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YIELD PERFORMANCE AND STABILITY OF CASTOR (*Ricinus communis* L.) ACROSS MULTIPLE ENVIRONMENTS IN INDIA

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ABSTRACT

Twelve castor genotypes were evaluated across ten environments in India during *kharif* 2022 to assess the genotype performance and to identify the stable and high-yielding genotypes. Genotype plus genotype x environment interaction (GGE) biplot for seed yield were employed to evaluate the genotype × environment interaction (GEI). The polygon view of GGE biplot revealed the "which-won-where" pattern of genotypes across different environments, with 'SHB-1082' and 'SHB-1083' occupying the vertices of the polygon. 'SHB-1083' emerged as the top performer in Bengaluru, while 'SHB-1082' excelled in S.K. Nagar for seed yield ha^{-1}. The genotypes 'ANDCH-1936' and 'SHB-1083', with the shortest vectors from the average environmental coordinates (AEC) line, were identified as highly stable across the test environments, exhibiting higher mean seed yield ha^{-1} as compared to the checks. In contrast, genotypes 'SKI-416' and 'DCS-107', positioned opposite to the AEC arrow, were identified as lower-performing across the environments. Among the genotypes, 'SHB-1082' and 'SHB-1083' stood out for their significantly higher seed yield potential and stability across the test environments, as demonstrated by GGE biplot analysis.

Keywords: AMMI, genotype x environment interaction, GGE-biplot, *Ricinus communis,* stability

INTRODUCTION

Castor (*Ricinus communis* L.) is a non-edible vegetable oilseed crop belonging to the family Euphorbiaceae. It is believed to be originated from the Ethiopian and East African region due to the presence of high genetic diversity (Vavilov, 1951; Moshkin 1986). The crop is mostly grown in tropical, subtropical and temperate parts of the world. Castor seed contains 42-58% oil. This oil has huge industrial importance due to the presence of high amount of ‘ricinoleic acid’ (up to 85%) which has anti-inflammatory effects (Vieira *et al*., 2000; Yamanura and Kumar, 2020b). It is mostly used as an efficient lubricant for high-speed engines and as an ingredient in several by-products *viz*., soaps, shampoos, cosmetics, ointments, etc. (Sadaiah *et al*., 2021). Though India is the largest producer of the crop; China, Brazil, Russia, Thailand, Ethiopia and Philippines also contribute to the global production (Yamanura and Kumar, 2020a). Despite phenomenal gain in productivity of castor over past few years, interestingly different castor growing regions of India exhibits significant variation in productivity. This could be due to several factors, with the main challenge being the absence of high-performing genotypes that can thrive in diverse environments (Kumar *et al*., 2021). To meet the growing demand for castor, the genetic improvement of the crop through development of high-yielding and climate-resilient genotypes is considered one of the most effective strategies (Sujatha *et al*., 2008; Dapke *et al*., 2016; Salihu *et al*., 2017).

Seed yield is an important quantitative trait governed by polygenes. Being a polygenic trait, yield variable changes in the environment due to high levels of genotype-environment interactions (GEI). Thus, identifying a genotype or a cultivar performing stable across the environments is challenging for researchers (Alwala, *et al*., 2010; Moghaddam, *et al*., 2013; Asungre *et al*., 2021). Analysis of genotype by environment data along with genotype main effect (G) plays a crucial role in identifying location-specific cultivars suitable for cultivation (Yan and Tinker, 2006). To address this objective, conducting multi-environment trials in different environments is essential (Alwala, *et al*., 2010). This allows to identify the response of targeted genotypes for changing environmental conditions which enables to identify high yielding and stable genotypes.

Several methods have been developed to understand the genotype environment interaction *viz*., Finlay and Wilkinson (1963), Eberhart and Russel (1966) and Perkins and Jinks (1968) using joint regression method. AMMI (additive main effect and multiplicative interaction) model analysis is considered one of the efficient and frequently used method of estimating GEI and to get the information regarding main and interaction effects including biplot (Annicchiaricom, 1997). However, it does not identify the close relation between high mean performance and stability. This was overcome by GGE biplot analysis (Yan *et al.,* 2000) which included both genotype main effects and GEI effects (Yan *et al.,* 2000). It is based on principal component analysis (PCA) and used graphical display of environmental interaction pattern of multi-environment trial data (Yan *et al*., 2000). The present multi-environment evaluation study was carried out using GGE bi-plot method to identify the stable genotype across diverse castor growing environments of India.

MATERIALS AND METHODS

The experimental material comprised of 12 castor genotypes including 9 hybrids & 3 varieties with pedigree, special attributes and sources as under:

Genotypes	Pedigree	Special attributes	Sources
ANDCH-1936(H)	ANDCP-16-1 x JI-424	Green stem, Triple bloom and spiny capsules in spike	AAU, Sansoli
SHB-1082(H)	SKP-106 x SKI-432	Red stem, Triple bloom and spiny capsules in spike	SDAU, S.K. Nagar
DCS-107(V)	DCH-177 x JI-133	Green stem, double bloom and spiny capsules in spike	ICAR-IIOR, Hyderabad
SKI-416(V)	Geeta x SKI-291	Red stem, double bloom and spiny capsules in spike	SDAU, S.K. Nagar
ICH-5(H)	DPC-25 x ICS-164	Red stem, Triple bloom and semi-spiny capsules in spike	ICAR-IIOR, Hyderabad
ICH-277(H)	DPC-25 x ICS-163	Red stem, Triple bloom and spiny capsules in spike	ICAR-IIOR, Hyderabad
SHB-1083(H)	JP-96 x SKI 291	Red stem, Triple bloom and spiny capsules in spike	SDAU, S.K. Nagar
ICH-66(H)	SKP-84 x ICS-164	Red stem, Triple bloom and semi-spiny capsules in spike	ICAR-IIOR, Hyderabad
JHB-1092(H)	SKP-106 x JI-449	Red stem, Triple bloom and spiny capsules in spike	JAU, Junagadh
SKI-401(V)	SKP-106 x SKI-299	Red stem, Triple bloom and spiny capsules in spike	SDAU, S.K. Nagar
GCH-8(H)	JP-96 x DCS-89	Red stem, Triple bloom and semi-spiny capsules in spike	SDAU, S.K. Nagar
JHB-1121(H)	SKP-84 x JI-473	Red stem, Triple bloom and spiny capsules in spike	JAU, Junagadh

These genotypes were evaluated in a randomized complete block design (RCBD) with three replications across the ten centres of All-India Coordinated Research Project (AICRP) on castor during *kharif* season 2022. The trial was conducted at five rainfed centers namely Bengaluru, Bhavanipatna, Palem, Raichur, and Yethapur and five irrigated centers namely Junagadh, Mandor, Navsari, Ahmedabad, and Sardar Krishi Nagar, representing the major castor-growing regions of the country. The site characteristics of each location is given in Table 1.

Table 1: The site characteristics of each site selected for the present study

S. No.	Parameters	Anand	Bawal	Bhavanipatna	Bengaluru	Junagadh
1.	Agro-ecoregion	Central (Malwa) highlands, Gujarat plains & Kathiawar peninsula, hot semi arid eco-region	Trans Gangetic plain, hot arid region	Eastern Plateau (Chotanagpur), eastern Ghats, hot sub humid eco-region	Eastern Ghats, Tamil Nadu up-lands & Deccan Plateau hot semi-arid ecoregion	Central highlands Gujarat plains and Kathiawar peninsula, semiarid eco-region
2.	Latitude	22°36’N	28°00'N	19°53'N	12°58’N	21°31’N
3.	Longitude	72° 55’E	76° 05'E	83°18'E	770 35E	70o, 33’ East
4.	Altitude (m masl)	45.1	266	262	930	61
5.	Soil taxonomic class	Udic Ustocrepts	Aridisol	Vertisols	Oxichaplustalf (Vijayapura series	Vertisol
6.	Soil texture	Sandy loam	Loamy desert soils	Loamy clay	Sandy loam to sandy clay loam	Clay type
	Sand (%)	86.49	82.0	6.8	52.5	22.5
	Silt (%)	6.25	10.0	33.2	7.4	13.5
	Clay (%)	4.75	8.0	59.1	36.6	63.9
7.	Soil physical parameters					
	Bulk density (g cm^{-1})	1.51	1.48	--	1.54	1.44
	Field capacity (%)	20.00	16.2	--	12-15	42
	Permanent wilting capacity (%)	9.80	8.3	18.1	6.5	19.5
8.	Soil chemical parameters					
	pH	7.8	7.9-8.5	7.1	5-5.5	7.62
	EC (dS m^{-1})	0.28	0.10-0.50	0.1	0.2	0.24
	Organic carbon (%)	0.15 to 0.38	0.17-0.25	0.45	0.4-0.75	0.65
	Av. N (kg ha^{-1})	260	Low	Low	250-275	225.0
	Av. P (kg ha^{-1})	75	Low-medium	Low	6-12	31.1
	Av. K (kg ha^{-1})	195	Medium-high	Medium	160-185	290.0
	Av. Fe (ppm)	4.30	Low-medium	Medium	3.44	10.31
	Av. Cu (ppm)	0.99	Medium-high	Medium	0.30	1.54
	Av. Mn (ppm)	12.07	Medium-high	Medium	20-25	15.06
	Av. Zn (ppm)	0.50	Low-medium	Medium	0.33	0.75
	Av. S (kg ha^{-1})	32.7	Low-medium	--	--	--

Table 1 Continued….

S. No.	Parameters	Mandor	Navsari	Palem	S.K. Nagar	Yethapur
1.	Agro-ecoregion	Western plain Kuchch and part of Kathiawar peninsula, hot arid eco-region	Western *ghats* and Coastal plain, hot humid to per humid eco-region	Deccan plateau (Telangana) and eastern Ghats, hot, semiarid ecoregion	Western plain, Kachchh and part of Kathiawar peninsula, hot arid eco-region	Eastern Ghats and Tamil Nadu uplands and Deccan Plateau, hot semi-arid ecoregion
2.	Latitude	26°15'N	20°57’N	16°35'N	24°19'N	11°35'N
3.	Longitude	73°00'E	72° 54’E	78°10'E	72°19'E	78°29E
4.	Altitude (M)	243	10	642	155	282
5.	Soil taxonomic class	Aridisol	Vertic Ustochrepts	Inceptisol	Typic Udipsamments	Typic Rhodustalf
6.	Soil texture	Loam sand	Clay	Sandy clay	Sandy loam	Sandy loam
	Sand (%)	73.4	12.80	36.2	87.0	--
	Silt (%)	14.8	24.64	35.4	6.0	--
	Clay (%)	8.8	62.56	28.4	6.8	--

7.	Soil physical parameters					
	Bulk density (g cm^{-1})	1.80	1.4	1.72	1.67	1.5
	Field capacity (%)	8.0	32.0	--	11.0	--
	Permanent wilting capacity (%)	3.0	18.0	--	2.35	--
8.	Soil chemical parameters					
	pH	8.2-8.6	7.5-8.3	6.2	7.5-8.5	6.7
	EC (dS m^{-1})	0.4-0.6	0.3-0.6	0.11	0.05-0.15	0.11
	Organic carbon (%)	0.10-0.29	Low to medium	0.15	Low	0.55
	Av. N (kg ha^{-1})	Low	Low	165	Low	218
	Av. P (kg ha^{-1})	Medium	Medium to high	14.4	Medium-high	7.5
	Av. K (kg ha^{-1})	Medium	High	98.3	Medium	680
	Av. Fe (ppm)	0.90	High	2.6	Low-medium	6.8
	Av. Cu (ppm)	0.27	High	2.2	Medium-high	0.8
	Av. Mn (ppm)	5.90	High	6.7	Medium to high	6.0
	Av. Zn (ppm)	0.68	Low to medium	1.6	Low to medium	0.8
	Av. S (kg ha^{-1})	25	Medium	--	Low-medium	Low

Rating chart of major nutrients for soil test data: Organic carbon: low: 0.5%, medium: 0.5-7.5%, high: > 0.75%, Available (Av.) nitrogen (N): low: < 240 kg ha^{-1}, medium: 240- 480 kg ha^{-1}, high: > 480 kg ha^{-1}; Available phosphorus (P): low: <11.0 kg ha^{-1}, medium: 11-22 kg ha^{-1}, high: > 22 kg ha^{-1}; Available potassium (K): low: < 110 kg ha^{-1}, medium: 110-280 kg ha^{-1}, high: > 280 kg ha^{-1}

Each genotype was sown in four 6 m long rows in rainfed condition and 9 m long row in irrigated conditions. The spacing adopted was 90 cm x 60 cm in rainfed situation and 120 cm x 90 cm in irrigated centres. The recommended agronomic and plant protection measures were followed during the entire crop growth period to raise good crop (AICRP Technical programme 2021-22). The data was collected in net plot area of 3.6 x 4.8 m (4 rows) under rainfed conditions and 4.8 x 7.2 m in irrigated conditions by eliminating boarder rows on all sides of the plot for seed yield (kg ha^{-1}). Data were taken according to the distinctiveness, uniformity and stability (DUS) guidelines of castor Protection of Plant Varieties and Farmer's Rights Act (2001), India.

The seed yield and related traits of all the locations were analysed through pooled analysis of variance wherein genotypes were considered as fixed and environments as random factors. The data were graphically analysed for interpreting GE interaction using GGE bi-plot (Yan, 2001). GGE bi-plot methodology, composed of two concepts *viz*., the bi-plot (Gabriel, 1971) and the GGE (Yan *et al*., 2000) models, were used to visually analyse the data. The graphs were generated based on (i) "which-won-where" pattern and (ii) ranking of genotypes on the basis of yield and stability (Yan *et al*., 2000). The statistical analyses were performed using Agricolae Package of R-software (Mendiburu and Yaseen, 2020). The analysis of variance (ANOVA) was used to identify the potential significant differences among the castor genotypes (Panse and Sukhatme, 1984).

The genotype + genotype × environment (GGE) bi-plot serves as a subjective and qualitative method for characterizing patterns of genotype-environment interaction (GEI) and evaluating the relative stability of test genotypes. This combines GGE concepts with the additive main effects and multiplicative interaction (AMMI) bi-plot methodology (Yan *et al*., 2000). The GGE bi-plot is recommended for visually interpreting patterns of GEI, assessing the representativeness and discriminating ability of environments, and gauging the relative stability of test genotypes. To assess GEI, the data from ten locations in a single year were considered, treating each location as a distinct temporal environment. The replication-wise mean seed yield data from these environments were analysed using GGE Bi-plot.

RESULTS AND DISCUSSION

The mean seed yield (Table 2) over locations and location-specific ANOVA demonstrated noteworthy mean squares associated with test genotypes across all the ten environments for seed yield ha^{-1} (Table 3a.b). This suggested substantial variations among the test genotypes in terms of seed yield ha^{-1} justifying their inclusion in the study. The Box-Whisker plots visually represent the range of seed yield ha^{-1} across the ten environments (Fig. 1).

Table 2: Mean seed yield (kg ha^{-1}) of castor genotypes tested at different locations in India during *Kharif,* 2022

Name of genotypes	S.K. Nagar (Gujarat)	Junagadh (Gujarat)	Navsari (Gujarat)	Sagarlaxmi (Gujarat)	Mandor (Rajasthan)	Yethapur (Tamil-nadu)	Palem (Andhra Pradesh)	Bengaluru (Karna-taka)	Bhawani patna (Odisha)	Raichur (Karna-taka)	Genotype mean across the environment
ANDCH-1936	3645	3337	2941	5155	3656	1623	1910	1534	1630	2132	2756
SHB-1082	5502	3182	2547	5392	4201	2087	1278	1440	1551	1786	2897
DCS-107	3539	3452	2817	5975	1869	1201	823	1427	1424	1743	2427
SKI-416	3986	3538	2094	3916	2107	1040	1286	1160	1304	1917	2235
ICH-5	3343	3003	2346	5763	3745	2312	1434	1806	1825	2093	2767
ICH-277	3974	2211	2128	5768	3612	1885	1611	1331	1044	2290	2585
SHB-1083	4116	3443	2514	5536	4023	2023	1338	2109	1746	2440	2929
ICH-66	4258	2745	2296	4225	3726	2120	1384	1405	1879	2502	2654
JHB-1092	4412	3157	2670	5634	2985	1587	1297	1544	1765	2018	2707
SKI-401	3443	3358	2784	4707	3251	1584	1059	1318	1530	1552	2459
GCH-8	4754	3656	2608	4866	4066	2042	1458	1787	1910	2945	3009
JHB-1121	3966	3496	3032	5285	3177	2172	1296	1820	1377	1350	2697
Mean	4078	3215	2565	5185	3368	1806	1348	1557	1582	2064	2677
$CD_{0.05}$	72.63	50.47	34.46	28.16	74.21	72.49	78.54	79.10	51.58	62.38	
SEm.±	213.02	148.04	101.08	82.58	217.65	212.59	230.56	232.00	151.28	182.95	
CV%	10.66	9.40	8.04	3.25	13.19	12.01	17.44	15.21	9.76	9.05	

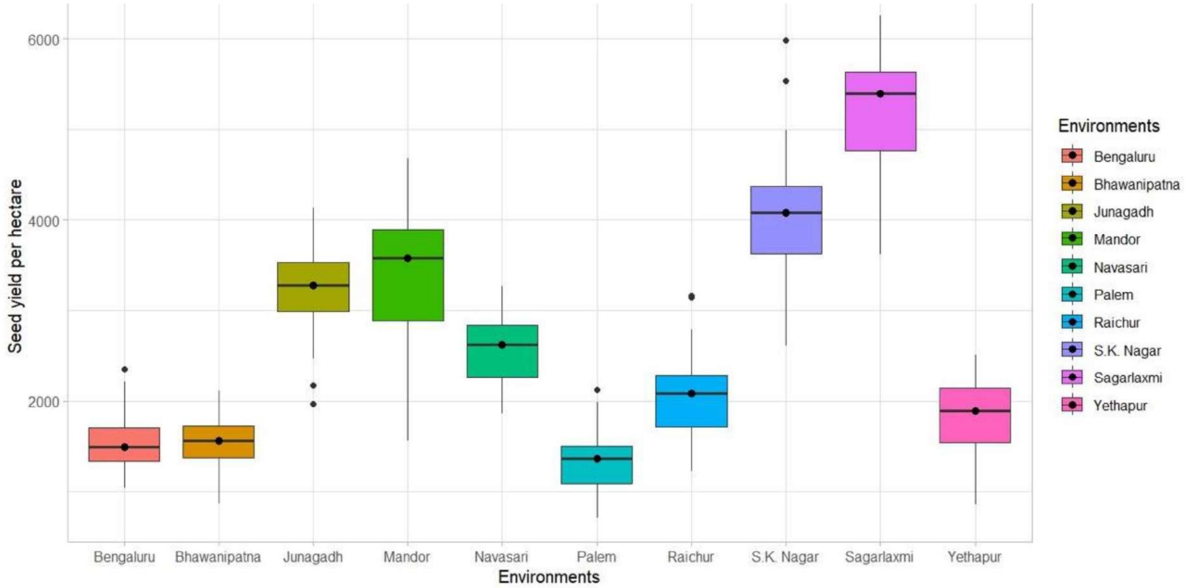


Fig. 1: Box-Whisker plots showing significant differences among various castor genotypes for seed yield ha^{-1}

Assessment of stability based on GGE Bi-plot

Ensuring the stability of test genotypes across temporal environments, as demonstrated in the present study, holds vital significance as it mitigates susceptibility to the unpredictable components of genotype-by-environment interaction (GEI) effects. The stability of test genotypes across ten temporal environments can qualitatively be assessed by visually representing them based on their first two IPCs in a GGE bi-plot (Yan *et al*., 2000). The GGE bi-plot serves as a multivariate analytical tool that visually illustrates the interaction between each genotype and environment, offering a two-dimensional graph for understanding the inter-relationships among environments and test genotypes.

Table 3a: Analysis of variance over locations for different characters (related to raceme) in castor

		DFF		DM		PH		NN		ELPR		NC	
	Df	MSS	F-value	MSS	F-value	MSS	F-value	MSS	F-value	MSS	F-value	MSS	F-value
Environment	9	1907.5**	72.5	4579.8	147.2**	11710.5**	42.16	160.3**	51.35	7297.7**	86.84	17612.1**	59.04
Rep (Env)	20	26.30**	1.89	31.12	1.43**	277.8**	1.97	3.12**	2.33	84.04**	2.59	298.3**	2.66
Genotype	11	60.51**	4.35	86.68	3.98**	2400.9**	17.05	10.24**	7.65	147.66**	4.55	768.7**	6.86
Gen x Env	99	27.89**	2.01	50.84	2.33**	512.2**	3.64	2.71**	2.02	81.91**	2.53	225.7**	2.01
Residual	220	13.89	-	21.78	-	140.8	-	1.33	-	32.43	-	112.1	-
Total	458	58.82	-	125.88	-	589.0	-	5.34	-	201.61	-	529.0	-

Table 3b: Analysis of variance over locations for different characters (growth & yield attributes) in castor

		NEBP		SY		HSW		OC	
	Df	MSS	F-value	MSS	F-value	MSS	F-value	MSS	F-value
Environment	9	565.10**	62.24	57551556**	473.98	172.25**	5.71	1655.83**	357.94
Rep (Env)	20	9.08**	3.55	121422**	1.59	30.17**	3.16	4.62**	1.75
Genotype	11	9.73**	3.80	1506101**	19.67	51.84**	5.43	16.34**	6.20
Gen x Env	99	7.27**	2.84	552119**	7.21	12.03**	1.26	9.66**	3.67
Residual	220	2.56		76568		9.54		2.63	
Total	458	15.59		1447869		15.40		38.57	

Df - Degrees of freedom; DFF = Days to flowering of primary raceme; DM = Days to maturity of primary raceme, PH = Plant height up to primary raceme, NN = No. of nodes up to primary raceme, ELPR = Effective length of primary raceme, NC = No. of capsules on primary raceme, NESP = No. of effective branches plant^{-1}, SY = Seed yield plant^{-1}, HSW = 100-seed weight; OC = Oil content; MSS = Mean square, *Significant at $p \leq 0.05$; **Significant at $p < 0.001$.

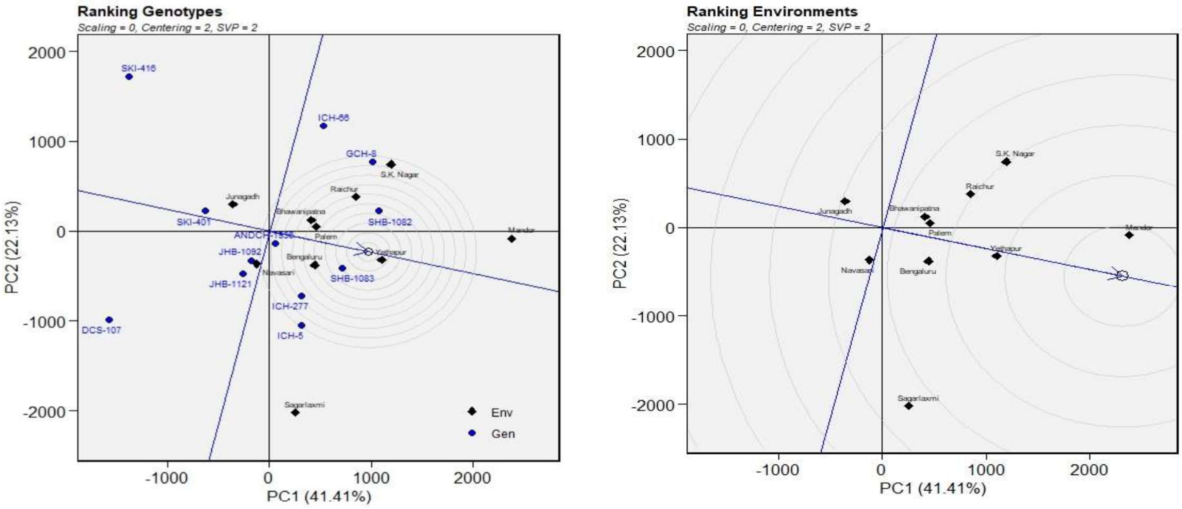
While there are various ways to utilize and interpret GGE bi-plot, four views are particularly relevant (Segherloo *et al*., 2010). (1) Average environment coordination (AEC) view, which employs test-genotype-focused scaling to rank test genotypes relative to the ideal genotype - a point located at the center of concentric circles in bi-plot. (2) Discriminating and representativeness of test environments view. (3) Polygon view, using symmetrical scaling to determine the 'which-won-where' pattern of test genotypes across test environments. (4) AEC view based on environment-focused scaling, offering insights into the mean performance of genotypes versus their stability patterns (Yan and Kang, 2003). The results derived from these four views of the GGE bi-plot provide valuable insights into the performance and stability patterns of test genotypes across the environments, facilitating informed decisions regarding genotype selection and recommendation for specific target environments.

Genotype(s) relative to ideal genotype

In the context of biplot, an ideal genotype is characterized by both high mean performance and high stability across the various test environments. Visualized in biplot, an ideal genotype is positioned precisely at the center of concentric circles, with an arrowed line, known as AEC, passing through it and originating from the origin (Yan and Tinker, 2006). The AEC represents the average environment, denoted by a small circle at the arrow's end. An ideal genotype sits precisely at the center of concentric circles, aligned with AEC, and its vector length equals the longest vector of genotype on the positive side of AEC. To aid visualization, several concentric circles are drawn around the ideal genotype, facilitating easy assessment of the distance between each test genotype and the ideal genotype. Genotypes positioned closer to the ideal genotype are considered stable. In the specific case of study, the test genotypes, 'SHB-1083' and 'SHB-1082', were identified as near-ideal due to their proximity to the ideal genotype, which is situated at the origin of biplot (Fig. 2).

Discriminative ability and representativeness of test environments

The dotted line connecting each test environment to the origin in biplot is termed the environment vector. Assessment of the length of these environment vectors and the angles they form with AEC aids in determining the discriminative ability and representativeness of the test environments. A discriminative environment effectively distinguishes the performance of test genotypes, while a representative environment accurately reflects the average performance of a mega environment among



(a) (b)

Fig. 2: GGE-biplot for the identification of test genotypes relative to ideal genotypes for seed yield [kg ha^{-1}] a) Average environment coordination (AEC) view b) Average environment coordination (AEC) view

others. Shorter environment vectors suggest lower discriminating ability, whereas longer vectors indicate higher discriminating ability of the environments. Additionally, the angle between each environment vector and the AEC signifies the representativeness of the environments. Smaller angles imply greater representativeness while larger angles denote lesser representativeness. The acute and obtuse angles between the environment vectors indicate similarity and dissimilarity between the test environments, respectively. In present study Mandor (Rajasthan) emerges as most discriminative environment due to its longer environment vector compared to others. Conversely, Yethapur (Tamil Nadu) serves as a representative of mega environment, as its vectors are oriented at acute angles relative to the AEC (Fig. 3).

Which-won-where view

The polygon view of GGE biplot serves to reveal the "which won where" pattern of genotypes across different environments. This view entails forming a polygon by connecting all the test genotypes that are farthest from the biplot origin, ensuring that all genotypes fall within the polygon. Perpendicular lines, known as equality lines, originate from the biplot origin and are drawn to each side of polygon. These equality lines partition the biplot into sectors. Each sector's vertex genotype represents the winning genotype for environments whose markers (points) fall within that respective sector (Yan *et al*., 2000). Therefore, environments with markers within the same sector share the same winning genotype, whereas environments in different sectors have different winning genotypes. Consequently, the polygon view of GGE biplot provides insight into the presence or absence of crossover genotype-by-environment interaction (GEI). In present study, test genotypes such as 'SHB-1082' and 'SHB-1083' occupied the vertices of polygon. 'SHB-1083' emerged as the winner in Bengaluru, while 'SHB-1082' was the winner in S.K. Nagar for seed yield ha^{-1} (Fig. 4).

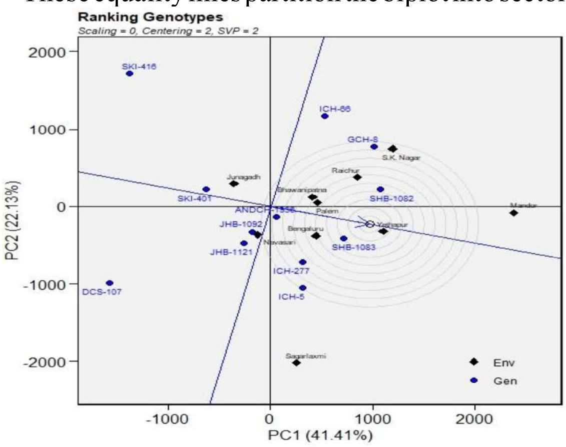


Fig. 3: Discriminative vs. representativeness view of GGE-biplot for seed yield (kg ha^{-1})

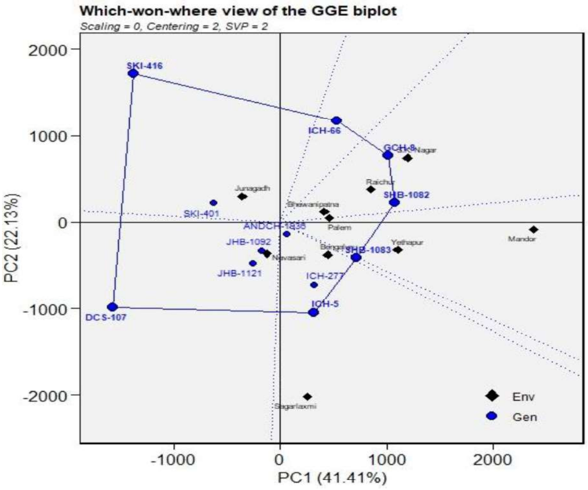


Fig. 4: Polygon view of GGE-biplot based on the symmetrical scaling for "which won-where" pattern of test genotypes and environments for seed yield (kg ha^{-1})

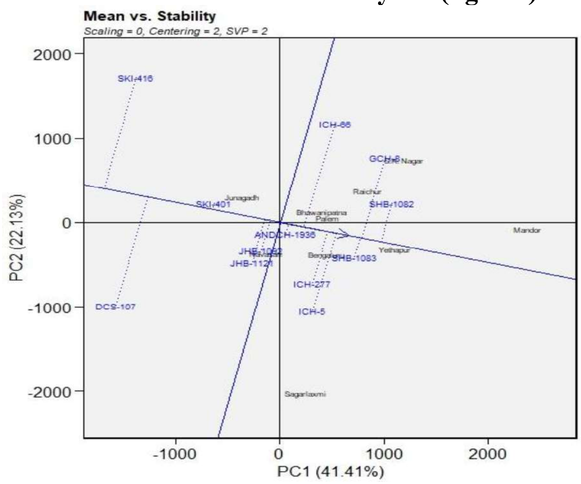


Fig. 5: Average environment coordination (AEC) view of GGE-biplot based on environment-focused scaling for the mean performance vs. stability of test genotypes for seed yield (kg ha^{-1})

Mean performance vs. stability patterns

In AEC view of GGE biplot, the mean performance and stability of genotypes are visually assessed on the basis of their positions relative to the AEC arrow. The single-arrowed AEC indicates the direction of higher mean performance of genotypes across the test environments (Yan, 1999). Genotypes positioned towards AEC arrow are deemed to exhibit high mean performance, while those located opposite to AEC arrow are considered lower performer. Moreover, the relative lengths of projections of genotypes from AEC indicate their stability. Shorter projections from AEC line signify greater stability, whereas longer projections suggest poorer stability (Yan and Kang, 2003). In present study, genotypes 'ANDCH-1936' and 'SHB-1083', with shortest vectors from AEC line, were identified as highly stable across test environments, exhibiting higher mean seed yield ha^{-1}. Conversely, genotypes like 'SKI-416' and 'DCS-107', located opposite to AEC arrow are regarded as lower-performing genotypes across the environments (Fig. 5).

Conclusion: The present study which evaluated superior castor entries from across the country revealed unique interpretations regarding genotype performance and stability. The "which-won-where" view from GGE biplot analysis indicated that entries 'SHB-1083' and 'SHB-1082' were near-ideal across the test locations, while genotypes 'ANDCH-1936' and 'SHB-1083', with shortest vectors from AEC line, were identified as highly stable across the test environments, exhibiting higher mean seed yield ha^{-1}. The results suggest that genotypes 'SHB-1083', 'SHB-1082' and 'GCH-8' were consistently stable and superior yielders across all locations. These findings imply that these hybrids can be further tested and potentially promoted across the castor-growing regions of the country.

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Author contributions: BY - Implemented the experiment and wrote the paper; KS - Executed the experiment, wrote the paper, proof reading; CL - Execution and supervision of the experiment and final proof reading; CS - Data analysis and interpretation; SS - Implemented the experiment, pooling of data from all the centres; RB - Executed the experiment and wrote the paper; AMP, SKM, GER, CJP, GKS, TM, SRV, PA, JMS, AP, AVSD and BS - Implemented the experiment, data collection and reporting to the coordinator.

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