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RESEARCH ARTICLE

Assessment of Wheat Genotypes for Spot Blotch and Other Traits under Normal and Diseased Conditions

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Abstract

Exploring the existing variability among wheat germplasm lines for trait of interest is of utmost importance for plant breeders to start the plant breeding activity under crop improvement programme. Hence, with this aim, 93 wheat genotypes were evaluated for spot blotch resistance and other traits in normal and artificial epiphytotic conditions during *rabi,* 2018-19 at Agriculture Research Farm, Institute of Agricultural Sciences, Banaras Hindu University. Findings revealed the presence of considerable variability among the genotypes for the studied traits grown in two different conditions hence, there is ample scope to develop superior genotypes along with spot blotch disease resistance. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) shows the minute difference for area under disease progress curve (AUDPC) and other traits in both conditions, indicating low environmental influence. High heritability with high genetic advancement for spot blotch disease resistance specified that its inheritance pattern may be additive in nature; therefore, direct selection could be effective in a breeding programme. In both conditions, genotype Raj 3814 had the lowest disease severity; in each environment, we identified 10 highly resistant genotypes. Thus, these genotypes can be used as resistant parent to breed the new source of resistance along with better yield. A negative correlation of AUDPC with seed yield per plant and other traits implies indirect selection of these traits to minimize spot blotch disease severity and increase crop yield.

Keywords: Wheat, Spot Blotch, AUDPC, *Bipolaris sorokiniana*, Resistance.

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Introduction

Among the major cereal crops, wheat (*Triticum aestivum* L.) is considered as one of the most paramount food crops in the world (Alzaayid and Aloush, 2021) as it is widely grown and also consumed as a food by huge people in the world. It is considered a staple food for more than 35% of the world's population (FAO, 2018) and because of the rapid population growth, the demand for wheat is expected to be high in 21st century as well (Prasad, 2022). Wheat is a major food crop in the world but is challenged by biotic and abiotic factors, which significantly lowered the crop yield (Kaur *et al*., 2021). In continuation, wheat crop is challenged by an important fungal disease viz., spot blotch which is causing by *Bipolaris sorokiniana* (Prasad, 2022 and Chandra *et al.* 2019). According to Kumar *et al.* (2019) it is known as the most crucial disease mostly in warm and humid region of South Asia and South America and this disease considerably reduces the crop yield, affect the quality of the crops in the country, especially in the Eastern Gangetic Plains of South Asia, which includes India, Nepal, and Bangladesh (Joshi *et al*. 2007a and Gupta *et al*. 2018). It remains more severe in the north eastern plain zone under late sown conditions where rice-wheat cropping system is followed. In South Asia, around 10 mha of land is affected by spot blotch, of which 9 mha exists in India alone, where rice-wheat cropping system has dominated since the time of green revolution (Joshi *et al*., 2007a). In severe conditions, disease may limts the yield upto 18 to 50% in the warmer and humid regions of the world (Gurung *et al*. 2014) and further yield loss could be reached up 100% under more severe/favorable conditions, if genotypes are lacking the resistance genes for spot blotch disease (Mehta, 1994 and Gupta *et al*. 2018). As per Yadav *et al.* (2015), around 25 million hectare of wheat land is badly affected by spot blotch disease, in continuation, spot blotch disease is known as one of the major constraints for wheat production in the globe, mainly the areas which is tagged as hot and humid climate (Tomar *et al*. 2021).

Severe condition of spot blotch disease is easily can be control by using fungicide but its repeated application involves additional cost to the growers, health hazard and the emergence of fungicidal resistance in the target pathogen. Further, there in still an unavailablity of completely resistant wheat genotypes to be cultivated to save the yield loss occurred by spot blotch because it is controlled by many genes (Gupta *et al*. 2018) and tagging the linked genes and its incorporation into single genotype to ensure the high level of resistance (Kumar *et al*. 2019). Therefore, exploring the available diverse germplasm lines and developing the resistance genotypes to save the yield loss that occurred by spot blotch is one of the eco-friendly approaches and continuing process (Prasad *et al*. 2013).

In this context, germplasm lines of wheat have been evaluated intensively by the researchers to find out the efficient donors or genotypes to be used in crossing program and further to obtain desirable segregants in later generations (Lamalaksmi *et al*., 2013). In recent past, resistance genotypes/genetic stocks have been identified by CIMMYT (Chowdhury *et al*. 2013 and Kumar *et al*., 2016), Prasad *et al*. (2013) in barley. Similarly, Kumari *et al*. (2018) also identified and reported some of the new source of resistance in wheat crop by screening the genotypes grown across the location and over the years; however, it is not up to the mark. So, screening of diverse wheat genotypes/germplasm for resistance to spot blotch and other desirable traits at large scale is a continuous process in field condition is vital because evaluation of huge genotypes under controlled conditions are not feasible (Duveiller and Sharma 2012, Lillemo et al. 2013 and Tomar *et al.* 2021). As per available reports, a number of genotypes are developed with better resistance to spot blotch disease, but this level of resistance is not enough to minimize yield loss because of slow progress and the polygenic nature of trait (Joshi *et al*. 2004b). Besides this, some morphological markers such as leaf angle, leaf wax and stay green have been reported which shows a positive association with spot blotch disease resistance hence, such reports could helps to breeders for selecting/developing resistance genotypes with better yielding during the breeding programme (Joshi *et al*. 2007b; Joshi and Chand (2002) and Prasad *et al*. (2013). Various genetic parameters, such as mean, range, and heritability, are used to measure the degree of genetic variability and know the genetic contribution of genotypes associated with spot blotch resistance is useful and practiced in crop improvement programme (Singh *et al*. 2007, Thakur *et al*. 2018). High heritability for a trait of interest shows the presence of additive gene action hence, and selection may be fruitful for crop improvement of these traits (Thakur *et al*. 2018).

It is therefore, by considering the above facts, experiment was desinded to explore the genetic information of a set of 93 diverse wheat genotypes grown in normal as well as in artificial ephiphytotic condition inorder to tag the superior genotypes having satisfactory yield, resistance and better other desirable traits for its utilization in plant breeding and producing the enough food grains for supplying the demand of growing population.

Materials and Methods

A set of 93 diverse wheat genotypes, comprised of national genetic stock nursery lines and released varieties for different zones *viz.,* North Eastern Plain Zone, North Western Plain Zone, Central Zone, Peninsular Zone and few exotic lines maintained by breeders department of Genetics and Plant Breeding, were screened for spot blotch disease, yield and other traits grown under normal as well as artificial epiphytotic conditions. The experient was carried during *rabi*, 2018-19 at Agriculture Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi in randomized complete block design. Each genotype was sown in a two rows of 2 m length in three replications in each condition and recommended agronomic practices were followed to raise the healthy crops.

Artificial Epiphytotic Conditions and Disease Assessment

Spore suspension of 10^4 spore/mL of *Bipolaris sorokiniana* fungus was uniformly sprayed at the time ear emergence Zadoks *et al*. (1974) during evening hours following the method of Chaurasia *et al*. (1999). After inoculation, experimental plots were irrigated immediately to provide a friendly environment of high humidity so that the pathogen can grow and multiply on the host (Joshi and Chand, 2002). The double-digit scoring (DD = 00-99) method was used to record the disease progress (Saari and Prescott, 1975) at three different growth stages of plant *viz*., GS 63 (beginning of anthesis to half-complete), GS 69 (anthesis complete) and GS 77 (late milking) following the Zadoks *et al.* (1974). The growth pattern (pure culture), conidia morphology of *B. sorokiniana* and disease symptoms (increasing order) are presented in Figure 1(a-c), respectively.

Data Recording and Statistical Analysis

Randomly five plants were tagged for each genotype in all the replication and data for the traits like days to 50% flowering, days to 75% maturity, grain filling duration, plant

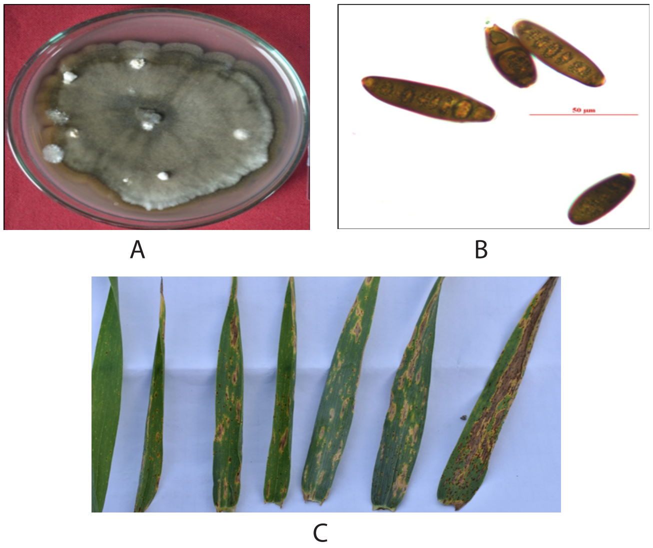

Figure 1(A): Pure culture of *Bipolaris sorokiniana* grown over PDA, **(B)** Spore of *B. sorokiniana* causing spot blotch disease in wheat, **(C)** Spot blotch disease severity on leaves in increasing order (left to right)

height, tillers per plant, peduncle length, spike length, awn length, biological yield per plant, seed yield per plant, harvest index, 1000 grain weight, and disease severity on plot basis was recorded for calculationg the AUDPC. The visual assessment of leaf angle and leaf waxiness was also assessed with aim to know its frequency among the population as these traits are associated with resistance to spot blotch. The disease severity in percent was calculated using double-digit score (Roelfs *et al*., 1992) to estimate the AUDPC.

The mean AUDPC was used to classify the 93 genotypes into different categories, i.e., resistant, moderately resistant, susceptible and AUDPC was calculated using following formula.

$$\text{AUDPC} = \sum_{i=1}^{n} [\{(Yi + Y(i+1)/2\} \times (t(i+1) - ti)]$$

where, Yi = disease level at time ti
t (i + 1) - ti = Time (days) between two disease scores
n = number of dates on which spot blotch was recorded

Leaf Angle and Waxiness

Leaf angle was measured just after an ear emergence (Nigam and Srivastava, 1976) using a protractor at the growth stage of 51 to 55 days (Zadoks *et al.* 1974). The genotypes were grouped into four classes like erect, semierect, semi-drooping. The leaf waxiness was recorded at growth stage 69 (Zadoks*et al.* 1974). Each genotype was grouped into waxy, semi-waxy, or non-waxy based on visual appearance of wax on the plant surface/leaf sheath (Prasad *et al.* 2013). The recorded data for 13 traits of two environments were subjected for statistical analysis using INDOSTAT Ver. 9.2 software.

Results and Discussion

Since spot blotch disease of wheat is one of the major constraints to global wheat production, mainly for hot and humid climate growing zones (Tomar *et al*. 2021) and it significantly limits the crop yield (Gupta *et al*. 2018) hence, the present study was designed with aim to explore genetic information of a set of 93 wheat genotypes and its use in plant breeding in order to develop the resistance/durable genotypes and save the yield loss of wheat crops through very effective and eco-friendly approach (Prasad *et al*. 2013, Gupta *et al*. 2018). The analysis of variance (ANOVA) showed significant differences for thirteen traits in 93 wheat genotypes studied under normal and artificial epiphytotic conditions (Tables 1 and 2). These findings indicate the presence of an enormous amount of phenotypic variability among the wheat genotypes for spot blotch disease, yield and yield contributing traits. Its exhibts that there is ample scope to breed the superior genotypes having low disease severity and desirable for other economically important traits by exploring such genotypes as parents donors or cultivars in future breeding programms.

The estimate of 13 traits of 93 genotypes (grown in normal and artificial condition) are presented in Tables 3 and 4. Which gives an idea about the relative importance of heritable and non-heritable variation (Thakur *et al*. 2018) while the environmental coefficient of variation gives an idea about non-heritable and non-fixable which is of non-significance in plant breeding. Present findings showed that the PCV value was slightly higher than the corresponding GCV for studied traits in both conditions. This indicates that appearance of variation among the genotypes for such traits is not only due to genetic makeup but also environmental effect. Moderate phenotypic variability was observed for traits such as 1000 grain weight, plant height, tillers per plant and peduncle length. Therefore, it is concluded that PCV and GCV for a majority of traits are moderate to high, which depicts considerable variation among 93 genotypes. Hence, exploitation of these traits in future breeding programmes can be done to enhance the crop output (Thakur *et al.* 2018; Thapa *et al.* 2018 ; and Chandra *et al.* (2019). The remaining traits, like days to 50% flowering, days to 75% maturity, grain filling duration and harvest index, exhibited less phenotypic variation, indicating that the environment less influences these traits.

The estimate of heritability and genetic advance also estimated to understand the inheritance pattern of spot blotch disease resistance and other traits of 93 genotypes grown in two environments. Studied characters exhibited higher heritability, accompanied by high genetic advance as percent of mean was also estimated for most of the characters *viz* seed yield per plant, 1000 grain weight, area under disease progress curve (AUDPC) and other traits. Our results indicate that high heritability of these traits could be

Table 1: Analysis of variance of 93 wheat genotypes for 13 traits grown under normal condition

Sources of variation	*DF*	*DM*	*GFD*	*PH*	*NTPP*	*PED L.*	*SL*	*AL*	*BYPP*	*SYPP*	*HI*	*1000GW*	*AUDPC*
Replicates	63.78	21.42	15.32	35.91	28.52	39.65	21.79	4.62	84.39	31.07	59.18	17.37	1521.15
Genotypes	32.43**	36.67**	17.87**	347.86**	7.26**	28.10**	4.04**	5.03**	33.76**	7.25**	18.84**	304.647**	26284.24**
Error	0.83	1.26	1.97	2.69	0.53	0.37	0.32	0.28	1.30	0.26	2.12	0.41	950.59
Mean	75.02	113.73	38.71	93.38	9.34	16.67	9.77	5.72	25.09	10.33	41.13	40.18	330.83
C.V.	1.22	0.99	3.63	3.76	4.80	3.65	5.86	5.34	7.55	8.99	3.54	1.50	13.32

Table 2: Analysis of variance of 93 wheat genotypes for 13 traits grown under artificial epiphytotic condition

Sources of Variation	*DF*	*DM*	*GFD*	*PH*	*NTPP*	*PED L.*	*SL*	*AL*	*BYPP*	*SYPP*	*HI*	*1000GW*	*AUDPC*
Replicates	60.52	60.24	37.60	59.40	37.09	28.47	22.60	9.28	94.04	10.28	12.13	26.90	3245.10
Genotypes	32.31**	43.03**	12.68**	331.34**	6.88**	25.71**	3.46**	5.92**	38.72**	8.07**	15.70**	56.69**	47680.93**
Error	0.88	1.35	2.12	3.09	0.49	0.68	0.35	0.18	1.48	0.36	1.800	0.30	1428.34
Mean	75.89	112.60	36.71	94.34	8.66	17.05	9.86	5.49	24.64	10.08	40.86	39.87	444.20
C.V.	1.24	1.03	3.97	3.19	5.17	4.86	6.01	4.77	8.94	7.97	3.28	1.40	15.51

*, ** Significant at 5 and 1% levels, respectively**,** CV=Coefficient of Variation (%)
Where, DF = Days to 50 % Flowering, DM = Days to 75 % Maturity, GFD = Grain Filling Duration (days), PH = Plant Height (cm), NTPP = Number of Tillers Per Plant, PED. L. = Peduncle Length (cm), SL= Spike Length (cm), AL = Awn Length (cm), BYPP = Biological Yield Per Plant (gm), SYPP = Seed Yield Per Plant (gm), HI = Harvest Index

Table 3: Estimation of genetic parameters of 93 wheat genotypes for 13 traits grown under normal condition

Parameters	*DF*	*DM*	*GFD*	*PH*	*NTPP*	*PED L.*	*SL*	*AL*	*BYPP*	*SYPP*	*HI*	*1000 GW*	*AUDPC*
Average Mean	75.02	113.73	38.71	93.38	9.34	16.67	9.77	5.72	25.09	10.33	41.13	40.18	257.78
Lowest Range	67.67	102.00	33.00	74.69	6.47	6.30	6.42	3.06	14.68	5.86	33.50	27.57	141.15
Highest Range	85.00	125.00	44.00	129.12	14.00	26.55	12.70	10.76	34.57	15.21	48.71	52.40	826.75
PCV (%)	4.49	3.18	6.97	11.62	17.83	18.60	12.81	23.90	13.88	21.60	6.75	11.47	29.30
GCV (%)	4.33	3.02	5.95	11.49	16.04	18.24	11.39	22.00	13.11	20.78	5.74	11.37	27.78
ECV (%)	1.22	0.99	3.63	1.76	7.80	3.65	5.86	9.34	4.55	7.99	3.54	1.49	9.32
h^2 (Broad Sense)	0.93	0.90	0.73	0.98	0.81	0.96	0.79	0.85	0.89	0.90	0.72	0.98	0.90
Genetic Adv. as % of mean	8.58	5.92	10.46	23.39	29.71	36.84	20.87	41.72	25.52	28.85	10.06	23.23	54.248

Table 4: Estimation of genetic parameters of 93 wheat genotypes for 13 traits grown under artificial epiphytotic condition

Parameters	*DF*	*DM*	*GFD*	*PH*	*NTPP*	*PED L.*	*SL*	*AL*	*BYPP*	*SYPP*	*HI*	*1000GW*	*AUDPC*
Mean	75.89	112.60	36.71	94.34	8.66	17.05	9.86	5.50	24.64	10.08	40.86	39.87	438.81
Lowest Range	68.33	101.67	31.67	75.25	5.53	6.72	6.65	3.47	12.27	4.75	32.32	27.50	184.36
Highest Range	84.33	123.33	41.00	126.42	13.53	25.36	12.57	12.03	36.30	15.73	46.27	51.90	1205.55
PCV (%)	4.44	3.47	6.47	11.24	18.73	17.63	11.95	26.35	15.13	22.00	6.21	10.96	29.22
GCV (%)	4.27	3.31	5.11	11.09	16.86	16.94	10.33	25.18	14.30	20.92	5.27	10.88	27.95
ECV (%)	1.24	1.03	3.97	1.87	8.17	4.86	6.01	7.77	4.94	7.97	3.28	1.40	8.51
h^2 (Broad Sense)	0.92	0.91	0.62	0.97	0.81	0.92	0.75	0.91	0.89	0.88	0.72	0.98	0.92
Genetic Adv. as % of mean	8.44	6.51	8.32	22.53	31.26	33.55	18.40	49.57	27.85	30.70	9.21	22.22	76.01

Where, DF = Day To 50 % Flowering, DM = Day To 75 % Maturity, GFD = Grain Filling Duration, PH = Plant Height, NTPP = Number of Tillers Per Plant, PED. L. = Peduncle Length, SL= Spike Length, AL = Awn Length, BYPP = Biological Yield Per Plant, SYPP = Seed Yield Per Plant, HI = Harvest Index.

due to additive gene action which supports the findings of Virender *et al.* (2015), Pandey *et al.* (2016), Turan *et al.* (2017), Chethana and Rudranaik (2017) and Chandra *et al.* (2019). It is, therefore, such a finding could be effective for direct selection of promising lines for targeted traits.

Categorization of Genotypes based on AUDPC

In the present study, AUDPC was calculated to identify the highly resistance genotypes with better yielding by grouping the genotypes into resistance, moderately resistance, moderately susceptible and susceptible classess.

Based on the genetic makeup of genotypes and severity level, plant breeders/researchers may choose these lines and design the research strategies to improve crop plants for trait interest. Similar results also published by Khan and Chowdhury (2011); Dibya *et al.* (2020); Kumar *et al.* (2020); and Mahapatra *et al.* (2020). Findings also showed that out of 93 wheat genotypes grown in normal condition, 31 genotypes fall into the resistance category having AUDPC ranging from 141.15 to 198.76 of which 10 best genotypes based on lower AUDPC presented in Table 5. Of which Raj 3814 and DBW 166 genotypes scored the lowest AUDPC value of 141.15 followed by FLW 10 (148.35), WR 544 (148.35), Chiriya#3 (155.90), HD 2285 (157.00), HD 3043 (161.32), Yangmai#6 (162.76), Mon/Ald (169.96), FLW 16 (171.40) and DBW 88 (175.52) with satisfactory yield and for other traits. Chandra *et al.* (2019) also published their findings, revealing that most genotypes were moderately resistant and susceptible.

Similarly, in artificial condition, 16 tagged as resistance genotypes having AUDPC ranged from 184.36 to 292.39 of which 10 best genotypes (RAJ (181.36), HI 8737 (218.93), Yangmai#6 (223.25), Ning 8201 (236.21), HD 2733 (236.32), LOK 1(237.65), DBW 168 (246.29), DBW 173 (249.29), Mon/Ald (252.06) and HI 8708 (262.14) scored lowest AUDPC with good yield (Table 6). The moderately resistant category consisted of 40 genotypes, moderately susceptible 27 and 10 susceptible genotypes, respectively. These findings agreed by Kumari *et al.* (2018), Dibya *et al.* (2020), Kumar *et al.* (2020) and Mahapatra *et al.* (2020).

Based on excellent findings, we have noticed that genotypes grown in normal condition differed for their resistance reaction as compared to the genotypes grown in artificial epiphytotic condition which could be because of more pathogenic load in artificially epiphytotic conditionthan and genetic makeup of genotypes too (Elliot *et al.*, 2002) and also consistency temperatures with 100% relative humidity which is favorable for diseae development (Duveiller *et al.* (1998). In both the conditions, genotype Raj 3814 exhibited very less disease severity hence, we considered this one as highly resistance genotype by comparing the performance of resistance checks like Ning 8201 and Yangmai#6 genotype, thus such resitance genotypes could be used as donor parent or even could b released as variety (Dhakal *et al.* 2020). Further, it is found that in both conditions, genotypes, namely HD 3171, HD 4730, HUW 468, HUW 55 and Sonalika, expressed severe symptoms and responses to higher degree of disease severity considered as highly susceptible genotypes. For crop improvement point of view, highly resistant and/or highly susceptible genotypes with potential role could be used as donor in hybridization programme for developing superior cultivars/genotypes.

Phenotypic traits such as leaf angle and waxiness indirectly play an important role in identifying the resistance genotypes against resistance to spot blotch disease. Our study evinced that out of 93, 35 genotypes showed erect leaf angle (37.63%), 28 were semi erect (30.10%), 20 genotypes were semi-drooping (21.50%) and 10 genotypes exhibited drooping pattern (10.75%). Similarly, for leaf waxiness 17 genotypes (18.27%) showed waxiness, 47 genotypes (50.53%) exhibited semi waxy pattern and 29 were non-waxy (30.20%). The frequency distribution of 93 genotypes based on leaf angle and waxiness is presented in Figure 2 (a-b), respectively. All 10 genotypes identified resistance in each environment exhibit either erect or semi-erect leaf stature except HD 2265 HI 8078 genotype. Similarly, most resistance genotypes confer waxy or semi waxy leaf for leaf waxiness except for HD 3043 genotype in normal and HI 77 in artificial conditions. The mechanism behind these phenotypes is that the presence of wax on leaf or stem does not allow water droplets to retain on leaf which could create humidity for spore germination and acts as a barrier for entry of the pathogen. Similarly, erect leaf stature drains out water drops and hinders spore germination. Thus, genotypes having either erect or semi erect leaves and waxy or semi waxy are positively associated with resistance to spot blotch hence, such genotypes could be exploited to breed the promising wheat genotypes (Joshi and Chand, (2002); Prasad *et al.* (2013) and Chandra *et al.* (2019) for human being.

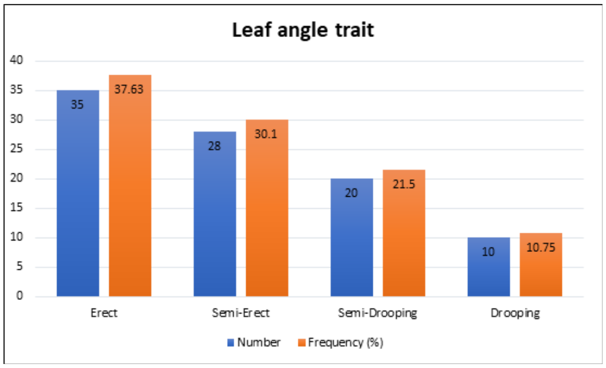

Figure 2a: Graphical representation of 93 wheat genotypes based on their leaf angle

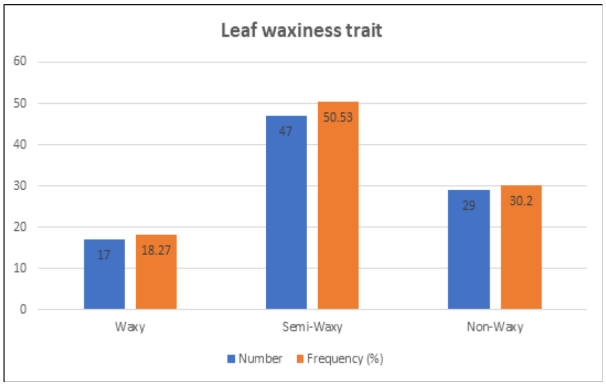

Figure 2b: Graphical representation of 93 wheat genotypes based on their leaf waxines.

Table 5: Mean performance of best 10 resistant genotypes based on AUDPC in normal condition

S. No.	*Genotype*	*DF*	*DM*	*GFD*	*PH*	*NTPP*	*PED L.*	*SL*	*AL*	*BYPP*	*SYPP*	*HI*	*1000 GW*	*AUDPC*	*Leaf angle*	*Leaf waxiness*
1	DBW 166	77.33	113.33	36.00	90.76	7.80	14.67	9.32	4.30	20.02	11.99	42.91	34.57	141.15	Semi Erect	Semi Waxy
2	RAJ 3814	80.00	116.33	36.33	122.85	10.07	22.59	7.62	6.53	23.18	9.21	39.69	41.77	141.15	Erect	Semi-Waxy
3	FLW 10	77.33	110.33	33.00	74.69	9.33	15.60	9.79	5.04	21.60	10.98	39.54	36.27	148.35	Erect	Waxy
4	WR 544	75.00	116.66	41.66	98.81	8.13	19.79	11.03	5.91	24.20	9.61	39.72	40.76	148.35	Erect	Semi Waxy
5	Chiriya#3	72.33	106.67	34.33	94.53	9.73	15.60	9.47	5.84	25.93	11.41	44.02	44.92	155.90	Semi Erect	Semi Waxy
6	HD 2285	69.00	111.00	42.00	83.99	10.00	13.08	10.31	5.94	23.37	9.75	41.70	44.97	157.00	Erect	Non-Waxy
7	HD 3043	77.00	114.67	37.67	96.02	9.73	17.91	9.40	6.97	25.07	9.93	39.58	42.67	161.32	Erect	Semi Waxy
8	Yangmai#6	75.00	112.67	37.67	114.07	11.00	15.66	7.22	5.44	27.63	12.44	45.03	43.93	162.76	Erect	Waxy

Table 6: Mean performance of best 10 resistant genotypes based on AUDPC in diseased inoculated condition

S. No.	*Genotype*	*DF*	*DM*	*GFD*	*PH*	*NTPP*	*PED L.*	*SL*	*AL*	*BYPP*	*SYPP*	*HI*	*1000 GW*	*AUDPC*	*Leaf angle*	*Leaf waxiness*
1	RAJ 3814	81.00	118.00	37.00	126.42	9.20	23.74	7.91	7.04	22.52	11.09	39.34	42.40	184.36	Semi Erect	Semi-Waxy
2	HI 8737 (D)	77.00	115.67	38.67	76.44	8.87	19.07	6.88	10.34	25.57	10.18	39.87	44.37	218.93	Semi Droop	Non-Waxy
3	Yangmai#6	74.67	111.33	36.67	113.13	11.00	14.56	7.10	5.44	27.86	11.74	42.17	41.14	223.25	Erect	Waxy
4	Ning 8201	76.33	111.67	35.33	111.34	11.97	19.00	12.14	5.16	28.26	11.91	41.87	41.44	236.21	Erect	Semi Waxy
5	HD 2733	81.00	115.00	34.00	88.26	8.53	13.90	10.48	4.54	24.57	9.74	39.66	41.43	236.32	Semi Erect	Semi Waxy
6	LOK 1	69.67	104.00	34.33	89.00	7.93	18.37	9.41	6.00	26.52	10.08	38.01	39.00	237.65	Semi Erect	Semi Waxy
7	DBW 168	80.00	115.67	35.67	94.77	7.67	18.16	9.04	6.67	17.96	7.17	39.93	46.57	246.29	Semi Erect	Waxy
8	DBW 173	76.67	114.00	37.33	92.19	6.33	13.78	10.24	4.47	22.50	8.58	38.13	42.00	246.29	Semi Erect	Waxy

Association of Spot Blotch Disease with Yield its Contributing Traits

The correlation results of 13 characters for 93 wheat genotypes grown in normal as well as in artificial epiphytotic conditions are presented in Table 7 and 8. Findings reveals that AUDPC established a negative correlation with important characters like seed yield per plant (r = -0.33), days to flowering (r = -0.27) and tillers per plant (r = -0.13) in normal condition. Similarly, in a diseased condition, it showed negative correlation with seed yield per plant (r = -20), days to 50% flowering (r = -0.17), days to 75% maturity (r = -0.13) and plant height (r = -0.20). However, seed yield per plant (gm) showed positive correlation with biological yield per plant (r = 0.89), number of tillers per plant (r = 0.55), harvest index (r = 0.45), plant height (r = 0.15) and grain filling duration (r = 0.12) in normal condition. Whereas, in diseased conditions, it showed positive correlation in highest magnitude with biological yield per plant (r = 0.92), tillers per plant (r = 0.55), harvest index (r = 0.47) and 1000 grain weight (r = 0.17) but negative and significant correlation with AUDPC (r = -0.20) and days to 50% flowering (r = -0.23) was manifested.

The above findings revealed that in normal conditions, negative correlation of AUDPC with seed yield per plant and other traits depicted that earliness would escapes the disease and intern increases grain yield by reducing disease progress. While the plat height is not common factor to correlate with disease spread as disease will progress from bottom to top of the plant and tall plant type will score less AUDPC. We have identified 10 genotypes expressed resistance reactions evinced tall height as given in Table 5. But earlier report says that increasing the plant height would reduces disease spread (Sharma, *et al*. (2006); Prasad *et al.* (2013); Singh *et al.* (2016) and Turan *et al.* (2017) which could

Table 7: Phenotypic correlation of spot blotch disease with yield and its component traits studied in normal condition

	DF	*DM*	*GFD*	*PH*	*SPP*	*PED L.*	*SL*	*AL*	*BYPP*	*HI*	*1000GW*	*AUDPC*	*SYPP*
DF	1.000	0.796**	-0 .103	0.091	-0.116	-0.016	0.153*	-0.069	-0.266**	-0 .017	-0.010	-0.178**	-0.230**
DM		1 .000	0.517**	0.129*	-0.069	0.054	0.160**	-0.049	-0.103	0.014	-0.011	-0.130*	-0.077
GFD			1.000	0.082	0.052	0.108	0.043	0.0128	0.207**	0.045	-0.004	0.037	0.197**
PH				1.000	0.209**	0.533**	0.185**	-0.060	0.188**	-0.158*	0.231**	-0.202**	0.100
SPP					1 .000	0.011	-0.020	0.0875	0.576**	0.111	0.087	0.063	0.550**
PED L.						1.000	0.005	0.241**	-0.038	-0.114	0.063	-0.052	-0.088
SL							1.000	-0.299**	-0 .073	0.026	-0.006	-0.094	-0.054
AL								1.000	0.110	-0.123*	0.154**	-0.205**	0.046
BYPP									1.000	0.108	0.209**	0.111	0.925**
HI										1.000	-0.033	0.022	0.473**
1000SW											1.000	-0.023	0.175**
AUDPC												1.000	-0.208**

Table 8: Phenotypic correlation of spot blotch disease, yield and its component traits studied artificial condition

	DF	*DM*	*GFD*	*PH*	*SPP*	*PED L.*	*SL*	*AL*	*BYPP*	*HI*	*1000 GW*	*AUDPC*	*SYPP*
DF	1.000	0.703**	0.306**	0.142*	-0.107	-0.0910	-0.047	-0.129*	-0.222**	-0.037	-0.099	-0.277**	-0.204**
DM		1.000	0.460**	0.079	-0.059	-0.0439	0.001	0.017	-0.076	0.071	0.107	-0.153	-0.101
GFD			1.000	-0.070	0.054	0.0549	0.061	0.185**	0.174**	0.048	0268**	0.141*	0.120*
PH				1.000	0.263**	0.5159**	0.017**	-0.153*	0.226**	0.082	-0.241**	0.108	0.159**
SPP					1 .000	0.1654**	0.101	0.071	0.561**	0.120*	-0.301**	-0.135*	0.5554**
PED L.						1.0000	0.063	0.156**	0.068	-0.123*	-0.025	-0.034	0.001
SL							1.000	-0.192**	0.108	-0.038	-0.157**	-0.071	0.081
AL								1.000	0.095	-0.160**	0.008	-0.175**	0.012
BYPP									1.000	0.022	-0.181**	-0.144*	0.899**
HI										1.000	-0.289**	-0.010	0.452**
1000 GW											1.000	-0.066	-0.290
AUDPC												1.000	-0.332**

*, ** Significant at 5 and 1% levels, respectively.

be better for plant breeders. Seed yield per plant showed strong correlation with biological yield per plant followed by number of tillers per plant and other studied traits in normal conditions which is also supported by Sharma *et al.* (2006) and Kumar *etal.* (2009). Similarly, in a diseased condition, a significant association was observed between seed yield per plant and biological yield per plant followed by the number of effective tillers per plant, harvest index and 1000 grain weight. Based on such findings/estimates, it is concluded that indirect selection of these traits may increase grain yield of the crops by applying strong selection pressure (Virender *et al.* (2015); Singh *et al.*(2016); Chethana *et al.* (2018); Kumari *et al.* (2018) and Chandra *et al.* (2019). Whereas, the negative association of grain yield found with days to 50% flowering and days to maturity, indicating completion of generation very early and may produce high grain yield in bread wheat, similar reports published by Chethana *et al.* (2018) and Chandra *et al.* (2019). Grain filling duration positively correlated with AUDPC as it is the period between spike emergence and maturity which is critical for spot blotch disease development. One of the excellent wheat genotype namely HUW 234 is early in flowering but it is also exhibit maximum spot blotch disease severity since it coincides with disease occurrence because of long grain filling duration and also has actual yield recovery property under diseased conditions.

Summary and Conclusion

Since spot blotch disease of wheat caused *B. sorokiniana* pathogen is one of the very destructive disease and there is the unavailability of enough resistance genotypes along with better yielding so, a set of 93 diverse wheat genotypes (most of them are released) are evaluated at the Agriculture Research Farm (known as hot spot for spot blotch), Institute of Agricultural Sciences, Banaras Hindu University in normal as well as artificial epiphytotic conditions inrder to identify the resistance and high yielding donors to be used for crop improvement. Present findings reveal a considerable variation for spot blotch disease resistance and other traits among 93 genotypes studied in normal and diseased conditions. Identified genotypes with potential grain yield are recommended for its use in resistance breeding programme to breed the desirable genotypes, saving the yield loss through an ecofriendly approach and enhancing the productivity of wheat crops to supply the demand of rapidly growing population. In spite of this, majority of genotypes that showed either resistance or moderately resistance reactions and having erect/semi-erect leaves as well as appearance of wax on plants, may be considered as strong morphological marker to select the resistance genotypes and incorporate genes for such traits into targeted genotypes during a breeding programme for crop improvement.

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References

Alzaayid DTJ and RH Aloush (2021) Effect of cytokinin levels on some varieties of wheat on yield, growth and yield components. *IOP Conf. Series. Environ. Earth Sci.,* 910:1-8.

Arya VK, J Singh, L Kumar, R Kumar, P Kumar and P Chand (2017) Genetic variability and diversity analysis for yield and its components in wheat (*Triticum aestivum* L.). *Indian J. Agric. Res*. 51(2): 128-134.

Chandra K, R Prasad, LC Prasad, K Madhukar, K Rashmi and P Thakur (2019) Genetic variability of barley germplasm (*Hordeum vulgare*) for spot blotch disease resistance in natural and artificial epiphytotic condition. *Electron. J. Plant Breed*. 10(4): 1352-1366.

Chandra K, R Prasad, LC Prasad, K Madhukar, K Rashmi and P Thakur (2019) Genetic variability of barley germplasm (*Hordeum vulgare* L.) for spot blotch disease resistance in natural and artificial epiphytotic condition. *Electron. J. Plant Breed.* 10(4):1352-1366.

Chaurasia S, AK Joshi, R Dhari and R Chand (1999) Resistance to foliar blight of wheat: A search. *Genet. Resour. Crop Evol.* 46:469-475.

Chethana CK and V Rudranaik (2017) Genetic variability for yield Parameters and Spot Blotch Resistance in F_2 Population of Durum Wheat (*Triticum turgidum* var *durum*). *Int. J. Agric. Sci*.9(7):843-3845.

Chowdhury AK, G Singh, BS Tyagi, A Ojha, T Dhar, PM Bhattacharya (2013) Spot blotch disease of wheat-a new thrust area for sustaining productivity. *J. of Wheat Res*. 5(2):1-11.

CIMMYT (2013) Research battles wheat spot blotch disease Informa No1851, CIMMYT Corporate Communications, Mexico.

Dhakal N, SN Shrestha, HK Manandhar, L Aryal, GC Sagar and KR Pant (2020) Screening of advance wheat genotypes against spot blotch disease (*Bipolaris sorokiniana*) under varying sowing dates at Chitwan, Nepal. *Fundam. Appl. Agric.* 5(3): 383-392.

Dibya SP, S Kumar, S Singh, M Kumar, KS Maurya and H Singh (2020) Evaluation of wheat genotypes for resistance against spot blotch disease. *J. pharmacogn. phytochem.* 9(6): 341-343.

Dubin HJ and MV Ginkel (1991) The status of wheat diseases and disease research in warmer areas. In: Wheat for the nontraditional warm areas, Proceedings of the International Conference,CIMMYT, Mexico. p. 125-45.

Duveiller E and L Gilchrist (1994) Production constraints due to *Bipolaris sorokiniana* in wheat: current situation and future prospects. In *Wheat in Warm Area, Rice-Wheat Farming Systems*. Dinajpur, Bangladesh. p. 13-15.

Duveiller E and RC Sharma (2012) In: Sharma I. editor. Disease resistance in wheat: Wheat resistance to spot blotch or foliar blight. CABI; p. 120-135.

Elliot SL, S Blanford and MB Thomas (2002) Host-pathogen interactions in a varying environment: temperature, behavioural fever and fitness. Proceedings of the Royal Society of London. Series B: *Biol. sci.* 269(1500): 1599-1607.

Gupta PK, R Chand, NK Vasitha, SP Pandey, U Kumar, VK Mishra and AK Joshi (2018) Spot blotch disease of wheat: the current status of research on genetics and breeding. *J. Plant Pathol.* 67: 508-531.

Gurung S, S Mamidi, JM Bonman, M Xiong, G Brown-Guedira and TB Adhikari (2014) Genome-Wide Association Study Reveals Novel Quantitative Trait Loci Associated with Resistance to Multiple Leaf Spot Diseases of Spring Wheat. *PLoS One,*9(9): 1-20.

Joshi AK and R Chand (2002) Variation and inheritance of leaf angle, and its association with spot blotch (*Bipolaris sorokiniana*) severity in wheat (*Triticum aestivum*). *Euphytica*. 124(3): 283-291.

Joshi AK, B Mishra, R Chatrath, G Ortiz Ferrara and RP Singh (2007a) Wheat improvement in India: present status, emerging challenges and future prospects. *Euphytica*.157: 431-446.

Joshi AK, G Ortiz-Ferrara, J Crossa, G Singh, G Alvarado, MR Bhatta and R Chand (2007b) Associations of environments in South Asia based on spot blotch disease of wheat caused by *Cochliobolus sativus*. *Crop Sci.* 47(3): 1071-1081.

Joshi SK, SN Sharma, DL Singhania and RS Sain (2004b) Combining ability in the F_1 and F_2 generations of diallel cross in hexaploid wheat (*Triticum aestivum* L. em. Thell). *Hereditas*. 141(2): 115-121.

Kaur J, J Kaur, GS Dhillon, H Kaur, J Singh, R Bala, P Srivastava, S Kaur, A Sharma and P Chhuneja (2021). Characterization and mapping of spot blotch in Triticum durum-Aegilops speltoides introgression lines using SNP markers, *Front. Plant Sci*. 12:1-13.

Khan H and S Chowdhury (2011) Identification of resistance source in wheat germplasm againstspot blotch disease caused by *Bipolaris sorokiniana*. *Archives of Phytopathology and Plant Protection.* 44(9): 840-844.

Kumar D, IS Panwar, V Singh and RR Choudhary (2020) Heterosis studies using Diallel analysis in bread wheat (*Triticum aestivum*L.). *International Journal of Communication Systems*. 8(4): 2353-2357.

Kumari J, S Kumar, N Singh, SS Vaish, S Das, A Gupta and JC Rana (2018) Identification of new donors for spot blotch resistance in cultivated wheat germplasm. *Cereal Res. Commun.*, 46(3): 467-479.

Lamalaksmidevi E, Swati, P Goel, M Singh and JP Jaiswal (2013) Heterosis studies for yield and yield contributing traits in bread wheat (*Triticum aestivum*L.). *The Bioscan*. 8(3): 905-909.

Lillemo M, A K Joshi, R Prasad, R Chand and R Singh (2013). Association of *Lr 34* and *Lr 46* with spot blotch resistance in wheat, *Theor. Appl. Genet.*, 126: 711-719.

Mahapatra S, HM Devi, S Kumar, D Mukherjee and S Das (2020) Performance and stability of different zone-specific genotypes evaluated against spot blotch of wheat. *Int. J. curr. microbiol. appl. sci.*, 9(6): 2968-2981.

Mehta YR (1994) Manejo integrado de enfermedadas de trigosanta cruz. CIAT/IAPAR, Bolivia, p 314.

Pandey AK, VK Mishra, C Ramesh and RK Singh (2016) Genetic assessment of CSISA-spot blotch lines of wheat (*Triticum aestivum*L.) for spot blotch resistance and yield traits. *Bangladesh J. Bot.* 45(5): 1187-1195.

Prasad R (2022) Cytokinin and its key role to enrich the plant nutrients and growth under adverse conditions-an update. *Front. Genet.* 13: 1-14.

Prasad R, LC Prasad, R Chand and AK Joshi (2013) Assessment of diversity for resistance to spot blotch disease and its association with certain phenotypic traits in barely. *Field Crops Res.* 154: 195-200.

Roelfs AP, RP Singh and EE Saari (1992) Rust Diseases of Barley: Concepts and Methods of Disease Management. CIMMYT, Mexico City, p. 1-81.

Saari EE and JM Prescott (1975) A scale for appraising the foliar intensity of wheat diseases. *Plant Disease Reporter.* 59:377-380.

Sharma RC, B Pandey, Chhetri and E Duveiller (2006) Heritability estimates of spot blotch resistance and its association with other traits in spring wheat crosses. *Euphytica*. 147: 317-327.

Singh CK, S Gupta, NK Tiwari and D Singh (2016) Evaluation of wheat genotypes for resistance against spot blotch. *Int. J. Plant Prot.* 9(1): 272-274.

Thakur P, P Upadhyay, K Rashmi, Namrata, R Prasad, K Chandra, K Madhukar K and LC Prasad (2018) Study of genetic variability, path analysis and diversity of selected germplasm lines of wheat (*Triticum aestivum* L.), under very late sown condition. *Int. I. bio-resour. stress manag.* 9(2):203-208.

Thakur P, P Upadhyay, K Rashmi, Namrata, R Prasad, K Chandra, K Madhukar and LC Prasad (2018) Study of Genetic Variability, Path Analysis and Diversity of Selected Germplasm Lines of Wheat, Under Very Late Sown Condition. *Int. j. bio-resour. stress manag.*, 9(2): 203-208.

Thapa RS, PK Sharma, A Kumar, T Singh and D Pratap (2018) Assessment of genetic variability, heritability and genetics advance in wheat genotypes under normal and heat stress condition. *Indian J. Agric. Res.* 53: 51-56.

Tomar V, D Singh, GS Dhillon, RP Singh, J Poland, and AK Joshi et al. (2021). New QTLs for spot blotch disease resistance in wheat (*Triticum aestivum*) using genome-wide association mapping. *Front.Genet.* 11:613217 doi: 10.3389/fgene.2020.613217.

Turan R, BS Tyagi, A Sharma, G Singh, V Singh and A Ojha (2017) Assessment of genetic variability and correlation among agro-morphological traits and spot blotch disease in a RIL population of wheat. *J. wheat res.* 9(2): 108-114.

Yadav B, R Singh and A Kumar (2015) Management of spot blotch of wheat using Fungicides. Bio-agents & Botanicals. *Afr. J. Agric. Res.* 10: 2494-2500.

Zadoks JC, TT Chang and CF Konzak (1974) A decimal code for growth stages of cereals. *Weed res.* 14:415-421.