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Research Article

Assessment stability and G x E interactions of baby corn hybrids for yield and yield contributing traits

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Abstract
The present study consisted of total 45 hybrids along with 18 parents and 2 checks. These entries were evaluated in randomized block design with three replications over three locations. Observations were recorded on ten characters to study *per se* performance, estimates genotype × environment interaction and stability parameters. The crosses × environment interactions were significant for all the characters indicating existence of non-linear response of crosses to the changing environments. The analysis of variance for individual environment indicated significant differences among genotypes for all the traits indicating the heritable nature of inheritance of these traits. The crosses EIQ-103 × EI-2156, EIQ-180 × EI-2518-4, and EIQ-103 × EI-670-2 were found to perform well across different environmental conditions for yield and yield-contributing traits. Specifically, the crosses EIQ-103 × EI-2156 and EI-1104-1 × EI-2156 demonstrated stability across various environments, while the crosses EI-2173 × EI-2156 and EIQ-235 × EI-2518-4 were particularly suitable for unfavourable conditions.

Keywords: Baby Corn, Stability Analysis, Eberhart & Russell, G x E Interactions

INTRODUCTION

Maize is one of the most important annual cereal crops, accounting for over 200 million hectares of farmland globally and contributing to approximately 1.2 billion tonnes of global food output in 2023-2024 (FAOSTAT, 2024). Maize breeding programs are designed to select new genotypes that exhibit both high yield potential and broad adaptation (Falconer & Mackay, 1996; Sibiya *et al.,* 2012). The increase in production of baby corn is necessary to meet the demand for vegetables for the burgeoning population of both human and animals (Kumar *et al.,* 2013; Sankar *et al.,*2023). To achieve these goals, newly introduced or developed inbred lines, hybrids, or open-pollinated varieties are evaluated in multi-environment trials (METs). In METs, sets of genotypes are grown across multiple environments to assess both the main effects and the interaction effects between genotype and environment (Mafouasson *et al.,* 2018; Yan & Tinker, 2006). Genotype environment interaction (GEI) is responsible for genotype sustainability. This process allows breeders to determine whether genotype-by-environment interaction (GEI) effects are significant. In METs, grain yield performance of a genotype can vary across different environments, which indicates the presence of high GEI. High GEI can alter the ranking of genotypes in different environments, a phenomenon known as cross-over interaction (Bocianowski *et al.,* 2019b). This

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adds complexity to the selection of superior genotypes for target environments. When GEI is absent, the superior genotype remains consistently the best performer across all environments (Tena *et al.,* 2019). Consequently, GEI presents significant challenges to plant breeders as it complicates the efficient selection and identification of superior cultivars (Mebratu *et al.,* 2019; Ndhlela *et al.,* 2014). Measuring GEI is crucial in optimizing breeding strategies for selecting cultivars that are well adapted to specific environments (Zewdu *et al.,* 2020). Although most GEI studies focus on evaluating maize testcross hybrids, this knowledge is equally important for parental inbred lines. Understanding the grain yield performance of hybrid parental inbred lines across environments is critical, as grain yield directly relates to seed producibility. Inbred lines with high productivity provide a solid foundation for the development of successful commercial hybrids (Worku *et al.,* 2016). Besides identifying high-yielding and stable genotypes across environments, METs also help identify experimental sites that best represent the target environment (Gasura *et al.,* 2015; Makumbi *et al.,* 2015). Therefore, this study aims to investigate the genotype-by-environment interaction (GEI) effects in maize breeding to enhance the selection and development of genotypes with high yield potential and stability across different environments. Specifically, it seeks to understand the grain yield performance of hybrid parental inbred lines, which is crucial for the successful production of commercial hybrids, and to identify experimental sites that best represent target environments for optimized breeding strategies.

MATERIALS AND METHODS

The present study was carried out to collect information on stability performance of hybrids and their parents in baby corn (*Zea mays* L.) over three locations. The trials were taken up during *Kharif*-2019 at Instructional farm, Rajasthan College of Agriculture, Udaipur (E1) and ARSS, Vallabh Nagar, MPUAT, Udaipur (E2) and during *Rabi* 2019-20 at Instructional farm, Rajasthan College of Agriculture, Udaipur (E3).

Geographically Udaipur is situated at 24^0-35' North latitude and longitude 73^0-42' East and at elevation of 582.17 meters above mean sea level. The climatic conditions of the area represent sub-tropical conditions with humid climate. The soil of both the experimental fields was clay loam, deep, well drained, alluvial in origin and fairly good moisture holding capacity.

The experimental material comprised of 15 inbred lines *viz.,* EI-2311-4, EI-2449-2, EI-2403, EIQ-103, EIQ-104, EI-1104-1, EI-561-2, EI-2173, EI-2177-2, EI-2509, EI-2518-2, EI-11-3, EIQ-180, EIQ-225, EIQ-235 and 3 testers EI-670-2, EI-2518-4, EI-2156 their 45 F_{1s} and two checks *viz.,* HM-4 and VL Baby Corn-2. These 45 F_{1s} were obtained by crossing 15 inbred lines and 3 testers in Line × Tester mating design. Pedigree of inbred lines, testers and checks are given in **table 1**. These 65 genotypes were planted in randomized block design with three replications Each treatment was sown in single row plot of 4m length maintaining crop geometry of 60 × 20 cm row to row and plant to plant spacing, respectively. The

Table 1 Details of inbred lines used as parents

S. No.	Symbol / Code	Inbred line	Origin
1.	L_1	EI-2311-4	AICRP on Maize, Udaipur
2.	L_2	EI-2449-2	AICRP on Maize, Udaipur
3.	L_3	EI-2403	AICRP on Maize, Udaipur
4.	L_4	EIQ-103	AICRP on Maize, Udaipur
6.	L_6	EI-1104-1	AICRP on Maize, Udaipur
7.	L_7	EI-561-2	AICRP on Maize, Udaipur
8.	L_8	EI-2173	AICRP on Maize, Udaipur
9.	L_9	EI-2177-2	AICRP on Maize, Udaipur
10.	L_{10}	EI-2509	AICRP on Maize, Udaipur
11.	L_{11}	EI-2518-2	AICRP on Maize, Udaipur
12.	L_{12}	EI-11-3	AICRP on Maize, Udaipur
13.	L_{13}	EIQ-180	AICRP on Maize, Udaipur
14.	L_{14}	EIQ-225	AICRP on Maize, Udaipur
15.	L_{15}	EIQ-235	AICRP on Maize, Udaipur
16.	T_1	EI-670-2	AICRP on Maize, Udaipur
17.	T_2	EI-2518-4	AICRP on Maize, Udaipur
18.	T_3	EI-2156	AICRP on Maize, Udaipur
19.	C_1	HM 4	CCSHAU, Uchani, Karnal
20.	C_2	VL Baby Corn-2	VPKAS- Almora

other recommended agronomical practices were used to raise a healthy crop. The phenotypic stability of genotype for different characters was estimated according to model proposed by Eberhart and Russell (1966).

RESULTS AND DISCUSSION

The stability analysis of 63 genotypes (45 F1 hybrids + 18 parents) was conducted using the Eberhart and Russell (1966) model. This model evaluates stability based on two main parameters: the regression coefficient (bi) of individual variety means on environmental indices, which measures responsiveness, and the deviation from regression (S2di), which assesses stability. A genotype is considered stable if bi is equal to 1.0, indicating that it responds proportionately to environmental changes, and S2di is zero, signifying that the genotype's performance does not deviate from the expected response across different environments. The analysis aimed to identify genotypes with high yield and stability, making them suitable for diverse environmental conditions.

The average interval between the first and last cob picking among the genotypes was 7.43 days, with a population mean of 5.61 days. Although none of the genotypes had a lower mean than the population mean with a bi value of 1.0 and S2di equal to zero, four genotypes—EI-11-3 × EI-2518-4, EIQ-180 × EI-2518-4, EIQ-225 × EI-2156, and EIQ-235 × EI-2518-4—exhibited a lower mean than the population mean, a bi value less than 1.0, and S2di equal to zero. These genotypes demonstrated above-average stability and wider adaptability, making them suitable for unfavorable environments. This result is consistent with previous studies that have highlighted the importance of identifying genotypes with stable performance across environments, particularly in stressful conditions (Eberhart and Russell, 1966; Lata *et al.,* 2010).

The population mean for the number of cobs per plant was 2.66. Two genotypes, EIQ-103EI-670-2 and EIQ-104EI-670-2, had higher means than the population mean (2.86), along with a bi value of 1.0 and S2di of zero, indicating average stability and adaptability to a variety of environmental conditions. This finding aligns with the stability criteria outlined by Finlay and Wilkinson (1963), who emphasized the importance of linear regression coefficients in assessing genotype adaptability. Additionally, three genotypes—EIQ-103EI-2156, EI-2177-2EI-2518-4, and EIQ-235EI-2518-4—exhibited greater stability and adaptability, making them desirable for unfavorable environments. These results underscore the value of identifying genotypes that perform well under suboptimal conditions, a key objective in plant breeding (Eberhart and Russell, 1966; Shahryar Inasab and Chogan, 2015).

The average husked cob weight was 44.69 grams. Twenty-six genotypes demonstrated instability by deviating from zero in the nonlinear component (S2di). However, three crosses—EIQ-103EI-670-2, EI-2518-2EI-2518-4, and EIQ-180EI-2518-4—had a higher mean than the population mean (47.41) with a bi value of 1.0 and S2di of zero, indicating resilience, adaptability, and suitability for a variety of environmental conditions. This finding is consistent with earlier studies that have shown the importance of both linear and nonlinear components in assessing genotype stability (Anley *et al.,* 2013; Matin *et al.,* 2017). Moreover, nine genotypes had a higher mean than the population mean, a bi value greater than 1.0, and S2di of zero, indicating adaptability to favorable conditions. This result highlights the potential of these genotypes to perform well under optimal conditions, a key consideration in crop improvement programs (Eberhart and Russell, 1966; Synrem *et al.,* 2017).

The average de-husked cob weight among the genotypes was 8.49 grams. Two genotypes, EIQ-180EI-670-2 and EIQ-180EI-2518-4, had higher means than the population mean (9.08), with a bi value of 1.0 and S2di of zero, indicating stability and adaptability across various environments. These findings align with previous research that has emphasized the need for genotypes with consistent performance across diverse environments (Sowmya *et al.,* 2018; Mebratu *et al.,* 2019). Additionally, six genotypes had higher means than the population mean, a bi value greater than 1.0, and S2di of zero, indicating their suitability for favourable conditions. These genotypes demonstrate lower-than-average stability but greater adaptability, which is crucial for maximizing yield under optimal conditions (Eberhart and Russell, 1966; Suthamathi and Nallathambi, 2016).

For the length of baby maize cobs, four genotypes—EIQ-103, EIQ-104, EI-1104-1, and EI-2173—had higher means than the population mean, with a bi value greater than 1.0 and S2di of zero. These genotypes demonstrated lower-than-average stability but greater adaptability, making them suitable for favourable environmental conditions. This result is consistent with the findings of Shahryar Inasab and Chogan (2015), who reported similar patterns in other crop species. Additionally, two genotypes, EIQ-180 and EIQ-2518-4, had a higher mean, a bi value less than 1.0, and S2di of zero, indicating superior stability and adaptability to unfavourable environments. These genotypes are ideal for harsh conditions, where stability is critical for maintaining yield (Eberhart and Russell, 1966; Synrem *et al.,* 2017).

The average circumference of baby corn cobs was 4.53 millimeters. The cross EIQ-103EI-2156 exhibited a higher mean than the population mean (4.97), with a bi value of 1.0 and S2di of zero, indicating sufficient stability and adaptability. This finding highlights the importance of stable genotypes for consistent performance across environments (Eberhart and Russell, 1966). Two other genotypes, EIQ-104EI-2156 and EI-2173EI-2156, had higher means, bi values greater than 1.0, and S2di of zero, indicating their adaptability to favorable conditions.

Table 2. Mean, regression coefficient (bi) and deviation from regression coefficient (S^2di) of traits

Genotypes	Days to first & last Cob Picking			No. of Cobs per Plant			Husked Cob Weight			De-Husked Cob Weight			Corn Cob Length		
	Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di
L1	7.4	1.21**	-0.75	2.23	1.88**	0	39.63	1.1*	5.02	7.87	0.89	1**	7.87	0.42	1.14**
L2	7.37	1.24**	-0.5	2.5	1.72**	0	36.67	0.69	2.47	7.1	0.76	0.12	7.43	0.72**	-0.05
L3	8.2	1.74**	-0.19	2.47	1.62**	-0.01	36.87	0.31≠	0.13	7.23	0.52	0.17	7.03	0.74	0.69**
L4	8.23	1.31**	-0.53	2.43	1.85**	-0.01	34.97	0.21	2.89	6.97	0.43**#	-0.07	6.97	0.69	0.8**
L5	5.77	0.57**≠	0.44	2.5	1.42**	0	36.83	-0.37	18.53**	7.33	0.04#	0	7.23	0.43	0.68**
L6	6.5	0.59**#	-0.34	2.5	1.75**	-0.01	41	0.18**#	-1.92	7.93	0.01#	-0.08	7.93	-0.09#	-0.02
L7	6.87	0.5**#	-0.53	2.63	1.52**	-0.01	37.43	-0.65	32.3**	7.17	-0.29	0.98**	7.7	0.83	0.19
L8	7.83	0.89**	0.71	2.53	1.46*	0.05*	39.9	-0.54	30.31**	7.7	-0.6	1.26**	7.93	0.6	2.88**
L9	8.37	1.54**	0.08	2.4	1.78**	0.02	34.53	-0.04	12.26**	7	-0.42#	0.01	6.93	0.91	1.06**
L10	6.37	0.5**#	-0.77	2.6	1.36**	0.02	37.2	-0.44	39.19**	7.37	-0.25	0.54**	7.3	0.56	0.74**
L11	6.7	0.7**#	-0.83	2.5	0.75	0.06**	35	-0.34#	3.78	7.07	-0.54#	-0.07	7.23	0.04#	-0.1
L12	8.47	1.36**	-0.68	2.33	1.55**	0.02	33.9	-0.08	10.65*	6.87	-0.19#	0	7.3	0.68*	0.05
L13	6.6	0.24#	0.78	2.53	1.85**	-0.01	40.2	1.38**	0.39	7.97	1.41**	-0.07	8.07	1.5**	-0.04
L14	6.77	0.93**	-0.65	2.43	1.49**	0	39.73	0.1#	-0.86	7.63	-0.11#	-0.01	7.47	0.8**	-0.05
L15	7.03	1.05**	-0.81	2.57	1.29**	-0.01	46.17	1.12	35.06**	8.6	0.51	0.1	8.43	0.89**	-0.11
T1	7.6	1.19**	-0.18	2.67	0.92**	-0.01	50.83	1.79**	1.6	9.4	1.27**	-0.09	8.67	1.11**	-0.05
T2	7.97	1.29**	-0.47	2.6	1.39**	-0.01	46.53	1.39**	-1.44	8.93	0.98	0.19	8.33	1.39**	-0.12
T3	6.7	0.39≠	1.23	2.63	0.76	0.04*	43.8	1.16	8.84*	8.73	0.83	0.17	8.2	1.26**	0.02
L1×T1	9.63	1.79**	-0.83	2.53	1.49**	0	43.77	2.15**	8.27*	8.23	1.67**	-0.07	8.63	2**	0.33
L1×T2	8.5	1.44**	-0.48	2.77	0.59**≠	-0.01	41.47	1.63**	-0.66	7.63	1.21	1.01**	7.93	1.41	1.16**
L1×T3	7.3	1.27**	0.02	2.6	1.75**	-0.01	46	1.65*	13.71**	8.73	1.73**	0.29*	8.57	1.68**	-0.11
L2×T1	9.17	1.67**	-0.84	2.57	2.31**	-0.01	48.47	1.72**	5.16	9.07	1.73**	-0.08	8.9	1.5**	-0.1
L2×T2	7.7	1.07**	-0.62	2.53	1.58	0.09**	46.8	1.23*	3.86	8.9	1.87**	0.18	8.4	1.72**	0.37*
L2×T3	8.47	1.52**	-0.75	2.5	1.69*	0.06*	46.03	1.42**	-1.32	8.73	1.37**	-0.06	8.73	1.24**	-0.03
L3×T1	6.1	-0.03#	-0.46	2.7	1.75**	-0.01	45.83	0.59**	-0.78	8.6	0.89**	-0.08	8.43	0.85	0.61*
L3×T2	6.23	-0.01#	-0.74	2.67	1.29**	-0.01	49.47	0.6	9.62*	9.13	0.19≠	0	9.17	0.07#	-0.08
L3×T3	8.37	0.83**#	-0.74	2.83	-0.23#	-0.01	45.9	0.15#	0.46	8.67	-0.19#	0	8.87	0.28≠	0.01
L4×T1	8.57	1.39**	-0.12	2.93	0.82**	-0.01	48.03	1.02*	3	9.17	1.36*	0.29*	8.77	1.15*	0.29
L4×T2	8.4	1.1**	-0.37	2.77	-0.13#	-0.01	45.53	0.91*	1.94	8.73	1.02	0.81**	7.67	1.24*	0.41*
L4×T3	8.8	1.37**	-0.78	2.9	0.01#	-0.01	51.9	2.09*	17**	9.7	1.6	0.54**	9.27	1.26*	0.23
L5×T1	7.3	0.72**	-0.22	2.9	1.06**	-0.01	42.33	-0.66	63.59**	8.23	-0.04	3.96**	8.77	0.74	1.65**
L5×T2	6.83	1.3**	-0.69	2.7	0.33#	0	42.63	0.32	71.08**	8.33	0.94	1.84**	9.3	0.83**≠	-0.11
L5×T3	8.23	1.03**	-0.84	2.77	0.23**#	-0.01	47.13	0.83**	-0.47	8.9	0.85	0.84**	9.47	1.39**	-0.06
L6×T1	7.73	1.31**	0.57	2.67	-0.1#	0	50.93	1.42**	-1.19	9.73	1.52**	-0.07	9.8	1.33**	-0.12

Table 2. Conitnued..

Genotypes	Days to first & last Cob Picking			No. of Cobs per Plant			Husked Cob Weight			De-Husked Cob Weight			Corn Cob Length		
	Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di
L6×T2	9.27	1.9**	0.42	2.67	0.89	0.02	49.13	1.6*	11.91**	9.17	1.59*	0.42*	9.1	1.2**	0.13
L6×T3	9.5	1.64**	-0.78	2.8	1.39**	-0.01	48.77	1.74**	0.78	9.1	1.75*	0.52**	9.9	0.77	2.49**
L7×T1	7.93	1.6**	-0.74	2.43	-0.32	0.16**	45.27	0.1	5.3	8.73	0.43	0.07	8.17	1.35*	0.35*
L7×T2	7.13	1**	-0.63	2.77	1.26**	0	48.17	1.14	8.96*	9.17	1.59*	0.42*	8.43	1.72**	-0.09
L7×T3	8.97	0.93*	3.82*	2.83	0.79**	0	44.23	1.36*	5.19	8.1	1.53**	0	8.4	1.42	1.42**
L8×T1	8.17	0.55**#	-0.73	2.77	-0.04	0.12**	49.67	3.34**	-0.91	9.13	2.94**	0.43*	8.9	2.59**	0.8**
L8×T2	6.53	0.69**#	-0.8	2.8	-0.33#	0	45.97	2.34**	2.72	8.67	2.18**	-0.09	8.63	2.05**	0
L8×T3	7.7	0.91**#	-0.86	2.8	0.06	0.07**	45.47	1.5**	1.25	8.87	1.68**	-0.05	9.43	1.57**	0.12
L9×T1	6.13	0.44*#	0.17	2.77	0.92**	-0.01	44.67	1.72**	-0.86	8.5	2.03**	0.15	9.2	1.74**	0.42*
L9×T2	7.33	0.69**#	-0.71	2.87	0.23**#	-0.01	47.23	1.55	77.51**	8.7	1.25	0.83**	9.07	0.68	0.59*
L9×T3	8.67	1.45**	-0.18	2.57	0.26	0.01	47.97	1.39	181.9**	8.97	0.75	2.73**	8.9	0.17#	-0.09
L10×T1	7.63	0.79**	-0.15	2.8	-0.3≠	0.04*	43.2	1.03	6.43*	8.2	0.85*	0.03	8.4	0.74	1.12**
L10×T2	6.97	1.15**	-0.86	2.77	0.23**#	-0.01	43.93	0.97	19.42**	8.13	1	0.72**	8.87	1.02*	0.1
L10×T3	5.63	0.87**	0.8	2.67	0.95**	0	43.2	1.34**	0.43	8.2	1.28*	0.26	8.93	0.83	2.44**
L11×T1	7.57	1.15**	-0.85	2.67	2.31**	-0.01	48.9	1.77**	6.77*	9.17	1.14**	-0.07	9.17	1.31**	-0.01
L11×T2	8.37	1.35**	0.27	2.73	0.49	0.01	48.23	0.85	2.75	9.03	0.45**#	-0.09	9	0.2**#	-0.12
L11×T3	8.27	1.37**	0.41	2.73	1.12*	0.02	47.8	1.23*	3.86	9.17	0.58**≠	-0.07	9.37	0.31	0.07
L12×T1	5.7	0.47**#	-0.52	2.8	0.33#	0	43.67	0.03#	-1.51	8.13	0.61	0.3*	8.37	0.48	2.25**
L12×T2	5.03	0.08#	-0.75	2.7	1.36**	0.02	48.2	1.78**	1.81	8.97	2**	0.09	8.07	1.2**	0.01
L12×T3	8.43	1.27**	0.54	2.67	1.29**	-0.01	50.07	2.88**	0	9.43	2.35**	0.53**	8.93	1.24	0.87**
L13×T1	5.67	0.5**#	-0.53	2.73	1.19**	0	47	0.65	6.92*	9	0.91	0.14	9.13	0.5	0.54*
L13×T2	5.37	0.27#	0.76	2.67	0.92**	-0.01	51.57	0.95**	-0.9	9.4	1.06*	0.16	9.3	0.59**#	-0.1
L13×T3	7.77	1.17**	-0.77	2.73	1.55**	0.02	54.47	1.62**	3.12	9.9	0.97	0.28*	8.97	0.54**#	-0.12
L14×T1	7.17	1.37**	1.8	2.57	2.28**	0.03*	42.63	1.12**	-1.65	8.37	2.04**	0.35*	8.57	1.07	4.07**
L14×T2	6.6	0.9**	-0.1	2.7	2.11**	0	47.47	1.67	33.87**	8.53	1.49**	0.18	8.27	1.09**	-0.06
L14×T3	5.47	0.56**#	-0.85	2.67	1.26**	0	44.23	0.84	4.83	8.6	1.36**	-0.08	9.03	0.92	0.62*
L15×T1	6.4	0.6**#	-0.38	2.83	-0.23#	-0.01	48.3	1.09	13.66**	8.93	1.88**	0.27*	8.77	1.26*	0.23
L15×T2	4.93	0.48**#	-0.86	2.87	0.23**#	-0.01	47.93	1.4*	9.23*	9	1.85*	0.42*	9.07	1.5	0.9**
L15×T3	9.57	1.86**	0.11	2.8	0.03≠	0.01	44.87	-0.07	16.3**	8.27	0.52	0.32*	8.9	0.76**	-0.01
C1	8.38	1.37**	-0.84	2.79	0.56**#	-0.01	48.38	0.86**	0.09	9.22	0.93	0.15	9.5	0.65	0.11
C2	9.55	1.77**	-0.49	2.71	0.76**	-0.01	46.95	1*	3.93	9.11	0.98**	-0.08	8.96	1.16*	0.36*
PM	7.43	-		2.66	-		44.69	-		8.49	-		8.51	-	
SE	0.66	0.14		0.07	0.4		0.98	0.77		0.21	0.71		0.24	0.64	
CD (5%)	1.82			0.2			2.72			0.59			0.68		

Table 2. Continue……

Genotypes	Corn cob girth			Husked cob yield per plant			De-husked cob yield per			De-husked to husked cob yield ratio per plant		
	Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di
L1	3.8	0.48	0.02	90.17	1.32**	134.03*	17.97	1.32	15.97**	0.199	-14.44#	0
L2	3.93	0.99**	-0.05	92.9	1.09**	34.3	18.1	1.15**	1.06	0.195	2.14*	0
L3	3.9	0.63	0.47**	90.67	0.83**#	-31.34	17.93	1.01**	1.97	0.197	-23.6	0*
L4	4.1	0.89	0.55**	85.2	0.92**	-12.72	16.97	1.02**	-1.37	0.199	-7.2	0
L5	3.97	0.57	0.56**	91.63	0.41**#	-19.01	18.37	0.63**#	-1.03	0.2	-16.33	0*
L6	4.33	0.62	0.13	102.77	0.91**	-13.42	19.87	0.87**	0.28	0.193	-1.44	0
L7	4.27	1.05**	-0.05	97.57	0.33	58.38	18.7	0.46	0.8	0.192	-3.87	0
L8	4.27	0.09**#	-0.05	99.33	0.5	329.46**	19.13	0.49	11.12**	0.193	0.31	0
L9	4.13	1.02	0.28*	81.97	0.69**#	-31.14	16.57	0.64**	-0.17	0.203	-17.29≠	0
L10	3.97	0.35**#	-0.04	96.37	0.45	379.23**	19.07	0.6	4.91*	0.199	-17.32≠	0
L11	3.9	0.3	0.13	87.97	0.11#	-5.95	17.77	0.07≠	3.17	0.202	-14.04#	0
L12	3.9	1.08	0.31**	78.5	0.51**#	-32.16	15.87	0.51	0.85	0.202	-15.61#	0
L13	4.17	1.49**	-0.04	102.77	1.44**	11.82	20.33	1.52**	-1.09	0.198	-4.1#	0
L14	4.1	1.33**	0.08	97.13	0.86**	-22.15	18.6	0.78**#	-1.2	0.192	-1.27	0
L15	4.63	1.51	0.43**	119.4	1.32	425.76**	22.07	1*	4.7*	0.188	13.86	0*
T1	4.47	0.72**	0	136.27	1.39**	-24.74	25.07	1.1**	-1.37	0.186	8.02	0*
T2	4.47	1.01**	-0.03	121.57	1.43**	-21.07	23.17	1.2**	0.5	0.192	9.73	0*
T3	4.4	1.22**	-0.05	115.3	0.98	417.78**	22.93	0.87	13.01**	0.201	-4.33	0
L1×T1	4.57	1.49**	-0.04	113.37	1.74**	-32.78	21.27	1.51**	-0.7	0.19	12.63	0*
L1×T2	4.17	0.56*	0.01	116	1.02**	-9.51	21.33	0.71	8.91**	0.185	23.73	0**
L1×T3	4.6	1.15**	0.06	121.83	1.68**	179.07*	23.17	1.68**	3.66	0.19	8.31**	0
L2×T1	5.1	0.81	0.18*	126.9	2.13**	-21.37	23.73	2.1**	-1.31	0.188	11.76**	0
L2×T2	4.63	0.8**	0.02	119.4	1.4	485.88**	22.63	1.62*	15.63**	0.189	4.82	0*
L2×T3	4.9	1.29	0.49**	116.63	1.68**	36.92	22.1	1.68**	0.8	0.19	2.52	0
L3×T1	4.9	0.51	0.11	123.67	1.21**	-34.17	23.3	1.3**	-1.25	0.188	-0.64	0
L3×T2	4.77	0.23**#	-0.05	132.13	1.07*	186.05*	24.4	0.83*	3.08	0.185	7.09	0
L3×T3	4.6	0.41**#	-0.05	130.7	-0.06#	4.48	24.73	-0.24#	-0.11	0.189	-1.27	0
L4×T1	4.97	1.37	0.46**	140.9	1**	18.37	26.93	1.18**	0.79	0.191	1.3	0
L4×T2	4.17	1.42**	-0.02	125.9	0.49**#	-31.73	24.13	0.63**	-0.03	0.191	-11.74	0
L4×T3	5	1**	-0.03	149.9	1.18**	47.9	28.07	0.92**	1.98	0.188	0.25	0
L5×T1	4.73	0.87**#	-0.05	122.03	0.07	342.69**	23.77	0.28	24.97**	0.194	14.08	0
L5×T2	4.67	0.97**	0	116.73	0.2	671.03**	22.83	0.5	22.45**	0.196	-3.4	0
L5×T3	5.07	1.79**	0.05	130.5	0.51**≠	-6.78	24.63	0.4	8.25**	0.189	20.12**	0
L6×T1	5.2	1.62**	0.15*	136.33	0.66**#	-28.94	26	0.68**#	-1.38	0.191	-2.54	0

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Table 2. Continue

Genotypes	Corn cob girth			Husked cob yield per plant			De-husked cob yield per			De-husked to husked cob yield ratio per plant		
	Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di
L6×T2	4.7	1.37**	-0.05	132.47	1.39**	-33.25	24.77	1.42**	-1.35	0.187	2.76	0
L6×T3	4.87	1.01*	0.08	139.03	1.65**	-24.81	25.97	1.69**	2.48	0.186	-7.26	0
L7×T1	4.63	1.06**	0.04	109.73	0.09	174.46*	21.17	0.25	9.04**	0.193	5.28	0
L7×T2	4.57	1.6**	0.22*	132.97	1.31**	-14.83	25.3	1.54**	-0.55	0.189	2.88	0
L7×T3	4.33	1.5**	-0.02	126.37	1.03*	155.93*	23.1	1.12**	3.28	0.182	-0.53	0
L8×T1	4.83	2.16*	0.53**	135.63	1.48**	178.93*	25.03	1.32	14.21**	0.185	-7.62	0
L8×T2	4.7	2.25**	0	128.23	0.95**	30.22	24.17	0.92**	-1.1	0.189	-6.6#	0
L8×T3	4.97	1.45**	-0.05	127.83	0.75	139.45*	24.9	0.79*	2.36	0.195	7.6**	0
L9×T1	4.9	1.81**	-0.04	124.03	1.37**	-34.08	23.6	1.45**	3.97*	0.19	21.87**	0
L9×T2	4.57	0.94*	0.13	136.8	1.13	421.85**	25.2	0.95*	2.61	0.186	17.31*	0
L9×T3	4.63	0.47**#	-0.05	123.7	0.99	1253.7**	23	0.65	21.97**	0.188	16.6	0*
L10×T1	4.53	0.54*≠	-0.01	120	0.25**#	-31.48	22.77	0.18**#	-1.37	0.19	-3.2	0
L10×T2	4.63	0.77	0.1	123	0.51	203.27**	22.83	0.52	7.26*	0.185	2.28**	0
L10×T3	4.57	1.38**	-0.01	116.5	1.18**	33.32	22.17	1.16*	5.01*	0.19	-6.04#	0
L11×T1	4.77	1.08**	-0.03	134.03	2.17**	33.74	24.9	1.87**	-0.81	0.188	10.24	0*
L11×T2	4.5	0.11#	-0.04	131.17	0.71	67.51	24.43	0.47*#	-0.46	0.187	7.8	0
L11×T3	4.6	0.45	0.1	131.07	1.35**	-33.85	24.97	1.03**	-0.05	0.193	11.91	0**
L12×T1	4.3	1.34	0.38**	121.4	0.19**#	-33.13	22.7	0.51**#	-0.53	0.187	-9.65	0**
L12×T2	4.77	1.53**	0.02	131.6	1.67**	-28.06	24.6	1.77**	-1.16	0.186	3.63	0
L12×T3	4.77	1.56**	0.1	136.73	2.12**	-31.84	25.73	1.94**	2.72	0.189	-8.72	0
L13×T1	4.6	0.48	0.01	129.67	0.87**#	-33.86	24.8	0.98**	-1.38	0.191	0.73	0
L13×T2	4.77	0.49**#	-0.05	136.77	1.03**	-13.62	24.97	1.03**	1.86	0.182	9.83**	0
L13×T3	4.83	0.58**#	-0.05	149.17	1.61**	-8.39	27.07	1.26**	-1.01	0.182	4.42	0*
L14×T1	4.17	1.49**	-0.04	110.4	1.68**	44.06	21.97	2.15**	-1.38	0.196	-13.05	0**
L14×T2	4.5	0.82	0.24*	130.03	1.92*	482.04**	23.27	1.72**	5.18*	0.18	14.89*	0
L14×T3	4.43	1.02**	-0.05	117.57	1.07*	100.46*	23	1.37**	-0.18	0.195	-9.22	0*
L15×T1	4.73	0.95**	0.04	137.27	0.51	33	25.4	0.88**	-1.19	0.185	10.09	0**
L15×T2	4.6	0.84	1.21**	137.67	0.7	107.6*	25.73	0.89	6.33*	0.187	6.06	0
L15×T3	4.6	0.33#	0	126.07	-0.11#	9.23	23.17	0.16#	-0.21	0.184	-1.52	0*
C1	4.92	0.74**#	-0.04	135.15	0.76**	-9.64	25.83	0.83**	0.96	0.19	0.33	0
C2	4.65	1.22*	0.26*	127.84	0.93**	38.46	24.79	0.89**	-0.81	0.2	8.25**	0
PM	4.53	-		119.8	-		22.73	-		0.19	-	
SE	0.16	0.44		4.14	0.42		0.83	0.41		0.0041	10.59	
CD (5%)	0.44			11.51			2.31			0.01		

*.** Significant at 5 % and 1%,respectively, ≠,# Significant at 5 % and 1%,respectively when tested against unity.

Twenty of the 63 genotypes exhibited significant deviations from zero in the nonlinear component (S2di), indicating instability. However, the hybrids EIQ-103EI-670-2 and EIQ-180EI-2518-4 had higher means than the population mean (131.31), with bi values of 1.0 and S2di of zero, indicating stability and adaptability across diverse environments. This finding is in line with previous studies that have identified genotypes with high yield potential and stability as crucial for crop improvement (Lata *et al.,* 2010; Anley *et al.,* 2013). Eight other genotypes had higher means than the population mean, with bi values greater than 1.0, indicating their adaptability to favourable conditions.

The average de-husked cob yield per plant was 22.73 grams. Seventeen of the 63 genotypes exhibited significant deviations from zero in the nonlinear component (S2di), indicating instability. Three genotypes—EI-2518-2EI-670-2, EIQ-103EI-2156, and EI-2177-2EI-2518-4—had higher means than the population mean (25.04), with bi values of 1.0 and S2di of zero, indicating average stability, adaptability, and environmental suitability. This result highlights the importance of selecting genotypes that are stable and adaptable across different environments (Eberhart and Russell, 1966; Matin *et al.,* 2017). Additionally, four other genotypes had higher means, bi values greater than 1.0, and S2di of zero, indicating their suitability for favourable conditions.

The average de-husked to husked cob yield ratio per plant was 0.19. None of the 45 hybrids was stable for this trait, but four lines EI-2177-2, EI-2311-41, EI-2311-42, and EI-2156 were stable, with higher mean values than the population mean (0.20), bi values less than 1.0, and S2di of zero. These genotypes exhibited lower-than-average stability, greater adaptability, and suitability for unfavourable environments. This finding underscores the importance of identifying genotypes that can maintain consistent performance under suboptimal conditions (Eberhart and Russell, 1966; Sowmya *et al.,* 2018).

The stability analysis revealed significant genotype × environment interactions for all the characters studied, indicating that environmental factors played a crucial role in determining genotype performance. The significant contributions of the environment linear and genotype × environment linear components to the interaction variance suggest that prediction across environments is possible for these traits. The identification of stable and adaptable genotypes is essential for improving crop yield and resilience, particularly in the face of changing environmental conditions. These findings align with previous research and reinforce the importance of stability analysis in plant breeding programs (Eberhart and Russell, 1966; Lata *et al.,* 2010).

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