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RESEARCH ARTICLE

# Stability analysis of promising winter maize (*Zea mays* L.) hybrids tested across Bihar using GGE biplot and AMMI model approach

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## Abstract

Multilocation evaluation facilitates the quantification of genotype-environment interaction (GEI) and the identification of high-yielding, stable hybrids along with partitioning the evaluating location into mega environments. Testing of 24 single cross hybrids and four checks across three environments revealed the significant GEI for all the studied traits. The environment contributed 12.90, 57.10, and 17.59% of the total variation for grain yield, anthesis silking interval, and days to maturity. The study indicated a negative genotypic correlation among grain yield and anthesis silking interval (-0.2244); days to maturity and anthesis silking interval (-0.019), whereas the positive correlation between grain yield and days to maturity (0.067). Location Sabour was found as the most representative environment for testing commonly adapted hybrids. Location Begusarai and Dholi are discriminatory and non-representative environments suitable for selecting location-specific genotypes. Both GGE biplot and AMMI analysis revealed that three hybrids, *viz.,* IMHSB1, IMHSB20, and IMHSB13 were high-yielding with average stability. The identification of superior and stable maize hybrids may contribute to farmers' income in Bihar.

**Keywords:** GEI, mega environment, winning genotype, correlation, heterosis

## Introduction

Maize is India's third most significant cereal crop, next to rice and wheat in acreage and production. Maize leads the cereals in terms of production (1046 MT) and area (191.90 mha), followed by wheat (218.28 mha) (Anonymous 2019). China (42.39 mha) and the United States (33.47 mha) account for 38.48 and 55.52% of global maize area and production, respectively. India with 5.32% (10.20 mha) of world maize area contributes roughly 2.2% (26.26 MT) to the global maize basket (FAOSTAT 2018). This magnitude of demand can be figured out only by using stable single cross hybrids (Kumar and Singh 2019; Singh et al. 2018). The country's thriving poultry sector consumes roughly 13–14 MT of maize per year. In addition to being a major food and animal feed, it is utilized in hundreds of industrial products. By 2025, maize demand is expected to reach 50 MT in India.

In India, maize is generally a *kharif* crop. Maize is currently grown throughout all three seasons due to its diversity and adaptability. In non-traditional places like Bihar, West Bengal, Karnataka, and others, winter maize outperforms kharif maize (Singh et al. 2020). Maize exploits significant heterosis, but hybrid performance differs region to region, suggesting instability due to genotype-

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**Table 1.** Details on hybrids used in the study

| S. No. | Hybrid Code | Pedigree |
|---|---|---|
| 1 | IMHSB1 | IMLSB-406-2×BML6 |
| 2 | IMHSB2 | IMLSB-428xBML6 |
| 3 | IMHSB3 | IMLSB-571-1xBML6 |
| 4 | IMHSB4 | IMLSB-592-1xBML6 |
| 5 | IMHSB5 | IMLSB-55xBML7 |
| 6 | IMHSB6 | IMLSB-83-1xBML7 |
| 7 | IMHSB7 | IMLSB-119-1xBML7 |
| 8 | IMHSB8 | IMLSB-133-1xBML7 |
| 9 | IMHSB9 | IMLSB-164-1xBML7 |
| 10 | IMHSB10 | IMLSB-173-2xBML7 |
| 11 | IMHSB11 | IMLSB-274-1xBML7 |
| 12 | IMHSB12 | IMLSB-285-1xBML7 |
| 13 | IMHSB13 | IMLSB-342-2-1xBML7 |
| 14 | IMHSB14 | IMLSB-343-3xBML7 |
| 15 | IMHSB15 | IMLSB-457-2xBML7 |
| 16 | IMHSB16 | IMLSB-976-2xBML7 |
| 17 | IMHSB17 | IMLSB-1299-5xBML7 |
| 18 | IMHSB18 | IMLSB-43-2xHKI-1128 |
| 19 | IMHSB19 | IMLSB-164-1xHKI-1128 |
| 20 | IMHSB20 | IMLSB-406-1xHKI-1128 |
| 21 | IMHSB21 | IMLSB-457-2xHKI-1128 |
| 22 | IMHSB22 | IMLSB-100xGPH-81 |
| 23 | IMHSB23 | IMLSB-801xIMLSB-406 |
| 24 | IMHSB24 | BML-7xIMLSB-457 |
| 25 | DHM 117 (C) | DHM-117 |
| 26 | BIO 9544 (C) | BIO-9544 |
| 27 | P 3396(C) | P-3396 |
| 28 | DKC 9081 (C) | DKC-9081 |

C= Checks

environment interaction (GEI). The performance of maize hybrids varies geographically, reflecting their instability due to GEI. GEI intensifies the breeder's task of identifying a genotype that performs consistently in a wide range of environments. Due to the presence of GE, it is worthwhile to evaluate genotypes' performance and stability in any genetic improvement programs (Ebdon and Gauch 2002). GEI may exhibit a low association among genotypic and phenotypic values, limiting the amount of progress made under selection and resulting in flaws in heritability estimates and genetic advance prediction. (Comstock and Holl 1963). Multilocation testing can assist in determining the genotype's stability in a range of environments. It helps to identify mega-environments and harness the specific adaptation of cultivars in the target environment. Winter maize in Bihar gives superior productivity and contributes greatly to the farmers' income. Multilocation evaluation facilitates the quantification of the GEI and the identification of high-yielding, stable hybrids, along with partitioning the evaluating location into mega environments. Keeping in view the importance of *rabi* maize in Bihar, a set of newly developed hybrids along with four checks in three locations was tested to assess their stable performance through GGE biplot and the AMMI model approach to quantify the GE in winter maize hybrids at multi locations, to identify high-yielding stable hybrids and partition the evaluating locations into mega environments.

## Materials and methods

A set of 24 newly developed hybrids and four checks, DHM-117, BIO 9544, P 3396, and DKC 9081 were tested and at three locations viz., Begusarai (BGS), Sabour (SBR), and Dholi (DOL) during *rabi* 2018-2019 and 2019-20 (Table 1). The material was planted in a randomized block design in three replications. Each genotype was planted in two rows of three meters each in a 60 x 20 $cm^2$ geometry. All the genotypes were assessed for grain yield (GY), days to maturity (DM), and anthesis silking interval (ASI). The AMMI (Agricolae) and GGE Biplot GUI packages of R software in RStudio were used to get AMMI and GGE biplots, respectively (RStudio 2020). As proposed by Yan and Tinker (2006), the analysis of multilocation trial data was performed without scaling ('Scaling 0' option) to obtain a tester-centered (centering 2) GGE biplot. Genotype-focused singular value partitioning (SVP = 1) was used with the GGE biplot software's 'Mean versus stability' option for genotype assessment, and environment-focused singular value partitioning (SVP = 2) was utilized with the 'Relation among testers' option for environmental evaluation (Yan 2001). The 'Which-won-where' function was utilized to evaluate the winning genotype in a range of locations.

## Results and discussion

### *Analysis of variance*

In terms of latitude, altitude, and macro-climatic factors, the climatic factors of the maize multilocation testing reflect the diversity of maize-producing ecosystems. In this study, combined ANOVA (Table 3) showed the significance of GEI for all three traits and demonstrated that G, E, and GE significantly affected each of the three attributes, except for the effect of E on GY. Table 3 shows the proportionate impact of each source to the total variation estimated using the sum of squares method. The environment contributed 12.90, 57.10, and 17.59% of the total variation for GY, ASI, and DM, respectively. The present finding implies that biplot graphics adequately describe the genotypes' GEI and the

**Table 2.** Year-wise and combined trait means of genotypes and environments and trait heritability over two years of testing

| Genotype/ location | GY (q/ha) | | | ASI | | | DM | | |
|---|---|---|---|---|---|---|---|---|---|
| Genotype | 2018-19 | 2019-20 | Combined | 2018-19 | 2019-20 | Combined | 2018-19 | 2019-20 | Combined |
| IMHSB1 | 92.61 | 110.37 | 101.49 | 4.44 | 3.44 | 3.94 | 155.89 | 151.06 | 153.47 |
| IMHSB2 | 72.96 | 82.72 | 77.84 | 3.78 | 3.94 | 3.86 | 155.11 | 151.06 | 153.08 |
| IMHSB3 | 81.71 | 101.78 | 91.74 | 4.44 | 3.78 | 4.11 | 156.67 | 152.61 | 154.64 |
| IMHSB4 | 74.76 | 86.82 | 80.79 | 4.11 | 4.00 | 4.06 | 153.78 | 151.44 | 152.61 |
| IMHSB5 | 72.21 | 50.89 | 61.55 | 3.78 | 3.83 | 3.81 | 157.11 | 152.50 | 154.81 |
| IMHSB6 | 91.15 | 81.61 | 86.38 | 3.78 | 2.56 | 3.17 | 158.78 | 154.83 | 156.81 |
| IMHSB7 | 81.74 | 92.42 | 87.08 | 4.22 | 2.56 | 3.39 | 158.00 | 155.28 | 156.64 |
| IMHSB8 | 78.57 | 61.83 | 70.20 | 3.89 | 3.06 | 3.47 | 158.56 | 155.78 | 157.17 |
| IMHSB9 | 96.69 | 92.12 | 94.40 | 3.78 | 3.83 | 3.81 | 160.00 | 158.28 | 159.14 |
| IMHSB10 | 91.02 | 86.68 | 88.85 | 3.89 | 4.11 | 4.00 | 157.89 | 155.89 | 156.89 |
| IMHSB11 | 89.05 | 74.74 | 81.89 | 3.89 | 2.78 | 3.33 | 159.56 | 154.67 | 157.11 |
| IMHSB12 | 80.03 | 81.00 | 80.52 | 4.78 | 3.33 | 4.06 | 158.33 | 156.67 | 157.50 |
| IMHSB13 | 89.54 | 86.15 | 87.85 | 3.56 | 3.11 | 3.33 | 159.67 | 155.44 | 157.56 |
| IMHSB14 | 93.90 | 92.71 | 93.30 | 3.67 | 2.78 | 3.22 | 159.44 | 155.00 | 157.22 |
| IMHSB15 | 75.40 | 88.25 | 81.82 | 4.00 | 4.00 | 4.00 | 160.78 | 156.22 | 158.50 |
| IMHSB16 | 79.72 | 79.76 | 79.74 | 4.56 | 2.78 | 3.67 | 156.56 | 155.61 | 156.08 |
| IMHSB17 | 83.51 | 108.96 | 96.23 | 3.89 | 3.17 | 3.53 | 160.44 | 157.67 | 159.06 |
| IMHSB18 | 76.35 | 79.74 | 78.04 | 3.33 | 3.78 | 3.56 | 158.56 | 155.28 | 156.92 |
| IMHSB19 | 74.28 | 92.42 | 83.35 | 4.22 | 3.72 | 3.97 | 160.44 | 157.33 | 158.89 |
| IMHSB20 | 105.36 | 101.41 | 103.38 | 3.33 | 3.00 | 3.17 | 158.67 | 153.61 | 156.14 |
| IMHSB21 | 89.71 | 85.57 | 87.64 | 4.00 | 2.56 | 3.28 | 161.22 | 156.06 | 158.64 |
| IMHSB22 | 78.72 | 95.27 | 86.99 | 3.44 | 3.17 | 3.31 | 154.78 | 149.50 | 152.14 |
| IMHSB23 | 87.42 | 80.67 | 84.04 | 3.78 | 3.44 | 3.61 | 154.67 | 153.00 | 153.83 |
| IMHSB24 | 65.12 | 72.62 | 68.87 | 3.44 | 3.94 | 3.69 | 160.89 | 156.67 | 158.78 |
| DHM 117 | 79.77 | 76.52 | 78.15 | 3.67 | 3.61 | 3.64 | 157.89 | 155.39 | 156.64 |
| BIO 9544 | 81.51 | 96.70 | 89.10 | 3.89 | 2.89 | 3.39 | 158.78 | 154.72 | 156.75 |
| P 3396 | 87.15 | 90.69 | 88.92 | 4.33 | 3.50 | 3.92 | 159.33 | 153.89 | 156.61 |
| DKC 9081 | 88.17 | 100.65 | 94.41 | 4.33 | 3.83 | 4.08 | 158.44 | 157.22 | 157.83 |
| Location Mean | | | | | | | | | |
| BGS | 91.62 | 88.26 | 89.94 | 3.25 | 3.71 | 3.48 | 158.96 | 153.50 | 156.23 |
| SBR | 87.03 | 74.90 | 80.96 | 5.19 | 3.82 | 4.51 | 157.79 | 152.94 | 155.37 |
| DOL | 71.86 | 97.31 | 84.58 | 3.37 | 2.59 | 2.98 | 157.90 | 157.76 | 157.83 |

GY = Grain Yield, ASI = Anthesis Silking Interval, DM = Days to Maturity, BGS = Begusarai, SBR = Sabour, DOL = Dholi

sum of squares. The contribution of genotype to the total variation was highest for DM followed by GY and ASI while the proportion of the variation explained by GE was highest for GY followed by ASI and DM, respectively. Environment contributed the most for ASI, followed by DM and GY. The contribution of G was highest for GY and DM, while the effect of E was highest for ASI (Table 3). In terms of location, the highest mean for GY was observed at BGS followed by DOL and SBR. The lowest location means for ASI was observed at DOL followed by BGS and SBR. Locations mean for DM was almost similar in all the locations (Table 2).

For GY, the G×E sum of squares was nearly three times greater than the genotype component, whereas for DM, they were roughly equivalent. The G component for GY

**Table 3.** Combined ANOVA and proportion of variation (G+E+GE) explained by genotype (G), environment (E) and GEI (genotype-environment interaction)of three traits across the location with mean

| Trait/year | Parameters | Source of variation | | |
|---|---|---|---|---|
| | | G | E | GE |
| GY | MS | 644.57*** | 2071.53 | 195.86** |
| | Proportion of G+E+GE (%) | 54.18 | 12.90 | 32.93 |
| ASI | MS | 0.836* | 47.57*** | 0.91** |
| | Proportion of G+E+GE (%) | 13.55 | 57.10 | 29.35 |
| DM | MS | 35.82*** | 131.40* | 4.892* |
| | Proportion of G+E+GE (%) | 64.73 | 17.59 | 17.68 |

*,** and ***: significant at the 0.05, 0.01, and 0.001 level of probability, respectively

was around four times larger than the E component. A little yield variation explained by environments suggested that environments were not highly variable, with genotypic effects accounting for the majority of GY variation. Balestre et al. (2009) and Rakshit et al. (2012) reported similar findings for location in maize and sorghum. For GY and DM, G explained a higher proportion of variation than GE. When the ratio of G to GE is larger, genotype performance is less environment-dependent, and testing locations do not have different mega environments. The environmental component for ASI was the largest of all three traits, demonstrating that even a minor environmental variation causes ASI variation. As a result, breeders must take this into account when devising breeding methods for their particular situations. A correlation study for these traits indicated a negative genotypic correlation among the GY and ASI; DM and ASI, and a positive correlation among GY and DM (Table 4).

### *Mean performance and stability of the genotypes across locations*

GGE biplots were used to graphically represent the genotypes' potential and stability under study (Figs. 1a, 1b, and 1c). The two highest-ranked principal components (PCs) accounted for a 90.47% variation for GY, 85.72% for ASI, and 92.26% for DM. The performance of hybrids for GY were observed as IMHSB20>IMHSB1>IMHSB17>DKC 9081> IMHSB3>IMHSB9>IMHSB14>BIO 9544> IMHSB22> IMHSB10>IMHSB13>P3396. The hybrids IMHSB20, IMHSB1, and IMHSB17 were yielding higher than the best check DKC 9081. It was followed by the hybrids, viz., IMHSB3, IMHSB9, and IMHSB14, yielding higher values than BIO 9544(C). The hybrids *viz.,* IMHSB22, IMHSB10, and IMHSB13 also performed better than P3396(C) in terms of GY. On the other hand, hybrids *viz.,* IMHSB5, IMHSB8, and IMHSB24 were the poor performers. Among high-yielding hybrids, IMHSB17, IMHSB9, IMHSB14, BIO9544(C), and IMHSB22 were least stable due to the increased projection from the AEC abscissa. Hybrids IMHSB20, DKC9081(C), IMHSB13, and P3396(C) were higher-yielding as well as stable. The hybrids *viz.,* IMHSB1, IMHSB3, and IMHSB10 showed intermediate stability. For ASI, the high-yielding and relatively stable hybrids *viz.,* IMHSB20, IMHSB1, IMHSB10, and IMHSB13 had lower ASI than the best check, DKC 9081, indicating the better synchrony in these hybrids (Fig. 1b). Based on DM, the observation for the high yielding hybrids and checks were IMHSB1<IMHSB3<IMHSB20 <BIO9544<P3396 <IMHSB10<IMHSB13<DKC9081. The highest-yielding hybrids, IMHSB20, IMHSB1, and IMHSB3, had lower DM than all the checks, indicating them to be early-maturing hybrids. These hybrids can be beneficial to the farmers as they can save at least one irrigation at the time of maturity, which is one of the most costly inputs to reduce the cost of production and, in turn, benefit the farmers. (Fig. 1c). Similar findings for high-yielding stable genotypes have been reported in maize by Kuchanur et al. 2015; Choudhary

**Table 4.** Correlation among studied traits (Genotypic correlation: above diagonal; Phenotypic correlation: below diagonal)

| Traits | GY | ASI | DM |
|---|---|---|---|
| GY | 0.00 | -0.2244 | 0.067 |
| ASI | -0.0149 | 0.00 | -0.019 |
| DM | 0.0233 | -0.0504 | 0.00 |

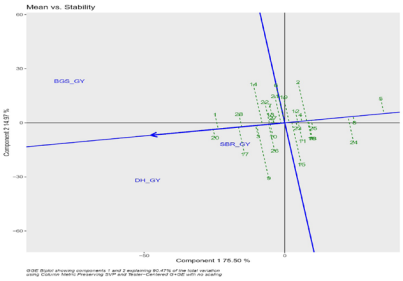


**Fig. 1a.** Mean Vs Stability (GY)

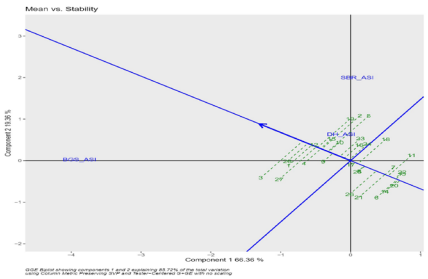


**Fig. 1b.** Mean Vs Stability (ASI)

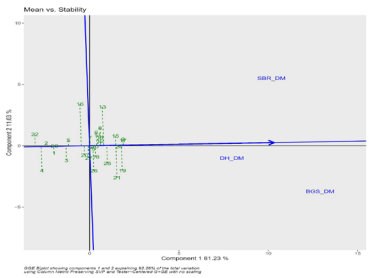


**Fig. 1c.** Mean Vs Stability (DM)

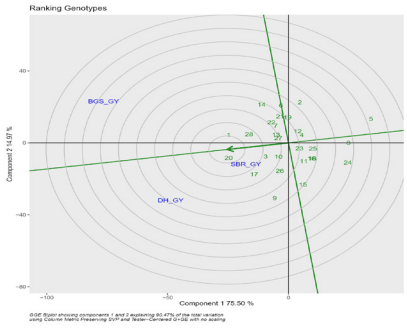


**Fig. 2a.** Ideal genotype (GY)

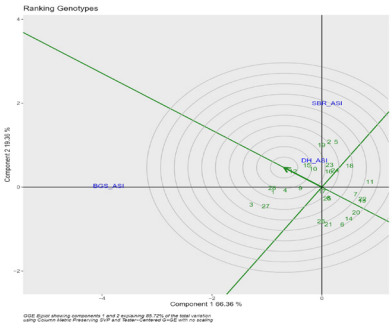


**Fig. 2b.** Ideal genotype (ASI)

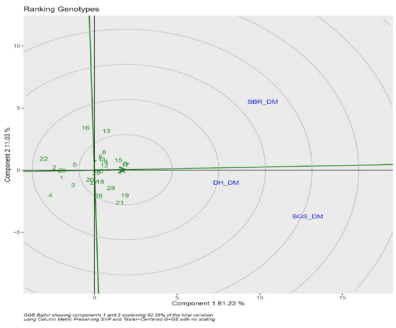


**Fig. 2c.** Ideal genotype (DM)

et al. 2019; Kumar et al. 2020.

An ideal genotype is defined as one that shows excellent performance while maintaining a level of stability across environments (Yan and Tinker 2006). Nonetheless, ideal hybrids were those representing high PC1 (high yield) and low PC2 (high stability) scores in the biplot to identify the best genotype. Fig. 2a, 2b, and 2c indicate the genotypes' ranking in terms of the ideal genotype for each of the three attributes. This study may assert that hybrid IMHSB20 is ideal and IMHSB1, IMHSB3 and check DKC 9081 were close to being ideal genotypes for GY. The ASI for high-yielding hybrid IMHSB20 was observed to be lesser (desirable).

### *Environmental evaluation*

An acute vector angle indicates that environments are more closely linked (Yan and Tinker 2006). The study revealed an acute angle for vectors reflecting all three locations, *i.e.,* BGS, SBR and DOL, among which SBR and DOL had least angle them (Fig. 3a, 3b, 3c). For ASI, there was also an acute angle between SBR and DOL and DOL and BGS and an obtuse angle between BGS and SBR. Thus, out of three locations, SBR and DOL were more correlated (Fig. 3a, 3b). The ability to distinguish genotypes in two environments is proportional to the distance between two environments. Thus, three locations might be categorized into two groups based on two traits (GY and ASI); one with SBR and DOL while other is represented solely by BGS (Fig. 3a, 3b).

Environments having lower angles with the average environment axis (AEA) are more reflective of the average test environments (Fig. 4a, 4b, and 4c). Thus, SBR, DOL and BGS had almost comparable projections from the AEA for GY while the angle was least of DOL for ASI and DM. BGS and DOL with longer vector lengths for GY were more discriminatory than SBR environment. Thus, a near-average location like SBR is the most representative and provides an excellent test environment for testing commonly adapted genotypes. On the other hand, since BGS and DOL are discriminatory and non-representative, they are advantageous for selecting genotypes that are especially suited for that particular location.

### *Which won where and mega environment identification*

A polygon formed by combining the most distant genotypes creates the which won where graph. The which-won-where graph for GY (Fig. 5) was found to be the most informative since it was able to distinguish environments with more accuracy and the polygon was well scattered and the hexagon has seven genotypes, IMHSB1, IMHSB20, IMHSB9, IMHSB24, IMHSB5, IMHSB2 and IMHSB14 at the vertices. It was observed that three locations might be partitioned into two separate mega-environments i.e., one mega-environment of SBR and DOL and another of BGS alone. For GY, IMHSB1 was winning in the BGS mega-environment while IMHSB20 was winning in the SBR, DOL mega-environment. Despite the fact that testing is being conducted in multilocations, almost identical findings might be obtained from one or two representatives of each mega-environment. However, multi-year and multi-environmental studies are needed to confirm this mega-environment pattern as conducted in maize (Kumar et al. 2023; Kuchanur et al. 2015), baby corn (Choudhary et al. 2019; Kumar et al. 2020).

### *AMMI analysis*

The ANOVA in AMMI showed significant differences ($p < 0.01$) for E, G, and GEI for all the three traits studied (Table 3). Fig. 6 and 7 exhibit biplot graphs of the AMMI1 and AMMI2. The environmental and varietal effects were scattered, revealing high environmental and genotypic variability (Figs. 6 and 7). AMMI1 evaluates stability in the y-axis (PC1), whereas AMMI2 reflects stable genotypes and environments near to the origin. Accordingly, IMHSB22 was most stable, and IMHSB2, IMHSB20, and IMHSB10 had intermediate stability for GY (Fig. 6). However, among these, IMHSB1,

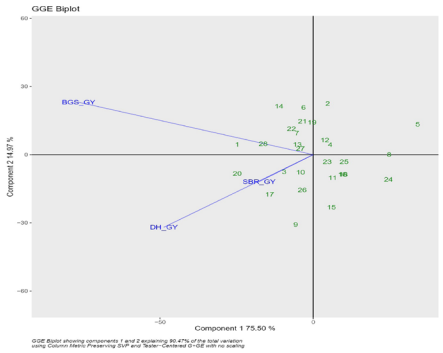


**Fig. 3a.** GGE Biplot (GY)

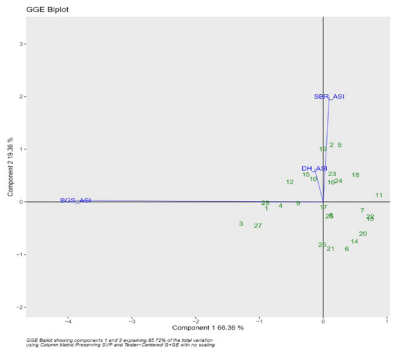


**Fig. 3b.** GGE Biplot (ASI)

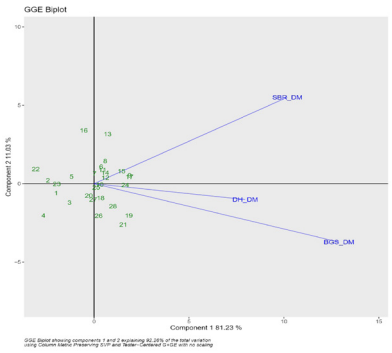


**Fig. 3c.** GGE Biplot (DM)

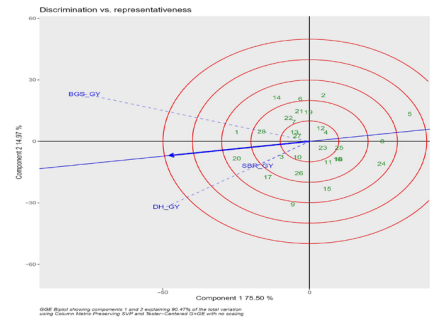


**Fig. 4a.** Discrimination vs Representativeness (GY)

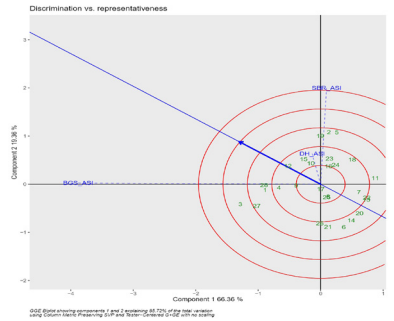


**Fig. 4b.** Discrimination vs Representativeness (ASI)

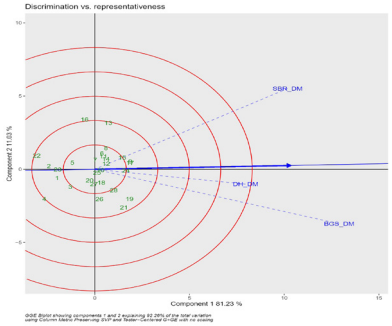


**Fig. 4c.** Discrimination vs Representativeness (DM)

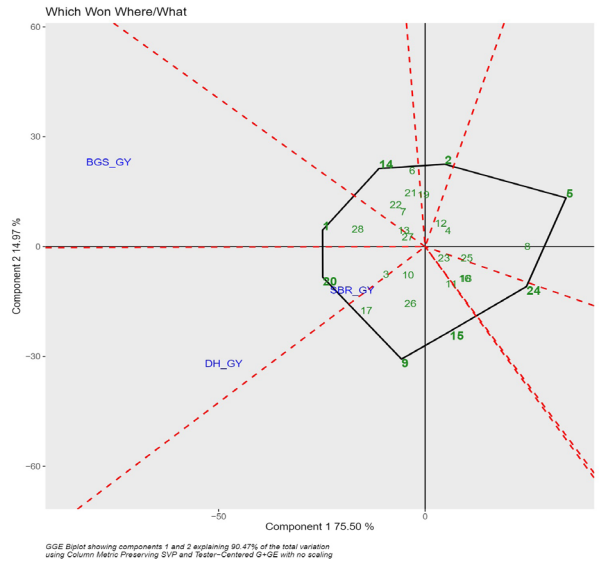


**Fig. 5.** Which won where (GY)

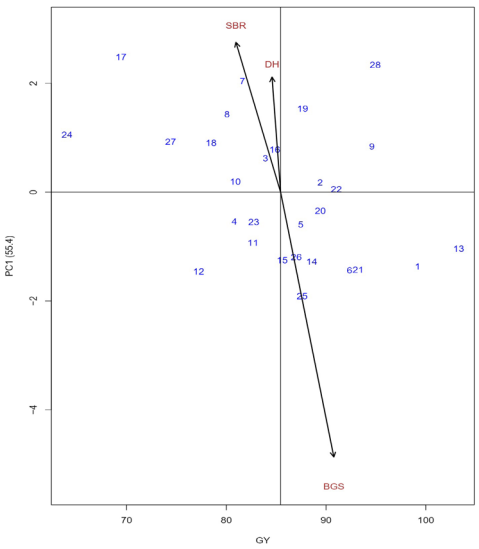


**Fig. 6.** AMMI (PC1 Vs GY)

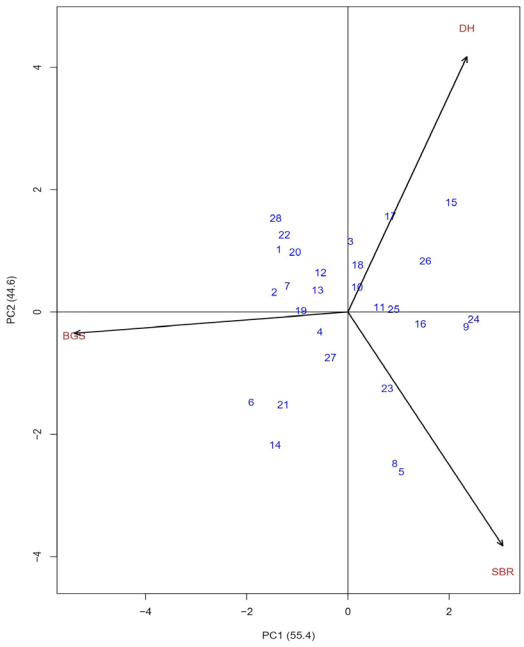


**Fig. 7.** AMMI (PC1 Vs PC2) for GY

IMHSB20, and DKC9081(C) were high yielder and relatively stable through GGE biplot, while by AMMI, only IMHSB20 was intermediately stable. Thus, for GY, IMHSB20, IMHSB1 and DKC 9081 were best. The hybrids IMHSB20 and IMHSB1 were identified as best from GGE biplot and AMMI. IMHSB20 was out yielding three checks and was relatively more stable, while IMHSB1 out yielded all the checks but showed average stability. The ASI of IMHSB20 and IMHSB1 was relatively the same as that of the best-yielding check DKC 9081. DM for these two high-performing hybrids was also lower in comparison to the checks. IMHSB13 was also identified as the high performer in terms of GY through AMMI, which had lower ASI and DM in comparison to checks.

AMMI2 biplot explained 100% G and G×E variation for all the three traits under study. The result revealed that the BGS environment was close to the biplot origin, which can be taken into consideration while selecting the genotypes with average adaptation. Based on AMMI2, hybrids *viz.*, IMHSB19, IMHSB11, and DHM117, were highly stable, while IMHSB2, IMHSB7, IMHSB13, IMHSB4, IMHSB16, IMHSB9 and IMHSB24 were found as intermediate stable (Fig. 7). Navrood et al. (2023) also followed both AMMI and GGE biplot models to select high-yielding and stable groundnut genotypes. Both GGE biplot and AMMI revealed that three hybrids, viz., IMHSB1, IMHSB20, and IMHSB13, were high-yielding and had average stability. The high-yielding and stable hybrids identified in this study could be tested in larger plot sizes at multilocations so that they may be recommended for commercial cultivation suited for an appropriate environment. The parents of these hybrids can be used with other elite inbred in crossing programs for developing high-yielding hybrids with average stability.

## Authors' contribution

Conceptualization of research (SBS); Designing of the experiments (SBS, SK, RK); Contribution of experimental materials (SBS); Execution of field/lab experiments and data collection (SBS, SK, BK, AK, RKK); Analysis of data and interpretation (SK, SBS, PK, GKC); Preparation of manuscript (SK, KRY, BSJ, MCD, SLJ).

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