Tropical Agricultural Research & Extension 23 (1 & 2): 2020

INVESTIGATION OF GENETIC VARIABILITY PARAMETERS FOR *Septoria tritici* BLOTCH RESISTANCE AND QUANTITATIVE TRAITS IN BREAD WHEAT GENOTYPES

Geleta Gerema[1]*, Dagnachew Lule[2] and Fikre Lemessa[3] and Tilahun Mekonnen[4]

[1]Bako Agriculture Research Center, Oromia, Ethiopia

[2]Oromia Agriculture Research Institute, Finfinne, Ethiopia

[3]Jimma University, Department of Horticulture and Plant Science, Jimma, Ethiopia

[4]Addiss Ababa University Institute of Biotechnology, Ethiopia

ABSTRACT

***Septoria tritici* Blotch (STB) is one of the most devastating diseases of wheat in Ethiopia and worldwide. The present study was conducted to assess the genetic variability of yield and yield parameters among different bread wheat genotypes grown under the stress of *Septoria tritici* Blotch. A total of 180 bread wheat lines, advanced genotypes and released varieties were included in the investigation. Genetic variance, heritability, correlation and ANOVA were estimated for *S.tritici*, and yield and yield parameters. The genetic variance was relatively high for grain yield, percentage of disease severity (% severity) and Septoria progress coefficient (SPC). Heritability and genetic advance were relatively higher for grain yield, and moderate heritability and high genetic advance were computed for disease parameters such as coverage of pycnidia, Septoria progress coefficient and % severity. A negative correlation was found between plant height and pycnidia coverage on the four uppermost leaves (PCD), SPC and severity. Days to maturity and heading inversely correlated with disease resistance parameters. This indicated that the genotypes having short plant height and short maturity period could be resistant to *Septoria tritici* Blotch. The results help researchers to utilize the promising genotypes of this study in future breeding programmers for narrowing the yield gaps between the potential and actual in the areas where the *Septoria tritici* Blotch infection is a problem.**

INTRODUCTION

Wheat is one of the food security crops at the global level with an annual volume of production and area coverage of 750 million tons and 220 million ha, respectively in 2017 (FAO 2017). Sub-Sahara Africa (SSA) produced wheat with an annual production of 7.5 million tons on a total area of 2.9 million hectares accounting for 40% and 1.4% of the total in Africa and at global levels, respectively (FAO 2017). Ethiopia is the second-largest wheat producer in Sub-Saharan Africa (SSA) next to South Africa (Tadesse *et al*. 2018). There is a broad range of factors affecting wheat productivity in Ethiopia. Actual productivity and yield stability of wheat in Ethiopia are influenced by abiotic factors such as climate change, increased intensity drought and heat, and biotic factors including weeds and several pathogens (Rezenne 1993; Hailu and Mengistu 1991; Hailu and Woldeab 2015; Tadesse *et al*. 2018). *Septoria tritici* blotch (STB), caused by *Zymoseptoria tritici*, is among the most devastating foliar diseases of wheat (Kidane *et al*. 2017). *S. tritici* causes premature death of wheat leaves, hampers photosynthesis, and ultimately reduces grain production (Kidane *et al*. 2017). Both farming practices and weather patterns influence *S.*

*Corresponding author: geletarabi@gmail.com

tritici disease severity, as *Zymoseptoria tritici* requires a moist leaf surface for a successful infection, and spreads throughout the crop canopy via rain splash (Gladders *et al*. 2001; Pietravalle *et al*. 2003). This disease impacts wheat production in Europe, Mediterranean area, Africa including Ethiopia, Americas, and Australia (Kosina *et al*. 2007; Ponomarenko *et al*. 2011; Dean *et al*. 2012; Fones and Gurr 2015) where, under favorable environmental conditions, can cause significant yield losses (Eyal 1999; Duveiller *et al*. 2007). The crop loss due to *S. tritici* may go up to 82% (Mengistu *et al*. 1991, Ayele *et al*. 2008) and 40% loss reported recently in Ethiopia (Abera *et al*. 2015). Severe epidemics of STB can reduce wheat yields by 35 to 50% (Ponomarenko *et al*. 2011). Fungicide application is one of the options for the management of *S. tritici* disease. The application of fungicides has some side effects such as it could lead to the rapid emergence of fungicide resistance strains and high costs in subsequent control of the disease (Cools and Fraaije 2013; Leroux *et al*. 2007; Torriani *et al*. 2009). Therefore, the development of resistant wheat cultivars is the most effective, economic and environmentally-safe strategy to control this disease (Eyal and Ziv 1974; Eyal 1999). Host plant resistance is the method of choice for the control of *S. tritici* (Cowger *et al*. 2000). Therefore, genetic diversity is a vital source for screening various disease resistance and high yielding genes. The dissimilar genetic sources provide desirable allelic variation in parental lines to produce new genetic combinations (Tar'an *et al*. 2005). Therefore, in this investigation, different genotypes were evaluated in an attempt to generate information and identify disease resistance that aid in the selection of better genotypes for further breeding activities. Therefore, the present study aims to: (1) study the level of genetic variability in bread wheat genotypes under the stress of *S. tritici* (2) assess the degree of correlation among yield and disease parameters. (3) identify *S. tritici* resistance bread wheat genotypes for utilization in the future breeding programs.

MATERIAL AND METHODS

Experimental materials and field management

One hundred and eighty (180) bread wheat genotypes consisted of improved varieties (11), candidate varieties (8) and lines (161) were collected from different Agricultural Research Centers in Ethiopia , the International Maize and Wheat Improvement Center (CIMMYT) and International Center for Agricultural Research in the Dry Areas (ICARDA) . The details of the genotypes are given in Tables 1 and 2. The genotypes were grown in alpha-lattice design with three replications at Gedo station of Bako Agricultural Research Center during the main season of 2017/18. Each plot consisted of four rows of 2.5m length with 20cm and 50 cm spacing between rows and plots, respectively. The seed rate of 150 kg ha -1 and fertilizer rate of 100 kg ha-1 of NPS and 100 kg ha-1 urea were used. NPS is a compound fertilizer containing nitrogen, phosphorous and sulfur with the ratio of 19% N, 38% P2O5 and 7% S. All other crop management and protection practices were undertaken following previous research recommendations for bread wheat production (BARC 2019).

To enhance *S. tritici* infection, in addition to natural infection, plants were inoculated by spreading chopped infected wheat straw between the rows. It is the cheapest and the easiest method to induce disease infection, as infected leaves are easily available in infected wheat farms and it couldn't need special techniques for application. Besides, a mixture of several susceptible varieties (Kubsa and Digalu) was planted around the experimental plots as infector/spreader rows to increase disease infection intensity.

Collection of data on Disease severity

The severity of *S. tritici* was examined using the double-digit scale (00–99) developed as a

Table 1. List of bread wheat lines used in the experiment

No	Acc no	Pedigree	No	Acc no	Pedigree
1	1092	MXI12-13\M47IBWSN/194	82	85	AON
2	6223	MXI12-13\M24ISEPTON\56	83	2122	MXI12-13\M25HRWSN\1148
3	6201	MXI12-13\M24ISEPTON\25	84	86	AON
4	61	AON	85	6220	MXI12-13\M24ISEPTON\36
5	2042	MXI12-13\M25HRWSN\1053	86	2014	MXI12-13\M25HRWSN\1012
6	6208	MXI12-13\M24ISEPTON\96	87	94	AON
7	1108	MXI12-13\M47IBWSN/247	88	1279	MXI12-13\M47IBWSN\779
8	20	Adap	89	6207	MXI12-13\M24ISEPTON\102
9	6239	MXI12-13\M24ISEPTON\26	90	6218	MXI12-13\M24ISEPTON\13
10	1102	MXI12-13\M47IBWSN/222	91	6203	MXI12-13\M24ISEPTON\63
11	6229	MXI12-13\M24ISEPTON\95	92	1299	MXI12-13\M47IBWSN\847
12	2	Adap	93	6241	MXI12-13\M24ISEPTON\66
13	2132	MXI12-13\M25HRWSN\1166	94	63	AON
14	6221	\\0	95	1179	MXI12-13\M47IBWSN\496
15	2034	MXI12-13\M25HRWSN\1041	96	9217	MXI12-13\M24ISEPTON\97
16	2083	MXI12-13\M25HRWSN\1100	97	2010	MXI12-13\M25HRWSN\1007
17	1096	MXI12-13\M47IBWSN/208	98	6219	MXI12-13\M24ISEPTON\44
18	80	AON	99	40	AON
19	1242	MXI12-13\M47IBWSN/655	100	1295	MXI12-13\M47IBWSN\830
20	1161	MXI12-13\M47IBWSN/415	101	2105	MXI12-13\M25HRWSN\1124
21	5	Adap	102	1034	MXI12-13\M47IBWSN\74
22	1141	MXI12-13\M47IBWSN/335	103	1097	MXI12-13\M47IBWSN\217
23	73	AON	104	6235	MXI12-13\M24ISEPTON\62
24	1087	MXI12-13\M47IBWSN/185	105	6242	MXI12-13\M24ISEPTON\73
25	1089	MXI12-13\M47IBWSN/188	106	51	AON
26	2106	MXI12-13\M25HRWSN\1127	107	6216	MXI12-13\M24ISEPTON\42
27	67	AON	108	2135	MXI12-13\M25HRWSN\1174
28	6205	MXI12-13\M24ISEPTON\89	109	6211	MXI12-13\M24ISEPTON\74
29	1265	MXI12-13\M47IBWSN\722	110	2131	MXI12-13\M25HRWSN\1162
30	2114	MXI12-13\M25HRWSN\1138	111	71	AON
31	6230	MXI12-13\M24ISEPTON\32	112	87	AON
32	1178	MXI12-13\M47IBWSN/492	113	6228	MXI12-13\M24ISEPTON\20
33	2082	MXI12-13\M25HRWSN\1099	114	2104	MXI12-13\M25HRWSN\1123
34	6240	MXI12-13\M24ISEPTON\85	115	6214	MXI12-13\M24ISEPTON\51
35	2123	MXI12-13\M25HRWSN\1150	116	52	AON
36	58	AON	117	2136	MXI12-13\M25HRWSN\1175
37	1103	MXI12-13\M47IBWSN\224	118	1294	MXI12-13\M47IBWSN\823
38	1293	MXI12-13\M47IBWSN\811	119	6210	MXI12-13\M24ISEPTON\71
39	2115	MXI12-13\M25HRWSN\1141	120	2133	MXI12-13\M25HRWSN\1169
40	2108	MXI12-13\M25HRWSN\1129	121	2113	MXI12-13\M25HRWSN\1137
41	1015	MXI12-13\M47IBWSN/25	122	1033	MXI12-13\M47IBWSN\73
42	1185	MXI12-13\M47IBWSN\517	123	70	AON

Table 1 continued

No	Acc no	Pedigree	No	Acc no	Pedigree
43	2058	MXI12-13\M25HRWSN\1074	124	1029	MXI12-13\M47IBWSN\64
44	6237	MXI12-13\M24ISEPTON\2	125	2121	MXI12-13\M25HRWSN\1147
45	4	AON	126	2011	MXI12-13\M25HRWSN\1008
46	1099	MXI12-13\M47IBWSN/220	127	1041	MXI12-13\M47IBWSN\95
47	6215	MXI12-13\M24ISEPTON\4	128	60	AON
48	1101	MXI12-13\M47IBWSN/221	129	6206	MXI12-13\M24ISEPTON\55
49	3	AON	130	1035	MXI12-13\M47IBWSN\78
50	6209	MXI12-13\M24ISEPTON\31	131	1236	MXI12-13\M47IBWSN\644
51	7	Adap	132	6202	MXI12-13\M24ISEPTON\12
52	82	AON	133	6246	MXI12-13\M24ISEPTON\16
53	1143	MXI12-13\M47IBWSN\345	134	2126	MXI12-13\M25HRWSN\1154
54	1030	MXI12-13\M47IBWSN\69	135	2125	MXI12-13\M25HRWSN\1152
55	95	AON	136	39	K6295-4A
56	62	AON	137	2117	MXI12-13\M25HRWSN\1144
57	6226	MXI12-13\M24ISEPTON\34	138	77	AON
58	6245	MXI12-13\M24ISEPTON\88	139	84	AON
59	66	AON	140	6238	MXI12-13\M24ISEPTON\58
60	1093	MXI12-13\M47IBWSN\196	141	2023	MXI12-13\M25HRWSN\1023
61	6213	MXI12-13\M24ISEPTON\18	142	72	AON
62	6224	MXI12-13\M24ISEPTON\99	143	2059	MXI12-13\M25HRWSN\1075
63	2107	MXI12-13\M25HRWSN\1128	144	55	AON
64	6227	MXI12-13\M24ISEPTON\65	145	12	AON
65	69	AON	146	31	AON
66	2033	MXI12-13\M25HRWSN\1040	147	1042	MXI12-13\M47IBWSN\96
67	6234	MXI12-13\M24ISEPTON\92	148	1172	MXI12-13\M47IBWSN\470
68	1162	MXI12-13\M47IBWSN\418	149	6222	\\0
69	2012	MXI12-13\M25HRWSN\1009	150	4	Adap
70	1241	MXI12-13\M47IBWSN\653	151	1037	MXI12-13\M47IBWSN\82
71	6243	MXI12-13\M24ISEPTON\69	152	2103	MXI12-13\M25HRWSN\1122
72	16	AON	153	79	AON
73	2134	MXI12-13\M25HRWSN\1170	154	6232	MXI12-13\M24ISEPTON\33
74	6225	MXI12-13\M24ISEPTON\83	155	44	K6290-Bulk
75	2013	MXI12-13\M25HRWSN\1011	156	89	AON
76	6204	MXI12-13\M24ISEPTON\86	157	83	AON
77	6244	MXI12-13\M24ISEPTON\70	158	1104	MXI12-13\M47IBWSN\225
78	6212	MXI12-13\M24ISEPTON\101	159	6236	MXI12-13\M24ISEPTON\50
79	74	AON	160	1032	MXI12-13\M47IBWSN\72
80	6231	MXI12-13\M24ISEPTON\23	161	6233	MXI12-13\M24ISEPTON\78
81	1036	MXI12-13\M47IBWSN\81			

Source: CIMMYT – The International Maize and Wheat Improvement Center

Table 2: Description of bread wheat genotypes (released and candidate varieties) used in the experiment

Sr No	Genotypes	Breeding Center	Year of release	Adaptation area (altitude, m asl)
1	Danda'a	EAIR/KARC	2010	2000-2600
2	ET-13A2	EAIR/KARC	1981	2200-2900
3	Alidoro	EAIR/HARC	2007	2200-2900
4	Huluka	EAIR/KARC	2011	2200-2600
5	Hoggana	EAIR/KARC	2011	2200-2800
6	Sofumar	OARI/SARC	1999/00	2300-2800
7	King bird	EAIR/KARC	2015	
8	Madda walabu	OARI/SARC	1999/00	1900-2800
9	Merero	OARI/SARC	-	-
10	Bika	EAIR/KARC	2014	
11	Pavon-76	EAIR/KARC	1982	750-2500
12	Acc//23	EAIR/KARC	NR	
13	Acc//24	EAIR/KARC	NR	
14	Acc//15	EAIR/KARC	NR	
15	Acc//25	EAIR/KARC	NR	
16	Acc//27	EAIR/KARC	NR	
17	Acc//255	OARI/SARC	NR	
18	Acc//9	OARI/SARC	NR	
19	Acc//12	EAIR/KARC	NR	

Key: Acc= Accession, HARC= Holeta Agricultural Research Center, KARC= Kulumsa Agricultural Research Center, NR= Not released, SARC= Sinana Agricultural Research Center.

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 vertical disease progress on the plant and the second digit (D2) refers to severity measured as diseased leaf area. Ten plants were randomly selected from each plot and tagged at the vegetative stage or before heading. Disease rating was done on the tagged plants continued until crops physiological maturity every 7 days intervals and thus assessed 7 times for all leave and 4 times for flag leaf.

Disease progress analysis and modeling

The area under disease progress curve (AUDPC) and growth curve models were developed for the disease progress data. An AUDPC value was calculated for each plot using the formula indicated below, which was stated by Campbell and Madden (1990).

$$\text{AUDPC} = \sum_{i=1}^{n-1} 0.5(x_{i+1} + x_i)(t_{i+1} - t_i)$$

Where n is the total number of assessment times, ti is the time of the ith assessment in days from the first assessment date, xi is the percentage of disease severity at i^{th} *assessment.*

Percentage of disease severity

Percent disease severity was estimated based on the formula adopted from Saari and Prescott (1975) as indicated below,

% Severity = (Y1/9) × (Y2/9) × 100

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).

Septoria progress of coefficient

To overcome some of the difficulties associated with plant growth habit (maturity and height) and the expression of symptoms, Eyal and Ziv (1974) have used the *Septoria* Progress Coefficient (SPC) together with an evaluation of disease severity. Plant and disease height (cm) were used to determine the *Septoria* Progress Coefficient. Disease height is the maximum height (cm) from the ground where pycnidia of the pathogen are found on the plant. The SPC was computed as follows,

SPC = Disease height (cm)/Plant height (cm) (Eyal and Ziv 1974)

Estimation of variance components

Environmental variance or error variance (δ2e), genotypic variance (δ2g) and phenotypic variance (δ2p) components and their coefficients of variation were estimated as suggested by Singh, (2001). The equations are as follows,

$$\textbf{Genotipic Variance } (\sigma^2 g) = \frac{\textbf{GMS} - \textbf{MSE}}{r}$$

Where; MSG=mean square of genotypes, MSE=mean square of error, r= Number of replication.

Phenotypic variance (δ^2p) =

$$\sigma^2 p = \sigma^2 g + \sigma^2 e \sigma^2 p = \sigma^2 g + \sigma^2 e$$

Where: δ2p= phenotypic variance, δ2g = genotypic variance, δ2e =Environmental variance or error variance.

The phenotypic (PCV) and genotypic (GCV) coefficients of variations were estimated as the percentage of the corresponding phenotypic (δ 2p) and genotypic (δ 2g) standard deviations of the grand mean of the trait. Hence,

$$\textbf{Genotypic cofficient of varation}(GCV) = \frac{\sqrt{\sigma^2 g}}{X} X100$$

$$\textbf{phenotypic cofficient of varation}(PCV) = \frac{\sqrt{\sigma^2 p}}{X} X100$$

Where x= population mean.

Estimate of heritability

Heritability (H2): Heritability in the broad sense for all characters was computed as per the formula adopted from (Allard, 1960).

$$H^2 = \frac{\sigma^2 g}{\sigma^2 p} X100$$

Where: δ2p= phenotypic variance, δ2g =genotypic variance, H2= broad sense heritability.

Estimation of expected genetic advance

Expected genetic advance under selection assuming a selection intensity of 5% was computed following the formula developed by (Allard 1960).

GA = (K) (δp) (H2), where GA = expected genetic advance, K= selection differential that varies depending upon the selection intensity and stands at 2.056 for selecting 5% of the genotypes, δp = phenotypic standard deviation and H2= heritability (in the broad sense)

Genetic advance as percent of mean was obtained as;

$$\textbf{GA (\% of mean)} = \frac{GA}{\bar{x}} \times 100\%$$

where GA=Expected genetic advance mean percentage, $\bar{\mathbf{x}}$ *= population mean for the trait considered.*

Correlation coefficients

The correlations between yield and related traits as well as disease parameters traits were estimated using the method described by (Miller *et al*. 1958).

$$rpxy = \frac{COVpxy}{\sqrt{\sigma^2 px.\sigma^2 py}}$$

Where: rpxy= phenotypic correlation coefficient between character x and y, COVpxy= phenotypic covariance between character x and y, $\sigma^2 px$*= phenotypic variance for character x.*

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) for agronomic and disease parameters

S. tritici was first observed 57 days after planting (DAP) at Zadoks growth stage (GS) (five leaves on the main shoot) on infector rows. The disease appeared slightly on most of the test genotypes. Whereas, it was observed on few genotypes gradually at the late heading stage (GS 65 and 72). These results are in agreement with Said, (2016) who reported that *S. tritici* was first observed and recorded at Zadoks growth stage (GS) of Z15, 23 (five leaves on main shoot & three tillers) from all treatments.

The analysis of variance was computed for disease parameters such as severity, area under disease development progress curve and *septoria* progress coefficient for 180 genotypes at the different phenological stages as presented in Tables 3 and 4. The results depicted that mean squares due to genotypes were significantly different for most *S. tritici* disease parameters such as area under diseases progress curve, disease severity and *Septoria* progress coefficient during the latter assessment periods or after the second assessment onwards for both all leaves (72 DAP) and flag leaf (88 DAP). This implied that there was significant variability among bread wheat genotypes in the response to *S. tritici* disease at both phenological stages and a clue to work further genetic analysis. This finding is in agreement with Abebe *et al*. (2015) and Mohammadi *et al*. (2012) those who reported a wide range of variability among wheat genotypes evaluated for S.tritici disease and other agronomic parameters. Gough (1978) also reported that a wide disease resistance variation occurred in different wheat genotypes for *S. tritici* and this variation is important for a breeding programme to develop high yielder and S.tritici resistant varieties. Developing *septoria* resistance varieties is one of the highest priorities in wheat breeding (Brown *et al*. 2015; Torriani *et al*. 2015).

The results of the analysis of variance for 180 bread wheat genotypes studied are presented in Table 5. The mean squares of the quantitative traits in the present study revealed that there is a highly significant difference ($P \leq 0.01$) among the tested genotypes (Table 5). This indicated the presence of adequate variability among the genotypes for all the traits studied. Similarly, several authors also reported the existence of an enormous amount of genetic variability for phenological and yield traits (Gerema *et al*. 2020; Kifle *et al*. 2016; Mesele *et al*. 2016). In the contrary to the present finding, Khan (2013) reported non -significant differences among bread wheat genotypes for grain yield, plant height and days to maturity. This disparity may be due to the environment-genotype interaction. The significant differences among studied bread wheat genotypes indicate the presence of genetic variability in the genotypes and it provides a good opportunity for selecting materials for wheat improvement programs.

Estimation of phenotypic and genotypic parameters

Estimation of variability Components

The estimated phenotypic coefficient of variation (PCV) and genotypic coefficients of variation (GCV) is presented in Table 6. The GCV value was ranged from 1.5% for days to maturity to 28.9% for grain yield, and PCV

Table 3: Mean squares from analysis of variance for Septoria tritici disease parameters of 180 bread wheat genotypes evaluated for all leaves

Parameters	Replica-tion (Df=1)	Geno-types (Df=179)	Block	Error (Df=149)	Mean	CV
Severity at 57 DAP (%)	0.04	0.185	0.17	0.09	1.35	19.05
Severity at 65 DAP (%)	83.10	0.328	0.37	0.14	3.29	20.00
Severity at 72 DAP (%)	0.96	0.616**	0.44	0.32	8.00	21.50
Severity at 80 DAP (%)	13.30	1.07**	1.64	0.55	18.34	12.00
Severity at 88 DAP (%)	0.73	1.69**	0.88	0.54	31.53	15.40
Severity at 96 DAP (%)	14.13	13.11**	10.22	12.96	50.12	9.30
Severity at 105 DAP (%)	0.15	1.55**	1.45	0.97	63.32	23.00
SPC	0.20	0.578*	0.60	0.56	1.10	18.00
AUDPC	24374.40	56330.18**	32360.87	30654.44	1001.90	9.30

N.T: Df=degree of freedom, CV= Coefficient of variation, AUDPC= Area under disease development curve, DAP=Days after planting, SPC=Septoria progress coefficient, * and **Significant difference at $p<0.05$, $P<0.01$, respectively.

Table 4: Mean squares from analysis of variance for *Septoria tritici* disease parameters of 180 bread wheat genotypes evaluated on flag leaves

Parameters	Repilica-tion (Df=1)	Geno-types (Df=179)	Block	Error (Df=149)	Mean	CV
Severity at 80 DAP (%)	13.30	1.63	1.07	0.55	18.34	13.30
Severity at 88 DAP (%)	63.95	60.24*	112.37	61.11	25.98	17.33
Severity at 96 DAP (%)	14.13	10.22**	13.11	12.96	49.06	18.10
Severity 105 DAP (%)	256.72	151.14**	110.58	69.79	63.09	14.31
AUDPC	19374.40	36330.18**	32360.8	30654.44	1001.90	9.30

NB: Df=degree of freedom, CV= Coefficient of variation, AUDPC= Area under disease development curve, AP=Days after planting, SPC=Septoria progress coefficient.

from 1.6% for days to maturity to 34.5% for grain yield. The GCV and PCV values were categorized as low (<10%), moderate (10 to 20%) and high (>20%) as indicated by (Deshmukh *et al*., 1986). Therefore, high PCV
and GCV were recorded for grain yield. Similar findings were reported by Geleta *et al*. (2020); Kifle *et al*. (2016); Mesele *et al*. (2016). Relatively moderate PCV and GCV values were recorded for *S. tritici* disease parameters such as SPC and % severity, indicating that there is variability among the genotypes studied and there is a possibility to select for *S. tritici* disease resistant.

Estimation of heritability and expected genetic advance

According to Singh (2001), the heritability of a character is very high if 80% or more, moderate if ranged from 40-80%, and low if less than 40%. In the present study, heritability was ranged from moderate (49.1%) for AUDPC to very high (88) for

Table 5: Mean square from analysis of variance for 4 quantitative traits of 180 bread wheat genotypes

Parameters	Rep	Block	Msg	Erorr(A. lattice)	Error (RCBD)	CV (A. lattice)
Days to maturity	9.4	0.4	4.8**	0.7	0.6	0.6
Plant height	28.8	44.3	83.5**	31.9	33.9	6.6
Grain yield	797067.5	2796054.6	1700082.1**	597044.0	666549.8	18.9

N B: Msg =mean of square for genotypes, A.lattice=alpha lattice

Table 6: Estimation of variance parameters, heritability and genetic advance for quantitative and Septoria tritici disease parameters of 180 bread wheat genotypes

Parameters	σ2g	σ2p	GCV	PCV	Her	GA	GA(%)
Percentage of disease severity	44.0	68.2	13.9	17.3	64.5	11.0	23.0
Septoria Progress Coefficient	1.4	2.2	36.1	46.2	61.1	1.9	58.1
Total Area under development progress curve	54.0	110.0	7.2	10.3	49.1	10.6	10.4
Days to maturity	4.6	5.2	1.5	1.6	87.3	34.7	22.6
Plant height(cm)	67.6	99.5	9.6	11.7	88.0	1130.3	13.2
Grain yield (kg/ha)	1401560	1998604	28.9	34.5	80.1	156869	38.3

NB: g2p = Genotypic variance, GCV = Genotypic coefficient of variation, H=Broad sense heritability, GA= genetic advance , GA(%) = Genetic advance as percent of mean, PCV = phenotypic coefficient of variance, δ2p =Phenotypic variance.

plant height (Table 6). High heritability was estimated for days to maturity, plant height and grain yield (Table 6). Gerema *et al*. (2020) also reported that high heritability was recorded for grain yield. High heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment. Moderate heritability was computed for disease parameters such as disease severity and *septoria* progress coefficient, which indicates the resistance genes to STB less influenced by the environment.

Heritability estimates along with genetic advances are normally more helpful in predicting the gain under selection than heritability estimates alone (Johnson *et al*. 1955). High heritability coupled with high genetic advance as percent of mean was observed for days to maturity and grain yield (Table 6). Moderate heritability coupled with high genetic advance as percent of mean was estimated for the percentage of disease severity and *Septoria* progress coefficient (Table 6). This indicated that these traits are controlled by additive genes and improvement through selection could be effective for days to maturity, grain yield, and resistance to *S. tritici* . Therefore, these traits should be taken into account while selecting superior and desirable plants for further improvement of grain yield and resistance to *S. tritici* disease.

High heritability associated with moderate genetic advance was exhibited for plant height. This could be because of the predominance of non-additive gene action in the expression of this character.

Correlation Coefficient Analysis

Correlation between grain yield and disease parameters

Association among disease resistance traits and some of the agronomic and phenological traits presented in table 7. Wheat yield was correlated with different disease parameters and those disease parameters were correlated with each other. The correlation coefficient analysis result revealed that percent coverage of disease, *Septoria* progress coefficient, and Percent disease severity had a negative association with the grain yield (Table 7). It implied that there is an inverse relationship between yield and disease parameters. The present finding is in agreement with Kidane *et al*. (2017) who reported grain yield conversely showed low correlations with all disease traits. Similarly, these disease parameters had non-significant and negative associated with plant height, 1000-kernels weight, grain filling period and days to heading (Table 7). This result shows that those genotypes with the short plant height (dwarf) and early grain-filled are less suffer with *S. tritici* disease infection. Similar results were reported by Danon *et al*. (1982). Abera *et al*. (2015) reported that plant height and thousand seed weight negatively correlated with severity. The number of seeds per spike and the grain size (reported as thousand-grain weight) is inversely correlated with SDS (Kidane *et al*. 2017). Days to maturity and heading had a negative and moderate association with disease parameters including SPC, PDC, and % severity. Genotypes having a shorter heading and maturity time have less infection, it could be contributed by disease escape mechanisms, i.e., early heading varieties escaping the disease spread and appearing more resistant as a consequence. The biological yield was negatively and moderately correlated with the severity of the disease and pycnidia but positively correlated with the *Septoria* progress coefficient (Table 7).

Table 7: Correlation coefficients of yield and other traits with STB disease for wheat genotypes

Parame-ters	DTH	GFP	DTM	PHT	SPC	PCD	%SEV	NPT	TSW	Gy/ha	By/ha
DTH	1										
GFP	0.713**	1									
DTM	0.406**	0.082	1								
PHT	0.098	-0.065	0.048	1							
SPC	-0.036	-0.028	-0.096	-0.111	1						
PCD	-0.034	-0.021	-0.097	-0.109	0.391**	1					
%SEV	-0.035	-0.046	-0.094	-0.19	0.568**	0.565**	1				
NPT	0.041	-0.097	0.059	0.216**	-0.005	0.048	0.009	1			
TSW	-0.134	0.151*	-0.0003	-0.058	-0.151	-0.055	-0.073	0.104	1		
Gy/ha	-0.032	0.119	0.146*	0.317**	-0.35	-0.46	-0.37	0.38**	0.166*	1	
By/ha	0.341	0.132	0.451	0.543	0.334	-0.432	-0.342	0.543	-0.541	0.0321	1

NB:DTH= Days to heading, DTM = Days to maturity, GFP= Grain filling period, NPT=Number of productive tillers, PHT=plant height, TSW=Thousand seed weight, By/ha =biological yield per hectare , Gy/ha= Grain yield per hectare, %SEV=Percent disease severity, PCD= pycnidia coverage , SPC= Septoria progress coefficient

CONCLUSION

The present study showed that the existence of considerable variability among the tested wheat genotypes for *S. tritici* resistance, yield and other parameters. Therefore, these traits should be taken into account while selecting superior and desirable plants for further improvement of yield and *S. tritici* resistance in the development of high yielding and resistant genotype in bread wheat.

REFERENCES

Abera T, Alemu L, Getaneh W, Endale, H and Bekele K. 2015 Status of wheat *Septoria* leaf blotch in southwest and western Shewa zones of Oromiya regional state, Ethiopia. Research in Plant Sciences. 3:43-48.

Abebe T, Muez M. and Legesse M 2015 Field Response of Wheat Genotypes to *Septoria tritici* Blotch in Tigray, Ethiopia.Journal of Natural Sciences Research. 5:1.

Allard RW 1960 Principles of Plant Breeding. John Wiley and Sons, New York,500p.

Ayele B, Eshetu B, Betelehem B, Bekele H, Melaku D, Asnakech T, Melkamu A, Amare A, Kiros M and Fekede A 2008 Review of two decades of research on diseases of small cereal crops. In: Abrham Tadesse (eds.) Increasing crop production through improved plant protection Vol. I. Proceedings of 14th annual conference of plant protection society of Ethiopia 19-22 Dec. 2006 Addis Ababa., Ethiopia. 375-416.

Brown JKM, Chartrain L, Lasserre-Zuber P and Saintenac C 2015 Genetics of resistance to *Zymoseptoria tritici* and applications to wheat breeding. Fungal Genetics Biology. 79: 33–41.

Bako Agricultural Research Center (BARC) 2019 Annual Research progress report (unpublished docs).

Campbell CL and Madden LV 1990 Introduction to plant disease epidemiology. John Wiley and Sons, New York. USA.

Cools H J and Fraaije B A 2013 Update on mechanisms of azole resistance in Mycosphaerella graminicola and implications for future control. Pest Management . Science. 69: 150-155. doi: 10.1002/ps.3348.

Cowger C, Hoffer ME and Mundt CC 2000 Specific adaptation by *Mycosphaerella graminicola* to a resistant wheat cultivar. Plant Pathology. 49:445–51.

Danon T, Sacks JM and Eyal Z 1982 The relationships among plant stature, maturity class and susceptibility to *Septoria* leaf blotch of wheat. Phytopathology. 72: 1037–1042.

Deshmukh SN, Basu MS and Reddy PS 1986 Genetic variability, character association and path Coefficients of quantitative traits in Virginia bunch varieties of groundnut. Indian Journal of Agricultural Science. 56: 515-518.

Dean R, Van Kan JAL, Pretorius ZA, Hammond-Kosack KE, Di Pietro A and Spanu PD 2012 The top 10 fungal pathogens in molecular plant pathology. Molecular Plant Pathology. 13: 414–430.

Duveiller E, Singh RP, and Nicol JM 2007 The challenges of maintaining wheat productivity: pests, diseases, and potential epidemics. Euphytica 157: 417–430. doi: 10.1007/s10681-007-9380-z.

Eyal Z and O Ziv 1974 The relationship between epidemics of *Septoria* leaf blotch and yield losses in spring wheat. Phytopathology. 64:1385-1389.

Eyal Z, Scharen AL , Prescott JM and Van Ginke M 1987 The *Septoria* diseases of wheat: Concepts and methods of disease management. CIMMYT. Mexico, DF

Eyal Z 1999 The Septoriatritici and Stagonosporanodorum blotch diseases of wheat. Eur. Journal of Plant Pathology. 105: 629-641.

FAO 2017 FAOSTAT Rome, available at: http://faostat.fao.org (accessed 16 January 2020).

Fones H and Gurr S 2015 The impact of *Septoria tritici* blotch disease on wheat: An EU perspective. Fungal Genetics and Biology. 79: 3–7. doi: 10.1016/j.fgb.2015.04.004.

Gerema G , Lule D, Lemessa F and Mekonnen T 2020 Morphological characterization and genetic analysis in bread wheat germplasm: A combined study of heritability, genetic variance, genetic divergence and association of characters. Agricultural Science & Technology, 12(4): 1313-8820.

Gladders P, Paveley ND, Barrie IA, Hardwick NV, Hims MJ and Langton S 2001 Agronomic and meteorological factors a□ecting the severity of leaf blotch caused by Mycosphaerella graminicola in commercial wheat crops in England. Annual Applied Biology. 138: 301–311.

Gough FG 1978 Effect of wheat host cultivars on pycnidiospore production by *Septoria tritici.* Phytopathology .68:1343–1345.

Hailu E and Woldeab G 2015 Survey of Rust and *Septoria* Leaf Blotch Diseases of Wheat in Central Ethiopia and Virulence Diversity of Stem Rust Pucciniagraminis f. sp. Tritici. Advance Crop Science. 5: 3-2.

Hailu G, Tanner DG and Mengistu H 1991 Bread wheat Breeding and Genetics Research in Ethiopia: A Historical Perspective, Addis Ababa, IAR/ CIMMYT.

Johnson HW, Robinson HF and Cornstock RE 1955 Estimates of genetic and environmental Variability in Soybeans. Agronomy Journal. 47: 314 -318.

Kidane YG, Hailemariam BN, Mengistu DK, Fadda C, Pè ME and Dell'Acqua M 2017 Genome-Wide Association Study of *Septoria tritici* Blotch Resistance in Ethiopian Durum Wheat Landraces. Frontiers in Plant Science. 8:1586.

Kifle Z, Firew M and Tadesse D 2016 Estimation of association among growth and yield-related traits in bread wheat (Triticum aestivum L.) genotype at Gurage Zone, Ethiopia. International Journal of Microbiology and Biotechnology. 1: 1-9.

Khan SA 2013 Genetic Variability and Heritability Estimates in F2 wheat Genotypes. International Journal of Agriculture and Crop Sciences. 5: 983 -986.

Kosina P, Reynolds M, Dixon J, and Joshi A 2007 Stakeholder perception of wheat production constraints, capacity building needs, and research partnerships in developing countries. Euphytica .157: 475–483.

Leroux P, Albertini C, Gautier A, Gredt M and Walker AS 2007 Mutations in the CYP51 gene correlated with changes in sensitivity to sterol 14 alpha-demethylation inhibitors in field isolates of Mycosphaerella graminicola. Pest Management Science. 63: 688–698.

Miller PA, Williams JC, Robinson HF, and Comstock RE 1958 Estimates genotypic implications in selection. Agronomic Journal. 50:126-131.

Mengistu H, Getaneh W, Yesh A, Rbka D and Ayele B 1991 Wheat pathology Research in Ethiopia. In: Hailu G, Tanner, DG, Mengistu H (eds). Wheat research in Ethiopia: A historical perspective. Addis Ababa. IAR/ CIMMYT, 173217.

Mesele A, Wassu M and Tadesse D 2016 Estimation of heritability and genetic advance of yield and yield related traits in bread wheat (Triticum aestivum L.) genotypes at Ofla District, Northern Ethiopia. International Journal Plant Breeding. 10: 31-37.

Mohammadi M, Ramezanpour S, Navabpour S, Soltanloo H, Kalateharabi M, Kia S 2012 Genetic analysis and heritabilities of resistance to Mycosphaerella graminicola in wheat. Crop Breeding Journal. 1:35-42.

Pietravalle S, Shaw MW, Parker SR, and van den Bosch F 2003 Modeling of relationships between weather and *Septoria tritici* epidemics on winter wheat: a critical approach. Phytopathology. 93: 1329–1339.

Ponomarenko A, Goodwin SB, Kema GHJ 2011 *Septoria tritici* blotch (STB) of wheat. Plant Health Instructor. doi:10.1094/PHI-I-2011-0407-01.

Rezenne F 1993 A review of weed science research activities on wheat and barleyin Ethiopia. pp. 121-148. In: Tsedeke Abate (ed.). A Review of Crop Protection Research in Ethiopia. Addis Ababa, Ethiopia:IAR

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

Said A and Hussein T 2016 Epidemics of *Septoria Tritici* Blotch and its Development over Time on Bread Wheat in Haddiya-Kambata Area of Southern Ethiopia. Journal of Biology, Agriculture and Healthcare. 6(1): 47-57.

SAS 2009Version 9.3.Inc. Carry, North California, USA.

Sharma RC and Duveiller E 2007 Advancement toward new Spot Blotch resistant wheat in south Asia.Crop Science. 47: 961-968.

Singh DN 2001 Heritability and genetic advances in linseed (L. usiataissimum L.).Journal of Research Birsa Agricultural Reserach. 13: 73-74

Tar'an B, Zhang C, Warkenting T , Tullu A and Vandenberg A 2005 Genetic diversity among varieties and wild species Accessions of pea (Pisum sativum L) based on molecular markers, and morphological and physiological characters. Genome. 48: 257-272.

Torriani SFF, Melichar JPE, Mills C, Pain N, Sierotzki H and Courbot M 2015 *Zymoseptoria tritici:* a major threat to wheat production, integrated approaches to control. Fungal Genetic Biology. 79: 8–12.

Tadesse W, Bishaw Z and Assefa S 2019 Wheat production and breeding in Sub -Saharan Africa: Challenges and opportunities in the face of climate change. International Journal of Climate Change Strategies and Management. 11 (5): 696-715.