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-Saharan 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.

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.

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

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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 | 93     | 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 | 17 | 7 | Adap |

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     | Sofumari           | 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= Kulumusa 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 \( i \)th 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 = \( \frac{(Y1/9) \times (Y2/9)}{100} \)

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,

\[
SPC = \frac{\text{Disease height (cm)}}{\text{Plant height (cm)}}
\]

(Eyal and Ziv 1974)

**Estimation of variance components**

Environmental variance or error variance (\( \delta^2 e \)), genotypic variance (\( \delta^2 g \)) and phenotypic variance (\( \delta^2 p \)) components and their coefficients of variation were estimated as suggested by Singh, (2001). The equations are as follows,

\[
\text{Genotypic Variance } (\sigma^2 g) = \frac{\text{MSG} - \text{MSE}}{r}
\]

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

Phenotypic variance (\( \delta^2 p \)) =

\[
\sigma^2 p = \sigma^2 g + \sigma^2 e \delta^2 p = \sigma^2 g + \sigma^2 e
\]

Where: \( \delta^2 p = \) phenotypic variance, \( \delta^2 g = \) genotypic variance, \( \delta^2 e = \) Environmental variance or error variance.

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

\[
\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\sigma^2 g}}{x} \times 100
\]

\[
\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\sigma^2 p}}{x} \times 100
\]

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).

\[
H^2 = \frac{\delta^2 g}{\sigma^2 p} \times 100
\]

Where: \( \delta^2 p = \) phenotypic variance, \( \delta^2 g = \) genotypic variance, \( H^2 = \) 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).

\[
GA = (K) (\delta p) (H^2)
\]

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, \( \delta p = \) phenotypic standard deviation and \( H^2 = \) heritability (in the broad sense)

Genetic advance as percent of mean was obtained as;

\[
GAN (\% of mean) = \frac{GA}{x} \times 100\%
\]

where \( GA = \) Expected genetic advance mean percentage, \( x = \) 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).

$$r_{pxy} = \frac{COV_{pxy}}{\sqrt{\sigma^2_{px} \cdot \sigma^2_{py}}}$$

Where: $r_{pxy}$= phenotypic correlation coefficient between character x and y, $COV_{pxy}$= 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 ($P\leq0.01$) 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                      | Replication (Df=1) | Genotypes (Df=179) | Block (Df=1) | 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                      | Replication (Df=1) | Genotypes (Df=179) | Block (Df=1) | 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 at 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    | Error (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 ProgressCoefficient      | 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 resistance 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**

| Parameters | DTH | GFP | DTM | PHT | %SEV | NPT | TSW | Gy/ha | By/ha |
|------------|-----|-----|-----|-----|------|-----|-----|-------|-------|
| DTH        | 1   |     |     |     |      |     |     |       |       |
| GFP        | 0.713** | 1   |     |     |      |     |     |       |       |
| DTM        | 0.406** | 0.065 | 0.048 |     |      |     |     |       |       |
| PHT        | 0.098 | 0.028 | 0.019 | 0.311** | 1   |     |     |       |       |
| %SEV       | -0.036 | -0.021 | -0.009 | 0.568** | 0.19 | -0.003 | 1   |       |       |
| NPT        | -0.034 | -0.046 | 0.059 | 0.216** | 0.019 | 0.055 | -0.515 | 1   |       |
| TSW        | 0.041 | 0.134 | 0.119 | 0.317** | 0.35 | -0.46 | -0.432 | -0.543 | 1   |
| Gy/ha      | -0.032 | 0.341 | 0.451 | 0.543 | 0.334 | -0.432 | -0.543 | 0.0321 | 1   |
| By/ha      | 0.341 | 0.132 | 0.451 | 0.543 | 0.334 | -0.432 | -0.543 | 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, 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.

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