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Study on Inheritance of Resistance to Cowpea Mosaic Disease in Cowpea (*Vigna unguiculata* L. Walp.)

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Abstract The inheritance pattern was studied in the cross C-152 (Susceptible) × HC-03-2 (Resistant) using per cent disease incidence in F_1 and other segregating generations, viz., F_2, F_3. BC_1P_1 and BC_1P_2. The expression of resistance reaction in F_1 generation is an indication of the role of dominant gene in controling cowpea mosaic virus in cowpea. Based on classification of plants into resistant and susceptible in F_2 segregating generation of the cross C-152 × HC-03-02, a good fit of 3:1 (388 Resistant: 138 Susceptible) ratio indicated the role of major dominant gene for field resistance. The F_3 population of this cross showed 1:2:1 ratio (55 Resistant: 83 Segregating: 42 Susceptible) and back cross generations BC_1P_1 and BC_1P_2 segregated in 1:1 (27 Resistant: 30 Susceptible) and 1:0 (56 Resistant: 3 Susceptible) test ratio respectively. The segregation pattern in different generations showed very good fit with the expected ratio confirmed the role of single dominant gene in controlling resistance to cowpea mosaic virus.

Keywords Cowpea, Cowpea mosaic virus, Inheritance, Resistant, Segregating generations.

Introduction

Cowpea (*Vigna unguiculata* L. Walp.), an annual legume among pulses, is one of the most ancient crops known to man. The largest production is in Africa, with Nigeria and Niger predominating, while Brazil, Haiti, India, Myanmar and Sri Lanka all have significant production. All parts of the plant in cowpea are used as nutritious food, providing protein, vitamins (notably vitamin B) and minerals. It is now a broadly adapted and highly variable crop, cultivated around the world primarily for seed, but also as a vegetable (for leafy greens, green pods, fresh shelled green peas and shelled dried peas), a cover crop and fodder.

The main production constraints of pulses in general and cowpea in particular are biotic and abiotic stresses. Diseases are prominent among biotic stresses know to affect the productivity. Fungi, bacterial and viral diseases are considered as major limiting factors for the production of cowpea in the tropical and subtropical countries. More than 20 viruses are reported from various cowpea growing areas worldwide. Among these viruses, cowpea mosaic virus (CpMV) is the most serious disease of cowpea. It may cause 80-100% yield reductions. Cowpea mosaic virus also severely affects vegetative parts of the plant. It may cause 14 to 54% decrease in plant height, 30 to 95% decrease in dry stem weight of cowpea.

Chemical management of these diseases is not economically feasible since cowpea is cultivated mostly on marginal land and in rainfed situations. Therefore, development of resistant varieties offer

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Table 1. Disease reaction of cowpea cultivars to cowpea mosaic virus disease under controlled conditions (Muniyappa et al, 1987). Where, HS=Highly susceptible, HR = Highly resistant.

Cultivars	Percentage foliage affected	Discase reaction
C-152 (P_1)	85	HS
HC-03-02 (P_2)	000	HR

best hope for farmers since, they are safe, eco-friendly and efficient means of combating the diseases. Use of resistant (R) varieties is cost-effective for farmers, but considerable time and cost may be involved in developing varieties with appropriate levels of resistance [1]. This calls for screening and evaluating the germplasm available for resistance to diseases in particular as a first step to know the source of resistance. After identifying the resistant source it becomes essential to understand the genetics of resistance that involves the identification of number of genes involved and nature of inheritance. Further, a good understanding of the inheritance of the traits that are correlated with disease is essential for successful disease resistance breeding program to evolve the resistance varieties.

(AICRP on Arid Legumes, ZARS, GKVK, Bangalore, provided the cowpea materials).

Materials and Methods

Plant material

The material used for the study includes three parental lines viz. C-152 (agronomically superior but susceptible for the diseases CpMV) and HC-03-02 (resistant to cowpea mosaic virus disease). They were selected based on the results of evaluation under both natural field conditions and in glass house screening (Table 1) and used for hybridization.

Crowing of segregating populations, F_1's and parents for study of inheritance

The experiment comprising six populations (viz., P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2) of the cross C-152 × HC-03-02 was laid out during *kharif* 2011 in randomized complete block design with two replication at ZARS, Bengaluru. The non-segregating populations (P_1, P_2 and F_1s) were grown in two row plots of 3.5 m length, while the segregating population viz., F_2, BC_1P_1 and BC_1P_2 were grown in two row plots in each replication, while F_2 were grown in six row plots in separate blocks. The entries were sown in plots of either two row or six rows spaced 60 cm apart and with a plant spacing of 15 cm in each row. The screening approach adopted was infector-row method. All the recommended package of practices was followed in raise a good and healthy crop.

The per cent disease incidence was considered for forming frequency distribution in F_1 and other segregating generations, viz., F_2,F_3, BC_1P_1 and BC_1P_2 (Table 2). The two parents involved in this cross showed distinctly different pattern for disease resistance incidence. This was used to classify plants as resistant (0-1 scale) and susceptible (3-9 scale) by using scoring method proposed by Muniyappa et al. [2].

Chi-square test

The inheritance pattern was studied in C-152 × HC-03-02 (for CpMV) and the disease resistance was classified into two groups, those with no apparent symptoms as resistant and those with visual expression of symptoms as susceptible. The reaction for the disease was recorded as resistant and susceptible on all individual plants of F_2 and back cross generations of the crosses. The recorded observations were subjected to chi-square test based on expected ratios. The goodness of fit between expected and observed segregation ratios were worked out. The chi-square was calculated by using the following formula :

$$\chi^2 = \Sigma \frac{(O-E)^2}{E}$$

Where, O = Observed frequency; E= Expected frequency.

The significance of Chi-square value was tested by comparing the calculated chi-square value with table value at 5% and 1% level of significance at appropriate degrees of freedom (n-1, where, n = number of classes of trait under consideration).

Table 2. Segregation for CpMV disease resistance and susceptibility in different generations of the cross C-152 ×HC-03-02.

Crosses/ generations	No. of plants								Test ratio R:S	Chi-square value	Table value
	Observed				Expected						
	Resistant (R)	Segregants	Susceptible (S)	Total	Resistance (R)	Segregants (S)	Susceptible	Total			
P_1	0	-	38	38	-	-	-	38	-	-	-
P_2	43	-	0	43	-	-	-	43	-	-	-
F_1	61	-	0	61	-	-	-	61	-	-	-
F_2	388	-	1.38	526	394	-	131	526	3:1	0.428	3.841
F_3	55	83	42	180	45	90	25	18	1:2:1	2.96	5.991
BC_1P_1 $(iP_1 \times F_1)$	27	-	30	57	28	-	28	57	1:1	0.157	3.841
BC_1P_2 $(P_1 \times F_1)$	56	-	3	59	59	-	0	59	1: 0	0.305	3.841

Results and Discussion

The segregation for disease resistance and susceptibility in different generations of this cross (C-152 × HC-03-02) is given in the Table 2. It was evident from the data that disease resistance was dominant over susceptibility. In F_2, the segregation pattern of 3:1 (388 resistant : 128 susceptible) was observed and showed very good fit with the expected ratio and chi-square values were non-significant at n-1 degrees of freedom (n-number of classes). In F_2 generation of the cross C 152 ×HC 03 02, a good fit of 3 : 1 (Resistant: Susceptible) ratio was an indication of major dominant gene controlling resistance to CpMV disease in cowpea.

The expression of resistance in F_1 generation is an indication of dominant gene controlling resistance of CpMV. The role of single dominant gene in controlling CpMV was evident from the F_2 segregating ratio of 3 resistant and 1 susceptible. The same was confirmed by the segregating behavior of 1:2:1 ratio (Resistant : Segregating : Susceptible) in F_3 population and test ratio back cross generations BC_1P_1 (1 Resistant : 1 Susceptible) and BC_1P_2 (1 Resistant : 0 Susceptible). The segregation pattern in different generations proved the resistance was under the control of single dominant gene.Similar findings were made earlier [3, 4] in cowpea. Similarly, in mungbean by Marappa [5] and Gupta et al. [6] in blackgram. On the contrary Taiwo et al. [7] and Arshad et al. [8] they observed single recessive controlling CpMV resistance/tolerance. But Ammavasai et al. [9] claimed that MYMV resistance was due to duplicate recessive genes. The findings of Reddy and Singh [10] reported that MYMV resistance was due to one dominant and one recessive gene may be due to the differential behavior of parental confirmations in their study. The another study Patel [11] reported that the inheritance was governed by interaction of two dominant genes. The study of Orawu et al. [12] reported that more than one recessive gene in eight population, but also revealed resistance to be conditioned by a single recessive gene in the other seven populations. Observation of continuous distribution of progenies for severity data in the F_2 populations also confirmed significance of quantitative inheritance for CABMV resistance. The genetics of resistance to in cowpea will help the breeders in the development of high yielding resistant varieties through simple selection in the segregating generations of crosses between resistant and susceptible genotypes.

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