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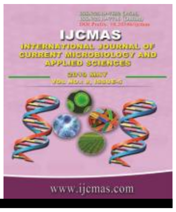

Original Research Article

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Genotype × Environment Interactions and Stability Analysis for Seed Yield and Yield Attributing Characters in Castor (*Ricinus communis* L.)

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ABSTRACT

Twenty six genotypes were evaluated for G × E interaction and stability analysis in three environments *viz.*, Castor-Mustard Research Station, S. D. Agricultural University, Sardarkrushinagar (E_1), Cotton Research Station, S. D. Agricultural University, Talod (E_2) and Agricultural Research Station, S. D. Agricultural University, Kholwada (E_3) (Gujarat, India) during *kharif-rabi* 2016-17. The partitioning of G × E interaction were significant for number of effective branches per plant, 100 seed weight, oil content and leaf area, which indicated that the genotypes under study responded differently to the environments. G × E linear component was significantly higher than its counterpart G × E non-linear component for number of effective branches per plant and leaf area. However, for 100 seed weight and oil content non-linear component was higher than linear component, which made them unpredictable. Among the three environments, higher number of effective branches per plant and leaf area was observed under E_1 location, hence, it was considered as better environment; whereas, less number of effective branches per plant was obtained under E_3 location, hence, it was considered as poor environment and E_2 location was considered as average environment.

Keywords

Stability analysis, G x E interaction, Grain yield, Castor genotype, Over environments

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Introduction

Castor (*Ricinus communis* L. 2n = 2X = 20) is one of the most important non-edible oilseed crop. It belongs to mono specific genus *Ricinus* of *Euphorbiaceae* family (Chaudhari *et al.*, 2019). It has cross pollination up to the extent of 50 per cent due to its *monoecious* nature.

Phenotype is defined as a linear function of Genotype (G), Environment (E) and G × E interaction effects. The study of G × E interaction serves as a guide for various environmental niches. A particular genotype does not exhibit the same phenotypic expression under different environments and different genotypes respond differently to a particular environment. This variation arising from lack of correspondence between the genetic and non-genetic effects is known as genotype × environment interaction. The crop yield is dependent on the genotype, environments and their interaction (Pagi *et* *al.*, 2017a,b). When interaction between genotype and environment is present, ranking of genotype will be different under different environments. The plant breeder always interested in the stability of the performance for the characters which are of economically important. The desirable hybrid should have low genotype × environment interaction for important characters, so as to get desirable performance of hybrids over wild range of environmental conditions. Such hybrids are said to be stable because for their stable performance under changing environments. The presence of G × E interaction is a major problem in getting a reliable estimate of heritability, difficult to predict with a greater accuracy rate of the genetic progress under selection for a given character. Hence, the knowledge of magnitude and nature of G × E interaction is very useful to plant breeders.

The statistical techniques to measure the G × E interaction developed by Finlay and Wilkinson (1963), Eberhart and Russell (1966) and Perkins and Jinks (1968) have been very useful in breeding programmes. In the present investigation, the approach of Eberhart and Russell (1966) was used to understand the G × E interaction and stability of different genotypes.

Materials and Methods

Twenty six genotypes of castor were selected for study. The field experiment was conducted at three different location *viz.*, Castor-Mustard Research Station, S. D. Agricultural University, Sardarkrushinagar (E_1), Cotton Research Station, S. D. Agricultural University, Talod (E_2) and Agricultural Research Station, S. D. Agricultural University, Kholwada (E_3) during *kharif-rabi* 2016-17 with spacing of 120 cm X 60 cm, in RBD with three replications. Standard agronomic practices were followed to raise the crop. The various quantitative traits *viz.*, Days to flowering (primary raceme), Days to maturity (primary raceme), Number of nodes up to the primary raceme, Effective length of primary raceme (cm), Plant height up to primary raceme (cm), Seed yield per plant (g), 100 seed weight (g), Number of capsules on primary raceme, Leaf area (cm^2) and Oil content (%) were included for study. Analysis of variance was performed and stability parameters were conducted following the model proposed by Eberhart and Russell (1966). The type of stability was decided on regression coefficient (b_i) and mean values (Finaly and Wilkinson, 1963).

Results and Discussion

The mean sum of squares due to genotypes was highly significant for all the 11 quantitative characters studied across the environments, which indicated the presence of substantial amount of variation in the material studied. The analysis also indicated significant variation among the environments for all the characters. The values of G × E interaction were significant for number of effective branches per plant, 100 seed weight, oil content and leaf area (Table 1), which indicated that genotypes interacted differently with environmental variations for the said characters. Highly significant values of mean square due to environments (linear) for all the characters indicated that environments differed considerably among different locations. The mean square values due to G × E (linear) and G × E (pooled deviation) were found to be significant for number of effective branches per plant, 100 seed weight, oil content and leaf area.

The stability parameters were worked out and interpreted only for the characters which had significant values of G × E mean square and greater magnitude of G × E (linear) component in respect to pooled deviation *i.e.* G × E (non-linear), thereby only two characters number of effective branches per plant and leaf area were considered for estimation of stability parameters. While, for 100 seed weight and oil content non-linear component (pooled deviation) was higher than linear component, which made genotypes unpredictable and prediction would be biased or less reliable. The stability parameters employed for identification of stable genotype were high or low mean value than population mean, a regression coefficient (b_i) equals to unity and a mean square deviation from regression coefficient statistically equal to zero (S^2di).

The higher number of effective branches per plant is desirable for higher seed yield. The results revealed that total 19 genotypes had non significant deviation from regression coefficient and 10 genotypes had higher number of effective branches per plant than mean, out of these, 18 genotypes were identified (b_i> 1 and significant: nine and b_i< 1 and significant: nine) as well adapted to different environments. Among the genotypes, nine genotypes GCH-2, GCH-7, SHB-1005, SHB-1019, SHB-1029, GNCH-1, GEETA, 48-1 and JI-96 had below average stability (Mean > genotypes mean; b_i> 1 and S^2d_i = 0 NS), thereby specifically adapted to favorable environment; while, nine genotypes GAUCH-1, GCH-4, SHB-1018, VP-1, SKI-352, SKI-370, SKI-372, SKI-373 and DCS-94 had above average stability (Mean > genotypes mean; b_i< 1 and S^2d_i = 0 NS), hence specifically adapted to poor environment (Table 2). Higher leaf area is desirable for higher seed yield. The results revealed that total 22 genotypes had non-significant deviation from regression coefficient and 10 genotypes had higher leaf area than mean. Out of 26 genotypes, nine genotypes were identified (b_i> 1 and significant: seven and b_i< 1 and significant: two) as well adapted to different environments. Among the genotypes, two genotypes GCH-6 and JP-65 had below average stability (Mean > genotypes mean; b_i> 1 and S^2d_i = 0 NS), thereby specifically adapted to favorable environment; while, genotypes GCH-4 had above average stability (Mean > genotypes mean; b_i< 1 and S^2d_i = 0 NS), hence specifically adapted to poor environment (Table 2).

The results partially confirmed the findings of Henry and Daulay (1985), Tank (2000), Patel (2001), Thakker (2002), Solanki and Joshi (2003), Kumari *et al.*,(2003), Chaudhari (2006), Patel and Pathak (2006), Sasidharan (2005), Patel *et al.*, (2010), Patel *et al.*,(2011), Dhedhi *et al.*, (2012) and Patel *et al.*, (2015). However, among the characters under consideration, five characters had higher magnitude of non-linear component (pooled deviation) than its counterpart linear component of G × E interaction; thereby it would not be possible to predict the performance of genotypes for different environments. Further, the significant G × E (linear) component for those characters indicated that the regression coefficients were statically differed and the variation in the performance of genotypes was due to environment induced in genotypes and hence performance of genotypes would be predictable. The results are in agreement with the findings of Henry and Daulay (1985), Thakker (2002), Solanki and Joshi (2003), Chaudhari (2006), Patel and Pathak (2006), Sasidharan (2005) and Patel (2009), Thakker *et al.*, (2010) and Patel (2010). However, pooled deviation variances were significant for number of effective branches per plant, 100 seed weight, oil content and leaf area. The results are also in partial agreement with reports of Patel *et al.*, (1984), Patel (2001), Thakker (2002),Solanki and Joshi (2003), Patel and Pathak (2006), Sasidharan (2005), Patel (2009), Thakker *et al.*, (2010) and Patel (2010).

Table.1 Analysis of variance for phenotypic stability for different characters

Source of variation	**d.f.**	**Days to flowering (primary raceme)**	**Days to maturity (primary raceme)**	**Number of nodes up to primary raceme**	**Seed yield per plant (g)**	**Effective length of primary raceme**	**Number of capsules in primary raceme**	**Number of effective branches per plant**	**100 seed weight**	**Oil content (%)**	**Plant height up to primary raceme (cm)**	**Leaf area (cm^2)**
Genotypes	25	88.81**	123.20**	14.43**	8868.08**	239.95**	947.97**	14.01**	15.83**	3600.70**	10.55**	**51600913.77****
Environments	2	9.16*	11.34**	3.44**	3878.20**	92.57**	239.1**	13.91**	20.73**	406.11*	7.56**	**73942126.65****
G x E	50	1.13	3.58	0.43	54.48	1.67	11.89	0.24**	1.05**	46.85	0.63**	**4493594.59****
Env.+ (Gen. x Env.)	52	1.44*	3.88	0.55	201.54**	5.17*	20.63	0.77**	1.81**	60.67	0.90**	**7164691.98****
Environments (Lin.)	1	18.31*	22.69**	6.87**	7756.39**	185.13**	478.2**	27.82**	41.45**	812.23**	15.13**	**147884253.30****
G x E (Lin.)	25	0.68	3.52	0.42	56.68	1.54	11.98	0.26**	0.61**	21.52	0.42**	**4775684.78****
Pooled Deviation	26	1.52	3.51	0.43	50.27	1.73	11.36	0.23**	1.44**	69.41	0.82**	**4049523.47****
Pooled Error	**150**	**0.97**	**6.39**	**0.70**	**248.33**	**3.38**	**12.78**	**0.11**	**0.26**	**96.50**	**0.27**	**1943771.96**

*, ** Indicate significant at 0.05 and 0.01 levels, respectively.

Table.2 Stability parameters of individual genotypes for number of effective branch per plant and leaf area (cm^2)

Sr. No.	Genotypes	Number of effective branch per plant			Leaf area (cm^2)		
		Mean	b_i	S^2d_i	Mean	b_i	S^2d_i
1	GAUCH-1	5.51	0.69*	-0.104	9306.60	0.67*	**-1625343.548**
2	GCH-2	8.18	1.07*	-0.049	9808.60	0.08	**12290286.129***
3	GCH-4	9.18	0.98*	-0.091	17224.95	0.99*	**-1430140.795**
4	GCH-5	11.82	1.37	0.733*	9668.86	-0.44	**2453512.157**
5	GCH-6	8.87	1.15	0.267	14379.70	2.23*	**-973101.749**
6	GCH-7	14.78	1.36*	0.167	11644.11	0.5	**-786097.617**
7	SHB-1005	10.38	1.66*	-0.004	11606.64	-0.14	**-1110514.754**
8	SHB-1018	9.00	0.92*	-0.099	13432.79	1.37	**7994919.588***
9	SHB-1019	12.22	1.87*	-0.102	11185.60	0.67	**838738.374**
10	SHB-1029	11.12	2.28*	0.062	18167.63	0.52	**14501160.418***
11	GNCH-1	10.44	1.14*	0.157	17221.76	0.56	**1073294.173**
12	VP-1	5.64	0.57*	-0.072	8650.98	0.45	**-1098805.252**
13	GEETA	11.29	1.18*	0.198	17163.74	0.67	**-437091.315**
14	JP-65	7.84	0.55	0.082	13886.30	1.13*	**-1188305.792**
15	SKP-84	8.31	0.75	0.376*	9394.85	0.92	**1989221.447**
16	VI-9	7.53	0.76	1.011*	16702.53	-0.67	**4897793.701**
17	JI-35	8.76	0.29	0.031	8654.87	1.8*	**2026587.796**
18	48-1	11.36	1.59*	0.234	27104.32	2.9	**12073768.38***
19	SH-72	8.47	0.47	0.405*	8974.80	-0.42	**-35226.164**
20	JI-96	8.07	1.19*	0.143	10722.39	0.96	**-69516.695**
21	SKI-215	9.71	0.51	0.351*	12281.03	2.04*	**-820716.022**
22	SKI-352	8.98	0.78*	-0.101	10830.72	1.79	**4626879.936**
23	SKI-370	8.18	0.96*	-0.091	10624.09	1.73*	**-1746194.105**
24	SKI-372	7.49	0.66*	-0.073	11532.73	1.89	**4662457.198**
25	SKI-373	10.73	0.70*	-0.069	13182.15	1.61*	**-1586709.844**
26	DCS-94	5.67	0.55*	-0.05	10112.52	2.18*	**-1771316.295**
General mean		**9.21**	-	-	**12825.59**	-	-
***, ** Indicate significant at 0.05 and 0.01 levels, respectively.**							

In conclusion, for number of effective branches per plant, genotypes GCH-2, GCH-7, SHB-1005, SHB-1019, SHB-1029, GNCH-1, GEETA, 48-1and JI-96 had below average stability (b_i> 1) and specifically adapted to favourable environment. Among genotypes, GAUCH-1, GCH-4, SHB-1018, VP-1, SKI-352, SKI-370, SKI-372, SKI-373 and DCS-94 had above average stability (b_i< 1) and well adapted to unfavorable environment. Genotypes, GCH-6, JP-65, JI-35, SKI-215, SKI-370, SKI-373 and DCS-94 had below average stability for leaf area (b_i> 1) and specifically adapted to favourable environment. Among genotypes, GAUCH-1 and GCH-4 had above average stability (b_i< 1) and well adapted to unfavorable environment for leaf area.

Out of the three environments, higher number of effective branches per plant and leaf area was observed under E_1 location, hence it was considered as better environment; whereas, less number of effective branches per plant was obtained under E_3 location hence, it was considered as poor environment and E_2 location was considered as average environment.

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