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Field Based Assessment of Spot Blotch (*Bipolaris Sorokiniana*) Disease of Wheat (*Triticum Aestivum* L.)

R. Basnet[1,2], S.M. Shrestha[2], D. Bhandari[1], H. K. Manandhar[2], D. B. Thapa[1]

[1]Nepal Agricultural Research Council, Kathmandu, Nepal
[2]Agricultural and Forestry University, Rampur, Chitwan

Corresponding Author: R. Basnet

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ABSTRACT

Wheat, the third major staple crop of Nepal has suffered from many diseases. Various diseases are the major limiting factors of considerable wheat production, one of them is Spot blotch. Spot blotch caused by *Bipolaris sorokiniana* is a major disease of wheat in warm and humid regions of Nepal. The fungus has a worldwide distribution but as a pathogen, it is the most aggressive under the conditions of high relative humidity and temperature associated with the low fertility of soils in South Asia, South America, Africa, and Australia. The yield loss due to the disease is very significant in Nepal. This experiment was conducted to identify the genotypes having a good level of resistance against spot blotch. The experiment set was received from CIMMYT comprises 52 entries and arranged in alpha lattice design with two replications in 2017/18 at Regional Agricultural Research Station, Parwanipur, Bara, Nepal. Each plot size was 8 rows of 2 meters long. Three times disease scoring was done in the double-digit method and calculated the Area under the disease progress curve (AUDPC). Heading days, days to maturity, plant height, number of grains per spike (NGPS), number of tillers per meter square (NTPM), mean AUDPC, thousand-grain weight (TGW), and grain yield were found highly significant. The genotype 8HLBSN24 was found the highest yielder (4999kg/ha) with a 208 mean AUDPC value. The grain yield and mean AUDPC was a strong negative correlation (-0.96). However, NGPS and NTPM found a positive correlation to grain yield.

Keywords: Foliar blight, AUDPC, Wheat, Genotype

INTRODUCTION

The average productivity of wheat in Nepal is very low than the potential yield. Various diseases are one of the major yield-limiting factors of wheat in Nepal. Among them, the major disease of wheat in Nepal was Foliar blight complex (spot blotch caused by *Bipolaris sorokiniana* Sacc) Shoem syn. *Drechslera sorokiniana* (Sacc.) Subrm and Jain (syn. *Helminthosporium sativum*, teleomorph (*Cochliobolus sativus*) and is considered one of the most destructive fungal diseases in humid and high-temperature regions; they not only affect wheat, but also several other small grains worldwide such as barley, rye, and triticale (Dubin and Rajaram,1996; Duveiller and Dubin,2002; Joshi and Chand,2002). The pathogen has a worldwide dispersal, but it is predominantly aggressive under warm, high relative humidity, and high temperature associated conditions with imbalanced soil fertility. Major yield losses are observed in the fields with lower inputs and under late-sown conditions (Chatrath *et al.*, 2007).

The spot pathogen can infect all plant organs, but particularly leaves and grain; thus, reducing plant photosynthetic efficiency and grain quality. It has a wide range of hosts among wild and cultivated

Poaceae species (Pandey *et al.,* 2005; Lozano-Ramirez *et al.*,2022). SB symptoms are characterized by light to dark brown lesions on leaves, oval to elongated in shape (Chand *et al.,* 2003), that extend and merge very quickly, resulting in tissue death. Stunting and reduced tiller may be observed in heavily infected plants, which may lead to premature death, resulting in white heads. Kernels become shrivelled and roots become dark brown and rotted. Yields may be reduced due to root rot even though symptoms are not well developed. Yellowing due to toxin production is sometimes observed (Singh *et al.,* 1998).

The infection of the spot is most severe when the crop's late post-anthesis phase coincides with a period of high relative humidity and high temperature. Globally, an estimated 25 million ha of the wheat area is affected by spot blotch (Van Ginkel & Rajaram, 1998), about 40% of which is grown in the Indian subcontinent (Joshi *et al.,* 2007a), where the crop losses due to spot blotch have been estimated to be in the range of 15–25% (Dubin & van Ginkel, 1991).

The importance of spot blotch in production losses has been widely documented. On average, yield loss of 15-20% due to spot has been reported in several countries under favorable climate conditions, yet the yield losses can reach up to 70% in susceptible varieties (Mehta *et al.*,1992; Acharya *et al.,* 2011; Lozano-Ramirez *et al.,* 2022). The disease also affects the end-use quality of harvested wheat grains (Mehta, 1998; Gupta *et al.,* 2018). The Fungicide trials confirmed that the losses from disease ranged from 10-25% in Nepal, Bangladesh, and India (Singh *et al.,* 1998), but were considerably larger (60%) in China (Chang and Wu, 1997). A study demonstrated that leaf blight by *Bipolaris sorokiniana* could be an important yield-limiting factor in the hot humid areas of the world. Besides grain yield, there were considerable losses in grain weight of up to 50%.

The genetic basis of spot blotch resistance has earlier been documented as eight major quantitative trait loci (QTLs), namely, QSb.bhu-2A, QSb.bhu-2B, QSb.bhu-2D, QSb.bhu-3B, QSb.bhu-5B, QSb.bhu-6D, QSb.bhu-7B, and QSb.bhu-7D (Kumar *et al.,* 2009, 2010). Sharma et al. (2007a) reported three microsatellite markers (Xgwm67, Xgwm570, and Xgwm469) linked with spot blotch resistance. The QTL QSb.bhu-5B, QSb.bhu-7D, and QSb.bhu-3B have been designated as genes Sb1, Sb2, and Sb3, respectively, in further studies (Lillemo *et al.,* 2013; Kumar *et al.,* 2015;). Lr34 and Lr46, the two broadly used genes conferring leaf rust resistance, have also been reported to contribute to spot blotch resistance. While the Lr34 gene has been reported to be the major locus on chromosome 7D explaining up to 55% phenotypic variation for spot blotch disease resistance, this locus was given the gene designation Sb1 (Lillemo *et al.,* 2013). Cultivar development for resistance to spot blotch is slow due to the quantitative nature of resistance and a limited number of genes are known to have a major effect. Four spot blotch resistance genes with major effects have been named to date, i.e., Sb1, Sb2, Sb3, and Sb4 (Lillemo *et al.,* 2013; Kumar *et al.,* 2015; 2016; Zhang *et al.,* 2020).

The management of spot blotch disease has become urgent to increase the production of wheat and to ensure food security. Effective management practices for farmers are still lacking. The application of fungicides is not only costly but also hazardous to human health. At the same time, effective resistance sources against this disease are still not clear. Therefore, the identification of the resistant source of genotypes and exploration against spot blotch is most crucial in reducing the leaf blight severity and attaining a higher yield. This research will be helpful to identify the spot blotch resistant/tolerant wheat.

MATERIALS AND METHODS

The experiment was carried out at Regional Agricultural Research Station (RARS), Parwanipur, Bara. Geographically, the station is located 105 meters above sea level

and 27°32' north latitude and 83°25' east longitude. The climate at RARS, Parwanipur is subtropical. The experiment was laid out in alpha lattice design with two replications and fifty-two entries. Each entry was planted in eight rows of two meters long. The cropping geometry was 25 cm by 25 cm. Chemical fertilizer 120 Kg N: 60 Kg P_2O_5:40 Kg K_2O per hector applied. Half dose of N and all P and K were applied at the time of planting while the remaining half dose of N was applied at the time of first irrigation and other cultural practices were used as general agronomic cultivation practices for wheat production. At the experiment site, the maximum and minimum temperatures recorded in November were 29.32^{0}C and 14.61^{0}C respectively and relative humidity was 82.13%. In December, the maximum and minimum temperature was recorded at 23.99^{0}C and 11.33^{0}C respectively and relative humidity was 91.25%. Similarly, in March maximum and minimum temperatures were recorded at 32.2^{0}C and 16.07^{0}C, precipitation was 5 mm and 67.19% relative humidity (Figure 1). The obtained data were analyzed R software and an excel sheet). For spot blotch, the rate of incubation period completion was described as a linear increase in rate with temperature up to approximately 29°C, then an exponential decline with temperature up to the maximum temperature of approximately 36°C in which disease development checked (Viani, *et al.*, 2013).

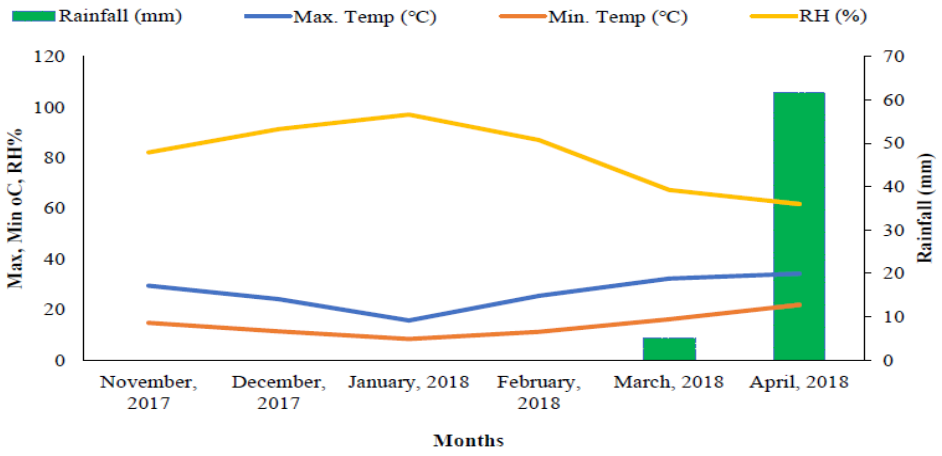

Figure 1: Meteorological Data Parwanipur, 2017-18

Since the disease severity increases very fast in the field and small differences indicating partial resistance need to be observed, disease evaluation is usually based on the area under the disease progress curve (AUDPC) calculated from a minimum of three field observations and it starts after the flowering stage of the crop. The severity of the disease was recorded by visually assessing with the double-digit method. Spot blotch severity can be visually scored for each plot at weekly intervals using the double-digit scale (00-99) developed as a modification of Saari and Prescott's severity scale to assess wheat foliar diseases (Saari and Prescott, 1975; Eyal *et al.*,1987). The first digit (D1) indicates the disease progress in height and the second digit (D2) refers to the severity measured by the diseased leaf area. For each score, the percentage of diseased leaf area (%DLA) was estimated based on the following formula: % DLA = ((D1/9) x (D2/9) x 100). Individual scores were recorded weekly over three weeks. The area under the disease progress curve (AUDPC) was calculated using the percent severity estimates corresponding to the three to four ratings as outlined by Das *et al.*, (1992) and shown below:

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

Where, xi = disease severity on the ith date, ti = ith day, and n= number of scoring dates. The AUDPC measures the amount of disease as well as the rate of progress and has no units.

RESULTS AND DISCUSSIONS

Days to heading, Days to maturity, and Plant height

Days to heading were found highly significant (P≤ 0.05) among the tested genotypes. The Mean heading was found to be 78 days. The first heading days were observed in 8HLBSN (72 days) followed by 8HLBSN31, 8HLBSN 27 (73 days), and 8HLBSN23 (74 days). However, the late heading days were observed in 8HLBSN29 and 8HLBSN3 (85 days) (Table 1). Days to heading were positively correlated with mean AUDPC value (0.23) but negatively correlated with grain yield (0.27) (Table 2).

Days to maturity were recorded after the development of yellowish color in the peduncle of 75% plant population. Days to maturity were found to be highly significant (P≤ 0.05) among the tested genotype (Table 1). The mean days to maturity was 110.3 days. Early maturity was observed in genotypes 8HLBSN31,8HLBSN23 and 8HLBSN19 (107 days) and late maturity was observed in 8HLBSN3 and 8HLBSN29 (117 days) (Table 1). Days to maturity and AUDPC were found to be week negatively correlated (-0.09) (Table 2). i.e., late maturity results in lesser development of the disease. This result is following the findings of Tewari et al. (2016) and Neupane et al. (2013). Genotypes with late maturity are more resistant and so lower disease severity than early maturing genotypes (Duveiller *et al.*, 2005).

Plant height was measured at the dough stage. The plant height was found to be highly significant (p ≤ 0.05) among the tested genotypes (Table 1). The genotype 8HLBSN21 had the highest plant height of 102 cm with an AUDPC value of 338. The plant height was then followed by 8HLBSN9 (99 cm) (Table 1). Plant height showed a weak negative correlation (-0.01) with AUDPC i.e., increase in plant height, and a decrease in AUDPC value (Table 2). Rosyara *et al.*, (2009), and Neupane *et al.*, (2013) found that there was a negative association between plant height and spot blotch resistance and there was no significant difference between AUDPC and plant height taken for different genotypes.

Number of grains per spike, Number of tillers per meter square, Thousand kernels weight, Grain yield, and Mean AUDPC

The number of grains per spike was found to be significantly different at (P≤0.05) among the tested genotypes. The lowest number of grains per spike was observed in 8HLBSN52 (27) followed by 8HLBSN51 (28) and the highest number of grains per spike was observed in 8HLBSN33 (58), 8HLBSN (58), and 8HLBSN7 (58) (Table 1). The mean of number grains per spike was 48.8 similarly, grain per spike is negatively correlated (-0.05) with AUDPC value i.e. lower the disease severity, the higher the grain per spike. (Table 2). This result is following the findings of Tewari *et al.*, (2016). This is because the lower grains per spike result from the higher diseased area and lower assimilation of carbohydrates.

Test weight (1000 kernel weight, TKW) Test weight was found to be highly significant among the tested genotypes at (P≤0.05). The mean test weight was 43.6 gm and ranged from 30 gm to 51 gm. The highest test weight was observed in 8HLBSN26 (51 gm) followed by 8HLBSN47, 8HLBSN25, 8HLBSN19, 8HLBSN23, 8HLBSN48, 8HLBSN49 (50gm) (Table 1). The lowest thousand grains weight (TKW) (30 gm) was observed in susceptible checks (8HLBSN51 and 8HLBSN52). The TKW and AUDPC value was found moderately negatively correlated (0.-0.63) (Table 2). Similar results were also reported by (2007), Tewari et al. (2016), and

Neupane et al. (2013). They found a negative correlation between TKW and AUDPC.

Table 1: Grain yield, mean AUDPC and other yield attributing character of wheat at Parwanipur, Bara during 2017/18

E. N	Genotypes	DTH (days)	DTM (days)	PH (cm)	NGPS	NTPM	Mean AUDPC	TGW (g)	Grain Yield (kg/ha)
24	8HLBSN24	76	108	88	50	496	208	45	4999
23	8HLBSN23	74	107	89	55	500	233	50	4992
31	8HLBSN31	73	107	97	47	591	236	44	4948
27	8HLBSN27	73	110	97	55	562	251	43	4944
46	8HLBSN46	75	109	90	56	441	171	46	4943
48	8HLBSN48	78	113	84	55	521	224	50	4938
5	8HLBSN5	74	109	97	49	312	221	42	4906
29	8HLBSN29	85	117	97	49	495	243	47	4883
42	8HLBSN42	76	109	91	52	365	278	45	4837
45	8HLBSN45	76	108	88	47	430	279	47	4837
4	8HLBSN4	80	113	93	49	377	273	45	4833
9	8HLBSN9	79	111	99	56	450	281	48	4805
37	8HLBSN37	79	113	79	51	448	320	39	4771
25	8HLBSN25	79	111	92	49	452	327	50	4754
21	8HLBSN21	76	112	102	54	435	338	45	4741
41	8HLBSN41	77	110	85	42	422	340	43	4733
15	8HLBSN15	76	109	87	52	440	359	44	4698
20	8HLBSN20	75	109	95	51	458	337	47	4691
19	8HLBSN19	75	107	98	49	433	379	50	4634
32	8HLBSN32	76	110	88	46	558	413	49	4625
47	8HLBSN47	76	112	88	48	396	376	50	4621
8	8HLBSN8	76	108	91	40	431	449	41	4605
33	8HLBSN33	78	109	99	58	510	432	42	4589
26	8HLBSN26	76	108	84	46	429	409	51	4547
35	8HLBSN35	77	109	84	55	485	433	44	4540
38	8HLBSN38	77	110	88	53	407	459	38	4523
1	8HLBSN1	74	112	99	54	442	453	37	4498
28	8HLBSN28	72	111	89	54	516	440	49	4485
22	8HLBSN22	78	113	52	43	424	457	48	4455
2	8HLBSN2	74	113	98	51	377	459	45	4439
13	8HLBSN13	77	110	89	51	395	470	42	4431
39	8HLBSN39	78	110	93	54	443	470	39	4427
49	8HLBSN49	75	109	86	58	413	495	50	4257
14	8HLBSN14	82	115	88	53	372	559	46	4210
16	8HLBSN16	76	108	95	44	377	498	44	4154
43	8HLBSN43	77	109	89	55	347	502	48	4043
40	8HLBSN40	81	115	87	45	352	542	40	3736
36	8HLBSN36	77	110	85	43	310	563	36	3637
3	8HLBSN3	85	117	86	47	428	556	42	3636
44	8HLBSN44	79	111	86	51	350	559	44	3607
34	8HLBSN34	79	111	95	43	377	597	43	3473
6	8HLBSN6	76	110	91	56	280	620	45	3426
12	8HLBSN12	75	108	91	45	334	605	45	3426
7	8HLBSN7	78	110	93	58	274	625	44	3399
18	8HLBSN18	79	112	85	49	314	645	46	3344
10	8HLBSN10	78	111	94	41	263	634	36	3286
11	8HLBSN11	80	114	96	41	347	631	39	3271
17	8HLBSN17	77	109	84	37	338	648	41	3244
30	8HLBSN30	80	114	88	34	190	719	39	2719
50	8HLBSN50	76	108	87	56	369	873	35	2686
52	8HLBSN52	76	108	92	27	233	915	30	2361
51	8HLBSN51	79	111	92	28	319	875	30	2083
Grand Mean		76.9	110.3	89.9	48.5	404.2	455	43.6	4204.9
LSD value		4.09	4.35	17.27	11.07	76.52	87	3.08	525.55
CV(%)		2.53	1.89	9.55	11.11	9.42	9.05	3.52	6.22
Genotype significance		<0.01	0.0005	0.001	<0.01	<0.01	0.001	0.0001	0.00001

DTH=Days to heading, DTM=Days to maturity, PH=Plant height, NGPS=Number of grain per spike, NTPM=Number of tillers per meter square, AUDPC=Area under disease progress curve, TGW=Thousand grain weight

The grain yield was found highly significant among the tested genotypes at ($P \leq 0.05$). The highest grain yield was found in 8HLBSN24 (4999 kg/ha) followed by the 8HLBSN23 (4992 kg/ha), 8HLBSN31 (4948 kg/ha) and 8HLBSN27 (4944 kg/ha) (Table 1). The

Grain yield was strongly negatively correlated with AUDPC (-0.96). This result is following the findings of Kandel *et al.*, (2014), Tewari *et al.*, (2016), and Lamsal *et al.*, (2017). This may be because of the reduced photosynthetic area of the plant to assimilate the carbohydrate in the seed due to the diseased leaf.

The mean AUDPC of different genotypes was found highly significant with each other at (P≤0.05). the grand mean of the mean AUDPC value was 455.The highest AUDPC value was 8HLBSN52, 8HLBSN51, and 8HLBSN50 915, 875, and 873 respectively (Table 1). The mean AUDPC values are strongly negatively correlated with grain yield. The mean AUDPC is negatively correlated with Plant height (-0.1), numbers of grain per meter square (-0.5), and, numbers of tillers per meter square (-0.7) (Table 2).

Table: 2. Simple linear correlation of AUDPC value with other yield attributing parameters.

	DTM	PH	NGPS	NTPM	Mean AUDPC	Grain Yield	TKW
DTH	0.75	-0.15	-0.20	-0.23	0.23	-0.27	-0.14
DTM		-0.12	-0.07	-0.12	0.09	-0.12	-0.05
PH			0.14	0.04	-0.10	0.06	-0.11
NGPS				0.46	-0.50	0.57	0.51
NTPM					-0.70	0.75	0.47
Mean AUDPC						-0.96	-0.63
Grain Yield							0.63

CONCLUSION

Genotypes with late maturity are more resistant and so lower disease severity than early maturing genotypes. There is no relationship between plant height and spot blotch development. The genotypes 8HLBSN47, 8HLBSN25, 8HLBSN19, 8HLBSN23, 8HLBSN48, 8HLBSN49 gave more thousand grain weight. The thousand-grain weight and mean AUDPC were negatively correlated. The grain yield and mean AUDPC were strongly negatively correlated. Identified genotypes having higher yield with higher thousand-grain weight, and low AUDPC will be the source of development of resistance to spot blotch and high yielding wheat varieties in Nepal.

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