



# GGE biplot analysis of genotype × environment interaction and identification of mega-environment for baby corn hybrids evaluation in India

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## Abstract

Baby corn has emerged as one of the most important sources to augment the farmer's income in peri-urban areas. It has diverse uses as vegetables, snacks, value-added products and assured supply of green fodder for livestock. The multi-location varietal trials mainly emphasize on the identification of new superior cultivars over commercial checks, while genotype × environment interaction (GEI) is ignored. In the current study, 13 baby corn hybrids were evaluated for green ear yield, baby corn yield and green fodder yield over eight locations (environments) in kharif seasons of 2015 and 2016 using GGE biplot analysis. The results revealed a higher proportion of the variation in the data is attributable to the environment (72.4-87.0%), while genotype contributed only 2.5-7.3% of the total variation. GEI contributed 10.5-24.1% of the total variation. Superior stable hybrids for green ear yield, baby corn yield and green fodder yield could be identified using a biplot graphical approach effectively. 'Which won where' plot for each of the traits partitioned testing locations into three mega-environments with different winning genotypes for different traits in respective mega-environments. Thus it can be concluded that similar inferences can be drawn from one or two representatives of each mega-environment instead of using several locations. Hence, the presence of extensive crossover GEI in baby corn multi-location trials clearly suggests the need to emphasize on smaller zonation of testing locations and location-specific breeding. Particularly in baby corn, this is the first study on GGE biplot analysis

to identify mega-environments for effective evaluation of baby corn trials.

**Key words:** Baby corn, stability analysis, GGE biplot, mega-environment, genotype-environment interaction

## Introduction

Corn (*Zea mays*) is one of the most economically valuable grain crops cultivated over 188 million hectares area globally and contributing ~50% (1,170 million metric tons) to the global food production (FAOSTAT 2018). About 60-70% of the cultivated area under corn lies in the domain of the developing world, with a predominant proportion in the low- and lower-middle income countries (Prasanna et al. 2018). Corn is the third most important cereal crop in India after rice and wheat (Yadav et al. 2015) and occupies 10.20 million hectares area with an annual production of 26.26 million tonnes (FAOSTAT, 2018). India is just preceded by the United States, China, Argentina and Brazil in terms of area and production. Corn has diversified uses in the form of food, feed, fodder, biofuel, and provides raw materials for various industrial applications. The changing food habits of the people have augmented the demand for corn by several folds,

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especially specialty corn. Among various specialty corns like sweet corn and popcorn, baby corn has emerged as the most important component due to its use as fresh and processed vegetables, value-added products and snack items (Yadav et al. 2015). Baby corn is the young and unfertilized ear of the corn plant harvested when the silks have either not emerged or just emerged (1 to 3 cm). The baby corn market is increasing day by day because of its use in diverse forms such as vegetables, snacks and other value-added products. Hence the importance of baby corn in augmenting income level of farmers in peri-urban areas has increased. The opportunity of earning foreign exchange by exporting the baby corn and its products through entrepreneurship development is increased by many folds. The successful example of baby corn as a platform for agribusiness can be cited from FieldFresh Foods Private Limited situated at Ludhiana. It produces the baby corn only for export purposes and is the leading baby corn seller brand in Europe (Pandey et al. 2010). After harvest of baby corn, the by-products such as tassel, young husk, silk, and green stalk aids to demand of green fodder for livestock production.

The multi-location and multi-year testing help in the identification of superior and stable genotypes (Rakshit et al. 2012). It also helps in the identification of discriminating environments (locations) through detecting differences among genotypes with minimal replications. The representative locations are characterized by the better performance of selected genotypes in target environments (Yan et al. 2011). The main focus of plant breeders aims at the development of widely adapted cultivars. However, identification of high yielding and stable genotypes that can perform better in less predictable and challenging environments remains a daunting task. Furthermore, the yield is not controlled by the same genetic system over diverse set of environments (Simmonds 1991; El-Soda et al. 2014). Therefore, breeders often target to harness the specific adaptations through development of genotypes for a particular environment (Samonte et al. 2005).

Multi-location testing of cultivars for grain yield is an integral part of any plant breeding programme. But in case of multi-location testing of baby corn trials the traits viz., green ear yield (corn with husk), baby corn yield (corn without husk) and green fodder yield are key traits for consideration. Multi-locations testing of baby corn trials aim at identifying the superior

performing genotypes that exceeds the commercial check for the target traits. However, the emphasis lacks on the most unpredictable component namely target environment and genotype-environment interaction (GEI). Hence, this can be taken care of by conducting multi-location trial (MLT). It can help to know the stability and adaptability of testing genotypes across environments (Scapim et al. 2000). The traditional statistical methods for handling the MLT data in GEI study have some limitations such as ANOVA being an additive model can only describe the main effects effectively (Snedecor 1980), whereas PCA only multiplicative components (Zobel et al. 1988). The purpose of mega-environment analysis relies on  $G \times E$  pattern-based identification of mega-environments (Yan et al. 2011).

Additive main effects and multiplicative interaction (AMMI) model addresses the limitations of ANOVA and PCA. The AMMI model effectively explains the GEI patterns (Zobel et al. 1988). Complex GEI can be understood in simpler and effective manner by use of graphics based biplot methodology (Gabriel 1971). The scatter plot visualization using two factors to explain underlying relationships and interactions is called as biplot. AMMI biplot and GGE biplot are the two most commonly used biplots for understanding GEI. (Cossa 1990; Gauch 1992; Yan et al. 2000; Yan and Kang 2003). Research studies exhibit a debate over the use of AMMI analysis and GGE biplot analysis for visualization and interpretation of MLT data, but the difference being the omission of E component in GGE biplot (Yan et al. 2000; Gauch 2006; Yan et al. 2007; Gauch et al. 2008). However, the comparison studies of GGE biplot with AMMI Models validate the equal efficiency of GGE biplot and AMMI models in understanding GEI (Dias et al. 2003; Ma et al. 2004). Several studies of GGE biplot based stability analysis have been conducted in field corn for understanding GEI (Balestre 2009; Shiri 2013; Boshev et al. 2014; Faria et al. 2017). However, to the best of our knowledge such types of studies are not available for baby corn. All India Coordinated Maize Improvement Project (AICMIP) is the nodal agency for testing the new corn cultivars across wide climatic and geographical conditions of the country. The AICMIP testing locations represent major baby corn growing locations as these are quite diverse in terms of climatic conditions like topography, rainfall, latitude and altitude. Hence, considering this, a study was planned to assess the GEI of 13 baby corn hybrids across eight locations for two years (rainy seasons of 2015

and 2016) using AMMI and GGE biplot graphical approach.

We measured baby corn yield components including green cob yield, baby corn yield and green fodder yield. The study aimed to (i) assess the GEI of baby corn hybrids, (ii) identify stable baby corn hybrids for yield (iii) classify testing locations into mega environments.

## Materials and methods

### Plant materials and experimentation

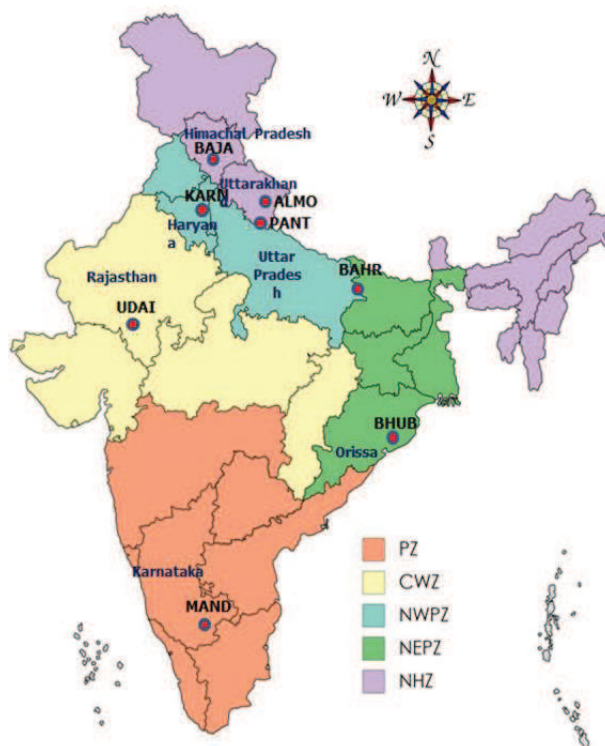
The data used in this study belongs to a sub-set of AICMIP *khari* 2015, 2016 (rainy season) baby corn database, in which 12 hybrids (Table 1) along with a

**Table 1.** Details information on genotypes used in the studied

S.No.	Hybrid code	Pedigree/original name	Source
1	IMR391	IMHB1532	IIMR, Ludhiana
2	IMR392	BVM2	BAU, Ranchi
3	IMR394	AH5021	IARI-New Delhi
4	IMR395	IMHB1538	IIMR, Ludhiana
5	IMR397	IMHB1525	IIMR, Ludhiana
6	IMR398	MBC11-15	TCA Dholi
7	IMR401	IMHB1531	IIMR, Ludhiana
8	IMR402	IMHB1537	IIMR, Ludhiana
9	IMR403	DMRHB1305	IIMR, Ludhiana
10	IMR404	GAYMH1	Godhra Gujarat
11	IMR405	IMHB1539	IIMR, Ludhiana
12	IMR406	IMHB1529	IIMR, Ludhiana
13	IMR408	HM4 (C)	CCSHAU, Hisar

(C)=Check hybrid

commercial check, HM-4 were evaluated in three replications across eight locations. The details on geographical location of testing environments have been given in Fig. 1, Information about the altitude, rainfall and dates of sowing are given in Table 2. The testing locations were distributed among seven states of the country with two locations in Uttarakhand and one each in Rajasthan, Haryana, Himachal Pradesh, Karnataka, Odisha and Uttar Pradesh. Based on the climatic conditions, the testing sites for baby corn hybrids under AICMIP has been grouped into five zones, viz., Northern Hill Zone (NHZ), North Western



**Fig. 1.** Geographical location of testing environments in five zones of AICRP Corn Network

Plain Zone (NWPZ), North Eastern Plain Zone (NEPZ), Peninsular Zone (PZ) and Central Western Zone (CWZ). Among the testing locations, Almora (ALMO) and Bajaura (BAJA) falls under NHZ, Karnal (KARN) and Pantnagar (PANT) falls under NWPZ, Bahraich (BAHR) and Bhubaneshwar (BHUB) comes under NEPZ, whereas Mandya (MAND) and Udaipur (UDAI) represents the PZ and CWZ, respectively. Depending upon the onset of monsoon, the sowing was done during the months of June and July (Table 2). The baby corn hybrids were evaluated in randomized complete block design with four rows each of 4 m length and 50 cm row to row and 20 cm plant to plant distance with standard crop management practices across all locations.

The 13 baby corn hybrids were evaluated for green ear yield (GEY) i.e., cob with husk, baby corn yield (BCY) i.e., cob without husk and green fodder yield (GFY) on plot basis. GEY and BCY data were recorded for weight of green ears (with husk) and baby corn weight (without husk i.e. dehusked) summed over multiple pickings. GFY was recorded after completion of all pickings by summing the weight of all plants. Finally, the plot yield data were converted from kg/m<sup>2</sup> to kg ha<sup>-1</sup> (Kumar et al. 2016).

**Table 2.** Geographical information, seasonal rainfall and sowing dates of baby corn trials across eight environments

Site (Code)	Elevation (metre) above (msl)*	Rainfall (mm)		Date of sowing	
		2015	2016	2015	2016
Almora (ALMO)	1600	264	647	Jul-14	Jul-04
Bajaura (BAJA)	1090	350	317	Jul-04	Jun-30
Karnal (KARN)	253	378	490	Jul-04	Jul-03
Pantnagar (PANT)	244	1168	988	Jun-24	Jun-29
Bahraich (BAHR)	126	386	908	Jul-04	Jun-26
Bhubaneswar (BHUB)	25.9	761	861	Jun-26	Jul-07
Mandya (MAND)	697	367	286	Jul-31	Aug-02
Udaipur (UDAI)	598	442	665	Jun-29	Jul-05

\* = mean sea level

**Statistical analysis**

The ANOVA for AMMI analysis was performed using Agricolae package of R studio for partitioning of variance to genotype, environment and  $G \times E$  components (RStudio, 2014). ANOVA indicated towards the significance of genotype  $\times$  environment interactions for target traits. Thus, additional statistics like AMMI and GGE biplots were done to identify the superior and stable as well as location specific best performers over eight environments. AMMI (Agricolae) and GGEBiplotGUI package of R statistical software were used to generate AMMI and GGE biplots, respectively (CRAN, 2014; RStudio, 2014). The AMMI and GGE biplot analysis were used to visually assess the presence of  $G \times E$  and rank genotype based on stability and mean (Yan et al. 2000; Yan and Kang 2003). The statistical theory of GGE methodology has been explained in detail by Yan and Kang (2003). The MLT data was analyzed as per the methodology of Yan and Tinker (2006) to generate a tester centered (centering 2) GGE biplot. The genotype evaluation and environment (location) evaluation were performed using the 'Mean versus stability' and 'Relation among testers' option of GGE biplot package, respectively (Yan 2001). The identification of winner or best genotypes in specific

**Table 3.** ANOVA and total variation (G+L+GE) explained by genotype (G), environment (E) and GE interaction for GEY, BCY and GFY across 2015 and 2016

Trait/year	Parameters	Source of variation		
		G	E	GE
GEY 2015	MS	9.6**	524.8**	5.4**
	Proportion of G+E+GE (%)	2.7	86.6	10.7
GEY 2016	MS	5.1**	311.6**	3.1**
	Proportion of G+E+GE (%)	2.5	87.0	10.5
GEY Combined	MS	3.8**	364.8**	2.5**
	Proportion of G+E+GE (%)	1.6	90.8	7.6
BCY 2015	MS	0.7**	22.3**	0.5**
	Proportion of G+E+GE (%)	4.2	74.1	21.7
BCY 2016	MS	0.4**	14.4**	0.4**
	Proportion of G+E+GE (%)	3.5	72.4	24.1
BCY Combined	MS	0.31**	15.7**	0.28**
	Proportion of G+E+GE (%)	2.7	80.3	17.0
GFY 2015	MS	135.7**	2588.9**	31.2**
	Proportion of G+E+GE (%)	7.3	81.0	11.7
GFY 2016	MS	87.9**	2341.2**	38.9**
	Proportion of G+E+GE (%)	5.1	79.1	15.8
GFY Combined	MS	90.5**	1925.4**	19.5**
	Proportion of G+E+GE (%)	6.7	83.2	10.1

\*\* P &lt; 0.01; GEY = Green ear yield; BCY = Baby corn yield and GFY = Green fodder yield; MS = Mean sum of square

environments and mega-environments was performed using 'Which-Won-Where' option.

## Results

### *Genotype × environment interaction*

The combined ANOVA indicated significant environment (E), genotype (G) and G×E (GE) effects for GEY, BCY and GFY in both the seasons (Table 3). The relative contributions of each source to the total variation (G+E+GE) are presented in Table 3. It was observed that environment played a most significant role (72.4-87%) in determining phenotypic variation and performance of genotypes. The large G×E along with small G effects were noticed in green ear yield (7.6 %; 1.6%), baby corn yield (17.0%; 2.7%) and green fodder (10.1%; 6.7%) yield, respectively (Table 3).

In 2015, the environment effect was relatively similar to 2016 for green ear and green fodder yield. However, for baby corn yield; it was relatively large during 2015. The environment (location) accounted for 90.8%, 80.3% and 83.2% of the variation in the combined analysis for green ear yield, baby corn yield and green fodder yield, respectively. Genotypes attributed for 1.6%, 2.7% and 6.7% of the variation for green ear yield, baby corn yield and green fodder yield, respectively. Similarly, the contribution of GE in green ear yield, baby corn yield and green fodder yield was 7.6%, 17% and 10.1%, respectively. For green ear yield, environment accounted for 86.6% of the variation in 2015 and 87% in 2016, while genotypes contributed 2.7% and 2.5% in 2015 and 2016, respectively. Proportions of variation explained by GE were 10.7% and 10.5% during 2015 and 2016, respectively. The year-wise and combined ANOVA values depicting the contributions of G, E and GE for all traits under study have been provided in Table 3. The contribution of environment to total variation ranged from 72.4% (minimum) for baby corn yield to 87% (maximum) for green ear yield in 2016. The heritability estimates of MLT data revealed high heritability for all the traits under study (Table 4).

The AMMI model helps better to identify the high yielding genotypes suitable for a single or multiple environment. The first three AMMI selections for each location for all three traits have been provided in Table 5.

### *Polygon view of GGE biplot*

The polygon (which-won-where) view of the GGE biplot

is based on making a polygon through connecting the extreme genotypes. The sides of polygon are dissected perpendicularly by rays to form sectors of biplots (Yan 2001). The falling of different environments into different sectors shows presence of GEI and hence indicating towards the presence of different winning genotypes in different sectors. The genotypes lying at the vertex of particular sectors spanning specific environment(s) are said to be won in that particular environment. In comparison to genotypes falling on vertex, genotypes lying inside polygon are reported to be relatively less responsive to the particular environment (Yan and Tinker 2006). Which-won-where biplots for green ear yield, baby corn yield and green fodder yield over 2 years are presented in Figs. 2a, 2b and 2c. A polygon view of the GGE biplot explained 62%, 71% and 71 % of the genotype and genotype × environment variation for the green ear yield, baby corn yield and green fodder yield, respectively (Figs. 2a, 2b and 2c). The polygon view indicates towards the presence of crossover G × E and mega-environments for all traits, but green ear yield having well distributed polygon was found to be the most informative due to its efficient ability to discriminate environments (Fig. 2a). The polygons for rest two traits had fewer vertices and hence locations were not well separated. All the traits had environments in three sectors with different winning genotypes (Figs. 2a, 2b and 2c). This confirms the existence of G × E for all the traits. For green ear yield, the polygon had five genotypes, viz., AH5021, IMHB1531, IMHB1537, GAYMH1 and IMHB1529 at the vertices. The hybrids AH5021 and GAYMH1 performed best in Udaipur, while IMHB1531 exhibited best performance at Bhubaneswar. Similarly, the hybrid IMHB1537 performed best at Mandya and Pantnagar, while IMHB1529 performed best at Bahraich. Biplot was divided into a total of five sectors, but all testing locations fall only under three sectors and hence representing three mega-environments: first represented by Udaipur with AH5021 and GAYMH1 as winning genotypes. Mandya and Pantnagar comprised second mega-environment with IMHB1537 as the winning genotype while rest of the locations constituted the third mega-environment with IMHB1529 as the winning genotype. For baby corn yield, BVM2 performed best at Bahraich, while IMHB1537 was the winning genotype at Pantnagar and Bajaura. The hybrids IMHB1532 and GAYMH1 performed best at Udaipur. The hybrid, IMHB1525 was poor performer in all the testing environments as no environment fall in its sector. For green fodder yield, AH5021 was the winning genotype at Pantnagar, Mandya and

**Table 4.** Year-wise and combined trait means of genotypes and environments and trait heritability over two years of testing

Genotype/location	GEY (tonnes per hectare)			BCY (tonnes per hectare)			GFY (tonnes per hectare)		
	2015	2016	Combined	2015	2016	Combined	2015	2016	Combined
<b>Genotype<sup>a</sup></b>									
IMHB1532	6.46	5.81	6.14	1.67	1.61	1.64	23.76	29.66	26.71
BVM2	5.91	6.48	6.19	1.45	1.54	1.50	17.28	22.58	19.93
AH5021	6.04	5.62	5.83	1.37	1.17	1.27	25.48	26.22	25.85
IMHB1538	6.05	6.15	6.10	1.47	1.65	1.56	19.43	24.67	22.05
IMHB1525	6.78	5.94	6.36	1.53	1.46	1.50	22.88	27.69	25.29
MBC11-15	7.21	5.15	6.18	1.49	1.36	1.43	23.83	23.71	23.77
IMHB1531	6.46	6.34	6.40	1.51	1.47	1.49	24.90	27.39	26.15
IMHB1537	7.05	6.09	6.57	1.68	1.44	1.56	20.64	25.42	23.03
DMRHB1305	6.95	6.78	6.87	1.52	1.65	1.59	19.61	23.62	21.62
GAYMH1	6.69	5.29	5.99	1.65	1.48	1.57	22.21	26.67	24.44
IMHB1539	6.31	5.75	6.03	1.65	1.37	1.51	22.44	24.86	23.65
IMHB1529	8.26	6.32	7.29	2.07	1.44	1.76	20.18	25.59	22.89
HM4 (C)	6.29	6.08	6.18	1.51	1.48	1.50	22.42	26.17	24.30
<b>Location<sup>b</sup></b>									
ALMO	8.34	3.94	6.14	1.68	0.91	1.30	37.73	33.20	35.47
BAJA	3.86	6.86	5.36	1.20	1.58	1.39	15.55	34.06	24.81
KARN	11.24	9.93	10.59	1.77	2.38	2.08	18.03	22.53	20.28
PANT	12.25	10.25	11.25	3.05	2.33	2.69	23.61	31.18	27.40
BAHR	4.60	3.48	4.04	1.46	1.15	1.31	27.49	23.29	25.39
BHUB	1.98	2.96	2.47	0.53	0.78	0.66	15.59	18.00	16.80
MAND	4.40	5.83	5.12	0.97	1.13	1.05	24.37	30.58	27.48
UDAI	6.53	4.63	5.58	1.99	1.50	1.75	13.04	12.85	12.95
Grand mean	6.65	5.99	6.32	1.58	1.47	1.53	21.92	25.71	23.82
$h^2_{bs}$	0.97	0.98	0.97	0.95	0.97	0.96	0.97	0.97	0.97

<sup>a</sup>Genotype means (in tonnes per hectare) are based on 8 location data over 2 years; <sup>b</sup>Location means (in tonnes per hectare) are based on 13 genotype data over 2 years; GEY = Green Ear Yield, BCY = Baby Corn Yield and GFY = Green Fodder Yield

Bhubaneswar, IMHB1531 performed best at Bajaura, Bahraich and Udaipur, while Almora was the best location for expression of IMHB1532. Hence, the testing locations were classified into three mega-environments for each of the traits.

#### **Additive main effects and multiplicative 2 interaction studies**

In AMMI2, first (PC1) and second (PC2) principal component are used to account for the variation. For green ear yield, baby corn yield and green fodder yield, AMMI2 accounted for explaining genotype and genotype × environment variation of 60%, 71% and

71%, respectively (Figs. 2d, 2e and 2f). Similar to GGE biplot, AMMI2 biplot is characterized by the presence of four sectors formed by the dissection of origin by horizontal and vertical lines. The genotypes lying in the location near biplot origin are considered to have average adaptability (Murphy et al. 2009). For all the three traits, different winning genotypes were identified in different sectors and hence validating the presence of GEI (Figs. 2d, 2e and 2f). The individual years data was also subjected to AMMI2 and Polygon View analysis; however, the general pattern of location grouping was found to be similar across years (Data not shown).

**Table 5.** First three AMMI selections per environment (location) for green ear yield (GEY), baby corn yield (BCY) and green fodder yield (GFY)

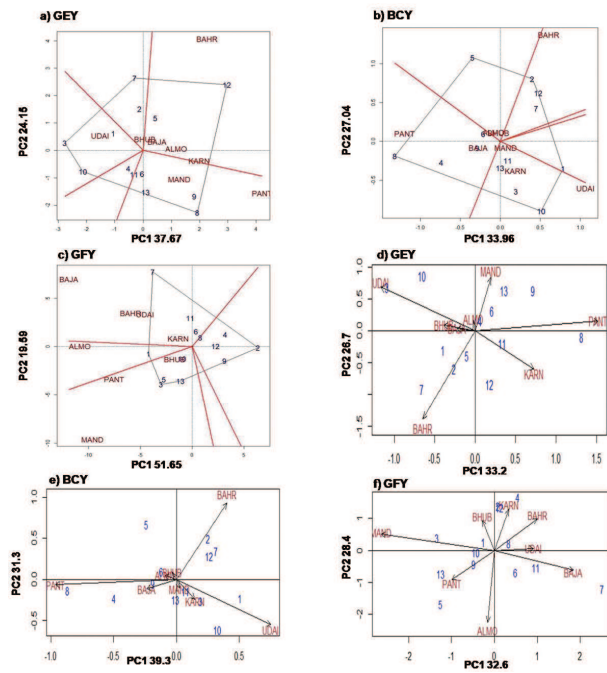
Location/ genotype	GEY 1 mean*	2	3	BCY 1 mean*	2	3	GFY 1 mean*	2	3	
ALMO	6.14	IMHB1529	DMRHB1305	BVM2	DMRHB1305	IMHB1537	35.47	IMHB1525	IMHB1531	HM4
BAJA	5.35	IMHB1529	DMRHB1305	DMRHB1305	IMHB1537	IMHB1538	24.81	IMHB1531	IMHB1532	IMHB1539
KARN	10.58	IMHB1529	IMHB1537	IMHB1525	IMHB1532	GAYMH1	20.28	IMHB1532	AH5021	IMHB1531
PANT	11.25	IMHB1537	DMRHB1305	IMHB1525	IMHB1537	IMHB1538	27.40	IMHB1525	AH5021	IMHB1532
BAHR	4.04	IMHB1529	IMHB1531	BVM2	IMHB1529	BVM2	25.39	IMHB1531	IMHB1532	AH5021
BHUB	2.47	IMHB1529	DMRHB1305	IMHB1532	IMHB1529	IMHB1532	16.80	IMHB1532	AH5021	GAYMH1
MAND	5.12	DMRHB1305	HM4	BVM2	IMHB1529	IMHB1532	27.48	AH5021	IMHB1525	IMHB1532
UDAI	5.59	AH5021	GAYMH1	IMHB1538	IMHB1532	IMHB1532	12.94	IMHB1531	IMHB1532	AH5021

\*Mean (in tonnes per hectare)

**Mean vs. stability and genotype comparison with ideal genotype views of GGE biplot**

The presence of significant G × E interaction for yield traits in baby corn hybrids indicated towards need for identification of high yielding and stable cultivars called as ideal genotypes. The “mean vs. stability” view of GGE biplot as presented in figure 3a, 3b and 3c helps in identification of ideal genotypes in each mega-environment (Yan et al. 2007). The arrow shown on the AEC abscissa points in the direction of higher trait performance of genotypes and rank the genotypes with respect to trait performance. Thus, hybrid IMHB1529 had the highest green ear yield and AH5021 had the lowest (Fig. 3a). Similarly, genotypes BVM2 and IMHB1532 had the highest baby corn yield and green fodder yield, respectively. AEC coordinates (Lines perpendicularly passing to the AEC via origin) are depicted as double-headed lines are passing through the biplot origin are referred to as AEC ordinate (Figure 3a, 3b and 3c). The greater the absolute length of the projection of a cultivar, the less stable it is. The projection of genotypes on the AEC vertical axis decides stability with the rule of closer the genotype to AEC abscissa (horizontal axis), more will be stable and vice-versa. Thus, the hybrid GAYMH1 was found to be the most stable and the hybrids IMHB1531 and IMHB1537 were the least stable for green ear yield (Fig. 3a). Similarly, BVM2 and IMHB1529 can be considered as most stable for baby corn yield as well as green fodder yield. Stability is useful only with high yield (Yan and Tinker (2006). In the Mean vs Stability biplot, the genotypes represented by a circle on the head of arrow on the AEC abscissa are considered to be ideal genotypes (Fig. 3a, 3b and 3c). For green ear yield, genotypes DMRHB1305 and IMHB1529 although relatively less stable but were highest grain yielder (Fig. 3a). Similarly, for baby corn yield BVM2, IMHB1531 and IMHB1529 were best (Fig. 3b). For green fodder yield, genotypes IMHB1532 was the best (Fig. 3c). The “comparison with ideal genotype” view of GGE biplot has concentric circles with the ideal genotype in the inner circle and the head of the arrow is the center of the circle (Fig. 3d, 3e and 3f). The genotypes grouped in the inner circle (ideal genotypes) are more desirable than the others. Thus, the hybrids BVM2 and IMHB1529 were the most desirable genotypes for baby corn yield (Fig. 3e). Similarly, for green ear and fodder yield, IMHB1532 was found to be the most desirable one. However, for green ear yield, no genotypes were found in the inner circle (Fig. 3d, 3e and 3f). Therefore, genotypes next to the ideal circle were desirable. Similar trend was observed in individual years as well. For green fodder yield, DMRHB1305 was the best performer over both the years, while IMHB1532 showed good performance in 2015 and was the best in 2016 for fodder yield.

Further, the study revealed the close relations among all locations except Bahraich with Udaipur and Pantnagar (Fig. S1 a, b and c). For green ear yield, Pantnagar, Bahraich and Karnal were most discriminating over Bhubaneswar and Bajaura as indicated from their highest vector length. Hence, these locations can be used for selecting specifically adapted genotypes. The near average

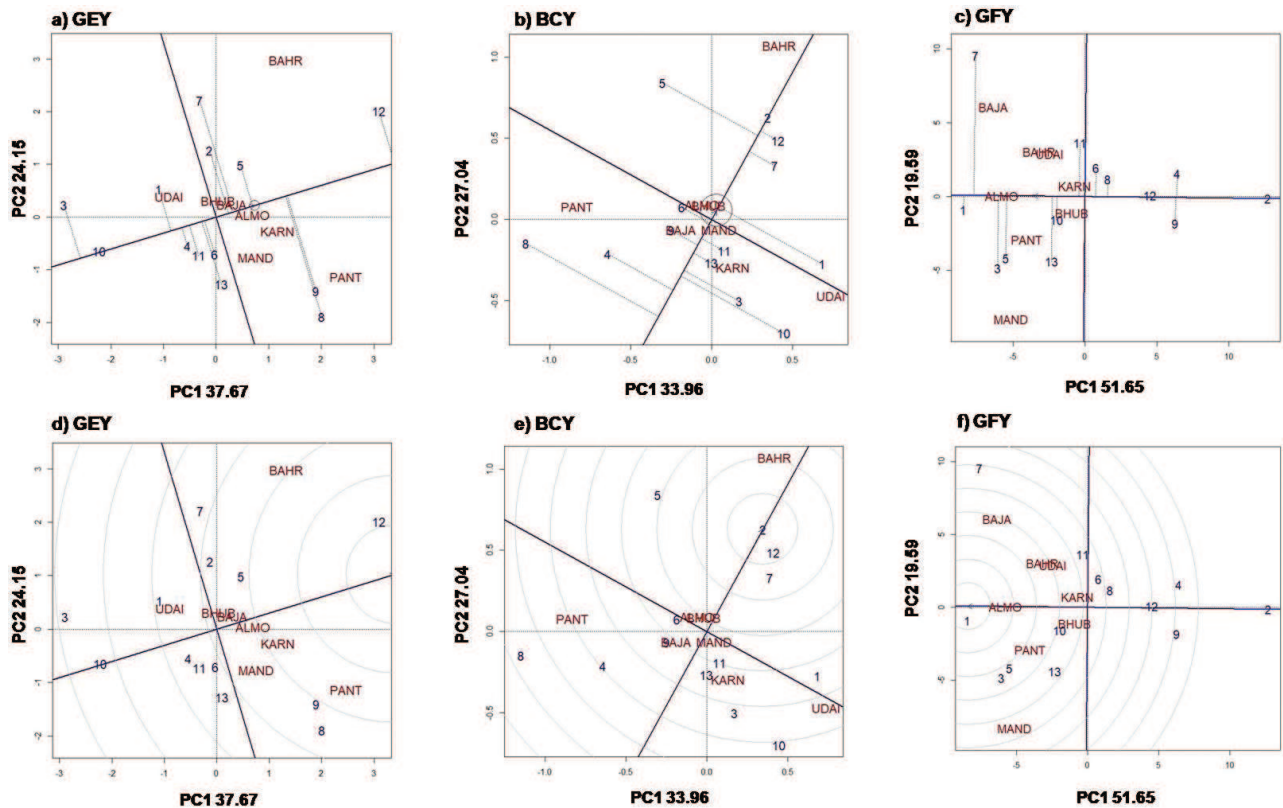


**Fig. 2.** GGE and AMMI biplots of 13 baby corn genotypes tested in 2 years and eight locations for green ear yield (GEY), baby corn yield (BCY) and green fodder yield (GFY). The polygon a-c (which-won-where) view), whereas d-f represents additive main effects and multiplicative interaction 2 (AMMI2) biplot

locations viz., Almora and Bajaura were most representative locations and good test environments for selecting generally adapted genotypes (Fig. S1a).

**Discussion**

India is a vast country with diverse agro-climatic conditions. The multi-location testing sites of AICMIP are representative locations for diverse baby corn production ecosystems in terms of their latitude, altitude and macro-climatic conditions. Suitable baby corn cultivars of various regions are to be identified. MLT are most suitable tool towards this direction. However, the MLT data are often not used to its fullest



**Fig. 3.** GGE Biplots for combined analysis of 13 baby corn genotypes tested over two years at eight locations for green ear yield (GEY), baby corn yield (BCY) and green fodder yield (GFY). The a-c represents mean vs. stability and d-f: shows comparison of genotypes with ideal genotype. The biplots were based on Scaling = 0, Centering = 2, and SVP = 1



potential (Rakshit et al. 2012). GGE biplot is an effective methodology to analyze MET data for simpler interpretation of complex GEI interaction (Yan and Tinker 2006). It is an effective graphical approach for detection of GEI and helps in delineating the testing locations into mega-environments (Yan et al. 2007). The stability analysis for studying the G×E for baby corn traits was carried out by Nahar et al. (2010) following regression approach but GGE biplot is more effective approach for stability analysis. However, considering the lack of any report on GGE biplot studies for baby corn, this is the first study on GGE biplot based analysis of baby corn MLT data. In current study, AMMI based ANOVA revealed that environment or location can contribute upto 87.0% of the total variation signifying towards very less contribution by genotypes and GEI (Table 3). The results agree with Zobel (1997) who also reported the contribution of about 80% by environment in MET Trials. Similarly, Rakshit et al. (2012) reported upto 89.9% of variation due to environment in sorghum MET trails. Kuchanur et al. (2015) also obtained similar pattern in single cross corn hybrids yield trials. In present study, GL was found to contribute more in total variation than G which signifies the presence of mega-environments (Yan and Hunt 2002). Hence, this holds true at all the corn growing ecologies globally and even in different crops. Thus, the baby corn breeders should also keep this point in mind and accordingly should target the key traits in their respective target environments.

GGE biplot analysis helps in getting an account of contribution of first two PCs to total variation. The biplot can be said to explain the total variation of G×E data effectively if over 60% and 10% of (G×GE) variability can be accounted by first two PCs and joint effects of (G×GE), respectively (Yan and Tinker 2006; Yan et al. 2010). The results of this study agree with above statement for all the traits as first two PCs explained over 62% of the variability and G and GL jointly explained more than 10% of total variation (Table 3) and hence the derived biplots effectively represent the variability in baby corn MLT data. The graphical presentation of PC1 and PC2 (Fig. 3a, 3b and 3c) has helped to simplify the complexity of data via biplot visualization. The genotypes projecting on the AEC abscissa are good yielders and those away from AEC ordinates indicate poor stability (Yan and Tinker 2006; Rakshit et al. 2012). Thus, it is evident from figure 3a that the highest green ear yielder (IMHB1529) was not stable, while the most stable one, GAYMH 1 was among the poorest yielders. Similarly,

for green fodder yield the most stable hybrids (BVM 2 and GAYMH 1) were poor yielders (Fig. 3c). However, in case of baby corn yield BVM 2 was highest yielder as well as most stable (Fig. 3b). Thus, it is evident that a genotype exhibiting good stability for one trait can be less stable for another trait and vice-versa because different set of genes govern different traits and environment has varying influence over different set of genes. Soil type and weather conditions are two most important influencing factors of environment (Lin and Binns 1988). Weather is relatively unpredictable factor for genotype expression as compared to soil as it exhibits variation over the years in same location. Hence, it is better to use GGE Biplot for partitioning of GE interaction to estimate cultivar × predictable variation (Allard and Bradshaw 1964; Lin and Binns 1988). The similar approach has been applied for GEI analysis in different crops like maize (Kuchanur et al. 2015), wheat (Kumar et al. 2018), sorghum (Rakshit et al. 2012), peanut (Lal et al. 2019) and watermelon (Dia et al. 2016).

The benefit of observing GEI graphically lies in the ease of identification of nearly ideal genotypes (lying close to ideal genotype). The ideal genotype is one which exhibits higher yield and greater stability. In graphical representation, the genotype with highest mean yield and nearly zero GEI, lying in the center of concentric circles, is called as ideal genotype. Breeders are mostly interested in selecting the ideal genotypes or genotypes lying closer to the ideal genotype. Thus, for baby corn yield, hybrids BVM-2, IMHB1529 and IMHB1531 can be considered as nearly ideal genotypes (Fig. 3d, 3e and 3f). For green fodder yield IMHB1532 was the closest to ideal genotype. However, for green ear yield, no genotypes were found in the inner circle. Therefore, genotypes next to the ideal circle were desirable. Hence, the hybrids IMHB1529, IMHB1525 and DMRHB1305 were the desirable genotypes for green ear yield (Figs. 3d, 3e and 3f). Thus, graphical approach helps in easy identification as compared to get it from mean table alone (Table 4). The performance of high yielding and stable genotypes in target locations agrees to a good level with the graphical interpretations of GGE Biplot. The ideal genotype, IMHB1529, exhibited highest baby corn yield at Pantnagar, while near average yielded at most locations, and lower than average yield at Bhubaneswar (Fig. 3e). The above results suggest high crossover GE interaction, i.e. order of genotypes based on their performance varied depending on the testing environment. Rakshit et al. 2012 also observed

high cross over GE interaction in sorghum multi-location trials and concluded with presence of three mega-environments. Similarly, crossover GE interaction was observed in watermelon cultivars tested at eight locations across the US (Dia et al. 2016).

Saeed and Francis (1984) reported significant effect of cropping season rainfall and temperature on grain yield, contributing to the GEI. Rakshit et al. (2012) also suggested pre-seasonal and cropping season rainfall and temperature regime to contribute to GEI sum of squares. The discriminativeness versus representativeness biplot graph helps in detection of representative and discriminating testing locations. For baby corn yield, Udaipur, Pantnagar, Bahraich and Karnal can be used to select the specifically adapted genotypes whereas Almora, Bajaura and Mandya were most representative locations (Fig. S1b). For green fodder yield Bajaura and Mandya were most discriminative testing environments (Fig. S1c). Such graphical representation helps in convenient identification of generally adapted- and specific-environment. The closer the test environments are related, more the similar information will be obtained from them and even removal of few such related environments don't affect output. This helps in removal of such similar information generating environments in future MLT of baby corn hybrids as well as decision making of future allocation of MLTs and hence aiding to the maximum utilization of scarce resources. For all the traits, some locations were found to have wide obtuse angles between their vectors indicating strong negative correlations among them and signifying the presence of crossover GEI (Figs. 3d, 3e and 3f), (Yan and Tinker 2006). In METs, with diverse multiple testing sites, prevalence of combination of crossover and non-crossover types of GEI is common (Kuchanur et al. 2015; Kumar et al. 2018; Rakshit et al. 2012; Dia et al. 2016). The genetic reason for mentioned fact may be attributed to combined properties of gene combinations as indicated from high responsiveness of some genotypes to particular change in environment, while others remain quite stable.

'Which-won-where' is the core component of GGE biplot, that eases the identification of crossover GE, mega-environment differentiation and specific adaptation by graphically projecting the GEI of MET data (Gauch and Zobel 1997; Yan et al. 2000; Yan and Tinker 2006; Putto et al. 2008). 'Which-won-where' analysis partitioned the testing locations into three mega-environments for green ear yield (Fig. 2a). The

winning genotypes, AH5021 and GAYMH 1 in Udaipur (first mega-environment), IMHB 1537 at Mandya and Pantnagar (second mega-environment) and IMHB 1529 in rest of the locations (third mega-environment) should be explored for their best performance in respective mega-environments only. Similarly, for the traits viz., baby corn yield and green fodder yield the testing locations were partitioned into three mega-environments (Figs. 2b and 2c). The findings indicate that in METs of baby corn hybrids conducted at several locations in different zones of the country, few representative environments in each mega-environment are quite good enough to provide the similar information as obtained from all testing locations of mega-environments. Thus dropping a few closely related locations in each mega-environment can help in reducing the testing cost in AICMIP baby corn METs through efficient utilization and optimal allocation of available resources. However, this should be adopted after verification or validation of mega-environments pattern over years and locations as realized from studies in wheat (Yan et al. 2000) and peanut (Putto et al. 2008). Therefore, persistence of good amount of crossover GEI in METs demand for reduction of testing locations in agricultural climatic zones for better utilization of resources and emphasizes to focus breeding efforts on stable as well location-specific expression of baby corn hybrids.

#### Authors' contribution

Conceptualization of research (BK, VM); Designing of the experiments (BK); Contribution of experimental materials (BK, MCK); Execution of field/lab experiments and data collection (SKG, NKS, RK, MCK, MV, RKS, PN and DS); Analysis of data and interpretation (MC, BK, PK, SR); Preparation of manuscript (MC, BK, SR).

#### Declaration

The authors declare no conflict of interest.

#### Acknowledgements

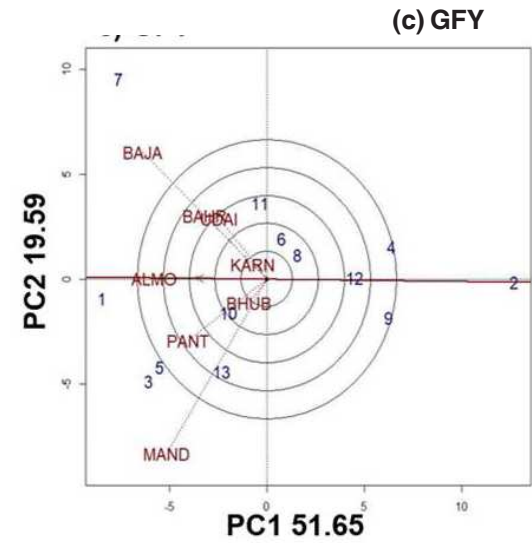
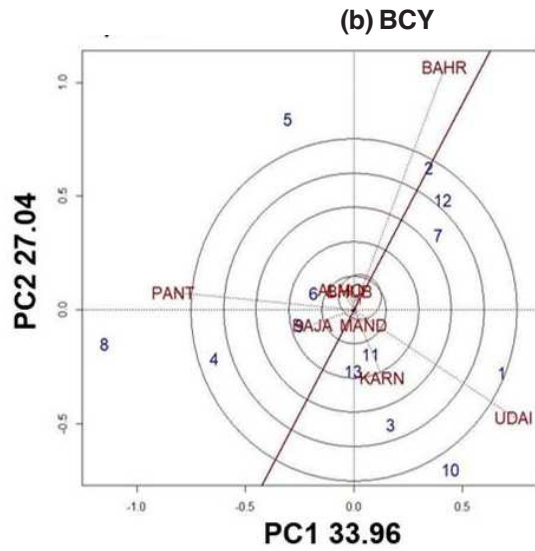
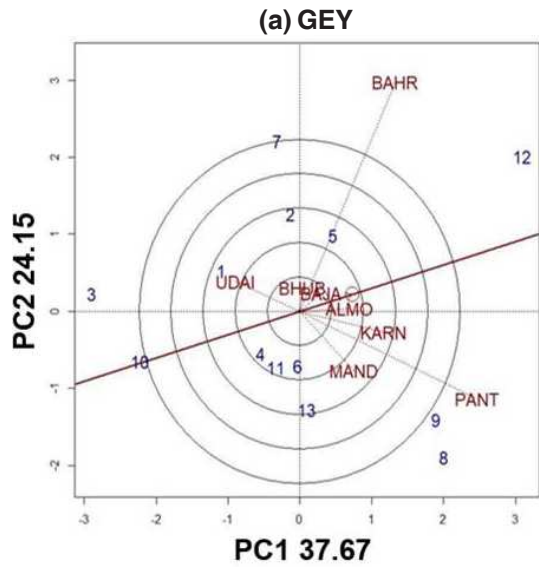
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Supplementary Fig. S1. Ranking of environments based on discriminating ability and representativeness for 13 baby corn genotypes tested over the two years and eight locations for a) green ear yield (GEY), b) baby corn yield (BCY) and c) green fodder yield (GFY)

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