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Estimation of Genotype×Environment Interaction and Stability Analysis of Carrot (*Daucus carota* L.) Genotypes under Different Nutrient Management Systems

P. Praanjal[1], J. C. Jana[1], S. K. Roy[2] and Prince Kumar[1]

[1]Dept. of Vegetable and Spice Crops, [2]Dept. of Genetics and Plant Breeding, Uttar Banga Krishi Viswavidyalaya, Pundibari, Cooch Behar, West Bengal (736 165), India

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Corresponding pranavapraanjal71@gmail.com

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ABSTRACT

The experiment was conducted during *rabi* season (October to March), 2022–23 and 2023–24 at the Horticultural Instructional Farm, Uttar Banga Krishi Viswavidyalaya, Pundibari, West Bengal, for evaluating 24 carrot genotypes under various nutrient management systems. 24 carrot genotypes under various nutrient management systems were evaluated to identify those with greater stability and adaptability for over two consecutive years. Pooled ANOVA results indicated significant differences among all yield and quality traits studied in carrot. AMMI ANOVA further revealed that genotype-×-environment interactions (GEI) significantly influenced the traits. Environmental effects were the major contributors to total variation across all traits, with notable genotype-×-environment interactions. AMMI analysis effectively captured these interactions, aiding in the identification of stable and high-performing genotypes. Based on lower AMMI stability values (ASV) and yield stability index, genotypes G_9, G_{10}, G_{12}, and G_2 consistently exhibited both high mean performance and stability across traits. Conversely, genotypes G_{24}, G_5, and G_{21} frequently showed poor performance and low stability. Therefore, G_9 and G_{10} were recommended as the most stable and high-performing genotypes across environments. The GGE biplot analysis was done on β-carotene content and yield which also confirmed the stability and adaptability of these genotypes. The environments E_5 and E_6 performed well for genotype evaluation. G_9 and G_{10} were recommended for breeding and cultivation in a range of growing conditions.

KEYWORDS: Carrot, stability, AMMI, GGE, nutrient management

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Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

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1. INTRODUCTION

Carrot is one of the most significant vegetables in the world which is recognised for their wide range of production, high market value, delicious flavour, and abundant nutritional makeup. The vegetable is an exceptional source of vitamins, carbohydrate, nutritional fibre, phenolic compounds, and carotenoids (Selvakumar et al., 2019, Yoo et al., 2020 and Chevalier et al., 2021). In India, carrot occupied an area of 1,26,000 ha with a production of 2,690,000 mt and average yield of 21.52 t ha^{-1} (Anonymous, 2024). The different root shapes of carrots-the Imperator, Danvers, Triangular, Chantenay, Kuroda, Nantes, Paris Market, and Ox-heart-allow them to be identified. Four pigments-carotene (orange carrot), lycopene (red carrot), anthocyanins (black/purple carrot), and lutein/xanthophyll (yellow carrot)-are abundant in carrot roots; rainbow carrots have a combination of these pigments, whereas white carrots are devoid of them (Arscott and Tanumihardjo, 2010; Sun et al., 2009, Kalia et al., 2023). A grown, fleshy tap root with an inner xylem core and an outside cortex makes up the edible part of a carrot. Carrots of high quality have more cortex than core. The carrot's larger fleshy and conical taproot stores a significant quantity of energy, which is required for flowering in the following year (Que et al., 2019). Traits in carrot genotypes are affected by various environmental factors. According to a static concept of stability which is generally used for quality characters, "a stable genotype is one that maintains consistent performance across different environmental conditions", showing little to no variation despite changes in the environment whereas dynamic concept state as "for key agronomic traits like yield, uniform performance across all environments is unlikely". Only low-yielding genotypes show consistent results, as they don't respond to favourable conditions. A dynamic stability concept addresses this by allowing performance to vary predictably across environments (Becker and Leon, 1988 and Hill et al., 1998). Plant breeders often choose cultivars based on how well they perform in terms of yield and related traits under different environmental conditions. Their main goal is to improve crops by ensuring stable yields, reducing risks, cutting costs, and ultimately increasing profitability. Factors like soil texture and fertility, temperature changes, rainfall patterns, and pest or disease outbreaks can all significantly affect carrot productivity and quality of carrots (Rosenfeld et al., 1997 and Saha, 2015). Environments can be considered as multilocation, or different sowing dates as well as manipulating soil with different fertilizer doses (Abdelrahman et al., 2022 and Kumawat et al., 2023). Genotypic stability is more important than genotypic mean, and the biplot's mean vs. stability view can help us locate the most stable genotype in various environments. The word "stability" refers to a geno¬type that performs consistently across different environments for a desired trait (Sharma et al., 2020). Phenotype results from the combined influence of genotype (G), environment (E), and their interaction (G×E). Unlike genotype, which remains constant, the environment varies significantly across seasons and locations, making it the primary factor influencing phenotypic expression (Prajapati et al., 2015). Several researches demonstrate the effect of soil composition on yield of carrots. Agyeman et al., 2015 highlighted the widespread application and effectiveness of the Additive Main Effects and Multiplicative Interaction (AMMI) and Genotype plus Genotype-by-Environment Interaction (GGE) biplot methods in overcoming challenges associated with analyzing multi-environment trial data. These techniques are particularly valued for their capability to manage the complexities of genotype-environment interactions, enabling clearer interpretation of genotype performance across varying environmental conditions. Hence, 24 carrot genotypes under various nutrient management systems were evaluated to identify those with greater stability and adaptability for over two consecutive years.

2. MATERIALS AND METHODS

2.1. Experiment location, experiment materials and design

Twenty-four carrot genotypes were cultivated during the rabi seasons of two consecutive years (October to March) of 2022–23 and 2023–24) at the Horticultural Instructional Farm of Uttar Banga Krishi Viswavidyalaya, Pundibari, situated at 26°19'2" N latitude, 99°23'2" E longitude, and 43 m above mean sea level. The field trial followed a randomized block design (RBD) with three replications, conducted under three different nutrient levels. Each plot measured 4.5 m^2, with a spacing of 30 cm between rows and 10 cm between plants. Hence, six different environments were created, as given in the following Table 1.

The 24 collected genotypes, collected from UBKV, Pundibari designated as G_1 to G_{24} and evaluated for different quantitative parameters during field investigation were, root length (cm), fresh weight of root (g), dry weight of root (g), yield (t ha^{-1}), TSS (°Brix) and β-carotene (mg 100 g^{-1}).

2.2. Statistical analysis

The data were analyzed using analysis of variance (ANOVA) in Statistical Analysis Software (KAU-GRAPES) to assess the variation among genotypes, environments, and their interaction. When the data violated model assumptions, Bartlett's Chi-square test was applied to identify a suitable transformation that would achieve an acceptable level of variance homogeneity across the main factors. The data collected on various yield components and root quality

Table 1: Environments of different sources of nutrients and years considered for the experiment

Environments	Source of nutrients	Season and year	Av. Temp		Av. Hum (%)		Rainfall (mm)
			Max.	Min.	Max.	Min.	
E_1	Organic nutrient management using, 25 t ha^{-1} of well-decomposed FYM and 7 t ha^{-1} of vermicompost+Azophos (3 kg ha^{-1})	*Rabi*, 2022–23	26.97	10.25	82.37	52.97	00
E_2		*Rabi*, 2023–24	26.07	12.55	83.00	54.82	0.1
E_3	Integrated nutrient management using, FYM at 15 t ha^{-1}, 135 kg of N, 135 kg of P_2O_5 and 150 kg of K_2O	*Rabi*, 2022–23	26.97	10.25	82.37	52.97	00
E_4		*Rabi*, 2023–24	26.07	12.55	83.00	54.82	0.1
E_5	INM+soil application of Borax and Zinc sulphate at 15 and 20 kg ha^{-1}, respectively	*Rabi*, 2022–23	26.97	10.25	82.37	52.97	00
E_6		*Rabi*, 2023–24	26.07	12.55	83.00	54.82	0.1

Av. Temp.: Average temperature; Av. Hum.: Average humidity

traits were analyzed using the AMMI model, following the statistical framework provided by Zobel et al. (1988). The sum of squares for the Genotype×Environment Interaction (GEI) was partitioned into Interaction Principal Component Axes (IPCA) scores and residuals. The IPCA I scores, along with the main effects of genotypes, were used to construct the AMMI biplot for identifying stable genotypes. AMMI Stability Values (ASV) was computed following the method proposed by Purchase et al., 2000 with the following formula.

$$ASV=\sqrt{[((SSIPCA1 / SSIPCA2)\times(IPCA1\ score)^2)+(IPCA2\ score)^2]}$$

Where, SSIPCA I and SSIPCA II were the sum of squares of IPCA I and IPCA II, respectively. IPCA I and IPCA II scores were the principal component scores of GEI obtained from the AMMI model.

In this study, the Average AMMI Stability Value (AASV) was computed and used as a benchmark to identify stable genotypes. Genotypes with ASV values equal to or less than the AASV were classified as stable.

AASV=Sum of ASV of all the genotypes/Total number of genotypes

The environment-centered data was subjected to Singular Value Decomposition (SVD), resulting in the first two principal component axes (IPCA I and IPCA II), which were then used to generate GGE biplots. These biplots captured both the genotype effects (G) and the genotype×environment interaction effects (G×E) as described by Yan et al., 2000, Yan, 2006 and Gauch et al., 2008. AAMI and GGE analysis were done using PBTOOL and GEA-R softwares.

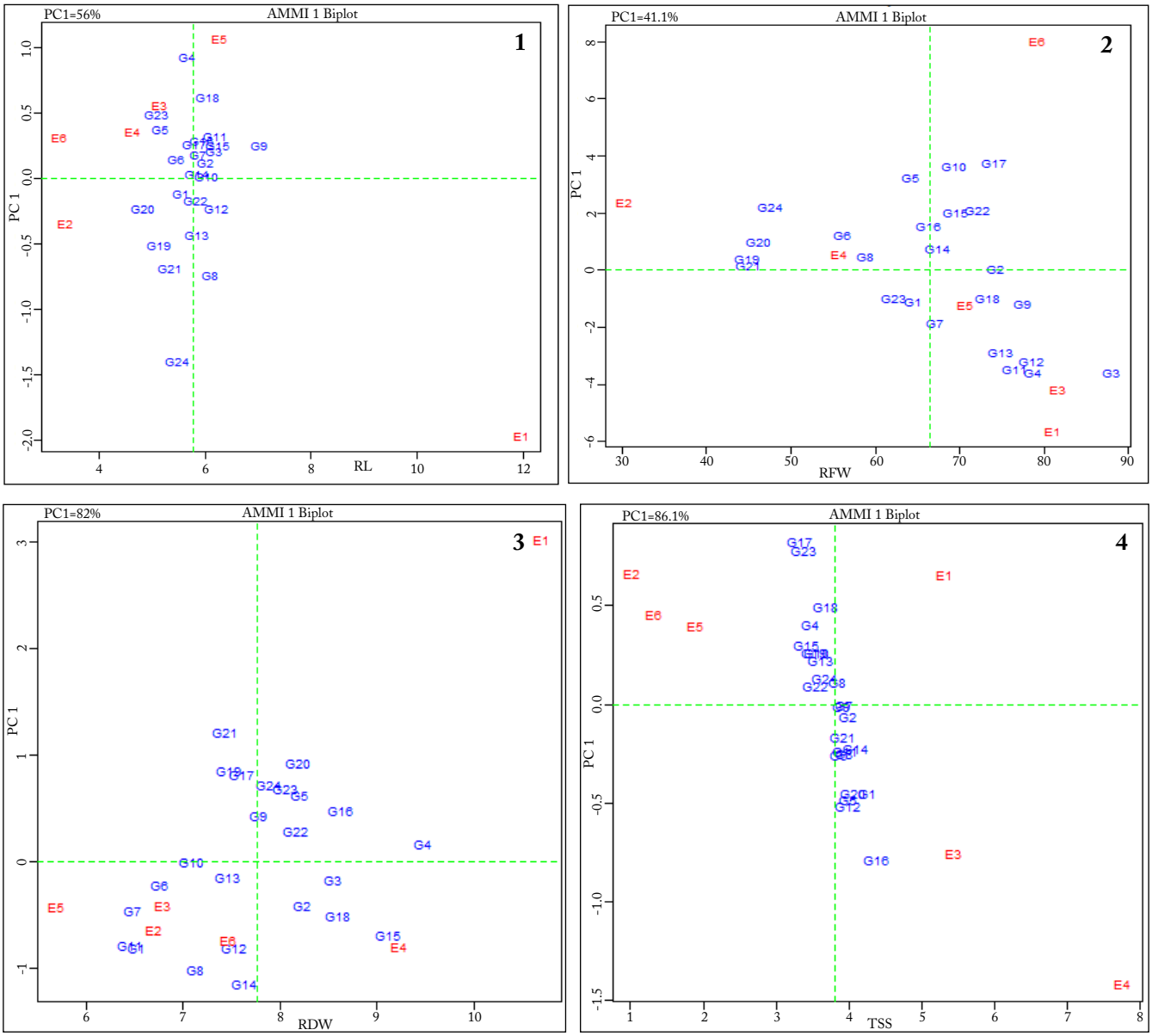
3. RESULTS AND DISCUSSION

3.1. AMMI analysis

The AMMI (Additive Main Effects and Multiplicative Interaction) analysis of variance (ANOVA) revealed significant effects of genotype, environment, and genotype-×-environment (G×E) interaction across all six traits studied: root length, root fresh weight, root dry weight, TSS, β-carotene, and yield.

For root length, the environment accounted for the highest proportion of total variation (93.45%), with a mean sum of squares (MSS) of 758.14, indicating strong environmental influence. Genotypic and G×E interaction effects contributed 2.33% and 4.22% respectively. The first principal component (PC1) captured 56.04% of the G×E interaction, and PC2 explained 20.74%, suggesting a well-structured interaction that could be effectively visualized using AMMI biplots (Figure 1). In the case of root fresh weight, the environment again dominated the variation, contributing 47.36%, while genotypic effects contributed 18.23% and G×E interaction 34.41%. Notably, G×E interaction here was quite substantial. PC1 and PC2 explained 41.11% and 27.03% of the interaction variance, respectively, suggesting complex interaction patterns among genotypes across environments (Figure 2). For root dry weight, the environmental effect was even more pronounced (63.30%), while genotype and G×E interaction contributed 13.60% and 23.09%, respectively. PC1 explained a dominant 82.04% of the G×E interaction variance, indicating that most of the interaction could be summarized effectively with the first principal component alone (Figure 3). Regarding total soluble solids (TSS), the environmental effect was overwhelming, accounting for 97.08% of the total variance; while genotype and G×E contributions were relatively minor (1.15% and 1.77%, respectively). PC1 captured 86.08% of the G×E interaction variance, highlighting the strong impact of environment on TSS expression (Figure 4). For β-carotene content, environment accounted for 57.84% of the variation, while genotype and G×E effects contributed 32.59% and 9.58%, respectively. PC1 and PC2 captured 73.04% and 14.36% of the G×E variation, respectively. These results emphasized considerable genotypic variability

for β-carotene, offering opportunities for selection based on both mean performance and stability (Figure 5). Finally, for yield, environment was again the major source of variation (47.35%), while genotype and G×E interaction accounted for 18.23% and 34.42%, respectively. The first two interaction principal components (PC1 and PC2) explained 41.12% and 27.02% of the G×E interaction sum of squares, respectively (Figure 6), indicating that both principal components are necessary for adequately modelling the interaction pattern (Table 2). The large proportion of G×E variance captured by PC1 (and PC2 in some traits) also indicated that AMMI1 and AMMI2 biplots would be effective tools for identifying stable and superior genotypes for each trait across multiple environments. Daemo and Ashango, 2024, worked on G×E interaction through AMMI on yield stability of 11 improved potato genotypes and they concluded considerable contributions of genotypes (62.40), environment (26.73) and G×E interaction (10.87) for potato tuber yield variation. Dhand and Garg, 2023, conducted an experiment for G×E interaction using AMMI analysis for growth and yield attributes of 30 radish genotypes. They found that the first two principal components accounted for 79.9% to 96.4% of the genotype-by-environment interaction variance across all traits. Their result revealed that four genotypes viz., G_5 (RL-9–1), G9, G17 (LSR-1–1-HP) and G_3 were selected as stable. Another experiment was done by Mohan et al., 2021, on 15 rice genotypes for identification of stable rice hybrids. The ANOVA revealed that environments contributed most to the total sum of squares (65.47%), followed by genotype×environment interactions (21.19%), highlighting the significant influence of environmental factors and their interactions in determining the final grain



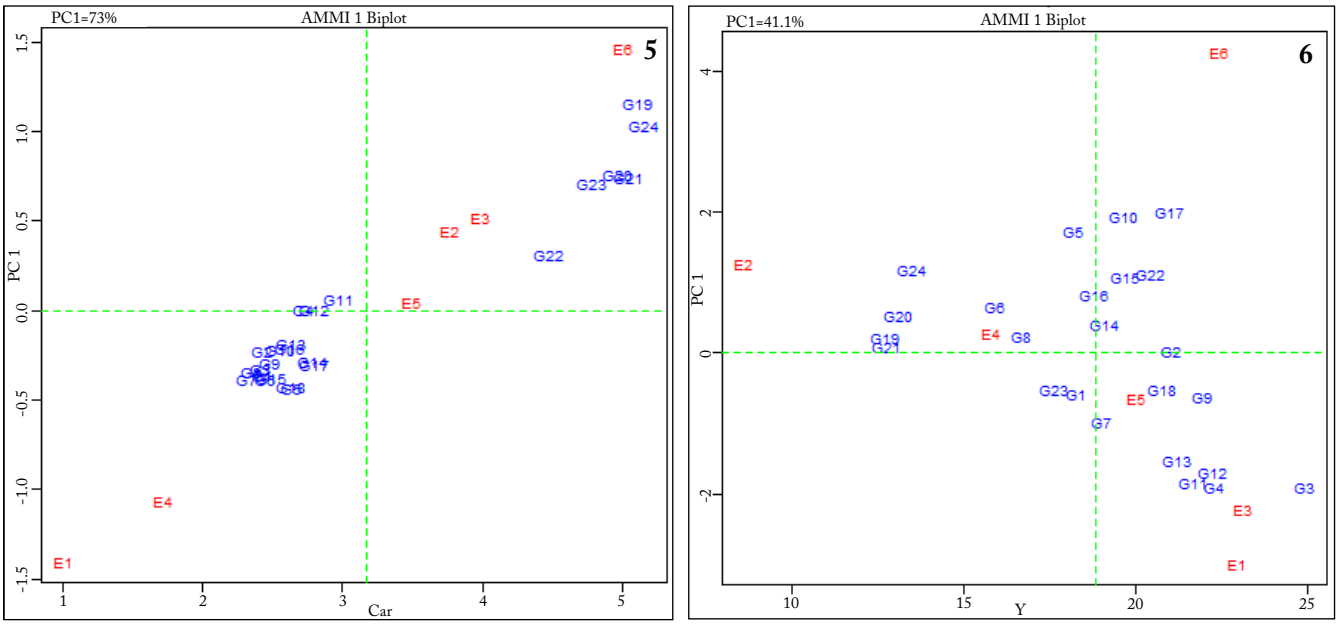


Figure 1–6: AMMI biplot for root length, root fresh weight, root dry weight, TSS, β-Carotene and yield

yield. They found that rice hybrids, G_8 and G_6 were most stable across environments with better yields.

3.2. *Stable genotypes*

Significant variation among genotypes was observed for root length, root weight, root dry weight, TSS, β-carotene, and yield, based on their means, AMMI Stability Value (ASV), and Yield Stability Index (YSI). Genotypes with lower ASV values were considered to be stable but genotypes coupled with lower ASV and higher mean values were considered to be desirable economically.

For root length, G_9 recorded the highest mean (15.99 cm, Rank 1), while G_{10} exhibited the best stability (lowest ASV 0.11, Rank 2) and the most desirable YSI (Rank 1). Genotypes G_{15}, G_{12}, and G_2 also showed a good balance between performance and stability. In contrast, G_{24} was the least stable with the highest ASV (3.78) and poorest YSI (Rank 24).

In root fresh weight, G_3 had the highest mean (113.07 g), but displayed poor stability (highest ASV 6.94, Rank 24). On the other hand, G_8 (ASV 0.91, Rank 2) and G_9 (ASV

Table 2: AMMI ANOVA table for various characters of carrot

Source of variation	Degrees of freedom	Root length (cm)		Root fresh weight (g)		Root dry weight (g)	
		MSS	Proportion	MSS	Proportion	MSS	Proportion
Genotype	23	4.11	2.33	2470.93	18.23	11.60	13.60
Environment	5	758.14	93.45	29528.28	47.36	248.25	63.30
G×E	115	1.49	4.22	932.95	34.41	3.94	23.09
PC1	27	3.55	56.04	1633.72	41.11	13.76	82.04
PC2	25	1.42	20.74	1159.83	27.03	2.71	14.94
Error	288	0.11	-	3.90	-	0.07	-
Source of variation	Degrees of freedom	TSS (°Brix)		β-Carotene (mg 100 g^{-1})		Yield (t ha^{-1})	
		MSS	Proportion	MSS	Proportion	MSS	Proportion
Genotype	23	1.42	1.15	19.93	32.59	198.40	18.23
Environment	5	552.01	97.08	162.74	57.84	2370.29	47.35
G×E	115	0.44	1.77	1.17	9.58	74.90	34.42
PC1	27	1.60	86.08	3.64	73.04	131.19	41.12
PC2	25	0.16	7.89	0.77	14.36	93.11	27.02
Error	288	0.02	-	0.01	-	0.31	-

1.91, Rank 7) were among the most stable. G_9 also achieved the best YSI rank (1), making it a top performer for root fresh weight stability, while G_{24} ranked the lowest in both mean and stability.

For root dry weight, G_4 stood out with the highest mean (13.28 g) and excellent stability (ASV 1.23, Rank 5; YSI Rank 1). G_3 also showed promising performance with a high mean and good stability (ASV 1.06, Rank 3). Conversely, G_{21} was the least stable with the highest ASV (6.68) and worst YSI (Rank 24).

In terms of TSS, G_1 recorded the highest mean (8.92 °Brix) but showed moderate stability. The most stable genotype was G_7 (lowest ASV 0.12, Rank 1) with the best YSI rank (1), making it ideal for selection. In contrast, G_{17} displayed the poorest stability (ASV 9.03, Rank 24).

Regarding β-carotene content, although G_{21} had the highest mean (8.59 mg $(100g)^{-1}$), the most stable genotype was G_{11} (lowest ASV 0.36, Rank 1; YSI Rank 1). G_{19} and G_7 was the least stable with high ASV and poor YSI rankings.

For yield, G_3 was the top performer (32.04 t ha^{-1}) but highly unstable (ASV 3.70, Rank 24). G_9 emerged as the most balanced genotype with a good mean (27.30 t ha^{-1}, Rank 5), high stability (ASV 1.01, Rank 7), and best YSI (Rank 1). G_5 and G_{24} were among the least stable (Table 3).

Overall, G_9, G_{10}, G_{12}, and G_2 consistently combined high mean performance and stability across all the traits. In contrast, G_{24}, G_5, and G_{21} often ranked among the least stable and poorest performing genotypes. Thus, G_9 and G_{10} were recommended as the most promising stable genotypes across environments.

Table 3: Stability analysis for 6 characters of 24 genotypes tested in 6 environments

Root length (cm)								Root fresh weight (g)							
SL. No.	Genotypes	Mean	Rank	ASV	Rank	YSI	Rank	SL. No.	Genotypes	Mean	Rank	ASV	Rank	YSI	Rank
1.	G_9	15.99	1	0.75	13	14	6	1.	G_3	113.07	1	6.94	24	25	11
2.	G_{15}	14.23	2	0.71	10	12	2	2.	G_{12}	99.63	2	4.86	17	19	5
3.	G_{11}	14.05	3	0.92	15	18	9	3.	G_2	99.30	3	3.28	13	16	3
4.	G_{12}	14.05	4	0.62	8	12	2	4.	G_4	98.43	4	6.34	23	27	15
5.	G_{18}	13.96	5	0.67	9	14	6	5.	G_9	96.36	5	1.91	7	12	1
6.	G_3	13.84	6	0.57	7	13	5	6.	G_{22}	95.73	6	5.45	19	25	11
7.	G_{10}	13.66	7	0.11	2	9	1	7.	G_{11}	95.15	7	5.55	20	27	15
8.	G_{16}	13.57	8	0.78	14	22	12	8.	G_{17}	94.80	8	5.80	22	30	20
9.	G_2	13.43	9	0.38	3	12	2	9.	G_{13}	94.70	9	4.35	16	25	11
10.	G_{17}	13.33	10	0.71	10	20	10	10.	G_{18}	93.11	10	1.56	5	15	2
11.	G_8	13.23	11	2.17	22	33	16	11.	G_{15}	89.19	11	2.41	9	20	6
12.	G_{22}	13.09	12	0.92	15	27	15	12.	G_{10}	88.90	12	5.58	21	33	21
13.	G_{14}	13.01	13	0.09	1	14	6	13.	G_7	86.41	13	2.83	11	24	9
14.	G_4	12.98	14	2.49	23	37	19	14.	G_{14}	84.85	14	1.47	3	17	4
15.	G_{13}	12.93	15	1.18	18	33	16	15.	G_{16}	83.41	15	2.41	9	24	9
16.	G_7	12.68	16	0.52	5	21	11	16.	G_1	82.75	16	3.09	12	28	17
17.	G_1	12.39	17	0.55	6	23	14	17.	G_5	80.55	17	5.12	18	35	23
18.	G_6	12.18	18	0.47	4	22	12	18.	G_8	80.34	18	0.91	2	20	6
19.	G_{23}	11.82	19	1.59	20	39	21	19.	G_{23}	79.18	19	4.28	15	34	22
20.	G_5	11.72	20	1.03	17	37	19	20.	G_6	72.03	20	2.20	8	28	17
21.	G_{21}	11.69	21	1.92	21	42	22	21.	G_{20}	62.11	21	1.53	4	25	11
22.	G_{24}	11.49	22	3.78	24	46	24	22.	G_{21}	61.43	22	0.47	1	23	8
23.	G_{19}	11.29	23	1.43	19	42	22	23.	G_{24}	59.99	23	3.41	14	37	24
24.	G_{20}	10.66	24	0.71	10	34	18	24.	G_{19}	57.89	24	1.56	5	29	19

*The genotypic means for the characters under study were obtained from non-transformed data. The ASV was calculated on the basis of the transformed (Aitkin's) data

Table 3: Continue...

Root dry weight (g)								TSS (°Brix)							
SL. No.	Geno-types	Mean	Rank	ASV	Rank	YSI	Rank	SL. No.	Geno-types	Mean	Rank	ASV	Rank	YSI	Rank
1.	G_4	13.28	1	1.23	5	6	1	1.	G_1	8.92	1	4.92	17	18	7
2.	G_{15}	12.98	2	3.86	14	16	7	2.	G_{16}	8.51	2	8.59	23	25	12
3.	G_{18}	12.22	3	2.84	11	14	4	3.	G_{14}	8.42	3	2.46	9	12	4
4.	G_3	12.05	4	1.06	3	7	2	4.	G_7	8.25	4	0.12	1	5	1
5.	G_{16}	12.05	5	2.74	10	15	6	5.	G_2	8.24	5	0.67	3	8	2
6.	G_2	11.59	6	2.26	7	13	3	6.	G_{11}	8.14	6	2.55	10	16	6
7.	G_5	11.40	7	3.47	12	19	9	7.	G_9	8.12	7	0.16	2	9	3
8.	G_{22}	11.36	8	1.56	6	14	4	8.	G_5	8.03	8	5.29	19	27	15
9.	G_{20}	11.20	9	5.07	21	30	15	9.	G_3	8.00	9	2.73	11	20	9
10.	G_{23}	11.19	10	3.73	13	23	12	10.	G_8	7.92	10	1.25	5	15	5
11.	G_{14}	11.05	11	6.34	23	34	18	11.	G_{20}	7.88	11	4.94	18	29	16
12.	G_{24}	10.87	12	3.95	15	27	14	12.	G_{21}	7.82	12	1.78	7	19	8
13.	G_9	10.80	13	2.41	8	21	10	13.	G_{12}	7.77	13	5.61	21	34	19
14.	G_{12}	10.76	14	4.47	18	32	16	14.	G_6	7.74	14	2.76	12	26	13
15.	G_{17}	10.48	15	4.52	19	34	18	15.	G_{24}	7.66	15	1.50	6	21	10
16.	G_{13}	10.46	16	0.92	2	18	8	16.	G_{13}	7.59	16	2.45	8	24	11
17.	G_{19}	10.22	17	4.69	20	37	20	17.	G_{18}	7.56	17	5.40	20	37	20
18.	G_8	10.20	18	5.58	22	40	23	18.	G_{19}	7.46	18	2.88	14	32	17
19.	G_{21}	10.13	19	6.68	24	43	24	19.	G_{23}	7.20	19	8.47	22	41	23
20.	G_{10}	9.89	20	0.11	1	21	10	20.	G_{10}	7.16	20	2.87	13	33	18
21.	G_6	9.50	21	1.21	4	25	13	21.	G_{17}	7.16	21	9.03	24	45	24
22.	G_1	9.27	22	4.45	17	39	21	22.	G_{22}	7.16	22	1.03	4	26	13
23.	G_{11}	9.14	23	4.39	16	39	21	23.	G_{15}	7.14	23	3.29	15	38	21
24.	G_7	9.13	24	2.57	9	33	17	24.	G_4	7.09	24	4.40	16	40	22
β-Carotene (mg 100 g^{-1})								Yield (t ha^{-1})							
SL. No.	Geno-types	Mean	Rank	ASV	Rank	YSI	Rank	SL. No.	Geno-types	Mean	Rank	ASV	Rank	YSI	Rank
1.	G_{21}	8.59	1	3.79	21	22	9	1.	G_3	32.04	1	3.70	24	25	10
2.	G_{24}	8.57	2	5.25	23	25	11	2.	G_{12}	28.23	2	2.59	17	19	5
3.	G_{20}	8.38	3	3.85	22	25	11	3.	G_2	28.13	3	1.75	12	15	2
4.	G_{19}	8.27	4	5.88	24	28	15	4.	G_4	27.89	4	3.37	23	27	15
5.	G_{23}	8.15	5	3.59	20	25	11	5.	G_9	27.30	5	1.01	7	12	1
6.	G_{22}	7.85	6	1.78	13	19	7	6.	G_{22}	27.12	6	2.90	19	25	10
7.	G_{11}	4.82	7	0.36	1	8	1	7.	G_{11}	26.96	7	2.96	20	27	15
8.	G_{17}	4.80	8	1.53	10	18	4	8.	G_{17}	26.86	8	3.09	22	30	20
9.	G_{14}	4.80	9	1.51	9	18	4	9.	G_{13}	26.83	9	2.32	16	25	10
10.	G_{18}	4.64	10	2.17	18	28	15	10.	G_{18}	26.38	10	0.83	5	15	2
11.	G_{12}	4.52	11	0.78	3	14	2	11.	G_{15}	25.27	11	1.96	14	25	10
12.	G_5	4.51	12	2.23	19	31	18	12.	G_{10}	25.19	12	2.97	21	33	21

Table 3: Continue...

β-Carotene (mg 100 g^{-1})								Yield (t ha^{-1})							
SL. No.	Geno-types	Mean	Rank	ASV	Rank	YSI	Rank	SL. No.	Geno-types	Mean	Rank	ASV	Rank	YSI	Rank
13.	G_{16}	4.39	13	1.10	5	18	4	13.	G_{7}	24.48	13	1.50	10	23	7
14.	G_{4}	4.37	14	0.57	2	16	3	14.	G_{14}	24.04	14	0.78	3	17	4
15.	G_{13}	4.36	15	0.96	4	19	7	15.	G_{16}	23.63	15	1.28	9	24	9
16.	G_{15}	4.30	16	1.96	15	31	18	16.	G_{1}	23.45	16	1.65	11	27	15
17.	G_{10}	4.25	17	1.12	6	23	10	17.	G_{8}	22.76	17	0.49	2	19	5
18.	G_{9}	4.18	18	1.50	8	26	14	18.	G_{23}	22.44	18	2.28	15	33	21
19.	G_{6}	4.16	19	1.96	15	34	21	19.	G_{6}	20.41	19	1.17	8	27	15
20.	G_{1}	4.11	20	1.85	14	34	21	20.	G_{5}	19.79	20	2.73	18	38	24
21.	G_{3}	4.02	21	1.74	11	32	20	21.	G_{20}	17.60	21	0.82	4	25	10
22.	G_{2}	4.01	22	1.18	7	29	17	22.	G_{21}	17.40	22	0.25	1	23	7
23.	G_{8}	3.94	23	1.74	11	34	21	23.	G_{24}	17.00	23	1.82	13	36	23
24.	G_{7}	3.94	24	1.96	15	39	24	24.	G_{19}	16.40	24	0.83	5	29	19

*The genotypic means for the characters under study were obtained from non-transformed data. The ASV was calculated on the basis of the transformed (Aitkin's) data

3.3. GGE bi-plot analysis

GGE biplots were powerful graphical tools used to visualize the patterns of genotype-by-environment interaction (GEI). GGE biplots was done for 2 most important characters i.e. β-carotene and yield. In this study, four distinct types of biplots were generated to select stable genotypes with superior performance and to identify ideal testing environments.

3.3.1. What-won-where" GGE biplot

For β-Carotene, genotypes G_{19}, G_{21}, G_{22}, and G_{24} emerged as winners across different environments. Environment E_5 was highly discriminative and favourable for selecting genotypes with higher β-Carotene content, while environments E_2 and E_3 were less suitable. The majority of the variation was explained by PC1 (93%), indicating strong reliability of the biplot interpretation (Figure 7).

In terms of yield, genotypes G_3, G_4 and G_{17} demonstrated superior performance across different environments. Environment E_5 was highly discriminative and rich for yield evaluation, followed by E_6 and E_1. In contrast, E_2 was identified as a poor environment, providing minimal genotype differentiation. The first two principal components captured 73% of the total variation, ensuring reliable biplot interpretation (Figure 8).

3.3.2. Idetification of test environments based on discriminativeness and representativeness

In the GGE biplot environment view for β-Carotene content, E_5 emerged as highly discriminative environments for differentiating among genotypes. E_6, in particular, combined both high discriminative power and representativeness, making it an ideal testing environment. In contrast, E_2 and E_3 displayed shorter vectors, suggesting their limited utility in genotype selection for β-Carotene content. The first two principal components explained 96.7% of the total variation, ensuring robust conclusions from the biplot (Figure 9).

For yield, environment E_3 was more discriminative while E_3 and E_4 were less discriminative for the genotypes. E_4 emerged as more representative while E_1 and E_6 had both high discriminative power and representativeness, making it an ideal testing environment. The first two principal components accounted for 73% of the total variation, providing a strong basis for reliable conclusions from the biplot (Figure 10).

3.3.3. Identification of stable and high-performing genotypes using GGE Biplot

In the genotype view of the GGE biplot for β-Carotene content, genotypes G_5, G_7, G_8, G_{11}, G_{13}, G_{15}, G_{16}, and G_{18} were identified as highly stable and high-performing. Among these, G_8 and G_{11} appeared particularly promising due to their proximity to the ideal genotype position. Genotypes G_{19}, G_{24}, G_{20} and G_{21} exhibited high β-Carotene content but with reduced stability across environments. The first two principal components explained 96.7% of the total variation, indicating a highly dependable visualization for genotype evaluation (Figure 11).

For yield, in the genotype view, the ideal genotypes were those positioned closer to the small circle along the average environment axis. Genotypes G_{14}, G_{15} and G_{16} were found very close to the centre of the concentric circles, identifying

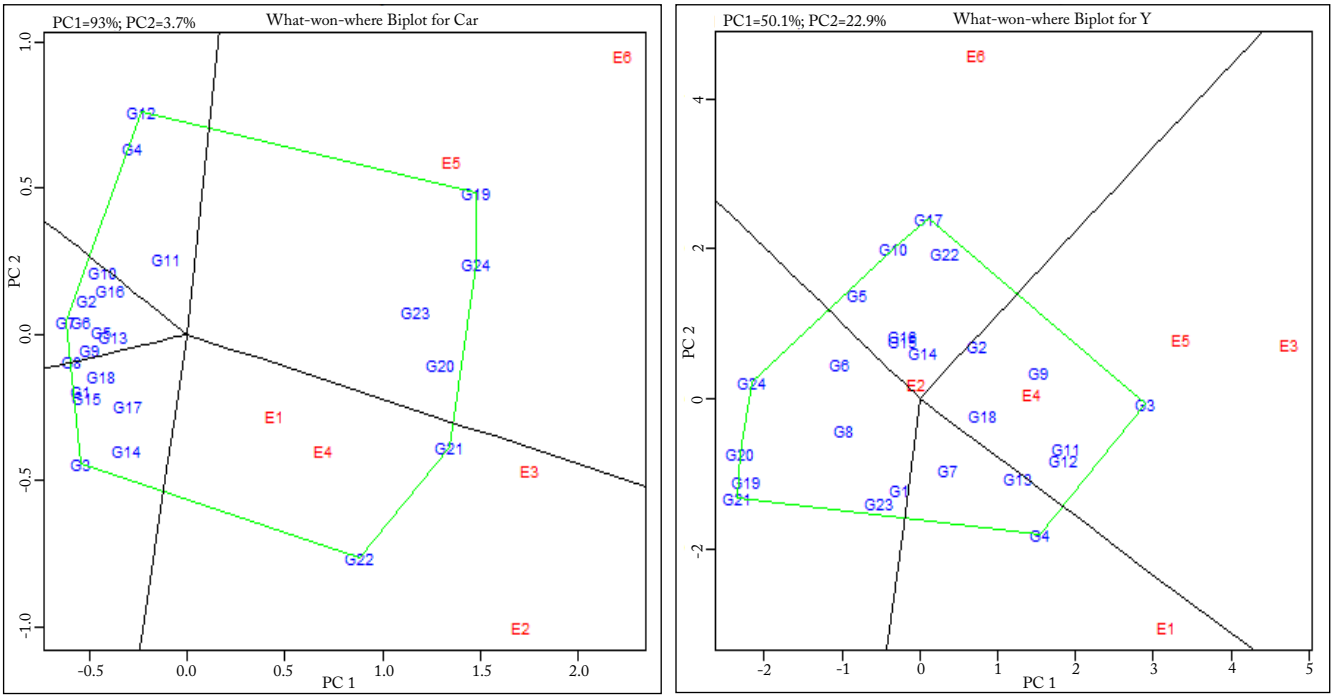


Figure 7 and 8: What won where plot for β-Carotene (left) and yield (right)

them as near-ideal for yield. In contrast, genotypes G_3, G_{21}, G_{19}, and G_{20} were located farther away from the centre of the concentric circles. The first two principal components explained 73% of the total variation, indicating a highly dependable visualization for genotype evaluation (Figure Praanjal et al., 2025 Praanjal et al., 2025 The finding was supported by the results of Daemo and Ashango, 2024, who evaluated 11 improved potato genotypes using AMMI, GGE biplot, and GSI analyses. Their study identified Gudanie and Gorebella as superior genotypes for tuber yield, consistently exhibiting high mean performance across various tested environments. Farwan et al., 2024 conducted

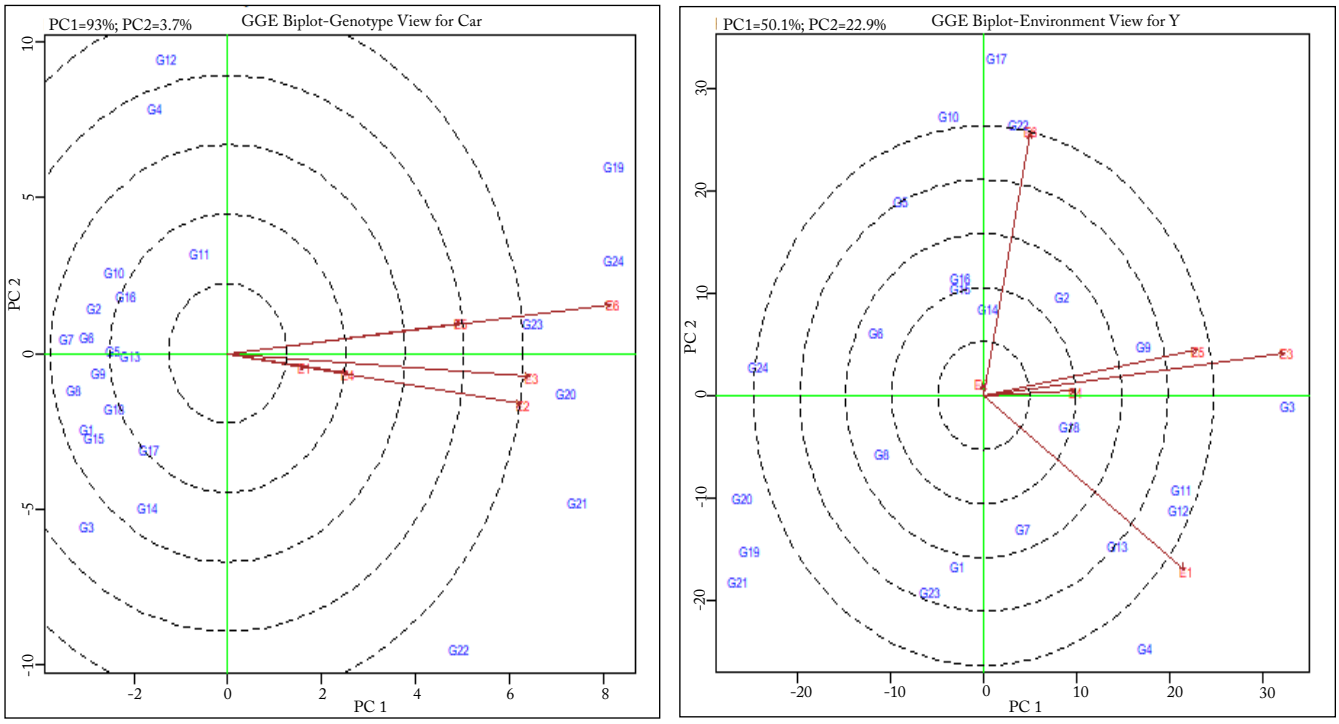


Figure 9 and 10: GGE biplot-environment view for β-Carotene (left) and yield (right)

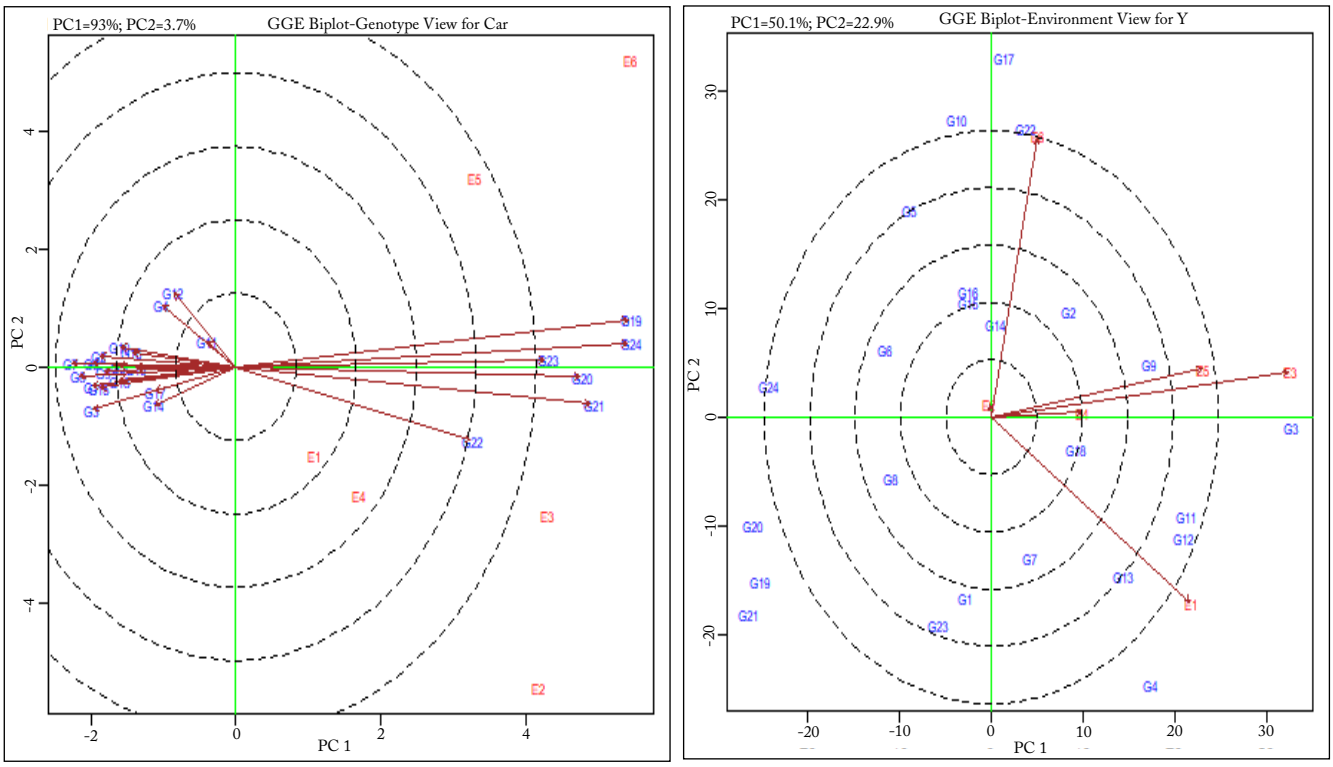


Figure 11 and 12: GGE biplot-genotype view for β-Carotene (left) and yield (right)

an experiment on the genotype x environment (G×E) interaction on the yield stability in twenty-eight genotypes of carrot was studied under eight environments. GGE biplot have given a mean vs stability and polygon view, which helps in the identification of the genotype with the highest mean performance and better adaptability. They found that genotypes G_6, G_3 and G_4 performed better for yield.

4. CONCLUSION

Using two seasons and three nutritional practices, this study assessed 24 carrot genotypes in six environments. On yield, root fresh weight, root dry weight and quality characters i.e TSS and β-carotene, the environment and genotype–environment interaction had a substantial impact. In addition to G_{12} and G_2, the genotypes G_9 and G_{10} showed great yield and stability. GGE and AMMI biplot analysis validated these trends. For genotype evaluation, environments E_5 and E_6 worked well. For breeding and cultivation under a variety of growth circumstances G_9, G_{10}, G_{11} and G_{12} were advised

5. ACKNOWLEDGEMENT

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6. REFERENCES

Abdelrahman, M., Alharbi, K., El-Denary, M.E., Abd El-Megeed, T., Naeem, E.S., Monir, S., Draz, A.S.E., 2022. Detection of superior rice genotypes and yield stability under different nitrogen levels using AMMI model and stability statistics. Plants 11(20), 2775.

Agyeman, A., Parkes, E., Peprah, B.B., 2015. AMMI and GGE biplot analyses of root yield performance of cassava genotypes in forest and coastal ecologies. International Journal of Agricultural Policy and Research 3(3), 122–132.

Anonymous, 2025. Ministry of Agriculture and Farmers Welfare. State horticulture estimates. Government of India. Retrieved, from: https://agriwelfare.gov.in/en/StatHortEst. Retrived on: March 21, 2025.

Arscott, S.A., Tanumihardjo, S.A., 2010. Carrots of many colours provide basic nutrition and bioavailable phytochemicals acting as a functional food. Comprehensive Reviews in Food Science and Food Safety 9(2), 223–239.

Becker, H.C., Leon, J.I., 1988. Stability analysis in plant breeding. Plant breeding 101(1), ISSN 0179–9541.

Chevalier, W., Moussa, S.A., Medeiros Netto Ottoni, M., Dubois-Laurent, C., Huet, S., Aubert, C., Geoffriau, E., 2021. Multisite evaluation of phenotypic plasticity for specialized metabolites, some involved in carrot

quality and disease resistance. PloS One 16(4), e0249613.

Daemo, B.B., Ashango, Z., 2024. Application of AMMI and GGE biplot for genotype by environment interaction and yield stability analysis in potato genotypes grown in Dawuro zone, Ethiopia. Journal of Agriculture and Food Research 18, 101287.

Dhand, A., Garg, N., 2023. Genotype×environment interaction using AMMI and MTSI analysis for growth and yield attributes of radish (*Raphanus sativus* L.) under high temperature stress conditions of north Indian plains. Scientia Horticulturae 313, 111880.

Farwan, K., Devi, R., Dhillon, T.S., 2024. GGE biplot analysis for yield performance and stability assessment of carrot genotypes (*Daucus carota* L.) under multi-environment trails (METs). Scientia Horticulturae 336, 113387.

Gauch, H.G., Piepho, H.P., Annicchiarico, P., 2008. Statistical analysis of yield trials by AMMI and GGE: further considerations. Crop Science 48, 866–889.

Hill, J., Becker, H.C., Tigerstedt, P.M.A., Hill, J., Becker, H.C., Tigerstedt, P.M.A., 1998. Stability, adaptability and adaptation. In: Quantitative and Ecological Aspects of Plant Breeding, 187–211.

Kalia, P., Singh, B.K., Patel, V., Selvakumar, R., 2023. Carrot: Breeding and genomics. Vegetable Science, 221–230.

Kumawat, C.K., Kulkarni, G.U., Sharma, L.K., 2023. Phenotypic stability analysis in Brinjal over environments. International Journal of Bio-resource and Stress Management 14(5), 709–718.

Mohan, Y.C., Krishna, L., Sreedhar, S., Chandra, B.S., Raju, C.D., Madhukar, P., Ramana, M.V., 2021. Stability analysis of rice hybrids for grain yield in Telangana through AMMI and GGE Bi-plot model. International Journal of Bio-resource and Stress Management 12(6), 687–695.

Prajapati, A., Tank, C., Gami, R., Ravindrababu, Y., Kanbi, V., 2015. G×E interaction and stability analysis in carrot (*Daucus carota* L.). Gujarat Agricultural University Research Journal 40(1), 23–27.

Purchase, J.L., Hatting, H., Van De Venter, C.S., 2000. Genotype×environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: stability analysis of yield performance. South African Journal of Plant and Soil 17(3), 101–107.

Que, F., Hou, X.L., Wang, G.L., Xu, Z.S., Tan, G.F., Li, T., Xiong, A.S., 2019. Advances in research on the carrot, an important root vegetable in the Apiaceae family. Horticulture Research 6, 69.

Rosenfeld, H.J., Baardseth, P., Skrede, G., 1997. Evaluation of carrot varieties for production of deep-fried carrot chips—IV. The influence of growing environment on carrot raw material. Food Research International 30(8), 611–618.

Saha, S., Kalia, P., Sureja, A.K., Sarkar, S., 2016. Breeding tropical carrots (*Daucus carota*) for enhanced nutrition and high temperature stress. Indian Journal of Agricultural Sciences 86(7), 940.

Selvakumar, R., Kalia, P., Raje, R. S., 2019. Genetic analysis of nutritional traits in tropical carrot (*Daucus carota* L.). Genetika 51(2), 641–660.

Sharma, S.P., Leskovar, D.I., Crosby, K.M., Ibrahim, A.M.H., 2020. GGE biplot analysis of genotype-by-environment interactions for melon fruit yield and quality traits. HortScience 55(4), 533–542.

Sun, T., Simon, P.W., Tanumihardjo, S.A., 2009. Antioxidant phytochemicals and antioxidant capacity of biofortified carrots (*Daucus carota* L.) of various colours. Journal of Agricultural and Food Chemistry 57(10), 4142–4147.

Yan, W., Hunt, L.A., Sheng, Q., Szlavnics, Z., 2000. Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Science 40, 597–605.

Yan, W., Tinker, N.A., 2006. Biplot analysis of multi-environment trial data: principles and applications. Canadian Journal of Plant Science 86(3), 623–645.

Yoo, K.S., Bang, H., Pike, L., Patil, B.S., Lee, E.J., 2020. Comparing carotene, anthocyanins, and terpenoid concentrations in selected carrot lines of different colours. Horticulture, Environment, and Biotechnology 61, 385–393.