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Short Communication

Combating leaf blight in wheat through resistance breeding

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Helminthosporium leaf blight (HLB) or spot blotch caused by *Bipolaris sorokiniana* is one of the most important diseases of wheat in hot and humid regions, resulting significant yield losses ranging 20-50% percent especially under rice-wheat cropping system [1]. The disease severity of HLB has increased due to crop intensification, growing wheat in non-traditional areas. It has been considered a major production constraint affecting nearly 12 million ha area under wheat in South Asia's intensive cropping systems. Most of the wheat varieties released for commercial cultivation posses only moderate to low levels of resistance thereby pressing the immediate need to identify cultivars with high genetic resistance that could be utilized as potential donors in the future breeding programmes. It has also been emphasized that the identification of parental stocks possessing adequate level of resistance to *B. sorokiniana* is urgently required [2]. An effective control of HLB can be achieved by introducing resistant cultivars as a major component of integrated disease management. Therefore, the present investigation was aimed at screening and identification of the HLB resistant lines in wheat through field and poly house testing and their sharing for effective and strategic utilization in the breeding programmes.

A set of 268 wheat germplasm lines collected from various national and international nurseries/trials were taken for the study. Three long term known susceptible checks namely Sonalika, HUW 234 and Kanchan were also included in the present study.

The genotypes were evaluated in RBD with three replications at Directorate of Wheat Research (DWR), Karnal, India during crop seasons 2004-05 and 2005-06. 100 seeds of each genotype were counted and dibbled in two rows plot of 4m length spaced at 23cm apart. The susceptible check Sonalika was also planted on borders as well as after every 20 test entries. All the recommended agronomic practices were followed to raise normal crop where preceding crop was rice.

The virulent strain of *B. sorokiniana* was maintained on potato dextrose agar (PDA) medium in the sterilized petridishes at 24 ± 1^{o}C at 12 h alternate light and dark cycles for 10 days. The spores were estimated and the spore suspension was adjusted to nearly 10,000 spores/ml. The spore suspension was sprayed as a fine mist on each plot using knapsack sprayer. The bulk inoculum was raised on autoclaved sorghum grains for 12 days at 24 ± 1^{o}C under 12 h alternate dark and light cycles and these were broadcasted in the field. A set of test lines were also planted in the plastic tunnel (poly house) in single row plot of 1 m length. The disease epiphytotic was created in the poly house following recommended procedure [3].

The disease score of HLB was recorded using double-digit scale [3]. The disease was recorded at three critical stages *viz.*, HLB 1 at stage 73 (early milk), HLB 2 at stage 77 (late milk stage) and HLB 3 at stage 83 (late dough) of Zadoks scale [4] and genotypes were categorized as immune or no blight (00), resistant (HLB score 01-23), moderately resistant (34-45), moderately susceptible (56-68), susceptible (78-89) and highly susceptible (89-99). The average of three stages for each genotype was calculated by taking mean of first and second digit separately.

The observations on ancillary attributes were recorded on 20 randomly selected plants from each plot as per standard procedures. The data of the crop seasons were pooled and analysis of variance (ANOVA) was carried out assuming year effects as random and genotypic effects as fixed [5]. Combined analysis of variance was done only for traits that have shown homogeneity of error variances. The variance components, phenotypic and genotypic coefficient of variations and genotypic correlation coefficients were also computed [6 & 7].

The results of pooled analysis across the years

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revealed significant differences for yield attributes and *Helminthosporium* leaf blight (HLB) under artificially inoculated field conditions at second and third stages. The disease score of genotypes for HLB incidence under poly house conditions was high as compared to field score. This might have been due to obvious reasons of higher disease incidence under poly house conditions wherein climatic factors affecting disease incidence were more conducive. However, in case of HLB-1, score under field conditions at initial stage, the genotypic differences were not very distinctive. The average effect of genotype was larger relative to the interaction effect for most of the traits particularly HLB score, revealing thereby that the precise ranking and grouping of genotypes over years is expected to be stable. The genotype x year effects was not significant for tillers/m, 1000-grain weight, grains/spike, HLB-2, HLB-3 and days to maturity, suggesting that genotypes have similar trend for expression of these traits over the years.

The mean, range, genotypic coefficient of variation (GCV), heritability (broad-sense) and genetic advance as percent of mean (GA) are presented in Table 1. The results indicated high degree of genetic variability as evident by mean and range for almost all the traits including HLB score. In general, a large number of modern high yielding genotypes of bread wheat had higher mean values for yield and yield determinants (tillers/m, grains/spike and 1000-grain weight) along with moderate score for HLB at second and third stage. It was also observed that wheat genotypes showed wide variation in almost all the traits particularly yield components like 1000-grain weight (22.7-52.8 g) and HLB score at third stage (13-99). This indicated that sufficient genetic variability exists for most of the traits in the material utilized and simultaneous improvement in these traits is possible through careful selection. In general the highest value of genetic advance as percent of mean (GA) was shown for spike length (95.4) followed by grains/spike, 1000-grain weight (46.0) and HLB-3 (43.5), suggest that there is possibility of improving these traits through direct selection. The highest estimates of heritability among yield attributes were observed for 1000-grain weight followed by grains/spike and spike length indicating that these traits are least influenced by environments and thus selection for these traits may be effective. However, the heritability estimates for HLB score at all three stages were moderate, thus indicating that HLB incidence to some extent is influenced by the environmental factors. Sharma *et al.* [8 & 9] reported that spot blotch resistance in wheat was quantitatively inherited with intermediate to high estimates of heritability. HLB resistance is lacking in wheat cultivars of south Asian countries [10 & 11].

Table 1. Mean, range, genotypic coefficient of variation (GCV), heritability and Genetic advance for HLB and yield components in different genotypes of wheat

Traits	Mean	Range	GCV	Herita-bility	GA as % of mean
Days to heading	78.2	70-103	23.87	0.69	17.55
Days to maturity	124.4	119-138	21.14	0.41	7.52
Plant height	92.1	78-118	9.85	0.33	17.30
Tillers/metre	148.6	118-194	31.25	0.78	11.60
Spike length	9.8	8.7-14.3	17.39	0.84	95.41
Grains/spike	43.9	34-78	33.63	0.89	46.00
1000-gr. weight	32.6	22.7-52.8	28.25	0.95	44.44
Yield/plot	456.9	145-870	30.45	0.63	11.02
HLB-1	13.0	00-35	27.14	0.42	15.84
HLB-2	35.0	01-78	24.82	0.55	43.54
HLB-3	46.0	13-99	19.96	0.36	35.19

HLB score of 268 wheat genotypes were recorded at three defined stages (HLB-1, HLB-2 and HLB-3) under field as well as under poly house conditions and were averaged for two years (Table 2). The most desired category of highly resistant genotypes consisted of only 39 genotypes (14.5 percent) from the total screened material, whereas about 35 percent each (total 70%) were in moderately resistant or susceptible category. The highly resistant genotypes for HLB namely, BH 1146, HRLSN-15, Nepal-1, Ning 8201, Chirya 1, Chirya 3, Chirya 7, BW/SH 16, Mayoor, Yangmai-6, ML 838, HRLSN 24 provide opportunity to incorporate HLB resistance by utilizing them in hybridization programme. Performance of most of these lines with respect to other economic traits like tillers/m, spike length, grains /spike and 1000-grain weight was within the desired limits. However, the duration of heading, maturity and plant height and yield potential might be improved by involving second parent as a good agronomic base.

Minor variations were recorded in the nature and magnitude of disease incidence in the crop seasons. However, these genotypes might be considered as stable sources as they have been screened for two seasons under extreme disease pressure. Moreover, the expectedly very high HLB score of susceptible checks indicated the perfection achieved for the screening techniques. The Indian wheat programme made efforts in identifying and sharing these HLB resistant wheat genotypes for effective and wider utilization as donors. Now visualizing the wider area under this disease and its impact on yield, major emphasis is being given on utilization of these diverse and highly resistant genotypes in the future wheat breeding programmes to incorporate multiple disease resistance. This will also cater the area specific needs of wheat improvement in South Asia focusing more on east and far eastern regions of India.

Table 2. Grouping of wheat genotypes based on their average incidence of HLB

Category	No. of genotype	HLB scale	Promising genotypes
Highly resistant	39	00-24	BL-1887, HRSN-7, BL-1835, BL-2655, HRLSN-15, HRLSN-22, NL-922, HRLSN-24, BH-1146, Nepal-1 Ning-8201, Chirya-1, Chirya-3, Chirya-7
Moderately resistant	95	34-46	HRLSN-6, BL-2623, BL-1915, BL-1866, BL-2127, HRLSN-19, HRSN-20, Senghai-7, PBW-373, PBW-475, PBW-492, PBW-493, BW-502, VL-738, VL-818, HPW-184, K-8027, K-9107, BW/SH-6, BW/SH-7, BW/SH-75, SENGHAI-158, BREEDSEL-85, BREEDSEL-105, BREEDSEL-110, BREEDSEL-116, BREEDSEL-246, BREEDSEL-978, BL-3047, EGPSN-90, NW-2026
Moderately susceptible	97	56-68	HRLSN-1, BL-2047, BL-2623, HRSN-8, BL-1905, BL-2727, BL-1910, BL-2537, CN079/RULLA, SW89-422, Nepal-5, PBW-443, UP-2425, HD-2733, HD-2687, HD-2770, HUW-468, HUW-533, HUW-541, NW-1012, NW-1014, BW/SH-77, PC-OE-BW-22, GW-273, BREEDSEL-334, BREEDSEL-906, EGPSN-40, EGPSN-41, BL-2983, BL-3002, PBW343, NL-966
Susceptible	33	78-89	BL-1882, NIAW-34, BL-1804, RAJ-3765, K-9006, Kanchan, HUW 234, LOK BOLD, GW-173, DL-788-2, SAWSN-131, BL3095, BL-3106, BL-3107
Highly susceptible	04	99	Raj 4015, BL-3263, Sonalika, HUW 234

Table 3. Mean performance of promising wheat genotypes for economic attributes along with HLB-3 screened under Indo-Gangetic plains of India

Genotype	Pedigree	Days to heading	Plant height	Tillers/ (m)	Spike length	Grains/ spike	1000-grain weight	Yield/ plot	Disease tole-rance level HLB-3*
BL 1887	SIDDHARTHA/NANZING8319//NEPAL297	87.0	96.0	154.0	13.0	42.0	38.0	768.0	24.0
BL 2655	BL1530/BL1095//NL297/CHIRYA-7	88.0	110.0	180.0	12.3	33.0	34.0	734.0	13.0
HRLSN-15	(205)/5/BP10*3/4/IAS5*4/CT14/23/3/IAS5S*4/ EG.AUS//IAS55	90.0	95.0	165.0	10.3	47.0	31.0	907.0	13.0
HRLSN-24	MILAN/SHA7	90.0	100.0	169.0	8.0	46.0	28.0	867.0	13.0
BH-1146	Ponta Grassa 1	86.0	100.0	220.0	9.0	21.0	44.0	345.0	13.0
Nepal-1	NL297/NING8201//BL1022	91.0	106.0	210.0	10.0	68.0	32.0	420.0	13.0
NING-8201	HLB resistant line from China	90.0	90.0	155.0	9.0	38.0	40.0	590.0	13.0
CHIRYA-1	HLB resistant line from CIMMYT/Nepal	89.0	89.0	175.0	10.0	37.0	39.0	725.0	23.0
CHIRYA-3	HLB resistant line from CIMMYT/Nepal	90.0	93.0	154.0	11.0	46.0	38.0	725.0	13.0
BW/SH-16	SABUF/7/ALTAR84/AE.SQUARROSA(224)// YACO	89.0	96.0	149.0	10.0	36.0	41.0	655.0	13.0
Mayoor	BW/SH 70	90.0	104.0	178.0	9.0	28.0	36.0	640.0	23.0
Yangmai # 6	HLB resistant line from China	88.0	102.0	131.0	7.0	56.0	36.0	395.0	23.0
MON'S/ALDS	Selection from progeny of cross MON'S/ALDS	90.0	105.0	180.0	13.0	39.0	41.0	520.0	23.0
BREEDSEL159	RDWG/3*BCN	93.0	92.0	125.0	12.0	44.0	45.0	455.0	23.0
BREEDSEL172	BOW/PRL//BUCK/3/PIDA	92.0	87.0	172.0	10.0	53.0	35.0	700.0	23.0
HRWYT-4	ERA F2000	88.0	102.0	145.0	9.0	38.0	37.0	795.0	24.0
HRWYT-33	MUNIA/ALTAR84//AMSEL	90.0	100.0	124.0	10.0	42.0	32.0	655.0	13.0
BL3124	BL1093/NL792/BL1907	90.0	107.0	142.0	12.3	46.0	40.0	720.0	23.0
BL3198	BL1761/BL1811V	88.0	110.0	162.0	12.0	39.0	41.0	740.0	23.0
EGPSN 103	SERI.1 B*2/3/KAUZ*2/BOW//KAUZ	92.0	88.0	135.0	9.3	41.0	37.0	680.0	23.0
IBWSN 26	BOW/FKG15	91.0	100.0	160.0	10.6	53.0	35.0	720.0	23.0
Sonalika (check)		75.0	90.0	136.0	8.6	40.0	38.0	452.0	99.0
HUW 234 (check)		72.0	91.0	129.0	9.0	41.0	36.0	368.0	99.0
Mean		90.2	98.07	162.5	10.3	42.6	37.7	645.5	23.4
LSD$_{0.05}$		1.02	2.34	5.28	0.47	1.10	2.03	45.87	1.21

*HLB score at most conducive crop stage (stage 83)

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