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RESEARCH ARTICLE

# Evaluating stability of corn (*Zea mays* L.) hybrids for fresh cob weight and quality across environments

**Devadharssini Obula Kannan[1], Subramanian Alagesan[1*], Ravikesavan Rajasekaran[1], Senthil Natesan[2], Gurusamy Kandasamy [3], Djanaguiraman Maduraimuthu[4] & Kumari Vinodhana Natarajan[1]**

[1]Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore 641 003, India

[2]Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore 641 003, India

[3]Department of Food Process Engineering, Tamil Nadu Agricultural University, Coimbatore 641 003, India

[4]Department of Crop Physiology, Tamil Nadu Agricultural University, Coimbatore 641 003, India

*Email: subramanian.a@tnau.ac.in

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## Abstract

Corn (*Zea mays* L.) is a major commercial crop cultivated worldwide. Recognizing its economic importance, corn breeding has gained considerable momentum, with a key focus on understanding how the environment influences genotype performance. This interaction, known as Genotype × Environment (G × E), plays a crucial role in identifying stable and high-performing varieties. This study analysed three critical quality traits, such as cob weight, total soluble solids and total sugars using advanced statistical tools, including AMMI (Additive Model and Multiplicative Index), GGE (Genotype and Genotype-Environment) and WAASB (Weighted Average of Absolute Scores) models. These approaches were applied to evaluate the performance of 40 sweet-field corn hybrids across multiple environments. Based on the study two promising hybrids 45530×UMI 1230$\beta^+$ and 45679×UMI 1200$\beta^+$, that consistently performed well across different seasons in Coimbatore were identified. The Which-Won-Where plot further characterized the mega-environment, identifying the most suitable genotype for each environment based on all traits. This comprehensive analysis provides valuable insights into the G × E interaction effects on key quality parameters of fresh corn. The findings of this study would help in focused breeding efforts for developing stable and better performing corn hybrids, ensuring they meet both production and quality demands across varying environmental conditions.

## Keywords

AMMI; corn; GGE;G × E; stability; WAASB

## Introduction

Corn is among the top three most consumed crop worldwide, serving both human and animal diets. It holds significant commercial value, being utilized in various industries and as a fuel source. Sweet corn is one of the specialty corn. It is the second-largest processing crop by production and value, trailing only tomatoes. In 2023, the total value of the sweet corn crop exceeded $774 million, with 75% designated for the fresh market and 25% for processing. The processing sector, which includes frozen and canned sweet corn, contributed $193 million to this total (1). Given its substantial market value and increasing demand, enhancing sweet corn production is essential for meeting consumer needs, in this context, sweet corn and corn breeding play a vital role. The genetic diversity of sweet corn is limited, as all modern sweet corn varieties

trace their lineage to a common progenitor. To enhance its genetic base, the integration of field corn is essential. This study explores the hybridization of sweet corn with field corn as a strategy to improve the germplasm of sweet corn.

In crop improvement programmes, evaluating genotype performance across diverse environments are critical for identifying stable and high-yielding genotypes. The interaction between genotype and environment (G × E) plays a significant role in influencing crop traits such as yield, quality and adaptability (2). This complexity is especially pronounced in crops like sweet corn and field corn, where hybrid performance can vary greatly across different agroecological conditions. To address this challenge, advanced statistical tools such as the Additive Main Effects and Multiplicative Interaction (AMMI) model, Genotype and Genotype-by-Environment Interaction (GGE) biplot analysis and Weighted Average of Absolute Scores (WAASB) analysis have emerged as powerful methods for dissecting G × E interactions. These approaches not only enhance the understanding of genotype performance but also aid in identifying stable genotypes and delineating mega-environments, which are regions with relatively homogenous environmental conditions (3–5). Sweet corn, prized for its high sugar content and sensory quality and field corn, valued for yield and industrial uses, both require careful multi-environmental evaluations to meet the demands of specific production systems. By applying AMMI, GGE and WAASB models, breeders can effectively visualize and interpret complex data, enabling informed decision-making in selecting hybrids that combine stability with superior performance (6-8).

Present study leverages multi-environmental data to assess sweet corn and field corn hybrids using the AMMI, GGE biplot and WAASB model. The objectives of the research were to evaluate the impact of G × E interactions, identify stable and high-performing genotypes and define mega-environments that facilitate targeted recommendations for cultivation. Such insights are vital for enhancing productivity and adaptability in the face of diverse growing conditions.

## Materials and Methods

### *Research materials*

Ten sweet corn inbreds and four field corn inbreds were sourced from Department of Millets, Tamil Nadu Agricultural University, Coimbatore, India. Among the four field corn inbreds, two (UMI 1200$\beta^+$ and UMI1230$\beta^+$) were β-carotene allele introgressed NILs of UMI 1200 and UMI1230, with seven-fold higher β-carotene as compared to their normal forms (10). The sweet corn parents had an average total sugar of around 17- 18%. The 10 sweet corn inbreds were considered as lines (females) and four field corn inbreds were considered as testers (males) and they were hybridised in Line x Tester fashion (9) to generate 40 hybrids (Table 1) . The 40 hybrids thus generated were raised in the fields of the Department of Millets, CPBG, TNAU, Coimbatore during three consecutive seasons *viz*., *Rabi* of 2022 (E1), Summer of 2023 (E2) and *Kharif* of 2023 (E3) (Table 2). The soil type was clay loamy soil and soil health were maintained uniformly for all seasons. The coordinates of the location is 11.02°N and 76.92°E. The hybrids were evaluated in a randomized block design (RBD) with two replications in each season. Each entry was raised in a two-row plot of row length 6.0 m adopting a spacing of 90 × 45 $cm^2$. All the recommended agronomic practices were adopted for good crop establishment and stand. Observations were recorded in five random plants for cob weight and quality characteristics namely total soluble solids and total sugars were measured at 22 days after anthesis. Fresh cob weight was measured in grams, after dehusking the cob harvested at 22 days after pollination (DAP). TSS was estimated in fresh seeds by using a hand refractometer (11), while total sugars (TS) were estimated by the anthrone method (12) and reducing sugars were estimated by following the Nelson-Somogyi method (13).

**Table 1.** Genotypes used in this study

| Sr. No. | Code | Genotype | Sr. No. | Code | Genotype |
|---|---|---|---|---|---|
| 1 | H1 | 45684 ×UMI 1200 | 21 | H21 | 45503×UMI 1200 |
| 2 | H2 | 45684 ×UMI 1200$\beta^+$ | 22 | H22 | 45503×UMI 1200$\beta^+$ |
| 3 | H3 | 45684 ×UMI 1230 | 23 | H23 | 45503×UMI 1230 |
| 4 | H4 | 45684 ×UMI 1230$\beta^+$ | 24 | H24 | 45503×UMI 1230$\beta^+$ |
| 5 | H5 | 12039-1 ×UMI 1200 | 25 | H25 | SC11-2×UMI 1200 |
| 6 | H6 | 12039-1 ×UMI 1200$\beta^+$ | 26 | H26 | SC11-2×UMI 1200$\beta^+$ |
| 7 | H7 | 12039-1 ×UMI 1230 | 27 | H27 | SC11-2×UMI 1230 |
| 8 | H8 | 12039-1 ×UMI 1230$\beta^+$ | 28 | H28 | SC11-2×UMI 1230$\beta^+$ |
| 9 | H9 | 12068-2 ×UMI 1200 | 29 | H29 | 45530×UMI 1200 |
| 10 | H10 | 12068-2 ×UMI 1200$\beta^+$ | 30 | H30 | 45530×UMI 1200$\beta^+$ |
| 11 | H11 | 12068-2 ×UMI 1230 | 31 | H31 | 45530×UMI 1230 |
| 12 | H12 | 12068-2 ×UMI 1230$\beta^+$ | 32 | H32 | 45530×UMI 1230$\beta^+$ |
| 13 | H13 | SC1107 ×UMI 1200 | 33 | H33 | 45679×UMI 1200 |
| 14 | H14 | SC1107×UMI 1200$\beta^+$ | 34 | H34 | 45679×UMI 1200$\beta^+$ |
| 15 | H15 | SC1107×UMI 1230 | 35 | H35 | 45679×UMI 1230 |
| 16 | H16 | SC1107×UMI 1230$\beta^+$ | 36 | H36 | 45679×UMI 1230$\beta^+$ |
| 17 | H17 | USC 12-3-1×UMI 1200 | 37 | H37 | SC17-3×UMI 1200 |
| 18 | H18 | USC 12-3-1×UMI 1200$\beta^+$ | 38 | H38 | SC17-3×UMI 1200$\beta^+$ |
| 19 | H19 | USC 12-3-1×UMI 1230 | 39 | H39 | SC17-3×UMI 1230 |
| 20 | H20 | USC 12-3-1×UMI 1230$\beta^+$ | 40 | H40 | SC17-3×UMI 1230$\beta^+$ |

The total sugar was calculated using the standard curve developed with glucose as standard.

*Total sugar in 100 mg sample (%) = (mg of glucose (x value) / volume of test sample) ×100*

### *Statistical analysis*

***Pooled Analysis of Variance (ANOVA) across environments:*** A simplified pooled ANOVA was constructed to identify the significance of genotype across different environments (seasons).

$$Y_{ijk} = \mu + G_i + E_j + GE_{ij} + B_{ij} + \varepsilon_{ijk}$$

**Table 2.** Location and its description

| Seasons | Code | Duration | Rainfall (mm/day) | Relative humidity (%) | Minimum temperature (°C) | Maximum temperature (°C) |
|---|---|---|---|---|---|---|
| *Rabi*, 2022 | E1 | 02.09.2022 - 21.12.2022 | 476.55 | 86.3 | 19.7 | 27.3 |
| Summer, 2023 | E2 | 02.02.2023 - 27.05.2023 | 219.4 | 60.5 | 22.5 | 34.2 |
| *Kharif*, 2023 | E3 | 12.06.2023 - 02.10.2023 | 77.1 | 67.9 | 23.5 | 32.6 |

Where μ represents the comprehensive mean of the analysed characteristic within the population, $G_i$ denotes the influence of the $i^{th}$ genotype, $E_j$ signifies the effectiveness of the $j^{th}$ environment, $GE_{ij}$ illustrates the interaction between the $i^{th}$ genotype and the $j^{th}$ environment, $B_{ij}$ indicates the impact of the $k^{th}$ replication in the $j^{th}$ environment and $E_{ijk}$ embodies the stochastic error.

To investigate the G × E interaction three models were adopted in this study. AMMI, GGE and WAASBY models considered to find out stability to evaluate under fixed and random effects and for better visualisation. The AMMI model works based on Principal Component Analysis (PCA) applied to the main effect and interaction effect using a fixed effect model. In contrast, the GGE model utilizes genotype and interaction effects, while the WAASB model is based on the BLUP prediction model using a random effect. The AMMI model is suitable when a comprehensive understanding of both main effects and interaction patterns is essential. The GGE model is employed when the focus is on genotype performance across environments and identifying mega-environments. The WAASB model is applied when balancing high productivity and stability is required, particularly for practical breeding decisions. The results of all these models can give a comprehensive view of selecting genotypes based on stability and productivity. Thus AMMI, GGE and WAASBY were optimal for investigating G × E interaction effects among different seasons under both fixed and random effects.

### *AMMI analysis*

The Genotype - Environmental interaction was estimated based on the Additive Model and Multiplicative Index (AMMI) model as suggested by Gauch (14). The AMMI model is a widely used statistical method in agriculture, particularly for analysing genotype-by-environment interaction (G × E) in multi-environment trials (METs). This method combines the ANOVA and principal component analysis (PCA) to effectively assess and interpret the interaction effects between genotypes and environments (4,15). To constitute the AMMI ANOVA, the following formula was used.

$$y_{ij}^{N} = \mu + g_i + e_j + \Sigma\lambda_k Y_{ik}\alpha_{jk} + \Sigma_{ij}$$

Where $y_{ij}$ represents the yield of the $i^{th}$ genotype within the $j^{th}$ environmental context, N denotes the number of principal components utilized in the AMMI model and μ signifies the overall mean across genotypes. In contrast, $g_i$ and $e_j$ represent the deviations of the genotype and environment from the overall mean, respectively. Furthermore, $\lambda_k$ is the eigenvalue corresponding to the PCA axis k, $Y_{ik}$ and $\alpha_{jk}$ are the principal component scores for genotypes and environments associated with axis k and $\Sigma_{ij}$ constitutes the residual value.

A mathematical formulation for AMMI analysis referred to as the AMMI stability value (ASV) was proposed by Purchase (16). The ASV is represented as the distance from the origin in a two-dimensional scatter plot depicting IPC1 (interaction PCA 1) in relation to IPC2. It is note worthy that IPC1 exerts a greater influence compared to IPC2; consequently, an adjustment must be incorporated into IPC1 to account for the symmetrical disparity with IPC2, ensuring that the contributions of IPC1 and IPC2 are appropriately represented (17). Within this framework, the genotypes and test environments exhibiting the highest stability are characterized by a minimum ASV (15,18).

The subsequent equation was employed to quantify and rank the genotypes and seasons:

$$ASV = \sqrt{\left[\frac{SSIPC1}{SSIPC2}(IPC1\ \text{score})^2\right] + (IPC2\ score)^2}$$

Another metric that can be derived from AMMI analysis is the genotype selection index (GSI). The selection based on stability does not invariably yield the optimal genotype in terms of performance. Consequently, the GSI for each genotype was determined by aggregating the rank of the genotype ($RY_i$) with the rank of the genotype ASV ($RASV_i$). A genotype possessing the lowest GSI is recommended as the most stable genotype (15,18,19).

$$GSI = RY_i + RASV_i$$

### *Weighted Average of Absolute Scores (WAASB)*

The WAASB can be derived from the singular value decomposition (SVD) of the matrix containing the best linear unbiased predictions (BLUPs) for G × E interaction effects, which are obtained using a linear mixed-effects model and the response variable(4,20). This can be calculated by the following formula.

$$WAASB_i = \frac{\sum_{k=1}^{p}|IPAC_{ik} \times EP_k|}{\sum_{k=1}^{p} EP_k}$$

Where $IPCA_{ik}$ is the score of the *i*th genotype in the *k*th Interaction Principal Component Axis (IPCA) and $EP_k$ represents the proportion of variance explained by the *k*th IPCA.

WAASBY is constructed using the WAASB value and the mean value of the variable. It gives a clear idea of genotype selection based on stability and mean performance.

$$WAASBY_i = \frac{(rY_i \times \theta_Y) + (rW_i \times \theta_S)}{\theta_Y + \theta_S}$$

Where, $rY_i$ is the rescaled mean of the variable, $rW_i$ is the rescaled $WAASB_i$ value, $\theta_Y$ and $\theta_S$ are the weights given to trait and stability respectively (4). Genotypes with higher $WAASBY_i$ are less interactive and better-performing genotypes (4,21).

### *GGE biplot analysis*

The Genotype and Genotype-Environment analysis was suggested by Gauch (14). GGE biplot analysis is applied when significant genotype × environment interactions complicate the direct identification of superior phenotypes. The most commonly used model for this analysis employs singular value decomposition (SVD), centred on either genotypes or environments (22). The process follows the formula:

$$\hat{Y}_{ij} = \mu + \beta_j + \lambda_1\xi_{il}\eta_{lj} + \lambda_2\xi_{iz}\eta_{zj} + \epsilon_{ij}$$

The term $\hat{Y}_{ij}$ represents the expected yield of the *i*th genotype in the *j*th environment. Here, μ is the overall mean yield, $\beta_j$ denotes the main effect of the *j*th environment and $\lambda_1$ and $\lambda_2$ are the singular values of the first two principal components, PC1 and PC2, respectively. Additionally, $\xi_{il}$ and $\xi_{iz}$ are the eigenvectors of the *i*th genotype for PC1 and PC2, while

$\eta_{ij}$ and $\eta_{zj}$ are the eigenvectors of the jth environment for PC1 and PC2. The term $\epsilon_{ij}$ accounts for the residual variation not explained by the genotype (G) or genotype × environment (GE) interaction effects. Which-Won-Where GGE biplot is used in this study to classify the winning genotypes of the mega-environment differentiated.

All the statistical analyses were carried out in Microsoft Excel (Version: 2410) and R software (4.4.1) using packages *metan*version 1.18.0.

## Results

### *Pooled ANOVA*

The ANOVA revealed highly significant differences between season, genotype and the interaction effect, genotype × season (G × E) at a 99.9% confidence level (p > 0.001) for all the characters. This indicates the presence of an interaction effect due to genotype and environment (Table 3). The G × E interaction can be substantiated using AMMI and GGE analysis. The same results were obtained in similar other studies (6,15,21).

### *AMMI model analysis of traits*

The results of AMMI ANOVA also revealed that genotype, season, G × E, PC1 and PC2 were significant at a 99.9% confidence level for all three traits. Replication was significant for the trait CW and non-significant for TSS and TS. The variance explained by PC1 and PC2 cumulatively contributed 100% in all three traits. In CW, PC1 and PC2 contributed 69.6% and 30.4% variance respectively. The variance contributed by PC1 and PC2 were 73.5% and 26.5% in TSS and 62.5% and 37.5% in the trait TS respectively (Table 4). This indicated the adequacy of PC1 and PC2 for AMMI analysis variance. Similar results were reported in several previous studies (6,15,21,23).

### *Mean performance, ASV, GSI, WAASB$_i$ and WAASBY*

The performance of genotypes across different seasons was assessed and ranked based on the pooled mean across seasons, as well as their ASV, GSI, WAASB$_i$ and WAASBY values for all three traits (Supplementary tables 1, 2 and 3). Genotypes with the lowest ASV, GSI and WAASBi and higher WAASBY values were selected, as they exhibit minimal interaction with the environment. This approach provides a clear understanding of genotypes that perform consistently well with reduced environmental influence(21,24,25).

**Table 3.** ANOVA for pooled analysis for cob weight, TSS and total sugar

| Source | df | Cob weight | TSS | Total sugars |
|---|---|---|---|---|
| Season | 2 | 9639.81** | 62.82** | 99.52** |
| Replication (environment) | 3 | 77.68** | 0.19 | 0.26 |
| Genotypes | 39 | 7214.07** | 8.64** | 12.27** |
| Genotypes × Season (G × E) | 78 | 62.25** | 1.16** | 1.36** |
| Pooled error | 117 | 7.53 | 0.23** | 0.15** |

Heavier cobs yield more kernels per unit area, leading to better economic returns for farmers. This is especially critical in sweet corn, where cob appearance and kernel quantity are key drivers of profitability. Fresh cob weight is the representative of the sweet corn yield. Thus, focusing on higher CW is key. The genotypes H21, H32, H12, H29 and H36 secured the top five spots based on the pooled mean across environments. The least interactive genotypes based on the ASV were H20, H28, H23, H37 and H14. The lesser the ASV, the lesser the G × E. GSI is a stability parameter that gives the result based on the ASV and mean value. Hence, the minimal value of GSI reveals genotypes that are least interactive with different seasons and good performers. For GSI, the top five stable and top-performing genotypes were in the order of H34>H23> H36> H32 > H3. Genotypes ranked based on WAASBi were similar to that of ASV, where the top five genotypes were H20 > H28 > H23 > H14 > H37. The WAASBY rank revealed the better performing and least interactive genotypes and the top five hybrids H32 > H34 > H36 > H23 > H20. Similar trend was seen by Patel *et al*., (6)(Supplementary table 1).

High TSS values often indicate superior genotypes for sweetness. This trait is essential for breeding programs to develop sweeter corn lines, especially for fresh market and processing purposes. The best-performing top five genotypes were in the sequence H22>H21>H24> H23>H32 based on the mean performance. The least environmentally interactive genotypes identified based on ASV were H27> H10>H12> H19> H14. Genotypes with lesser environmental interaction and above the average mean were H21 > H24 >H16> H22>H14 identified based on GSI values. The genotypes with the lesser G × E, as determined by WAASB$_i$ values, were identified in the following order: H27> H14> H10>H19> H12. This trend was observed to be similar to ASV. The top five genotypes based on the values of WAASBY are H22 > H21 > H24 > H32 > H16 (Supplementary table 2). Results of Patel *et al*., were similar to the current study (6).

The total sugar level is a crucial quality parameter. It reflects the biochemical composition of the kernels, which directly contributes to flavour. It is especially important in distinguishing sweet corn from field corn and other maize types. Based on the mean performance H32 > H22 > H23 > H21 > H29 performed better across three seasons. H24> H37> H35> H31> H25 were identified as stable genotypes based on the ASV. Stable and better-performing hybrids were in the

**Table 4.** AMMI ANOVA for cob weight, TSS and total sugar

| Source | df | Cob weight | TSS | Total sugars |
|---|---|---|---|---|
| Season | 2 | 9639.81** | 62.82** | 99.52** |
| Replication (environment) | 3 | 77.68** | 0.19 | 0.26 |
| Genotypes | 39 | 7214.07** | 8.64** | 12.27** |
| Genotypes x Season (G × E) | 78 | 62.25** | 1.16** | 1.36** |
| PC1 | 40 | 84.53** | 1.66** | 1.66** |
| PC2 | 38 | 38.80** | 0.63** | 1.05** |
| G×E explained (%) for PC1 | | 69.6 | 73.5 | 62.5 |
| G×E explained (%) for PC2 | | 30.4 | 26.5 | 37.5 |
| Cumulative (%) for PC1 | | 69.6 | 73.5 | 62.5 |
| Cumulative (%) for PC2 | | 100 | 100 | 100 |
| Residuals | 117 | 7.53 | 0.23 | 0.15 |
| Total | 317 | 982.50 | 2.12 | 2.86 |

sequence H24 > H34 > H31 > H37 > H12 and identified based on GSI. The less interactive genotypes identified based on $WAASB_i$ values were H24 > H35 > H11 > H37 > H12. The sequence of top performing hybrids based on WAASBY were H24 > H32 > H22 > H34 > H31. Parameters of AMMI model resembled the parameters of WAASB model in all traits studied. Similar pattern were reported by Verma and Singh in wheat, Arshad *et al*., in pigeon pea(26,27)(Supplementary table 3).

### *AMMI, GGE and WAASBY biplots*

AMMI 1 biplot was constructed based on the interaction of the mean of the variable and the first principal component (PC1). AMMI 1 biplot can be annotated based on the position of genotypes on the biplot. If the genotype is on the right side of the ordinate, then the mean of the variable could be considered to be above average. Abscissa remains to be the least interactive position on the AMMI 1 biplot. Thus, the genotypes from such positions can be chosen for better performance and stability (15). In the AMMI 2 biplot, genotypes positioned near the origin are the least interacting genotypes (4,15). The Which-Won-Where (WWW) plot is a GGE biplot which reflects the G × E crossover, winner of the specific environment, characterization of mega environments, etc. In WWW, a polygon is constructed using the farthest vertices of the biplot and the mega environment is differentiated based on the perpendicular line drawn from the origin to the sides of the polygon. These vertices are considered the winner of the mega environment from which it is hailed (3). The visualization of the WAASB model was performed using the mean and WAASBY biplot (Y × WAASBY biplot). This biplot can be annotated based on the quadrants where the genotypes are placed. Genotypes located in the first quadrant are highly unstable and perform below the mean. In the second quadrant, genotypes exhibit lower stability and a higher mean. The third quadrant contains genotypes with high stability and a low mean, while the fourth quadrant consists of stable genotypes with a higher mean (24,28,29). From Y × WAASBY biplot, five best performing and stable hybrids were picked from fourth quadrant.

In the present study, from the AMMI 1 biplot, H32, H12, H36, H34, H23 were five better hybrids with higher mean than average performing genotype and lesser G × E for the trait CW (Fig. 1). Whereas the stable genotypes identified from AMMI 2 biplot were H20, H23, H28, H2, H4 (Fig. 2). The results of WWW biplot for CW revealed the presence of two mega environments. The first mega environment consisted of E1 and second mega environment consisted of E2 and E3. The winners of the first mega environment were H30, while the winners of the second mega environment were H32, H21, H13 and H22 (Fig. 3). From the Y× WAASBY biplot, H32, H36, H34, H23 and H17 were found in the fourth quadrant (Fig. 4).

In the case of TSS, based on AMMI 1 biplot (Fig. 5), the genotypes H22, H21, H24, H32 and H16were observed to exhibit higher mean values compared to the average-performing genotype and demonstrated lower G × E interaction. The AMMI 2 biplot (Fig. 6) revealed that the genotypes H2, H12, H8, H35 and H27 were stable. The WWW biplot indicated the presence of two mega-environments: the first comprising E1 and E2 and the second including E3. In the first mega-environment, the winning genotypes were H23 and H22, whereas, in the second mega-environment, H26was identified as the winner (Fig. 7).H22, H21, H24, H32 and H16 were found to be stable and better performing in the Y× WAASBY biplot (Fig. 8).

Further, the AMMI 1 biplot (Fig. 9) indicated that the genotypes H32, H24, H34, H31 and H37 had higher mean values than the average-performing genotype and exhibited lower G × E interaction for the trait TS. In contrast, the AMMI 2 biplot (Fig. 10) highlighted H37, H27, H24, H12 and H31 as the most stable genotypes. According to the WWW biplot for TS, two mega-environments were identified, the first consisting of E1 and the second comprising E2 and E3. The genotypes H22 and H15 were the winners in the first mega-environment, while H32 was the winner of the second mega-environment (Fig. 11).Stable and better performing five hybrids identified from Y× WAASBY biplot were H32, H24, H22, H34 and H31 (Fig. 12)

This study employed different approaches to identify genotypes that demonstrate better performance as well as stability across all seasons. Among the genotypes identified from GSI and WAASBY, which can be considered selecting since these parameters are constructed based on mean and stability index (6,26). AMMI biplots and Y× WAASBY biplot visualisation was in anology with the indices GSI and WAASBY. From the results, hybrids H32 and H34 stood out as stable and better performing for all the traits. The coincidence of AMMI analysis and WAASB is seen in this study. A similar pattern was reported by Pranthi*et al*., in pigeon pea and Verma and Singh in wheat(26,30). Admist of employing both random effect and fixed effect models in studying the G × E interaction effects, results were similar for both methods. Thus application of these methods in heterotic sweet corn hybrid analysis can be used in future. Hybrid H32 and H34 outperformed other hybrids and shown its stability over environment in weight and quality traits. Better performance of these hybrids may attributed to their heterosis and better combining ability.

## Conclusion

Sweet corn is a highly marketable crop that is consumed either fresh or frozen. Fresh cob weight, total soluble solids and total sugars are the important traits accounting for its marketability. These traits are heavily influenced by the environment. The same pattern was noticed in the current study. From the assessment, a few hybrids were found to be better performing and stable across environments. The hybrids 45530 × UMI 1230$\beta^+$ and 45679 × UMI 1200$\beta^+$ were found to be stable and better performing for all the traits studied, owing to which they can be exploited after large scale evaluation. Further, selection from segregants of these hybrids could result in sweet corn inbreds with enhanced β-carotene. Improvement of the above promising inbred lines for their biotic and abiotic stress tolerance could result in development of promising hybrids with better nutritional quality and stress resistance.

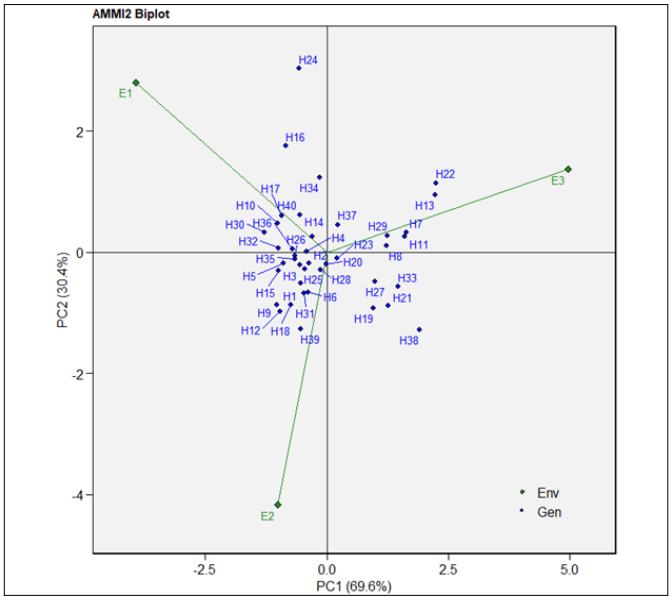


**Fig. 1.** Biplot of PC1 *vs.* cob weight (gm) in AMMI analysis.

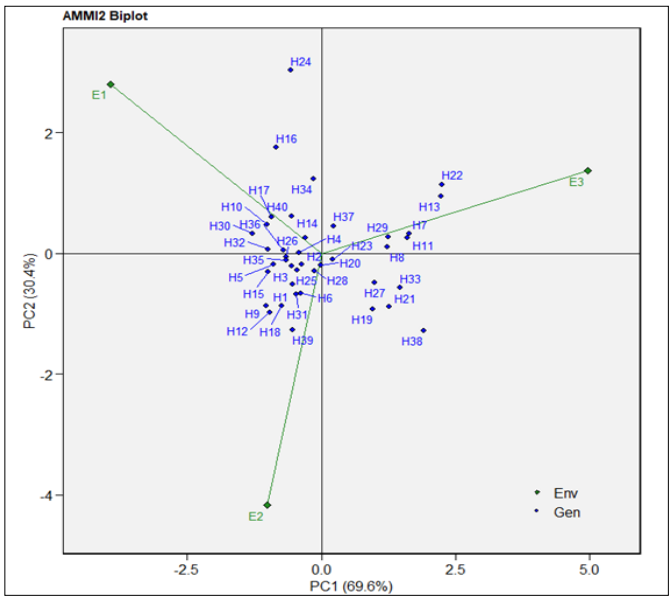


**Fig. 2.** Biplot of PC1 *vs.* PC2 in AMMI analysis of cob weight (gm).

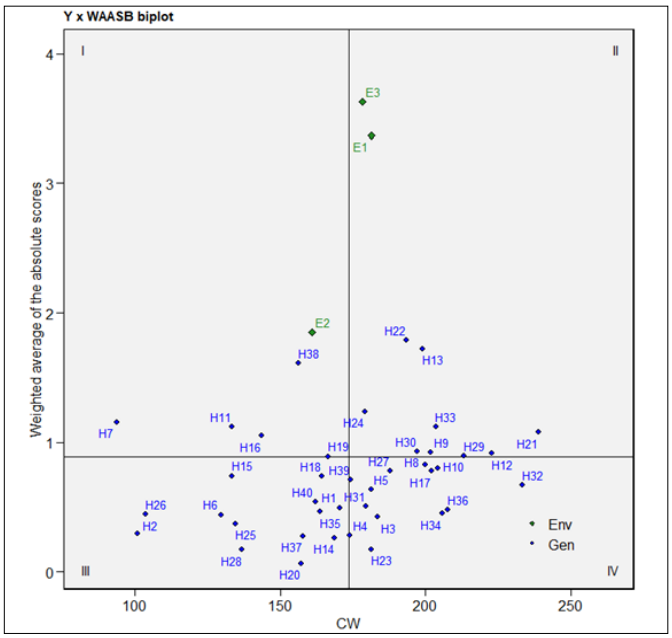


**Fig. 3.** Which-Won-Where plot of cob weight (gm) in AMMI analysis.

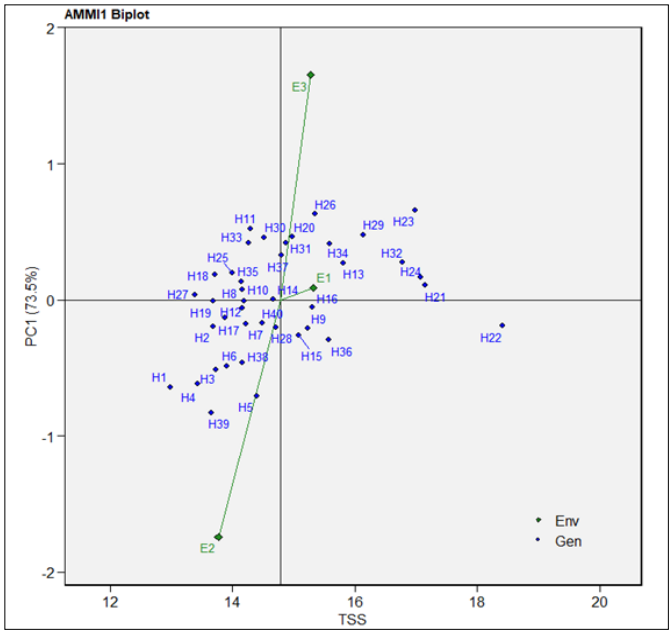


**Fig. 4.**WAASB scores Vs. Cob Weight (gm) biplot in WAASB analysis.

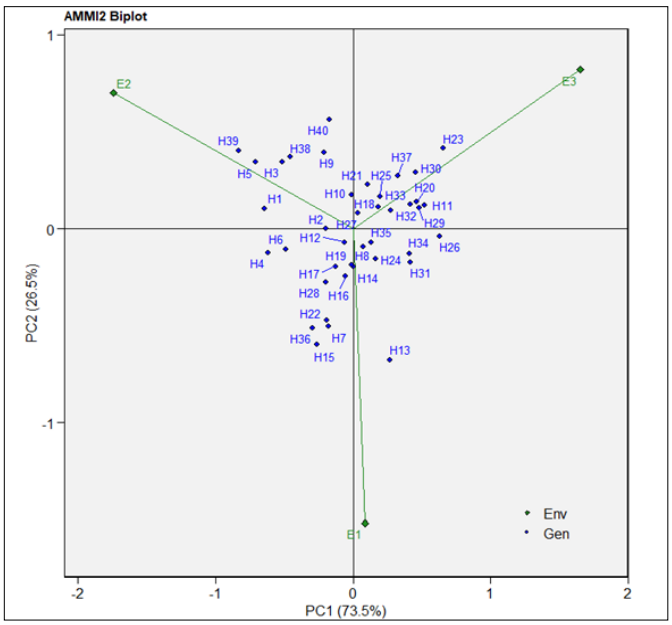


**Fig. 5.** Biplot of PC1 *vs.* Total soluble solids (°) in AMMI analysis.

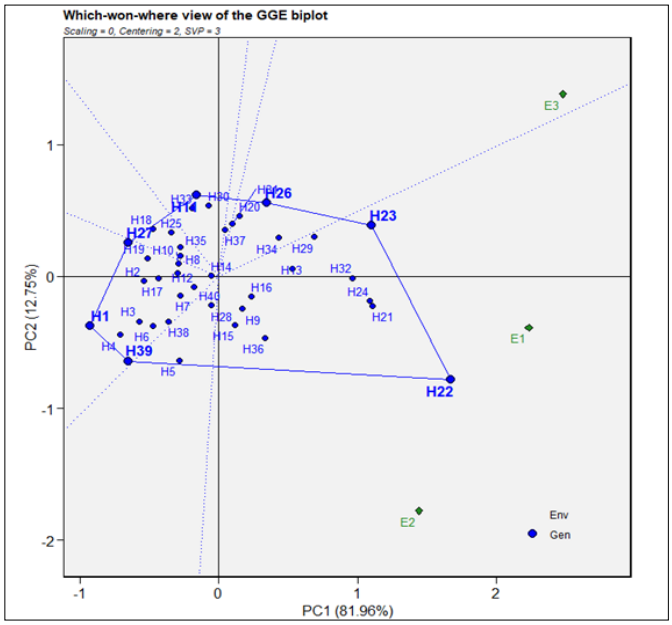


**Fig. 6**. Biplot of PC1 *vs*. PC2 in AMMI analysis of Total soluble solids (°).

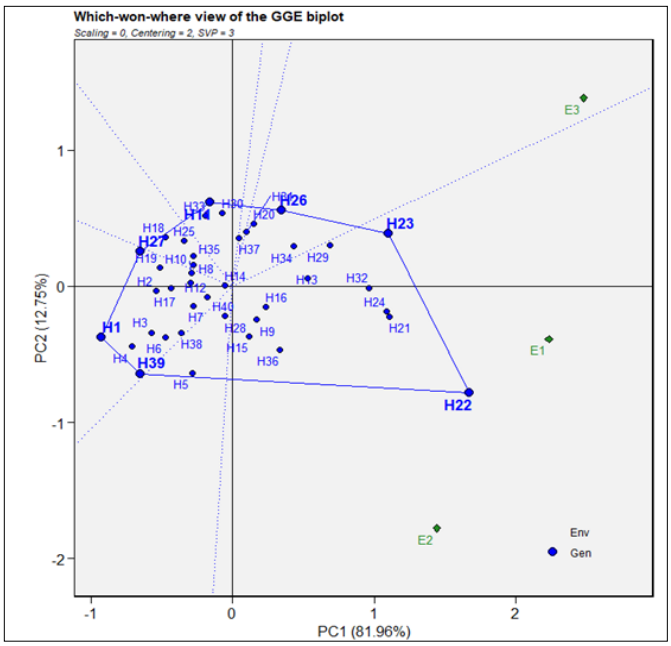


**Fig. 7.** Which-Won-Where plot of Total soluble solids (°) in AMMI analysis.

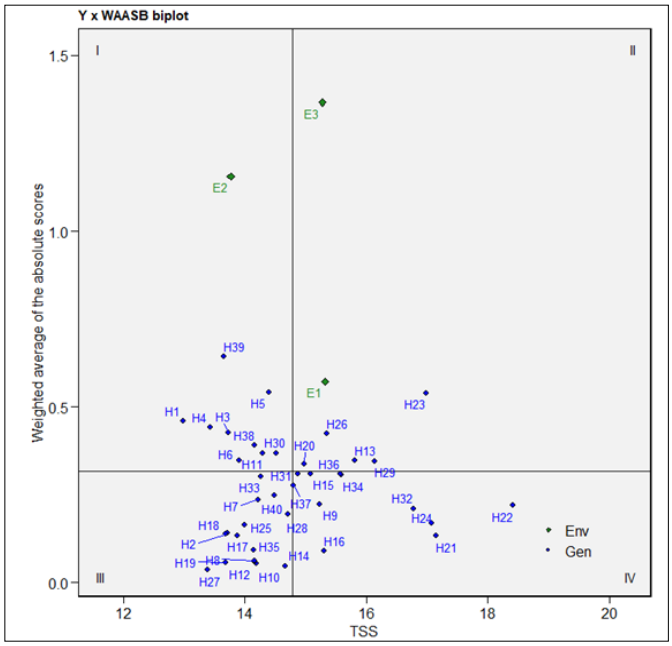


**Fig. 8.**WAASB scores Vs. Total soluble solids (°) biplot in WAASB analysis.

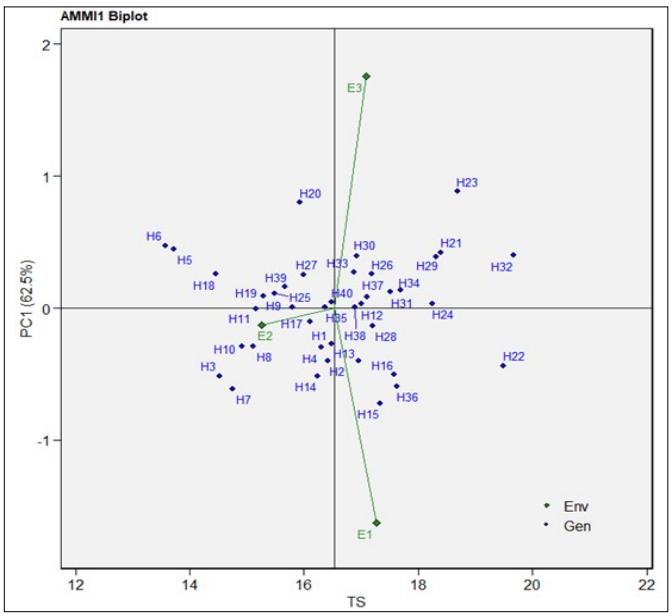


**Fig. 9.** Biplot of PC1 vs. Total sugars (%) in AMMI analysis.

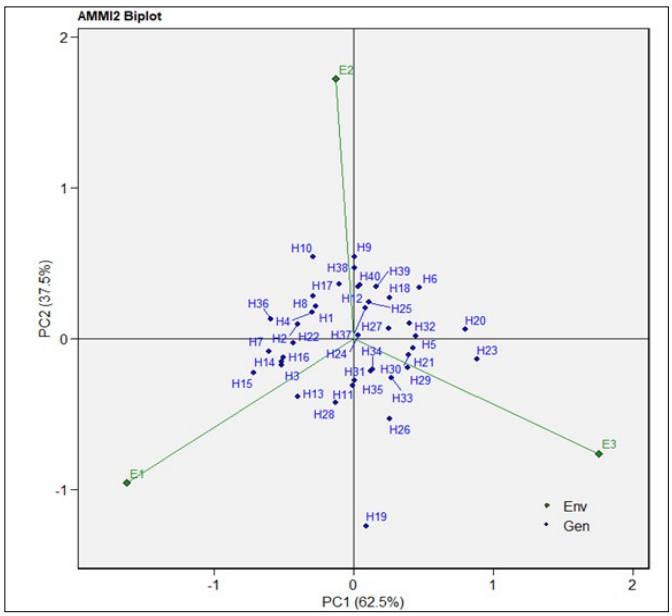


**Fig. 10.** Biplot of PC1 vs. PC2 in AMMI analysis of Total sugars (%).

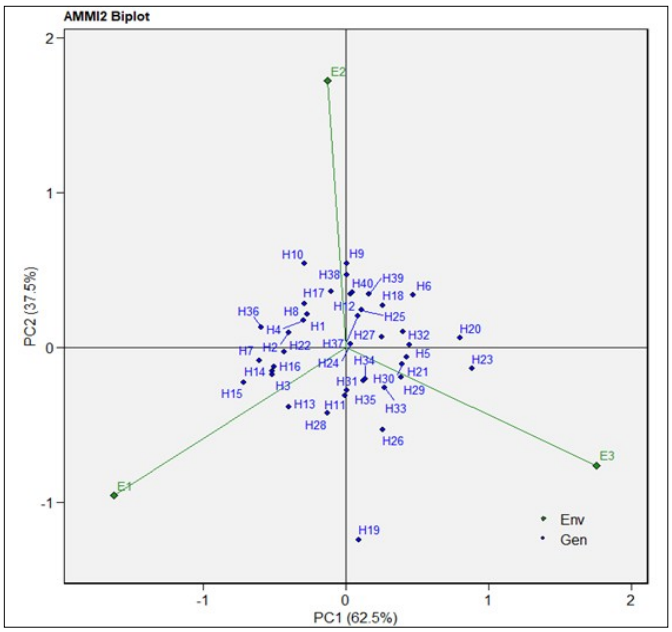


**Fig. 11.** Which-Won-Where plot of Total sugars (%) in AMMI analysis.

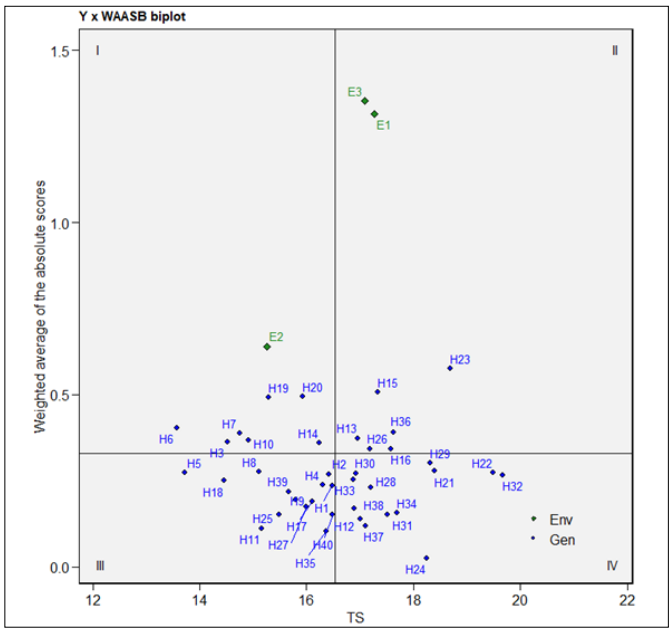


**Fig. 12.** WAASB scores Vs.Total sugars (%) biplot in WAASB analysis.

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## Authors' contributions

DOK, designing experiments, execution of field/lab experiments, data collection, data analysis and interpretation and manuscript preparation. SA, supervised and conceptualised and formulated the research, experimental design and manuscript preparation. RR, provided research material, conceptualised and formulated the research and reviewed the article. SN: Provided facility to conduct laboratory experiments, guided research and reviewed the manuscript. GK and DM, member of the committee, guided in conducting experiments and laboratory procedures. KVN, helped in experimental layout and characterisation of traits.

## Compliance with ethical standards

**Conflict of interest:** Authors do not have any conflict of interests to declare.

**Ethical issues:** None

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