Genetic Variability in Cardamom (*Elettaria cardamomum* Maton.)

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Small cardamom (*Elettaria cardamomum* Maton.), popularly called "Queen of Spices", is an important export oriented spice crop. India has a rich wealth of genetic resources of cardamom as the crop originated in the tropical forests of Western Ghats. Cardamom being cross-pollinated crop, abundant diversity exists in the population which can be exploited both for commercial and scientific interest. Assessment of variability for the yield and its components becomes absolutely essential before planning for an appropriate breeding strategy for genetic improvement. Parameters such as genotypic and phenotypic coefficient of variability are useful in detecting the amount of variability present in the germplasm. Heritability and genetic advance help in determining the influence of environment on the expression of genotype and the reliability of characters. Hence, present investigation was undertaken to quantify the available variability in small cardamom (*Elettaria cardamomum* Maton.) based on nine quantitative characters, to identify desirable genotypes based on performance, and to select promising donors for various characters which may be used in hybridization programme to obtain useful recombinants and to create genetic variability.

The study was conducted at Indian Institute of Spices Research, Cardamom Research Centre, Appangala, Madikeri, Kodagu (Dt.), Karnataka, which is located in heavy rainfall region (2500-3500 mm/annum) at an elevation of 1000 MSL. The experimental material comprised 119 Malabar (prostrate panicle types) accessions spaced at 2m x 2m between the rows and plants. The accessions, represented collections and distinct morphotypes from cardamom growing tracts such as Waynad, Anamalais, Manjoli Hills, Nelliampathy, Lower Pulneys, Meghamalai and Cardamom Hills. Uniform suckers were planted during 1997 and the observations were recorded during 1999-2000 crop season on plant height, total tillers, bearing tillers, panicle length, number of nodes/panicle, internodal length, number of capsules/plant and yield/plant as recommended in IPGRI descriptor 1994. The mean value obtained were used for determining phenotypic coefficient variation (PCV) and genotypic coefficient of variation (GCV) (Comstock and Robinson, 1952), heritability (Allard, 1960) and expected genetic advance (Johnson *et al.* 1955).

The analysis of variance (ANOVA) for nine characters indicated that there is a considerable variation in respect to all the characters studied. However, absolute variability in different characters cannot be the criteria for deciding, as to which character is showing the highest degree of variability. For this, computation of phenotypic variance (Vp), genotypic variances (Vg) and coefficient of variation was done. Table 1 shows that maximum variation in Malabar type was exhibited by number of capsules/plant followed by yield/plant and number of panicles both at genotypic and phenotypic levels. Similar observations were recorded by Gopal *et al.* 1995. The

Table 1. Genotypic, phenotypic variances, coefficient of variation, heritability and genetic advance for various characters

Character	V_p	V_g	PCV %	GCV %	Heritabilty % (Broad sense)	Genetic Advance	GA (% of mean)
Plant height	0.22	0.13	27.92	21.46	59.09	0.57	0.01
Total tillers	203.17	132.58	52.25	41.40	65.26	19.16	5.32
Bearing tillers	32.42	18.63	71.18	53.95	57.46	6.69	0.53
Number of panicles	1586.64	955.67	94.95	73.69	60.23	49.23	20.65
Panicle length	298.16	214.14	49.36	41.83	71.82	25.55	8.93
No. of nodes/panicle	49.96	35.00	43.05	36.03	70.06	10.19	1.67
Internodal length	3.52	0.99	62.30	33.06	28.13	1.08	0.03
No. of capsules/plant	89526.79	66622.56	138.86	119.78	74.42	458.57	222.10
Yield/plant	68606.87	52297.75	148.77	129.89	76.23	411.32	233.62

variance was very low for characters like plant height and internodal length.

In the present study (Table 1), GCV was less compared to that of PCV for all the characters indicating a considerable influence of the environment on their expression. The GCV, which exhibits the extent of genetic variability in the population, ranged from 21.46 (plant height) to 129.89 (yield/plant). The GCV values were considerably high for characters such as yield/plant, number of capsules/plant and number of panicles. The above mentioned characters having higher range of variation have a better scope for improvement through selection.

Characters such as plant height, panicle length and number of nodes/panicles had nearly equal PCV and GCV values indicating least influence of the environment on their expression. In such a situation, selection can be effective on the basis of the phenotype alone with equal probability of success.

On the basis of GCV alone, it is not possible to determine the amount of heritable variation. It can be found out with greater degree of accuracy when heritability in conjunction with genetic advance is studied (Dudley and Moll, 1969). Hence, both heritability and genetic advance were determined to study the scope of improvement in various characters through selection. The heritability estimates ranged from 28.13% for internodal length to 76.23% for yield/plant (Table 1). High heritability values were observed for yield/plant, number of capsules/plant, panicle length and number of nodes/panicle indicating less influence of environment on these traits. Moderate to low heritability for other characters indicating that environmental effects constitute a major portion of the total phenotypic variation and hence, selection for these characters will be less effective.

Expected genetic advance and its estimated percentage mean for various characters (Table 1) revealed that yield/plant and number of capsules/plant exhibited the highest genetic advance. Though characters like panicle length, number of nodes/panicles and total tillers exhibited moderate to high heritability values, their GCV was comparatively less, resulting in less genetic advance. This confirms to findings of Burton (1952), that GCV together with heritability estimates would give a better picture of genetic advance to be expected from selection. The characters like yield/plant and number of capsules/plant possessing high GCV, heritability and genetic advance could be effectively used in selection, as it has been suggested that characters with high heritability coupled with high genetic advance would respond to selection better than those with high heritability and low genetic advance.

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