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RESEARCH ARTICLE

Genotypic evaluation and stability analysis of chilli (*Capsicum* species) for yield and capsaicin content using AMMI and GGE biplot

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Abstract

Chilli (*Capsicum* species) is a widely cultivated crop valued for its economic and nutritional significance. However, (G x E) genotype-by-environment interactions often cause variability in yield and biochemical characters, necessitating stability analysis to identify genotypes with consistent performance. The study evaluates 6 chilli genotypes (5 breeding lines and 1 check variety, PLR-1) for yield and capsaicin content across 3 environments in Tamil Nadu: Paiyur, Udumalpet and Yethapur. The study was conducted during the 2023-24, using a randomized block design (RBD) with 4 replications. Agronomic traits including fruit yield per plot and capsaicin content, were recorded. Statistical models, viz. Additive Main Effects and Multiplicative Interaction (AMMI) and Genotype + Genotype x Environment (GGE) biplot, were employed to assess G × E interactions and determine genotype stability. Analysis of variance (ANOVA) revealed significant G x E interactions for both traits, reinforcing the need for stability assessment. PC1 contributes 98 % and 65.5 %, PC2 contributes 2 % and 34.5 % for the 2 characters for the trait yield and capsaicin respectively. G1 (CC-CBE-003) exhibited superior yield (22.87 kg) and high capsaicin content (120451.00 SHU) with stability across locations, making it suitable for fresh and industry purposes. Yethapur (E3) emerged as the most discriminative environment for genotype testing. These findings aid breeding programs in improving productivity and adaptability in chilli.

Keywords: AMMI; chilli; GGE biplot; G x E interactions; stability analysis

Introduction

Chilli (*Capsicum* species), a vital crop of the Solanaceae family, is one of the most economically significant crops globally. It is a diploid ($2n = 2x = 24$) species, cultivated for its diverse applications as a vegetable, spice and medicinal ingredient (1, 2). Five species, *C. annuum* L., *C. chinense* Jacq., *C. frutescens* L., *C. baccatum* L. and *C. pubescens*, out of the more than 30 species in the genus *Capsicum*, are domesticated and grown (3, 4). Central America, particularly Mexico and Guatemala, is recognized as the center of diversity for *Capsicum* and it is believed that the Portuguese introduced it to India in the 17th century (5, 6).

India dominates global chilli production, contributing approximately 38 % of the total output and fulfilling nearly 50 % of global demand as both a major consumer and exporter (7). India's top chilli-producing states are Andhra Pradesh, Tamil Nadu, Karnataka and Maharashtra, with diverse agro-ecological conditions influencing the crop's yield and quality.

Beyond its culinary relevance, chilli possesses significant nutritional and pharmaceutical properties. Fresh fruits are rich in bioactive compounds including phenols, flavonoids, capsaicinoids and ascorbic acid, which contribute to their antioxidant potential. Capsaicinoids, responsible for the pungency of chilli, have been widely studied for their medicinal properties, including pain relief, metabolism enhancement and anti-inflammatory effects. Ascorbic acid (vitamin C) content in chilli ranges between 50-120 mg/100g, playing a crucial role in human nutrition, post-harvest quality maintenance and shelf-life extension (8). However, both yield and nutritional parameters exhibit considerable variation across different agro-climatic conditions, posing a significant challenge for breeding programs aimed at developing superior, stable genotypes (9).

The genotype and environment interaction (G x E) is a key consideration in crop improvement, especially in areas with diverse climatic conditions. Variations in soil type, temperature, rainfall and other environmental factors influence phenotypic expression, making it essential to assess stability to identify consistently high-performing cultivars. Inconsistent performance across different environments can hinder large-scale adoption of promising genotypes, underscoring the necessity for stability analysis in breeding programs (10, 11).

Despite extensive research on chilli, the stability of both yield and biochemical traits, particularly capsaicin content, has received limited attention. Since chillies are grown across a variety of agro-ecological zones in Tamil Nadu, this gap is particularly pertinent here, making the identification of genotypes with consistent production and nutritional quality necessary (12, 13).

Statistically advanced models, AMMI (14) and the GGE biplot approach (15), widely used for dissecting complex G x E interactions, are employed to identify genotypes exhibiting superior performance for both yield and capsaicin content. By integrating multi-environmental testing with robust stability analysis, this research aims to provide valuable insights into developing climate-resilient, nutritionally enriched chilli varieties suited for sustainable cultivation in diverse environments.

The findings from this study will be instrumental for breeders, farmers and policymakers in selecting stable and high-yielding chilli genotypes, ultimately contributing to enhanced production, improved marketability and greater nutritional security. Additionally, understanding the stability of key biochemical traits will support breeding efforts for functional foods and pharmaceutical applications, reinforcing the role of chilli as a versatile crop in both agricultural and industrial domains.

Materials and Methods

Experimental material and locations

Six chilli genotypes, including 5 breeding lines CC-CBE-003 (G1), CA-CBE-202 (G2), CA-CBE-205 (G3), CA-CBE-199 (G4), CA-CBE-213 (G5) and 1 check variety PLR-1 (G6), were evaluated across three diverse environments in Tamil Nadu, India during 2023-24, viz. E1- Paiyur (Krishnagiri district, 12°21' N, 78°18' E, 490 m Mean Sea Level), E2- Udumalpet (Tiruppur district, 10°33' N, 77°16' E, 215 m MSL) and E3- Yethapur (Salem district, 11°35' N, 78°29' E, 282 m MSL). These locations represent environments with varying soil characteristics and weather conditions (Table 1).

Experimental design and cultural practices

RBD was adopted to experiment, with 4 replications at each location. Plants were spaced at 60 x 45 cm, with approximately 25 plants per plot. Standard agronomic practices were followed as per the Tamil Nadu crop production guide. Forty-five-day-old seedlings of 15 cm height were transplanted in early January 2024 across all locations.

Yield parameter

For fruit yield per plot, fully ripe fruits from all plants in each plot were harvested and then weighed, with the total weight per plot recorded as the yield was expressed in kg.

Capsaicin content analysis

The capsaicin values reported represent the mean of 5 replicates per genotype, analyzed using High-Performance Liquid Chromatography (HPLC) (16). Dried chilli fruits were ground into a fine powder, mixed with methanol and subjected to extraction at 80 °C for 4 hr. After filtration, 2 mL of supernatant was stored for analysis. Capsaicin concentration was determined by injecting 10 µL of the sample into the HPLC system, with analytical standard capsaicin from Sigma-Aldrich used for calibration. The stock solution was diluted with methanol to create working standard solutions (5 ppm). Using the American Spice Trade Association (ASTA) formula (1985), Scoville Heat Units (SHU) were calculated where ppm H was derived from the peak areas of capsaicin and dihydrocapsaicin and converted to SHU by multiplying by a factor of 15.

$$\text{ppm H} = \frac{[\text{Peak area of capsaicin} + (0.82 \times \text{peak area of dihydrocapsaicin})]\ (\text{ppm standard})\ (\text{mL acetonitrile})}{\text{Total capsaicin peak area of standard}\ (\text{g sample})}$$

Statistical analysis

The data were subjected to individual environment analysis followed by pooled analysis across environments using the software Statistical Tool for Agricultural Research (STAR) Version 2.0.1. Stability was analysed using both AMMI and GGE biplot analyses models through Plant Breeding Tools (PB Tools) Version 1.3 software. While the AMMI model distinguished additive variance and multiplicative variance, the GGE biplot analysis helped visualize genotype performance and stability across environments.

Table 1. Location and description of the environment and soil conditions of test locations

Location/ environment		**Paiyur**	**Udumalpet**	**Yethapur**
District		Krishnagiri	Tiruppur	Salem
Altitude (m MSL)		490	215.21	282
Latitude		12.21° N	10.33 ° N	11.35 ° N
Longitude		78.18° E	77.16 ° E	78.29 ° E
Sowing date		24.12.2023	22.12.2023	28.12.2023
Transplanting date		08.01.2024	06.01.2024	12.01.2024
		Meteorological data		
Mean temperature*	Max (°C)	35	36	35
	Min (°C)	21	18	23
Precipitation (mm)		3	63	38
		Soil data		
Soil type		Sandy loam	Red soil	Red sandy loam
pH		7.76	7.5	6.5
EC (dSm^{-1})		0.12	0.26	0.8

MSL = Mean Sea Level, EC = Electrical Conductivity, dSm^{-1} = deciSiemens per meter, °C = degree Celsius, mm = millimeter, pH = potential of hydrogen. Mean temperature values are averages for the study period (January–June 2024).

For AMMI analysis, the following model was used:

$$Y_{ij} = \mu + g_i + e_j + \Sigma\ \lambda k\ Yik\ \alpha jk + \Sigma ij$$

Where,

Y_{ij} is the yield of i^{th} genotype in j^{th} environment, μ is the overall mean, g_i and e_j are genotype and environment deviations, λk is the eigenvalue of PCA axis k, Yik and αjk are principal component scores of genotype and environment and Σij is the residual. The interpretation of stability was based on AMMI biplot analysis (Interactive Principal Component Axes (IPCA)1 vs. means) and GGE biplot analysis for identifying stable, high-performing genotypes across environments.

Results

Per se performance

Yield per plot (kg)

The evaluation of yield per plot revealed that G1 (CC-CBE-003) exhibited the highest yield across all environments: 25.65 kg at E1, 19.98 kg at E2 and 22.98 kg at E3. The lowest yield was consistently observed in G2 (CA-CBE-202): 7.15 kg at E1, 4.52 kg at E2 and 5.53 kg at E3, as shown in Table 2. In Paiyur (E1), yield per plot ranged from 7.15 kg for G2 (CA-CBE-202) to 25.65 kg for G1 (CC-CBE-003), with a mean of 8.87 kg. Udumalpet (E2) showed a range from 4.52 kg for G2 (CA-CBE-202) to 19.98 kg for G1 (CC-CBE-003), averaging 8.77 kg. In Yethapur (E3), the range was from 5.53 kg for G2 (CA-CBE-202) to 22.98 kg for G1 (CC-CBE-003), with a mean of 9.32 kg. The pooled data across all locations indicated an overall range of 5.73 kg for G2 (CA-CBE-202) to 22.87 kg for G1 (CC-CBE-003) for yield per plot, with a mean of 8.99 kg for all genotypes.

Capsaicin content (SHU)

The assessment of capsaicin content showed that G1 (CC-CBE-003) had the highest content across all environments: 123289.00 SHU at E1, 117075.75 SHU at E2 and 120988.25 SHU at E3. The lowest content was observed in G5 (CA-CBE-213) at E1 with 22595.25 SHU, at E2 with 16440.50 SHU and at E3 with 20685.00 SHU, as presented in Table 3.

In Paiyur (E1), capsaicin content ranged from 22595.25 SHU for G5 (CA-CBE-213) to 123289.00 SHU for G1 (CC-CBE-003), with a mean of 42528.92 SHU. Udumalpet (E2) showed a range from 16440.50 SHU for G5 (CA-CBE-213) to 117075.75 SHU for G1 (CC-CBE-003), averaging 35994.87 SHU. In Yethapur (E3), the range was from 20685.00 SHU for G5 (CA-CBE-213) to 120988.25 SHU for G1 (CC-CBE-003), with a mean of 40064.92 SHU. The pooled data across all locations revealed an overall range of 19906.92 SHU for G5 (CA-CBE-213) to 120451.00 SHU for G1 (CC-CBE-003) for capsaicin content, with a mean of 39529.57 SHU for all genotypes.

ANOVA

ANOVA was performed, taking into consideration 2 characters, viz. fruit yield per plot (kg) and capsaicin (SHU) in the individual locations. Since both the traits showed significance for genotype, it was further proceeded for combined analysis. In the combined analysis, a pooled ANOVA for the 3 locations' data, considering these 2 characters, was studied and is presented in Table 4. ANOVA showed significant values ($p < 0.05$) for genotype, environment and genotype x environment components for both the characters. Hence, it was further proceeded to conduct stability analysis for the two characters using AMMI and the GGE biplot model.

Table 2. *Per se* mean and pooled performance of chilli genotypes for fruit yield per plot in different environments

Genotype code	Fruit yield per plot (kg)			Mean across locations
	E1	E2	E3	
G1	25.65	19.98	22.98	**22.87**
G2	7.15	4.52	5.53	**5.73**
G3	9.36	6.27	8.07	**7.90**
G4	8.06	6.96	10.10	**8.37**
G5	13.87	8.75	11.87	**11.50**
G6 (Check)	23.58	7.18	10.97	**13.91**
Mean across genotypes	**8.87**	**8.77**	**9.32**	**8.99**
Maximum value	**25.65**	**19.98**	**22.98**	**22.87**
Minimum value	**7.15**	**4.52**	**5.53**	**5.73**
SED	0.10	0.04	0.06	-
CD 5 %	0.22	0.08	0.13	-
CV (%)	1.01	0.58	0.76	0.88

E1 = Paiyur, E2 = Udumalpet, E3 = Yethapur, SED = Standard Error of Difference, CD = Critical Difference, CV = Coefficient of Variation, kg = kilogram. Mean across locations indicates pooled mean over three environments.

Table 3. *Per se* mean and pooled performance of chilli genotypes for capsaicin content in different environments

Genotype code	Capsaicin (SHU)			Mean across locations
	E1	E2	E3	
G1	123289.00	117075.75	120988.25	**120451.00**
G2	28110.50	20276.75	26224.75	**24870.67**
G3	26593.25	22925.50	25102.00	**24873.58**
G4	29608.75	21337.75	24520.00	**25155.50**
G5	22595.25	16440.50	20685.00	**19906.92**
G6 (Check)	24976.75	17913.00	22869.50	**21919.75**
Mean across genotypes	**42528.92**	**35994.87**	**40064.92**	**39529.57**
Maximum value	**123289.00**	**117075.75**	**120988.25**	**120451.00**
Minimum value	**22595.25**	**16440.50**	**20685.00**	**19906.92**
SED	336.40	687.84	333.38	-
CD 5 %	717.02	1466.09	710.57	-
CV (%)	1.12	2.70	1.18	1.72

E1 = Paiyur, E2 = Udumalpet, E3 = Yethapur, SHU = Scoville Heat Units, SED = Standard Error of Difference, CD = Critical Difference, CV = Coefficient of Variation. Capsaicin content expressed in SHU.

Table 4. Pooled analysis of variance

Source of variation	DF	Fruit yield per plot (kg)		Capsaicin (SHU)	
		SS	MS	SS	MS
Genotype	5	2289.67	457.93*	66977.59	13395.58*
Environment	2	386.19	193.10*	189.08	94.54*
Replication within location	9	0.09	0.01	13.41	1.49
Genotype x Environment	10	374.70	37.47*	101.41	10.14*
Pooled error	45	0.43	0.01	53.49	1.19
Total	71	3051.09	-	67334.98	-

DF = Degrees of Freedom, SS = Sum of Squares, MS = Mean Square

Stability study by AMMI model

For the trait yield and capsaicin, PC1 contributes 98 % and 65.5 %, PC2—2 % and 34.5 % for the 2 characters respectively, whereas the 3rd component showed no interaction for both the traits (Table 5).

AMMI biplot 1 for yield and capsaicin content

IPCA scores for genotype and environment main effects were plotted against the mean yield per plot in AMMI biplot 1 (Fig. 1a) and for capsaicin (Fig. 1b). High-yielding genotypes are found on the farthest right, while low-yielding genotypes are found on the farthest left. Here, Genotype G1 was to the farthest right and G2 was to the farthest left for fruit yield per plant (kg). For capsaicin content, genotype G1 was at the farthest right and G5 to the farthest left. Genotypes G1, followed by G5 and G3, were near the horizontal axis. Capsaicin G1, followed by G5 and G6, were near the horizontal axis. Out of the 3 environments, E3 (Yethapur) had less IPCA interaction than the 2 locations, E1 (Paiyur) and E2 (Udumalpet) positioned near the horizontal axis for both the traits.

AMMI biplot 2 for yield and capsaicin content

IPCAs 1 and 2, which described the overall G x E interaction, were plotted against one another in AMMI biplot 2. The genotypes within and near the circle are stable. Here, G1 and G5 were near the origin and dotted circle (Fig. 2a, b) for both yield and capsaicin content.

Stability study by GGE biplot model

GGE biplot - environment view

In this study, the vector of environment E3 comparatively makes a lesser angle with average environment axis (AEA), followed by E2 and E1 (Fig. 3a) for the trait fruit yield per plot. All 3 environment vectors made a smaller angle with the AEA, among which E3 falls on the AEA (Fig. 3b) for the trait capsaicin content. E1 has a longer vector, followed by E3 and E2 for both yield per plot and capsaicin content (Fig. 3c, d).

Table 5. PC values for the traits fruit yield per plot and capsaicin content

Genotype/ environment code	Fruit yield per plot (kg)			Capsaicin (SHU)		
	Mean	PC1	PC2	Mean	PC1	PC2
G1	22.87	-19.0326	3.337302	120451.00	-140160	-9.70977
G2	5.73	10.55286	0.133659	24870.67	25391.56	887.2378
G3	7.90	6.823343	0.671439	24873.50	25381.78	-2069
G4	8.37	6.334577	2.88857	25155.50	24898.13	1178.889
G5	11.50	0.463085	0.549491	19906.92	33987.02	-318.569
G6	13.91	-5.14128	-7.58046	21919.75	30501.74	331.1495
E1	14.61	-0.70301	-0.70773	42528.88	-0.57635	0.704916
E2	8.94	-0.47461	0.540152	120451.00	-140160	-9.70977
E3	11.59	-0.52965	0.455356	24870.67	25391.56	887.2378

PC1 = Principal Component Axis 1, PC2 = Principal Component Axis 2, kg = kilogram, SHU = Scoville Heat Units, G1–G6 = genotype codes, E1–E3 = environment codes.

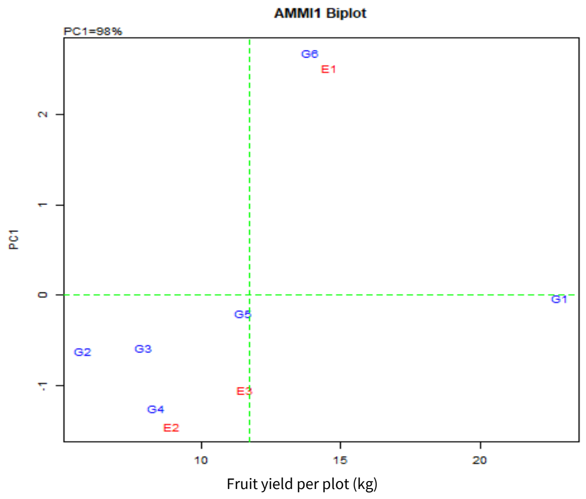

Fig 1a. AMMI biplot 1 for fruit yield per plot.

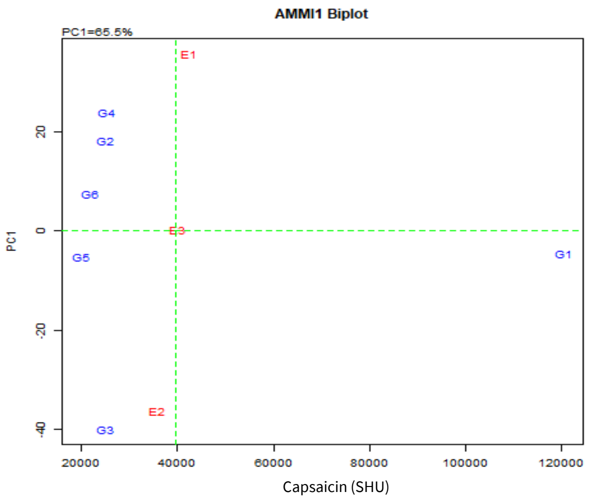

Fig 1b. AMMI biplot 1 for capsaicin content.

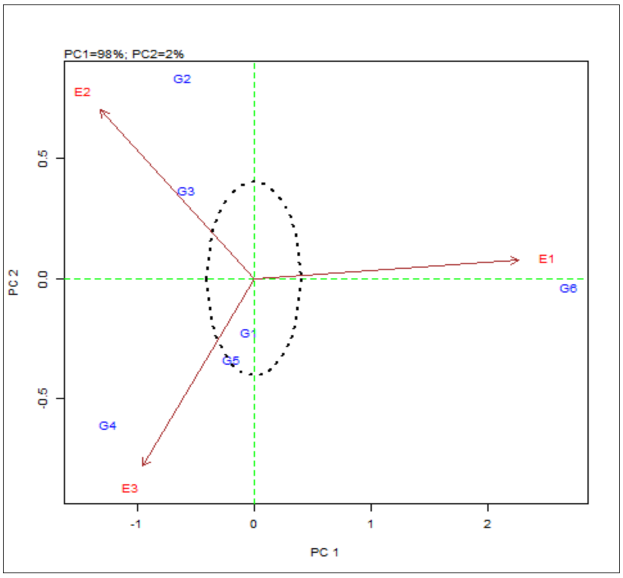

Fig 2a. AMMI biplot 2 for fruit yield per plot.

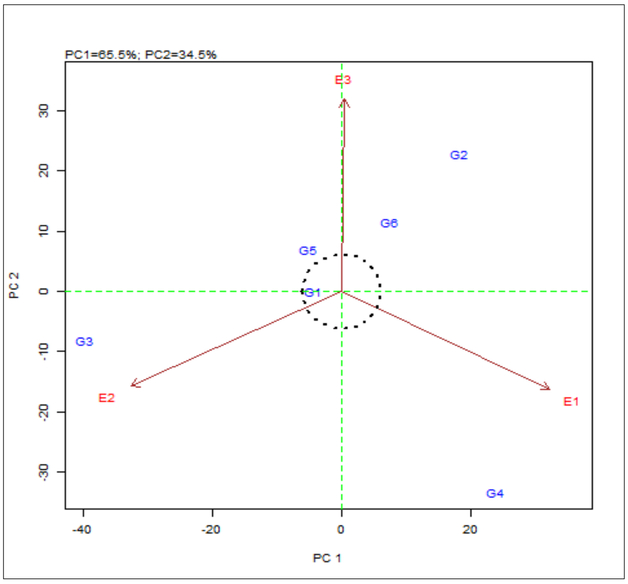

Fig 2b. AMMI biplot 2 for capsaicin content.

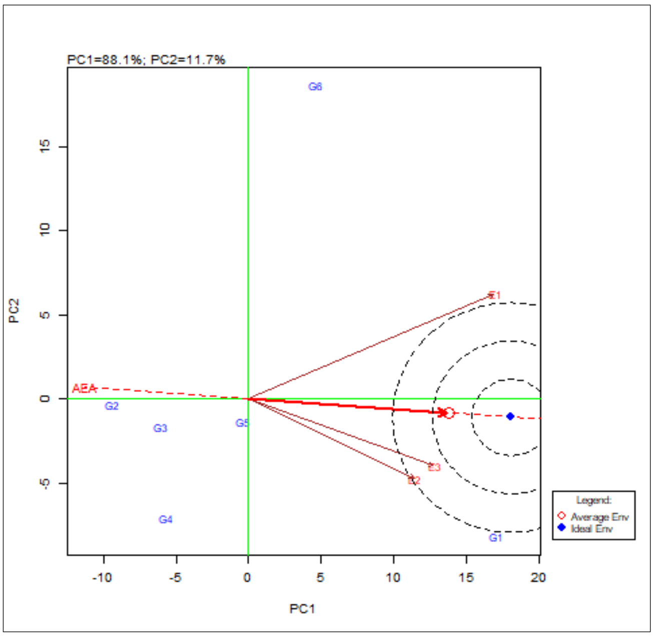

Fig 3a. GGE biplot - environment view 1 for fruit yield per plot.

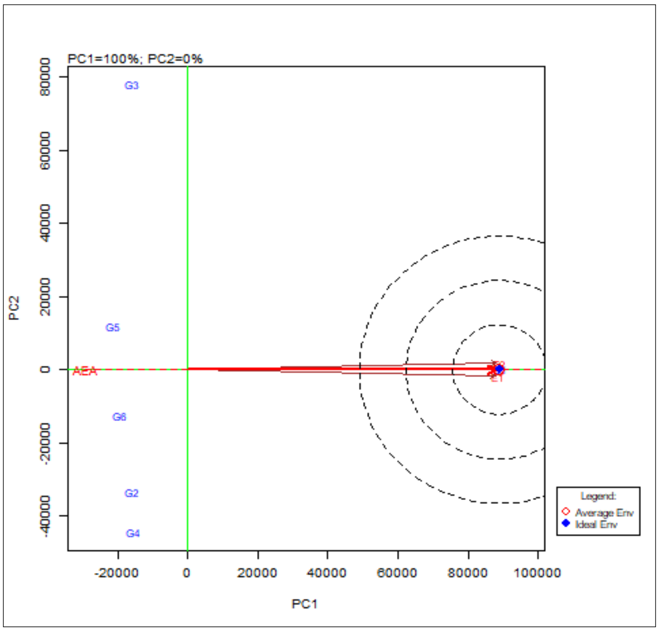

Fig 3b. GGE biplot - environment view 1 for capsaicin content.

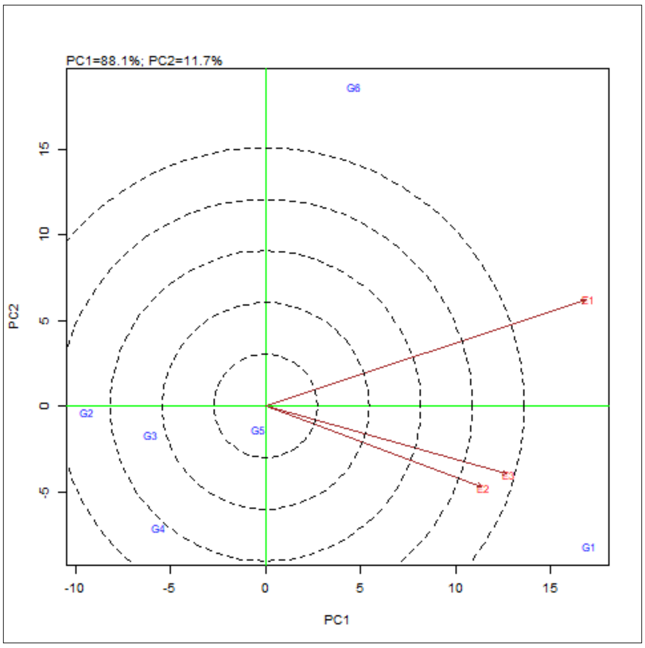

Fig 3c. GGE biplot - environment view 2 for fruit yield per plot.

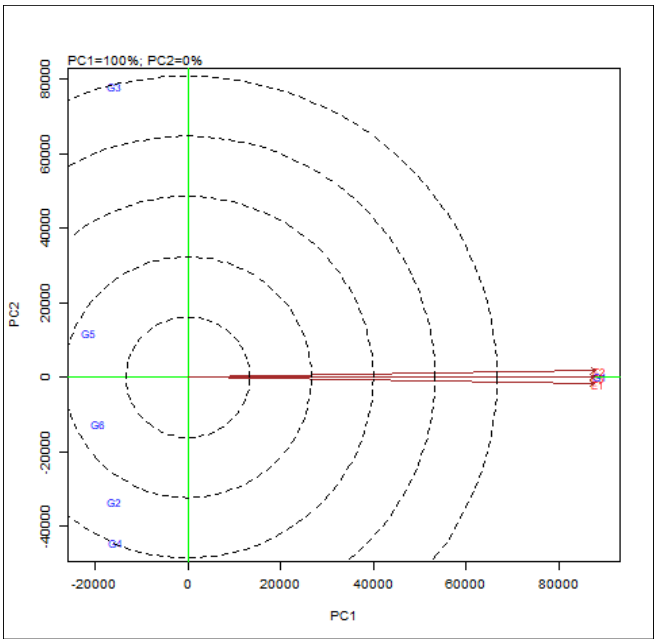

Fig 3d. GGE biplot - environment view 2 for capsaicin content.

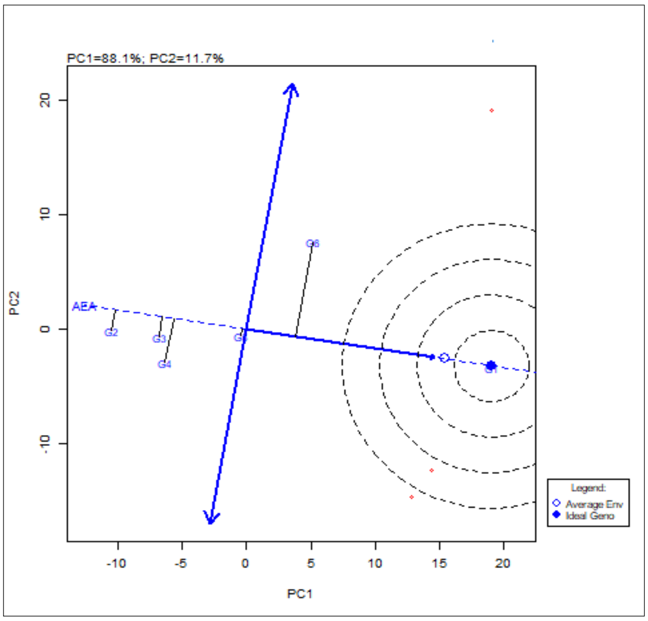

Fig 4a. GGE biplot - genotype view 1 for fruit yield per plot.

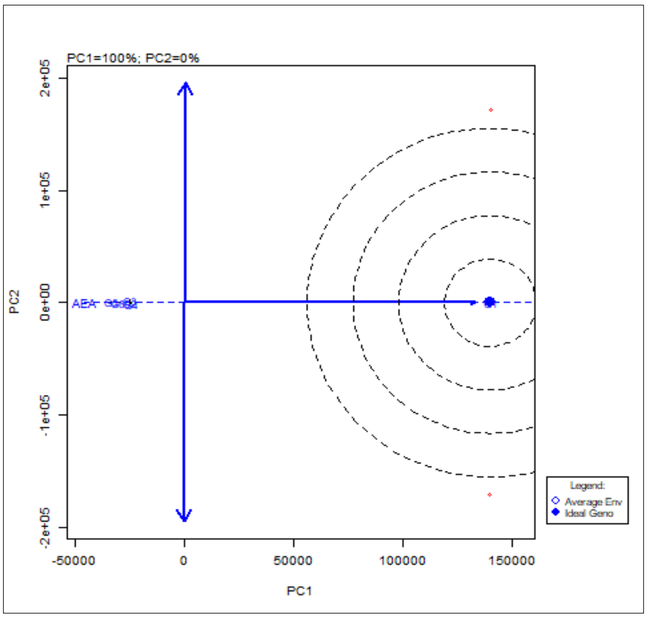

Fig 4b. GGE biplot - genotype view 1 for capsaicin content.

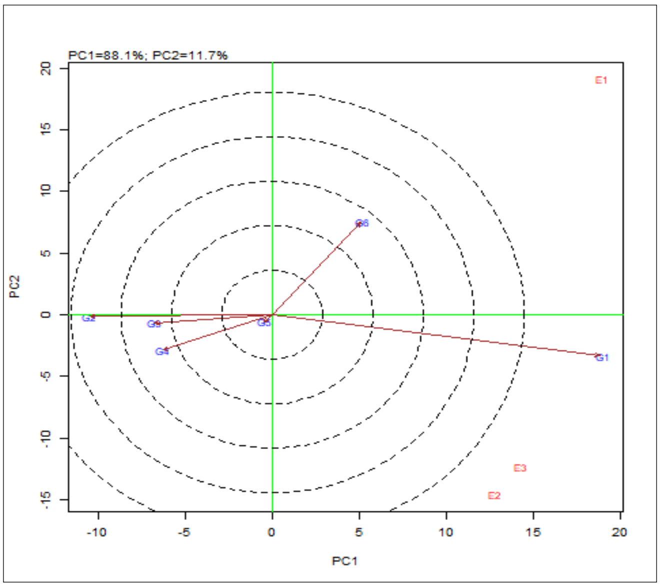

Fig 4c. GGE biplot - genotype view 2 for fruit yield per plot.

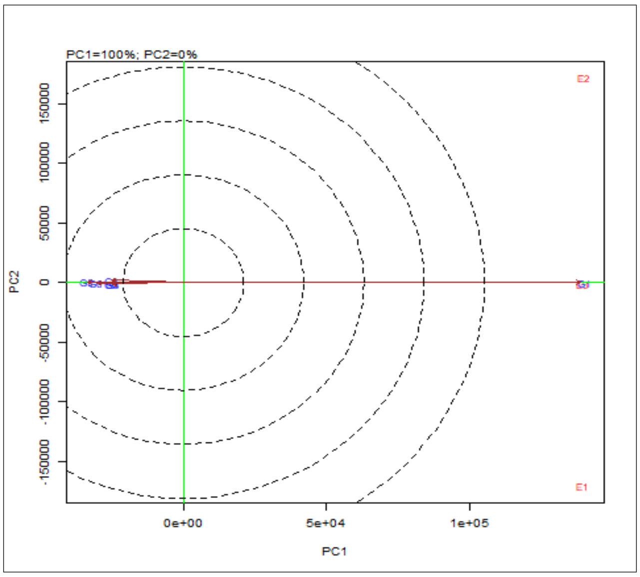

Fig 4d. GGE biplot - genotype view 2 for capsaicin content.

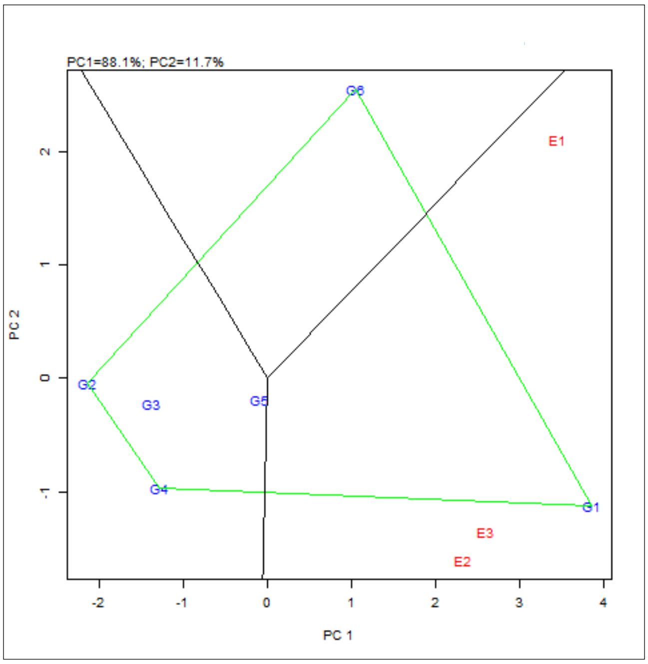

Fig 5a. What won where biplot for fruit yield per plot.

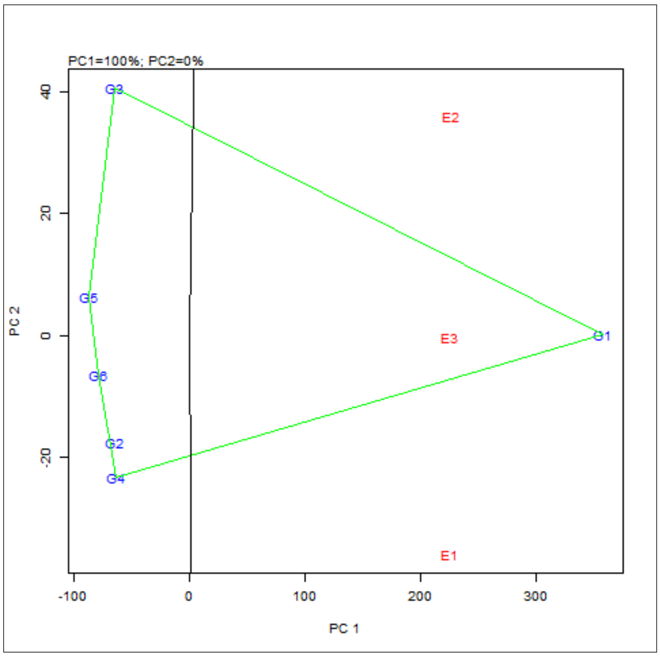

Fig 5b. What won where biplot for capsaicin content.

GGE biplot – genotype view

Genotype, G1, fell in the concentric circle, for both the traits across all the 3 environments. G1 and G6 are to the right of AEA axis and G1 is present near the horizontal axis, with less projection (Fig. 4a). In a similar way, genotype G1 was present closer to the x-axis for capsaicin content (Fig. 4b).

G1 has a lesser angle with E3, followed by E2 and E1 vectors; G6 vector made a lesser angle with E1 vector, followed by E3 and E2 and other genotypes—G2, G3, G4, G5, made wider angles for fruit yield per plot (Fig. 4c). G1 was near E3, followed by E2 and E1 then other genotypes for capsaicin content, then the remaining other genotypes (Fig. 4d).

What won where biplot

In this study, it is found that G1 was present in the sector having all the environments (Fig. 5a, b). The genotypes G2, G3, G4, G5 and G6 were present in other sectors. Each sector groups the environments into mega-environments. E1, E2 and E3 fall in the same sector, forming 1 mega environment.

Discussion

Per se performance

G1 (CC-CBE-003) demonstrated the highest fruit yield per plot with a pooled mean of 22.87 kg, while G2 (CA-CBE-202) had the lowest with 5.73 kg. The wide range of 22.87 kg to 5.73 kg suggests substantial genetic variability for this trait. This variation could be due to differences in fruit number, fruit size and overall plant vigor, which are regulated by genetic factors. Similar variability in fresh fruit yield was reported in evaluation studies on chilli genotypes (17-19).

The consistently low yield observed in certain genotypes, particularly G2 (CA-CBE-202), with a mere 5.73 kg fruit yield per plot, can be attributed to multiple factors. This poor performance likely stems from unfavourable genetic architecture affecting key yield components such as fruit setting efficiency, fruit retention capacity and source-sink relationships within the plant (17). The limited adaptability of G2 across testing environments suggests its genetic makeup may be poorly suited to the prevailing agroecological conditions of the test locations. Unlike G1 (CC-CBE-003), which demonstrated remarkable stability alongside high performance, G2 and other low-yielding genotypes may possess genetic backgrounds that favour vegetative growth at the expense of reproductive development, resulting in poor fruit set and yield.

The analysis of capsaicin content revealed substantial variation among the genotypes across different environments. Genotype G1 (CC-CBE-003) consistently had the highest capsaicin content, with an impressive mean of 120451.00 SHU across all locations. In contrast, G5 (CA-CBE-213) demonstrated the lowest capsaicin content with a mean of 19906.92 SHU. The significant difference in capsaicin content among genotypes can be attributed to genetic factors and their interaction with environmental conditions. The consistently high capsaicin content in G1 (CC-CBE-003) across all environments suggests a strong genetic predisposition for this trait (20, 21).

Stability study using AMMI model

The AMMI ANOVA revealed that, G x E interaction was further explained by the interaction of genotypes into 3 IPCAs (12). The first 2 principal components together explained more than 80 % of the total variation. Thus, the first 2 IPCAs were used to plot the graphs.

AMMI biplot 1 for yield and capsaicin content

The IPCA scores for both genotype and environment main effects were plotted against the mean yield per plot in Fig. 1a and against capsaicin content in Fig. 1b. Genotypes positioned farthest to the right exhibit high yield, while those on the farthest left show low yield (12). Accordingly, genotype G1 showed the highest mean values and G2 showed the lowest value for fruit yield per plant (kg). For capsaicin content highest mean value was observed for genotype G1 and the lowest for G5. While genotypes with greater IPCA scores, whether positive or negative, are adapted to certain environments, those with an IPCA1 score closer to 0 are considered to be stable across environments. Therefore, genotypes G1, followed by G5 and G3, which were near the x-axis, were stable. For capsaicin G1, followed by G5 and G6 were stable performing genotypes. Out of the 3 environments, E3 (Yethapur) had IPCA interaction less than the 2 locations, E1 (Paiyur) and E2 (Udumalpet), which had lower IPCA interaction for both the traits, indicating favorable circumstances for genotypes in E3 for yield and capsaicin content and also contributed to higher yield.

AMMI biplot 2 for yield and capsaicin content

In AMMI biplot 2, the genotypes within and near the circle are stable. Accordingly, G1 and G5 were stable performing genotypes for both yield (Fig. 2a, b) and capsaicin content. Similar results were obtained in previous studies using the AMMI model (22, 23).

Stability study by GGE biplot model

GGE Biplot - environment view

Stability and mean parameters for the 3 locations are reflected in the AEA. The arrow pointing in the direction of AEA indicates the ideal location (22). The environmental vector or spike that makes a lesser angle with AEA is considered the representative environment or location for all the locations (24).

In this study, E3 is considered as the representative environment for fruit yield per plot as vector of environment E3 comparatively makes lesser angle with AEA, followed by E2 and E1 shown from Fig. 3a. E3 (Yethapur) is an ideal representative environment for the trait capsaicin content (Fig. 3b) as all the three environment vectors made less angle with the AEA among which E3 falls on the AEA.

The standard deviation within an environment is represented by the length of the environment vector, which indicates the environment's capacity for discriminating. The magnitude of the vector length indicates how effectively an environment can differentiate between genotypes (25). E1, having a longer vector, indicated more interaction, followed by E3 and E2 for yield per plot and capsaicin content (Fig. 3c, d). Similar results were obtained in previous studies on stability analysis using the GGE biplot (26, 27).

GGE biplot – genotype view

The AEA in GGE biplot indicates or points towards the high-yielding region. In all 3 environments, the genotypes within these concentric circles show higher average yield values. The genotypes are separated into those with above-average yield on the right and below-average yield on the left, by the double-headed arrow in the center. The length of each genotype's projection indicates how stable the genotypes are. The projection of unstable genotypes is longer than that of stable genotypes (24).

Accordingly, genotype G1, falling in the concentric circle, has higher average values for both traits across all 3 environments. G1 and G6 have above-average yield in all the environments and G1 has above-average capsaicin content in all 3 environments. Genotypes G1 and G6 are considered ‘stable genotypes’ as the length of the projection is less for these two. In a similar way, genotype G1 is stable for capsaicin content (Fig. 4a, b). The genotype vectors that have less angle with an environment vector, performs well in that particular environment (26). In this regard, G1 performed well in E3 followed by E2 and E1, G6 performed best in E1 followed by E3 and E2 and other genotypes—G2, G3, G4, G5 exhibited comparatively lower yield performance across all three environments. G1 performed best in E3, followed by E2 and E1 than other genotypes for capsaicin content, than the remaining other genotypes (Fig. 5b). These findings were in corroboration with the stability study in *C. chinense* Jacq. genotypes (28).

What won where biplot

All of the genotypes found on the outer sides are connected to make a polygon. The genotypes at this polygon's vertices will yield a lot in the same sector as the environment (15). This biplot explicitly portrays the genotypes suitable for specific environments. It says which genotypes perform best and become a ‘winner’ in which environment.

In this study, it is found that G1 is suitable in all the 3 locations studied and also G1 is the best performing genotype in all the 3 environments (Fig. 5a, b). Sectors without any environment will contain genotypes that yield poorly in either specific locations or across all locations (24). The genotypes G2, G3, G4, G5 and G6 were present in the sectors containing no environments that are low yielders in all the 3 locations. Each sector groups the environments into mega-environments. E1, E2 and E3 fall in the same sector thus falling in a single mega environment (Fig. 5a, b). These results conformed with previous G x E studies in chilli (28-35).

Conclusion

High yield and capsaicin content, along with stable performance of these characters, are most important for chilli growers for industry purposes and for breeders to develop robust varieties. Considering these, the current study was conducted to assess the consistency of the two economically important traits, viz. fruit yield per plot and capsaicin content performance in 3 variable environments. This was performed using the advanced statistical models AMMI and GGE biplot. Based on the study, genotype G1 was found to be a high-yielding and stable performer. Yethapur (E3) was found to be the better-performing environment. All the 3 environments are considered as 1 mega environment for these traits. Hence, any one of these 3 environments can be considered for further studies. These lines can be used for further breeding programs or to be utilized to release as a variety.

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Authors' contributions

SS contributed to the literature search, writing of the original draft and preparation of tables and figures and HUND was responsible for conceptualization, resources, supervision, validation and writing-review and editing.

Compliance with ethical standards

Conflict of interest: The Authors do not have any conflicts of interest to declare.

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