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Research Article

Variability and stability analyses for yield and related traits of baby corn (*Zea mays* L.) genotypes grown under NE region of India

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Abstract
Baby corn is gaining preference as a vegetable across different parts of India but the availability of varieties specific to baby corn purposes is limited. To increase production, it is essential to study the variability and stability of genotypes that can be used for baby corn purposes across different environments. Assessment of genetic variability among 12 baby corn genotypes for nine quantitative traits revealed that days to 50% silking and cob weight are essential traits for increasing baby corn yield. Environment plays a predominant role in determining the stable performance of genotypes. AMMI and GGE biplot analysis provided a clear idea of genotype and environment interaction. The results of the present study showed the influence of environments on the evaluated genotypes across seasons. Which- won- where biplot revealed that pre *kharif* season was better for higher baby corn yield and also the genotype GAYMH-4 was stable across the three evaluated environments with respect to baby corn yield without husk.

Keywords: Baby corn, AMMI, GGE, GEI, Silking.

INTRODUCTION

Among the cereal crops, maize has the highest yielding potential and currently, around 1147.7 million MT of maize is being produced in over 170 countries with average productivity of 5.75 t/ha (FAOSTAT, 2020). In India maize is mainly cultivated for food, feed and industrial products like starch, alcoholic beverages, oil, cosmetics etc. Recently maize is gaining importance as a vegetable crop across the world. Specialty corns like baby corn are young finger-like unfertilized maize consumed as a vegetable in early crop stages. It is considered a safe vegetable as it is harvested without any chemical residues. In nutritional aspects, baby corns are a rich source of iron, calcium and vitamins (Shahi and Gayatonde, 2017; Magudeeswari *et al*., 2019) which attracts consumers. However, the cultivation area and production are restricted to few places like Delhi, Uttar Pradesh, Haryana, Maharashtra, Karnataka, Andhra Pradesh, Telangana and hilly areas like Manipur, Meghalaya. India is a country with diverse environments and varied climatic conditions and hence crop variety should express stable performances across varied environmental conditions. The northeastern region of India holds maximum diversity for maize landraces and its cultivation if favoured by environment and soil (Devi *et al*., 2022). The weather and seasonal differences in this region especially in the Manipur favor the potential cultivation of baby corn.

Environment plays an important role in determining the stability of the genotypes. Multi-environment testing (MET) helps in detecting the influence of environment on the character expression of genotypes (Kivuva *et al*., 2014; Ruswandi *et al*., 2022). It is a common observation that quantitative characters are often affected by environments, hence the resultant genotype by environment (G X E) interaction often complicates the interpretation of results obtained and reduces the efficiency of selecting the best genotypes (Annicchiarico and Perenzin, 1994, Ruswandi *et al*., 2020). The relative performance of an individual will change across the environments due to changes in edapic, climatic and biotic factors (Dixon and Nukenine, 1997; Katsenios *et al*., 2021). Therefore, it is essential to know the influence of G X E on character expression so that the same can be minimized to get the inherent performance of an individual.

Several methods have been proposed to study the G X E interaction and its quantification. The most commonly used stability analyses methods are proposed by Eberhart and Russel (1966), Finlay and Wilkins (1963) etc. Additive main effects and multiplicative interactions or AMMI analysis is being followed mostly now-a-days, as it helps in understanding the interactions graphically (biplot) than other methods. The GGE biplot also provides a clear understanding of the GEI among the genotypes (Yan *et al*., 2000, Yan*,* 2001). Here the GGE refers genotype (G) as a main factor and interaction (GE) as the major source of variation.

These analyses help in the identification of genotypes that perform well under the different agronomic zone, which help in regionalized recommendation and selection of test sites (Gauch and Zobel, 1996; Gauch *et al.,* 2011; Gauch, 2013). With the available information, the AMMI and GEI analysis was performed on baby corn genotypes to find the variability among the genotypes and the performance of different genotypes under varied environmental conditions. With the objective of identifying association among yield contributing traits and stable baby corn genotypes suitable for North East India, a study was carried out involving 12 baby corn genotypes.

MATERIALS AND METHODS

A total of 12 baby corn genotypes *viz*, IMHB 1538, IMHB1525, IMHB 1531, AH-7043, IMHB1539, AH 5021, IMHB 1537, GAYMH -1, IMHB 1532, BVM -2, DMRHB 1305 and HM 4, obtained from All India Coordinated Research Project (AICRP) were evaluated in three different seasons *i.e., kharif* 2016 (E1), *rabi* 2017 (E2), pre *kharif* 2017 (E3) in the college farm of Central Agricultural University, Manipur, India. The field is geographically located at 24.81˚N latitude, and 93.89˚E longitude with average of 97.2 rainy days and average annual rainfall of 1387.8mm per year (https://www.weather-atlas.com/en/india/imphal-climate#rainfall). The total rainfall, maximum, and minimum temperature data recorded during the crop period is presented in **Fig.1**. The experiment was carried out in Randomized Block Design (RBD) with three replications and each genotype was planted in four row plots. In all three seasons, uniform spacing of 60 cm row to row and 20 cm plant to plant was followed. The observations were recorded on randomly selected five plants in each genotype for the following traits *i.e*., plant height (cm), no of cobs per plant, cob length (cm), cob girth (cm), cob weight (g), baby corn yield with husk (g/plant), baby corn yield without husk (g/plant) and observations on days to 50% pollen shedding and days to 50% silking were observed on plot basis.

Individual and pooled season correlation analysis were performed and a correlogram was made using *metan* package (Olivoto and Dal`Col Lucio, 2019) in R studio. The stable performing genotypes were identified using AMMI and GGE biplot analysis. The AMMI analysis which can differentiate the source of variation in to genotype, environment and G x E interaction was performed using STAR software version 2.0.1. The GGE biplot both provide the visual representation of biplots helps in analysing the G x E interaction, genotype ranking and their performances (Yan and Kang, 2003) and the same were obtained by using GEA-R software (CIMMYT).

RESULTS AND DISCUSSION

The mean baby corn yield per plant of 12 genotypes studied under three seasons and pooled mean is presented in **Table 1**. The pooled mean for baby corn yield without husk per plant ranged between 17.11g (BVM-2) to 10.25g (IMHB 1525). Among the twelve genotypes studied, five genotypes (IMHB 1532, GAYMH-1, BVM-2, AH 5021, HM-4) recorded higher average mean baby corn yield without husk per plant. Pooled analysis of variance showed the genotypes were significantly different for all the traits except cob girth and no. of cobs per plant. Variability studies revealed that highest genotypic coefficient of variation (GCV) was observed for yield without husk per plant (46.95%) followed by cob weight (27.71%), cob length (27.06) and the lowest was observed for days to 50% pollen shedding (3.31%) and cob girth (4.8%). Phenotypic coefficient of variation (PCV) was highest for yield without husk per plant (50.54%) followed by cob weight (35.14%), yield with husk per plant (34.44%) and lowest for days to 50% pollen shedding (4.33%) and days to 50% silking (5.57%) (**Fig. 2**). Generally, GCV values are considered most reliable to use in breeding programmes. The traits with high GCV to PCV are mostly preferred and in our study yield without husk and cob weight were observed to record highest GCV and PCV values suggesting the selection of genotypes based on these traits could be advantageous.

Highest heritability was observed for yield without husk per plant (86.28%) followed by plant height (82.62%), days to 50% silking (78.45%) and the lowest was observed for cob girth (27.21%). The genetic advance as percentage of mean was observed to be highest for yield without husk per plant (89.83%) followed by cob length (52.89%), cob weight (45.02%) and lowest observed for cob girth (5.16%) and days to 50% pollen shedding (5.21%) (**Fig.2**). The traits with high heritability and genetic advance are controlled by additive gene action. For such traits, selection method of breeding would provide the

Table 1. Pooled mean data of baby corn genotypes evaluated for nine quantitative traits

	Genotypes	Days to 50% pollen shedding	Days to 50% silking	Number of cobs per plant	Plant height (cm)	Cob length (cm)	Cob girth (cm)	Cob weight (g)	Yield with husk (g/plant)	Yield without husk (g/plant)
G1	IMHB 1538	65.44	69.223	1.8	114.447	14.135	9.21	41.357	76.71	98.47
G2	IMHB1525	66.33	69.777	1.58	119.797	17.3525	9.483	50.11	80.11	92.21
G3	IMHB 1531	65.56	69.78	1.71	113.77	15.89	9.563	47.22	83.44	110.36
G4	AH-7043	65.33	69.443	1.8	108.747	16.275	9.44	50.797	91.71	119.26
G5	IMHB1539	65.78	70.553	1.67	120.87	19.07	9.453	53.667	96.11	102.99
G6	AH 5021	67.11	71.667	1.64	127.287	18.76	9.313	57.553	84.56	119.03
G7	IMHB 1537	65.33	70.777	1.71	128.93	17.8025	9.033	46.223	70.56	135.99
G8	GAYMH -1	66.78	72.33	1.84	123.487	17.475	9.19	51.333	89.22	140.62
G9	IMHB 1532	67.22	72.113	1.84	120.713	15.935	9.76	55.11	98.89	146.76
G10	BVM -2	67.11	72.337	1.76	112.28	16.7825	9.57	58.887	100.22	154.01
G11	DMRHB 1305	66.11	71.11	1.58	108.8	20.4325	9.483	60.113	90	103.94
G12	HM4	68.44	74	1.64	116.093	16.795	9.697	46.447	76.44	107.7

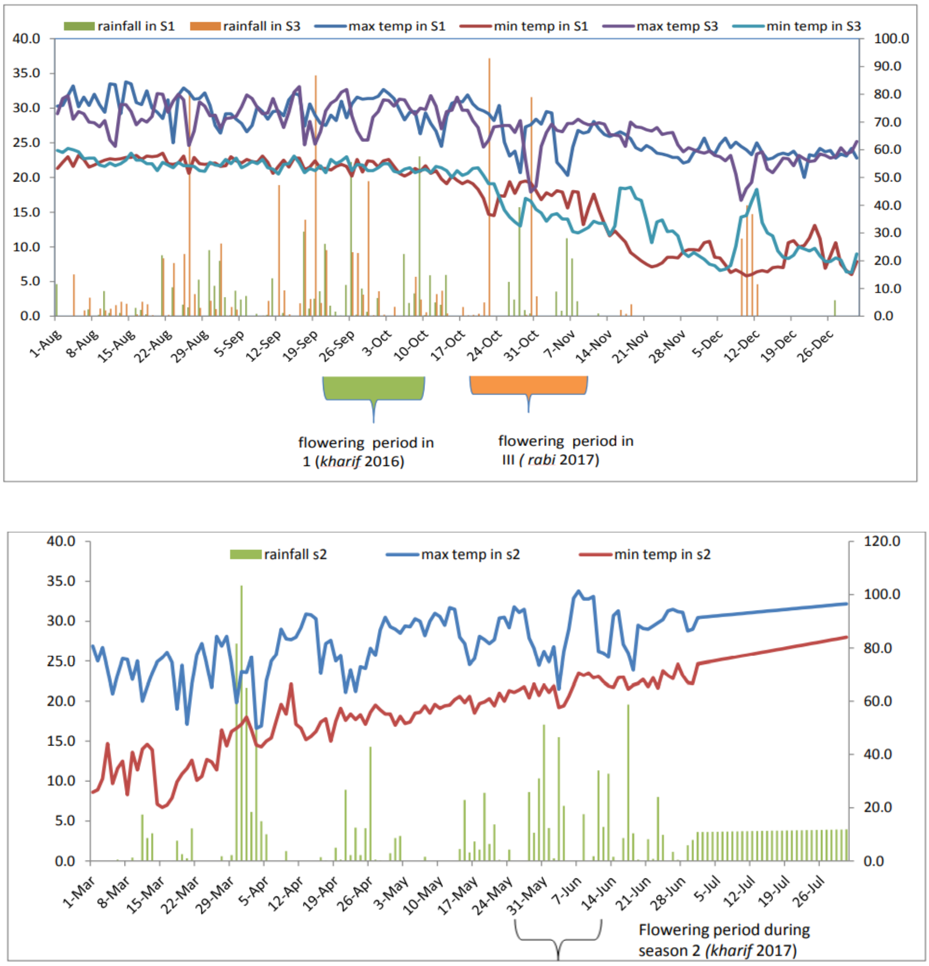

Fig. 1. Weather data (temperature and rainfall) recorded during the crop season *Kharif* 2016 (E1), *Rabi* 2017 (E2) and pre *Kharif* 2017 (E3).

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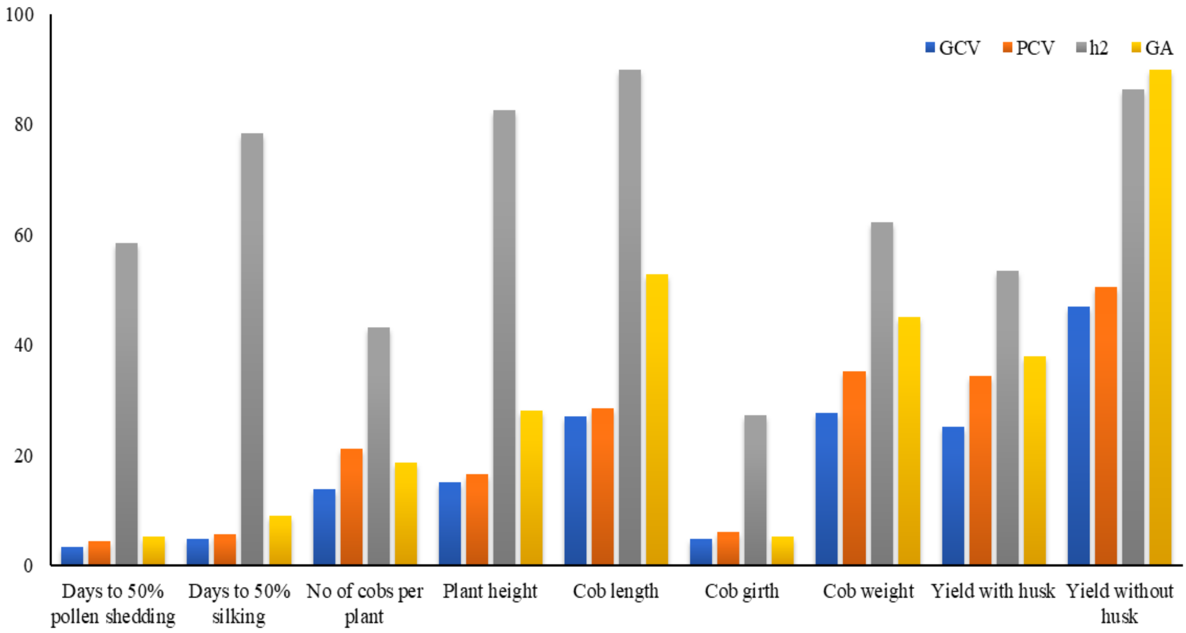


Fig. 2. Coefficient of variation, heritability and genetic advance of nine quantitative traits studied on baby corn genotypes

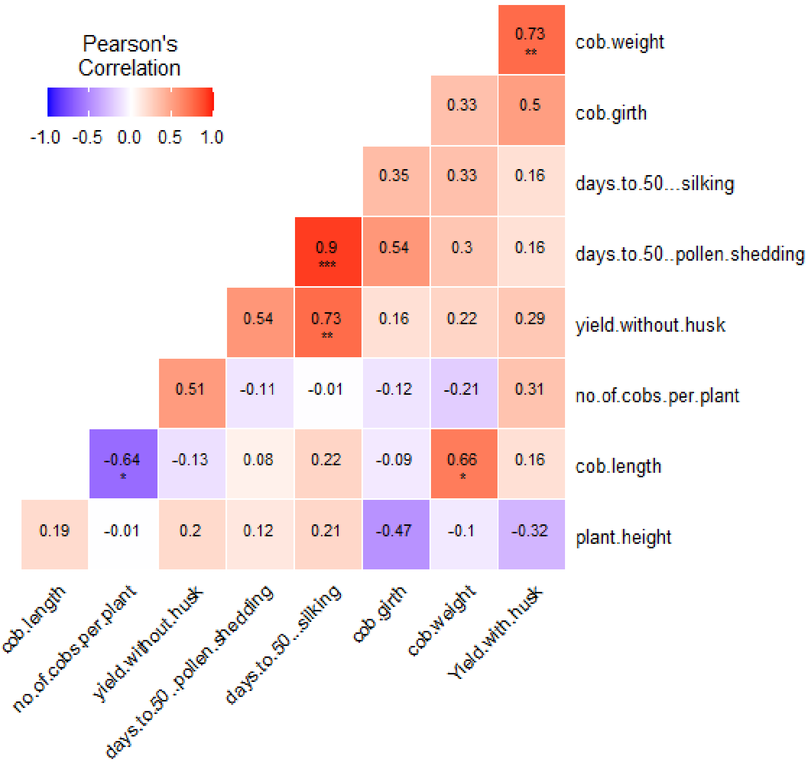
significant results. As per the suggestion of Najeeb *et al*. (2009), heritability and genetic advance are not always linked but the combination of two would result in effective picking of a superior genotype for the traits under study.

Correlation analysis between nine morphological traits revealed a positive significant association between days to 50% tasselling and days to 50% silking (0.9), days to 50% silking and baby corn yield without husk (0.73), cob weight and baby corn yield with husk (0.73) and cob length (0.66) (**Fig.3**). So, selection of these traits will pave a way for the indirect selection of better genotypes.

Genotype and environment interaction (GEI) is an important source of variation for all crops. The stability of genotype represents a stable response across environmental conditions. Based on this idea the genotype with minimum variance for traits across different environments are considered as stable genotype (Becker and Leon, 1988). So, analysing G x E interaction is necessary for the breeders in order to plan the distribution of new varieties and also it is an urge to identify the genotypes with specific and general adaptation across the environment (Farshadfar *et al.,* 2012; Chandrasekhar et al., 2020; Patil et al., 2020; Kumawat et al., 2023).

ANOVA of AMMI analysis revealed that environments were significantly different for all the traits. Significant difference among genotypes was observed for all traits except for number of cobs per plant and cob girth (**Table 2**). The proportion of variation due to environments was highest indicating significant differences among environments and their influence on genotypes. The G x E interaction was found significant for most of the characters except number of cobs per plant. The mean sum of square value for G x E interaction was higher than genotype mean sum of square indicating the differential response of genotypes on environments. AMMI analysis showed that above 90% variation was contributed by environments for days to 50% pollen shedding (98.24), days to 50% silking (96.11), cob girth (92.14) and plant height (95.58), while it was above 50% for number of cobs per plant (66.88), cob length (56.25) and yield without husk (62.81). In case of the remaining traits environmental contribution was observed to be low. The contribution of G x E component to the total variation was above 20% for number of cobs per plant (21.48), cob weight (52.01) and yield with husk (43.61). The genotypic contribution to total variation observed was above 10% for number of cobs per plant (11.65), cob length (24.09), cob weight (28.24), yield with husk (17.66) and yield without husk (18.83).

The large sum of square (SS) values for environments indicates that the three seasons were diverse for all the studied traits. The presence of large difference among environments causes most of the variation to the trait. This variation might be due to varied rainfall pattern, minimum and maximum temperature across the seasons (**Fig. 1**) which could have impacted baby corn yield and other traits. Furthermore, the significant genotype and environment interaction specify the differential expression of genotypes on the seasons studied. Hence,



* $p < 0.05$; ** $p < 0.01$; and *** $p < 0.001$

Fig. 3. Correlation studies on nine quantitative traits of baby corn genotypes

Table 2. AMMI analysis of variance for nine quantitative traits in 12 baby corn genotypes

Source of variance	Degrees of freedom	Mean sum of square								
		Days to 50 % pollen shedding	Days to 50% silking	Number of cobs per plant	Plant height (cm)	Cob length (cm)	Cob girth (cm)	Cob weight (g)	Yield with husk (g/plant)	Yield without husk (g/plant)
Rep/ environment	6	4.51	7.54 *	0.08	367.03 **	12.48 *	0.59	288.07 **	610.35 **	16.00 *
Environment	2	9347.90 **	8028.18 **	2.58 **	111248.1 **	574.38 **	212.07**	1133.80 **	9728.27 **	848.08 **
Genotypes	11	8.49 *	18.78 **	0.08	402.34 **	44.72 **	0.41	294.68 **	806.78 **	46.22 **
G X E	22	11.01 **	20.19 **	0.08	266.73 **	18.26 **	1.44 *	271.31 **	995.94 **	22.54 **
IPCA 1	12	10.51	26.59	0.10	374.14	27.93	1.98	374.97	1472.64 **	28.36
IPCA 2	10	11.63	12.48	0.04	137.75	6.63	0.80	146.93	423.96	15.54
Error	70	2.78	2.69	0.06	53.69	3.49	0.33	101.09	336.16	5.01
% Of treatment SS due to G	11	0.49	1.24	11.65	1.90	24.09	0.98	28.24	17.66	18.83
% Of treatment SS due to E	2	98.24	96.11	66.88	95.58	56.25	92.14	19.76	38.73	62.81
% Of treatment SS due to G X E	22	1.28	2.66	21.48	2.52	19.67	6.88	52.01	43.61	18.36
% Of G X E SS due to IPCA 1	12	52	71.9	74.5	76.5	83.5	74.9	75.4	80.7	68.7
% Of G X E SS due to IPCA 2	10	48	28.1	25.5	23.5	16.5	25.1	24.6	19.3	31.3

* 5% level of significance; **1% level of significance

it necessitates the study of genotype responses for different seasons.

The AMMI model retrieves the part of the sum of squares (SQG×E) that determines the G×E interaction, which is called the standard portion (the genotype and environment effect), and a residual part, which corresponds to unpredictable and un interpretable responses from the model (Cornelius *et al*., 1996). Thus, the genetic variation can be explained by the different AMMI models. In the present study, the contribution of IPCA1 was higher for days to 50% silking, number of cobs per plant, plant height, cob length, cob girth, cob weight (more than 70%)

AMMI biplot for baby corn yield without husk is presented in **Fig.4**. The x-axis represents mean values and the y-axis represent the IPCA1 values. IPCA1 explains around 68 % of the variation. The results revealed that IMHB 1538, IMHB 1525, HM-4 were having low yield and also low PC1 values. IMHB 1532, IMHB 1537 were high yielders but unstable (low PC1 values). GAYMH-1 was to be average yielder and also less interactive with environments.

The biplot analysis of genotype and environment interaction provides best way of visualizing the interaction pattern of genotypes and environments (Gauch and Zobel,1996; Yan *et al*., 2000) and also results a possible existence of different environment groups in a region (Yan and Kang, 2003). The GGE biplots were constructed using the principal components 1and 2 (PC1 and PC2). The biplot analysis based on performance of baby corn for three seasons, with respect to yield and yield attributing traits indicated that 76.3% of variation was explained by PC1 and 19.7% variation was explained by PC2 for yield without husk.

The grouping of different environments and their best suited or yielding genotypes (**Fig.5**) revealed that E3 (pre *Kharif* 2017) had the highest mean baby corn yield without husk and the genotypes IMHB1532, IMHB1537 were the highest yielders (high PCA 1 score) but they were unstable due to large PCA 2 scores. The genotypes HM-4, IMHB 1539, IMHB 1538, DMRHB 1305, IMHB 1525 yielded below average yield and also their PCA 1 score <0. So, these genotypes were considered as unstable or non-adaptable genotypes. The genotypes IMHB 1532 and IMHB 1537 were having PCA1 score >0 and are considered as high yielding genotypes. The genotypes AH 7043 and AH 5021 were having almost low PCA1 scores (Low yielding) and also low PCA2 score (high stable) across environments and also, they were found within the polygon. Hence they were considered as less responsive to the environments. The genotype GAYMH-1 having PCA1 score >0 and also having low PCA2 score was identified to be stable. Genotype ranking based on their performance under the environments explained by

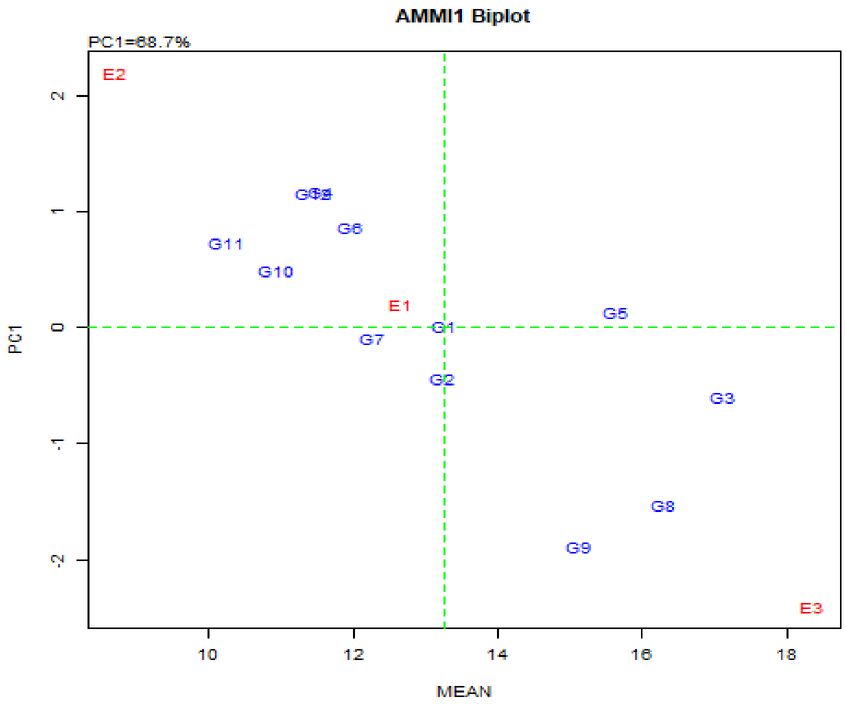


Fig. 4. AMMI biplot analysis of 12 baby corn genotypes evaluated under different environmental conditions. [The environments (E1, E2, E3) are same as mentioned in materials and methods section and the genotypes (G1-G12) names are the same as mentioned in Table 1]

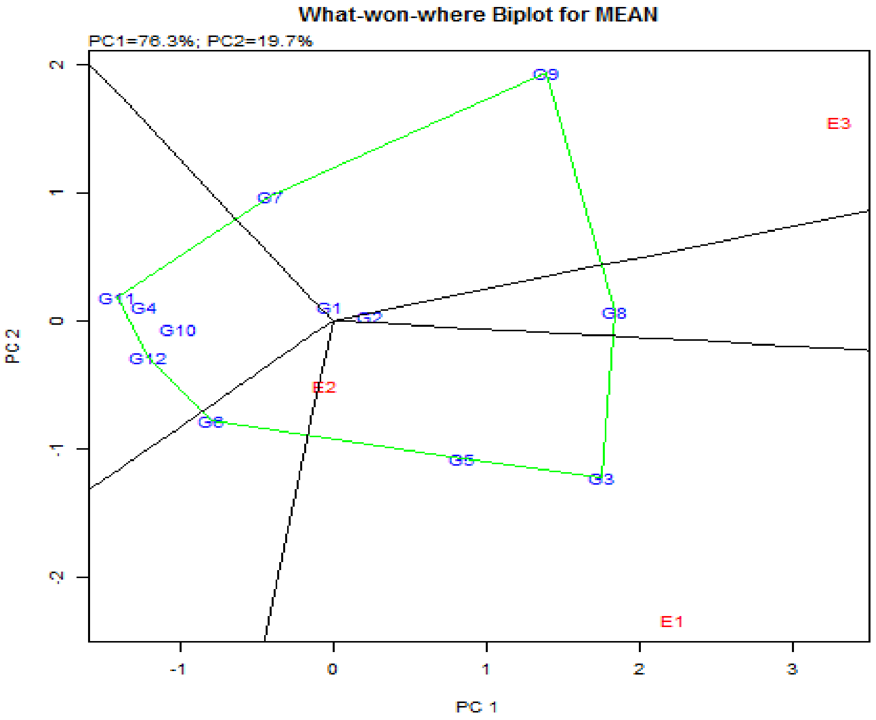


Fig. 5. GGE biplot analysis (Which –Won-Where biplot) for baby corn yield of 12 genotypes evaluated under different environment conditions

[The environments (E1, E2, E3 are same as mentioned in materials and methods section and the genotypes (G1-G12) names are the same as mentioned in Table 1]

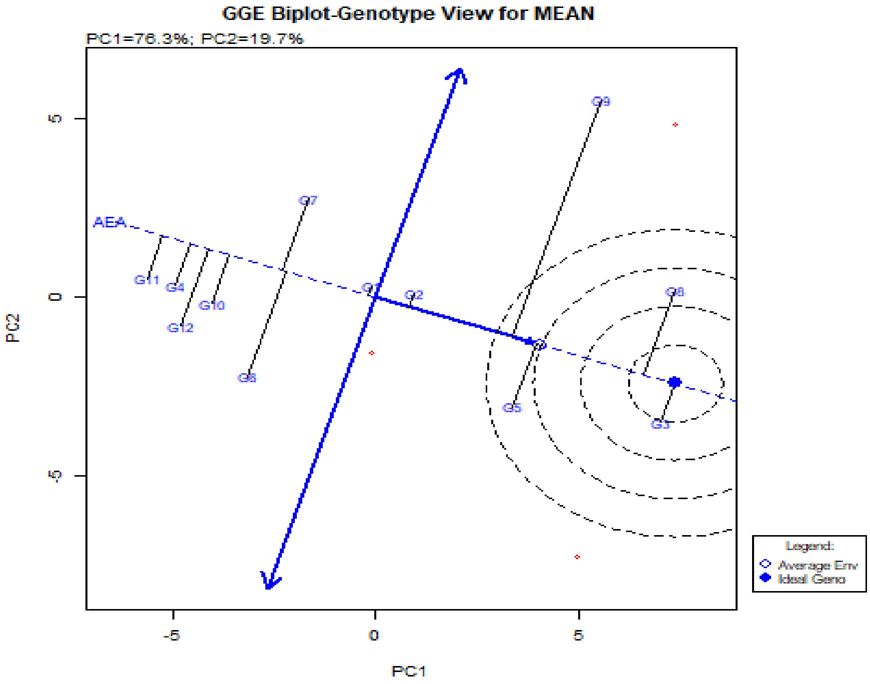


Fig 6. Mean performance and stability of baby corn genotypes evaluated under different environmental conditions

[The environments (E1, E2, E3) are same as mentioned in materials and methods section and the genotypes (G1-G12) names are the same as mentioned in Table 1] a line drawn that passes through the biplot origin and environment (**Fig. 6**) indicates that the genotypes AH 7043 and AH5021 are the low yielders (further way from AEC x axis) and genotypes IMHB1532, IMHB 1537 and BVM-2 were high yielders (closer to AEC x axis arrow). Even though IMHB1532, IMHB1537, BVM-2 were having long projections from AEC x axis, they were unstable genotypes. The genotypes AH7043 and AH5021were having very less projections and were found stable genotypes. GAYMH-4 is considered as desirable genotype with average yield of baby corn without husk. Similarly for cob weight also genotypes GAYMH-4 and AH 5021 were found desirable ones.

This study suggested that the trait yield without husk per plant, in baby corn, was controlled by additive gene action and hence could be improved by selection method of breeding. The above trait was positively influenced by days to 50% silking. Hence selection for earliness could favourably influence yield. The existence of significant amount of variation due to GE interaction among the baby corn genotypes for yield as explained by GGE and AMMI biplots. Both biplots indicated that GAYMH-1 was found to have higher yield on an average and it was also a stable genotype, which could be exploited in future breeding programs.

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