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Screening of Bread Wheat (*Triticium astivum L.*) Genotypes against Septoria tritici Blotch (*Mycosphaerella graminicola*) in North Gondar, Ethiopia

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ABSTRACT

Bread wheat is one of the most important cereal crops grown in different parts of Ethiopia. However, its production was affected by foliar diseases. Mycosphaerella graminicola is among the most important ones. Therefore, screening of wheat genotypes was conducted at Dabat, during the 2021 main cropping season to identify the source of resistance for Septoria tritici blotch. One hundred genotypes were evaluated in a simple lattice design with 2 replications. The result revealed that none of the genotypes were immune. The majority (61%) of wheat genotypes were had an infection that ranged from highly resistant to moderately resistant and gave a better yield (>5 t-1). About 28% of the genotypes were moderately susceptible. The remaining limited genotypes were within the range of susceptible. All of the studied yield and yield components were negatively correlated with AUDPC and TRS values. Hence, further research is needed under different agroecologies for additional years for the development of disease resistant variety, and to increase the production and productivity of bread wheat in the country.

1. INTRODUCTION

Bread wheat (Triticum aestivum L, 2n=6x=42) is the most commonly cultivated wheat species (Randhawa et al 2013). It is estimated that more than 75% of the world's population consumes wheat as part of their daily diet. Bread wheat accounts for approximately 20% of the total consumed human food calories and provides the most stable food for 40% of the human population (Kumer et al 2011). The production and productivity of wheat in Ethiopia increased over the last few years, but when we compared it to the other wheat-producing countries it is still low. The average productivity of bread wheat in Ethiopia is estimated to be 3.04 t ha-1 (CSA 2020), which is lower than the average world yield productivity of 3.5 t ha-1(FAO 2017) (FAO 2017). The low productivity of bread wheat is attributed to several factors, including biotic (diseases, insect pests, and weeds), abiotic (moisture stress, soil-physical-chemical properties, and temperature), and socio-economic factors (Abera 2017). Among these diseases, septoria leaf blotch caused by the ascomycete fungus Mycosphaerella graminicola (asexual stage: Zympseptoria tritici) is currently the most important foliar disease of wheat in many regions of the world (Eyal et al 1987; Alamirew et al 2020b). In Ethiopia, STB was reported to be the most important disease, followed by stem rust and yellow rust caused by Puccinia spp.

Epidemics of SLB 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 and Duveiller 2007). It is one of the major constraints on wheat in all wheat-growing areas of Ethiopia, causing 42% economic loss annually (Abebe et al 2015; Abebe et al 2015; Said and Hussein 2016). The strategies to control this pathogen includes cultural practices (crop rotation, use of balanced fertilizers, and framework of planting dates), use of resistant varieties, and fungicide application (Wondimagegn and Abera 2021; Alamirew et al 2020a). Moreover, use of genetic resistance is the most effective, economic and environmentally friendly method to manage septoria tritici blotch disease. Many host resistance studies of wheat to Septoria tritici blotch have been done but no variety or line has been identified with a high level of resistance (Nigir 2013; Abebe et al 2015). Moreover, wheat genotypes resistant in one part of the country may show susceptibility elsewhere, even within regions of the country difference observed in virulence may be associated with fungal genetic variability (Eyal et al 1987). Thus, the objective of this experiment was to identify resistant bread wheat genotypes for Mycosphaerella graminicola under field condition.

2. MATERIALS AND METHODS

2.1. Discretion of the Study Area

The study was conducted at Dabat Agricultural Research station in Dara Kebelle, under Gondar Agriculture Research Center (GARC) during the 2021/2022 main cropping season. Dabat Research 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 unimodal rainfall. According to the available digital data, the mean annual rainfall for the area ranges from 1250 to 1565 mm. The rainy months extend from June to the end of September, and the dominant soil in the area is Vertisol (Demelash 2013).

2.2. Experimental Materials

Hundred bread wheat genotypes including one standard variety (Alidoro) that are listed for Septoria leaf blotch resistance were tested for the present experiment. These genotypes were obtained from Kulumsa Agricultural Research Center, Ethiopia.

2.3. Experimental Design and Procedure

The treatments were laid down using a 10 x 10 simple lattice design with two replications. Each genotype was planted in a plot size of 1 .5m2 (2.5m x 0.6m). The gap between replications, blocks, plots and rows was 2m, 1m, 0.5m, and 0.2m respectively. The seeding rate was 125 Kg per hectare and recommended fertilizer rates, of 64 and 46 Kg ha per hectare N and P2O5, were applied respectively. All NPS fertilizer was applied at planting while nitrogen fertilizer was applied in split (½ at planting, ¼ at tillering, and ¼ at head initiation. Harvesting was done manually using hand sickles at the harvesting stage. Weeding and other agronomic management practices were done as per the recommendation for bread wheat (MOARD 2012).

2.4. Data Collected

2.4.1 Disease Parameters

Disease Severity; the severity of Septoria leaf blotch was assessed 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). It was assessed on 10 randomly selected pre-tagged plants per plot at ten-day intervals from the time of disease appeared until the crop attained its physiological maturity. About three scorings were done. The average severity from the 10 plants per plot was used for analysis. The first digit (D1) indicates vertical disease progress on the plant and the second digit (D2) refers to severity measured as diseased leaf area. Percent disease severity is estimated based on the formula: % Disease severity (PDS) =

Where D1 and D2 represent the score recorded (00-99 scale) and Y1 and Y2 represent the maximum score on the scale (9 and 9) (Sharma and Duveiller 2007). Genotypes were classified into seven categories; immune (00), highly resistant (11 -14), resistant (15-34), moderately resistant (35-44), moderately susceptible (45-64), susceptible (65-84) and highly susceptible (85-99) (Eyal et al 1987). AUDPC: Area under Disease Progress Curve (AUDPC) values were calculated for each plot using the equations as follows

$$\text{AUDPC} = \sum_{i=1}^{n-1} (0.5(X_i + X_{i+1}))\,(t_{i+1} - t_i)$$

Where Xi is the severity percentage of the disease at i^{th} assessment, ti is the time of the i^{th} assessment in days from the first assessment date and n is the total number of disease assessments

2.4.2. Agronomic Data

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). Plant height (cm): The average height of five plants was randomly taken from each plot at physiological maturity and measured from the ground to the tip of the panicle excluding the awns. Days to physiological maturity (days): It is calculated as the number of days from emergence to 95% maturity which is the number of days to maturity minus the number of days to emergence.

2.4.3. Crop Yield Traits

Spike Length (SL): the length (cm) of main spikes from the five sampled plants. Number of Spikelet Spike-1 (SPS): Total numbers of spikelets on the main spike of all five plants from the three rows were counted at the time of maturity and the average was recorded and used for analysis. Number of Kernels per spike (NKPS): The numbers of grains of the main tillers of each of the five randomly taken plants for each experimental unit were recorded and the average of the five plants were used for analysis. Thousand Kernel Weight (TKW) (g): One thousand grains selected at random were weighed in grams for each experimental unit. Grain yield per plot (g): Grain yields were taken from all three rows harvested at full maturity with appropriate moisture content on a plot basis (0.6m x 2.5 m =1.5 m2). The yield per plot was weighed and converted into kilogram per hectare at 12.5% moisture content.

$$\left(\frac{D1}{Y1} X \frac{D2}{Y2}\right) X100$$

2.5. Data Analysis

The calculated diseases data (severity and area under disease progress curve) for each assessment date and yield and yield components of bread wheat from the field experiment were subjected to analysis of variance (ANOVA) using SAS (9.0) and interpretations were drawn following the procedure described by Gomez and Gomez (1984). Mean separation was done using the least significant difference (LSD) test at a 5% probability level as described by Gomez and Gomez (1984) for a difference among genotypes for traits.

3. RESULTS AND DISCUSSION

The analysis of variance (ANOVA) revealed that there was a highly ($p<0.0001$) significant difference among the tested bread wheat genotypes in all phenological, agronomic, and disease parameters except spike length which was not significantly affected by the genotypes (Table 1). A study which was conducted by Azene et al (2020) revealed that the tested genotypes were significant differences in their most phenological and agronomic traits, which might be due to their genetic makeup.

3.1. Diseases Intensity of Bread Wheat Genotypes

The tested genotypes were grouped into seven categories based on their mean terminal severity value, according to Abebe et al (2015). This study confirmed that none of the bread wheat genotypes was completely resistant or immune to Septoria leaf blotch (Tables 2). Hence, the present finding is consistent with previous findings in that, even though many host resistance studies of bread wheat to Septoria leaf blotch, no variety or line has been identified with a high level of resistance (Bekele 1986).

Table 1: The response of bread wheat genotypes against Septoria tritici blotch

S/N	Number of Observation	Reaction level	Host response
1	0	0	IM
2	2	14-Nov	HR
3	22	15-34	R
4	37	35-44	MR
5	28	45-64	MS
6	10	65-84	S
7	0	85-99	HS
	Check	28.4	R
S/N	Number of Observation	Reaction level	Host response
1	0	0	IM
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4	37	35-44	MR
5	28	45-64	MS
6	10	65-84	S
7	0	85-99	HS
	Check	28.4	R

Note: IM – Immune, HR-Highly Resistant, R-Resistant, MR-Moderately Resistant, MS-Moderately Susceptible, S-Susceptible, HS-highly Susceptible

However, a clear difference in the degree of resistance was noted among the genotypes. For this reason, where resistance is not effective, tolerance can be sought (McKendry et al 1995).

The ANOVA revealed that the terminal severity ranges from (11.1 to 77.8%) which is from high resistance to susceptible level. Out of 100 bread wheat genotypes, only two (G-89 (EBW197639) and G-91(EBW192481)) exhibited high resistance to the disease. Similarly, more than 22% of tested genotypes including the standard check (Alidoro) were show a resistance response and high yield (5.4 to 7.3 t ha^{-1}) than other tested genotypes. Contrary to the present finding, Badebo et al (2008) and Nigir (2013) reported that as with other diseases, however, satisfactory result(s) on resistance was not found in the SLB in Ethiopia. More than half of the tested genotypes (61%) were found highly resistant and moderately resistant to the disease (Table 2). Likewise, 38% of the tested bread wheat genotypes were moderately susceptible to susceptible to Septoria tritici blotch (Table 2). This result revealed that the bread wheat tested genotypes were in the range of high resistant to moderately resistant.

The rest-tested genotypes about 10% exhibited maximum severity, show a susceptible reaction to the pathogen, and attained lower yield as compared to other genotypes (Table 2). The result further revealed that all bread wheat genotypes including the standard check were affected by Septoria leaf blotch at varying intensity levels. This condition could be due to favorable environments (frequent rain and moderate temperature) for the development of the pathogen in the study area. This result is in line with that of Lakachew and Hassenfa (2018) who reported that an epidemic of STB in wheat is associated with favorable weather conditions (frequent rains and moderate temperatures), specific cultural practices, availability of inoculum, and the presence of susceptible wheat cultivars.

3.1. Area Under Diseases Progress Curve for the Tested Genotypes

ANOVA revealed that there was a highly significant difference ($P<0.0001$) among the tested genotypes in the AUDPC value of Septoria tritici blotch (Table 2). The mean range of AUDPC for the tested genotypes was from 222.2 to 1337.4 %- days. The value of AUDPC on highly resistance genotypes was 222.2 % days. Similarly, the lowest mean value of AUDPC (263.9 to 611.2 % days) was recorded from genotypes, which were categorized as resistant and moderately resistant (Table 2). On the other, hand the highest AUDPC value (1370.4 % days recorded from genotype EBW110820 followed by genotype EBW171262, EBW186388, EBW140186, and EBW188072 (Table 2). From this result, we can conclude that the highest value of AUDPC has been categorized as a moderately susceptible and susceptible response. Genotypes that have less AUDPC value indicate more resistance and moderate resistance to Septoria tritici blotch (Azene et al 2020). This is because of AUDPC value and severity of Septoria tritici blotch of bread wheat is always a direct correlation. The genotypes, which recorded higher AUDPC values, showed severe necrotic blotches of the foliage that was filled with the asexual and sexual fructifications and categorized as susceptible (Shaw and Royle 1989). Generally, genotypes that have less AUDPC value indicate resistant and moderate resistant to Septoria tritici blotch.

Table 2: Mean yield and yield related traits, resistance levels, TRS and AUDPC of bread wheat genotypes in 2021 at *Dabat*

Genotypes	DH	DM	PH	SL	SPS	KPS	GY (t ha^{-1})	TSW	TRS (%)	AUDPC
EBW110272	63.5	126.5	84	7.4	17.8	37.7	4.9	39.9	50.0MS	847.2
EBW112564	61.5	131.0	94.8	7.9	17.5	41	5.9	39.7	33.3R	805.6
EBW113287	65.0	133.5	97.2	8.1	17.4	47.5	6.9	40.7	42.0MS	782.4
EBW114362	69.5	133.0	92	8	17.7	40.3	4.8	42.7	55.6MS	944.5
EBW115124	61.0	131.5	87.8	7.8	17	40.3	5.6	47.9	55.6MS	972.2
EBW116532	69.5	128.0	89.9	7.6	18.2	45.7	6.4	40.4	40.5MS	740.8
EBW110543	63.0	129.0	93.3	8.6	17.5	41.2	4.4	37.8	38.9MR	828.7
EBW110891	66.5	126.0	97.5	7.9	17.8	45.9	7.7	36	38.9MR	495.4
EBW110417	67.5	126.5	90.3	7.3	18.1	43.3	6.1	33.1	44.4MR	740.7
EBW113285	69.5	124.0	81.3	8.1	18.5	39.9	5.1	39.5	44.5MR	888.9
EBW110820	63.0	124.0	81.9	7.8	17.7	41.6	4.1	36.8	66.7S	1370.4
EBW110211	66.5	126.5	89	8	18.1	43.9	6.8	36.7	22.2R	509.3
EBW119101	63.0	126.0	88.6	7.8	17.5	42.1	5.5	42.6	27.8R	476.9
EBW116926	69.5	133.0	89.7	7.6	17.7	45.4	5.6	37.6	44.5MR	888.9
EBW119843	66.0	131.0	89.4	7.7	17.8	42.3	5.6	40.5	44.4MR	731.5
EBW120165	66.0	133.5	89.4	8	17.5	39.4	3.7	43.3	61.1MS	819.4
EBW120954	61.0	128.0	94.3	7.4	17.8	43.4	4.9	35.4	61.1MS	856.5
EBW120101	62.5	131.0	98.4	8.6	18.6	42.9	5.8	42.5	33.3R	824.1
EBW120672	63.5	131.5	95	8.4	17.9	42	5.9	45.3	38.9MR	597.3
EBW128801	64.0	124.0	90.8	7.9	16.7	42.1	5.7	43.1	27.8R	773.2
EBW126028	69.5	133.0	89.5	7.9	17.3	44.5	5.5	39.4	38.9MR	495.4
EBW120732	66.5	133.5	90.2	7.5	18	42.5	4.8	40.9	44.4MR	472.2
EBW128682	66.0	131.0	84.9	8	17.6	40.2	4.7	46.9	50.0MS	643.6
EBW12006	66.5	131.5	93.2	8.2	17.3	36.9	4.8	43.4	50.0MS	717.6
EBW128109	69.5	131.0	94.7	8.2	17.7	43.9	5.8	44.5	38.9MR	560.2

EBW124327	70.0	135.0	96	8.5	18.6	43.2	3.8	35.3	44.4MR	768.5
EBW123624	66.5	135.0	93.4	8.1	18	38.7	3.2	42.6	55.6MS	925.9
EBW126328	69.5	128.0	90.7	8.6	18.3	35.1	4.2	44.4	72.2S	838
EBW120951	65.0	131.0	86.5	8.1	18.5	39.8	5.9	41.9	55.6MS	620.4
EBW122896	71.0	131.0	85.9	7.8	18	42.1	7.2	40.9	22.2R	370.4
EBW129901	71.5	132.5	91.3	8.1	18.5	40.9	7.7	41.9	27.8R	731.5
EBW120136	61.0	131.0	91.9	7.8	17.8	41.7	5.7	35.1	27.8R	606.5
EBW128375	71.5	128.0	90.4	8	18.8	42.4	6.4	39.6	22.2R	370.4
EBW128361	73.5	133.5	95.7	8.4	17.9	40.7	6.7	41.3	30.0R	513.9
EBW124022	67.5	131.0	90.4	8.2	17.8	39.3	6.2	41.3	44.5MR	629.6
EBW130019	71.0	133.0	91.2	7.9	18.1	37.3	6.8	37.5	33.3R	453.8
EBW130081	63.0	129.0	90.6	8.3	18.2	37.8	5.6	41.6	44.4MR	1027.8
EBW130120	69.0	133.0	97	7.9	18.4	39.7	7.4	43	33.3R	666.7
EBW130615	65.5	126.5	91.2	8.1	19	42.2	4.9	30.2	50.0MS	1069.5
EBW140282	66.0	135.0	91.7	7.6	18.4	43.9	5.7	35.7	33.3R	796.3
EBW140323	66.0	131.0	95.7	8.6	19.5	41.3	7.2	50.2	27.8R	365.8
EBW146602	69.5	133.0	93.3	7.9	18.2	37.3	5.2	43	38.9MR	560.2
EBW148863	64.0	124.5	98.1	8.2	18.3	37.2	3.3	44.3	72.2S	1097.2
EBW140928	71.5	131.0	96.3	8.3	19.4	42.7	6.1	45	35.0MR	708.4
EBW140631	71.0	129.0	97.8	8	18.3	42.7	6.1	42.1	38.9MR	430.6
EBW147262	69.5	128.0	97.9	7.6	17.7	43.4	6.5	44.2	44.4MR	611.2
EBW142642	69.5	131.0	100.6	8	18.4	45	6.8	41.1	22.2R	370.4
EBW141219	71.0	128.0	97.7	8.3	18.9	45.5	6.2	44.7	33.3R	388.9
EBW146207	69.5	131.0	95.9	8	17.9	41.2	6.5	47.2	33.3R	388.9
EBW149272	66.5	126.0	94.8	8.1	17.7	40.3	7.3	43.8	38.9MR	430.6
EBW143783	69.5	133.0	98.6	8.3	19	44.1	6.9	41.5	16.7R	263.9
EBW140186	61.0	124.0	82.6	7.6	17.6	38.7	3.6	46.2	55.6MS	1129.6

EBW149827	64.0	126.0	89.1	7.8	17.5	41.8	4.9	48.7	61.1MS	810.2
EBW150562	71.0	131.0	92.8	7.9	18.6	40.5	6.7	39.7	35.6MS	620.4
EBW150989	71.5	131.0	94.5	8.1	18.5	40.6	5.8	38.8	27.8R	421.3
EBW151817	71.5	135.5	98.9	8.3	19	41.4	6.2	36.5	41.4MR	449.1
EBW150287	66.5	128.0	92.7	8.4	18.5	39.8	5.3	50.5	38.9MR	430.6
EBW156151	71.0	131.0	95	8.1	18.5	40	5.5	40.8	38.9MR	449.1
EBW150864	66.5	135.0	88.9	7.8	18.6	31.1	3.3	35.2	66.7S	935.2
EBW169612	64.0	133.0	92.3	7.9	18.2	37.8	5.2	40.8	66.7S	842.6
EBW160083	71.0	133.0	101.3	7.9	17.9	40.6	7.6	44.8	16.7R	365.8
EBW160061	66.0	126.5	88.9	7.9	17.9	39.7	5.3	48.4	50.0MS	791.7
EBW160065	64.0	128.0	93	8	18.3	40.4	4.6	47.1	44.4MR	731.5
EBW160904	64.5	133.0	92.7	8.2	17.5	39.8	4.7	42	55.6MS	685.2
EBW160709	66.0	131.0	90.8	7.7	18.6	38.5	4.5	42.6	55.6MS	703.7
EBW170906	62.5	128.0	94.6	7.8	17.9	37.2	6.2	42.6	38.9MR	504.7
EBW171262	63.0	124.0	92.5	8.1	17.9	36.9	3.5	33.4	72.2S	1217.6
EBW170187	69.5	128.0	91.7	8.4	18	41.4	4.6	42.8	55.6MS	787.1
EBW170856	69.5	131.0	96.6	8.3	18.1	37.9	4.4	46.6	55.6MS	703.7
EBW170923	69.0	124.0	92.8	8	18.7	42.5	3.8	41.8	61.1MS	875
EBW179826	69.5	133.5	103.4	8.4	18.4	47.8	7.7	46.3	27.8R	541.7
EBW171873	70.5	131.0	93.1	8.1	18.3	41.3	4.7	34.6	50.0MS	958.4
EBW180069	71.0	135.0	97	8.4	18.3	42.2	3.9	43.5	50.0MS	791.7
EBW182376	66.0	131.0	95.5	8	18.9	38.9	3.7	37.3	66.7S	1027.8
EBW180987	69.5	128.0	100.4	8.4	18.5	44.5	5.7	37.4	50.0MS	662
EBW180028	71.0	130.5	90.9	7.6	18.3	41.9	6.2	40.8	44.5MR	481.5
EBW186893	64.5	143.5	93	8	18.1	40.6	4.3	39.5	61.1MS	1088
EBW188072	66.0	124.0	89.4	8	16.7	43.9	3.8	30	72.2S	1106.5
EBW186388	66.5	128.0	92.3	8.2	19.1	40.3	4.2	37.4	66.7S	1148.2

EBW189383	66.0	126.0	92.6	7.7	17.7	36.4	3.6	34.7	61.1MS	1023.2
EBW180272	66.0	128.0	98.2	7.6	17.7	48.6	7.7	36	44.5MR	629.7
EBW180674	71.0	131.0	98	8.2	17.7	41.1	4.8	41.5	44.4MR	685.2
EBW191027	64.5	131.5	95.7	7.6	18.1	35.8	3.9	46.5	50.0MS	791.7
EBW191826	66.5	126.0	92.1	8.3	17.7	39.5	4.4	34.1	66.7S	1092.6
EBW192312	66.5	128.0	92	7.6	17.4	40.3	6.7	41.2	38.9MR	708.4
EBW191421	64.0	127.0	96.2	8.1	17.6	43.8	4.8	37.8	44.5MR	879.7
EBW191204	64.0	126.0	94.4	8.2	18.6	41.5	6.2	45.8	38.9MR	560.2
EBW191138	71.0	128.0	93.3	8	18.5	44.1	6.3	41.4	50.0MS	588
EBW197639	71.5	133.0	92.4	7.7	18.2	43	7.4	35.8	11.1HR	222.2
EBW193256	63.0	132.0	96.4	8.4	18.1	47.8	7.5	45.5	46.9MS	685.2
EBW192481	69.5	131.0	93	8.1	18.1	45.7	6.5	41.5	11.1HR	222.2
EBW192712	71.0	133.0	100.1	7.9	19.3	45.2	7.9	42.8	41.4MR	449.1
EBW192863	74.7	133.0	111.7	7.7	17.5	43.9	6.7	37	28.4R	265.5
EBW192754	69.0	128.0	93	8.1	18.8	43.4	5.1	38	50.0MS	810.2
EBW193471	69.5	131.0	93.4	8.4	18.5	46.3	7.6	39.3	22.2R	379.7
EBW192432	64.5	126.0	88.4	8.2	17.9	46.1	5.5	39.3	44.5MR	861.1
EBW192437	64.0	126.0	95.5	8.2	18.3	44.1	4.9	36.9	50.0MS	1088
EBW192762	66.5	128.0	95.2	8.2	17.9	46.5	7.4	44.2	44.4MR	537.1
EBW192880	69.5	131.5	94.6	7.9	18.8	43.3	6.4	43.6	40.0MR	884.3
EBW192336	64.0	127.0	92.8	7.6	17.3	45.5	6.9	38.1	50.0MS	782.4
Mean	67.1	129.9	93.01	7.99	18.09	41.56	5.6	40.9	45.2	704.7
CV (%)	0.75	1.71	3.09	5.22	3.62	6.69	11.01	6.9	28.5	21.5
LSD (5%)	1	4.4	5.71	0.83	1.3	5.53	1.2	5.61	25.7	301.6
Sig.	<0.0001	<0.0001	<.0001	0.6214	0.0499	<.0001	<.0001	<.0001	<.0001	<.0001

G=Genotype, HR-Highly Resistant, R-Resistant, MR-Moderately Resistant, MS-Moderately Susceptible, S-Susceptible, LSD=Least Significant difference, CV = coefficient of variation,Sig=Significant level, DH =Days to heading, DM = Days to Maturity, PH = Plant Height, SL=Spike length, SPP = Spikelet per spike, KPS = Kernel per spike, TSW = Thousand Seed Weight, GY = Grain yield, TRS=Terminal Severity. AUDPC=Area under Disease Progress curve

3.2. Crop phenological and yield-related parameters

The ANOVA revealed that except spike length all crop phenological, growth and yield-related

parameters were a highly significant differences (P<0.0001) among the tested genotypes. While spikelet per spike showed significant difference among the tested genotypes (P<0.05) (Table 2).

Days to heading, the range of days to heading ranges from 61 to 74.7 days and the mean heading date was 67.8 days. Extended days to heading were observed on the standard check followed by genotype 34 (Table 2). While the shortest days to heading (61 days) were observed on genotypes 5, 17, and 52. The high variation among bread wheat tested genotypes for days to heading was also reported by Kefale and Menzir (2019) which is in agreement with the present result. The correlation analysis revealed that days to heading are negatively correlated with STB disease intensity (TRS and AUDPC (-0.26 and -0.51)) value, which means that late heading results in less development of disease. While early heading results in more disease development. This result agrees with that of Azene *et al* (2020). 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).

Days to 90% maturity; Days to maturity were found to be highly significant ($p \leq 0.001$) among the tested genotypes (Table 2). The average mean of days to maturity was 129.9 days and ranged from 124-143.5 days. Genotypes EBW140186, EBW171262, EBW110820, EBW128801, EBW188072, EBW170923 and EBW113285 took the shortest days (124) to mature as compared to other tested genotypes while genotypes EBW151817 and EBW186893 show the longest day (135.5 and 143.5) for their physiological maturity (Table 2). The variations of physiological maturity among the tested genotypes should be attributed to the difference in their genetic makeup. This result is in agreement with Shahzad *et al* (2007), who reported that the days to physiological maturity of wheat cultivars, varies due to inherent differences between cultivars.

The ANOVA revealed that the plant height was found to be highly significant ($p \leq 0.001$) among the tested genotypes (Table 2). The standard check had the tallest plant height 111.7 cm followed by genotype EBW160083 and EBW179826 (101.3 and 103.4cm) respectively, which were resistant to disease response. The shortest plant height was recorded from genotype EBW113285 and EBW110820 (81.3 and 81.9cm) respectively (Table 2). These semi-dwarf genotype exhibits maximum (888.9 and 1370) AUDPC value and lower yield as compared to other tested genotypes. The present finding is in agreement with Tavella (1978) who reported that plant height was negatively correlated with wheat STB disease severity and AUDPC. This finding also revealed that the disease intensity was inversely correlated with the plant height or it's affected by the growth parameter since most short genotypes show moderate to susceptible response, while the tallest genotypes show resistant response.

This should be attributed to the lower distance between consecutive leaves facilitating the contact between newly emerging leaves and splashed pycnidiospores leading to an earlier occurrence of pycnidia in upper parts of dwarf cultivars (Simón 2005). Reduced plant height was usually associated with more necrosis due to the highest necrosis percentage of the shortest lines. Alternatively, the variation may be due to the genetic makeup of the genotypes.

The ANOVA revealed that both yield components were highly (P<0.001) significantly different among the tested genotypes (Table 2). The mean values of kernels per spike and thousand seed weight were found to be 41.6 and 40.9g respectively. The lowest number of kernels per spike was observed in genotype EBW150864 (31.1), and the highest number of kernels per spike was observed in genotype EBW180272 (48.6). In thousand seed weight, maximum seed weight (50.5 g) and the minimum (30g) were recorded from genotypes EBW150287 and EBW188072 respectively (Table 2). The variation in thousand seed weights of the tested genotypes might be due to the varietal character of genotypes possessing bold type grains. On the other hand, this study revealed that kernel per spike and thousand seed weight; were show a negative correlation with STB intensities (TRS and AUDPC value) (Table 2). So, this result is in agreement with previous findings of Sharma and Duveiller (2007) who showed that necrosis was highly correlated with the reduction of the kernel weight.

The ANOVA for the mean grain yield

indicated that highly significant differences (P<0.0001) were observed among the tested genotypes. The mean grain yield was 5.6 t ha^{-1}. Minimum and maximum (3.2 and 7.9 t ha^{-1}) grain yield was recorded from genotypes EBW123624 and EBW192712. The result further revealed that about 22% of the tested genotypes show high yield (6.7 to 7.9 t ha^{-1}) than the standard check (6.7 t ha^{-1}). Considering yielding about 64 genotypes, show a yield greater than 5 t ha^{-1}, however, their response to the disease is variable. Most of them were moderately resistant and resistance reaction in Septoria tritici response. Some genotypes such as genotype EBW126328 and EBW148863 have high AUDPC value and give a reasonable yield, it may be suggested that genotypes were resistant and tolerant. In addition, some of the tested genotypes showed a low level of disease intensity (AUDPC and TRS) and a high yielder than the other genotypes. This is because grain yield was highly negatively correlated with AUDPC which indicates that when the grain yield is decreased with an increase in AUDPC value (Kandel and Mahato 2014).

Considering grain yield and disease intensity about 18 genotypes showed the highly resistant and resistant reaction and above 5 t ha^{-1} yield and compared to the standard check (Alidoro, R). On the other hand, majority of tested genotypes (61%) were sustained infection responses that ranged from highly resistant to moderately resistant and gave a better yield (>5 t ha^{-1}). Genotypes with tolerant/resistant reaction will be advanced for further breading purposes. The development of disease resistance variety is considered the most effective and environmentally safe control strategy for Septoria tritici blotch (Azene et al 2020).

Correlation coefficients between STB intensities with yield and yield-related traits of genotypes: The analysis showed that Septoria tritici blotch terminal severity and AUDPC with yield and most agronomic parameters of tested genotypes were negatively correlated (Table 3). This is in agreement with the study of Vrapi et al (2012) “there were high negative correlations between wheat crop yield and Septoria tritici blotch. The correlation between kernels per spike, grain yield, and thousand seed weight with STB intensities (TRS and AUDPC) showed that there was a significant negative correlation (Table 3). The maximum correlation coefficient (r = -0.63 and -0.69) was shown on grain yield with TRS and AUDPC values respectively. The study further revealed that the result of correlation analysis of STB severity recorded at the terminal growth stage and its AUDPC showed a significantly negative correlation with yield and most yield-related components. This finding is supported by the results of Alamirew et al (2020b).

Table 3: The correlation of SLB intensity with other yield and yield-related traits of tested genotypes

	DH	DM	PH	SL	SPS	KPS	GY	TSW	TRS	AUDPC
DH	1	0.31**	0.35	0.14ns	0.37***	0.16ns	0.33**	-0.02ns	-0.26**	-0.51**
DM		1	0.29**	0.09ns	0.18ns	-0.03ns	0.14ns	0.09ns	-0.15ns	-0.27**
PH			1	0.28**	0.22*	0.31**	0.34***	0.06ns	-0.27**	-0.38**
SL				1	0.32ns	0.03ns	-0.03ns	0.22*	-0.01ns	-0.04ns
SPS					1	0.01ns	0.13ns	0.04ns	-0.08ns	-0.16ns
KPS						1	0.56**	-0.12ns	-0.41**	-0.31**
GY							1	0.13ns	-0.63**	-0.69**
TSW								1	-0.11*	-0.27**
TRS									1	0.77**
AUDPC										1

*Note: *, ** significant at 5% and 1% level of probability, respectively, ns= not significant*

4. CONCLUSION AND RECOMMENDATION

The findings revealed that there exists a high genetic variation among genotypes in most of the studied traits and the Septoria tritici blotch evaluation. Moreover, the analysis of variance

showed that none of the genotypes were completely resistant or immune to Septoria leaf blotch. However, a clear difference in the degree of resistance was noted among the tested genotypes. The majority (61%) of bread wheat genotypes were sustained infection responses that ranged from highly resistant to moderately resistant and gave a better yield (>5t ha^{-1}). These genotypes with tolerance characteristics could be considered in a breeding program and an important component in integrated management of Septoria tritici blotch in the study area. The development of disease resistant variety is considered the most effective management strategy for Septoria tritici blotch and should be a routine activity in a breeding program. About 28% of the tested genotypes were moderately susceptible and the remaining limited genotypes were within the range of susceptible reaction. Since grain yield and disease intensity assessment is the most important and economic parameters for the screening study, the genotypes (61%) showing the best response to the pathogen and maximum yield (>5t ha^{-1}) would be advanced for further breading purpose. However, the experiment was executed under field condition in natural infection of the pathogen and there might be variability in inoculum distribution among plots, so further investigation of genotypes will be done by artificially inoculating the pathogen.

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