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Field response and identification of bread wheat genotypes to *Septoria tritici* blotch in the highlands of North Gondar

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Abstract
STB is among the fungal disease which threatens wheat production and its reported to be major wheat production threaten factor worldwide causing considerable yield loss every year. It is an economically important foliar disease in the major wheat-growing areas of Ethiopia. This research was conducted during 2019/2020 at Dabat research station under Gondar agricultural research center. The experiment was conducted to advance high yielding and septoria resistant bread wheat varieties suitable for studied environments. The experimental field was designed in simple lattice design with two replications and 100 genotypes used as treatment. The analysis of variance showed a highly significant difference ($p \leq 0.001$) for most of the yield and yield contributing traits among the tested genotypes. Out of 100 genotypes, 60 were found to be moderately resistant and forty were in the range of moderately susceptible. Area under progress curve (AUDPC) value was calculated for days to heading, grain filling period, days to maturity, plant height, spike length, spikelets per spike kernels per spike, thousand seed weight, and grain yield. The lowest AUDPC value was recorded from genotypes BW120044 (535.8), followed by genotypes, BW172938, BW120056, and BW120063 (553.1, 566.1, & 596.3) respectively, which are resistance to the disease. Genotype BW172082 showed the highest AUDPC value (1512.3) followed by genotype BW173214, BW120012, and BW120074 (1451.9), these genotypes are more susceptible to the disease. All of the studied yield and yield contributing traits were negatively correlated with AUDPC value except plant hight. Which indicated that the highest values of AUDPC impact on grain yield directly or indirectly. The development of disease resistance variety is considered as the most effective control strategy for *Septoria tritici* blotch.

Keywords: bread wheat, septoria, screening, AUDPC

Introduction

Wheat (*Triticum aestivum*) is one of the important cereal crops 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 (Ali *et al*., 2009) [1]. According to FAO, world wheat production in 2017 was 756.8 million tons which were reduced as compared to 2016 which was 757.2 million tons. (FAO, 2018) [5].

Wheat production constrained by various biotic and abiotic factors. Among the biotic factors, fungal diseases are one of the most important biotic constraints threatening wheat production in Ethiopia (Hailu, 1991) [9] Mengistu. Recently, rusts (stem yellow and leaf rust) and septoria leaf blotch and fusarium head blight are significantly threatening wheat production in most of the wheat-producing agro-ecologies (Hailu, 2003) [10].

STB is among the fungal diseases which threaten wheat production and it is reported to be major wheat production threatening factor worldwide causing considerable yield loss every year (Eyal, 1987) [4] and (Haile and Kasa, 2015) [8]. STB occurs in wheat-producing areas of all continents and results in serious crop losses in many wheat-growing regions of the world with crop losses in some areas, such as North Africa and southern Brazil, being devastating. The disease causes serious yield loss and losses attributed to a heavy infestation in fields planted with wheat susceptible cultivars have been reported to range from 30% to 40% (Wahl and Eyal, 1975) [37]. Epidemics can be particularly devastating in developing countries, such as those in East Africa, and severe epidemics of STB can reduce wheat yields by 35 to 50% (Sharma, 2012) [32].

To alleviate these constraints challenging wheat production, wheat breeding program wheat breeders have been working on the development of wheat varieties with high yield potential and resistance to major wheat diseases.

The development of high yielding varieties requires a thorough knowledge of the existing genetic variation for yield and its components. The successful process of wheat breeding is based on the knowledge of characteristics of genotypes, environment, and interaction. The ideal cultivar for high grain yield or for any other desirable traits needs to express genetic potential with the low value of variance in different environmental factors of growing. Therefore, the objective of this study was to advance high yielding and septoria resistant bread wheat varieties suitable for studied environments.

Materials and Methods

Description of the Study Area

The experiment was conducted in the 2019/2020 cropping season at Dabat Agricultural Research Station under Gondar Agriculture Research Center (GARC). The experimental site is located at 248 km distant from Bahir Dar (the capital city of Amhara Regional State) and 809.09 km from Addis Ababa to the Northern part of the country, and 75.8 km from Gondar town.

Dabat Research Site/Station is located at "12°59′03″N latitude and " 37°45′54″E longitude, with an altitude of 2607 m.a.s.l. The minimum annual temperature ranges between 4.6 °C and 24.5 °C. Dabat has a unimodal rainfall. According to the available digital data, the mean annual rainfall for the area ranges from 1250 to 1565mm. The rainy months extend from June to the end of September, and dominant soil in the area is Vertisol (Nigus Demelash, 2013) [24]

Experimental materials

A Total of 100 bread wheat genotypes that are listed for septoria resistance were used for the present experiment. These genotypes were obtained from kulumsa agricultural research center.

Experimental Design and Procedure

The trial was laid down using a 10 x 10 simple lattice design. Each genotype was planted in a plot size of $1m^2$ (2.5m x 0.4m). The distance between replications, blocks, and plots was 2m, 1m, and 0.3m respectively**.** The seeding rate was 150kg /ha and recommended fertilizer rate, 100kg DAP, and 150 kg Urea was used.

All DAP fertilizer was applied at planting while nitrogen fertilizer was applied in split (½ at planting, ¼ at tillering, and ¼ at head initiation (MOARD., 2012) [21]. Weeding and other agronomic management practices were done as per the recommendation for durum wheat.

Data to be collected

Days to heading (days): The number of days was recorded from the date of emergency to the stage when the spikes of 50% of the plants are fully visible (exerted*).*

Grain filling period (days): The grain filling period in days was computed by subtracting the number of days to heading from the number of days to maturity.

Days to physiological maturity (days): It is calculated as the number of days from emergence to 95% maturity that is the number of days to maturity minus the number of days to emergence.

Yield and Yield Related Traits

Plant height (cm): The average height of ten plants randomly taken from each plot at physiological maturity and measured from the ground to the tip of the panicle excluding the awns.

Biological yields (t/ha): It will record by weighing the total above-ground yield harvested from the two rows of each experimental plot at the time fully dried.

Thousand kernels weight (gm): The weight of one thousand randomly taken kernels from each experimental plot.

Grain yield (t/ha): The grain yield per plot was measured in gram using sensitive balance after moisture of the seed is adjusted to 12.5%. The total dry weight of grains harvested from the two rows was taken as grain yield per plot and expressed as a ton per hectare for analysis.

Kernels per spike: Number of kernels per spike was counted from ten randomly taken plants and the average was worked out.

Spikelet per spike: Number of spikelets per spike was counted from ten representative spikes per plant and average was worked out.

Spike length (cm): The average spike lengths of ten plants on the main Culm from the base of the spike to the top of the last spikelet excluding awns.

Disease data: The major wheat diseases mainly (septoria and rust) was recorded based on the standard recording methods.

Disease Scoring Method

Double-Digit Scoring (Septoria)

The severity of *Septoria tritici* blotch was examined using the double-digit scale (00-99) developed by the modification of Saari & Prescott's Scale, measures overall foliar infection on the whole plant on the basis of two digits (Saari and Prescott, 1975) [29], where; The first digit (D1) indicates disease progress in canopy height from the ground level and the second digit (D2) refers to the severity of the disease based on the diseased leaf area (Nagarajan, 1998) [22]. D1 represents a vertical extent and D2 represents a horizontal extent. The assessment was done through the whole plots and the evaluation was carried out three times interval at the booting stage, heading stage, and maturity stage. For each score the percentage disease severity can be calculated by the following formula:

SDS (%) = (D_1/Y1× D_2 /Y2 × 100), where D1 and D2 represent the score recorded from (00-99), and Y1 and Y2 represent the maximum score on the scale (9 and 9) (Sharma and Duveiller, 2007) [31].

Scales for the height of infection (vertical extent)

1 = lowest leaf, 2 = second leaf from the base, 3-4 = second leaf up to below middle of the plant, 5 = up to the middle of the plant, 6-8 = from the center of the plant to below of the flag leaf, and 9 = up to flag leaf and spikes.

Scales for severity infection (horizontal extent): 1 = 10% coverage, 2 = 20% coverage, 3 = 30% coverage, 4 = 40% coverage, 5 = 50% coverage, 6 = 60% coverage, 7 = 70% coverage, 8 = 80% coverage, 9 = more than 90% coverage

Scale for Disease Reaction and Host Response: The genotypes were classified into six categories which are immune (00), resistance (10-14), moderately resistant (15-35), moderately susceptible (36-55), susceptible (56-79), and highly susceptible (>79) (Singh *et al*., 2014) [35].

Estimating Area Under Disease Progress Curve (AUDPC)

The area under the disease progress curve (AUDPC) was calculated in order to know the progress of the disease for all genotypes (Shaner Finney, 976) [30] by the following formula.

$$\text{AUDPC}=\sum_{1=1}^{n=1}(Yi+1+Yi)0.5(Ti+1-Ti)$$

Where,

Yi=disease severity in the ith date

Ti= date on which the disease was scored

n=number of dates on which disease was recorded

Statistical Analysis

Analysis of variance (ANOVA) was computed to test the presence of significant differences among the genotypes for studied traits. The data were collected for each quantitative trait and would be subject to analysis of variance using Proc Glm of SAS version 9.0, (SAS Institute, 2008).

Fisher’s protected least significant difference (LSD) 5% level of significance will be used for mean comparisons, whenever the Analysis of Variance (ANOVA) result showed a difference among genotypes for traits.

Results and Discussions

The analysis of variance (ANOVA) showed that there was a highly significant difference among the genotypes of most of the studied traits. Results obtained on screening assessments among genotypes for yield and yield-related traits, disease (septoria & rust), and genetic variation are presented hereunder. Implications of such studies in bread wheat improvement and breeding programs for higher grain yield, disease resistance, and other traits of interest are also discussed.

Table 1: The mean and range values of phenological, yield and yield-related traits and disease data of bread wheat genotypes

Traits	Range	Mean	CV	Sig
DH	56-72	64.24	2.81	***
GFP	46-65.5	55	3.73	***
DM	118-124.5	120	0.88	***
BY	1.2-1.9	1.5	13.76	ns
GY	6-2-107.5	6078.8	16.29	***
TSW	9.9-42	33	7.70	***
PH	72.6-138	86.1	4.06	***
SL	7.7-9.9	8.67	5.18	**
SPS	15.5-19.5	16.86	4.09	***
KPS	12.1-99.1	54.16	12.09	***
SEP	18.3-50.41	34.56	18.78	***
StR	0-90	1.75	40.41	***
AUDPC	535.8-1512.3	1010.38	18.68	***

DH=days to heading, GFP=grian filling period, DM=days to maturity, BY=biological yield GY=grain yield, TSW=thousand seed weight, PH=plant height, SL=spike length, SPS=spiklet per spike, KPS=kernels per spike, SEP=septoria, STR=stripe rust, AUDPC= area under progress curve, CV=coefficient of variation, sig=significant level

This study was carried out aiming at the screening of bread wheat genotypes including standard and local checks for *Septoria tritici* blotch resistance/tolerance. The results on disease intensity and host response are presented in (Table 3). From this study, none of the bread wheat genotypes were completely immune or resistant to *Septoria tritici* blotch. For this reason, where resistance is not much effective, tolerance can be sought according to (McKendry and Henke, 1994) [20]. Out of bread wheat genotypes, sixty were within the range of moderate resistance while the rest of forty were moderately susceptible. This indicated that the bread wheat genotypes were in the range of moderate resistance to moderately susceptible. And the disease *Septoria tritici* blotch is one of the devastating diseases that curtails the production and productivity of wheat nationwide (Abebe Teklay *et al.*, 2015) [1].

Table 2: The mean values of all studied traits and diseases data

Accessions	DSH	GFP	DSM	BY	GY	TSW	PH	SL	SPS	KPS	SEP	AUDPC
BW173120	67.00	53.00	120.00	1.55	5331.26	26.22	79.55	7.90	16.70	54.25	38.89	1119.1
BW173123	56.00	63.00	119.00	1.25	6104.53	34.36	72.55	8.85	16.75	53.10	37.45	1119.1
BW172846	64.00	57.00	121.00	1.40	7291.60	37.53	84.85	9.60	17.05	52.10	28.81	846.9
BW172862	65.00	53.00	118.00	1.46	5357.24	38.26	79.75	8.90	16.30	54.95	27.37	786.4
BW172864	67.50	51.50	119.00	1.40	5658.38	38.55	78.45	8.80	16.40	55.60	39.92	989.5
BW172867	65.00	53.00	118.00	1.50	5903.32	26.02	83.15	9.25	17.85	66.10	35.80	933.3
BW172872	68.00	54.00	122.00	1.45	4544.81	30.67	81.85	8.65	16.70	61.45	38.68	1054.3
BW172936	66.00	55.00	121.00	1.80	6519.78	36.68	85.95	9.10	16.40	59.50	28.81	816.7
BW172938	64.00	60.50	124.50	1.50	5712.24	36.16	81.60	8.90	16.30	52.80	22.02	553.1

BW172949	56.00	62.00	118.00	1.50	6791.63	32.51	75.00	7.70	15.50	56.00	46.71	1425.9
BW172082	64.00	59.50	123.50	1.65	6349.34	30.34	89.80	9.55	17.05	53.20	50.41	1512.3
BW172969	68.00	50.00	118.00	1.35	5545.80	39.25	83.15	8.70	16.10	56.55	36.01	1028.4
BW172996	64.00	58.00	122.00	1.25	6370.69	37.85	79.70	8.70	16.65	56.60	31.69	937.7
BW173001	64.50	56.50	121.00	1.50	5952.27	36.75	80.05	8.55	16.00	55.35	29.84	747.5
BW173006	64.50	53.50	118.00	1.35	5129.56	29.05	86.55	8.95	15.95	60.90	43.21	1270.4
BW173013	68.00	54.00	122.00	1.35	5080.51	33.73	76.05	8.80	15.85	62.00	34.98	1041.4
BW173016	63.50	54.50	118.00	1.35	5335.06	32.23	80.10	8.60	15.85	56.40	27.37	786.4
BW173415	68.00	56.50	124.50	1.15	4855.12	33.80	77.55	9.20	17.05	62.65	20.16	604.9
BW173436	63.00	58.00	121.00	1.35	5821.06	31.07	82.10	8.20	15.50	51.80	34.57	1028.4
BW173353	57.00	64.00	121.00	1.60	6940.74	36.17	80.35	8.05	15.60	55.85	38.68	1054.3
BW173366	61.00	61.00	122.00	1.75	9125.97	33.26	82.45	9.00	17.25	59.60	21.40	600.6
BW173372	67.00	54.00	121.00	1.50	4968.60	35.63	84.75	9.10	16.85	58.15	28.81	816.7
BW173378	64.50	54.50	119.00	1.55	5347.36	38.05	79.55	7.80	15.95	58.00	33.13	998.1
BW172319	58.00	65.50	123.50	1.50	6607.92	40.69	75.90	8.75	16.10	57.30	26.34	674.1
BW172324	60.00	60.00	120.00	1.50	4782.34	31.62	78.35	8.70	16.35	57.70	32.92	842.6
BW172353	68.00	54.00	122.00	1.65	6361.59	42.01	83.80	9.00	16.70	49.25	28.81	846.9
BW172390	58.00	60.00	118.00	1.25	6672.20	34.07	79.60	8.75	16.45	99.05	36.01	1088.9
BW172392	58.00	60.00	118.00	1.50	6247.14	34.35	76.55	8.40	15.85	61.25	37.45	1149.4
BW172393	62.00	58.00	120.00	1.60	6470.02	35.54	81.40	8.10	16.05	57.80	33.13	998.2
BW172440	63.00	57.00	120.00	1.50	6723.39	32.75	81.15	8.30	15.65	49.05	34.57	1028.4
BW172474	58.00	61.00	119.00	1.45	5987.09	30.37	83.60	9.00	16.25	52.50	46.09	1391.4
BW172479	68.50	54.50	123.00	1.45	4170.67	30.00	81.85	8.40	16.85	56.40	34.36	903.1
BW172486	65.00	58.00	123.00	1.75	7805.85	38.94	80.65	8.90	16.75	51.85	25.93	756.2
BW172487	68.00	56.50	124.50	1.60	6129.68	39.42	84.25	8.75	17.95	53.75	34.57	1028.4
BW172495	68.00	50.00	118.00	1.65	5450.75	32.12	84.05	8.55	16.50	58.55	33.13	967.9
BW172509	65.00	53.00	118.00	1.55	7155.36	33.75	82.50	8.60	16.75	61.15	28.81	816.7
BW172516	59.00	59.00	118.00	1.40	6378.47	33.55	81.10	8.60	16.40	57.35	36.01	1088.9
BW172548	59.00	59.00	118.00	1.60	5914.35	29.62	77.10	8.25	16.00	54.95	34.57	1058.6
BW172550	61.50	56.50	118.00	1.25	5143.96	29.67	83.10	8.65	16.85	59.25	38.89	1149.4
BW172558	63.00	55.00	118.00	1.50	7158.46	40.47	81.40	8.55	16.60	53.90	28.81	846.9
BW172559	65.50	54.50	120.00	1.75	7869.79	35.35	91.05	9.25	17.70	59.00	44.65	1330.9
BW173202	64.00	55.00	119.00	1.70	6716.33	35.05	86.40	8.70	16.55	58.65	34.36	993.8
BW173207	62.00	56.00	118.00	1.80	7583.56	33.04	84.30	7.90	15.85	52.70	36.01	1028.4
BW173208	69.00	52.00	121.00	1.65	7301.95	28.52	85.20	8.50	16.60	52.70	30.04	812.3
BW173214	57.00	61.00	118.00	1.25	4921.35	27.20	75.65	8.35	16.00	57.65	48.97	1451.9
BW173252	60.00	58.00	118.00	1.50	5382.43	33.42	82.05	8.60	16.80	56.55	43.21	1270.4
BW173261	59.00	59.00	118.00	1.40	6361.45	31.26	76.15	8.15	15.70	56.50	41.77	1240.1
BW173263	59.00	59.00	118.00	1.65	6940.32	34.52	85.30	8.55	16.50	57.90	33.13	967.9
BW173265	61.50	57.50	119.00	1.50	6421.27	28.75	82.85	8.35	16.65	58.05	28.81	816.7
BW173270	64.00	57.00	121.00	1.55	6481.05	33.19	83.90	8.25	16.55	59.15	44.65	1300.6
BW173284	59.00	59.00	118.00	1.40	6174.18	30.89	81.10	8.75	16.55	52.80	36.01	1058.6
BW173285	58.00	62.00	120.00	1.45	5889.45	35.23	80.60	8.75	18.40	55.65	33.13	998.1
BW173287	60.00	58.00	118.00	1.45	6030.39	31.33	83.40	8.60	17.70	59.45	33.13	998.2
BW173288	59.00	59.00	118.00	1.45	7782.38	37.86	83.75	8.65	17.65	61.50	37.45	1119.1
BW173290	64.00	58.00	122.00	1.75	7574.14	35.82	83.95	9.00	18.55	62.25	28.81	846.9
BW173292	64.00	58.00	122.00	1.50	7566.20	36.71	80.95	7.95	16.45	61.35	30.25	907.4
BW173317	60.00	58.00	118.00	1.85	7041.51	34.46	81.70	8.25	17.15	55.50	22.84	600.6
BW173318	58.00	60.00	118.00	1.55	5738.48	34.56	80.55	7.90	16.45	56.20	25.93	725.9
BW173340	64.00	55.00	119.00	1.60	6420.30	40.46	80.40	7.95	16.35	56.75	34.57	998.2
BW173342	67.00	53.00	120.00	1.40	6913.80	34.18	86.95	8.50	16.60	55.25	33.13	967.9
BW174170	68.50	49.50	118.00	1.50	4436.01	26.01	82.60	9.30	17.35	54.30	37.45	1149.4
BW174172	67.00	53.00	120.00	1.40	3828.80	25.08	77.60	8.70	16.20	52.95	38.89	1179.6
BW174214	60.00	58.00	118.00	1.35	5062.39	31.05	77.15	8.65	16.75	55.05	40.33	1179.6
BW174226	57.00	61.00	118.00	1.55	6384.32	26.38	79.60	8.25	16.50	50.70	36.01	1088.9
BW174252	63.00	57.00	120.00	1.30	4538.89	26.33	79.50	8.50	16.50	54.05	34.57	1028.4
BW174277	60.00	60.00	120.00	1.65	6358.13	30.74	78.40	8.70	17.00	54.60	27.37	816.7
BW120002	64.00	55.00	119.00	1.55	6458.27	33.97	84.35	8.55	16.70	53.60	43.21	1300.6
BW120003	64.50	54.50	119.00	1.85	6644.76	27.15	91.90	8.40	16.60	58.40	41.77	1240.1
BW120004	64.50	53.50	118.00	1.25	5130.72	26.62	90.85	8.25	16.70	53.45	43.21	1270.4
BW120007	65.50	54.50	120.00	1.45	4714.65	28.38	84.55	8.20	16.30	55.60	34.57	1028.4
BW120008	68.50	54.50	123.00	1.40	4817.14	34.57	96.75	8.85	17.70	49.60	36.01	1088.9
BW120009	69.00	51.00	120.00	1.60	6691.39	32.74	93.80	8.80	17.45	49.45	31.69	967.9
BW120011	65.00	55.00	120.00	1.50	6166.37	29.60	92.10	8.90	17.50	52.25	41.77	1270.4
BW120012	63.00	55.00	118.00	1.20	4399.94	26.53	83.95	7.95	16.20	54.90	48.97	1451.9
BW120015	67.00	56.00	123.00	1.65	5674.57	32.72	89.40	8.20	16.50	50.55	46.09	1361.1
BW120019	68.50	54.50	123.00	1.50	5041.84	34.94	86.90	8.65	17.20	51.20	38.89	1179.6
BW120030	69.00	53.00	122.00	1.50	6147.00	32.75	90.55	9.00	17.10	54.35	30.04	872.8

BW120039	66.00	53.00	119.00	1.50	4665.18	29.10	86.00	8.30	16.65	47.55	40.33	1179.6
BW120041	69.50	53.50	123.00	1.50	7142.77	34.44	100.70	9.60	18.80	50.45	30.25	907.4
BW120042	70.00	53.00	123.00	1.60	7253.49	35.81	102.10	9.70	18.77	44.05	28.81	877.2
BW120044	63.00	60.00	123.00	1.90	10746.97	40.47	97.40	8.30	17.75	46.15	18.31	535.8
BW120049	68.50	52.50	121.00	1.65	6993.40	35.80	94.60	8.60	17.45	48.20	25.10	708.6
BW120052	64.50	54.50	119.00	1.40	5099.87	30.67	89.05	8.75	17.05	59.20	34.57	1028.4
BW120053	66.00	53.00	119.00	1.45	6994.68	37.89	91.75	8.80	17.45	49.70	31.69	967.9
BW120054	68.50	53.50	122.00	1.50	6056.67	38.01	92.40	8.85	17.75	54.45	34.57	1028.4
BW120055	64.50	56.50	121.00	1.50	6239.26	38.65	95.75	9.15	18.10	51.00	31.69	967.9
BW120056	70.00	52.00	122.00	1.75	7364.29	31.87	91.35	8.80	17.90	47.40	22.63	566.1
BW120060	64.00	56.00	120.00	1.45	5497.90	33.59	94.35	8.85	17.60	47.55	31.69	907.4
BW120061	60.00	58.00	118.00	1.55	6260.13	35.93	90.95	8.55	16.50	49.80	36.01	1088.9
BW120062	67.50	54.50	122.00	1.35	6284.49	32.77	94.70	8.90	17.65	57.85	28.81	877.2
BW120063	68.00	54.00	122.00	1.80	9439.85	34.72	93.20	8.90	17.45	44.70	25.51	596.3
BW120068	64.00	57.00	121.00	1.60	6703.19	35.01	99.30	9.05	17.05	46.35	31.69	907.4
BW120069	67.00	52.00	119.00	1.45	6727.13	34.91	89.75	8.65	17.10	53.80	33.13	998.2
BW120072	66.00	53.00	119.00	1.35	5645.25	35.15	94.20	8.60	16.90	48.60	41.77	1209.9
BW120073	68.50	54.50	123.00	1.40	5980.07	34.61	92.80	8.75	17.65	37.80	33.13	998.2
BW120074	72.00	46.00	118.00	1.50	2463.33	35.65	113.55	9.35	18.70	43.35	48.97	1451.9
BW120076	69.50	48.50	118.00	1.30	619.61	9.88	107.50	8.75	17.20	12.10	30.04	1084.6
BW120070	68.00	50.00	118.00	1.40	4104.30	26.75	103.50	8.90	17.50	35.40	46.09	1361.1
Check	71.50	51.50	123.00	1.50	7743.26	35.76	100.45	9.90	19.45	50.20	34.36	933.3
Local	72.00	52.00	124.00	1.55	5054.68	35.54	137.65	9.05	17.70	35.35	40.33	1240.1

DH=days to heading, GFP=grian filling period, DM=days to maturity, BY=biological yield GY=grain yield, TSW=thousand seed weight, PH=plant height, SL=spike length, SPS=spiklet per spike, KPS=kernels per spike, SEP=septoria, AUDPC=area under progress curve

Table 3: The response of bread wheat genotypes for *Septoria tritici* blotch

Disease	No. Observation	Reaction level	Host Response
Septoria	00	00	IM
	00	01-14	RS
	60	15-35	MR
	40	36-55	MS
	00	56-79	SS
	00	>79	HS
	Check	34.6	MR
	Local	40.33	MS

IM=immune, RS=resistance, MR=moderately resistance, MS=moderately susceptible, SS=susceptible, HS=highly susceptible

Description

IM: No visible infection

RS: lesions absent or small without chlorosis

MR: lesions small but with some chlorosis

MS: lesions large with extensive chlorosis but little or no coalescence

SS: lesions large and coalescence with chlorosis

HS: lesions large and extensive coalescence with severe chlorosis Key

One hundred bread wheat genotypes were studied including standard and local checks. There was a highly significant difference among the genotypes for Days to heading, grain filling period, days to maturity, plant height, grain yield, thousand seed weight, spike length, spikes numbers of spikelets per spike, and Kernels per spike. The significant difference among genotypes for the traits indicates that there was the presence of genetic variation among the genotypes which in turn suggests that selection of lines can be effective in improving both yield and quality traits (Kumar *et al.*, 2009). The main objective of this research was to identify/screen the genotypes which are resistance/tolerance to wheat disease particularly for septoria trite blotch and rust diseases as well high grain yield was vital. The disease data were recorded at different stages of wheat growth (to estimate the disease occurrence time and yield loss), based on this double-digit method is the best way to score septoria trite blotch. Most of the genotypes are ranged from 15-35%, which indicates that the genotypes response to diseases is resistant to moderate resistance.

Area Under Progress Curve (AUPDC)

AUDPC value was found to be a highly significant difference ($p \leq 0.01$) among the tested genotypes (Table 2).The lowest AUDPC value was obtained from genotype BW120044 (535.8) followed by genotypes BW172938, BW120056, and BW120063 (553.1, 566.1, & 596.3) respectively, Genotypes that have less AUDPC value indicate more resistance and moderate resistance to *Septoria tritici* blotch. Genotype BW172082 showed the highest AUDPC value (1512.3) followed by genotype BW173214, BW120012, and BW120074 (1451.9) (Table 2).

Days to Heading: days to heading found to be highly significant ($p \leq 0.01$) among the tested genotypes (Tabe 1). The mean of heading date was found to be 64.24 days. Among the tested genotypes, the first heading was observed in genotype BW173123 and BW172949 (56 days), followed by genotype BW172867, BW173353, and BW173214 (57 days). Late days to heading was recorded from genotype 96 and 100 (72 days) (Table 2). The difference level of pathogen aggressiveness on susceptible genotypes as compared with less susceptible ones can be explained by differences in variations of aggressiveness when the pathogen is on different host genotypes (Pandey *et al.*, 2018) [25]. Days to heading is negatively correlated with AUDPC (-0.11072) value, which means that late heading results in less development of disease (Table 4). While early heading results in more disease development. This result agrees with that of (Latwal *et al.*, 2019) [17]. Genotypes late in heading have lower disease severity, it is due to slower plant development and shorter period of exposure of the plant to the pathogen (Pandey *et al.*, 2018) [25].

Grain Filling Period: Grain filling period founds to be a highly significant difference (p≤0.01) among the tested genotypes (Table 2). The mean values of the grain filling period were 55 days and it ranged from 46 days to 65.5 days. The shortest days for grain filling period were recorded from genotype BW120074 (46 days) and the longest days were obtained from genotypes BW172319, BW173353, and BW173123 (65.5 days, 64days, and 63 days) respectively. Grain filling period is negatively correlated with AUDPC value (-0.07669). This means that the shortest days for the grain filling period results in the more development of disease (Table 2). While the longest days for grain filling results in less disease development. Hence, days to grain filling period and days to maturity are positively correlated (0.04388) (Table 4). So late grain filling genotypes mature lately and they have lower disease severity. This result is in accordance with the finding of (Neupane *et al*., 2013) [23]

Days to maturity: Days to maturity were recorded at the stage of full physiological matured of genotypes. Days to maturity was found to be highly significant (p≤0.01) among the tested genotypes (Table 1). The average mean of days to maturity was 120 days ranged from 118-124.5 days. The early maturity was observed in BW172486 genotypes (118 days) and late maturity was observed in genotypes BW172938, BW173415, and BW172487 (124.5 days) (Table 2). Days to maturity was negatively correlated with AUDPC (-0.35576) (Table 4). Which means that late maturity results in less development of the disease. This result is in line with similar findings (Tewari *et al*., 2016) [36] and (Neupane *et al*., 2013) [23]. Genotypes with late-maturing are more resistant and lower disease severity than early maturing genotypes (Duveoller *et al*., 2005). Hence, days to heading and days to maturity are positively correlated (0.46349) (Table 4). So, late heading genotypes mature lately and they have lower disease severity. This result is in accordance with the finding of (Neupane *et al*., 2013) [23].

Plant height: plant height for wheat genotypes was measured at physiological maturity stage. The plant height was found to be highly significant (p≤0.01) among the tested genotypes (Table 1). The local check had the highest plant height 137.65cm followed by genotype BW120074 & BW120074 (113.55cm and 107. 50cm respectively. The lowest plant height was recorded from genotype BW173123 (72.55cm) (Table 2). The mixture of genotypes gene rotation and other resistance placement strategies useful for obtaining the stability of resistance to *Septoria tritici* blotch (Paraschivu *et al*., 2013) [27]. Previous studies showed that plant height and heading date reduce the chance of contact between pathogens and host by different escaping mechanisms ((Parelviliet, 1977) [28]; (Jlibene M., 1992) [12]; (Simón, 2004) [19] and (Simon, 2005) [34], these mechanisms should be taken in to account.

Reduce plant height was usually associated with more necrosis due to the highest necrosis percentage, while, the highest plant height was strongly associated with reduced AUDPC values in the tested wheat genotypes mixture leading to the finalizing that vertical progress of septoria from lower to upper leaves is affected by the distance between consecutive leaves. So for tall genotypes, the septoria progress was lower comparatively with dwarf and semi-dwarf cultivars (Paraschivu *et al.*, 2013) [27]. Plant height showed a positive correlation (0.11206) with AUDPC which indicates that an increase in plant height, increases in AUDPC values (Tbabe 4). This idea disagrees with (Chedli *et al*., 2018) [3]; (Li *et al*., 2016) [18] and (Neupane *et al*., 2013) [23] found that there was a 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 is in line with (Joshi *et al*., 2002) [13]s

Spikelet's per spike: Spikelet per spike was found to be a highly significant difference (p≤0.01) among the tested genotypes (Table 1). The mean of spikelet per spike was found to be 16.86cm. it ranged from 15.5cm-19.5cm. The highest spikelet per spike was recorded fro the stsndard check 'Alidoro' (19.45) followed by genotypes BW120041, BW120042, BW120074, BW173290, BW173285, and BW120055 (18. 80cm, 18.77cm, 18.70cm, 18.55cm, 18.40cm, and 18.10cm respectively (Table 2). While the lowest spikelets per spike were recorded from genotypes BW17949 and BW174336 (15.50cm) followed by genotypes BW173353, BW172440, and BW173261 (15.60cm, 15.65cm, and 15.70cm) respectively. The correlation between spikelet per spike and AUDPC value was negatively correlated (-0.13670) table cor..6. this result is supported by the findings of (Tewari *et al*., 2016) [36].

Grain yield: There was a highly significant difference (p≤0.001) among the tested genotypes (Table 1). Grain yield was taken after the harvest of wheat genotypes and measured at the standard moisture content (12.5) of wheat. The mean grain yield was 6078.8t/ha. The highest grain yield was observed from genotype BW120042 (10746.97t/ha) followed by genotypes BW120063 and BW173366 (9439.85 and 9125.97t/ha) respectively. While the lowest grain yield was found to be genotype BW120076 (619.61t/ha) followed by genotypes BW120074 and BW174172 (2463.33 and 3828.80t/ha) respectively (Table 2). Grain yield was highly negatively correlated with AUDPC (-0.42269) which indicates that when the grain yield is decreased with an increased in AUDPC value (Table 4). This result is similar to previous findings of (Kandel & Mahato, 2014) [14]; (Tewari *et al*., 2016)) [36], and (Pandey *et al*., 2018) [25].

This may be because of the reduced photosynthetic area of the plant to assimilate the carbohydrate in seed due to the diseased leaf. Most yield studies on septoria tricitici blotch showed relationships between disease severity on the upper one and three leaves and yield (King *et al*., 1983a, 1983b) [15, 16]. The greatest risk to a crop is the occurrence of conditions that favor spore dispersal during and shortly after flag leaf emergence. (James, 1974) [11] showed that crop losses are related to total leaf area infected including necrotic lesion and chlorotic flakes. Some genotypes have high AUDPC value and give a reasonable yield, it may be suggested that genotypes were more resistance and tolerance.

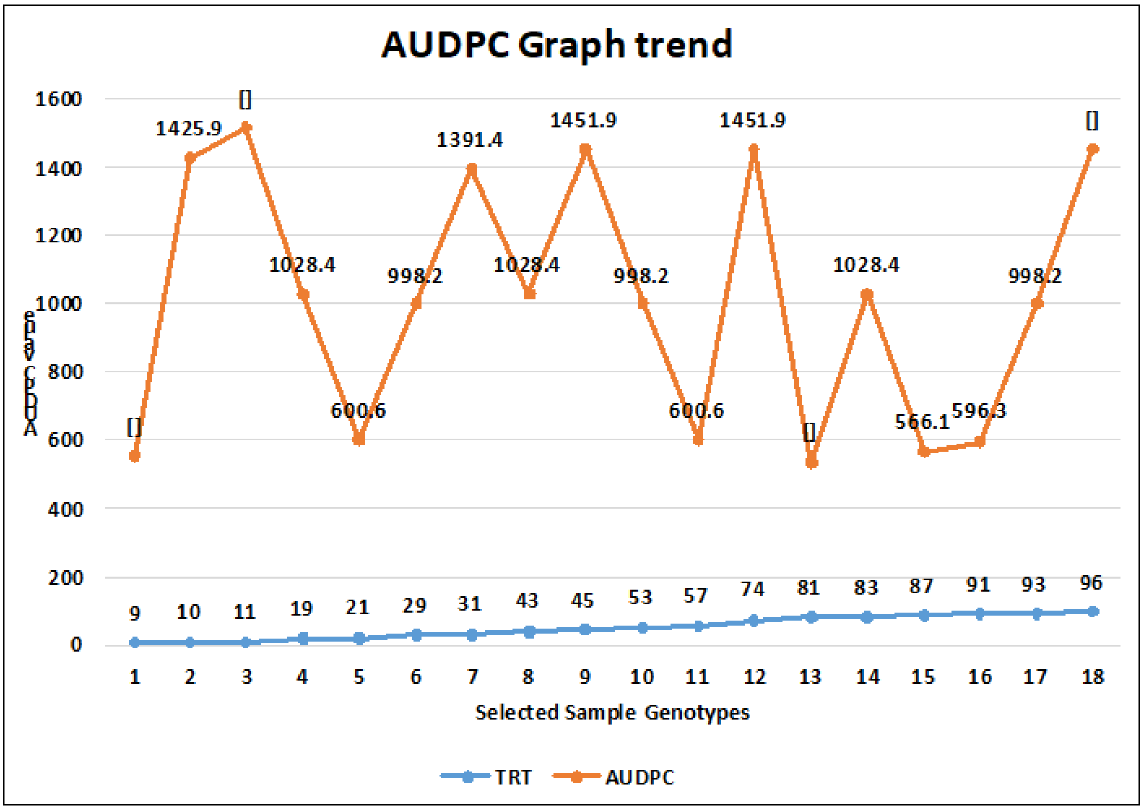

Fig 1: The graph shows the trend of relationship between AUDPC and 17 genotypes which were selected from the minimum, medium, and maximum AUDPC values

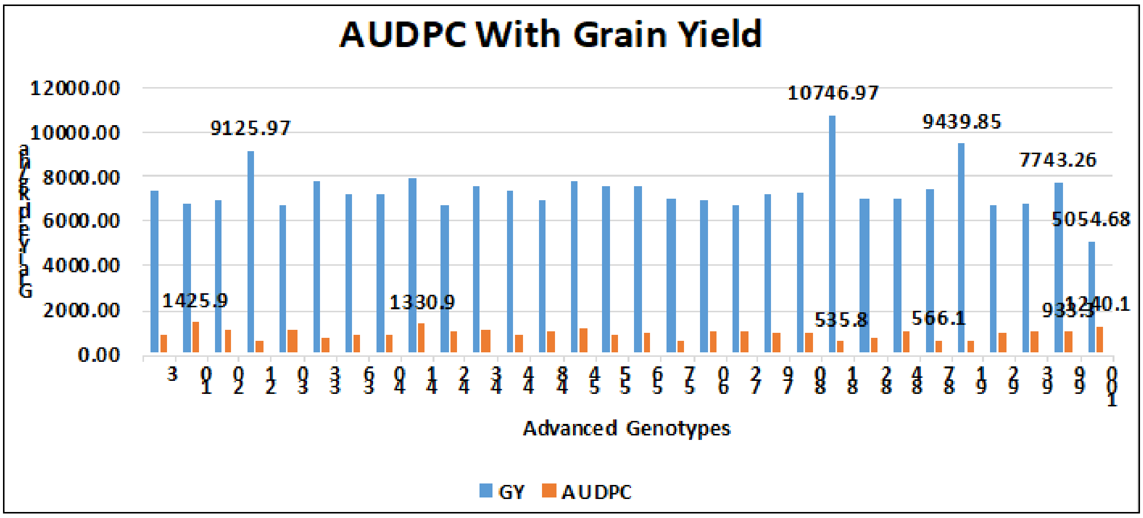

Fig 2: The graph shows that the relationship between AUDPC values and the grain yield of selected/advanced genotypes to preliminary yield trials

Thousand Kernels weight: Thousand Kerneles weight was showed a highly significant difference (p≤0.001) among the tested genotypes (Table 1). The mean thousand Kernels weight was 33gm and ranged from 9.9gm to 42.1gm (Table 2). The highest thousand Kernels weight was observed in genotype BW172353 (42.01gm) followed by the genotypes BW172319, BW120041, BW172558, and BW173340 (40.69, 40.47, 40.47, and 40.46gm) respectively. While the lowest thousand Kernels weight was observed in genotype Bw120076 (9.9gm). The thousand Kernels weight and AUDPC value found to be negatively correlated (-0.36290) (Table 4). This result was observed due to the varietal character of genotypes possessing bold type grains. So, this result was in agreement with the finding of (Sharma and Duveiller, 2007) [31]; (Tewari *et al.*, 2016) [36] and (Neupane *et al.*, 2013) [23]. They found that there was a negative correlation between thousand Kernels weight and AUDPC. Previous findings showed that necrosis was highly correlated with the reduction of kernel weight (Forrer and Zadoks, 1983) [7].

Kernels Per Spike: Kernels per spike was found to be highly significant different (p≤0.001) among the tested genotypes (Table 1). The mean values of kernels per spike were found to be 54.16, and it ranged from 12.1-99.1. The lowest number of kernels per spike was observed in genotypes BW120076 (12.01), and the highest number of kernels per spike was observed from genotype BW172390 (99.05) followed by genotypes BW172867, BW173415, BW173290, and BW173013 (66.10, 62.65, 62.25 and 62.00) respectively (Table 2). Similarly, kernels per spike are negatively correlated (-0.04543) with AUDPC value which means that when the disease severity becomes lower, higher the kernels per spike (Table 4). This result is in accordance with the findings of (Tewari *et al*., 2016) [36]. This is because the lower kernels per spike are resulted in a higher diseased area and lower assimilation of carbohydrates.

Spike Length: Spike length showed a highly significant difference (p≤0.01) among the tested genotypes (Table 1). The mean values of spike length were found to be 8.67cm and ranged from 7.7cm to 9.9cm. The longest spike length was recorded from the standard check Alidoro (9.9cm) followed by genotype BW120042, BW120041, BW172846, and BW172082 (9.7, 9.6, 9.6, and 9.55cm) respectively. While the lowest spike length was observed from genotypes BW172949 (7.7) followed by genotype BW173378 (7.8cm) (Table 2). There was a negative correlation between spike length and AUDPC value (-0.12574) (Table 4). AUDPC has a negative correlation with yield and yield-related traits of wheat including spike length. These findings completely agreed with (Sharma *et al*., 1997) [33] and (Fellahi *et al*., 2013) [6].

Table 4: The correlation of AUDPC values with other yield and yield attributing traits

	AUDPC	DSH	GFP	DSM	BY	GY	TSW	PH	SL	SPS	KPS
AUDPC	1	-0.11ns	-0.08ns	-0.36**	-0.32**	-0.42***	-0.36**	0.11ns	-0.13ns	-0.14ns	-0.05**
DSH		1	-0.86***	0.46***	0.07ns	-0.19*	0.01ns	0.59***	0.43***	0.47***	-0.39***
GFP			1	0.04ns	0.03ns	0.35**	0.18ns	-0.52***	-0.28**	-0.34**	0.35**
DSM				1	0.20ns	0.22*	0.33**	0.26**	0.36**	0.35**	-0.16ns
BY					1	0.58***	0.27**	0.15ns	-0.02ns	0.17ns	-0.09ns
GY						1.0	0.55***	-0.08ns	0.03ns	0.14ns	0.24**
TSW							1	-0.03ns	0.13ns	0.11ns	0.23ns
PH								1	0.41***	0.61***	-0.59***
SL									1	0.65***	-0.13ns
SPS										1	-0.27ns
KPS											1

DH=days to heading, GFP=grian filling period, DM=days to maturity, BY=biological yield GY=grain yield, TSW=thousand seed weight, PH=plant height, SL=spike length, SPS=spiklet per spike, KPS=kernels per spike, AUDPC= area under progress curve

Conclusions and Recommendations

In this investigation, a sufficient amount of genetic variability was observed in the germplasm accessions for septoria disease reaction. On the basis of findings, accessions were grouped into moderate resistance to moderately susceptible categories under field conditions. The genotypes showing low AUDPC values were considered as resistance and high AUDPC as susceptible. The negative association between AUDPC value and important yield components revealed its impact on yield and yield contributing traits. From one hundred genotypes including local and standard check, sixty were found to be moderately resistant including standard check and forty genotypes including local check were found to be moderately susceptible to *Septoria tritici* blotch. This result leads us to conduct further research to check more resistance and tolerance ability of different genotypes. Hence, this information from the studied traits and disease evaluation among different genotypes indicated that there was found to be high existing genetic variation among genotypes. Based on this information, disease, yield, and yield contributing traits and field stand assessment twenty-eight genotypes were advanced to the next breeding step PYT.

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