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Research Article

Screening of Bread Wheat (*Triticum aestivum* L.) Genotypes for Septoria Tritici Blotch in Central Highland of Ethiopia

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Abstract

Septoria tritici blotch is a major disease that limits wheat yields globally. This study aimed to identify Septoria-resistant bread wheat genotypes for use in future breeding and variety development programs. A total of 49 genotypes were evaluated in the first year and 60 in the second year, selected from an international nursery and evaluated during the 2016–2018 cropping seasons. The experiments were conducted in both research and farmers' fields during the 2018/19 and 2019/20 cropping seasons. The trial used an alpha lattice design with three replications. Data on yield and related traits were analyzed using SAS version 9.3 software. The results indicated significant (P < 0.01) variation among the genotypes for all phenotypic traits measured at Holetta over the two years. Similarly, significant differences (P < 0.01) were observed at Weliso for all traits except for Septoria disease severity, thousand kernel weight, and grain yield. Across the two locations, the highest grain yield recorded was 5.4 t/ha, while the lowest was 1.8t/ha. Therefore, the study findings indicated that some genotypes showed the best performance and a good opportunity to incorporate a variety of development of wheat breeding programs.

Keywords

Alpha Lattice, Genotypes, Major Disease, Septoria Tritici, Wheat

1. Introduction

Global wheat production relies almost exclusively on two main species: hexaploid bread wheat (Triticum aestivum L., 2n = 6X = 42, AABBDD) and tetraploid durum wheat (Triticum turgidum subsp. durum, 2n = 4X = 28, AABB) [9]. Wheat is capable of growing in the Ethiopian highlands, which lie between latitudes 6° and 16°N and longitudes 35° and 42°E, at altitudes ranging from 1500 to 3000 meters above sea level (m.a.s.l.). However, the most ideal elevation range for wheat cultivation in this region is between 1900 and 2700 m.a.s.l. [3].

Wheat is used not only for producing bread, biscuits, and pastries, but also for making starch and gluten [5]. Wheat

(*Triticum aestivum L.*) is a key staple food for a significant portion of the global population, including Ethiopia. In Ethiopia, wheat is one of the most important cereals, grown on a total area of 2.1 million hectares—1.7 million hectares under rain-fed conditions and 0.4 million hectares irrigated. The country produces 6.7 million tonnes of wheat, with average yields of 3.0 tonnes per hectare for rain-fed and 4.0 tonnes per hectare for irrigated land [4].

Wheat production in Ethiopia is limited by various biotic and abiotic factors, with fungal infections being among the most significant biotic constraints [6, 7]. Septoria tritici is a major disease of wheat in all wheat-growing areas of the

world when climatic conditions are favorable. Wheat is vulnerable to infections throughout its growth stages, from seedling to mature plant. Mild infections may result in only a few scattered lesions, while more severe infections can lead to significant grain loss by damaging leaves, spikes, or even the whole plant [12]. These diseases reduce yield by causing grains to shrink and become lighter [13].

Septoria tritici blotch (STB) caused production losses of up to 82% in sensitive wheat types cultivated in hotspot locations in Ethiopia [15]. In the central highlands of Ethiopia, where the disease was 100% prevalent, recent studies also revealed that nearly all bread wheat varieties under production were susceptible to STB, with yield losses of up to 41% and 48% reported at the Holeta [1] and Areka [14] Agricultural Research Centers, respectively [11].

At present, a majority of bread wheat genotypes are significantly impacted by Septoria tritici blotch disease, leading to substantial yield losses and poor grain quality. One effective approach to mitigate these losses is through resistance breeding. The first step in this process is identifying genotypes with resistance to the disease. Consequently, the purpose of this activity is to evaluate bread wheat genotypes with resistance to Septoria for future breeding programs and variety development.

2. Materials and Methods

2.1. Description of the Experimental Site

The genotypes were evaluated at two locations namely; Holetta and Weliso in Ethiopia the year 2018 to 2019 cropping seasons. Holetta Agricultural Research Center (HARC) is located in the Oromia regional state in the central highlands of West shawa region. HARC is located at 09°04'12"N latitude and 38°29'45"E longitude with an altitude of 2,400 m.a.s.l. The minimum and maximum temperature of the area is 6.05°C and 22.41°C respectively. The mean annual rainfall of HARC is 1102 mm. The soil in the area consists of nitosols and vertisols, with a pH level of 6.0 [10]. Weliso is situated in the Southwest Shewa Zone of the Oromia Region in Ethiopia, 114 km southwest of Addis Ababa. Its coordinates are 8°32' N latitude and 37°58' E longitude, at an elevation of 2,063 meters above sea level.

2.2. Experimental Material

In the first and second years, 49 and 60 bread wheat genotypes, respectively, including selected materials from CIMMYT along with control varieties (both susceptible and resistant), were assessed for resistance to Septoria and Fusarium diseases. The experiment was conducted in the field using an alpha lattice design with three replications, and natural infestation was used for disease testing.

2.3. Data Collected

The data were collected based on plant and plot basis those are; days to heading and maturity, plant height, agronomic score, number of tillers, biomass yield thousand kernel weight, hectoliter weight, grain yield, and disease data.

2.4. Statistical Analysis

The data analysis was subjected to analysis of variance (ANOVA) according to the general linear model using SAS 9.3@ version [8]. The ANOVA for individual locations followed the model:

$$P_{ijk} = \mu + g_i + b_k(j) + r_j + e_{ijk}$$

Where: Pijk represents the phenotypic value of the ith genotype in the jth replication and the Kth incomplete block within replication j; μ is the grand mean; gi is the effect of the ith genotype; bk (j) denotes the effect of the Kth incomplete block within replication j; rj is the effect of replication j; eijk is the residual or random error effect.

3. Result and Discussion

Analysis of Variance

F-max tests were conducted to verify the heterogeneity of error variances. Both locations exhibited heterogeneity in error variances. As a result, the data were analyzed separately by location and year. The outcomes of the separate analysis of variance for the two locations and years are presented in Tables 1, 2, 3, and 4.

The separated analysis of variance: the analysis conducted over the two years revealed statistically significant (P < 0.01) variations among the genotypes for all phenotypic traits. Namely; DTH, DTM, PHT, SDS, AgrSc, TKW, HLW, and GYLD considered in this study. The detailed information is presented (Tables 1, 2). The significance of the traits suggested a high level of genetic variability in growth and yield characteristics. Based on the study conducted at Holetta; the maximum and minimum grain yield obtained was 5.4 t/ha and 2.6 t/ha from the first year while 5.3 t/ha and 1.8 t/ha from the second year respectively. The finding of this study is similar to previous findings [2] it was conducted on" Field response and identification of bread wheat genotypes to Septoria tritici blotch in the highlands of North Gondar." The finding of this study is similar to previous findings for plant height, tausand kernel weight and grain yield [16].

Table 1. Separated analysis of variance for grain yield and yield-related character of bread wheat genotypes grown in Septoria screening trials at Holetta, 2018/19 cropping season.

Traits (Y)	MSG (48)	MS Rep (2)	MS Blk (Rep)	MSE (78)	Mean	CV (%)	R2	LSD (5%)
DTH	20.17**	2.15ns	3.26ns	174.36	65.2	2.3	0.87	2.43
DTM	31.10**	14.41*	4.31ns	4.55	139.12	1.53	0.84	3.47
PHT	43.87**	0.19ns	9.97ns	15.90	96.61	4.13	0.67	6.48
SDS	0.08**	0.03*	0.02ns	0.01	0.43	21.59	0.88	0.15
AgrSc	0.84**	0.53ns	0.39*	0.19	3.48	12.57	0.79	0.71
TKW	59.79**	3.93ns	7.42ns	5.78	42.95	5.60	0.89	3.91
HLW	10.13**	2.24ns	2.20ns	1.12	78.44	1.35	0.87	1.72
GYLD	97023.51**	85533.10**	61080.50**	16752.43	1222.64	10.59	0.82	210.39

(*, **, and ns) indicate highly significant at 1%, significant at 5%, and non-significant, respectively. The numbers in parentheses represent degrees of freedom. MSG refers to Mean Squares for Genotypes, MS Rep to Mean Squares for Replications, MSBlk to Mean Squares for Blocks, MSE to Mean Squares for Error, and CV to Coefficient of Variation. Abbreviations used: DHT = Days to Heading, PTH = Plant Height, SDS = Septoria Disease Severity, AgrSc = Agronomic Score, BMY = Biomass Yield, TKWT = Thousand Kernel Weight, HLW = Hectoliter Weight, GYLD = Grain Yield.

Table 2. Separated analysis of variance for grain yield and yield-related character of bread wheat genotypes grown in Septoria screening trials at Holetta, 2019/20 cropping season.

Traits	MSG (59)	MS Rep (2)	MS Blk (Rep)	MSE (91)	Mean	CV (%)	R2	LSD (5%)
DTH	15.89**	1.35ns	4.48**	1.93	69.10	2.01	0.889	2.2537
PHT	52.34**	6.54ns	5.19ns	6.05	94.05	2.61	0.88	3.9892
SDS	516.89**	18.34ns	202.64**	92.21	31.01	30.97	0.85	15.574
FHB	1.31**	0.02ns	0.58**	0.19	2.02	21.84	0.89	0.7143
AgrSc	0.48**	0.34*	0.12ns	0.10	2.96	10.84	0.82	0.5206
TKW	75.76**	157.51**	28.13**	10.55	33.54	9.69	0.87	5.2689
HLW	29.04**	156.51**	5.62ns	3.67	75.55	2.54	0.89	3.1074
GYLD	157985.14**	203026.96**	52043.51**	15755.07	1117.73	11.23	0.91	203.58

Y = The abbreviations are defined in Table 1.

The separated analysis of variance conducted in 2018/19 at Weliso showed statistically significant (P < 0.01) highly significant differences among the genotypes for all phenotypic traits except SDS and GYLD considered in this study (Table 3). While conducted in 2019/20 at Weliso it was statically highly significant for all phenotypic traits (Table 4). The significance of the traits indicated the existence of an enormous amount of genetic variability for growth and yield-related attributes. From this experiment conducted at Weliso, the maximum, and minimum grain yields obtained were 3.0 t/ha and 1.5 t/ha from the first year while 4.5t/ha and 1.8t/ha from the second year respectively. This result is also in line with the findings of [2].

The first-year grain yield interactions of almost all the genotypes of the grain yield observed at Holetta performed better than Weliso at the farmer field as indicated (Figure 1). The second-year grain yield result of the majority of the genotypes revealed that the Holetta location was better performed than the Weliso location (Figure 2). This indicated that there were significant differences across the years and locations.

Table 3. Separated analysis of variance for grain yield and yield-associated character of bread wheat genotypes grown in Septoria screening trials at Weliso 2018/19 cropping season.

Traits	MSG (48)	MS Rep (2)	MS Blk (Rep)	MSE (78)	Mean	CV (%)	R2	LSD (5%)
PHT	106.17**	248.02*	38.48ns	60.33	86.57	8.97	0.59	12.63
SDS	169.65ns	116.72ns	283.61*	160.24	54.57	23.20	0.51	20.58
AgrSc	0.56**	0.12ns	0.11*	0.15	3.20	11.96	0.74	0.62
TKW	0.50ns	0.96ns	0.46ns	0.41	10.27	6.24	0.56	1.04
HLW	2.18**	0.19ns	0.25ns	0.29	80.98	0.66	0.84	0.87
GYLD	19066.97ns	416851.45**	18978.06ns	14423.26	705.61	17.02	0.69	195.22

Y = The abbreviations are defined in Table 1.

Table 4. Separated analysis of variance for grain yield and yield-associated traits of bread wheat genotypes grown in Septoria screening trials at Weliso, 2019/20 cropping season.

Traits	MSG (59)	MS Rep (2)	MS Blk (Rep)	MSE (91)	Mean	CV (%)	R2	LSD (5%)
DTH	13.88**	3.27**	0.61ns	0.57	74.17	1.02	0.95	1.23
PHT	59.92**	222.64**	29.10ns	19.07	87.14	5.01	0.74	7.08
SDS	258.83**	3.28ns	28.27ns	24.87	17.22	28.95	0.90	8.09
AgrSc	0.18**	0.56**	0.12*	0.07	3.036	8.46	0.74	0.42
TKW	26.06**	32.25**	12.28**	5.49	40.03	5.85	0.82	3.80
HLW	3.26**	61.32**	5.53**	2.03	80.39	1.77	0.76	2.31
GYLD	46368.75*	680301.95**	63259.38**	31834.52	871.14	20.48	0.70	289.38

Y = The abbreviations are defined in Table 1.
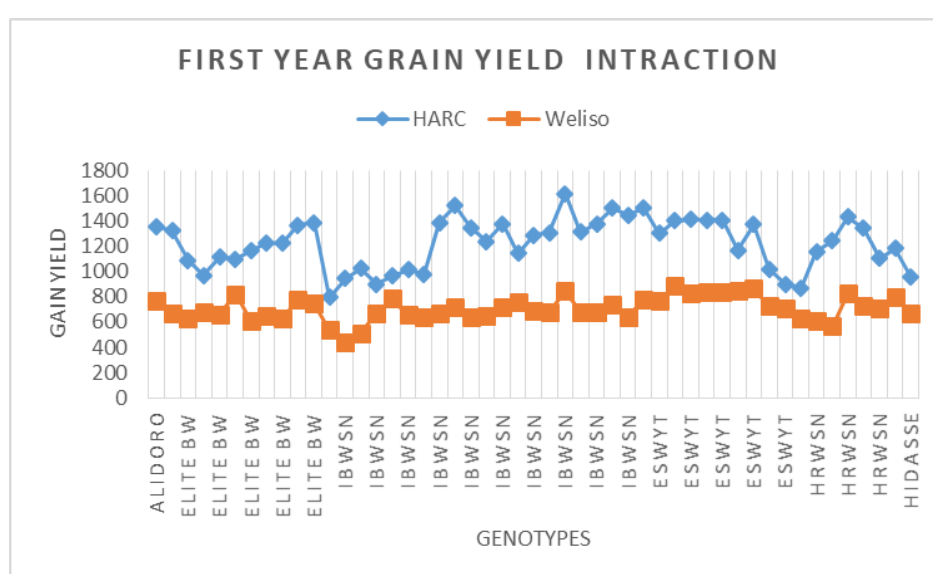
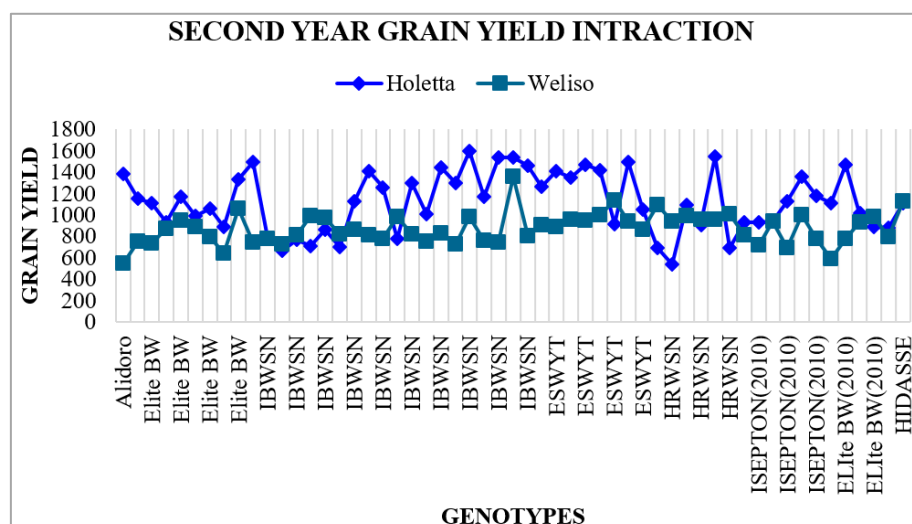*Figure 1. Interactions of mean grain of grain yield of bread wheat genotypes from two locations.*

Figure 2. Interactions of mean grain of grain yield of bread wheat genotypes from two locations.

4. Conclusions

In this study, substantial genetic variation was found in the germplasm accessions evaluation experiment for Septoria disease response, especially the Holetta site. This result prompts us to do more studies to assess the resistance and tolerance abilities of various genotypes. As a result, the information from the researched attributes and diseases evaluation among various genotypes revealed that there was a significant level of genetic diversity between genotypes. Based on disease, yield, and yield-contributing attributes the top-performing genotypes proceeded to the next breeding stage as a preliminary yield trial. Therefore, the study findings indicated that some genotypes showed the best performance and a good opportunity to incorporate a variety of development of wheat breeding programs. In conclusion, this study shows that more research is necessary to properly utilize the genetic potential found in wheat, even though it offers insightful information on the genetic variation for agronomic qualities and resistance to Septoria disease. Future research will be crucial for developing wheat varieties that can satisfy the demands of global food security in the face of persistent biotic and abiotic challenges by extending our understanding of the genetic variables determining disease resistance and yield.

Abbreviations

ANOVA	Anlaysis of Varianve
CIMMYT	International Maize & Wheat Improvement Center
t/ha	Tone Per Hactare
IBWSN	Internatinal Bread Wheat Scrrining Nursery
HRWSN	High Rain Fall Screening Nursery
ISEPTON	International Seproria Observation Nursery

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Author Contributions

Endashaw Girma is the single author of this work. The author reviewed and approved the final manuscript.

Conflicts of Interest

The author declares no conflicts of interest.

References

[1] Abera, T., Alemu, L., Bekele, K., Getaneh, W. and Endale, H., "Estimated Yield Loss Assessment of Bread Wheat (Triticum aestivum L.) due to Septoria Leaf Blotch Septoria tritici (Roberge in Desmaz) on Wheat in Holetta Agricultural Research Center, West Shewa, Ethiopia." Research in Plant Sciences, vol. 3, no. 3 (2015) 61-67.

[2] Azene, Y., Fentaw, B. and Adugna, Y., Field response and identification of bread wheat genotypes to Septoria tritici blotch in the highlands of North Gondar. JCRFS 2020; 1(2) 09-17. https://doi.org/10.7176/jbah/10-10-01

[3] Bekele H, Verkuiji W, Mawangi T. (2000). Adaptation of improved heat technologies in Addaba and Doddola Worede's of the Bale highlands of Ethiopia. CIMMYT/EARO, Addis Ababa, Ethiopia.

[4] Central Statistics Agency for Ethiopia. Agricultural sample survey of area and production of major crops. Available from https://www.statsethiopia.gov.et/ Accessed 2022 Jul 15.

[5] Hanson H, Borlaug NE and Anderson RG, 1982. Wheat in the third world. West view press. 192p. https://doi.org/10.1007/978-1-349-06163-1_11

[6] Hailu. Wheat Research in Ethiopia A Historical perspective. In Cimmyt. Org 1991.

[7] 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.

[8] SAS. 2012. Statistical analysis system, version 9.3 editions. SAS Institute Inc. Cary, NC.

[9] Sears, E. R., 1966. Nullisomic-tetrasomic combinations in hexaploid wheat. In Chromosome Manipulations and Plant Genetics The contributions to a symposium held during the Tenth International Botanical Congress Edinburgh 1964 (pp. 29-45). https://doi.org/10.1007/978-1-4899-6561-5_4

[10] Tamene, T. Gemechu, K. and Hussein, M. 2015. Genetic progresses from over three decades of faba bean (*Vicia faba* L.) breeding in Ethiopia. *Australian Journal of Crop Science*, 9(1), p. 41.

[11] Yitagesu Tadesse, Alemayehu Chala and Bekele Kassa 2020. Yield Loss Due to Septoria tritici Blotch (Septoria Tritici) of Bread Wheat (Triticum aestivum L.) in the Central Highlands of Ethiopia. Journal of Biology, Agriculture and Healthcare ISSN 2224-3208 (Paper) ISSN 2225-093X (Online) Vol. 10, No. 10, 2020. https://doi.org/10.7176/jbah/10-10-01

[12] Azanaw, A., Ebabuye, Y., Ademe, A., Gizachew, S. and Tahir, Z., 2017. Survey of Septoria Leaf Blotch (Septari atritici Roberge in Desmaz) on Wheat in North Gondar, Ethiopia. *Abyssinia Journal of Science and Technology*, *2*(2), pp. 11-18.

[13] Suffert, F., Sache, I. and Lannou, C., 2011. Early stages of septoria tritici blotch epidemics of winter wheat: build‐up, overseasoning, and release of primary inoculum. *Plant Pathology*, *60*(2), pp. 166-177. https://doi.org/10.1111/j.1365-3059.2010.02369.x

[14] Said, A. and Hussein, T., 2016. Epidemics of Septoria tritici blotch and its development overtime on bread wheat in Haddiya-Kambata area of Southern Ethiopia. *Journal of Biology, Agriculture and Health Care*, *6*(1), pp. 47-57.

[15] Badebo, A., Bekele, E., Bekele, B., Hundie, B. and Degefu, M., 2006. Review of Two Review of Two Decades of Decades of Decades of Research on Research on Diseases Diseases Diseases of Small Cereal Crop Cereal Crop Cereal Crops. *Increasing Crop Production through Improved Plant Protection–Volume I*, p. 375.

[16] Binalf, L., Shifa, H. and Tadesse, W., 2024. Association mapping of septoria tritici blotch resistance in bread wheat in Bale and Arsi highlands, Ethiopia. *Heliyon*. https://doi.org/10.2139/ssrn.4516021