Genetic analysis for quantitative characters in cardamom (Elettaria cardamomum Maton)

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Genetic analysis for quantitative characters in cardamom (*Elettaria cardamomum* Maton)

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Cardamom (*Elettaria cardamomum* Maton) popularly called "Queen of Spices", is a perennial rhizomatous crop belonging to the family Zingiberaceae. The average productivity of cardamom is low in India compared to other countries, mainly due to non-availability of disease tolerant high yielding varieties. In India, cardamom is susceptible to disease such as cardamom mosaic disease (*katte*) and rhizome rot. Cardamom mosaic disease, which is caused by a virus, causes severe yield losses (up to 68 %) to cardamom [1]. Resistant sources to the above diseases were identified by collecting disease escapes from hotspots [2]. So there is a need to exploit the heterosis in cardamom to develop high yielding hybrids by combining disease resistant and high yielding lines. Practically very little information on combining ability is available in cardamom. Hence, an attempt was made to study the estimates of combining abilities in cardamom by using var. CCS-1 (high yielding), RR-1 (rhizome rot tolerant) and NKE-3, NKE-9, NKE-12, NKE-19, NKE-27 and NKE-34 (*Katte* resistant) to make crosses in all possible combinations in June-Sep 1997. Fifty six F_1 hybrids along with parents were planted at 1.8 × 1.8 m spacing in a randomised block design with three replications during 1998. Standard management practices were adopted to ensure good crop growth. Observations were recorded on 10 randomly selected plants in each replication during 1999-2000 cropping season on plant height, total tillers, bearing tillers, number of capsules per plant and yield per plant. The combining ability estimates were calculated according to model suggested by Griffing [3] and model I (fixed effects) from which the additive and dominance components of genetic variances were also estimated.

Analysis of variance for combining ability effects (Table 1) of different characters showed that general (gca) as well as specific combining ability (sca) were highly significant for all the characters indicating that both additive and non additive (dominance) gene action played important role in the expression of all the characters.

As the positive gca effects can be utilized for improvement of the character concerned, NKE-19 was found to be the best general combiner for total tillers (2.74**) and bearing tillers per plant (1.50**). For yield per plant NKE-9 (35.20**) NKE-12 (45.60**), NKE-34 (44.77**) and CCS-1 (58.87**) were found to be good general combiners.

Table 1. Analysis of variance for combining ability for different characters

Source of Variation	df	Plant height	Total tillers	Bearing tillers	No of capsules per plant	Yield per plant
gca	7	351.26**	38.50**	7.48**	110541.37**	72774.09**
sca	28	384.26**	19.5 1**	4.62**	115879.36**	67215.88**
Error	126	118.36**	10.47**	2.64**	5288.12**	799.67**

*Significant at 5% level and ** significant at 1% level

The estimates of specific combining ability for top three crosses are presented in Table 2. Total number

Table 2. Top three crosses selected on the basis of sca effects and *per se* performance

Character	Significant crosses	sca effects	Mean
Plant height (cm)	NKE-3 × RR-1	31.45**	167.0
	RR-1 × NKE-12	29.13**	169.0
	NKE-12 × NKE-27	20.37**	189.0
Total tillers	NKE-9 × NKE-3	7.93**	28.5
	NKE-19 × NKE-12	6.73**	28.5
	RR-1 × NKE-12	6.10**	23.5
Bearing tillers	NKE-19 × NKE-12	4.33**	15.8
	CCS-1 × NKE-34	3.06**	14.3
	NKE-12 × NKE-27	2.46**	10.6
No. of capsules	RR-1 × NKE-12	571.17**	1205.3
	NKE-9 × NKE-3	471.33**	958.7
	NKE-12 × NKE-27	433.04**	1105.0
Yield/plant (g)	NKE-34 × NKE-12	541.17**	1100.7
	RR-1 × NKE-12	394.33**	819.3
	NKE-34 × RR-1	379.92**	985.0

of crosses showing significant positive sca for plant height was 6. NKE-3 × RR-1 was observed as the best specific combiner, derived from poor x poor general combiners, followed by RR-1 × NKE-12 and NKE-12 × NKE-27 which were the products of poor x poor and poor x good general combiners.

Crosses showing significant sca for total tillers were 14 amongst which four combinations were in positive direction. NKE-9 × NKE-3 was the best general combiner followed by NKE-19 × NKE-12, RR-1 × NKE-12, which was the products of good x poor, poor x poor and poor x poor general combiners respectively. As for as bearing tillers concerned, NKE-19 × NKE-12, CCS-1 × NKE-34, NKE-12 × NKE-27 and NKE-27 × NKE-12 had good specific cross effects. These combinations involved good x poor and poor x poor combiners indicating the involvement of dominance and complimentary epistasis. For number of capsules per plant, RR-1 × NKE-3, NKE-9 × NKE-3 and NKE-12 × NKE-27 had the highest specific combing ability. These crosses involved poor x poor combing parents showing role of complimentary gene action. Among 54 cross combinations, high sca values coupled with good *per se* performance in respect of yield per plant were observed in NKE-34 × NKE-12, RR-1 × NKE-12 and NKE-34 × RR-1. The three good specific combiners for yield were the product of good x poor, moderate x poor and good x moderate general combiners showing role of dominance and additive gene action.

The genetic parameters calculated after Griffing [3] model 1 are presented in Table 3. Since the mean sum of square due to gca and sca do not provide clear picture regarding the relative magnitude of additive and non-additive components, the unbiased estimates

Table 3. Estimates of genetic parameters for five quantitative characters in cardamom

Character	$\sigma^2 g$	$\sigma^2 s$	$\sigma^2 e$	$\sigma^2 A$	$\sigma^2 D$	$\sqrt{D/A}$
Plant height	23.72	148.91	118.36	47.44	148.91	1.77
Total tillers	1.20	5.06	10.47	2.40	5.06	1.45
Bearing tillers	0.18	1.08	2.65	0.36	1.08	1.73
No. of capsules/ plant	212.38	62086.31	5288.12	424.60	62086.31	3.92
Yield/plant	420.31	37192.00	46786.50	840.62	37192.00	6.6

of components of variances due to gca $(\sigma^2 g)$ and sca $(\sigma^2 s)$ are very important. The characters to have high $\sigma^2 s$ than $\sigma^2 g$ indicating preponderant role of non-additive gene action for their expression. The magnitude of non-additive $(\sigma^2 D)$ gene action was invariably larger than the additive component $(\sigma^2 A)$ for all the five traits. Average degree of dominance, which was found to be more than one for these characters, confirmed the results of the above findings and also suggested that dominance or over dominance influenced the manifestation of these characters

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