity and nutritional pool, nevertheless crop breeding program have given little attention over genetic improvement of this "alternative crop".

The aptness to develop prominent high yielder and stable genotypes over wide environment is an unambiguous motto in pragmatic plant breeding programme (Boshev et al., 2014). Assorted environments can diminish the steadiness of plant varieties (Hebert et al., 1995). Genotype $\times$ environment interaction (GE) have shown there supremacy for delineating stability of genotypes and have partitioned variation that better aid for selection of consistent stable genotypes in many different studies (Dehghani et al., 2006; Yan et al., 2007; Sabaghnia & Sabaghpour, 2008). There are several methods for stability analysis among which GGE biplot analysis was used in the present study to deduce stability of the crop with aim to investigate the stability of seed yield in amaranths and graphically summarize and considerate the assets of G and GE interaction (Yan & Kang, 2003; Samonte et al., 2005; Dehghani et al., 2009; Balestre et al., 2009; Oliveira et al., 2010; Tonk et al., 2011).

Present study was undertaken for the first time to gather information about GE interaction of different amaranth genotypes for high seed yield using three year data using GGE biplot analysis.

2 Materials And Methods

2.1 Experimental site and materials

The experiment was carried out at the Crop Improvement Research Station (24°12' N, 72°12' E and 154.5 m), Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat, India. Thirteen genotypes viz., Annpurna, Durga, BGA-2, GA-1, GA-2, GA-3, PRA-1, PRA-2, PRA-3, RMA-4, RMA-7, Suvarna and VL-344 from diverse backgrounds were sown in randomized block design (RBD) design with three replications in six rows of 4 meter length with 45 $\times$ 15 cm spacing for each genotype. All the genotypes were grown during the *Rabi* season in 2012-13, 2013-14

and 2014-15 to access their stability for grain yield across variable environments. The size of unit plot was 4.0 $\times$ 1.8 msq. Plots were thinned duly ensuring a single plant per hill. Two rows of each plot were harvested at maturity, siliques were shelled, dried out and grain yield was measured in each plot.

2.2 Statistical analysis

Statistical computations and estimations were carried out using INDOSTAT software. Analysis of variance was carried out to partition the variation due to genotypes, environment and GE interaction. Stability analysis of data was carried out by employing Eberhart & Russell model (1966). The untransformed data of each genotype from field trials were subjected to G $\times$ E biplot analysis for deduction of GE interaction using PBTools software version 1.4 (PBTools, 2014). The GGE biplot is a multi-faceted most comprehensive tool and produce lucrative informative graphs depicting (i) "what-won-where" pattern, (ii) ranking of amaranth genotypes with respect to yield and stability, (iii) environment vectors, and (iv) assessment of environment to ideal environment (Yan & Kang, 2003). The GGE biplot study execute by using singular value decomposition (SVD) model that presents the first two principal components (PC1 and PC2, referred as primary and secondary effects, respectively) resulting from environment centered yield data (yield discrepancy due to GGE) based on symmetric scaling $f=0.5$ (Yan et al., 2000). Each environment is characterized by its vector (the line that connects it with the origin of the biplot), the length of the vector was used to determine the discriminating ability of each of the test environments, with a shorter vector implying that the environment was not well represented by PC1 and PC2 (Yan et al., 2007). The angle between environments vectors were used to judge correlations (similarities/dissimilarities) between pairs of environments (Yan & Kang, 2002).

3 Results and Discussion

Development of a stable variety is one of the major goals for all breeding programme because phenotypically stable genotypes are usually required for commercial production of crop plants. Hence, to find out stable genotypes for different characters, stability analysis was employed as suggested by Eberhart & Russell (1966) was employed. Accordingly, three kinds of linear responses (b_i) viz., $b_i < 1$, $b_i = 1$ and $b_i > 1$ have been considered in which $b_i = 1$ is average stability and widely adaptable to different environments; $b_i > 1$ is below average stability, increasing sensitivity to environmental changes and well adapted to favourable environment and $b_i < 1$, above average stability, greater tolerance to environmental changes; thereby genotypes would have the specific adaptability to poor yielding environment.

Based on ANOVA it was concluded that all the thirteen amaranth genotypes significantly differed from each other indicating the presence of substantial variation among them (Table 1). Further, the performance of all the genotypes varied under all the environments and it is depicted in figure 1. Based on mean yield data, each genotype was ranked which is given in table 2.

Figure 1 Yield performance of different amaranth genotypes across three environments

The set of thirteen genotypes was evaluated under three environments. The data of analysis of variance for different characters are presented in table 1. The $G \times E$ interaction was found significant for all the characters except for inflorescence length, which revealed that genotypes interacted differently with environmental variations for days to flowering, days to maturity, plant height, test weight, inflorescence length, plant stand at harvesting, fodder yield and grain yield characters. The variances due to $G \times E$ were further partitioned into components, (i) $G \times E$ (linear) and (ii) $G \times E$ (non-linear) *i.e.*, pooled deviation. Pooled deviation, the non-linear component of $G \times E$ interaction was observed significant for the traits, days to flowering, days to maturity, plant height, test weight, inflorescence length and grain yield, whereas plant stand at harvesting and fodder yield were

Table 1 Analysis of variance (mean squares) for stability pertaining to various characters in amaranth genotypes

Characters									
Source of variation	Degree of Freedom	Days to flowering	Days to maturity	Plant height	Test Weight (10ml/g)	Inflorescence Length (cm)	Plant stand at harvesting	Fodder yield (kg/plot)	Grain yield (kg/plot)
Genotypes (G)	12	432.66**	238.22**	3,756.04**	0.01	418.64**	143.90	3,770,923**	165,246**
Environments (E)	2	555.52**	248.23**	6,239.14**	0.39**	2101.35**	4177.14**	229,989,508**	3,152,549**
G x E	24	8.66*	7.20*	122.72**	0.01*	81.03	123.15**	1,335,427**	334,988**
Environment (Linear)	1	1111.05**	496.45**	12,478.29**	0.77	4202.69**	8354.28**	459,979,017**	6,305,098**
G x E (Linear)	12	15.81**	11.23**	154.31	0.01**	145.60**	245.20**	2,348,038**	34,541*
Pooled deviation	13	1.40**	2.92*	84.12**	0.01**	15.20**	1.01	297,984	30,863*
Pooled error	72	1.32	1.08	11.42	0.01	6.89	160.66	686,233	48,935

*, ** Significance at 5 and 1 per cent probability levels, respectively

Table 2 Mean grain yield (Kg/ha) of thirteen amaranth genotypes across three environments at E₁, E₂ and E₃ their average seed yield

Name of genotype	Genotype code	E1	E2	E3	Average grain yield (Kg/ha)	Rank
Annpurna	G1	658.40	902.72	1212.04	924.39	12
Durga	G2	1078.13	1120.30	2148.77	1449.07	3
BGA-2	G3	710.25	1023.08	2072.53	1268.62	5
GA-1	G4	1382.64	944.38	1736.73	1354.58	4
GA-2	G5	1351.78	1347.14	2247.84	1648.92	1
GA-3	G6	1189.24	1182.79	1999.69	1457.24	2
PRA-1	G7	754.28	490.71	1390.43	878.47	13
PRA-2	G8	588.45	773.10	1477.78	946.44	11
PRA-3	G9	711.90	892.54	1507.72	1037.39	10
RMA-4	G10	684.32	923.55	1549.69	1052.52	9
RMA-7	G11	537.83	1138.82	1918.83	1198.49	7
Suvarna	G12	563.34	969.85	1758.95	1097.38	8
VL-344	G13	771.56	1064.75	1836.11	1224.14	6

unpredictable due to non significant of pooled deviation as well as lower magnitude than linear component. The non-linear effect must be significant and of lower magnitude than linear component to predict the performance of genotype and its stability. This reflected greater importance of linear portion in building up total $G \times E$ and the possibility of prediction across the environments for these characters. The seasonal variation in these characters may be due to micro-environmental conditions i.e., differences in climatic or soil factors among environments, during the grain filling stage. The variation in meteorological parameters viz., temperature ($^{\circ}\text{C}$) and relative humidity (%) are represented in figure 2. The genotypes $\times$ environment interaction was highly significant for mean grain yield, which revealed that genotypes interacted differently with environmental variations in character.

On analyzing SVD based GGE biplot analysis, the GGE biplot revealed that component PC1=73.6% and PC2=21.5% explaining total 85 percent of environmental centred variation of mean grain yield. The observed high magnitude of $G \times E$ (linear) component could lead to the identification of genotypes adapted to different environmental conditions on the basis of deviation from the regression line of unit slope (Figure 3).

3.1 What-won-where Biplot for vertex/ideal genotype

The biplot (Figure 3) represents a polygon, where some of the genotypes were placed on the crests, while the rest were surrounded by the polygon. As the genotypes placed on the peak had the longest detachment from the biplot origin and they were expected to be the most responsive. The genotypes at the crests of the polygon could be called the vertex/ideal genotype.

In present study, the genotypes G_4 in E_1 are the vertex genotype, which had the highest grain yield. The two environments (E_2 and E_3) were to be found in the same sector on the graph, which recommended that these environments did not differ significantly among themselves. The genotype G_5 is the only apex genotype for environment E_2 and E_3 environments. None of the environments fell in the sectors with genotypes, G_1 , G_7 , G_9 and G_{11} , representing that these genotypes were not appropriate for growing in these environments.

In an "ideal" view (Figure 4), it was observed that the genotype G_5 (1648.92) was in close proximity to the ideal genotype, followed by G_6 (1457.24 Kg/ha) and G_4 (1354.58 Kg/ha), respectively. According to Yan & Kang (2003), a model genotype could be described as one which was the uppermost yielding across tested environments and is utterly stable in its performance.

3.2 Average yield and stability of genotypes

The average grain yield and stability of the genotypes presented in Figure 4. The AEAaxis (average environmental axis, AEA) passes

across the biplot origin. The point of average environment coordinates for environments was indicated by open blue circle with an arrow. An "ideal" genotype was represented by closed blue dot in Figure 4. The higher yielding genotypes located closer to the circle; the stable genotypes are lie on the upper area of the line, and unstable are those in the lower fraction of the biplot. Considering

Figure 2 Meteorological parameters of three environments (RH-1: Relative Humidity at 0700 LMT, RH-2: Relative Humidity at 0700 LMT, Av. RH: Average Relative Humidity, $T_{\max}$: Maximum Temperature, $T_{\min}$: Minimum Temperature, T_{mean} : Average Temperature)

Figure 3 A genotype + (genotype $\times$ environment) interaction biplot showing genotype performance in each environment.

Figure 4 Comparison of genotypes with the ideal genotype showing the environmental axis (AEA) the GGE biplot. Environments and genotypes are denoted by 'E' and 'G', respectively. AXIS1 and AXIS2 are the first and second principal components, respectively.

this, the highest projection on the performance line holding by genotype G₅ has the highest average grain yield (1648.92 Kg/ha), followed by G₆ (1457.24 Kg/ha) and G₄ (1354.58 Kg/ha) which are positioned very close to the genotype G₅ (Figure 4).

3.3 Environment evaluation based on GGE biplot

The cosines of the angle between parents were used for the analysis of the interrelationship between entries / testers:

$$\cos [a_{ij}] = r_{ij},$$

Where, a_{ij} is the angle between environments i and environments j and r_{ij} is the correlation coefficient between both the environments.

If the angle between their vectors is $<90^\circ$ considering the two environments are positively correlated, if the angle is $>90^\circ$ they are negatively correlated, and independent if the angle between them is 90° . The angle of 0° specifies that the correlation [r] is 1 and the angle of 180° represents that the correlation is -1 . The more discriminating entries exist testers with longer vectors, while less discriminating has short vectors and those position at the biplot origin are not discriminating Rastogi et al. (2011).

The environments were presented in Figure 5 has discriminating ability and representativeness. The representative environment of

all other environments has longest distance between the marker of the environment to the biplot origin, is a measure of its discriminating ability considered as ideal environment, that is most discriminating for genotypes and shortest projection from the marker of location onto the AEA Y-axis is the measurement of its representativeness (Yan, 2001; Yan & Kang, 2003).

Considering this, E₃, as it is, as E₃ is far away from the plot origin and had the shortest projection onto AEA Y-axis was the most discriminating as well as the most typical environment, respectively. The other favorable environment E₂ was positioned close to E₃, which indicates that stable production of amaranths is possible in this environment. The pattern of environments on the biplots suggested that all the environments were positioned in different concentric circle (Figure 5). In present study, as the angle between E₂ and E₃ environments was less than 90° , it revealed that $G \times E$ was moderately small and these environments tend to discriminate among genotypes in a similar manner and have a strong relationship. Corresponding environments were considered as the best environments for genetic discrepancy of genotypes under study (Tonk et al., 2011; Miah et al., 2015). Besides, the environment which is not far away from the origin of biplot did not have the discriminating ability and was not illustrative (E₁), as the AEA Y-axis shown large projection (Figure5).

Figure 5 Comparison of environments with an ideal environment. The genotypes and environments are indicated by G and E, respectively.

3.4 Relationship among the environments

The correlation between the test environments is represented by the vectors of all three environments that facilitate the determination of the relationship between environments (Figure 6). In biplot environment view, the vectors of three environments depicting the relationship between environments while cosine of the angle between two environments shows the relationship among them (Yan, 2001). Both, E_1 and E_3 had the longer vectors thus, they were the best for genetic discrimination of genotypes but on considering the angle between these two environments they are comparatively less discriminating than E_2 . The environment E_2 was the least representative environment in this investigation because it has shorter vector. Minimum angle between the vectors of E_1 and E_2 has shown that they had robust correlation.

An essential target in a breeding program is to accommodate authentic indication that will gratify as a guide for selection of the best genotypes that have to be planted in the following seasons and to be capable to forecast yield as exactly as possible based on limited experimental data. The objective of any breeding experiment is to put up authentic clue that will gratify as a guide for selection of the model genotypes and ability for projection of yield as exactly as likely based on restricted experimental data. The amaranth genotypes effectively identified by means of GGE biplot which should be considered for growing in E_2 . Moreover, by means of this method, it was apparently established that high and

stable yields could be attained only in specific environment. Other researchers observed that GGE biplot analysis is a suitable device for detecting experimental environments to select best genotypes in field crops as well (Balestre et al., 2009; Ilker et al., 2009; Oliveira et al., 2010; Tonk et al., 2011; Khalil et al., 2011; Beyene et al., 2011; Nzuve et al., 2013; Mortazavian et al., 2014; Miah et al., 2015).

Conclusion

In the present study, the genotype G_4 was the vertex genotype in E_1 whereas, G_5 was vertex genotype in E_2 and E_3 , with the highest seed yield. From “ideal” view it was reported that genotype G_5 was the next to the ideal genotype, followed by G_6 and G_3 , respectively. With regard to the environments, E_3 was the most discriminating as well as the most typical environment. The stable production of amaranths is possible in favorable environment E_2 as it was positioned close to E_3 . Hence, it was concluded that GGE biplot could be efficiently used to predict stable and high yielding genotypes as well as best performing environments for the cultivation of amaranth.

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Figure 6A genotype + $G \times E$ interaction biplot showing relationships among three environments.

Conflict of interest

Authors would hereby like to declare that there is no conflict of interests that could possibly arise.

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