

## **A Generalized AMMI Model to Study $G \times E$ Interaction for Cobs Count in Maize**

**Baishali Mishra and B.K. Hooda**

*Chaudhary Charan Singh Haryana Agricultural University, Hisar*

*Received 10 December 2021; Revised 09 August 2022; Accepted 18 November 2022*

---

### **SUMMARY**

Additive main effects and multiplicative interaction (AMMI) models have been used to analyze genotype-by-environment interactions (GEI). Applicability of AMMI model depends on the assumption of normally distributed error with a constant variance. However, in case of count data, the appropriateness of AMMI model may be inappropriate as it does not conform to these statistical assumptions. It can be handled by introducing multiplicative terms for interaction in wider class of modeling, Generalized Linear Models known as Generalized AMMI (GAMMI) model. In this paper, GAMMI model with Poisson distribution and log link function has been used to analyze GEI data for number of cobs in maize during Kharif season for 32 genotypes grown over 13 locations across India. Here, Generalized AMMI model replaces the classical AMMI to model GEI in case of count data. For genotype by environment ( $G \times E$ ) interaction in cobs count data, GAMMI model has been applied and compared with the usual AMMI model for original as well as squared root transformed data. The performance of the GAMMI model was compared with the classical AMMI model and the AMMI model applied to transformed (square-root) data. The criterion used for comparison was explained variability in terms of number of axes which were determined by Gollob test. On comparison of results it was found that maximum variation was explained by the first three axes in case of GAMMI model i.e., 63.13 percent.

*Keywords:* GEI, AMMI, Number of cobs, GAMMI, Log link, Poisson distribution.

---

### **1. INTRODUCTION**

A differential response of genotypes across environments is frequently observed in multiple-environment trials (METs) and is known as genotype by environment interaction. The data from these trials are usually summarized in a two-way table with genotypes in rows and environments in columns, or vice versa. GEI is manifested by change in ranking of genotypes across environments; Detection and analysis of GEI is essential for identifying genotypes with stability and/or adaptability to specific environmental conditions. One can use either parametric or non-parametric stability measures to study  $G \times E$  interaction. The parametric measures make use of statistical assumptions about distribution of genotype, environment and  $G \times E$  interaction effects. Whereas, the non parametric measures make no such assumptions. Gabriel (1971) coined the word “biplot”, where the prefix bi refers to

the simultaneous display of both rows and columns of a two-way table. Kempton (1984) proposed the use of bi-plots in explaining GEI in crop variety trials. The additive main effects and multiplicative interaction (AMMI) model given by Gauch (1988) is one of the most widely used tool to study and analyze the  $G \times E$  interaction in METs. The AMMI model combines the features of analysis of variance (ANOVA) and singular value decomposition (SVD). Initially ANOVA is used for estimation of additive main effects of the two-way data table and then SVD is applied to the residuals from the additive ANOVA model to decompose  $G \times E$  interaction into a sum of multiplicative terms i.e. the interaction principal components (IPCs). Later on, adding the genotype mean to the GEI to measure genotype performance in each environment, Yan *et al.* (2000) applied another type of multiplicative decomposition and displayed its results as biplot

(GGE-biplot). The GGE classes of models are obtained by accounting main effect of genotypes and  $G \times E$  interaction effect and applying SVD to the data matrix centered on the environmental means.

The AMMI model represents observations as main effects and interaction effect through multiplication of interaction components, apart from random error component. AMMI model is used to analyze stability and adaptability in  $G \times E$  interaction studies. AMMI provide an additive model for main effects of genotype and environment plus complete multiplicative terms for the interaction effects. Basically, the interaction terms was modeled by a statistical technique of reduction dimension called Singular Value Decomposition. With SVD, the interaction terms will have complete parameters, a parameter for every single cell of the two ways table. SVD visualizes the interaction terms by way of Biplot and makes the GEI analysis easier. With this feature of Biplot, AMMI is said to be most powerful model for GEI analysis (Hadi *et al.* (2010)).

AMMI model can only be applied when the response variable  $Y$  follows a normal distribution with a homogeneous variance. However, agronomic and plant breeding data do not always conform to these statistical assumptions. For non-normal data, multiplicative interaction terms would very likely reflect both heterogeneity of variance and real multiplicative interaction (Snee, 1982; Hinkley, 1985). Transformation of data does not guarantee a complete solution to these problems. In the case of linear regression and analysis of variance a transformation is expected to produce homogeneity of variance, approximate normality of errors and additivity of systematic effects. One transformation will seldom meet all three requirements. And even after transformation of the data, estimated multiplicative terms are likely to reflect mixtures of heterogeneity of variance and multiplicative interaction.

The advantages of AMMI model for the GEI analysis, together with its limitation on normality assumption, encouraged many statisticians to develop AMMI to be more generalized by introducing GLM to AMMI model. Van Eeuwijk (1995) proposed multiplicative model in terms of GLM as an extension of AMMI model called as Generalized AMMI (GAMMI) model. Introduction of multiplicative terms for interaction in generalized linear models removes the restriction of normally distributed error. GAMMI also

keep the feature of Biplot visualization of GEI. Hadi *et al.* (2010) applied Generalized AMMI Models to leaf pest count data for assessing the endurance of soybean against leaf pest. Acorsi *et al.* (2016) analyzed GEIs for severity and incidence of grey leaf spot, a foliar disease in maize caused by *Cercospora zea-maydis*, using a generalized AMMI model.

This paper aims to evaluate the  $G \times E$  interaction for number of cobs in maize for 32 genotypes in 13 location/environment using GAMMI models. The results of GAMMI model have been compared with the classical AMMI model and AMMI model applied to transformed (square-root) data. This study is expected to provide useful information to study the GEI in multi environment trials when the assumption of normality is violated.

## 2. MATERIALS AND METHODS

### 2.1 Genotype $\times$ Environment data used

Data on cobs count at harvest for the present study were obtained from the annual report of AICRP on Maize during Kharif 2019. Based on climatic conditions, different breeding trials for maize cultivation in the country is carried out in various zones. In AICRP, field corns trials were conducted in three maturity groups (early, medium and late). For this study, data on Trial No. 666 NIVT (Early) evaluated at 3 zones namely NWPZ, NEPZ and CWZ were used. In this trial, 32 early type genotypes of maize were evaluated at 13 locations NWPZ (Delhi, Karnal, Ludhiana, Pant Nagar), NEPZ (Varanasi, Bhubaneswar, Dholi, Ranchi, Sabour) and CWZ (Ambikapur, Chindwara, Godhra, Udaipur) in a randomized complete block design with three replications.

### 2.2 Generalized AMMI models

The AMMI model for a random variable  $Y_{ij}$  occurring in  $i_{th}$  row and  $j_{th}$  column of a two-way table is as follows:

$$Y_{ij} = \mu + \alpha_i + \beta_j + \sum_{n=1}^k \lambda_n \gamma_n \delta_{nj} + \theta_{ij} \quad (1)$$

$$\theta_{ij} \sim N(0, \sigma^2); \quad i=1,2,\dots,G; j=1,2,\dots,L$$

Where  $Y_{ij}$  = mean yield of  $i_{th}$  genotype in the  $j_{th}$  environment/ location

$\mu$  = general mean

$\alpha_i$  =  $i_{th}$  genotypic effect

$\beta_j$  =  $j_{\text{th}}$  location effect

$\lambda_n$  = eigen value of the  $n_{\text{th}}$  IPCA axis

$\gamma_{ni}$  and  $\delta_{nj}$  are the  $i_{\text{th}}$  genotype  $j_{\text{th}}$  environment IPCA scores for the axis  $n$

$\theta_{ij}$  = residual

$k$  = number of PCA axis retained in the model

The residual combines the PCA scores from the  $N-k$  discarded axes, where  $N = \min(G-1, L-1)$ .

For many practical situations, the number of PCA axes to be retained is determined by testing the mean sum of square of each axis with the estimate of residual through F-statistics (Gollob, 1968 and Gauch, 1988). The mean sum of squares of each PCA axis is equal to the ratio of square of the corresponding eigen value and the degree of freedom of each axis obtained as  $G+L-1-2n$ . An AMMI model is a GAMMI model with identity link and constant variance.

Van Eeuwijk (1995) describes an alternating GLM procedure, using iteratively reweighted least squares to estimate the parameters of the GAMMI model with specified link and variance function.

Fixing the values of  $\beta_j$  and  $\delta_{nj}$  reduces model (1) to a GLM over the rows, whereas fixing the values of  $\alpha_i$  and  $\gamma_{ni}$  reduces model (1) to a GLM over the columns. This property of the GAMMI model provides the basis for devising a procedure for estimation of the parameters.

### 2.2.1 Forming Initial Values for the Environment Main and Interaction Effects

When a GAMMI model with  $k$  axes is to be fitted and no results are available from fits with  $m < k$  axes, fit a main effects model to the two-way table,  $Y_{ij} = \mu + \alpha_i + \beta_j$  and save the estimates  $\hat{\beta}_j$  of the column main effects. Also choose arbitrary column scores,  $\hat{\delta}_{nj}$ , for the axes 1 to  $k$ . These scores must not be all equal and should be standardized and orthonormalized;

$$\sum_{j=1}^L \hat{\delta}_{nj} = 0, \sum_{j=1}^L \hat{\delta}_{nj}^2 = 1, \quad \text{for } n = 1, \dots, k$$

$$\sum_{j=1}^L \hat{\delta}_{nj} \hat{\delta}_{n'j} = 0, \quad \text{for } n \neq n'$$

When parameter estimates are available for GAMMI models with  $m < k$  axes, the values of  $\hat{\beta}_j$  and  $\hat{\delta}_{nj}$ , with  $n$  now from 1, ...,  $m$ , can be used as initial

values for the GLM of the next step. For the  $\hat{\delta}_{nj}$  values belonging to the axes  $m+1, m+2, \dots, k$ , arbitrary values can again be chosen.

### 2.2.2 Genotype Main and Interaction Effects estimation

Put  $b_j = \hat{\beta}_j$  and  $d_{nj} = \hat{\delta}_{nj}$  and fit the row regression

$$Y_{ij} = \mu + \alpha_i + b_j + \sum_{n=1}^k \gamma_{ni} d_{nj}.$$

Here the values of  $b_j$  are supposed to be known and do not need to be estimated known as offsets in GLM. The  $d_{nj}$  values represent concomitant variables on the column factor. They are called offsets in GLM. The parameters  $\alpha_i$  and  $\gamma_{1i}, \gamma_{2i}, \dots, \gamma_{ki}$  are the intercept and slopes for the regression of the entries of row  $i$  on the variables  $d_1, d_2, \dots, d_k$ . The row main effects,  $\hat{\alpha}_i$ , need not necessarily be centered within the iteration process, this may just as well be done after convergence.

### 2.2.3 Centering and Orthogonalizing the Genotype Interaction Effects

$$\sum_{i=1}^G \hat{\gamma}_{ni} = 0, \quad \text{for } n = 1, 2, \dots, k$$

$$\sum_{i=1}^G \hat{\gamma}_{ni} \hat{\gamma}_{n'i} = 0, \quad \text{for } n \neq n'$$

### 2.2.4 Environment Main and Interaction Effects estimation

Put  $a_i = \hat{\alpha}_i$  and  $c_{ni} = \hat{\gamma}_{ni}$  and fit the column regression

$$Y_{ij} = \mu + a_i + b_j + \sum_{n=1}^k c_{ni} \delta_{nj}$$

Now the  $a_i$  values form offsets, while the  $c_{ni}$  values represent concomitant variables on the row factor. The parameters  $\hat{\beta}_j$  and  $\delta_{1j}, \delta_{2j}, \dots, \delta_{mj}$  are the intercept and slopes for the regression of the entries of column  $j$  on the variables  $c_1, c_2, \dots, c_m$ . Again, there is no need to center the column main effects,  $\hat{\beta}_j$  within the procedure.

### 2.2.5 Standardizing and Orthonormalizing the Environment Interaction Effects

For the calculations involved in the standardization and orthonormalization of the column interaction effects, see Section 2.2.1. If convergence has occurred,

stop, otherwise go back to Section 2.2.2 using the values for  $\hat{\beta}_j$  and  $\hat{\delta}_{nj}$ , from Sections 2.2.4.

Change in deviance of either or both the row and column regression can be used as the convergence criterion, or changes in estimates of either or both row and column parameters. Upon convergence the residual deviance of the row regression will be equal to that of the column regression.

The number of multiplicative terms to be retained in GAMMI models can be assessed by generalizing well-known tests for AMMI models. A simple test, proposed by Gollob (1968), attributes  $(G - 1) + (L - 1) - (2n - 1)$  degrees of freedom to the eigenvalue corresponding to axis  $n$ , this being the difference between the number of parameters to be estimated and the number of identification constraints imposed. Goodman (1981) arrived at an equivalent number of degrees of freedom for the interaction terms in log-bilinear models. The corresponding mean square is then tested against an estimate of error. However, in the presence of multiplicative interaction which clearly dominates noise, Gollob's rule has been shown to be satisfactory (Goodman and Haberman, 1991; Gauch, 1992).

**Testing of assumptions:** The Shapiro–Wilk multivariate normality test and the Bartlett test for homogeneity of variance were used to determine whether to apply an AMMI model or a GAMMI model to analyze the  $G \times E$  interactions for Cobs count data in maize.

For fitting GAMMI model alternating regression between row and column regressions was performed, where each regression includes GLM class that is done iteratively by using iterative reweighted least square (IRLS) method.

**Analysis of Deviance:** In AMMI model (ANOVA in general) we test effect of factors by using sum of squares while in GAMMI model (GLM in general) we use deviance (Dobson 2002). We use F test to determine multiplicative axis by comparing ratio between mean deviance component tested and error mean deviance to F table value.

**Appropriateness of Model:** We investigate appropriateness of model by using error diagnostics visually, i.e., errors plot. Q–Q plots are used to determine if the choice of distribution is appropriate or not.

**Analysis of Stable Genotypes:** Information about stable genotype can be obtained through biplot configuration. Biplot gives row and column scores plot simultaneously. Both the genotype vectors and the environment vectors are drawn so that the specific interactions between a genotype and an environment (i.e., the performance of each genotype in each environment) can be visualized. The interpretation rule is: the performance of a genotype in an environment is better than average if the angle between its vector and the environment's vector is less than  $90^\circ$ ; and it is near average if the angle is about  $90^\circ$ . The angle determines the direction of the interaction, i.e., above or below average in the specific environment; the magnitude of the interaction is determined by both the cosine of the angle and the length of the vectors.

Analysis and graphics were obtained using R Studio version 1.2.1335.

### 3. RESULTS AND DISCUSSION

The first step in applying the GAMMI methodology was to determine variances for the number of cobs for location and genotype. There was a larger variability

**Table 1.** Variances of number of cobs estimated for 32 maize genotypes grown in 13 environments during Kharif 2019

Genotypes	Variance	Genotypes	Variance	Genotypes	Variance	Genotypes	Variance
AH 8178	34.269	DH 329	49.025	JH 32006	41.358	KNMH 4193	21.974
AH 8323	37.935	DH 330	32.423	JH 32328	27.974	LMH 1946	20.974
AH 8622	45.834	DKC 7204	23.001	JH 32375	22.423	Rasi 50252	31.923
AH1608	32.923	EH 3524	35.935	JH 32385	54.564	VEH18-1	31.935
AH3254	66.423	EH 3571	57.526	JH 32391	38.411	Bio 605 (C)	45.192
BAU-MH-18-1	36.807	FH 3912	26.411	KH 102E	26.089	DKC7074 (C)	27.269
BYMH-13-5	33.923	HKH 370	60.912	KMH 18-13	29.256	Vivek Hybrid 45	34.166
DH 321	33.589	IMHSB-19K-1	27.436	KMH 18-15	33.001	Vivek Hybrid 51	26.192

in number of cobs among environments. For environments, variances for number of cobs ranged from 1.515 (BHUB) to 20.221(CHIND) (Table 2) and the variances for number of cobs among genotypes ranged from 20.974 (LMH 1946) to 66.423 (AH3254) (Table 1).

**Table 2.** Variances of number of cobs estimated for 13 environments with 32 maize genotypes grown during Kharif 2019

Environment	Variance
AMBI	15.732
CHIND	20.221
GODH	19.419
UDAI	13.192
BHU	10.318
BHUB	1.515
DHOL	7.467
RANC	4.119
SABOU	12.458
IARI	13.805
KARN	1.733
LUDH	5.081
PANT	12.483

### Testing of assumptions

The initial assumptions of normality and homoscedasticity of the data were checked using the Shapiro-Wilk test and Bartlett test, respectively. The results of the Shapiro-Wilk test (W) indicated that the data were not normally distributed ( $W = 0.9835$ ,  $p < 0.0001$ ).

Also, the hypothesis of equality of variances from different locations was rejected (D.F. = 12;  $\chi^2 = 102.23$ ;  $p < 2.2 \times 10^{-16}$ ) based on result of the Bartlett test and for genotypes it was accepted (D.F. = 31;  $\chi^2 = 16.931$ ;  $p < 0.981$ ).

### Fitting of GAMMI model with Poisson distribution and log link function

The GAMMI model for cob count data in maize was fitted using poisson distribution with the log link function. Analysis of deviance is given in Table 3. The ANODEV with the log link function was significant for genotype and environment and also for the first three axes of the  $G \times E$  interaction. GAMMI model with three axes is appropriate because mean deviance ratio of axis 3 is significant at p-value. Axis 1, axis 2 and axis 3 accounted for approximately 26.12%, 20.43% and

16.58% of variance associated with this interaction, respectively (Table 4).

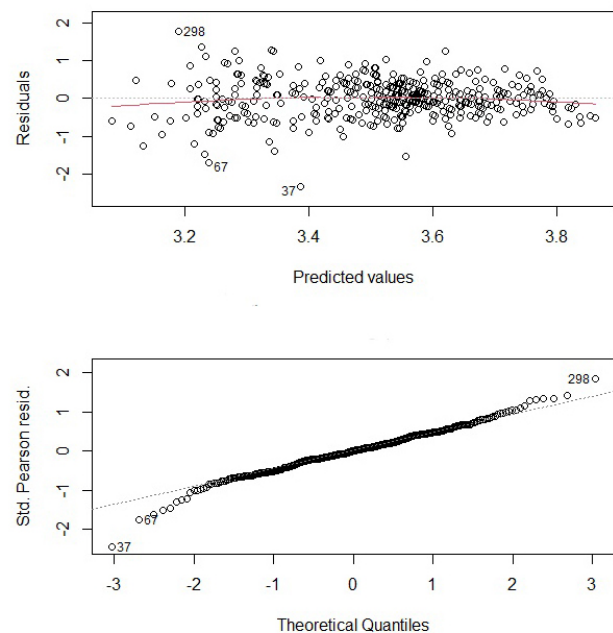
**Table 3.** Analysis of deviance (ANODEV) for number of cobs in maize data

Source	D.F	Deviance	Mean deviance	Fcal	P>F
Genotype	31	38.14	1.23	7.63	< 0.001*
Environment	12	320.69	26.72	140.53	< 0.001*
Axis 1	42	25.72	0.61	3.79	< 0.001*
Axis 2	40	20.42	0.51	3.16	< 0.001*
Axis 3	38	16.58	0.43	2.38	< 0.001*
Residual	252	38.77	0.15		
Total	415	117.87			

**Table 4.** Deviance proportion in relation to the proposed axes for the mean values of number of cobs

Axes	Deviance	Deviance proportion	Cumulative proportion
Axis 1	25.72	0.26	0.26
Axis 2	20.42	0.20	0.46
Axis 3	16.58	0.16	0.62
Residuals	38.77	0.38	1

Plots of deviance residuals versus predicted values and normal QQ plot for GAMMI model with log link function are depicted in Fig 1. Plotting of errors residuals versus predicted values shows that there is no anomaly. Plotting of Normal Q-Q plot indicates



**Fig. 1.** Error plot for cobs count data: Residuals vs predicted values plot and Normal Q-Q plot for GAMMI model

improperness of link function, if the plot is non linear. The influence of error was minor, as can be seen in the Normal QQ plot and it is almost near to a straight line so, GAMMI model with Poisson distribution and log-link function fits our data well.

The relative contribution of genotype and environment to the interaction is shown through GAMMI Biplot in Fig. 2 with the first and second axis explaining 26.12 and 20.43% of the interaction sum of squares. It describes the variability associated with the first two axes.

Most of the genotypes showed higher specific adaptability for environments BHU, BHUB, DHOL, RANC, SABOU, LUDH, PANT and KARN. AH3254, AH8622 showed no specific adaptability to any environment. Genotype fac1.UDAI is adapted to environment UDAI, it indicates a high mean productivity of genotype in selected environment. As regards the environments, poor contributions were presented by the environments GODH, CHIND and IARI (Fig. 2).

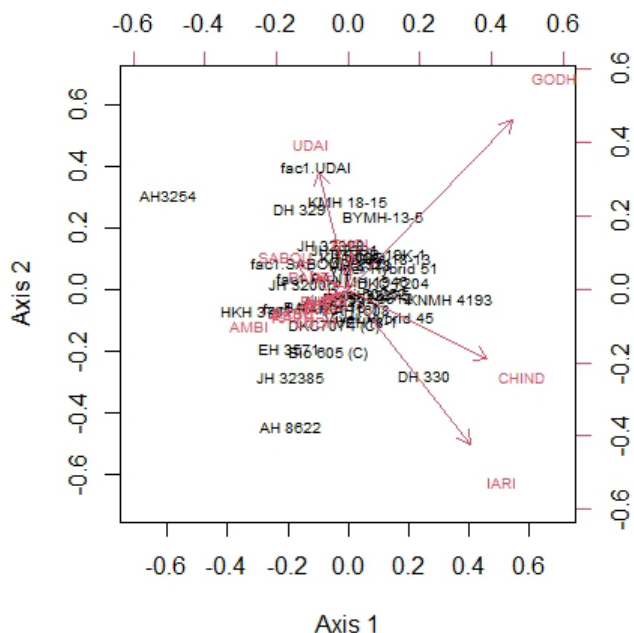


Fig. 2. GAMMI Biplot for cobs count data with logarithm link function

**Fitting of AMMI model to G×E data**

Next, we analyzed the same data with a classical AMMI model. Interaction was again determined by three multiplicative axes which are called as Interaction principal component analysis axes in AMMI.

The AMMI ANOVA (Table 5) indicates that maximum contribution towards variation (71.65%) was made by environment effect followed by G×E interaction (19.86%) and genotypic variation (8.48%). The GEI was partitioned into three interaction principal components analysis axes (IPCA). All the three axes IPCA1, IPCA2 and IPCA3 were found significant using the Gollob’s F-test. IPCA1, IPCA2 and IPCA3 of the AMMI model captured 22.65%, 17.98% and 15.56% of the GEI sum of squares (SS), respectively.

Table 5. Analysis of variance for AMMI model fitted to maize (number of cobs) data

Source	D.F	Sum of squares	Mean square	Fcal	Sum of squares %
Genotype	31	1276.12	41.16	5.12	8.48
Environment	12	10777.04	898.08	111.84	71.65
G×E interaction	372	2987.89	8.03	1.55	19.86
IPCA1	42	676.96	16.12	3.11	22.65
IPCA2	40	537.33	13.43	2.59	17.98
IPCA3	38	465.10	12.23	2.36	15.56
Residual	252	1308.49	5.19		
Total	415	15041.04			

The relative contribution of genotype and environment to the interaction is shown through AMMI Biplot in Fig.3 with the first and second axis explaining 22.65 and 17.98% of the interaction sum of squares.

Here, most of the genotypes showed higher specific adaptability for environments BHU, BHUB, RANC and KARN. AH3254, AH8622 showed no specific adaptability to any environment. Genotype JH 32385 is adapted to environment AMBI, it indicates a high mean productivity of genotype in selected environment. As regards the environments, poor contributions were presented by the environments GODH, CHIND, AMBI and IARI (Fig. 3).

**Fitting of AMMI model to the transformed G×E data**

Data was first transformed with the help of square root transformation and then analyzed by an AMMI model. The AMMI ANOVA (Table 6) indicates that maximum contribution towards variation (69.85%) was made by environment effect followed by G×E interaction (21.26%) and genotypic variation (8.85%). In this case also all the three axes IPCA1, IPCA2 and IPCA3 were found significant using the Gollob’s F-test. These axes accounted for (25.29%), (20.19%) and (14.01%) of the GEI sum of squares (SS), respectively.

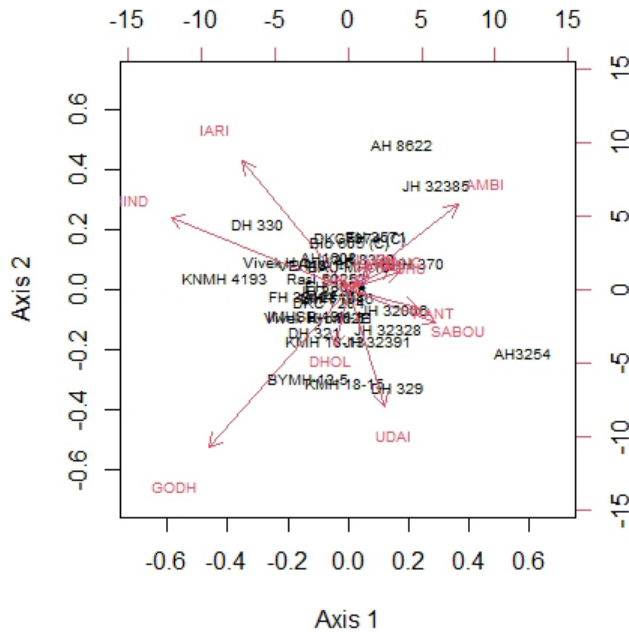


Fig. 3. AMMI Biplot for cobs count data

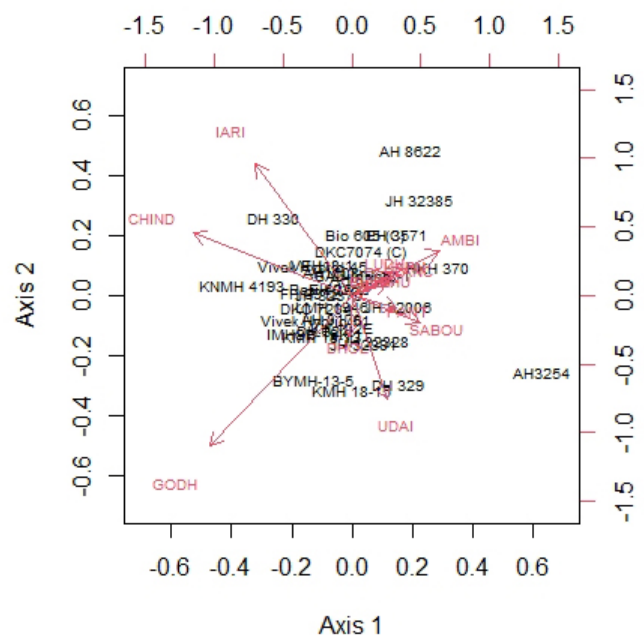


Fig. 4. AMMI Biplot for transformed data

Table 6. Analysis of variance for AMMI model fitted to square root transformed maize (number of cobs) data

Source	D.F	Sum of squares	Mean square	Fcal	Sum of squares %
Genotype	31	10.43	0.34	4.85	8.85
Environment	12	82.39	6.86	98	69.89
G×E interaction	372	25.06	0.07	1.75	21.26
PCA1	42	6.34	0.15	3.75	25.29
PCA2	40	5.06	0.13	3.25	20.19
PCA3	38	3.51	0.09	2.25	14.01
Residual	252	10.15	0.04		
Total	415	117.87			

The relative contribution of genotype and environment to the interaction is shown through AMMI Biplot in Fig.4 with the first and second axis explaining 25.29 and 20.19% of the interaction sum of squares. From Fig. 4, it is evident that most of the genotypes showed higher specific adaptability for environments BHU, BHUB, RANC, DHOL, LUDH, PANT and KARN. In these locations, most of the genotypes can be grown. AH3254, AH8622 and JH 32385 showed no specific adaptability to any environment. As regards the environments, poor contributions were presented by the environments GODH, CHIND and IARI. These can be considered examples of unfavorable environments.

### Comparison of models

Table 7 shows the comparison among the three models applied to G×E data of number of cobs in maize in terms of variability explained by the first three axes. From the table it is evident that maximum variability (63.13%) explained by the axes is in GAMMI model followed by AMMI model applied to square root transformed data (59.49%) and the least variability (56.19%) was explained in the case of classical AMMI model. Therefore, a GAMMI model fitted with Poisson distribution with log link is most appropriate for the count data as in our case.

Table 7. Comparison of models in terms of explained variation by their first three axis

Models	Axes	Variability explained (%)	Cumulative Variability explained (%)
GAMMI	Axis 1	26.12	26.12
	Axis 2	20.43	46.55
	Axis 3	16.58	<b>63.13</b>
AMMI	IPCA 1	22.65	22.65
	IPCA 2	17.98	40.63
	IPCA 3	15.56	<b>56.19</b>
AMMI with transformed data	IPCA 1	25.29	25.29
	IPCA 2	20.19	45.48
	IPCA 3	14.01	<b>59.49</b>

#### 4. CONCLUSION

AMMI analysis is of great importance in agricultural data; but in case of non-normally distributed data, the appropriateness of AMMI model is being doubtful. In such cases, data can be handled by introducing multiplicative terms for interaction in wider class of modeling, Generalized Linear Models which is called as Generalized AMMI model. The present study used GAMMI model with Poisson distribution and log link function for studying  $G \times E$  interaction data for number of cobs in maize during Kharif season. Biplot of Poisson GAMMI model with link function logarithm gives additional information about  $G \times E$  interaction. Further the results of GAMMI model were compared with classical AMMI model and AMMI model applied to transformed (square-root) data. The criterion used for comparison was explained variability in terms of axes which was highest (63.13%) in case of GAMMI models as compared to other two models. It was observed that GAMMI with Poisson distribution and log link function can be applied to count data when the assumption of normality is violated. Biplot interpretation also showed that highest adaptability of genotypes in most of the environments was in case of GAMMI-Biplot. Hence, GAMMI model would help the researchers to study  $G \times E$  interaction data well if the data is not normally distributed.

#### REFERENCES

- Acorsi, C.R.L., Guedes, T.A., Coan, M.M.D., Pinto, R.J.B., Scapim, C.A., Pacheco, C.A. P. and Casela, C.R. (2016). Applying the generalized additive main effects and multiplicative interaction model to analysis of maize genotypes resistant to grey leaf spot. *The Journal of Agricultural Science*, **155**(6), 939-953.
- Dobson, A.J.A. (2002). *Introduction to Generalized Linear Models*. New York, USA: Chapman & Hall CRC.
- Gabriel, K.R. (1971). The biplot graphic display of matrices with application to principal component analysis. *Biometrika*, **58**(3), 453-467.
- Gauch Jr, H.G. (1988). Model selection and validation for yield trials with interaction. *Biometrics*, 705-715.
- Gauch, H.G., Jr. (1992). *Statistical Analysis of Regional Yield Trials: AMMI Analysis of Factorial Designs*. Amsterdam: Elsevier.
- Gollob H.F. (1968). A statistical model which combines features of factor analytic and analysis of variance techniques. *Psychometrika*, **33**, 73-115.
- Goodman, L.A. (1981). Association models and canonical correlation in the analysis of cross- classifications having ordered categories. *Journal of the American Statistical Association* **76**, 320-334.
- Goodman, L.A. (1991). Measures, models and graphical displays in the analysis of cross-classified data. *Journal of the American Statistical Association* **86**, 1085-1138.
- Hadi, A.F., Mattjik, A.A. and Sumertajaya, I.M. (2010). Generalized AMMI models for assessing the endurance of soybean to leaf pest. *Journal Ilmu Dasar*, **11**(2), 151-159.
- Hinkley, D. (1985). Transformation diagnostics for linear models. *Biometrika* **72**, 487-496.
- Kempton, R.A. (1984). The use of biplots in interpreting variety by environment interactions. *The Journal of Agricultural Science*, **103**(1), 123-135.
- Snee, R.D. (1982). Nonadditivity in a two-way classification: is it interaction or nonhomogeneous variance. *Journal of the American Statistical Association* **77**, 515-519.
- Van Eeuwijk, F A. (1995). Multiplicative interaction in generalized linear models. *Biometrics* **51**, 1017-1032.
- Yan, W., Hunt, L A., Sheng, Q. and Szlavnic, Z. (2000). Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Science*, **40**(3), 597-605.