



GGE biplot based stability analysis of experimental hybrids for baby corn purpose and green fodder

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Abstract

The multi-location testing puts emphasis mainly on identification of new superior cultivars over commercial cultivars, while giving very less importance to genotype × environment interaction (GEI). In the present study, performances of 37 baby corn cross combinations (including three checks) were evaluated for green ear yield, baby corn yield and husk yield over three locations (environments) in kharif season of 2018. Environment (51-74%) attributed highest proportion of the total variation followed by GEI (14-29%) and genotype (12-19%). Superior stable hybrids for green ear yield, baby corn yield and husk yield could be identified using GGE biplot graphical approach effectively. 'Which won where' plot for each of the traits partitioned testing locations into two mega-environments with different winning genotypes for different traits in respective mega-environments. This clearly indicated that though the testing was being conducted in many locations, similar conclusions could be drawn from one or two representatives of each mega-environment. Thus the stability analysis could help to classify the stable as well as location specific baby corn hybrids.

Keywords: Baby corn, Fodder, GEI, GGE biplot, Stability analysis

Introduction

Maize (*Zea mays* L.) being of erratic nature crop, is adapted to a wide range of production environments (Gerpacio and Pingali, 2007). Maize is the leading crop among cereals contributing more than 1046 million tons annually to the global food basket (FAOSTAT, 2018). India globally shares around 2.2% with annual production of 26.26 million tons from 10.20 million hectare (FAOSTAT, 2018). The projected demand for maize in India is

expected to be 45 million tons by the year 2022 (FICCI, 2018). Maize has diverse uses in the form of human food, livestock feed and as raw materials for a number of industrial products like starch, pharmaceuticals, alcoholic beverages, oil, cosmetics, textiles etc. Baby corn, a special type of normal maize refers to whole unfertilized immature cob harvested at the silk emergence stage (silk length of about 1-3 cm) (Galinat, 1985). It is the dehusked tender ear of the female inflorescence of maize plant (Pandey *et al.*, 2000; Kapoor, 2002). Young and tender ears of 4.5"10 cm length and 0.7"1.7 cm diameter (in dehusked condition) and having regular row arrangement are handpicked (Bar-Zur and Sadi, 1990). Baby corn has the immense potential to fetch foreign currency because of its huge demand in international market for its taste, nutritive value, and consumed fresh as it is free from pesticide residues. Besides being consumed fresh it is used in preparation of many diverse food products and the remaining plant part after harvest *viz.*, stem with leaf and husk serves as excellent green fodder for livestock production. Hence baby corn can help in boosting the income of farmers in peri-urban areas. The farmers easily adopt baby corn cultivation as the net income from baby corn is also very high, around four to five times higher than field corn crop. In addition, the net income from baby corn can be enhanced by taking 3-4 crops of baby corn in a year (Joshi and Chinwal, 2018). The early maturity hybrids facilitate crop diversification and hence increasing overall cropping intensity in a year leading to higher profitability. Therefore, in order to meet the increasing demand for baby corn, there is need to develop early maturing and high yielding prolific single cross hybrids. India has emerged as one of the potential baby corn producing countries because of its low cost of production as compared to other countries. Maize is an important source for grain as well as fodder, and also

called dual purpose maize (Kumar *et al.*, 2018), but baby corn provide the fodder at early stage in the form of husk, tassel and stem.

Maize being a highly cross-pollinated crop offers great scope for exploitation of heterosis, but the performance of hybrids is not similar across the locations. Hence the plant breeders focus on hybrids which perform consistently well across all the environments. The phenotypic expression of hybrid is the result of Genotype (G) × Environment (E). However, G × E interaction effects act as barrier in the selection of stable hybrids. Multi-location testing (MLT) of cultivars for grain yield stability is an integral component of any crop breeding programme. But in case of multi-location testing of baby corn trials, the traits *viz.*, green ear yield (GEY, cob with husk), baby corn yield (BCY, cob without husk) and husk yield (HY, difference of yield between GEY and BCY) are the important traits. Multi-location testing of baby corn hybrids is aimed at identification of superior performing genotypes that exceeds the commercial check for the target traits. The presence of GEI makes it necessary to measure both performance and stability for genotypes being evaluated in breeding programs (Magari and Kang, 1993; Ebdon and Gauch, 2002). Presence of GEI interaction deviates the correlation among phenotypic and genotypic values, thereby reducing progress under selection. This leads to biasness in the estimation of heritability and prediction of genetic advance (Comstock and Holl, 1963). Various statistical models proposed to estimate the GEI have been described by Yan and Kang (2003) which includes Analysis of variance (ANOVA), linear regression (LR) and principal component analysis (Rakshit *et al.*, 2014). However, these methods have some shortfalls like, being an additive model; it can only describe main effects effectively (Snedecor and Cochran, 1980), while PCA can only illustrate the multiplicative components.

A biplot is a scatter plot based on two factors that explain the underlying relationships and interactions among factors. There are two types of commonly used biplot to understand GEI, the AMMI biplot (Crossa, 1990 and Gauch, 1992) and the GGE biplot (Yan *et al.*, 2007; Yan and Kang, 2003). The main difference in GGE (GGE) biplot and AMMI biplot is that GGE biplot eliminates the E component and integrates G with GE interaction effect of a GEI dataset (Yan *et al.*, 2000). Several studies of GGE biplot and AMMI model based stability analysis have been made in field corn for revealing GEI (Faria *et al.*, 2017; Balestre *et al.*, 2009), but such types of studies have not

been carried out for baby corn. The objectives of this study was to estimate the GEI of baby corn genotypes, and identify high yielding baby corn genotypes with high stability.

Methods and Materials

Plant materials and experimentation: The study was carried out on 37 baby corn hybrids along with three commercial checks *i.e.* IHMB1532, IHMB1539 and HM4 at three testing location *i.e.* Ludhiana (LUDH), Pantnagar (PANT) and Ambikapur (AMBI) in *Kharif* 2018 (Table 1) The three locations represent the three states with different climatic conditions. The experiment design followed was complete randomized block design with two replications. Trial was laid in 50 × 20 cm² crop geometry and each genotype was sown in two rows each of three-meter length in each replication. All the recommended package of practices for the crop management was followed as per standard practices across all locations. The observations were on green ear yield (GEY) *i.e.* cob with husk, baby corn yield (BCY) *i.e.* cob without husk and husk yield (HY) *i.e.* difference of yield between GEY and BCY plot basis. GEY and BCY data were recorded for weight of green ears (with husk) and baby corn weight (without husk *i.e.* dehusked), respectively and summed over multiple pickings. HY (GEY-BCY) was calculated by subtracting the BCY from total GEY after completion of all pickings.

Data analysis: The AMMI and GGE biplots were analyzed using the AMMI (Agricolae) and GGE biplot GUI package, respectively, of R statistical software in R Studio (R Development Core Team, 2007; CRAN, 2014; R Studio, 2014). The AMMI and GGE biplot analysis were used to visually assess the presence of G×E and rank genotype based on stability and mean (Yan *et al.*, 2000; Yan and Kang, 2003). The multi-location testing data was analyzed without scaling ('Scaling 0' option) to generate a tester centered (centering 2) GGE biplot as suggested by Yan and Tinker (2006). For genotype evaluation, genotype-focused singular value partitioning (SVP=1) was used using the 'Mean versus stability' option of GGE biplot software, while for environmental evaluation, environment-focused singular value partitioning (SVP=2) was employed (Yan 2001) using 'Relation among testers' option. 'Which-won-where' option was used to identify the winner genotype in a given set of environments.

Results and Discussion

Analysis of variance: Overall ANOVA representations

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along with the proportionate magnitude for the traits were recorded (Table 2). Analysis of variance clearly showed the significant effect of G, E and GE for all the traits studied (Rajora *et al.*, 2017). Relative contributions of each source to the total variation were also recorded. It was observed that environment was the most important source of variation for HY (74%) and GEY (73%), followed by GEI (14%) for both the traits, and 13 and 12% of genotypic effect, respectively. For BCY, environment contributed 51%, followed by 29% of GEI and then genotypic effect 19%. In terms of location wise mean, highest yield (q/ha) for respective traits *viz.*, GEY, BCY and HY was observed at Ambikapur (130.23, 24.56, 105.26) followed by Pantnagar (76.97, 23.11, 53.86) and Ludhiana (34.97, 6.62, 31.00) (Table 2). Gauch and Zobel (1997) reported that environment generally contributes more than 80% of the total variation in multi environment data. Similar results were found in different earlier studies by Kaya *et al.* (2006) and Rakshit *et al.* (2012) where environment contributed upto 81% and 89.9% of total variation in wheat and sorghum, respectively. Dehghani *et al.* (2006) also observed similar results for barley yield trials in Iran. In this study, G explained relatively higher proportion of the variation than GE for all the three traits. Higher proportion of G as compared to GE indicated that performances of genotypes rely up to lesser extent on the environment suggesting the existence of relatively lesser number of mega-environments (Mohammadi *et al.*, 2009).

Mean performance and stability of the genotypes across locations:

Performance and stability of the genotypes was visualized graphically through GGE biplot (Fig 1a-c). This was evaluated by average environment coordination (AEC) method (Yan, 2001; 2002). The first two Principal components (PC) explained 92.61% variation for GEY, 94.53% for BCY and 97.61% for HY. In figure (Fig 1a-c), the line with single arrow head is called AEC abscissa. AEC abscissa crosses the biplot origin and marker for average environment and moves towards higher mean values. The average environment has generally average PC1 and PC2 scores over all environments (Yan, 2001). The line perpendicular to the AEC passing through the biplot origin is known as AEC ordinate. These ordinates are depicted as double arrowed lines in figures (Fig 1a-c). The longer length of the projection of the cultivar shows the less stability. Furthermore, the average yield of any genotype is approximated by the projections of their markers from the AEC abscissa (Kaya *et al.*, 2006; Rakshit *et al.*, 2012; Rakshit *et al.*, 2014). Thus genotypes BCH 8, BCH 27, BCH 25 and BCH 40 were the best performers in terms

Table 1. Details of genotypes used in the study

Hybrid code	Pedigree
BCH-1	0631C1-30 × 0591C1-30
BCH-2	0673C1-30 × 0591C1-30
BCH-3	0627C1-30 × 0591C1-30
BCH-4	0555C1-30 × 0591C1-30
BCH-5	0547C1-30 × 0591C1-30
BCH-6	0499C1-30 × 0591C1-30
BCH-7	0569C1-30 × 0591C1-30
BCH-8	0673C1-30 × 0613C1-30
BCH-9	0598C1-30 × 0613C1-30
BCH-10	0555C1-30 × 0613C1-30
BCH-11	0544C1-30 × 0613C1-30
BCH-12	0569C1-30 × 0613C1-30
BCH-13	0555C1-30 × 0673C1-30
BCH-14	0598C1-30 × 0627C1-30
BCH-15	0555C1-30 × 0627C1-30
BCH-16	0635C1-30 × 0627C1-30
BCH-17	0544C1-30 × 0627C1-30
BCH-18	0598C1-30 × 0491C1-30
BCH-19	0499C1-30 × 0491C1-30
BCH-20	0544C1-30 × 0491C1-30
BCH-21	0598C1-30 × 0651C1-30
BCH-22	0555C1-30 × 0651C1-30
BCH-23	0499C1-30 × 0651C1-30
BCH-24	0544C1-30 × 0651C1-30
BCH-25	0555C1-30 × 0598C1-30
BCH-26	0499C1-30 × 0598C1-30
BCH-27	0544C1-30 × 0598C1-30
BCH-28	0569C1-30 × 0598C1-30
BCH-29	0635C1-30 × 0555C1-30
BCH-30	0544C1-30 × 0635C1-30
BCH-31	0569C1-30 × 0635C1-30
BCH-32	0499C1-30 × 0547C1-30
BCH-33	0544C1-30 × 0547C1-30
BCH-34	0569C1-30 × 0547C1-30
BCH-35	0544C1-30 × 0499C1-30
BCH-36	0569C1-30 × 0499C1-30
BCH-37	0569C1-30 × 0544C1-30
BCH-38 (C1)	IMHB1532
BCH-39 (C2)	IMHB1539
BCH-40 (C3)	HM4

of GEY, whereas BCH 9, BCH 4 and BCH 1 were the poorest yielders (Fig 1a). In terms of stability, genotypes BCH 1, BCH 7, BCH 13, BCH 15, BCH 18, BCH 34, BCH 37 and BCH 39 were the most stable, whereas BCH 27, BCH 5, BCH 31 and BCH 33 exhibited least stability for GEY. Although BCH 1, BCH 7, BCH 13, BCH 15, BCH 18, BCH 34, BCH 37 and BCH 39 were relatively more stable but were poor performers in terms of GEY. However,

Table 2. ANOVA and proportion of variation (G+E+GE) explained by genotype (G), environment (E) and GE interaction of three traits across the location with mean

Traits	MS value and % proportion of G, E & GE	Source of variation			Location wise mean (q/ha)		
		G	E	GE	AMBI	PANT	LUDH
GEY	MS	1607.71***	183799.63**	889.90***	130.23	76.97	34.97
	Proportion of G+E+GE (%)	13	74	14			
BCY	MS	154.60**	7947.79***	116.11*	24.56	23.11	6.62
	Proportion of G+E+GE (%)	19	51	29			
Husk Yield	MS	1054.42***	125272.86**	632.27***	105.26	53.86	31.00
	Proportion of G+E+GE (%)	12	73	14			

*(P<0.05); **(P<0.01); ***(P<0.001); AMBI: Ambikapur; LUDH: Ludhiana; PANT: Pantnagar

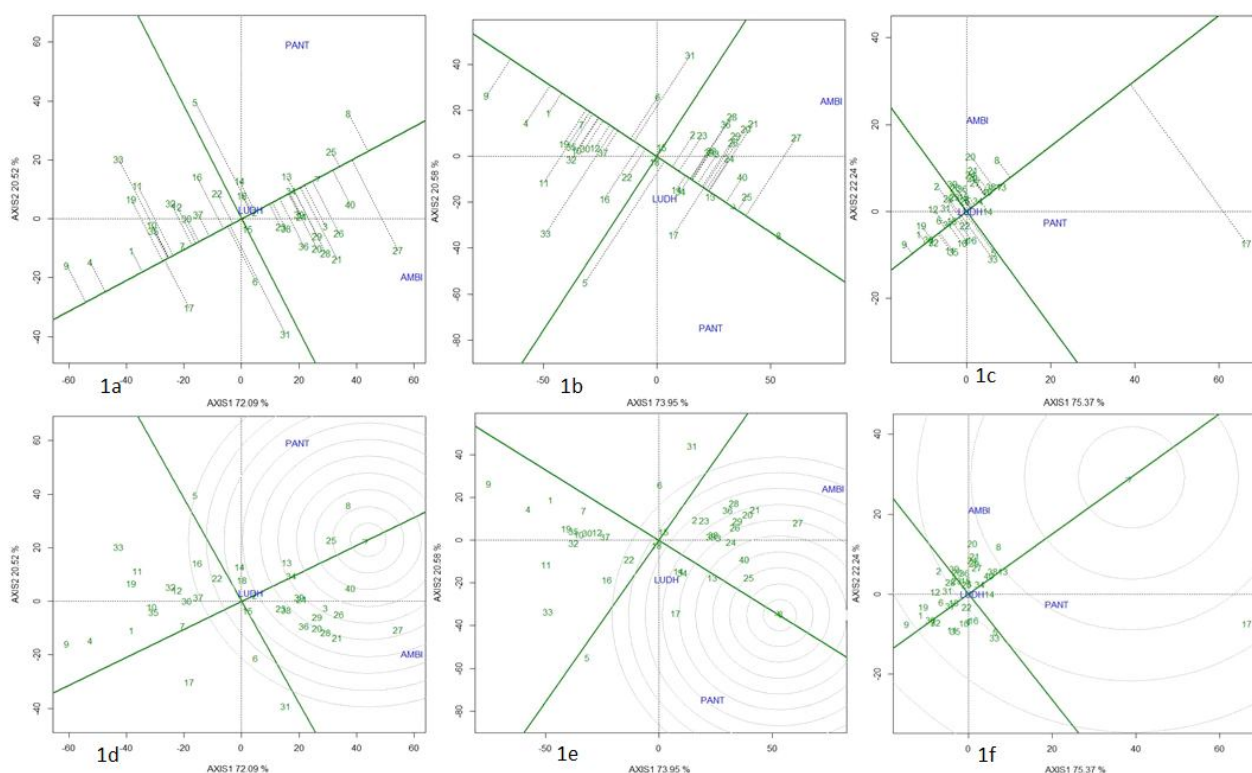


Fig 1. Mean vs. stability graph for GEY (1a), BCY (1b) and HY (1c) and graph for ranking of genotype for GEY (1d), BCY (1e) and HY (1f)

genotypes BCH 25 and BCH 34 exhibited better stability along with high GEY. In case of BCY genotypes BCH 8, BCH 27, BCH 25 and BCH 40 were the best performers and genotypes BCH 13, BCH 25, BCH 34 and BCH 14 exhibited good stability along with high BCY (Fig 1b). Similarly for HY genotypes BCH 8, BCH 13, BCH 38, BCH 40 and BCH 14 were found to exhibit average stability and high HY (Fig 1c). Thus, the GGE biplots might safely be decoded as effective graphical portrayal of the variability in the multi-location data. Figures (Fig1a-b) indicated that genotype BCH 25 exhibited average stability and high yielding nature for GEY and BCY which might be explained on the basis that both traits are governed by same set of genes. The high mean and low stability of

BCH 8 might be attributed to the influence of testing environment on the cumulative expression of different set of genes. Soil and weather of testing locations were key factors that could influence the performance of a genotype (Lin and Binns, 1988). Lin and Butler (1988) analyzed fixed components (soil) by taking average of a set of cultivar x location means over years assuming that GEI structure over years might get improved substantially if grouping of locations are based on fixed component. So use of GGE biplot was justifiable as cultivar x predictable variation was controllable (Dehghani *et al.*, 2006). Following similar approach, several authors reported high performing and stable genotypes in many crop species like barley (Dehghani *et al.*, 2006), lentil

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(Sabaghnia *et al.*, 2008), rapeseed (Dehghani *et al.*, 2008) and wheat (Kaya *et al.*, 2006).

An ideal genotype is that which exhibits high performance for concerned trait along with high stability across environments (Yan and Tinker, 2006). An ideal genotype could be identified through genotype comparison with ideal genotype view of GGE biplot. The genotypes that lie in the innermost concentric circle are considered as ideal. Figure (Fig 1d) indicated that genotype BCH 8 and BCH 25 could be considered as nearly ideal for GEY. In case of BCY, genotype BCH 8 was found to be ideal (Fig 1e). This finding agreed with the results of highest mean yield and stability exhibited by these genotypes for concerned traits (Fig 1a-b). However, for HY, no genotype was found to be ideal (Fig 1f). 'Which-won-where' is the very important feature of GGE biplot, which graphically explains crossover GE, mega-environment differentiation, specific adaptation etc. (Gauch and Zobel, 1997; Yan *et al.*, 2000; Yan and Tinker, 2006; Rao *et al.*, 2011).

Which won where (polygon view): The relationships among the test environments were analyzed by environment centered preserving of data (SPV=2) without scaling. The correlation among them was indicated by the Cosine of the angle between two vectors (Yan and

Tinker, 2006). Presence of wide obtuse angles between environment vectors, which suggested strong negative correlations among the test environments indicating existence of strong crossover GE across some locations (Yan and Tinker, 2006). Analysis for target traits showed acute angle for the vectors representing all the three locations *i.e.* Ludhiana, Pantnagar and Ambikapur (Fig 2a-c). Acute vector angles indicated the closer relationship among the environments (Yan and Tinker, 2006). The angle between Ludhiana and Pantnagar was much closer as compared to that of Ambikapur indicating the high correlation between Ludhiana and Pantnagar. Similarly Ambikapur and Ludhiana exhibited fewer angles between them indicating good correlation. However, Ambikapur and Pantnagar exhibited right angle between them indicating the distinctness (low correlation) among them (Fig 2d-f). Projections of the environments with respect to concentric circles were indicative of discriminating ability (Yan, 2001). The environments with higher and smaller vector lengths were considered to be discriminating and representative testing locations, respectively. In other words, environments with smaller angles with the AEA were most representative of the average test environments (Yan, 2001). Thus Ludhiana was closest to the AEA followed by Pantnagar and Ambikapur which had almost equal projection from the AEA for all traits. Hence for all three

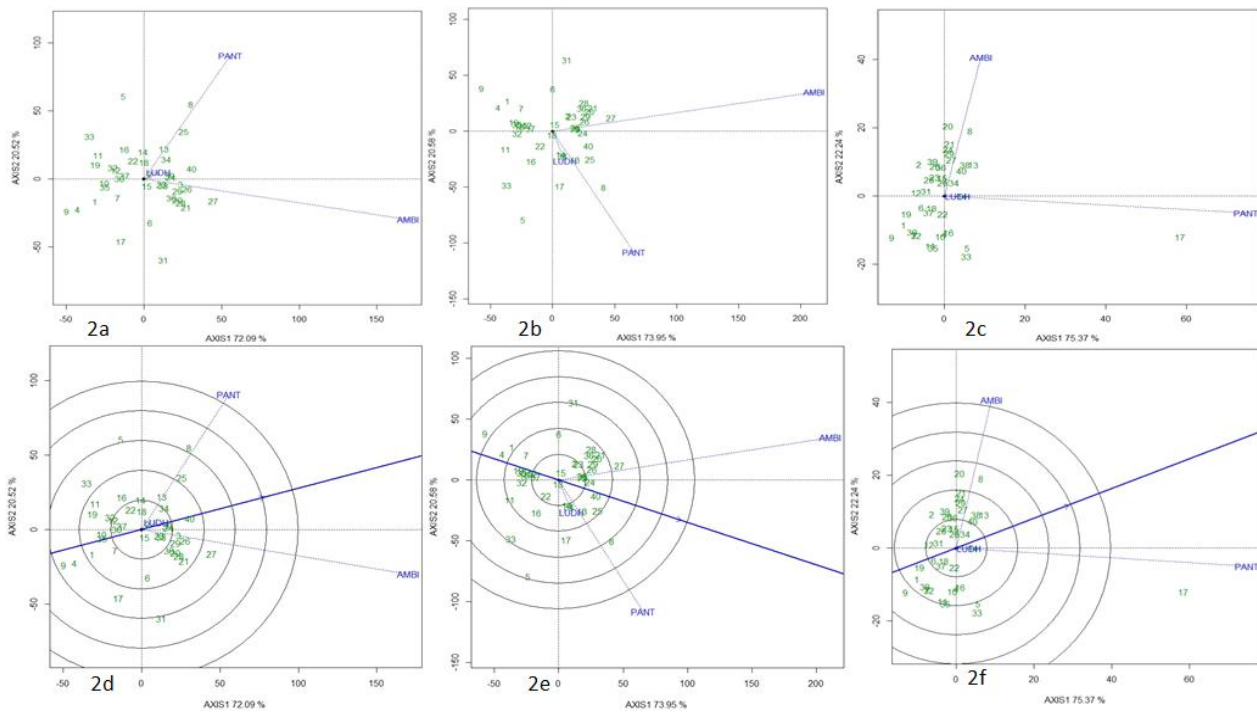


Fig 2. GGE Biplot for GEY (2a), BCY (2b) and HY (2c) and discriminativeness vs. representativeness graph for GEY (2d), BCY (2e) and HY (2f)

traits, Ambikapur and Pantnagar having highest vector length could be considered as discriminating environments for testing of location-specific genotypes. On the other hand, Ludhiana with least vector length could be used as representative location for testing of generally adapted genotypes (Fig 2d-f). This revealed that genotypes performing better in one environment could perform poor in another environment, while closer relationships among different locations indicated non-existence of crossover GE which suggested that ranking of genotype did not change from location to location (Kaya et al., 2006; Fan et al., 2007; Sabaghnia et al., 2008; Rao et al., 2011). This might be due to the fact that some genotypes were highly responsive to variation in the growing environment, while others might show stability since response to environment was purely based on combined properties of their gene combinations.

The environments with higher and smaller vector lengths were considered to be discriminating and representative testing locations, respectively. In terms of representativeness of average test environment, Ludhiana was closest to the AEA followed by Pantnagar and Ambikapur having almost equal projection from the AEA for all traits. Thus Ambikapur and Pantnagar with higher vector lengths were discriminative testing environments, whereas Ludhiana with shortest vector length was least discriminative (most representative) (Fig 2d-f). Hence, Ambikapur and Pantnagar should be explored for testing of specifically adapted genotypes, whereas Ludhiana should be used for testing of generally adapted genotypes.

Conclusion

The study clearly aided in the identification of stable and superior hybrids in a graphical manner. GGE biplot helped in easy detection of mixed crossover effects, of which baby corn breeders should take care of for development of adapted genotypes. The genotypes exhibiting location-specific adaptation should be targeted for cultivation in specific locations for expression at its fullest, while genotypes exhibiting wider adaptation could be released as mega-variety. 'Which-won-where' analysis demonstrated the existence of mega-environments indicating the possibility of grouping similar information generating locations (although geographically distant). Existence of extensive crossover GEI clearly suggested that the existing procedure did not realistically depict the actual situation. Hence, consideration of multi-location based stability analysis is expected to help in identification of location-specific as well as generally adapted elite genotypes.

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