scientists and are safely preserved in germ plasm repository of Directorate of Wheat Research. A few of them were found to be tested for their response to Karnal bunt and those found resistant are listed in Table 2.

Table 2. Response of synthetic hexaploids and fixed prebreeding lines to the Karnal bunt pathogen (*Tilletia indica*) under artificial inoculated conditions. An * indicates the fixed prebreeding lines developed at the DWR, Karnal, the other lines are CIMMYT synthetic hexaploids.

Pedigrees of wheat lines categorized as resistant (up to 5% coefficient of infection).

DVERD-2 / *Ae. tauschii* (214) / OPATA
YUMAI 13 / 2*KAUZ
BCN / CROC-1 / *Ae. tauschii* (662)
ALTAR 84 / *Ae. tauschii* (219) // 2* LOXIA /3/ KAUZ
*EVD 2-1 1012 / Kauz // WH 542
*FASAN / CROC_1 / *Ae. tauschii* // KAUZ
*HD 2329 / CHOIX // RAJ 3777
*PBW343 / FIOS-1
*AGA / 2*CMH74A.582 / CMH76A.912 / CMH79.681 / BOW // RAJ 3777

Pedigrees of wheat lines categorized as moderately resistant (5–10% coefficient of infection).
XIANG82.2661 / 2*KAUZ
BCN // SORA / *Ae. tauschii* (323)
OPATA // CROC-1 / *Ae. tauschii* (879)
ALTAR 84 / *Ae. tauschii* (219) // SERI
CHEN / *Ae. tauschii* (TAUS) // FCT /3/ STAR
*HD 2329 / CHOIX // RAJ 3777
*PBW 343 // HE1 / 5*CNO79 / BORLAUG 95

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An inheritance study of spot blotch (Bipolaris sorokiniana (Sace) Schoem) resistance in bread wheat.

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Abstract. We studied the inheritance of resistance to spot blotch on six *T. aestivum* cultivars. Artificial epiphytotic conditions in the field were developed in the material, which was evaluated in a six parameter model and consisted of P_1, P_2, F_1, F_2, BC_1, and BC_2 generations. A total of 66 entries were evaluated from the six generation material. Disease scoring was recorded on the flag and penultimate leaf using double-digital rating. The resistance showed its dominance over susceptibility in all the F_1 material. The F_2 segregation ratio of the pathogen in 60% of the crosses involving 'resistant / resistant' and 'resistant / susceptible' cultivars was 15 resistant :1 susceptible. We showed that resistance is conditioned by two dominant genes with duplicate gene interaction. On the other hand, the segregation ratio of 9 resistant :7 susceptible in 40% of the crosses indicated complementary gene action. The BC_1 and BC_2 segregation pattern of 3 resistant : 1 susceptible further supplement the finding of the F_2 results. The genes controlling resistance and susceptibility in these parents are different.

Introduction. India, a major wheat-producing country, occupies second place after China in terms of area and production on global level. Three wheat species, *T. aestivum, T. turgidum* subsp. *durum,* and *T. turgidum* subsp. *dicoccum* are successfully cultivated in different parts of the country. Among the biotic stresses, rusts, smut, and foliar blight are the major diseases damaging the wheat crop at different stages with various intensity. Foliar blight is considered as a complex, because a number of pathogens causing blight, blotch, and spot are associated with wheat in India (Misra 1973; Joshi et al. 1978). *Drechslera sorokiniana* (Syn. *Helminthosporium sativum*; perfect stage *Cochliobolus sativus*) appears to be the major pathogen, along with *D. tritici repentis* and *D. tetramera* and *Alternaria triticina* and *A. alternata* (Joshi et al. 1974). The chief fungus causing blight or blotch is *B. sorokiniana* (Singh et al. 1980; Meena Kumari 1985). *Bipolaris sorokiniana* has been found to infect barley, oats, rice, and 12 other grasses (Misra 1973). Foliar blight is a problem in North Western Plains (Singh et al. 1993), the North Eastern Plains (Nagarajan and Kumar 1997; Chattopadhyay and Chakarabarty 1968; Narain et al. 1973), the Peninsular zone, and Nepal (Singh et al. 1998). A thick canopy and the profuse tillering of high-yielding cultivars favours the build up of a congenial microclimate for the development of this fungus (Joshi et al. 1983; Singh et al. 1986). The distribution of *A. triticina* is comparatively less than that of spot blotch. *Bipolaris sorokiniana* affects the wheat crop more occasionally than *A. trticiana* (Singh et al. 1993). More humid conditions during the growing period are conducive for establishment and subsequent spread of this disease. *Bipolaris sorokiniana* is a dominant species and is fast emerging as one of the major disease on national level (Singh et al. 1995).

Most of the present day wheat cultivars are susceptible to one or the other pathogen of this disease. Information on the inheritance of resistance to spot blotch is still scanty. A systematic program to breed spot blotch-resistant cultivars is needed and could be effectively undertaken if the donors imparting resistance to this pathogen and inheritance to this pathogen are studied on a sound footing. In the present study, *T. aestivum* material selected on the basis of multilocation screening against spot blotch was used to study the inheritance of resistance to this pathogen.

Materials and Methods. The present study was conducted with six wheat cultivars/breeding lines of diverse origin (Table 1). Among them, HD 2733, HD 2881, and DW 1293 were the resistant parents and Sonalika, DW 1277, and DW 1282 were highly susceptible to spot blotch. These parents were selected from Plant Pathological Screening Nursery (PPSN), which evaluates material on multilocation testing that are spread out through the hot spot. These six wheat lines were crossed in a half diallel to develop F_1, F_2, BC_1, and BC_2 generations. Three crop season were needed to develop the experimental material. The summer nursery facility at the IARI Regional Station, Wellington, Nilgiri, Tamilnadu, India, was utilized to advance the breeding material. The genetics of resistance to spot blotch was determined from breeding material comprised of P_1, P_2, F_1, F_2, BC_1 and BC_2 generations.

Table 1. Parental lines and pedigrees used in this study.

Parent	Pedigree
HD 2733	ATTILA /3/ TU1 / CARC // CHEN / CHTO /4/ ATTILA
HD 2881	KS / *T. turgidum* // HD 1999 // SKA*3 / *T. turgidum* subsp. *carthilicum* // HD 2204
DW 1293	HD 2402 // ALDAN / PF70534 // 2*Kauz /3/ HD 2657 / CPAN 2009
DW 1277	Kauz /3/ Tob / BAU / Bb /4/ ALD'S" /5/ Opata /6/ ToB /7/ HD2631
DW 1282	J-155 / HD 2007 // TRAP /3/ HD 2329N
Sonalika	II54.388 / AN /3/ Yt-54 / NIOB / LR64

The experimental material consisted of 66 entries (six parents, 15 F_1s, 15 F_2s, 15 BC_1, and 15 BC_2s). These lines were planted in three replications using a randomized block design at the research farm of the Indian Agricultural Research Institute, New Delhi, India, during crop seasons rabi 2003–04. Two rows of the parental lines, four rows each of the F_1s; six rows each of the BC_1 and BC_2, and ten rows each of the F_2 generations were grown with a row-to-row distance of 23 cm and 10 cm plant-to-plant. Recommended agronomic practices were followed to raise a good crop.

For effective screening against spot blotch, inoculum spraying was according to the standard techniques at 60 DAS to create sufficient disease pressure. Scoring of disease symptoms was on the flag and penultimate leaves using a double-digit rating system at the seventh day of growth stage 59 (Zadock scale) as proposed by Kumar et.al. (1998), which rated both severity and response and an improved field scale over the 0–9 scale suggested by Sarri and Prescot (1975). Plant were scored based on percent leaf area covered on flag and penultimate leaf as 0 (immune); 01–13, very resistant (VR); 14–35, resistant (R); 36–57, moderately susceptible (MS); 58–78, susceptible; and 79–99, highly susceptible (HS). In the experimental population, plants showing either of the categories (reactions) were the basis to proceed further. All the plants in different generations were observed carefully, counted, and a probable genetic ratio was fit for each cross. A chi-square test, as outlined by Stansfield (1969), was used to test the goodness-of-fit for the appropriate genetic ratio in all 15 crosses.

Results and Discussion. A half diallel between spot blotch resistant and susceptible lines comprised of 15 crosses was evaluated in the F_1, F_2, BC_1, and BC_2 in a randomized block design to study the inheritance (Table 2, p. 69). Disease attained full severity in these lines at the late milky stage and disease severity recorded. These parents were selected on basis of their diverse origin, distinct parentage, and distinct response to leaf blight.

The segregation ratio with respect to crosses involving the resistant parent HD 2733 and the remaining five parents (HD 2881, DW 1293, Sonalika, HD 1277, and DW 1282); HD 2881/DW 1293; HD 2881/DW 1277; and HD 2881/DW 1282 were 15:1. The calculated X^2 values in these crosses varied from 0.02 to 1.82 (Table 3, p. 70). The X^2 analysis revealed that the observed ratios were in agreement with the expected ones with a high degree of confidence (P value ranges from 0.016 to 2.71), indicating that resistance in these crosses is controlled by two genes with a duplicate type of gene interaction. This finding is in accordance with Adlakha (1984) who found that the inheritance of resistance to spot blotch is simple and is governed by one or two dominant factors. Three crosses involving 'susceptible / susceptible' parents, i.e., 'Sonalika/DW 1277', 'Sonalika/DW 1282', and 'DW 1277/DW 1282' show the segregation ratio as 9:7 suggesting that either of the parents contributed a dominant resistance factor in the F_1s. In earlier studies, the resistance to spot blotch in Sharbati Sonora and E 4858 was established as two complimentary genes. Two pairs of dominant, complimentary genes for susceptibility to *A. triticina* in NP 891 and one pair of dominant independent genes were reported by Kulshreshtra and Rao (1976). Three cross combinations were made with one susceptible parent, namely 'HD 2281/Sonalika', 'DW 1293/Sonalika', and 'DW 1293/DW 1277'. The segregation pattern/ratio was 9:7 (R:S). In these crosses, the calculated X^2 value ranges from 0.11 to 1.84, which fits with the table value ranges from 0.15 to 2.71 at one degree of freedom (Table 3, p. 70) indicating complementary gene interaction.

Table 2. Half-diallel cross combinations, parents, and segregation ratio for spot blotch resistance in the F_2 populations (R = resistant, S = suceptible parent).

Cross	Type of cross	Segregation ratio (F_2)
HD 2733 / HD 2887	R / R	15:1
HD 2733 / DW 1293	R / R	15:1
HD 2733 / Sonalika	R / S	15:1
HD 2733 / DW 1277	R / S	15:1
HD 2733 / DW 1282	R / S	15:1
HD 2881 / DW 1293	R / R	15:1
HD 2881 / Sonalika	R / R	9:7
HD 2881 / DW 1277	R / R	15:1
HD 2881 / DW 1282	R / S	15:1
DW 1293 / Sonalika	R / S	9:7
DW 1293 / DW1277	R / S	9:7
DW 1293 / DW 1282	R / S	15:1
R X S		
Sonalika / DW 1279	S / S	9:7
Sonalika / DW 1282	S / S	9:7
DW 1277 / DW 1282	S / S	9:7

Furthermore, the appearance of resistance in F_1 material indicated that resistance is dominant over susceptibility. The segregation pattern of spot blotch in 'resistant/resistant' parents and 'resistant/susceptible' crosses is observed as 15:1 (resistant : susceptible) in 60% of the cases, an indication that resistance is conditioned by two dominant genes with duplicate gene interaction. These results agree with the findings of Gopalakrishnan et al. (2003) showing interaction of two dominant genes modifying the Mendelian ratio. On the other hand, a 9:7 (R:S) ratio in 40% of the crosses indicated complementary gene action. The fact that the BC_1 and BC_2 generations were 3R:1S further support the results obtained from the F_2 generation. Finally, it is worth noting that the gene/s conditioning resistance and susceptibility in the parents used in this study were different showing variation in the expression.

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Table 3. Reaction to spot blotch in of F_2 and BC_1 populations of the different crosses. For the frequency distribution, 0, 1–13, and 14–35 are resistant classes and 36-57 and 58-78 and greater are susceptible reactions.

Cross	Generation	Frequency distribution 0	01-13	14-35	36-57	58-78 and >	Observed frequency (R:S)	Total plants observed	Expected frequency (R:S)	Expected segregation ratio	X^2 value	Table X^2 value	Probability (P)
HD 2733/HD 2887	F_2	—	84	20	9	—	104:9	113	105.95:7.06	15:1	0.93	0.46-1.07	0.30-0.50
	BC_1	—	40	18	16	—	58:16	74	55.50:18.50	3:1	0.45	0.15-0.46	0.50-0.70
HD 2733/DW 1293	F2	—	90	13	5	—	103:5	108	101.25:6.75	15:1	0.48	0.46-1.07	0.30-0.50
	BC1	—	39	5	17	—	54:17	71	53.25:17.70	3:1	0.04	0.016-0.15	0.70-0.90
HD 2733/Sonalika	F_2	—	50	40	7	—	90:7	97	90.94:6.06	15:1	0.16	0.016-0.15	0.70-0.90
	BC_1	—	7	74	14	2	51:16	67	50.25:16.75	3:1	0.04	0.016-0.15	0.70-0.90
HD 2733/DW 1277	F_2	—	42	54	10	—	96:10	106	99.38:6.63	15:1	1.82	1.64-2.71	0.10-0.20
	BC_1	—	18	30	13	5	48:18	66	49.50:16.50	3:1	0.18	0.15-0.46	0.50-0.70
HD 2733/DW1282	F_2	—	45	40	7	—	85:7	92	86.25:5.75	15:1	0.29	0.15-0.46	0.50-0.70
	BC_1	—	15	30	18	—	45:18	63	47.25:15.75	3:1	0.43	0.15-0.46	0.50-0.70
HD 2881/DW1293	F_2	—	80	20	5	2	100:7	107	100.31:6.69	15:1	0.02	0.004	0.95
	BC_1	—	36	22	15	—	58:15	73	54.75:18.25	3:1	0.77	0.46-1.07	0.30-0.50
HD 2881/Sonalika	F_2	—	60	9	45	3	69:48	117	65.80:51.19	9:7	0.20	0.15-0.46	0.50-0.70
	BC_1	—	29	20	18	—	49:18	67	50.25:16.75	3:1	0.12	0.016-0.15	0.70-0.90
HD 2881/DW1277	F_2	—	61	46	8	—	107:8	115	107.80:7.19	15:1	0.11	0.016-0.15	0.90-0.70
	BC_1	—	36	20	18	4	56:22	78	58.50;19.50	3:1	2.34	1.64-2.71	0.10-0.20
HD 2881/SW 1282	F_2	—	49	42	6	2	91;8	99	92.80;6.19	15:1	0.55	0.46-1.07	0.30-0.50
	BC_1	—	8	35	18	—	43:18	61	45.75;15.25	3:1	0.66	0.46-1.07	0.30-0.50
DW 1293/Sonalika	F_2	—	45	21	41	5	66;46	112	63.00:49.00	9:7	0.32	0.15-0.46	0.50-0.70
	BC_1	—	18	31	14	6	49:20	69	51.75:17.25	3:1	0.58	0.46-1.07	0.30-0.50
DW 1293/DW 1277	F_2	—	60	7	45	1	67:46	113	63.56:49.44	9:7	0.43	0.15-0.46	0.50-0.70
	BC_1	—	26	18	19	—	44:19	63	47.25:15.75	3:1	0.89	0.46-1.07	0.30-0.50
DW 1293/DW1282	F_2	—	47	55	9	—	102:9	111	104.6:6.94	15:1	0.65	0.46-1.07	0.30-0.50
	BC_1	—	17	33	16	7	50:23	73	54.75:18.25	3:1	1.65	1.64-2.71	0.10-0.20
Sonalika/DW 1279	F_2	—	7	41	10	30	48:40	88	49.50:38.50	9:7	0.11	0.016-0.15	0.70-0.90
	BC_1	—	5	37	9	13	42:22	64	48.00:16.00	3:1	3.0	2.71-3.84	0.05-0.10
Sonalika/DW 1282	F_2	—	2	43	19	24	45;43	88	49.50:38.50	9:7	0.94	0.46-1.07	0.30-0.50
	BC_1	—	6	40	6	15	46:21	67	50.25:16.75	3:1	1.44	1.07-1.64	0.20-0.30
DW 1277/DW 1282	F_2	—	7	41	8	36	48:44	92	40.25:40.25	9:7	1.84	1.64-2.71	0.10-0.20
	BC_1	—	8	36	3	16	44:19	63	47.25:15.75	3:1	0.89	0.46-1.07	0.30-0.50

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Development of a genetic stock carrying multiple rust and powdery mildew resistance genes.

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Yellow or stripe rust is one of the important rust diseases causing considerable yield loss in India, particularly in the North Western Plains and the Northern and Southern Hill regions. The *T. turgidum* subsp. *dicocoides*-derived yellow rust-resistance gene *Yr15*, present in the Israeli stock V763-2312, confers high degree of resistance against widely prevalent races in India, especially races 78S84 (virulent on *Yr9*), 46S119 (virulent on PBW 343), and I (Southern Hills) (Vinod et al. 2006). The line V 763-2312 is used widely as donor for the development of resistance lines at IARI, Regional Station, Wellington, India. The Australian stock Cook, carrying the *Th. ponticum*-derived, linked genes *Lr19* + *Sr25* and *T. timopheevii*-derived, linked genes *Sr25* + *Pm6*, confers a high degree of resistance against most prevalent races of the leaf and stem rust and powdery mildew pathotypes in India, although a new pathotype is reported virulent on *Lr19*. This stock is used effectively in developing several NILs of popular Indian bread wheat cultivars at the IARI, Regional Station, Wellington.

The availability of stocks carrying these genes in a spring wheat background will immensely help the breeders develop lines resistant to these pests. V763-2312 was crossed to Cook and the line HW 6001, which is resistant to leaf, stem, and yellow rust and powdery mildew, was obtained at the BC_3F_4 stage. The gene *Sr36* confers a very high degree of resistance against the widely occurring stem rust pathotypes in India and also to race Ug99, which is virulent on *Sr31* and becoming a threat to wheat production worldwide. Therefore, this stock with resistance genes *Lr19* + *Sr25*, *Sr36* + *Pm6*, and *Yr15* developed at Wellington will be very useful for the breeders in wheat-improvement programs for developing resistant wheat cultivars (Table 1).

Table 1. Characteristics of parental lines and HW 6001, a genetic stock with multiple rust and powdery mildew resistance genes.

Line/Cultivar	Black rust	Brown rust	Yellow rust	Powdery mildew
V763-2312	R	80S	R	2 (0–4 scale)
Cook	R	R	F (undesignated)	R
New line HW 6001 with *Lr19*+*Sr25*, *Sr36*+*Pm6*, and *Yr15*	R	R	R	R