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Short communication

Inheritance of cardamom mosaic virus (CdMV) resistance in cardamom

D. Prasath [a,*], M.N. Venugopal [a], V.A. Parthasarathy [b]

[a] Indian Institute of Spices Research, Cardamom Research Centre, Appangala, Madikeri, Kodagu (Dt), Karnataka 571201, India
[b] Indian Institute of Spices Research, P.B. No. 1701, Marikunnu (P.O.), Calicut, Kerala, India

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ABSTRACT

Cardamom lines, NKE 9 and NKE 12, resistant to Cardamom Mosaic Virus (CdMV) was crossed to two susceptible genotypes, viz., CCS 1 and RR 1 to determine the nature of inheritance of resistance. It was revealed from the results that the CdMV resistance in NKE 9 and NKE 12 is genetically governed. The F_1 hybrids between resistant and susceptible genotypes were resistant. The segregation pattern for disease reaction in F_2 and BC_1 generations of the two crosses suggested that CdMV resistance in NKE 9 and NKE 12 could be controlled by two dominant complementary genes. Over all it could be hypothesized that the resistance to CdMV is quantitative, with possibly two major factors, and dependant on gene dosage with completely dominant gene action. This is the first report of CdMV inheritance in cardamom.

1. Introduction

Cardamom (*Elettaria cardamomum* Maton), "Queen of Spices" ($2n = 2x = 48$) is an important spice crop and is native of evergreen forests of Western Ghats of South India (Purseglove et al., 1981). In spite of its prominence in world trade from time immemorial, cardamom received attention for genetic upgradation only in the second half of this century. Three major types, viz., Malbar, Mysore and Vazhukka are grown in the country. The Vazhukka is more important in terms of area and production. However, the average dry capsule production is India is only 142 kg ha^{-1} (Anon, 2008). The low productivity is mainly due to low yielding local cultivars, which are susceptible to viral diseases especially mosaic or *katte* disease caused by *Cardamom mosaic virus* (CdMV), which is an aphid (*Pentalonia nigronervosa* f. *caladii*) transmitted poty virus, widely prevalent in all cardamom growing tracts of India with incidence ranging from 0.01 to 99 per cent (Venugopal, 2002). CdMV was reported as reason for rapid decline of cardamom in Guatemala, India and Sri Lanka (Dimitman, 1981; Dimitman et al., 1984; Gonsalves et al., 1986).

The disease cannot be controlled by chemical means. Uprooting of infected plants is not practical and economical because of heavy infection rate in the field. So only practical solution of this problem is to develop resistant varieties. Therefore, an extensive search for resistance in cultivated cardamom was started by screening available germplasm (Subbarao and Naidu, 1981). Study was also undertaken to create resistant source through induced mutation. No desirable mutant has so far been obtained. Sterility (Pillai and Santhakumari, 1965) and lack of macro-mutations in the M_1 generation (ICRI, 1987) were also reported. Resistant sources to *katte* disease were identified by collecting 134 disease escapes (Natural *katte* Escapes) from hotspots of virus infection in South India and screening them in green house, sick plot and hot spots. Testing of promising collections in four hotspots and also against natural infection confirmed the resistant nature of 17 collections. Further evaluation of these 17 collections led to identification of three lines, viz., NKE 9, NKE 12 and NKE 19 with mosaic resistance combined with good capsule characters (Venugopal, 1999). There is no report on type of resistance/tolerance in cardamom, therefore, it is important to know the genetics of the resistance for proper maintenance of the genotype, and to explore the possibility of utilizing the character in future cardamom breeding programmes.

2. Materials and methods

2.1. Plant materials

Two cultivated lines susceptible to CdMV, viz., CCS 1 and RR 1, were crossed with the CdMV resistant lines, NKE 9 and NKE 12, respectively, (NKE 9 × CCS 1, NKE 12 × RR 1) during 2002–2003. The ploidy level of the parental lines is $2n = 2x = 48$ and other details are given in Table 1. The dry capsule yield among the parents was recorded and categorized as low (<500 kg/ha), moderate (500–750 kg/ha), high (750–1000 kg/ha) and very high (>1000 kg/ha). In general cardamom flowers on the third year of planting, the two F_1s were selfed and back crossed to both the parents during 2005–2006. All the parental lines, 2 F_1s using resistant female parent, their F_2s and back cross-generations (Table 2) were established in poly bags under screen house and screening

* Corresponding author. Fax: +91 495 2731410.
E-mail address: dprasath@gmail.com (D. Prasath).

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Table 1
Description of parental lines used in the cross.

Parents	Collection no.	Yield level	Mosaic resistance
CCS 1	IC 349589	Moderate	Susceptible
RR 1	IC 349591	Moderate	Susceptible
NKE 9	IC 349600	Low	Resistant
NKE 12	IC 349599	Low	Resistant

was carried out during 2006–2007. The experiment was carried out at Indian Institute of Spices Research, Cardamom Research Centre, Appangala, Karnataka, India (latitude 12°42′N, longitude 77°35′E and altitude 1000 m amsl) during 2002–2007.

2.2. Screening hybrids against mosaic disease

The seedlings of all the parental materials, 2 F_1s, their F_2s and back cross-generations were inoculated with viruliferous aphids (*Pentalonia nigronervosa* f. *caladii*) carrying local severe isolate of mosaic virus. In each plant, two leaves of actively growing tillers were rolled to make the leaf funnels and 5 aphids/tiller were released. The inoculants were assessed for symptoms up to 45–50 days and the screening was repeated thrice at an interval of 50 days (Venugopal, 1999). The disease symptom starts with prominent, discontinuous yellowish stripes running out from the midrib to the margins on young leaves and the symptoms were unmistakable (Fig. 1).

Table 2
Disease symptom and segregation pattern of CdMV resistance in F_1, F_2 and back cross-populations of cardamom.

Generation	Resistant	Susceptible	Total	Ratio	χ^2	p
Parents (resistant)						
NKE 9	36	–	36	–	–	–
NKE 12	36	–	36	–	–	–
Parents (susceptible)						
RR 1	–	36	36	–	–	–
CCS 1	–	36	36	–	–	–
Hybrids						
NKE 9 × CCS 1	36	–	36	–	–	–
NKE 12 × RR 1	36	–	36	–	–	–
F_2						
NKE 9 × CCS 1	36	29	65	9:7	0.047	0.83
NKE 12 × RR 1	15	10	25	9:7	0.159	0.69
BC_1						
(NKE 9 × CCS 1) × NKE 9	40	16	56	1:0	∞	–
(NKE 9 × CCS 1) × CCS 1	34	90	124	1:3	0.075	0.78
(NKE 12 × RR 1) × NKE 12	61	23	84	1:0	∞	–
(NKE 12 × RR 1) × RR 1	11	19	30	1:3	0.126	0.72
All F_2	51	39	90	9:7	0.028	0.78
All BC_1 (R)	101	39	140	1:0	∞	–
All BC_1 (S)	41	113	154	1:3	0.055	0.87

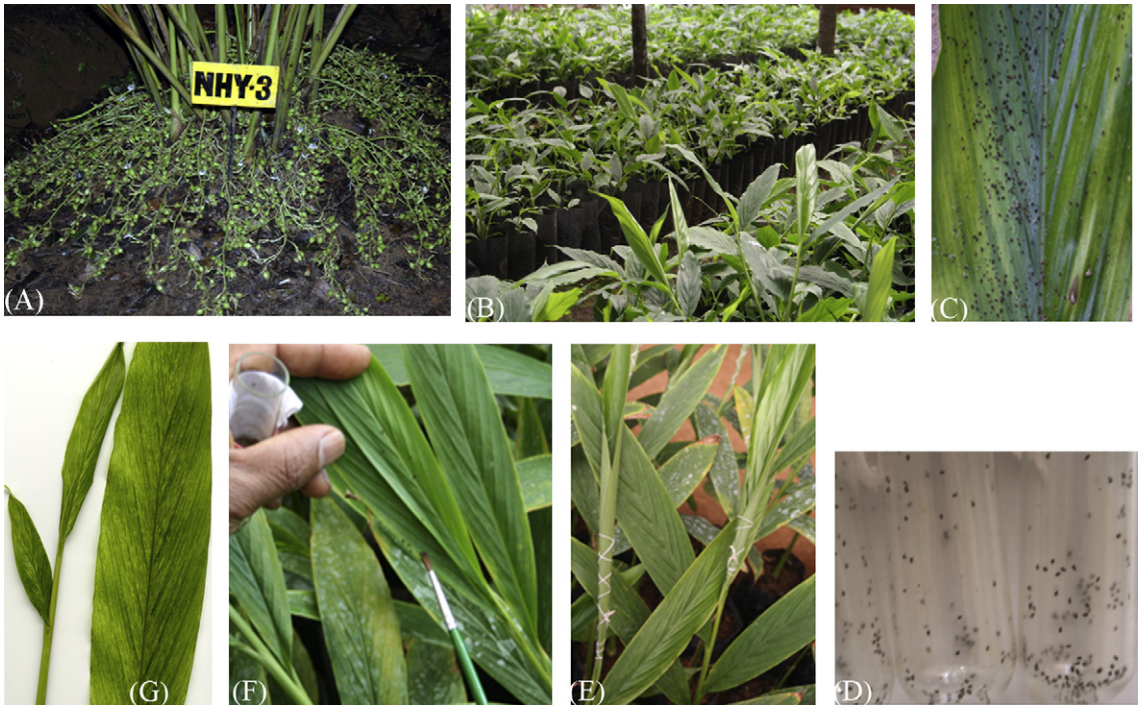

Fig. 1. CdMV screening methodology, (A) Hybrid (NKE 12 × RR 1), (B) F_2 and back cross-progenies, (C) Aphids (*Pentalonia nigronervosa* f. *caladii*), (D) pre-acquisition fasting of aphids, (E) leaf funnel to release aphids, (F) collection of aphids after feeding and (G) characteristic mosaic symptom.

2.3. Data analysis

Reactions of CdMV inoculated plants were classified into two categories: resistant (R) and systemic susceptible (S). Plants verified as resistant showed no mosaic symptoms on inoculated leaves nor did they have systemic symptoms on subsequent leaves. Plants categorized as susceptible showed typical mosaic symptoms on leaves, but there was a slight difference among the susceptible plants: a large majority of susceptible plants expressed typical symptoms on the inoculated and subsequent leaves 7–10 days after inoculation, whereas the some susceptible plants showed a delay in systemic infection and the symptoms kept stable at the final rating (45–50 days). Data on disease reaction were recorded on individual plants considering the above categories. The data were analysed by the χ^2-test using Statistica 5.1 (Statsoft, 1997).

3. Results and discussion

Under natural epiphytotic and artificial screening conditions of CdMV disease appearance, the CdMV resistant lines and its F_1 hybrids with susceptible varieties were free from disease symptoms while the lines RR 1 and CCS 1 showed CdMV symptoms. This indicated the dominant nature of the resistance in NKE 9 and NKE 12.

In the cross NKE 9 × CCS 1, all the progenies of segregating generations (F_2 and back cross) were observed for disease reaction. The data on segregation pattern for disease reaction were compatible with digenic control, with a 9 resistant:7 susceptible ratio in F_2 and in BC_1 (F_1 × CCS 1) a ratio of 1 resistant:3 susceptible (Table 2). However, the segregation pattern of the progenies of other BC_1 progeny (F_1 × NKE 9) did not fit with the expected ratio (1 resistant:0 susceptible). The progenies of the segregations in the cross NKE 12 × RR 1 exhibited the same segregation pattern as NKE 12 × CCS 1.

Data on segregating generations from the two one-way crosses were summed up and grouped into tolerant and susceptible. Segregation pattern for disease reaction in F_2 and BC_1 (back cross with susceptible lines) generations revealed 9 resistant:7 susceptible and 1 resistant:3 susceptible, respectively. But the progenies of the BC_1 (back cross with tolerant line) did not fit the expected ratio.

Observations on F_2 and BC_1 generations of back cross with susceptible lines suggested that resistance to CdMV in NKE 9 and NKE 12 could be controlled by two dominant complementary genes. But the segregation pattern of the progenies of BC_1 generations of back cross with resistant line did not agree with the pattern. According to the hypothesis, all the progenies of BC_1 generation should have exhibited resistance to CdMV. Some progenies of all BC_1 (back cross with resistant line) exhibited susceptibility to CdMV. This deviation denotes the possibility of the presence of a few more factors in the resistance system of NKE 9 and NKE 12 and/or the contribution of minor tolerance factors by the susceptible parents. Considering the overall segregation ratio, it could be hypothesized that the inheritance of tolerance is quantitative, with possibly two major factors, and dependant on gene dosage. Venugopal et al. (1999) reported that the colonization of aphids on all *katte* escape lines indicates that the resistance of cardamom accessions to *katte* virus is not due to deterrence to vector but due to some other factors. The oligogenic nature and gene dosage dependency characterize resistance as incompletely dominant rather than fully dominant. Fraser (1990) reported oligogenic resistance in some crops against viruses and supported by the hypothesis that gene dosage dependant resistance is incompletely dominant.

4. Conclusion

Over all it can be concluded from this study that the resistance to CdMV in cardamom is quantitative, with possibly two major factors, and dependant on gene dosage with completely dominant gene action.

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