CHAPTER-5

DISCUSSION
5. DISCUSSION

Breeding a resistant variety to a natural biotic or abiotic hazards require some of the important materials and information. The first essential prerequisite is the resistance source and the other one is the knowledge of the inheritance/genetics of the character. In the present context a project to work out genetics of resistance to *M. phaseolina* and *R. solani* in cowpea was envisaged. Although, the resistant source to these fungi was not available either within the cultivated cowpea or as a wild type. Therefore, the present research work includes a survey of resistant source as well. In order to recover a resistant cowpea strain a large enough germplasm was collected and subjected to screening for resistance.

1) Screening for Resistant Sources:

A collection of 283 germplasm lines was screened for resistance/susceptibility to *M. phaseolina*, *R. solani* on the basis of penetrance of the pathogen. Penetration and expressivity are two important visible parameters to ascertain extent of disease in the host. While screening for resistance with an objective of searching a resistant source it is always advisable to bank on penetrance only. 'Penetrance' of a disease may be defined as the percentage of individuals showing the disease symptoms. 'Expressivity' of a disease is the extent of expression of a symptom in the host. While searching a resistant source opting for penetrance only and ignoring expressivity is advantageous in the sense that the resultant selected material does not show even an insignificant expression of
a disease symptom and it is completely free from the disease in that
generation. Another reason, which favours for selection of
individuals only on penetrance basis is that the selected individual
types may be required a long travel from generation to generation
to be used as the resistant ones, selection of a individual showing
even a least expressivity may lead to show a greater
expression/variable expression in the next generation. For this
very fact a search of resistant source was opted through a selection
of individuals with zero penetrance. Study of penetrance of the
fungi singly or in mixture was done under artificial epiphytotic as
detailed in materials and methods. The inoculation, however, was
supported by natural infection. As a consequence three parents
namely C-87, C-1 and C-21 have been selected as resistant to either
one or both the fungi and or 1:1 mixture as detailed in the previous
chapter.

Few attempts had been made elsewhere earlier for screening
of sources of resistant. A field screening considering natural
infection a *M. phaseolina* was attempted and two lines out of thirty
one were selected as moderately resistant to *M. phaseolina*, (Miglo
for resistance to *M. phaseolina*. None was completely resistant to
disease although 5 varieties were moderately resistant (Pusa-1, V-
38, CO-1, RC-48 and C-152).

Field resistance of cowpea varieties to anthracnose
(*Colletotrichum lindemuthianum*) and stem blight (*M. phaseolina*),
diseases was studied. 141 cultivars tested, 21 were resistant to *C.
lindemuthianum* and 4 to *M. phaseolina* (Sohi and Rawal 1983,
1984).
2) **Variation within the parents and F1s:**

The parents and F1s are supposed to be genetically homogeneous, however, some variation for resistance to *M. phaseolina*, *R. solani* and 1:1 mixture of both the parents was observed in parents and F1s in the same environment (table 3.1, 3.2 and 3.3). This variation could be due to environmental factors. The results for minor intra hybrid variability are in conformity with Schroeder *et al.* (1960), who studied the symptom expression of bean virus-2 in pea and found that the plants heterozygous for resistance were determined by temperature; phenotypic resistance being dominant at air temperature of 65 °F below and recessive at 80 °F or above. The symptom expression was delayed between these two temperatures.

3) **Dominance pattern in F1:**

In all the crosses involving resistant and a susceptible parent, irrespective of whether the resistant parents had a greater degree of resistance or low degree of resistance (moderately resistant) and irrespective of fungus whether *M. phaseolina* or *R. solani* or 1:1 mixture thereof the susceptibility appeared to be dominant over resistance. The susceptibility as dominant over resistance has also been reported for MYMV in soybean (Malick, 1976); bean yellow mosaic virus (Reeder *et al.*, 1972) and cowpea chlorotic mottle virus (Roger *et al.*, 1973) in cowpea; bean yellow mosaic virus and watermelon mosaic virus-2, (Schroeder *et al.* 1971). Pea leaf roll virus (Drijfhout, 1969), bean virus-2 (Schroeder *et al.*, 1960), pea mosaic virus, (Yen and Fry, 1957). Pea seed-borne mosaic virus (Hagedorn and Gritton, 1973) in pea and bean yellow mosaic
virus in the interspecific crosses of *Phaseolus vulgaris* *X* *P. coccineus*, (Baggett 1956). Variation within the closes noticed to be not much enough and it could not affect the dimension of a particular class category.

4) **Genetics of resistance:**

There have been two approaches to deal with the inheritance of a character. One of them is Mendelian School of thought and another Galton’s School. The segregating generations showing discrete variations wherein distinct groups/classes are formed the research on inheritance is dealt with Mendelian School and in continuous variations, wherein cumulative action of genes causes variation the problem is dealt with the Galton’s School of thought (Mather and Jinks 1971).

Segregation patterns for resistance to *M. phaseolina* in F2 generation (table 4.1) indicated that the character, resistance is governed by two recessive genes. The modified F2 ratios indicated duplicate dominant epistasis in the crosses C-1xC-70, C-1xC-201, C-1xC-21, C-87xC-19, C-87xC-70 and C-87xC-21. In two of the crosses, the interallelic gene interaction was noticed to be recessive epistasis showing a genetic ratio of 13 susceptible; 3 dominant. These crosses are C-1xC-19 and C-87xC-21. The results were duly confirmed by back cross/test cross generations as the expected genetic ratios for back cross and test cross segregation gave a good fit. Although, the ‘P’ values in this case appeared to be a little less than the F2 generations. The interesting observation in back cross is that in the genetic ratios where one of the expected value is zero there is ample possibility for the observe frequencies
a very high and immeasurable significance even if there is a little
value of observed frequency recorded for expected frequency of
zero. The $\chi^2$ value in this case is bound to happen to be zero, in all
the cases if Yate's correction is not applied. In case of application
of Yate's correction the observed frequency exceeding one for
expected frequency of zero would yield infinite value of $\chi^2$.
Because of this reason a little variation in the observed frequencies
may lead to a situation from which a fruitful inference may hardly
be drawn. This suggested that in the inheritance studies one should
prefer to study test crosses instead of back crosses. The value of $\chi^2$
infinity was observed in case of C-1xC-201xC-201. The further
confirmation was obtained from F$_3$ progenies wherein the expected
genetic ratios gave a good fit as the values of 'P' were quite high.
The total number of progenies however were low. A cross look at
F$_2$ generation, backcross and F$_3$ progenies indicated that substantial
plant population was study in F$_2$. Backcross and F$_3$ progenies
contained low number. Accordingly, the precisions of results are
so expected in the descending order from F$_2$ to backcross to F$_3$
progenies. The Mendelian inheritance involving one dominant
gene for resistance to Fusarium oxysporum was reported by earlier
workers, (Rigert, 1986). The duplicate dominant epistasis and
recessive epistasis involving two recessive genes conferring
resistance to mung bean yellow mosaic virus (MYMV) has also
been reported by Shukla (1977); Shukla, et.al. (1978) and Shukla
and Pandya (1985). The double recessive resistance worked out in
case of M. phaseolina in the present study is also in conformity
with the double recessive inheritance of resistance to MYMV
reported by Malick (1976) in soybean. The inheritance pattern for
resistant to *R. solani* in F2 generation as presented in table 5.1 is analogous to the inheritance of resistance to *M. phaseolina*. Resistance to *R. solani* was also noticed to be governed by double recessive gene wherein seven crosses out of eight showed a duplicate dominant epistasis whereas only in the one cross namely C-87xC-1, a recessive epistasis showing a genetic ratio of 13 susceptible: 3 resistant was observed. The 'P' values showed a medium to high range as 0.50-0.30 to 0.90-0.80, meaning thereby the goodness of fit is adequate. The back cross generations also showed the results similar to that of *M. phaseolina*. In all backcrosses two of the crosses namely C-21xC-19xC-21 and C-87xC-19xC-87 were the test crosses and rest were the back crosses. In this case as well one of the crosses namely C-21xC-70xC-70 showed $x^2$ value to the infinity. Such segregations may hardly be explained through statistical tools. The F3 progenies in this case also warranted the results obtained in F2 and backcross/test cross progenies. The degree of precision in the case also flows in the descending order from F2 to back cross to F3 progenies as in case of *M. phaseolina*.

The segregation pattern observed was having only one consideration that number of damped plants showing symptoms of any one of the disease was taken on one hand and disease free plants on the other (table 6.1).

As per expectations only three of the crosses C-21xC-70, C-21xC-19 and C-21xC-201 should have shown segregation for resistance to *R. solani* and entire population should have shown susceptibility to *M. phaseolina* similarly the crosses C-1xC-19, C-1xC-70 and C-1xC-201 should have shown segregation for
resistance to *M. phaseolina* and susceptibility to *R. solani*. The crosses C-87xC-19, C-87xC-70 and C-87xC-201 should have shown segregation for resistance to both the fungi, *M. phaseolina* and *R. solani*. But such observations could not be practically recorded. When the relative penetrance was observed on the same plant population, it could be evident that penetrance of *M. phaseolina* was much greater ranging from 80% - 90%, while penetrance of *R. solani* was noticed to be 10-20% in all the cases namely F2 back cross and selected sample population from each F3 progenies. In F3 progenies the penetrance of *R. solani* was a bit higher up to 40% and in few cases 50% and in one case 68% (table 7.1, to 7.3). In a broad spectrum of relative penetrance of both the fungi it is evident that in majority of the cases *M. phaseolina* overpowers the infection of *R. solani*. Similar antagonistic biological effects have been observed in the co-infection of nematode *Meloidogyne javanica* and *Rhizoctonia* as it is evident available in the literature (Kanwar *et al.* 1987, 1988; Varshney *et al.*, 1987; Khan & Hussain, *et al.* 1990; Gupta and Mehta, 1993). In such biological antagonisms *Meloidogyne* species may be used as a tool for biological control of the co-existing fungus. Contrary to this *M. phaseolina* may hardly be utilized to check the invasion of *R. solani*, since *M. phaseolina* is itself a hazard to cowpea and that too greater hazardous than *R. solani*.

Considering total infection of both the fungi in an individual whether infection of one fungus contributes in the total infection or not the genetic segregation was worked out for diseased : disease free plants. Eventually, the F2 segregation has shown two types of segregation one is digenic and other one monogenic as mentioned
above. Amongst the inter allelic interaction the duplicate dominant epistasis, recessive epistasis and complementary epistasis were observed. In the crosses of such resistant x resistant crosses two of the crosses showed complementary epistasis and the remaining one monogenic inheritance. In all the cases the susceptibility was recorded in greater proportion except C-87xC-1 wherein reverse complementary epistasis could be observed.

The back cross/test cross generation and F3 progenies by and large showed conformity to the results obtained in F2 generation. The study of resistance to mixture of pathogenic fungi, manifests more than one possibilities as far as the interaction of genes for conferring resistance is concerned. One of the possibilities is that a gene responsible for resistance to *M. phaseolina* may interact with the gene responsible for resistance to *R. solani*. Another possibility is that a pleiotropic gene or genes are responsible to resist combined infection of the two fungi at a time.