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RESEARCH ARTICLE

Inheritance of alternaria blight resistance in sesame

■ **RENUKA GOUDAPPAGOUDAR, R. LOKESHA AND VANISHREE**

SUMMARY

In order to study inheritance of alternaria blight resistance in sesame, straight and reciprocal crosses were made between RT-273 (resistant) and Gulbarga local black (susceptible) during *Kharif*-2007. Screening of F_2 and F_3 progenies against *Alternaria* blight, and segregation analysis showed that resistance is governed by single dominant gene. Further screening of F_4 families under field condition during *Kharif*-2010 confirmed the single dominant gene governing the *Alternaria* blight resistance in cultivated sesame.

Key Words : Sesame, F_4 families, Alternaria blight resistance, Dominant gene

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Alternaria blight of sesame (*Sesamum indicum*) caused by *Alternaria sesami* is a major fungal disease distributed throughout the sesamum growing areas of India which causes seed rot, pre and post–emergence death of seedlings and infect all the above ground parts resulting in considerable yield loss both qualitatively and quantitatively (Naik *et al*., 2003). Upto 73 per cent yield loss has been recorded in North-Eastern zone of Karnataka (Dolle, 1981).

Use of chemicals to control the disease certainly increases the cost of production besides polluting environment. As sesame is grown by many small and marginal farmers, they can't bear the increased cost of production. Using resistant varieties would be more effective, cheap and eco-friendly method to combat sesame alternaria blight as compared to chemical control. Development of resistant variety requires the knowledge on genetics and inheritance of the resistance. Work pertaining to inheritance of alternaria blight resistance is scarce. Some of the studies have reported that resistance to alternaria sp. is governed by single gene (Thomas *et al.*, 1990). Thus, the present study was under taken with an aim to understand the inheritance pattern of alternaria blight resistance in cultivated sesame.

MEMBERS OF THE RESEARCH FORUM

VANISHREE, Department of Genetics and Plant Breeding, University of Agricultural Sciences, G.K.V.K., BENGALURU (KARNATAKA) INDIA
Email: vanishreegpb@gmail.com

Address of the Co-authors:
RENUKA GOUDAPPAGOUDAR AND R. LOKESHA, Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences, RAICHUR (KARNATAKA) INDIA

MATERIALS AND METHODS

Straight and reciprocal crosses were made between RT-273 (alternaria blight resistant) and Gulbarga local black (GLB; alternaria blight susceptible) during *Kharif*-2007 at University of Agricultural Sciences, Raichur, Karnataka. F_1 was raised during *late Kharif*-2007. During *Kharif*-2008, F_2 was screened against alternaria blight in net house by Eshwarappa (2010) and reported that alternaria blight resistance is controlled by single dominant gene (3R:1S). Deepa (2010) screened F_3 families under field condition during *Kharif*-2009 and reported the same segregation ratio. To confirm this segregation ratio, F_4 families were further screened against alternaria blight during *Kharif*-2010 under field condition. One hundred and twenty F_4 families were raised in augmented design with spacing of 45 cm between rows and 20 cm between the plants and were scored for alternaria blight using 0-5 disease scale (Table A).

Only segregating F_4 families with respect to alternaria blight were selected for inheritance study (ten F_4 families from straight cross and seven from reciprocal cross). From these segregating F_4 families, plants showing resistant reaction (0, 1 and 2 scores) were pooled into one class as resistant while the plants showing susceptible reaction (3, 4 and 5 scores) were pooled in to another class as susceptible and the

Table A: Disease scale used for scoring alternaria blight of sesame

Grade scale (0-5)	% infection	Disease reaction
0	0	Immune
1	1-10	Resistant
2	11-25	Moderately resistance
3	26-50	Moderately susceptible
4	51-75	Susceptible
5	>75	Highly susceptible

segregation ratio was derived. Chi-square analysis was used to test the goodness of expected segregation ratio.

RESULTS AND DISCUSSION

In the present study only those F_4 families segregating with respect to *Alternaria* disease were selected for inheritance study from both straight and reciprocal crosses.

Straight cross :

From straight cross (RT-273 x GLB), ten segregating F_4 families were obtained which included a total of 50 plants. Out of 50 plants, 37 plants were resistant (pooling of plants with 0, 1 and 2 scores) and 13 plants were susceptible (pooling of plants with 3, 4 and 5 scores).

Reciprocal cross :

From reciprocal cross (GLB x RT-273), seven segregating F_4 families were obtained with a total of 35 plants. Out of 35 plants, 26 plants were resistant (pooling of plants with 0, 1 and 2 scores) and 9 plants were susceptible (pooling of plants with 3, 4 and 5 scores). Disease score of 50 plants from straight cross and 35 plants from reciprocal cross is depicted in Table 1.

However, pooling of plants showing resistance reaction into one class as resistant and plants showing susceptible reaction into another class as susceptible gave segregation ratio for alternaria blight resistance as 2.96R:1.04S in case of straight cross and 2.97R:1.03S in case of reciprocal cross, which were very close to a monogenic ratio 3R:1S. Chi-square analysis of these segregation ratios (Table 2) showed no significant difference between observed ratios (2.96R:1.04S and 2.97R:1.03S) and expected ratio (3R:1S) at both 1per cent and 5 per cent level of significance indicating that alternaria blight resistance in sesame is controlled by single dominant gene. Thus, the result obtained in the present study is in line with the findings of Lokesh (2006), Eshwarappa (2010) and Deepa (2010). Since the inheritance studies on alternaria blight resistance in sesame are limited, the results of present study may provide useful information for further investigation.

Table 1 : Disease score of plants from segregating F_4 families of straight (RT-273 x GLB) and reciprocal cross (GLB x RT-273) for alternaria blight in sesame

Score	Disease reaction	No. of F_4 plants of straight cross	No. of F_4 plants of reciprocal cross
0.	Immune	0	0
1.	Resistant	18	10
2.	Moderately resistant	19	16
3.	Moderately susceptible	9	7
4.	Susceptible	3	2
5.	Highly susceptible	1	0
Total		50	35

Table 2 : Chi-square analysis of segregation ratios for alternaria blight resistance in F_4 generation of straight and reciprocal crosses between RT-273 and GLB

Type of cross	Total no. of F_4 plants scored	No. of resistant F_4 plants (pooling of 0, 1 and 2 scores)		No. of susceptible F_4 plants (pooling of 3, 4 and 5 scores)		Segregation ratio		Calculated $\chi 2$ value	Table $\chi 2$ value at 1 d.f	Significance level
		Observed	Expected	Observed	Expected	Observed	Expected			
Straight cross	50	37	37.5	13	12.5	2.96R:1.04S	3R:1S	0.0266	6.635 (P=0.01)	Non significant
Reciprocal cross	35	26	26.25	9	8.75	2.97R:1.03S	3R:1S	0.0094	3.841 (P=0.05)	Non significant

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