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Research Article

Screening of Bread Wheat (*Triticum aestivum* L.) Genotypes for Waterlogged Area in Highlands of Ethiopia

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Abstract

Due to a serious waterlogging issue, Ethiopia's agricultural productivity has been severely limited, yielding much lower than expected results. In this study conducted on screening of 49 for first year and 60 for second year bread wheat genotypes selected from international nursery. An experiment was undertaken at two locations namely, Ginchi Agricultural Research Sub Center and Tulu Bolo farmer field in Ethiopia in 2018/19 and 2019/20 cropping seasons. The main objective of this study was to select best performed genotypes in waterlogged areas for next variety development and future breeding program. The experiment was conducted using apha lattice with three replications. Data on yield and associated traits were collected and analyzed using SAS version 9.3 software. The results revealed that the separate analysis of variance over the two years conducted at Ginchi showed statistically significant ($P \leq 0.01$) differences among the genotypes for all phenotypic traits except Septoria disease severity, Number of tiller and biomass yield considered in this study. The results revealed that the separate analysis of variance over the two years conducted at Tulu bolo showed statistically non-significant ($P \leq 0.01$) differences among the genotypes for all phenotypic traits except days to heading, plant height, Septoria disease severity agronomic score, hectoliter weight and thousand kernel weight considered in this study. In general from the two locations the maximum and minimum were revealed 29.85qt/ha and 2.32qt/ha respectively. This indicated that almost all genotypes were showed low performed and the wheat breeder give more attentions to provide resistance genotypes for waterlogging.

Keywords

Alpha Lattice, Bread Wheat, Low Oxygen, Waterlogging

1. Introduction

World wheat production is almost totally reliant on two modern species: hexaploid bread wheat (*Triticum aestivum* L., 2n = 6X = 42, AABBDD) and tetraploid wheat (*Triticum turgidum* subsp. durum, 2n = 4X = 28, AABB) [9]. Wheat may be grown in Ethiopia's highlands, which are located between 6° and 16° N, 35° and 42° E, and longitude at altitudes ranging from 1500 to 3000 m.a.s.l. Wheat's optimal altitude is from 1900 to 2700 meters above sea level [2]. Wheat is not only for making bread, biscuit and pastry products, but also for the Production of starch and gluten [6]. Wheat (*Triticum aestivum* L.) is the staple food for a large part of the world population including Ethiopia. It is one of the most important cereals cultivated in Ethiopia. It is cultivated on a total area of 2.1 million hectares (1.7 million ha rain-fed and 0.4 million ha irrigated) with a total production of 6.7 million tonnes of grain at an average productivity of 3.0 and 4.0 t/ha under rain-fed

and irrigated conditions, respectively [3].

Water-logging is a significant limitation that impacts crops worldwide. The primary cause of this stress is when water from precipitation or irrigation accumulates in the soil profile for an extended length of time as a result of excessive rainfall, soil compaction, flat topography, or poor drainage systems [12]. Wheat (*Triticum aestivum* L.) is one of the most intolerant crops to waterlogging [11]. The primary problem of watered logged soils is a lack of oxygen. Underground roots, like other tissues, require oxygen to respire. In a typical soil, gas exchange occurs easily through air-filled gaps between soil particles. The rate of oxygen transport in water is extremely slow, and as a result, waterlogged soils are almost completely deoxygenated [7].

Currently, almost all of the bread wheat genotypes are highly affected by waterlogging problems. This results in high yield loss. Resistance breeding is a solution to prevent this loss. Identifying the resistant materials is the basic thing for resistance breeding. Therefore; the activity was designed to select best performed genotypes in waterlogged areas for next variety development and future breeding program.

2. Material and Methods

2.1. Description of the Experimental Site and Materials

Tulu Bolo is located in the Southwest Shewa Zone of the Oromia Region in Ethiopia, 80km from Addis Ababa on the way to Jimma. It is located at 8° 40''N latitude and 38° 13''E longitude with an elevation of 2193 m.a.s.l. While, Ginchi is located in the west Shewa Zone of the Oromia Region in Ethiopia. It is located at 09° 30''N latitude and 38° 30''E longitude with an elevation of 2200 m.a.s.l. The first year 49 and the second year 60 bread wheat genotypes selected from introduced materials from CIMMYT lines. The field experiment was laid down on alpha lattice design with three replications.

2.2. Data Collected

The data were collected based on plant and plot basis those

are days to heading and, plant height, agronomic score, number of tillers, biomass yield, thousand kernel weight, hectoliter weight, grain yield and diseases data.

2.3. Statistical Analysis

Using SAS 9.3@ version [8], the data analysis was conducted to an ANOVA based on a general linear model. The ANOVA for each location conforms to the model:

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

Where; P_{ijk} = phenotypic value of ith genotype under j^{th} replication and K^{th} incomplete block within replication j; μ = Grand mean; g_i = the effect of the ith genotype; $bk_{(j)}$ = the effect of incomplete block "K" within replication "j"; r_j = the effect of replication "j"; e_{ijk} = the residual/random error effect.

3. Results and Discussion

Analysis of Variance

F max tests were used to confirm heterozygosity in error variances. The two locations had heterozygous error variances. As a result, data were collected and analyzed independently based on location and year. The results of the separated analysis of variance across the two location and year are presented on (Tables 1, 2, 3 and 4).

The separated analysis of variance conducted, 2018/19 at Ginchi showed statistically significant (P≤0.01) highly significant differences among the genotypes for all phenotypic traits except Septoria tritici blotch considered in this study. While conducted 2019/20 at Ginchi showed that statistically highly significant except Septoria disease, biomass yield and number of tillers. From this studied conducted at Ginchi the maximum and minimum were observed 7.54qt/ha and 2.32qt/ha from the first year while 29.85qt/ha and 9.74qt/ha from the second year respectively. The finding of this study is similar to previous findings for grain yield and plant height [1, 4, 10]. The finding of this study is similar to previous findings for grain yield [5] it was conducted on" Yield response of restricted-tillering wheat to transient waterlogging on duplex soils."

Table 1. Mean squares results from the separate analysis of variance for yield and associated traits of wheat genotypes assessed at Ginchi, 2018/19 cropping season.

Traits [(y)]	MSG /48/	MS Rep /2/	MS Blk /Rep/	MSE /78/	Mean	CV (%)	R2	LSD (5%)
PTH	48.200847**	425.170068**	36.585477ns	23.817794	59.32	8.23	0.68	7.9331
SDS	52.128324ns	119.047619ns	98.400399ns	76.80382	93.95	9.33	0.44	14.246
NT	0.51053470*	0.49884354ns	0.59716284*	0.30230831	3.14	17.50	0.61	0.8938
AgrSc	0.60191653**	1.52714286**	0.80907900**	0.24156785	2.28	21.52	0.71	0.7989
TKW	16.3534714**	12.7259864*	13.6729305**	2.899256	33.21	5.13	0.84	2.7678

Traits [(y)]	MSG /48/	MS Rep /2/	MS Blk /Rep/	MSE /78/	Mean	CV (%)	R2	LSD (5%)
GYLD	3746.0952**	1813.5580ns	3579.3196ns	2098.6094	142.05	32.25	0.60	74.466

(*, ** and ns) = highly significant @ 1%, significant @ 5% and non-significant respectively.
// parenthesis indication of degrees of freedom. MSG = Genotypes Mean squares, MS Rep = Replications Mean Square, MSBlk = Block Mean square, MSE = Error Mean Squares, CV = Coefficient of variation.
Abbreviations: DHT = Days to heading, PTH = Plant Height, SDS = Septoria Disease Severity, AgrSc = Agronomic Score, NT = Number of Tiller, BMY = Biomass yield, Thousand Kernels Weight, HLW = Hectoliter weight, GYLD = Grain yield.

Table 2. *Mean squares results from the separate analysis of variance for yield and associated traits of wheat genotypes assessed at Ginchi, 2019/20 cropping season.*

Traits	MSG /59/	MS Rep /2/	MS Blk /Rep/	MSE /91/	Mean	CV (%)	R2	LSD (5%)
DHT	21.998534**	1.688889ns	2.526015ns	2.187763	67.94	2.18	0.90	2.3989
PTH	45.794783*	350.138889**	41.109176ns	29.924261	71.78	7.62	0.67	8.8721
SDS	21.096429ns	62.751936*	25.157039ns	19.864004	10.99	40.54	0.56	7.2285
AgrSc	0.24313565**	4.09305556**	0.35156390**	0.12258238	2.49	14.07	0.75	0.5678
NT	0.39474340ns	1.68888889*	0.45970676ns	0.47849970	2.83	24.46	0.50	1.1219
BMY	0.33084466ns	8.13872722**	0.52256717ns	0.33374174	1.66	34.86	0.64	0.937
TKW	36.003740**	10.006722ns	17.021634*	9.373950	35.77	8.56	0.79	4.9657
HLW	40.557375**	1.514056ns	22.244720**	10.985195	73.49	4.51	0.76	5.3755
GYLD	35888.656**	109781.264**	67392.547**	19584.766	562.23	24.89	0.72	226.97

y = abbreviations refer to table 1.

The separated analysis of variance conducted 2018/19 at Tulu-bolo showed statistically significant (P≤0.01) non-significant differences among the genotypes for all phenotypic traits except thousand kernel weight considered in this study. While conducted 2019/20 at Tulu-bolo showed that statistically highly significant except grain yield, biomass yield and number of tillers. The detail information's are presented (Tables 3, 4). The significant of the traits indicated that the existence of enormous amount of genetic variability for grain yield and yield attributes. From this studied conducted at Tulu bolo the maximum and minimum were observed 23.36 qt/ha and 7.08qt/ha from the first year while 25.40qt/ha and 12.38qt/ha from the second year respectively. The finding of this study is similar to previous findings for days to heading and plant height [1, 10].

The first year grain yield interactions almost all the genotypes of the grain yield was observed at Tulu bolo better performed than Ginchi (Figure 1). The second year grain yield the of the genotypes of the grain yield was revealed at Tulu bolo equal performed with Ginchi (Figure 2).

Table 3. *Mean squares results from the separate analysis of variance for yield and associated traits of wheat genotypes assessed at Tulu-bolo, 2018/19 cropping season.*

Traits	MSG /48/	MS Rep /2/	MS Blk /Rep/	MSE /78/	Mean	CV (%)	R2	LSD (5%)
PHT	29.507773ns	269.695578**	104.631273**	25.768110	67.60	7.51	0.70	8.2515
SDS	77.712143ns	31.422433ns	129.468431ns	64.13564	13.11	61.08	0.54	13.018
AgrSc	0.32192203ns	0.93367347*	1.09466434**	0.26617985	2.10	24.54	0.70	0.8386
TKW	31.412318**	69.955397**	33.724583**	8.631548	41.50	7.08	0.79	4.7757
HLW	70.546267ns	96.503929ns	261.781460**	48.36552	68.82	10.11	0.71	11.305

Traits	MSG /48/	MS Rep /2/	MS Blk /Rep/	MSE /78/	Mean	CV (%)	R2	LSD (5%)
GYLD	19319.960ns	81095.754ns	87459.863**	20903.992	353.18	40.94	0.67	235.02

y = abbreviations refer to table 1.
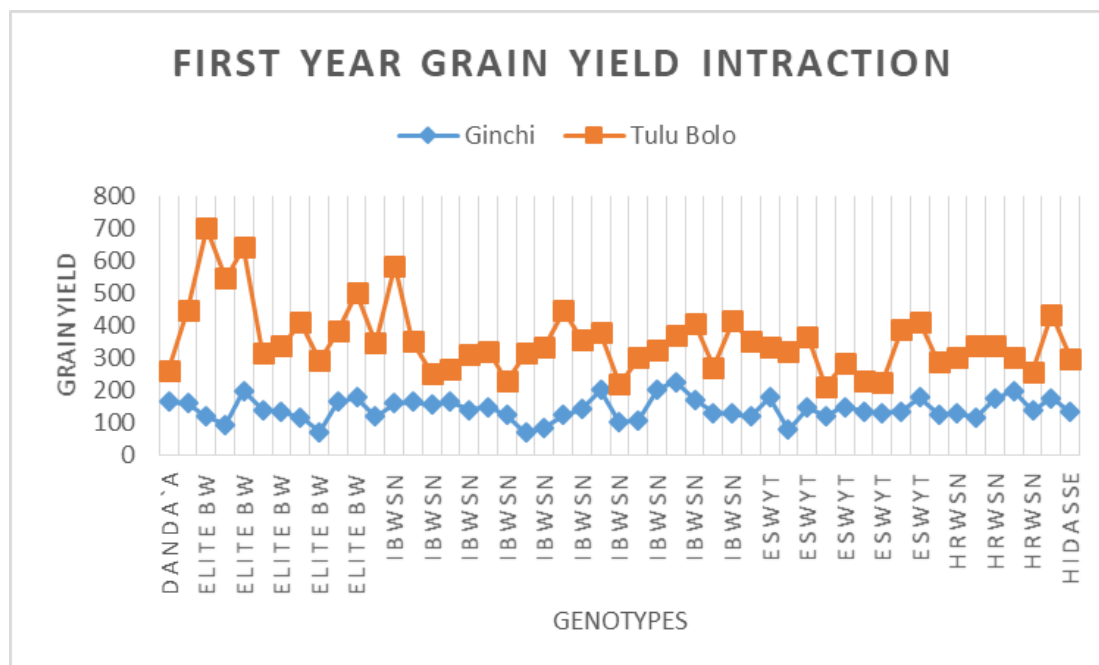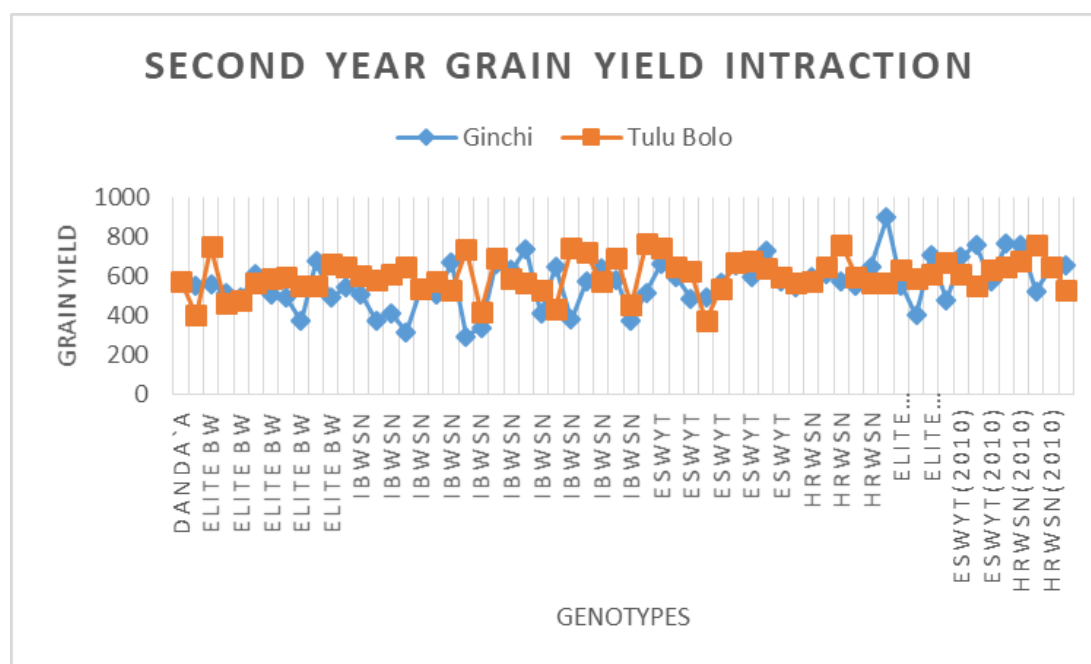

Figure 1. Interactions of mean grain of grain yield of bread wheat genotypes from two locations.

Table 4. Mean squares results from the separate analysis of variance for yield and associated traits of wheat genotypes assessed at Tulu-bolo, 2019/20 cropping season.

Traits	MSG /59/	MS Rep /2/	MS Blk /Rep/	MSE /91/	Mean	CV (%)	R2	LSD (5%)
DHT	8.4936059**	3.0055556*	0.7695668ns	0.7019478	71.06	1.18	0.90	1.3588
PTH	58.029244**	55.972222ns	91.177073**	25.197157	82.56	6.08	0.76	8.1413
SDS	48.198014*	84.752761ns	33.678239ns	31.578602	10.23	54.92	0.59	9.1141
AgrSc	0.26926318**	0.08888889ns	0.24538579**	0.10655831	3.01	10.84	0.72	0.5294
NT	1.44992206ns	10.15555556**	2.27410953ns	1.4537135	4.54	26.56	0.58	1.9555
BMY	0.22672808ns	0.41921056ns	0.37503897ns	0.19784022	1.85	24.05	0.59	0.7214
TKW	22.097706**	4.546889ns	7.232008*	3.868593	33.99	5.79	0.83	3.19
HLW	17.171893**	4.956292ns	15.444858ns	9.910490	76.34	4.12	0.61	5.1058
GYLD	17920.150ns	74288.237**	64260.077	14081.945	602.19	19.71	0.72	192.46

y = abbreviations refer to table 1.

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

4. Conclusion

The waterlogged area-based screening technique was effective in distinguishing wheat genotypes, making it appropriate for early tolerance testing. It can also be applied to the crossing program. This finding encourages us to conduct additional research to test the resistance/tolerance capacities of various genotypes. Tolerance in specific genotypes is important for identifying cultivars for particular conditions and future use in wheat breeding program. The screening results for waterlogged tolerance of wheat genotypes are based on the particular environmental conditions of the Ginchi site. They may vary in different waterlogged regions; thus, waterlogged tolerance should be evaluated in specific areas of importance. More research is urgently needed to investigate the tolerance genotypes for waterlogged soil situations.

Abbreviations

ANOVA: Analysis of Variance
CIMMYT: International Maize and Wheat Improvement
            Center
t/ha: Tone Per Hectares
m.a.s.l.: Meters Above Sea Level

Acknowledgments

Author Contributions

Endashaw Girma is the sole author. The author read and approved the final manuscript.

Conflicts of Interest

The author declares no conflicts of interest.

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