VARIETAL SCREENING OF WHEAT GENOTYPES AGAINST SPOT BLOTCH DISEASE (*Bipolaris sorokiniana*) UNDER FIELD CONDITION AT BHAIRAHAWA, NEPAL

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ABSTRACT

A field experiment was conducted to evaluate the performance of wheat genotypes against spot blotch disease from November 2016 to April 2017. Experimental field was designed in Alpha Lattice Design with 2 replications and 20 genotypes as treatments. Area Under Disease Progress Curve (AUDPC) value, days to heading, days to maturity, plant height, spike per m^2, grain per spike, Thousand Kernel Weight (TKW), grain yield were examined. Negative correlation was observed between yield of different genotypes and AUDPC i.e. -0.17322. Genotype BL 4699 and NL 1247 were found to be resistant with AUDPC value 141.7 and 140.6 and yield 3.335MT/ha and 3.604MT/ha respectively. Similarly, genotype BL 4708, NL 1327 and BL 4707 were found to be tolerant with AUDPC value 567.2, 570.6 and 274.6 and yield 3.761MT/ha, 3.642MT/ha and 3.681Mt/ha respectively. So, resistant and tolerant genotypes BL 4699, NL 1247, BL 4708, NL 1327 and BL 4707 could be suggested to incorporate into the breeding program.

Keywords: Wheat, Spot Blotch, AUDPC, Yield

INTRODUCTION

Wheat (*Triticum aestivum*) is the one of the important cereal crop of the world along with rice and maize. It is grown on more land area than any other commercial food. Globally, it occupies approximately 240 million ha with the production of approximately 600 million tones (Jaiswal, 2009). According to FAO, world wheat production in 2017 was 756.8 million tons which was reduced as compared to 2016 i.e. 757.2 million tons (FAO, 2018).

However, demand is exceeding supply, the main reason for this is population growth. Population is expected to be doubled by 2050 so current food production should be increased to satisfy the hunger of growing population (Kendall and Pimentel, 1994). But, there are some biotic and abiotic constraints that hinder the productivity of wheat. Among various fungal disease, spot blotch of wheat is creating great threat in the global wheat production.

Spot Blotch (*Bipolaris sorokiniana*) causing substantial damage to wheat and wheat yield, is most notably observed in those areas with warm and humid condition, and commonly observed in areas such as Latin America, South East Asia, Nepal, China, and Africa. (Raemakers 1991; Saari 1998). It attacks seedlings, leaves, roots, nodes, spikes and grains during various stages of development. Symptoms are first observed at the seedling stage, but the number of airborne conidia and leaves infected by pathogens remains low for several weeks till lower temperature prevails. As the temperature increases sharp rise in infestation can be observed (Duveiller *et al.,* 2004). Spot blotch is the number one disease of wheat in the Eastern Gangetic Plains, seriously damaging the crops of farmers who are mostly smallholders, covering 9 million hectares in total (CIMMYT, 2013). In Nepal, the loss was reported up to 23.8% (Shrestha *et al.,* 1997) but Duveiller and Gilchrist (1994) and Mehta (1998) said that spot blotch causes substantial yield loss up to 20-100%. Similarly, yield losses up to 2-22% in Bangladesh was reported by Siddique *et al*. (2006). Duveiller *et al.*

(2005) reported yield loss of an average of 30% by combined effect of spot blotch and tan spot HLB complex. Being an important disease, breeding resistant cultivars against spot blotch is a research priority (Villareal *et al*., 1995).

In South Asia, the best leaf blight resistance varieties of wheat were reported to be late maturing and tall. Various studies done by different scientists clarify that spot blotch resistance is less in short varieties with early maturity (Dubin *et al*., 1998, Sharma *et al*., 1997). Unfortunately, most of the identified promising spot blotch resistant genotypes were found to be with some undesirable agronomic trait (Sharma and Duveiller, 2007).

Spot blotch disease can be managed by good cultural practices, soil fertility management and effective use of fungicides. Changing climatic factor is giving a pressure on disease severity and so there is continuous need to introduce and identify new resistance sources for spot blotch resistant wheat (Sharma *et al*., 2007). With progress in developed genotype against spot blotch since 1983 disease severity and yield reduction due to disease is lowering (Siddique *et al*., 2006).Thus, this study was conducted to find out the severity of spot blotch on different genotypes of wheat, to determine the effect of spot blotch in the grain yield of wheat and to find out resistant and tolerant varieties among selected 20 genotypes at Bhairahawa condition.

MATERIALS AND METHODS

Seed collection

Twenty genotypes were collected from National Wheat Research Program (NWRP), Bhairahawa, Nepal. Among them, some were released and some were pipeline genotypes. Gautam was used as resistant check whereas RR-21 was used as susceptible check.

Experimental site

The research experiment was conducted in research field of National Wheat Research Program (NWRP), Bhairahawa, Rupendehi, Nepal during November-April, 2016-17. NWRP is located at 105m above the sea level at latitude of 27°32' north and longitude of 83° 25' east. It is 300 km west of Kathmandu and 21 km west of Lumbini. The recorded maximum temperature in summer is 44.6°C and minimum temperature in winter is 4.8°C. The average annual rainfall is 1700mm.

Design of experimental site

The experimental field was designed in Alpha Lattice design with two replications. Each replication consists of five blocks with four plots. Each plot with an area of 2.5m X 4m containing 10 rows. The row-row spacing was 25cm and continuous within the same row. The spacing between the two plots was 50cm and the spacing between two replications was 1m. Border distance from all four sides was 1m. The recommended dose of fertilizer was used (100:50:25 NPK kg/ ha). Irrigation was given during the critical stages of wheat.

Disease assessment

Plants were evaluated against natural disease occurrence (without artificial inoculation). Disease from each plot was recorded starting with the appearance of first spot blotch disease symptoms, when susceptible check (RR-21) showed 50% disease symptom, at an interval of 5 days. Scoring of disease was carried out following double digit and single digit scoring.

Single digit scoring

For single digit scoring, we observed the symptoms in flag leaf (F) and penultimate leaf (F-1) after the completion of heading in all genotypes. Single digit scoring was carried out in each plot of both replication following the standard diagram of CIMMYT (Muzeeb – Kaazi *et al.,* 1996). Five disease scoring data were collected with the same procedure to calculate the AUDPC value.

(%) Disease intensity = (sum of numeric rating/ total numbers of plant observed) ×100

Double digit scoring

Double Digit Scoring scale measures the overall foliar blight on whole plot on the basis of two digits (D1 and D2). First digit, D1, denotes the average height of infection on the plant of a plot while second digit, D2, denotes the average disease severity within that height. Its value ranges from (00-99). Leaf severity of disease in accordance to the double digit scoring was carried out following Saari – Prescott (0-9) scale (1975). Double digit scoring was taken to calculate the area under disease progress curve.

The disease severity was calculated for each genotype using the formula given (Duveiller *et al*., 2005).

Disease severity = $(D_1/9)$ X $(D_2/9)$ X 100

Where,

D_1 = 1st digit (vertical disease progress)

D_2 = 2nd digit (severity of infection)

The disease severity was used to calculate the area under disease progress curve (AUDPC) value for each genotype.

Estimating Area Under Disease Progress Curve (AUDPC)

The area under disease progress curve (AUDPC) was calculated in order to know the progress of disease. AUDPC for flag leaf (F), Penultimate leaf (F-1) and double digit scoring was calculated separately. Formula for it was given by Das *et al.* (1992).

$$\text{AUDPC}= \sum_{I=1}^{n-1}(Y_{i+1}+Y_i)0.5(T_{i+1}-T_i)$$

Where,

Y_i = Disease severity in the i^{th} date

t_i = Date on which the disease was scored

n = number of dates on which disease was recorded

Agronomic traits

Agronomic traits such as, days to heading, days to maturity, plant height, spike per m^2, grain per spike, TKW and grain yield were recorded during the research.

Data analysis

Recorded data were analyzed using softwares; Crop stat version 7.2 for analysis of variance (ANOVA) and MS-Excel version 2013 for deriving correlation between AUDPC, plant height, days to heading, thousand kernel weight (TKW) and other parameters.

RESULT AND DISCUSSION

Plant height

Plant height for wheat was measured at dough stage. The plant height was found to be highly significant ($p \leq 0.05$) among the tested genotypes (Table 1). The genotype BL4699 had the highest plant height of 105.1 cm with AUDPC value of 141.7. The plant height was then followed by BL4335 (96.92cm), NL1244 (95.27cm), BL4708 (95.13cm) and NL1211 (93.95cm). And their AUDPC value was 731.2, 259.8, 567.2 and 265.8, respectively (Table 2). Lowest plant height was of Bhrikuti (79.8cm).

Plant height showed positive correlation (0.147345) with AUDPC i.e. increase in plant height, increases in AUDPC value (Table 2). In contrary, Rosyara *et al.* (2009), Basnet (2016) and Neupane *et al.* (2013) found that there was negative association between plant height and spot blotch resistance and there was no significant difference for AUDPC and plant height taken for different genotypes. This result was also supported by Joshi *et al.* (2002).

Days to Heading

Days to heading was found to be highly significant ($P \leq 0.05$) among the tested genotypes (Table 1). Mean heading was found to be 78 days. Among the tested genotypes, first heading was observed in BL4335 at 74 DAS, followed by NL 1326 and Gautam in 75 DAS. Late heading was observed in NL1207 and NL1328 (82 DAS) (Table 1).

Days to heading was negatively correlated with AUDPC value (-0.28296) i.e. late heading results in the lesser development of disease (Table 2) while early heading results in more disease development. This result is alike to findings of Sharma.*et al.* (1995), Shrestha *et al.* (1998), Duveiller, E. and Dubin, J. (2002), Tewari *et al.* (2016). Genotypes late in heading have lower disease severity. It is due to slower plant development and shorter period of exposure of plant to pathogen. (Duveiller *et al.,* 1998).

Days to Maturity

Days to maturity was recorded after the development of yellowish color in peduncle of 75% plant population. Days to maturity was found to be highly significant ($P \leq 0.05$) among the tested genotype (Table 1). Mean days to maturity was 113 days ranged from 113 to 116 days. The early maturity was observed in genotype BL 4335 and Bhrikuti in 113 days followed by NL 1244, NL 1253, BL 4708, NL 1325, NL 1327, RR 21 and Gautam in 116 days and late maturity was observed in NL 1207, NL 1211, NL 1202, NL 1254, NL 1307, and NL 1328 in 117 days.

Days to maturity and AUDPC were found to be negatively correlated (-0.06619) (Table 2). i.e. late maturity results in lesser development of the disease. This result is in accordance to 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). Since, days to heading and days to maturity are positively correlated (0.819781) (Table2), so late heading varieties mature lately and they have lower disease severity. The result is in accordance to the finding of Neupane *et al.* (2013)

Spike per m^2

Spike per m^2 was found to be significantly different ($P \leq 0.05$) among the tested genotypes (Table 1). The mean spike per m^2 was found to be 85.68. It ranged from 73 to 102 spikes per m^2. The highest spikes were observed in NL 1328 (102) followed by BL 4707(94), NL 1326 and Gautam

(91) whereas the AUDPC value for the same genotype was found to be 166.4, 274.6, 307, 1790 respectively. The lowest spikes were found in BL 4335 (73), followed by NL1207 (76) and NL 1327(79) while their AUDPC values were found to be 731.2, 495.4 and 570.6 respectively (Table 1). Similarly, the correlation between spike per m^2 and AUDPC value were found to be negatively correlated (-0.37875) (Table 2) and the result is supported by the finding of Tewari *et al.* (2016). This means higher disease severity leads to the lesser spikes per m^2 area.

Grain per spike

Grain per spike was found to be significantly different at ($P \leq 0.05$) among the tested genotypes(Table 1).The lowest number of grain per spike was observed in NL 1328 (37) followed by RR 21 (38) and BL 4335 (38), NL 1307 (40), Gautam (41) and highest grain per spike was observed in NL 1327 (56), followed by NL 1253 (48), BL 4708 (48), NL 1325 (48) and NL 1325 (48).(Table 1). The mean of grain per spike was 44 and ranged from 56 to 37.

Similarly grain per spike is negatively correlated (-0.26474) with AUDPC value i.e. lower the disease severity, higher the grain per spike. (Table 2). This result is in accordance to findings of Tewari *et al.* (2016). This is because the lower grains per spike is resulted by the higher diseased area and lower assimilation of carbohydrate.

Test weight (1000 kernel weight, TKW)

Test weight was found to be highly significant among the tested genotypes at ($P \leq 0.05$). The mean test weight was 44.97gm and ranged from 39 gm to 53 gm. The highest test weight was observed in BL 4335 (53gm) followed by NL 1211 (51gm), Gautam, NL 1327and BL 4699 (48.5gm) with AUDPC value 731.2, 265.8, 1790, 570.6 and 141.7 respectively (Table 1). Lowest TKW was observed in NL1326.

The test weight and AUDPC value was found to be positively correlated (0.165164) (Table 2). This result was observed due to varietal character of genotypes possessing bold type grains. But, this result was in contrast to findings of Sharma *et al.* (2007), Tewari *et al.* (2016) and Neupane *et al.* (2013). They found negative correlation between TKW and AUDPC.

Grain yield

Grain yield was taken after the harvest of wheat. There is significance difference between the grain yield of different genotypes ($1 < p = 0.1226 > 0.05$) (Table 1). Mean grain yield was 3.337 ton/ha. Highest grain yield was given by BL4708 (3.761 ton/ha) followed by NL1325 (3.726 ton/ha), BL4707 (3.681 ton/ha) and NL1327 (3.642 ton/ha). Lowest grain yield was recorded in NL1328 (2.57 ton/ha), NL1247 (2.99 ton/ha) and NL1244 (3.035 ton/ha) (Table 2).

Grain yield was negatively correlated with AUDPC (-0.17322) which means, grain yield decreases with increase in AUDPC value (Table 1). This result in accordance to findings of Kandel *et al.* (2014), Tewari *et al.,* (2016) and Lamsal *et al.,* (2017). This may be because of reduced photosynthetic area of the plant to assimilate the carbohydrate in seed due to the diseased leaf.

Disease assessment

AUDPC of double digit scoring

AUDPC value of double digit scoring of different genotypes was found to be highly significant with each other at 5% level of significance. Highest AUDPC value was recorded in RR21 (1960) and lowest value was recorded in NL1202 (140.6) followed by BL4699 (141.7). Genotypes NL1202, BL4699, NL1328 and BL4707 had lower AUDPC with satisfying yield. Resistant check (Gautam)

had second highest AUDPC (1790). It may suggest that genotypes which were used were more resistant and tolerant than Gautam.

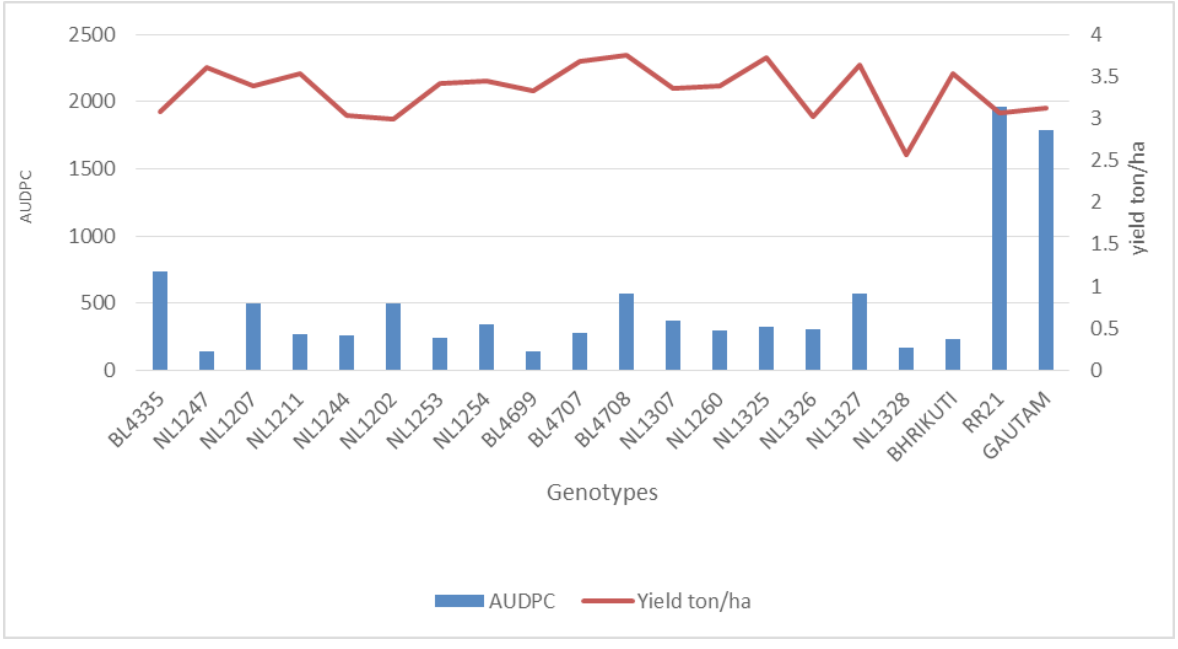

Figure 1: Relationship of yield in response to AUDPC of 20 Genotypes.

AUDPC on Flag leaf

Similarly, AUDPC value of flag leaf of different genotypes was also found to be highly significant with each other at 5% level of significance. Highest AUDPC value was recorded in genotype RR21 (264.1). Lowest AUDPC value of flag leaf was recorded in BL499 (4.398) followed by NL1244 (6.713).

AUDPC on Penultimate leaf

AUDPC value of penultimate leaf (F-1) of different genotypes was found to be highly significant with each other at 5% level of significance. Highest AUDPC value was recorded in RR21 (657.9). Lowest AUDPC value of flag leaf was recorded in BL499 (45.6) followed by NL1307 (92.82).

Table 1: Average of different yield attributing parameters of wheat at Bhairahawa

Parameters ENTRY	*Days to heading*	*Days to maturity*	*Plant height*	*Spike/m²*	*Grain/spike*	*TKW*	*Yield ton/ha*	*AUDPC*	*AUDPCF*	*AUDPCF-1*
BL4335	74	113	96.92	73	38	53	3.077	731.2	47.92	192.8
NL1202	79.5	116	83.91	81	43	47.5	3.604	499.9	64.35	141.4
NL1207	82	117	88.37	84	43	43	3.393	495.4	121.1	219.7
NL1211	80.5	116.5	93.95	76	44	51	3.542	265.8	98.61	243.3
NL1244	81	116	95.27	92	43	40.5	3.035	259.8	6.713	45.6
NL1247	81	115.5	86.42	91	47	40.5	2.990	140.6	175.9	270.1
NL1253	76.5	115.5	83.3	85	48	46.5	3.412	241.3	96.99	190.5
NL1254	80	116.5	84.52	88	42	46.5	3.447	342.8	49.54	138.2
BL4699	79.5	115.5	105.1	80	47	48.5	3.335	141.7	4.398	183.3
BL4707	79.5	115.5	92.04	94	45	44	3.681	274.6	156	286.6
BL4708	78	116	95.13	90	48	46.5	3.761	567.2	98.84	214.5
NL1307	79	117	90.1	81	40	46	3.366	366.6	40.51	92.82
NL1260	76	114.5	91.12	88	46	42.5	3.386	290.8	237.5	338
NL1325	76	115.5	83.32	90	48	41	3.726	325.6	84.72	180.1
NL1326	75	113	92.32	93	46	39	3.020	304	57.64	146.5
NL1327	79	115.5	89.3	79	56	48.5	3.642	570.6	146.5	228.7
NL1328	81.5	117	82.9	102	37	40.5	2.570	166.4	126.6	217.4
BHRIKUTI	75	113	79.8	90	44	40.5	3.543	233.5	82.64	296.3
RR21	76	115.5	91.87	78	38	45.5	3.068	1960	264.1	657.9
GAUTAM	78	116	92.37	91	41	48.5	3.130	1790	26.62	358.3
Grand Mean	78.35	115.5	89.9	85.68	43.72	44.97	3.337	498.4	99.36	232.1
F-test at 5%	HS	HS	HS	S	S	HS	S	HS	HS	HS
	3.18E-06	2.21E-07	3.18E-05	0.1497	0.2735	1.32E-08	0.1226	7.16E-10	8.95E-04	9.90E-04
CV% at 5%	1.426974	0.425477	3.377398	9.294663	12.41681	2.951753	9.518957	6.747272	1.64053	0.702297
LSD	2.236068	0.982853	6.072561	15.92733	10.85726	2.654807	635.2952	3.01264	3.260061	3.260061

TKW = Thousand kernel weight, HS= highly significant, AUDPC= Area under Disease Progress Curve, AUDPCF= AUDPC of flag leaf, AUDPCF-1= AUDPC of penultimate leaf

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

	HD	*MD*	*PL HT*	*S/M2*	*G/S*	*TKW*	*Y KG/ HA*	*AUDPC*
HD	1							
MD	0.819781	1						
PL HT	0.012975	-0.07876	1					
S/M2	0.20737	0.065852	-0.38595	1				
G/S	-0.0229	-0.10536	0.02745	-0.00403	1			
TKW	-0.05667	0.084169	0.421074	-0.82625	-0.01263	1		
Y KG/HA	-0.11283	0.051588	-0.0552	-0.27282	0.559216	0.311349	1	
AUDPC	-0.28296	-0.06619	0.147345	-0.37875	-0.26474	0.165164	-0.17322	1

HD= Days to heading, MD= Days to maturity, PL HT= Plant Height, S/M² = Spike per meter square, G/S= Grain per Spike,TKW= Thousand Kernel Weight, Y KG/HA= Grain Yield in Kg/ Hectare, AUDPC= Area Under Disease Progress Curve

CONCLUSION

Lower AUDPC value gives higher grain yield. Lowest mean AUDPC value was observed in NL 1202 (140.6) and highest was observed in RR21 (1960). Negative correlation was observed between AUDPC value and grain yield.

All the genotypes had lower AUDPC value than RR-21 (susceptible check) and Gautam (resistant check). Genotypes NL 1202, BL 4699, NL 1328, BL4707 had lower AUDPC value with satisfying grain yield. These genotypes could be further included in breeding programs. Among genotypes screened, NL 1202, BL 4699 and NL 1328 were found to be resistant and BL 4708, 1327, BL 4707 were found to be tolerant. This opens the way to conduct further research to check resistance and tolerance ability of different genotypes.

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