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Interpreting Genotype by Environment Interaction Using Weather Covariates

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Abstract

Understanding genotype by environment interaction (G*E) has always been a challenge to statisticians and plant breeders. Recently site regression analysis has emerged as a powerful analysis tool to understand G*E, specific and general adaptability of genotypes and grouping of environments into mega-environments. This paper attempts to enhance power of site regression by using environmental covariates in tandem to explain G*E better. In this present study, performances of eighteen genotypes were investigated across five environments during the year 2008 rainy season. Three traits, namely grain yield, harvest index and dry fodder yield were used for analysis purpose. Biplot analysis identified two major groups of environments, first group of environments included Karad and Coimbatore and second group consisted Udaipur, Palem and Surat. SPH 1615 and SPH 1609 were identified as winning genotypes for first mega-environment whereas SPH 1596, SPH 1611 and CSH 16 were winners for second mega-environment for grain yield. High yielding genotypes, SPH 1606, SPH 1616 and CSH 23 performed consistently well across all environments and should be considered for general adaptability. Genotype SPH 1596 was identified for both specific and general adaptability. By superimposing GGE biplots for different traits, genotypes SPH 1596 and CSH 23 were identified as stable for all three traits. Climatic data on average maximum temperature and minimum temperature at early (June-July) and late phase (August) of plant growth was incorporated to study G*E by using factorial regression. Average maximum temperature and minimum temperature at early phase and average minimum temperature during late phase were found significantly affecting genotype performance.

Genotypic sensitivities for each genotype were estimated. Genotype SPH 1606 with negative genotypic sensitivity was found to perform better in Karad with below average maximum temperature during early phase. Genotype CSH 16 with negative genotypic sensitivity for average minimum temperature during early phase and positive genotypic sensitivity average minimum temperature during late phase performed better in Palem.

Keywords: **AEA** (Average Environment Axis); biplot; Factorial regression**; G*E** (Genotype by Environment interaction); **GGE** (Genotype plus Genotype by Environment); **MET** (Multi-Environment Trial); **PCA** (Principal Component Analysis); stability, Site regression; **SVD** (Singular Value Decomposition).

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1 Introduction

Releasing genotypes from breeding programs suffers primarily due to variability present in target environments and their interaction with breeding material. Understanding the performance of genotypes over diverse environments has always been an important goal and challenge before plant breeding community. To understand this, usually Multi-Environment Trials (MET) are planned and data from several environments and/or years are gathered systematically. Various statistical models are used to study genotype by environment interaction (G*E). If a statistical model is able to explain pattern of G*E to a meaningful extent, genotypes are released accordingly. However, in most cases this task is not easy and straightforward and need lots of exploration of data. Since early 1960s several efforts were made by various researchers to explain G*E by use of different statistical models. Towards this direction initial efforts were mainly centered towards using regression based approaches. Most commonly regression based stability models were given by Wricke (1962), Finlay and Wilkinson (1963), Eberhart and Russell (1966), Perkins and Jinks (1968), Freeman and Perkins (1971), Shukla (1972) and Franchis and Kannenberg (1978). Out of these Eberhart and Russell (1966) stability model has been exploited by breeders widely. Their model assumes that the genotypes have a linear response to change with environments. According to this model, a genotype is said to be stable having high mean yield, with coefficient of regression (b_i) equal to one and deviation from linear regression(S_{di}^2) equal to zero. Wricke (1962) suggested using G*E for each genotype as a stability measure, which is termed as ecovalence (W_i^2). Shukla (1972) presented a statistic called stability variance (σ_i^2) that partitions G*E and assigns it to individual genotype. Franchis and Kannenberg (1978) used the environmental variance (S_i^2) and the coefficient of variation (CV_i) to define a stable genotype. Soon it was realized that G*E pattern always cannot be explained by using additive models and hence another important milestone in studying G*E was introduction of multiplicative models (Zobel et al., 1988) and use of biplots (Gabrial, 1971). Biplots

are used to graphically summarize G*E pattern mostly on a two-dimensional graph, depicting relationship between genotypes and environments. This graphical representation has been found extremely helpful in selecting specific and generally adapted genotypes. Two types of biplots, the AMMI biplot (Crossa et al., 1990 and Gauch, 1992) and the GGE biplot (Yan et al., 2000; Yan and Kang, 2003; Joshi et al.,2007) are the most commonly used biplots. Two dimensional biplots apply multivariate techniques such as Singular Value Decomposition (SVD) to approximate multidimensional information into two dimensions to address the issue of genotype recommendation in multi-environment trials through graphical visualization.

To strengthen genotype recommendation, a usual practice among breeders is to repeat trial over years and revalidate recommendations again. In this approach many times because of change in climatic conditions at specific environment, crossover (Yang, 2007) kind of G*E are observed frequently, which makes it difficult to take decision for genotype adaptability. Biplots over multiple years and environments may be useful for such situations, however many time this becomes very difficult to give recommendations and also to understand change in performance of genotypes. To understand such behavior one may use techniques where data on various environmental variables which are supposed to influence genotype performance like temperature, precipitation, sunshine, relative humidity and other important weather parameters are carefully recorded. Once such information is available one may try to explain performance of specifically adapted genotypes to individual environments based on these climatic parameters. Such studies come under a wider class of techniques named factorial regression (Eeuwijk et al., 1966). Factorial regression with environmental covariates has been proved extremely helpful in understanding G*E relation to environmental covariates (Voltas et al., 2005). In factorial regression, environment variables are tested for their possible association with the genotypes performance across environments. Once these variables are identified it becomes easier and more confident to recommend genotypes for specific adaptation.

In addition to above breeders are often more interested in studying common stability of various traits together to screen and recommend genotypes to targeted regions. The objective of the present study is also to identify adaptable genotypes for targeted environments by using weather covariates and use of multiple traits.

2 Material and Methods

Experimental material and environment - Data used for this study was taken from All India Coordinated Sorghum Improvement Project, where eighteen genotypes were evaluated under Advanced Varietal and Hybrid Trial (AVHT) during the year 2008 rainy season. Experiment was conducted at nineteen environments across India, however five

environments *viz.*, Coimbatore (COIM), Karad (KARA), Palem (PALE), Surat (SURA) and Udaipur (UDAI) were considered for study as consistent environmental weather data was available for these environments. These environments mainly covered the western and southern-east region of India (Fig 1). The materials included 10 test hybrids, 2 test varieties, 2 hybrid checks (CSH 16, CSH 23), 3 variety checks (SPV 1616, SPV 462, CSV 15) and to these one absolute check was also included. Details of the genotypes are presented in Table 1. Detail information on environments relative to area/state, latitude, longitude, altitude, date of sowing and harvesting is given in Table 2. The experimental design at each environment was a randomized complete block design with eighteen genotypes replicated thrice. Field management practices such as application of fertilizers and use of pesticides were standard across all environments. Planting started during middle of June and ended by the first week of July across all environments. Data were recorded on grain yield (GY) and dry fodder yield (DFY). Another statistic, harvest index (HI) was calculated as the ratio of grain mass to total above ground biomass and was used to measure the proportion of grain yield value to total biomass collected and was used for analysis purpose. Grain yield ranged from 1456 kg/hectare to 6311 kg/hectare and dry fodder yield ranges from 3704 kg/hectare to 22072 kg/hectare across five environments.

Table 1: Information on the genotypes used in the study

Genotypes Names	Genotypes Code	Contributing sector
SPH 1596	G1	Private
SPH 1603	G2	Private
SPH 1604	G3	Private
SPH 1605	G4	Public
SPH 1606	G5	Private
SPH 1609	G6	Private
SPH 1610	G7	Private
SPH 1611	G8	Private
SPH 1615	G9	Private
SPH 1616	G10	Private
SPV 1616	G11	Public
SPV 1786	G12	Public
SPV 1817	G13	Public
SPV 462	G14	Public
CSH 16	G15	Public
CSH 23	G16	Public
CSV 15	G17	Public
Absolute Check	G18	-

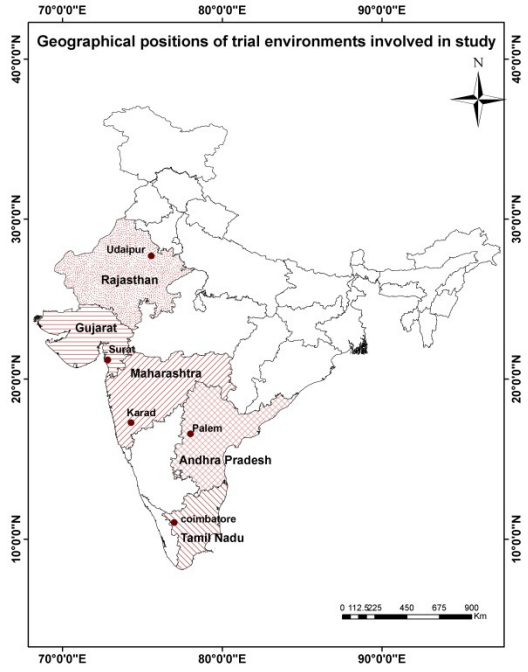

Fig 1. Geographical position of the trial environmentsinvolved in study

Table 2: Information on the trial environments

Environments (Code)	Area/States	Latitude	Longitude	Altitude (msl)	Date of sowing	Date of harvest
Coimbatore (COIM)	Tamil Nadu	11° 02' 00" N	76° 59' 00" E	412	16th June 2008	04th Oct 2008
Karad (KARA)	Maharashtra	17° 16' 26" N	74° 17' 02" E	597	29th June 2008	08th Oct 2008
Palem (PALE)	Andhra Pradesh	16° 35' 00" N	78° 00' 00" E	642	28th June 2008	27th Oct 2008
Surat (SURA)	Gujarat	21° 11' 45" N	72° 49' 52" N	1340	08th July 2008	26th Oct 2008
Udaipur (UDAI)	Rajasthan	27° 42' 00" N	75° 33' 00" E	598	01st July 2008	15th Oct 2008

Statistical Analysis - Analysis of variance was carried out for grain yield using proc *glm* procedures of SAS software version 9.3 for Windows (SAS Institute Inc., 2008). To pool data, homogeneity of error variance across five environments was tested using Bartlett test (Gomez and Gomez, 1984) and the chi-square statistic was found significant. Aitken's transformation was used to make error variances homogeneous. In order to determine the contribution of environment, genotype and their interaction following statistical model was used:

$$Y_{ijk} = \mu + g_i + e_j + r_{jk} + (ge)_{ij} + \varepsilon_{ijk}$$

where, Y_{ijk} is the yield of genotype *i* in block *k* for environment *j*, μ is the grand mean, g_i and e_j are the main effects of i^{th} genotype and j^{th} environment respectively, r_{jk} is the k^{th} replicate effect in j^{th} environment, $(ge)_{ij}$ is the interaction effect between i^{th} genotype and j^{th} environment and ε_{ijk} is the error effect.

Site regression (GGE) using Biplot - A standard biplot is the scatter plot that graphically displays both the row factor and column factors of a two-way table data. A biplot graphically displays a matrix with application to principal component analysis (Kroonenberg, 1995). For generating a biplot, a two-way table representing two factors was subjected to singular value decomposition. The singular value decomposition of a matrix X= $(x_{ij})_{vxs}$ is given by

$$x_{ij} = \sum_{k=1}^{r} u_{ik} \lambda_k v_{kj}$$

where, (u_{ik}) is the element of the matrix U_{vxs} characterizing rows, λ_k's are the singular values of a diagonal matrix L_{sxs}, v_{kj} is the element of the matrix V_{sxs} characterizing the columns and *r* represents the rank of matrix X≤min(v,s). Principal component scores for

row and column factors were calculated after singular value partitioning of $(x_{ij})_{vxs}$ (Yan et al., 2002). Biplot was obtained using first two components and percentage of variation explained by them is calculated.

The fixed effect two-way model for analysing multi-environments genotype trials is as follow:

$$E(Y_{ij}) = \mu + g_i + e_j + (ge)_{ij}$$

where, μ is the grand mean, g_i and e_j are the genotype and environmental main effects respectively, $(ge)_{ij}$ is the G*E effect. The sites regression model is given by (Crossa and Cornelius, 1997; Yan and Kang, 2003):

$$E(Y_{ij}) = \mu + e_j + \sum_{n=1}^{r} \xi_{in}^{*} \eta_{jn}^{*}$$

where, r = number of principal components (PCs) required to approximate the original data. ξ_n^{*} and η_{jn}^{*} are the i^{th} genotype and the j^{th} environmental scores for PCn, respectively. In the site regression method, PCA is applied on residuals of an additive model with environments as the only main effects. Therefore, the residual term $\sum_{n=1}^{r} \xi_{in}^{*} \eta_{jn}^{*}$ contains the variation due to G and G*E. A two dimensional biplot (Gabriel, 1971, Parsad et.al, 2007) derived from above 2-way table of residuals is called GGE biplot (G plus G*E) (Yan et al., 2000). A GGE biplot graphically depicts the genotypic main effect (G) and the G*E effect contained in the multi-environment trials. GGE biplots have been found very useful in understanding G*E, mega environment identification and genotype recommendation. All five environments data was fitted using site regression model and which-won-where and ranking biplot were generated.

Factorial Regression - For better understanding of G*E pattern, inclusion of environmental covariates into study is always useful. The most common technique to explain G*E by environmental covariates is factorial regression. The general form for a factorial regression model with *H* environmental covariates is given by (Denis, 1988; Van Eeuwijk et al., 1996):

$$E(Y_{ij}) = \mu + g_i + e_j + (\sum_{h=1}^{H} \beta_{ih} E_{jh} + \delta_{ij})$$

where β_{ih} to β_{iH} are sensitivities of i^{th} genotype to environmental variables E_1 to E_H, *H* being the number of covariates included in the model and δ_{ij} is the component of deviation from regression.

After fitting the main effects □ , g_i, and e_j, environmental variables are included on the levels of environmental factor to describe the G*E interaction as $ge_{ij} = \sum_{h=1}^{H} \beta_{ih} E_{jh} + \delta_{ij}$

Now the ge_{ij} effect for each genotype i, can be regressed on to environmental covariates E_h (h = 1 to H) to obtain the sensitivity coefficients for that genotype .A usual way of determining weather covariates influencing genotype performance is to fit factorial regression model by fitting all possible linear models and are select best combination by using some statistical criteria. A commonly used method for selection of best model in factorial regression is Mallows' Cp selection criteria and adjusted R-square value (Draper and Smith, 1981). After fitting the main effects μ, g and e_j, the environmental variables are introduced in an attempt to describe G*E interaction by fitting of regression line for individual genotype corresponding to environmental variables that resulted in estimation of genotypic sensitivities. During present study four weather covariates were included and Mallows' Cp selection criteria were used for selecting significant covariates. Selected covariates were standardized to facilitate interpretation and the genotypic sensitivities were estimated by least square method.

3 Results and Discussions

*Analysis of Variance and study of crossover type of G*E*

Homogeneity test for error variance was computed to pool multi-environments trial data with five environments and 18 genotypes for grain yield using Bartlett chi-square test. Bartlett test resulted in a highly significant chi-square value (χ^2 =55.04**). Hence, data were transformed to make error variance homogeneous. Transformed data was analyzed using analysis of variance technique (Table 3). All sources of variation (i.e., due to E, G and G*E) were found to contribute significantly towards yield variation. The total amount of variation (i.e., E+G+G*E) accounted by environment (E), genotype (G) and genotype by environment interaction (G*E) were 88.21%, 5.64% and 6.15%, respectively. Mean plot (Fig 2) of genotypes across environments was drawn to visualize the ranking of genotypes based on yield performance. The rank of genotypes was changing across environments, which suggested existence of crossover G*E.

Table 3: Combined Analysis of Variance of grain yield data (transformed) of 18 genotypes tested across 5 environments

Source of Variation	Degrees of Freedom	Mean Square Error	Proportion of (E+G+G*E)
Environment	4	1129.60**	88.21
Genotype	17	16.99**	5.64
Genotype * Environment	68	4.64**	6.15
CV (%): 12.46	**R^2: 0.97**		

denotes significance at p<0.01; **CV: Coefficient of Variation; **R^2:** Coefficient of Determination

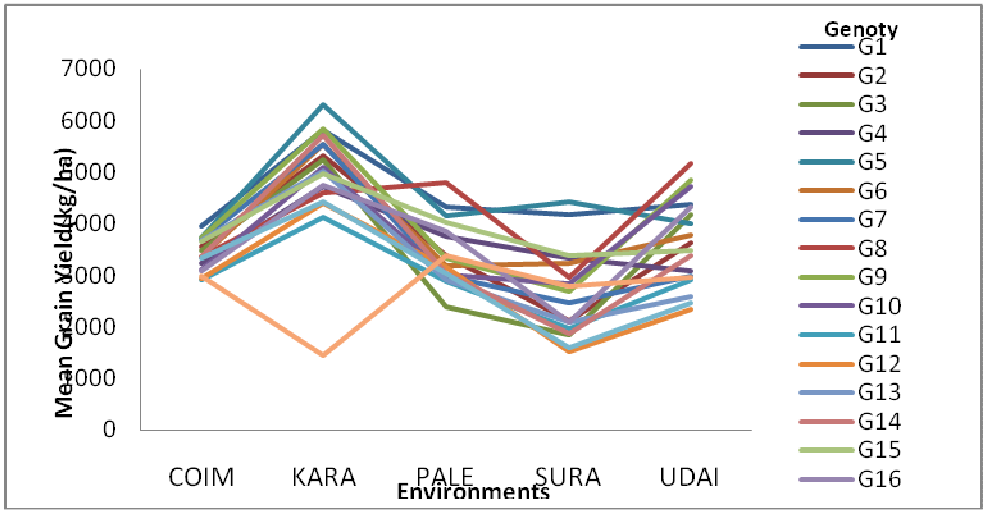

Fig 2: Graphical representation of mean yield for genotypes against environment means showing their rank change

Yield stability analysis using GGE biplot

The GGE biplot explained 80.21% of the total variation (53.43% and 26.78% by PC1 and PC2, respectively). Fig 3a represents the which-won-where pattern of multi-environment trial data that helps to recognize the specific and general adaptability of genotypes across environments. The lines connecting the test environments to the biplot origin are called environment vectors. The cosine of the angle between two environment vectors approximates the correlation between them. An acute angle between two test environments indicates close association between them suggesting that the same

information about the genotypes ranking could be attained. Environment vectors at right angle indicate no correlation and at wide obtuse angles (i.e., strong negative correlations) indicates strong crossover G*E. 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 a measure of the discriminating ability of the environments. Test environments that are non-discriminating provide little information on the genotypes. Fig 3a presents UDAI, SURA and PALE are positively associated and are at obtuse angle with KARA. KARA is the most discriminating among all environments whereas COIM could not differentiate much among genotype performances. An "Average-Environment Axis" (AEA) has also been included in the same biplot. The Average Environment Coordinate (AEC) represented by the small circle at the end of the arrow, has the average coordinates of all test environments, and AEA is the line that passes through the average environment and the biplot origin. A test environment that has a smaller angle with the AEA is more representative than other test environments. Test environments that are both discriminating and representative are good test environments for selecting generally adapted genotypes. Fig 3a suggested that UDAI can be considered as an ideal test environment. Performance of genotypes can also be visualized using which-won-where view of GGE biplot. A genotype performance in an environment will be better if the angle between the genotype and the environment's vector is <90°; it is poorer than average if the angle is >90°; and it is near average if the angle is about 90°. Fig 3a represents that G9 and G6 can be considered as the winning genotypes for KARA and COIM whereas G1, G15 and G8 seem the winning genotypes for UDAI, SURA and PALE. Fig 3b represents the ranking biplot that helps in the identification of stable genotypes. Genotype with high/low mean (based on trait under consideration) and positioned close to AEA is considered as stable genotype. Line drawn perpendicular to AEA helps to measure the degree of stability. The more a genotype deviates from AEA, the higher the degree of instability. Genotypes at right side of this perpendicular line were above average performer and which are left were below average performer, while the genotypes which are close to this perpendicular line are average performer. Genotype G5 seems the most high yielding and stable genotypes across all environments. In addition to G5, genotypes G10 and G16 were also found stable and above average performer. G1 can also be considered as a general adaptable genotype because of its high performance and moderately smaller angle with AEA. G18 seemed to be a highly unstable genotype whereas G11 seems a very stable genotype however it was a below average performer.

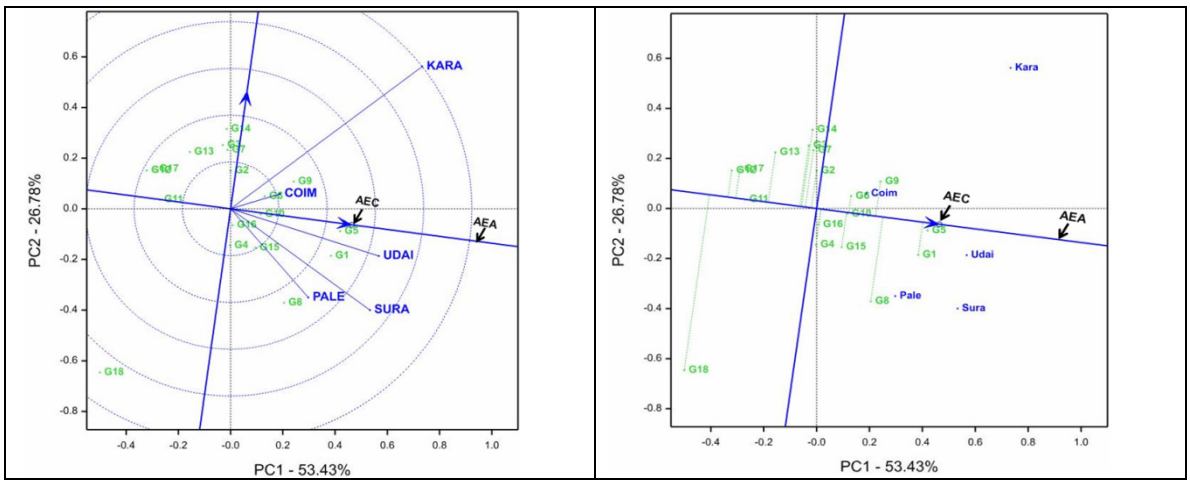

Fig 3a: Which-won-where view of GGE Biplot of grain yield

Fig 3b: Ranking of genotypes based on grain yield & stability

*Incorporating weather parameters for studying G*E using factorial regression*

Factorial regression analysis using environmental covariates helps to relate the genotype performance to the environmental variables which may directly or indirectly affect the crop. Table 4a indicates four weather parameters, i.e., average maximum and minimum temperature recorded at five environments at early (June-July) and late phase (August) of plant growth that were used for factorial regression analysis. Out of these covariates, average maximum temperature and average minimum temperature during the early phase and average minimum temperature during late phase were found to significantly affect genotype performance using Mallows' Cp selection criteria and adjusted R-square value. Contribution of each covariate in explaining G*E was calculated and genotypic sensitivities were also estimated for each significant covariate that gives the amount of variation in yield value for a unit change in covariate value. Furthermore, the estimates of genotypic sensitivities for specifically adapted genotypes were also studied. This analysis revealed basis of genotypes performance and their behavior as affected by significant covariates.

Table 4a: Average environmental characteristics for the early and late crop development phases at 5 environments

Environment	Early Phase (June-July)		Late Phase (August)	
	Min Temp (^oC)	Max Temp (^oC)	Min Temp (^oC)	Max Temp (^oC)
	MITE	***MXTE***	***MITL***	***MXTL***
COIM	23.33	31.60	22.13	31.33
KARA	20.78	29.41	19.58	27.75
PALE	23.41	31.52	22.58	28.98
SURA	26.58	31.72	25.61	30.47
UDAI	24.71	31.99	22.90	30.10

Abbreviations for environmental covariates:
MITE - Average minimum temperature during early phase (June-July)
MXTE - Average maximum temperature during early phase (June-July)
MITL - Average minimum temperature during late phase (August)
MXTL - Average maximum temperature during late phase (August)

Sum of squares due to G*E split into components that is explained by significant environmental covariates MITE, MXTE and MITL, when regressed on it, and rest remained unexplained by these variables. Modeling of G*E with significant environmental covariates explained nearly 87.4% of G*E sum of square (in Table 4b). Genotypic sensitivities measured the expected variation in yield for genotypes exposed to unit change in selected environmental covariates. Using Table 4c, among the genotypes under consideration, at 5% level of significance, G18 was found to response simultaneously to all selected environmental variables. Other genotypes showed specific response to MITE (G15, G9 and G12), MXTE (G5) and to MITL (G15, G9 and G12).

In this study, the main objective of factorial regression was to draw vivid information about the adaptability of specifically adapted genotypes. From factorial regression analysis, we found a significant negative genotypic sensitivity for genotype G5 for MXTE indicating that it could response better to environments with below average maximum temperature during early phase. The average yield value of G5 in KARA (6311 kg/hectare) and which-won-where pattern of GGE biplot, suggests that G5 has ability to response better for MXTE in KARA. Also the results indicate that genotype

G15 (negative genotypic sensitivity for MITE and positive genotypic sensitivity for MITL) would perform better in PALE because of below average MITE and above average MILT.

Table 4b: Proportion of G*E explained by significant environmental covariates

Environmental Covariates	Proportion of sum of squares explained to the total G*E sum squares
MITE	38.99
MXTE	22.21
MITL	26.21

Table 4c: Estimates of genotypic sensitivities (βi) and corresponding p value to selected environmental covariates

	MITE		**MXTE**		**MITL**	
Genotype	β_i	p-value	β_i	p value	β_i	p value
G1	-1.55	0.99	-411.73	0.19	273.37	0.4
G2	37.83	0.79	85.91	0.42	-218.72	0.28
G3	1593.69	0.22	-157.47	0.71	-1660.73	0.19
G4	-861.42	0.08	-177.56	0.21	1049.98	0.06
G5	-28.61	0.86	**-944.92**	0.05	463.65	0.16
G6	601.68	0.17	-637.86	0.09	-336.75	0.26
G7	-223.26	0.85	-330.33	0.65	200.14	0.86
G8	188.16	0.94	727.62	0.61	-320.2	0.88
G9	**1488.87**	0.04	-246.57	0.14	**-1479.09**	0.04
G10	1732.48	0.16	-345.89	0.39	-1520.95	0.16
G11	-273.34	0.28	193.95	0.23	208.56	0.32
G12	**-1128.63**	0.04	316.44	0.08	**867.57**	0.05
G13	-674.41	0.65	-14.66	0.99	530.32	0.69
G14	283.32	0.45	-250.2	0.33	-437.6	0.3
G15	**-802.99**	0.02	6.11	0.76	**890.3**	0.02
G16	336.43	0.82	445.12	0.61	-534.74	0.69
G17	-973.33	0.35	389.87	0.46	693.18	0.42
G18	**-1294.91**	0.004	**1352.17**	0.002	**1331.71**	0.004

Selection of agronomical stable genotype based on multiple traits

An important aspect of crop breeding experiment is to select genotypes based on several traits under consideration. Although grain yield is the most important characteristics of plant breeding, there are many other traits which equally contribute to breeding objectives. Hence, genotypic advancement based on multiple trait data can aid in a more advance way of selection criteria and hence it is an inevitable issue for plant breeders. Individual GGE biplots for each trait were drawn to see the genotypic behavior in terms of their magnitude and stability. While looking for some commonality between genotype performances, Fig 4c suggested that the genotypes G5, G1, G16 and G10 which are good for grain yield in terms of mean yield and stability were also good for harvest index. This is quite expected since grain yield and harvest index were highly correlated traits (Table 5). From GGE biplot for dry fodder yield (Fig 4b), we could also find some similar genotypes which were good performer and quite stable for grain yield and harvest index (G1 and G16) were also stable for dry fodder yield. However their performances in terms of mean value were below average. Table 5 suggested that DFY is significantly negatively correlated with GY and HI. This advises for collective performance of similar genotypes for all three traits in terms of stability but in terms of mean performance they performed opposite for DFY. Most importantly from individual traits GGE biplot we could also discover that environments were grouped in the same fashion. Hence, grouping of environments identified appeared more reasonable. Therefore studying G*E effect with several traits resulted in more robust identification of stable genotypes and grouping of environment.

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Table 5: Test of significance of correlation coefficient between grain yield, harvest index and dry fodder yield in each environment

Environment	**COIM**	**KARA**	**PALE**	**SURA**	**UDAI**
GY vs HI	0.483**	0.839**	0.840**	0.926**	0.693**
GY vs DFY	0.485^{ns}	-0.501*	-0.303^{ns}	0.475*	0.022^{ns}
HI vs DFY	-0.585**	-0.884**	-0.757**	-0.756**	-0.689**

^{ns}: non-significant; ** Significance at p <0.01; * Significance at p<0 .05

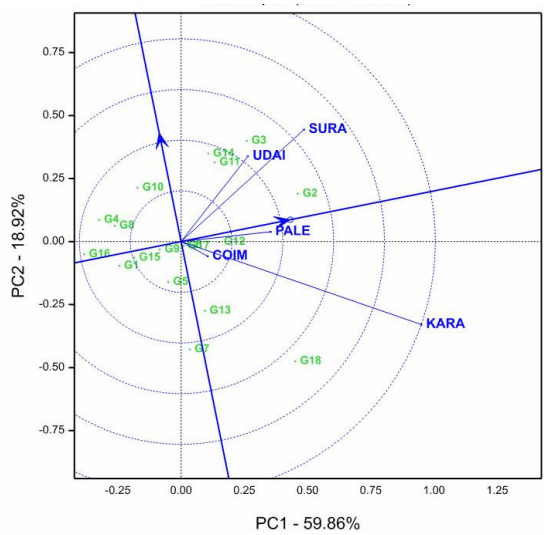

Fig 4a: Which-won-where view of GGE Biplot for dry fodder yield

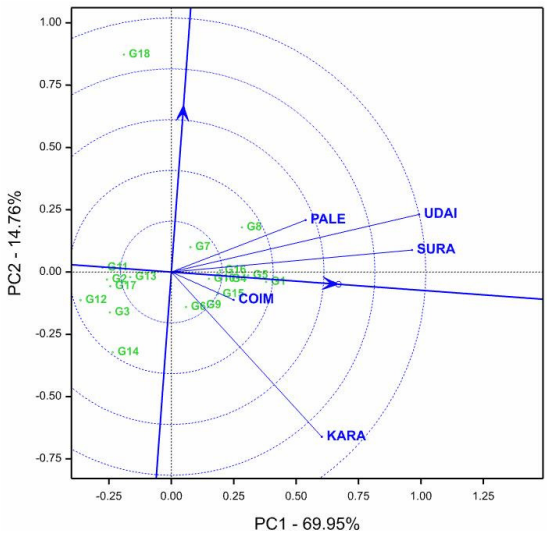

Fig 4b: Which-won-where view of GGE Biplot for harvest index

4 Summary and conclusion

GGE biplot is well-known and powerful technique for the visual analysis of multi-environmental trials. Its capabilities include recommendation of specific and general adaptable genotypes and grouping of similar performing environments into mega environments. This technique becomes even more powerful when it is clubbed with weather covariates to explain specific adaptability of genotypes. In present study, for three traits, grain yield, dry fodder yield and harvest index a GGE biplot analysis accounted for 80.21%, 78.78% and 84.71% of total (G+G*E) variation respectively. Based on these biplots specific and general adapted genotypes were identified for individual traits. Further, to identify genotypes stability for all three traits, biplots were visually superimposed over each other. Genotype G1 and G16 were identified as highly stable and high performer genotypes for GY, HI and DFY, however G5, G1, G16 and G10 was identified winning genotypes only for GY and HI. We could also identify that for GY, genotype G9 and G6 were specifically adapted for environments KARA and COIM and genotype G1, G15 and G8 for UDAI, SURA and PALE.

To understand adaptation pattern of these genotypes further, weather data on average maximum and minimum temperature at early and late phase of plant growth was used for factorial regression. Out of these, average maximum, average minimum temperature during the early phase and average minimum temperature during late phase of crop growth period were significantly associated with the genotype performance. Factorial

regression could explain a significant proportion (87.4 %) of total G*E. Factorial regression revealed that the most general adapted genotype G5 for GY performed best in KARA because of its affinity to below average maximum temperature (negative genotypic sensitivity for MXTE) during early phase of crop development. Factorial regression could also explain specific adaptability of genotype G15 in PALE. Genotype G15 was having negative genotypic sensitivity for MITE and positive genotypic sensitivity for MITL. PALE has a below average MITE and above average MITL. However we also found that few specific adaptations (G9) could not be explained properly by use of weather covariates. We understand that there are many other important factors influencing performance of genotypes in different environments which we could not capture by studied weather covariates. This also indicates that partitioning G*E with significant weather variables was not sufficient for complex environmental interaction of G9. We recommend that multi-environment trials should pay more emphasis on collection of weather data on various important weather parameters at regular duration of interval. Availability of sufficient weather data with good quality standards will ease in taking decision on specific and general adaptations.

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