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LINE × TESTER ANALYSIS FOR SEED YIELD AND ITS COMPONENTS IN CASTOR (*RICINUS COMMUNIS* L.)

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ABSTRACT

A line × tester set was obtained by crossing 3 females (100% pistillate lines) with 20 diverse males in castor. Sixty F_1 along with their parents were evaluated for 10 quantitative characters under north Gujarat conditions. Additive genetic variance predominantly governed the expression of days to flowering, days to maturity, total and effective branches, and 100-seed weight, whereas nonadditive genetic variance chiefly controlled the inheritance of seed yield, plant height, nodes up to primary spike, length of primary spike, and number of capsules on primary spike. Variety VP 1 was a superior female parent for seed yield, total and effective branches, and 100-seed weight. Varieties VH 28/2, JI 16, and JI 21 were good general combiners for seed yield and several yield components, whereas EC 103745 and 1379 were good combiners for earliness and dwarfness. Crosses CNES 1 × VH 28/2, CNES 1 × 201, JP 58 × GAUCH 1, JP 58 × 2-73-11, JP 58 × JI 16, and VP 1 × EC 103745 exhibited desirable sca effects and can be exploited by further breeding for developing superior genotypes in castor.

Key words: *Ricinus communis*, castor, line × tester, combining ability.

The availability of 100% pistillate lines has helped in developing and release of superior castor hybrids, viz. GCH 3, GAUCH 1 and GCH 2, for general cultivation in Gujarat. For improving the yield potential of varieties and hybrids, the decision should be made about the choice of the right type of parents for hybridization. Combining ability analysis is frequently employed to identify the desirable parents and to study the nature of genetic variation. Out of several methods, line × tester analysis helps in testing of large number of varieties besides being more comprehensive for understanding the genetical basis at population level. The present study, therefore, aims to analyse the combining ability through line × tester analysis involving 3 females and 20 diverse males of castor (*Ricinus communis* L.).

MATERIALS AND METHODS

The experimental material comprised 60 F_1 hybrids, derived by crossing 20 diverse males with 3 females (100% pistillate lines), and all the 23 parents. The

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experiment was laid out in randomized block design with three replications at the Experiment Station, Gujarat Agricultural University, Vijapur. Each entry was represented by a single row of 9.0 m length with 90 × 60 cm spacing. Five competitive plants/plot were randomly taken for observations of 10 quantitative traits (Table 1). The mean values were analysed statistically. The combining ability analysis was done following Kempthorne [1].

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences for all the characters among the entries evaluated (Table 1). The mean squares due to parents also differed significantly, indicating great deal of diversity among them. Highly significant differences were also observed for the variance component, viz. parents vs crosses for all the characters, except length of primary spike. This showed expression of heterosis for these characters. Significant mean squares for all the characters, except effective branch number due to males; all but days to maturity and nodes up to primary spike due to crosses; and for seed yield, total and effective branch number, length of primary spike, capsules on primary spike, and 100-seed weight due to females revealed wide range of variability for these characters. Mean squares due to males × females interaction were significant only for length of primary spike, capsules on primary spike, and 100-seed weight (Table 1).

The analysis of combining ability indicates the preponderance of nonadditive gene action for seed yield, plant height, nodes up to primary spike and length of primary spike, whereas additive gene action was predominant for days to flowering, days to maturity, total and effective branches, and 100-seed weight (Table 1). The

Table 1. ANOVA for line × tester analysis in castor

Source	d.f.	Mean sum of squares									
		seed yield per plant	plant height	days to flowering	days to maturity	total branches	effective branches	nodes to primary spike	length of primary spike	capsules per spike	100-seed weight
Replications	2	20593.1**	843.9**	2581.5**	383.7	4.4*	2.4	0.4	108.8	30.2	19.7
Treatments	82	5458.6**	768.5**	267.9**	1245.4**	8.1**	6.9**	14.5**	196.9**	326.5**	52.7**
Parents	22	11210.9**	1754.9**	469.2**	3452.4**	11.1**	10.7**	36.0**	369.7**	565.6**	119.6**
Parent vs crosses	1	77274.6**	3064.7**	1332.3**	4038.9**	94.9**	70.5**	60.7**	138.3	354.2**	65.9**
Crosses	59	2096.5**	361.7**	174.8**	375.1	3.9**	4.4**	5.8	150.4**	236.9**	27.5**
Lines (females)	2	8951.9**	70.3	80.3	361.1	57.5**	67.1**	0.3	263.5**	891.0**	240.1**
Tester (males)	19	3765.4**	874.5**	315.3**	627.1**	3.9**	2.9	8.9*	244.5**	453.7**	33.7**
Lines × testers	38	1401.3	120.7	109.6	249.9	1.1	1.9	4.5	71.1*	94.0*	13.3*
Error	164	1039.6	90.5	107.2	499.3	1.4	1.4	4.3	43.8	63.6	8.3
σ^2 gca		82.62	5.86	1.47	4.07	0.49	0.552	0.003	3.047	9.639	2.060
σ^2 sca		120.55	10.063	0.8047	−83.11	−0.0847	0.1513	0.055	9.114	10.155	1.6687
σ^2sca/σ^2 gca		1.459	1.72	0.55	—	—	0.274	18.333	2.991	1.054	0.810

*P = 0.05; ** P = 0.01.

data revealed that both additive and nonadditive genetic variances were of equal importance for capsules on main spike. The results further revealed that appreciable additive genetic variance was also present for seed yield, plant height, and length of primary spike, whereas nonadditive genetic variance was also observed for days to flowering and 100-seed weight, suggesting the importance of both additive and nonadditive gene actions for the inheritance of these traits. Our observations indicating the importance of both additive and nonadditive gene actions for seed yield and its components and predominance of nonadditive gene action for seed yield are in agreement with earlier reports [2–4]. The results of Patel et al. [5] were similar to the present findings for days to flower and plant height, but not for days to maturity, although only nonadditive gene action for yield and yield components in castor has also been reported to be more important [6].

The estimates of combining ability effects indicated that VP 1 was the most desirable female which contributed significant positive gca effect for seed yield, total and effective branches, and 100-seed weight (Table 2). It should be utilized in evolving highly productive hybrids. This observation is further substantiated by the fact that this female line has already been used in the development and release of two most productive hybrids, viz. GAUCH 1 and GCH-2, in Gujarat. CNES 1, on the other hand, showed its superiority for capsules on primary spike, 100-seed weight, and early maturity. Among male parents, VH 28/2, JI 21 and JI 16 were superior general combiners for seed yield. Besides, VH 28/2 for plant height, total and effective branches, and 100-seed weight; JI 16 and JI 21 for length of primary spike, and capsules on primary spike; 6-219-22 for plant height and capsules on primary spike; HC 1 for plant height and 100-seed weight; and GAUCH 1 for length of primary spike also showed significant desirable gca effects. VI 14, VH 66,2/4, 201, EC 103745, EC 97706, 38534, 1-4-13, and 1379 had significant negative gca effects for plant height, suggesting that these lines are good combiners as a source of genes for dwarfness.

Since early maturity and low node number up to primary spike are desirable traits, parents with negative gca effects should be preferred for these characters. It was observed that EC 103745 and 1379 were the best parents for these traits (Table 2), since they gave highly significant negative gca effects for days to flowering, days to maturity, and nodes up to primary spike. This observation further emphasizes the need for selection of genotypes forming spikes at lower nodes to evolve early maturing hybrids/varieties in castor.

The per se performance of the parents and their gca effects were generally in close correspondence, which indicated that per se performance of the parents could possibly be taken as a criterion for selection of parents. This conclusion is also supported by earlier reports [5, 6].

The line × tester component of variance of crosses was significant only for three characters, viz. length of primary spike, number of capsules/spike, and 100-seed weight (Table 1). Accordingly, the sca effects for these characters are presented and discussed here. Crosses VP 1 × EC 103745, VP 1 × 961, VP 1 × VI 14, JP 58 × EC 97706, and CNES 1 × VH 64 for length of primary spike; VP 1 ×

Table 2. General combining ability effects of the parents for different characters in castor

Parents	Seed yield per plant	Plant height	Days to flowering	Days to maturity	Total branches	Effective branches	Nodes to primary spike	Length of primary spike	Capsules per primary spike	100-seed weight
Females:										
VP-1	12.9*	0.8	-1.2	2.1	1.09**	1.1**	-0.06	-2.4**	-4.4**	-1.2**
CNES-	-1.6	-1.2	1.1	-2.7	-0.79	-1.0	0.07	1.3	2.8**	1.1**
JP-58	-11.4**	0.4	0.03	0.6	0.31**	0.2	-0.02	1.1	1.6	-2.3**
SE ±	5.1	1.2	1.3	2.9	0.15	0.2	0.27	0.9	1.0	0.4
Males:										
GAUCH-1	11.6	5.2	-6.2	-2.9	-2.23**	-0.1	0.05	4.5*	4.8	-1.4
VH-28/2	35.2**	8.5**	-1.8	-1.0	1.67	1.5**	-0.69	2.6	-1.7	2.9**
VI-3-2	1.7	3.9	-2.7	-4.0	-0.73	-0.6	-0.36	7.5**	4.3	-0.8
VI-14	-6.0	-11.0**	-4.6	-4.2	0.37	0.2	-0.37	-3.9	-2.6	-1.4
VH-64	6.8	2.0	6.8*	8.1	0.14	-0.2	0.44	2.3	4.9	0.4
VH-66, 2/4	-18.7	-6.6*	-4.9	-7.1	-0.68	-0.3	-0.68	2.4	4.1	-3.4**
JI-16	27.7*	16.1**	8.7*	11.2	0.01	-0.1	0.54	7.6**	11.0**	0.5
JI-21	33.0*	16.1**	3.6	10.5	0.07	-0.5	0.71	8.2**	8.1**	-1.9*
6-219-22	15.7	8.5**	1.1	7.8	0.67	0.6	0.40	3.4	7.0**	0.4
201	-21.0	-4.6	2.5	1.1	-1.05**	-0.8*	-0.36	-1.2	-1.9	2.0*
EC 103745	-29.2*	-11.4**	-10.1**	-17.1*	-1.03**	-0.8*	-2.07**	-9.7**	-14.9**	1.7
HC-1	14.2	7.1*	7.0*	3.0	-3.39**	0.3	0.25	-2.1	-3.0	-3.4**
EC-97706	-8.4	-12.4**	-3.1	-1.7	0.37	0.3	0.96	-0.01	-9.6**	0.2
38534	-8.8	-15.1**	4.6	-09.3	-0.25	0.1	2.62**	-3.1	-1.2	1.6
EB-16	-22.8	0.9	7.6*	1.2	-0.05	-0.4	0.24	-0.8	-6.7*	1.5
2-73-11	12.4	5.4	2.6	8.4	0.74	0.5	0.48	2.0	8.4**	2.3*
1-4-13	-27.2*	-7.4*	-0.3	-0.1	-0.43	0.1	-0.49	-6.4**	-5.2	2.1*
827	11.9	5.8	-1.2	2.2	0.06	0.6	0.02	1.6	-0.4	1.8
1379	-29.0*	-15.1**	-13.0**	-16.9*	-0.68	-0.6	-1.95**	-11.9**	-12.4**	-2.4*
961	1.0	4.9	3.9	10.8	0.34	0.3	0.20	-0.8	3.3	-0.3
SE ±	13.1	3.2	3.5	7.5	0.39	0.4	0.69	2.2	2.7	1.0
SE (gi-gj) lines	7.2	1.7	1.9	4.1	0.22	0.2	0.38	1.2	1.5	0.5
SE (gi-gj) testers	18.5	4.5	4.9	10.5	0.56	0.6	0.98	3.1	3.8	1.0

*P = 0.05; **P = 0.01.

2-73-11, VP 1 × EC 103745, CNES 1 × 961, CNES 1 × 38534, and CNES 1 × EB 16 for capsules on primary spike; and VP 1 × EC 103745, CNES 1 × 2-73-11, CNES 1 × VI 14, and JP 58 × VI 3-2 for 100-seed weight exhibited desirable superior sca effects. It is evident that crosses involving at least one high general combiner exhibited high sca effects, indicating that additive × dominance type of interaction was involved. However, few crosses between low × low general combiners produced higher sca effects, suggesting epistatic gene action which may be due to genetic diversity in the form of heterozygous loci. These crosses would be utilized for the improvement of the above three characters through single plant selections as they seem to have good potential to produce transgressive segregants for these characters.

The best crosses selected on the basis of sca effects and per se performance were the same as for 100-seed weight, suggesting a close relationship between yield potential and seed size.

The study, in general, indicated that in view of the preponderance of nonadditive gene action for seed yield and some important yield components, commercial exploitation of hybrid vigour is the most appropriate method for utilizing such gene action. But for overall improvement, random mating among several elite lines, viz. VH 28/2, JI 16, JI 21, for seed yield and length of primary spike; EC 103745 and 1379 for earliness; and 6-219-22 and 2-73-11 for capsules on main spike and 100-seed weight, should be done to incorporate desirable genes at a time using genetic male sterility and reciprocal recurrent selections, as described by Doggett [7] in sorghum to exploit both types of gene action.

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