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Inheritance studies on spot blotch of wheat caused by *Bipolaris sorokiniana*

Hanif Khan[1]*, S. M. S. Tomar and S. Chowdhury

Division of Genetics, Indian Agricultural Research Institute, New Delhi 110 012

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Abstract

Spot blotch of wheat caused by *Bipolaris sorokiniana* (Sacc.) Shoem, is one of the most important disease constraints to wheat cultivation in the north-eastern and eastern plain zones of India. Genetics of resistance to spot blotch was studied in seven resistant wheat lines *viz*., Chirya-3, Mayoor, Shanghai-4, Suzhoe 128-OY, Suzhoe 1-58, Longmai and Chuanmai #18, by crossing them with two susceptible varieties Sonalika and HD-2329. Studies under both artificial inoculation and natural epiphytic condition in F_1, F_2 and backcross generations indicated that resistance in Chirya-3 and Mayoor is governed by two dominant genes. The test of allelism showed that the resistance genes in the Chirya-3 and Mayoor are allelic. The continuous nature of frequency distribution for AUDPC of spot blotch reaction in F_2 generation involving resistant parents of Chinese origin did not suggest any simple Mendelian inheritance. The type of resistance among the resistant parents of Chinese origin Shanghai-4, Suzhoe 128-OY, Suzhoe 1-58, Longmai and Chuanmai #18 appears to be additive with polygenic control as the F_2 populations of the susceptible x resistant crosses exhibited different degrees of disease reaction of all categories, *viz*., resistant, moderately resistant, susceptible and highly susceptible.

Key words: Genetics, spot blotch, resistance, *Bipolaris sorokiniana*, wheat

Introduction

Spot blotch of wheat caused by *Bipolaris sorokiniana* (Saac) Shoem [syn. *Drechslera sorokiniana* (Saac) Subram & Jain], the perfect stage *Cochliobolus sativus* (Ito & Kuribay), has assumed alarming proportions, especially in the North Eastern and Eastern plain zones of India. Increase in temperature, coupled with a high relative humidity favour the outbreak of disease, especially under rice-wheat cropping system [1]. Yield losses between 20% and 80% were reported [2] and may be 100% under most severe conditions of infection [3]. Studies on genetics of resistance to spot blotch have been inconclusive so far. Previous studies have reported the resistance to be qualitatively [4-8], as well as quantitatively [9-11] governed.

In view of growing importance of spot blotch, lack of resistance to it and scant availability of information on underlying genetic mechanism of resistance, studies were conducted on the genetics of plant resistance in wheat to the pathogen *B. sorokiniana*.

Materials and method

Wheat germplasm screening was carried out at I.A.R.I. Regional Station, Pusa, Bihar, a 'hot spot' location to identify spot blotch resistant sources. Out of four hundred twenty two diverse genetic stocks of wheat including different accessions of elite lines and cultivars screened, the top 20 lines with high resistance were tested under artificial epiphytotic conditions in polyhouse at the Division of Genetics IARI, New Delhi to find out highly resistant and highly susceptible lines for inclusion in the genetic studies.

Crossing programme

Seven resistant wheat lines namely, Chirya-3, Mayoor, Shanghai-4, Suzhoe 128-OY, Suzhoe 1-58, Longmai and Chuanmai #18, were crossed with two susceptible varieties *viz*., Sonalika and HD-2329 to produce test material for studying mode of inheritance and gene action. A part of F_1 seeds collected from the crossed spikes was planted along with parents in the growth chambers at National Phytotron Facility (NPF), New Delhi. The seeds from selfed spikes were harvested on individual plant basis as F_2 seeds. The F_1 were also backcrossed with susceptible and resistant parents. The F_1 hybrids, their F_2's, backcrosses and parents were

*Corresponding author's e-mail: hanif.gene@gmail.com
[1]Present address: Scientist (Plant Breeding), Central Institute for Arid Horticulture, Beechwal, Bikaner
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planted in the field at Pusa Bihar during *Rabi* 2003-04 in the rows of 2m length, with 25 cm row spacing and 10cm distance between seed to seed. The standard agronomic practices were followed while epiphytotic condition was created in the field.

Creation of epiphytotic conditions in the field

Late sowing was done to provide maximum chance of disease spread during flowering time. While the field at Pusa Bihar was located in 'hot spot' region for spot blotch of wheat, the populations of the experimental material were also provided additional inoculum artificially. Spot blotch was induced by artificially inoculating spreader rows at required intervals in parental lines, F_1s, F_2s and backcross populations. A pure culture of local most aggressive isolate of *B. sorokiniana* (Pusa isolate) was multiplied on sorghum grains and spores were harvested in water. A spore suspension of fixed concentration (10^4 spores/ml) was uniformly sprayed at three stages *viz*., tillering, flag leaf emergence and anthesis during evening hours, following standard method [12]. Plots were irrigated immediately after inoculation to maintain a high relative humidity, which facilitate spore germination and disease development.

Disease Assessment

The disease was measured using spot blotch severity (%) using double-digit scoring method [13, 14]. As the disease progressed from the bottom to the top of the plant, the diseased area on leaf below flag (flag-1) leaf was greater than that of flag leaf. Three disease readings were recorded at 85, 95 and 105 days after sowing. The area under disease progress curve (AUDPC) was calculated using the percent severity estimates corresponding to the three ratings [15].

$$AUDPC = \sum_{i\ 1}^{n-1} [(x_i + x_{i\ 1})/2](t_{i\ 1} - t_i)$$

Where x_i is the disease severity on the i^{th} date, t_i is the i^{th} day; n is the number of scoring dates. The AUDPC measures the amount the disease as well as the rate of progress, and has no units.

Segregation analysis

The segregation for the disease response was analysed by χ^2 analyses to determine the goodness of fit of the observed segregation with the expected ratios.

$$\chi^2 \quad \sum \frac{(O-E)^2}{E}$$

Where O is the observed frequency, E is the expected frequency in a particular class of distribution and Σ is Summation over all classes. The plants, which scored up to 3,4 were pooled as resistant whereas the plants, with >5,6 score were pooled as susceptible. In many crosses where F_1s were showing intermediate values and F_2's were showing continuous variation were not subjected to chi-square analyses. The calculated χ^2 values were compared with the table value for d.f. at 5% level of significance.

Results and discussion

Pattern of inheritance of resistance to spot blotch was not uniform in all the resistant parents involved in crosses. Two resistant genotype *viz*., Chirya-3 and Mayoor showed complete dominance of resistance in F_1 generation in the crosses with susceptible parents Sonalika and HD 2329. Both the Chirya-3 and Mayoor are synthetic wheat lines whose spot blotch resistance has been derived from *Thinopyrum curvifolium.* Five other resistant parents namely, Shanghai-4, Suzhoe 128-OY, Suzhoe 1-58, Longmai and Chuanmai #18 showed lack of dominance or partial dominance for resistance to spot blotch in crosses with the susceptible parents.

The segregation analysis in F_2 generation of the four crosses supported the observation in F_1 hybrids involving resistant parents Chirya-3 and Mayoor with susceptible parents that resistance to spot blotch is dominant (Table 1). In these four crosses the data showed good fit to the segregation ratio of 15 resistant: 1 susceptible. This suggested that the spot blotch resistance in Chirya-3 and Mayoor was under control of two pairs of dominant genes Fig. 1(i) & 2(i). The backcross progenies from the four crosses (F_1 x susceptible parents) fell in the category of 3 resistant: 1 susceptible validating and supporting the hypothesis that the resistance is governed by two dominant genes (Table 1). To find out whether Chirya-3 and Mayoor possess similar genes for resistance, a test of allelism was conducted. Both the genotypes Chirya-3 and Mayoor were crossed with each other and the F_2 population was analyzed. All the F_2 plants of the cross Chirya-3 x Mayoor were resistant indicating the presence of same alleles for resistance to spot blotch. The resistance to spot blotch in another synthetic wheat line Chirya-1, a sister-line of Chirya-3 has been reported to be controlled by two dominant genes against spot blotch isolate from the American subcontinent. Similarly, Cugap, also derived from *Th. curvifolium* carries two dominant genes for resistance against Mexican isolate

Table 1. Segregation for spot blotch resistance in F_2 and BC_1 generation in four crosses

Cross	Total no. of plants	Reaction to spot blotch		Ratio tested	Observed χ^2 value	P value
		Resistant	Susceptible			
Sonalika x Chirya-3						
P_1	60	0	60			
P_2	60	60	0			
F_1	47	47	0			
F_2	252	231	21	15:1	1.867	0.5-0.1
BC_1	68	49	19	3:1	0.314	0.7-0.5
HD 2329 x Chirya-3						
P_1	60	0	60			
P_2	60	60	0			
F_1	42	42	0			
F_2	237	219	18	15:1	0.732	0.5-0.1
BC_1	62	44	18	3:1	0.538	0.5-0.1
Sonalika x Mayoor						
P_1	60	0	60			
P_2	60	60	0			
F_1	46	46	0			
F_2	228	211	17	15:1	0.566	0.5-0.1
BC_1	65	45	20	3:1	0.154	0.7-0.5
HD 2329 x Mayoor						
P_1	60	0	60			
P_2	60	60	0			
F_1	38	38	0			
F_2	269	247	22	15:1	1.707	0.5-0.1
BC_1	71	50	21	3:1	0.793	0.5-0.1
Chirya-3 x Mayoor						
P_1	60	60	0			
P_2	60	60	0			
F_1	41	41	0			
F_2	218	218	0			

of spot blotch [1]. The donor species *Th. curvifolium* has been postulated to carry about eight different genes for spot blotch resistance [16]. However, the resistance genes identified in the present study may be different from the other ones reported earlier. It may be presumed that both the set of resistance genes may belong to eight potential genes identified in *Thinopyrum curvifolium* derived wheat lines. The resistance in wheat against spot blotch has been variously characterised as a dominant [1, 4], recessive [8, 11] and no dominance to partial dominant [17, 18].

Five resistant parents of Chinese origin, namely, Shanghai-4, Suzhoe 128-OY, Suzhoe 1-58, Longmai and Chuanmai #18 showed absence of full dominance of the resistance in F_1's of the susceptible x resistant crosses. All the F_1's showed moderate resistance to spot blotch as compared to F_1's involving Chirya-3 and Mayoor, which showed complete resistance. F_2 populations of the susceptible x resistant crosses involving resistant parent of Chinese origin exhibited different degree of disease reaction of all categories *viz*., resistant, moderately resistant, susceptible and highly susceptible. The double-digit score of the disease could not be used to draw any inference about inheritance pattern. Therefore the double-digit score of individual plants taken at three stages (two intervals) was converted into Area Under Disease Progress Curve (AUDPC). The F_2 populations derived from the crosses involving Sonalika with Shanghai-4, Suchoe 128-OY, Suzhoe 1-58, Longman and Chunmai #18 showed continuous variation for spot blotch reaction in terms of

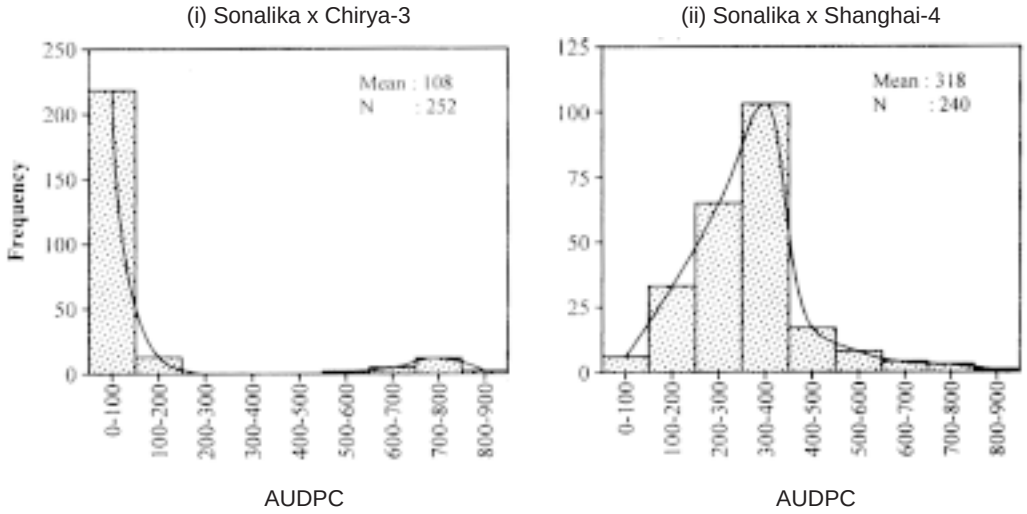

Fig. 1. Frequency distribution in F_2 generation of crosses involvingh susceptible (Sonalika) x resistant varieties for AUDPC to spot blotch showing (i) discontinuous and (ii) continuous variations

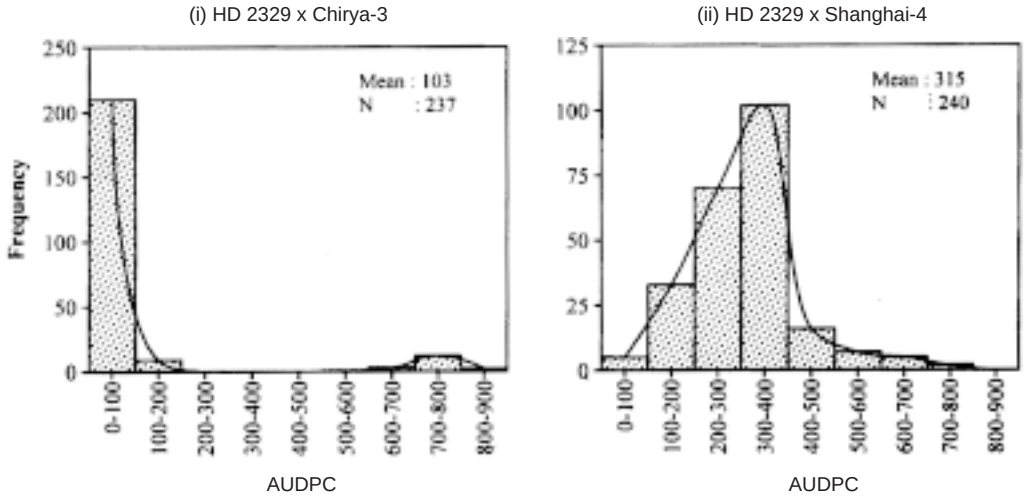

Fig. 2. Frequency distribution in F_2 generations derived from susceptable (HD 2329) x resistant crosses for AUDPC to spot blotch showing (i) discontinuous and (ii) continuous variations

AUDPC (Figs. 1 (ii) & 2(ii)). Similar trend was also observed in the croses involving in HD 2329 and above mentioned resistant parents (Fig. 2(i & ii). The continuous nature of frequency distribution as indicated by the AUDPC of spot blotch reaction in the F_2 segregating generations susceptible x resistant crosses involving Chinese resistant parent did not suggest simple Mendelian inheritance. The maximum frequency in the F_2 crosses was of moderately resistant plants. The type of resistance among the resistant parents, Shanghai-4, Suzhoe 128-OY, Suzhoe 1-58, Longmai and Chuanmai #18 appears to be additive with polygenic control. Studies on some other genotypes of Chinese origin such as Yangmai 6 and Longmai 10 indicated that the resistance to spot blotch is under polygenic control with additive gene action [2, 19, 20]. The Area Under Disease Progress Curve (AUDPC) for spot blotch in F_2 populations of susceptible x resistant crosses involving resistant parents Shanghai-4, Suzhoe128-OY, Suzhoe1-58, Longmai and Chuanmai#18 showed continuous frequency distribution with skewness towards resistant parents which implies that resistance is under polygenic control involving both additive and dominance gene action. Joshi *et al.* [21] also reported lack of dominance in F_1 generation of crosses of three resistant genotypes, ACC. No. 8226, Mon/Ald, Suzhoe#8 with susceptible parent Sonalika.The resistant genotype Chirya 3 showed strong expression of stay green trait and the F_1 crosses involving it exhibited absence of dominance as reported earlier [22].

They evaluated F_3, F_4, F_5 and F_6 generations under induced epiphytotic conditions and reported that the resistance was under control of three additive genes.

One of the important reason for the slow progress in breeding for spot blotch resistance has been suggested to be the quantitative nature of resistance [19] and absence of suitable resistant parents. However, by selecting for spot blotch resistance in F_3 and F_4 generations, a substantial gain in resistance can be achieved.

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