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Genotype x environment interaction and stability analysis across environments for yield related traits of carrot (*Daucus carota* sub spp. *sativus*) cultivars in North Karnataka

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Abstract

Carrot (*Daucus carota* L.) is a popular root vegetable crop suitable for tropical and temperate climate, grown throughout the world. The success of carrot crop improvement and production activities can be enhanced with scientific information generated from genotype-environment interactions (GEI). The present research was carried out to find the stable and adaptable carrot genotypes under three different agro-ecologies. Seven genotypes were evaluated in randomized complete block design (RCBD) with three replications. Eberhart and Russell model stability indices were used to evaluate stability and genotype by environment performances. Combined analysis of variance (ANOVA) for yield components traits revealed highly significant ($P \leq 0.01$) differences for genotypes, environments and their interaction. The significant interaction showed genotypes respond differently across environments. None of the genotype was found stable for all the traits across all the environments and stability of each trait was independent from one another in three different locations.

Keywords: Adaptability, environment, genotype, stability

Introduction

Carrot (*Daucus carota* var. *sativus*) is a biennial vegetable in the family of *Apiaceae* (Peirce, 1987) [19]. This vegetable is among the top-ten most economically important vegetable crops in the world after potato (Simon *et al.*, 2008; Spooner *et al.*, 2019) [29, 30] and it is the most widely grown and important vegetable across tropical and temperate regions (Simon *et al.*, 2008; Kulkarni *et al.*, 2019a; Kulkarni *et al.*, 2019b) [29, 14, 15]. Carrot, including its undomesticated and domesticated forms, has wide phenotypic and molecular variation (Simon 2008; Chaitra *et al.*, 2020) [29, 8]. The first widely accepted evidence of cultivation of modern-day carrot comes from Afghanistan/Central Asia in tenth-century, where cultivation of this root vegetable spread throughout Asia and Europe (Bradeen and Simon 2007) [7].

Cultivated carrots are divided into two groups: (1) Asian/tropical group that has characteristic root color such as yellow, black purple/anthocyanin type or light orange flesh with strong xylem, phloem patterning and lateral branching of roots, slightly soft texture, low sweet roots. Plants are with pubescent leaves having annual habitat as they bolt easily with less or no vernalization requirement. Hence, widely adapted to warmer temperature; and (2) European/temperate group that has deeply pigmented orange roots, yellow, or white root in color, firm textured, sweet, less pubescent green leaves, slow bolting and acclimated to cool temperature (Rubatzky and Yamaguchi 1997; Que *et al.*, 2019; Chaitra *et al.*, 2020) [25, 22, 8].

Carrot root color is observed in various colors orange, yellow, red, purple and white (Nicolle *et al.*, 2004; Surlis *et al.*, 2004) [18, 31]. Orange carrots contain predominantly β -carotene (45-80%) accompanied by α -carotene that together constitute up to 95% of total carotenoids (Rubatzky *et al.*, 1999; Arango *et al.*, 2014; Perrin *et al.*, 2016; Kulkarni *et al.*, 2019a; Kulkarni *et al.*, 2021b) [24, 3, 20, 14, 12]. Carrot contains 495 mg of β -carotene, vitamins, and minerals and a good source of calcium, potassium and magnesium (Hager and Howard 2006) [11]. Moreover, carrot also contains phenolic compounds, and other antioxidant micronutrients (Que *et al.*, 2019) [22].

Light orange colour Asiatic type and deeply pigmented dark orange European types vegetative phase can be successfully grown in tropical climatic region. Hence, the genotypes adaptability, and stability are important measures for understanding the cultivar performance under varied environmental conditions.

The phenotype of an individual plant is decided by both genetic make-up and environmental influences. Genotype \times environment interaction is regarded as an important source of divergence in any crop, and Eberhart and Russell model of stability analysis have been used to distinguish carrot genotypes for their behaviour in three different environmental conditions. GEI reduces the association between phenotype and genotype which result in relative ranking and stability differences of genotypes across environments (Prabhakaran and Jain 1992; Ayalneh *et al.*, 2014) [21, 5].

For analysis of GEI, among seven carrot genotypes across three environments, Linear Regression model (bi) and deviation from regression mean square (S^2di) of Eberhart and Russell (1966) [10] model was used to identify stable genotype across environments in the present study.

Material and Methods

The materials for stability analysis consisted of seven carrot cultivars as listed in Table 1a, six representing Asiatic types and one representing European type were utilized. The study was conducted over three environments during Aug-Dec 2019. Details of climatic factors of three environments is presented in Table 1b. The information on climatic conditions during the crop season was recorded in Division of

Agrometeorology at each experimental site. Experiments were laid out in randomized block design with three replications. Plot sizes of 1m \times 10 m and 10 cm \times 30 cm spacing plant to plant and between rows were used respectively. Minimum hundred plants per replication were maintained for each cultivar. All recommended agronomic practices and management were applied uniformly. Seven morphological traits as listed in Table 1c were recorded from five randomly selected plants for each cultivar per replication. Linear regression model of stability suggested by Eberhart and Russell (1966) [10] was employed and the data was analysed using OPSTAT software (Sheoran *et al.*, 2010) [28] for stability parameters.

Table 1a: List of elite genotypes used for multi-location evaluation

S. No	Name of genotype	Tropical/Temperate adapted
1.	UHSBC-32-2	Tropical
2.	UHSBC-17	Tropical
3.	UHSBC-117	Tropical
4.	UHSBC-67	Tropical
5.	UHSBC-23-1	Tropical
6.	UHSBC-34-1	Tropical
7.	UHSBC-100	Temperate

Table 1b: Summary of climatic factors for multi-location trial conducted during the present investigation

Particulars of three environments		Environments		
		Bagalkot (E1)	Arabhavi (E2)	Devihosur (E3)
Geographical position	Latitude (N)	16° 12' N - 16° 46' N	15° 51 '01.30 "N	14°47'59.85"N
	Longitude	74° 59' E 76° 20' E	74° 30'16.81" E	75°23'59.92"E
Soil type		Red sandy loam (Laterite)	Red soils	Red Shallow Soils
Altitude (AMSL)		533 m	836 m	563m
Rainfall average (mm)		585	823	777
Temperature average (°C)		30	31.8	26
Agro-climatic Zone (NARP)		Northern Dry Zone	Northern Dry Zone	Northern Dry zone
Season		Kharif	Kharif	Kharif

Table 1c: List of traits for stability analysis of carrot cultivars used for multi-location evaluation

S. No	Trait
1	Root length (cm)
2	Root width(mm)
3	Root weight (g)
4	Shoot length (cm)
5	Number of petioles
6	Shoot weight (g)
7	Shoulder width (mm)

Results and Discussion

The combined analysis of variance across three environments means sum of squares due to genotypes (Table 2) was significant for shoot length, Number of petioles, shoot weight, shoulder width, root length and root width traits indicating the presence of genetic variability among the genotypes involved in the study. Therefore, partition of these characters was done as per Eberhart and Russell model (1966) [10] in order to know magnitude of linear and non-linear components of variation. The environment and GEI component can also be subdivided into environment (linear), G \times E (linear) and pooled deviations from regression. Variation due to G \times E interaction has been partitioned in such a way that, predictable component is due to linear regression and the unpredictable one is due to pooled deviations from regression. ANOVA

(Table 2) showed that the sources of variation for Environment + (G \times E) was found highly significant. Highly significant ($P < 0.01$) variation was observed in environment and genotype \times environment interaction. A significant ($p < 0.05$) variation is also noted in genotypes. Significance of GEI is an indication for inconsistency of genotypes in response to changing climatic conditions across locations due to genotype-environment interaction. Similar results were obtained by Das *et al.* (2010) [9], Tiawari *et al.* (2011) [32] and Zerihun (2011) [33], Matin *et al.* (2017) [17], Kulkarni *et al.* (2021a) [13]. Higher variation was observed across environment similarly as reported by Letta (2009) [16] and Das *et al.* (2010) [9]. The magnitude of variation instigated by environment reveals that complex external factors (biotic and abiotic) are number one challenges in crop improvement. The larger variation observed in GEI, discriminate the correlation between phenotype and genotype, hence, it is hard to evaluate the genetic potential of particular genotype whose performance changed in different environments. The three stability parameters *viz.*, mean (μ), regression coefficient (β_i) and deviation from linearity (σ^2di) were estimated for seven characters and the result obtained are presented character wise in table 3a and 3b. According to Eberhart and Russel (1966) [10] the desirable and stable genotypes is one with the high mean yield, bi close to unity and low and non-significant σ^2di . However, the condition may

vary with respect to selection of characters.

For shoot length, genotypes UHSBC-34-1 (G6) and UHSBC_67 (G4), had higher mean yield, unit regression coefficient ($b_i=1$) and non-significant S^2d_i . Thus, they were stable, high yielding genotypes which can be adapted to all the environments. Genotypes UHSBC_23-1 (G5) and UHSBC_117 (G3) had higher mean than overall mean, b_i significantly greater than 1, non-significant S^2d_i . Therefore, UHSBC_23-1 (G5) and UHSBC_117 (G3) are stable and well adaptable to favourable environments. UHSBC_100 (G7) exhibited non-significant deviation from regression and regression coefficient value less than unity ($b_i<1$) with mean value lower than the population mean indicating their stability under unfavourable environments. Genotypes, UHSBC_32-2 (G1), UHSBC_17 (G2) were found unstable due to their significant S^2d_i values.

For number of petioles, UHSBC_117 (G3) and UHSBC_67 (G4) had higher mean yield and regression co-efficient around unity and non-significant S^2d_i . Thus, are found to be adaptable to all the environments across environments. UHSBC_17 (G2) had regression coefficient greater than unity with non-significant deviation from regression line and higher overall population mean which indicates its adaptation to favourable environment. UHSBC_23-1 (G5), UHSBC_34-1 (G6), UHSBC_100 (G7) genotypes showed regression coefficient lesser than unity ($b_i<1$) with non-significant deviation from regression line so are suitable under unfavourable environment. Genotype UHSBC_32-2 (G1) and which are comparable to higher population mean showed regression coefficient greater than one ($b_i>1$) with significant deviation from regression line, hence found unstable due to their significant S^2d_i values.

For shoot weight, genotypes UHSBC_17 (G2) presented unit regression coefficient ($b_i=1$) and non-significant S^2d_i . Therefore, it is regarded as stable genotype across all environments. UHSBC_32-2 (G1) and UHSBC_67 (G4) had regression coefficient greater than unity with non-significant deviation from regression line and higher overall population mean which indicates its adaptation to favourable environment. UHSBC_117 (G3), UHSBC_23-1 (G5), UHSBC_34-1 and (G6) UHSBC_100 (G7) showed regression coefficient less than unity ($b_i<1$) with non-significant S^2d_i . Hence, are suitable under unfavourable environments. None of the genotypes had significant S^2d_i values for shoot weight, therefore no genotypes were found unstable.

For shoulder width, genotypes UHSBC_117 (G3), UHSBC_67 (G4), UHSBC_23-1 (G5) and UHSBC_100 (G7)

had $b_i>1$ and non-significant S^2d_i indicating adaptation to favourable environment. UHSBC_17 (G2) and showed regression coefficient ($b_i=1$) significant S^2d_i and regarded as unstable genotype across environments. Genotypes UHSBC_32-2 (G1), UHSBC_34-1 (G6) showed regression coefficient less than unity ($b_i<1$) with non-significant S^2d_i . Hence, are suitable under unfavourable environments.

For root length, UHSBC_32-2 (G1), UHSBC_17 (G2), UHSBC_117 (G3), UHSBC_67 (G4), and UHSBC_23-1 (G5) genotypes were superior over average mean, showed regression coefficient close to one with non-significant deviation from regression line (S^2d_i) reflecting its stability over changing environments. Genotype UHSBC_100 (G7) had $b_i>1$ and non-significant S^2d_i indicating its adaptability to favourable environment. Genotypes UHSBC_32-2 (G1), UHSBC_34-1(G6), showed regression coefficient less than unity ($b_i<1$) with non-significant S^2d_i . Hence, UHSBC_34-1 (G6), suitable under unfavourable environments. None of the genotypes evaluated in the study showed significant S^2d_i for root length and found unstable across environments.

For root width, UHSBC_100 (G7), showed superior population mean and with regression coefficient close to one with non-significant deviation from regression line indicates adaptation to all the environments. UHSBC_67 (G4), had $b_i>1$ and non-significant S^2d_i indicating adaptable to favourable environment. UHSBC_17 (G2), UHSBC_117 (G3), UHSBC_34-1 (G6), had $b_i<1$ with non-significant S^2d_i , so are suitable under unfavourable environments. Remaining UHSBC_32-2 (G1), UHSBC_23-1 (G5), genotypes were considered to be unstable as they had significant S^2d_i .

For root weight, none of the genotypes showed unit regression coefficient ($b_i=1$) and non-significant S^2d_i and found adaptable to all the environments. UHSBC_23-1 (G5), UHSBC_34-1 (G6) and UHSBC_100 (G7) genotypes exhibited superior performance coupled with regression coefficients lesser than unity ($b_i<1$) with non-significant deviation from regression line so are suitable under unfavourable environment. Yet, UHSBC_17 (G2), and UHSBC_117 (G3) had ($b_i>1$) with non-significant deviation from regression line reflecting its adaptation under favourable environments. However, UHSBC_32-2 (G1) and UHSBC_67 (G4) possess regression co-efficient more than one and display significant S^2d_i . Hence, are regarded as unstable across environments (Seboksa *et al.*, 2001; Akcura *et al.*, 2005 and Arshad *et al.*, 2003) [1, 4]. These results are in conformity with Mane *et al.*, (2010) [9].

Table 2: Mean Squares due to different source of variation for various quality traits in carrot (*Daucus carota L*)-ANOVA for Eberhart and Russel Model across locations

Source of Variation	DF	Shoot length	Shoot weight	Shoulder width	Number of petioles	Root length	Root width	Root weight
Replication within Environment	6	15.103	0.785	419.146 **	10.587	3.349 *	7.471	262.667
Genotypes	6	526.415 ***	10.305 ***	2913.404 ***	110.161 ***	1.523	10.502	136.831
Environment+ (Genotype × Environment)	14	60.598 *	7.766 ***	1418.167 ***	8.354	39.012 ***	8.129	168.859
Environments	2	324.700 ***	36.058 ***	6763.322 ***	6.68	268.798 ***	26.355 *	133.756
Genotype × Environment	12	16.582	3.051 *	527.308 **	8.633	0.714	5.091	174.71
Environments (Lin.)	1	649.401 ***	72.115 ***	13526.640 ***	13.36	537.597 ***	52.710 **	267.513
Genotype × Environment (Linear)	6	18.936	5.471 **	1000.664 ***	12.843	0.726	6.652	121.578
Pooled Deviation	7	12.194	0.541	46.244	3.791	0.601	3.026	195.292
Pooled Error	36	12.571	1.458	274.505	5.28	2.297	5.557	127.261
Total	20	200.343	8.528	1866.738	38.896	27.765	8.841	159.251

* Significant at 5% level of significance, ** significant at 1% level of significance

Table 3a: Mean value, regression coefficient (bi) and variation due to deviation (S^2di) for seven carrot genotypes across locations

	Genotypes	Shoot length			Number of petioles			Shoot weight			Shoulder width		
		μ Mean	β_i	S^2di	μ Mean	β_i	S^2di	μ Mean	β_i	S^2di	μ Mean	β_i	S^2di
1	UHSBC_32-2	64.044	0.99	30.4	12.444	2.24	0.24	126.02	2.07	-244.48	37.349	-3.214	-5.99
2	UHSBC_17	61.444	1.15	1.31	10.356	1.64	-0.78	107.507	1.09	-293.43	43.057	0.34	11.2
3	UHSBC_117	61.741	1.54	-12.68	9.157	1.03	-1.14	82.827	0.75	-177.22	39.001	1.22	-3.05
4	UHSBC_67	58.711	0.98	-1.49	8.956	0.91	-0.45	83.343	1.78	-165.1	39.856	5.31	-0.3
5	UHSBC_23-1	56.778	1.2	-11.82	9.578	0.58	-1.34	77.596	0.85	-293.37	39.576	2	-5.93
6	UHSBC_34-1	62.467	1.07	-5.38	10.022	0.49	-0.92	104.542	0.44	-284.55	39.053	-0.41	-5.89
7	UHSBC_100	26.407	0.07	-5.51	6.256	0.12*	-1.36	28.204	0.02*	-284.31	24.274	1.76	-5.76
	Population Mean	55.942			9.538			87.148			37.452		

*Significant at 5% level of significance, ** significant at 1% level of significance

Table 3b: Mean value, regression coefficient (bi) and variation due to deviation (S^2di) for seven carrot genotypes across locations

	Genotypes	Root length			Root width			Root weight		
		μ Mean	β_i	S^2di	μ Mean	β_i	S^2di	μ Mean	β_i	S^2di
1	UHSBC_32-2	20.744	0.97	-2.31	25.691	0.71	2.63	90.731	2.05	115.52
2	UHSBC_17	22.178	0.96	-1.51	27.06	0.53	-4.93	94.491	2.84	-50.25
3	UHSBC_117	20.489	0.97	-2.42	24.537	0.03	-5.78	85.804	1.69	-146.01
4	UHSBC_67	21.862	1.01	-2.37	21.795	2.66	-4.05	90.266	2.6	642.01*
5	UHSBC_23-1	20.516	1.02	-1.69	27.365	1.88	0.75	87.931	-0.5	-40.02
6	UHSBC_34-1	20.667	0.87	-2.03	25.858	0.28	-3.78	87.118	-1.97	-137.76
7	UHSBC_100	21.644	1.19	-0.59	26.028	0.91	-4.48	73.191	0.29	-42.68
	Population Mean	21.157			25.476			87.076		

*Significant at 5% level of significance, ** significant at 1% level of significance

Table 4: Character wise classification of genotype for stability and adaptability under different environment

Characters	Poor/Unfavourable environments $bi < 1$	Rich/favourable environments $bi > 1$	Overall environments $bi = 1$
Shoot length	UHSBC_100 (G7)	UHSBC_23-1 (G5), UHSBC_117 (G3)	UHSBC_34-1 (G6), UHSBC_67 (G4)
Number of petioles	UHSBC_23-1 (G5), UHSBC_34-1 (G6), UHSBC_100 (G7)	UHSBC_17 (G2)	UHSBC_117 (G3), UHSBC_67 (G4)
Shoot weight	UHSBC_117 (G3), UHSBC_23-1 (G5), UHSBC_34-1 (G6) UHSBC_100 (G7)	UHSBC_32-2 (G1), UHSBC_67 (G4)	UHSBC_17 (G2)
Shoulder width	UHSBC_32-2 (G1), UHSBC_34-1 (G6)	UHSBC_117 (G3), UHSBC_67 (G4), UHSBC_23-1 (G5), UHSBC_100 (G7)	-
Root length	UHSBC_32-2 (G1), UHSBC_34-1 (G6)	UHSBC_100 (G7)	UHSBC_32-2 (G1), UHSBC_17 (G2), UHSBC_117 (G3), UHSBC_67 (G4), UHSBC_23-1 (G5)
Root width	UHSBC_17 (G2), UHSBC_117 (G3), UHSBC_34-1 (G6)	UHSBC_67 (G4)	UHSBC_100 (G7)
Root weight	UHSBC_23-1 (G5), UHSBC_34-1 (G6), UHSBC_100 (G7)	UHSBC_17 (G2), UHSBC_117 (G3)	-

Conclusion

Eberhart and Russell (1966) ^[10] model considers both linear (bi) and non-linear (S^2di) components of genotypes x environment interaction for predicting the performance of a genotype, an ideally stable/adaptable genotypes would be the one having unit regression coefficient ($bi \approx 1$) and deviation from regression non-significantly deviate from zero ($S^2di=0$) with high mean performance over the population mean. The value $bi \approx 1$ indicates that the genotype is less responsive to the environmental changes and therefore is more adaptive. However, if bi is less than unity ($bi < 1$), the genotype is likely to perform well under poor environmental condition and if bi value more than unity ($bi > 1$), the genotype will perform better under favourable environment conditions. Significant deviation from regression (S^2di) will invalidate for the linear prediction, whereas non-significant S^2di indicate that the performance of a genotype in a given set of environmental condition may be predicted.

Character wise classification of genotypes used in the present investigation (Table 4) clearly revealed that, UHSBC_34-1 (G6) exhibited non-significant deviation from regression and regression coefficient less than unity ($bi < 1$) with mean value close to the population for all traits except shoot length indicating its stability under unfavourable environments. Whereas, UHSBC_100(G7), showed stable performance across all environments for shoot length, number of petioles, shoot weight, root weight. Genotype UHSBC_23-1(G5), was found stable for number of petioles, shoot weight and root weight across all environments. Thus, these genotypes can be used for general cultivation across all environments. UHSBC_117(G3), for shoot length, shoulder width and root weight and UHSBC_67(G4), for shoot weight, shoulder width and root weight traits, showing stability under favourable environments showing non-significant deviation from regression and regression coefficient around unity ($bi > 1$) along with mean value close to the population mean.

Genotypes UHSBC_32-2(G1), UHSBC_17(G2), UHSBC_117G3), UHSBC_67(G4) and UHSBC_23-1(G5), were having unit regression coefficient ($b_i \approx 1$) and deviation from regression non-significantly deviate from zero ($S^2_{di}=0$) with high mean performance over the population mean for root length across all environments, thereby indicating their stability and adaptability under all environments. Data further revealed that, UHSBC_67 (G4) genotype had stability for shoot length and number of petioles as well across three different environments. Similar findings were reported by Sharma *et al.* (2012), Arain *et al.* (2011) [2], Aydin *et al.* (2010) [6]. None of the carrot cultivars were stable across changing environments across three locations for all seven traits under northern dry zone of Karnataka. Climatic factors, as well as soil conditions play prominent role in the vegetative growth period of carrot. Therefore, the present work reveals the necessity of understanding G×E interactions and its effect on co-inheritance of traits for development of environment specific cultivars to tropical climates. G×E interaction, coupled with high mean performance indicate that the genotypes are suitable for general adaptation in the range of environments considered.

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