Among the oilseed crop grown during winter season, linseed is next to rapeseed and mustard both in acreage and production. The crop has an area of 3.526 lakh hectares with the production of 1.480 lakh tones and productivity 420 kg/hectare. The crop yield is lowest in India, as most of it is rainfed and host to a number of diseases (5). Alternaria blight once considered minor has become serious. Eastern India being hot and humid has become epidemic to this disease. It causes yield loss from 40.6 to 60% (8,9,10) and infected plants bear spots on leaves, branches and stem. Though the disease in India was first reported as early as in 1933 (2) only little work has been published from this area (5,6). The long lasting, achievable and economical method to combat disease is varietal resistance. Despite the fact that considerable efforts have been made to develop resistant variety this has not been fully achieved due to the reasons that the genetics of resistance of the host is not explored and exploited to the fullest. The present paper describes the inheritance of disease resistance in 3 crosses involving 3 resistant and 1 susceptible genotypes (Table 1) to Alternaria blight in linseed.

The experimental material consisted of three resistant genotypes, Polf-5, Ayogi, ES-44 and one susceptible genotype, Chambal. The resistant genotypes gave consistent resistant reaction more than 5 years of testing (7,9). To study the inheritance of resistance, 3 crosses were made between resistant and susceptible genotypes to generate sufficient F1 seeds at Student's Instructional Farm of Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad, U.P. during winter 2004-05. During the same year F1 seeds of these 3 crosses were sown at Kukumsheri for generation advance to get F2 seeds. During 2005-06 fresh F1s were also made. F2 seeds of each cross procured from Kukumsheri (HP) were planted to get F3 seeds. In this year also few F1 seeds of all the crosses were sown in November 2006 at Kumarganj. Row length was kept two meters and spaced 40 cm. apart. Within row plants were maintained at 15cm. Normal agronomic practices were followed to raise a good crop. In India Kumarganj is considered as one of the hot spots for the incidence of Alternaria blight in linseed in the country. The disease usually attacks the crop every year in mild to severe form. In order to facilitate uniform incidence of Alternaria blight in the epidemic form, an epiphytic condition was created by inoculating entire test materials and planting infector rows, grown all around the experiment and in between the test rows. All the test lines were inoculated with the spore suspension of Alternaria lini with the spore concentration of 20-25 conidia/microscopic field thrice in crop season. First spray was given at seedling stage 25 Day after sowing (DAS), second at flower initiation (75 DAS), third at capsule formation (100 DAS). After each inoculation the crop was irrigated immediately to maintain the humidity in field. In the beginning only infector rows were inoculated and once 20-25% foliage of plants in infector rows was covered with blighting of fungus, the process was repeated on the test materials. The disease observations were recorded when the disease severity was stabilized and there was no further increase in severity following 0-5 scale (1) The middle, upper and lower infected leaves were collected from every plants. The plants were categorized on the basis of blighted leaf area in following ways: 0= No disease (Immune), 1= 1-10% leaf area infected (Resistant), 2=10.1-25% leaf area infected (Moderately resistant), 3=25.1-50% leaf area infected (Moderately susceptible), 4=50.1-75% leaf area infected (Susceptible), 5= More than75% leaf area infected (Highly susceptible). For genetic study, scale 0-2 collectively categorized as resistant (R) whereas, scale 3-5 were taken as susceptible (S) plants. Segregation in F2 at F3 generation into resistance and susceptible classes were tested for goodness of fit to the expected segregating ratio by Chisquare method.

The characteristic features of the parents are given in table 1. In general the genotypes showing resistant towards Alternaria blight disease were taller and late maturing type than the susceptible parent, i.e. Chambal. The confounding effects of the stature of the plant and phonological traits with disease resistance to Alternaria blight have also been reported earlier (4). The F1s plants of all the 3 crosses in the present study were resistant indicating disease resistance

Table 1. Characteristic feature of the parent plants

<table>
<thead>
<tr>
<th>Name of the genotypes</th>
<th>Days to flowering</th>
<th>Days to maturity</th>
<th>Plant height (cm)</th>
<th>Disease reaction</th>
</tr>
</thead>
<tbody>
<tr>
<td>Polf-5</td>
<td>92</td>
<td>149</td>
<td>89</td>
<td>Resistant</td>
</tr>
<tr>
<td>Ayogi</td>
<td>87</td>
<td>143</td>
<td>56</td>
<td>Resistant</td>
</tr>
<tr>
<td>ES-44</td>
<td>83</td>
<td>147</td>
<td>90</td>
<td>Resistant</td>
</tr>
<tr>
<td>Chambal</td>
<td>65</td>
<td>130</td>
<td>42</td>
<td>Susceptible</td>
</tr>
</tbody>
</table>
dominant over susceptibility in these genotypes (Table 2). In F2 population of the cross Polf-5 x Chambal of the total 198 plants, 149 were resistant and 49 susceptible; in Ayogi x Chambal of the total 148 plants, 112 were resistant and 36 susceptible and ES-44 x Chambal of the total 153 plants, 115 were resistant and 38 susceptible; giving a good fit to a ratio of 3:1 indicating that resistance is governed by one dominant gene. Furthermore, resistant plants of all the 3 crosses, F3 plant progenies resulted in true resistant segregating and susceptible progenies which had good fit to the expected 1:2:1 ratio, which further clarify that Alternaria blight resistance was under monogenic dominant control in materials tested. These findings confirmed the earlier report of Islam (3) and Singh et al. (8). Since inheritance of resistance against Alternaria blight in linseed is dominant and monogenic, therefore, simple back cross breeding may be used to transfer resistant genes from resistant genotypes to agronomically superior otherwise susceptible cultivars.

REFERENCES