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ABSTRACT

Ethiopia is one of the high wheat-producing countries in Africa. Production has increased over the years, but the country imports about 25 % of its internal consumption. To be wheat self-sufficient, the government of Ethiopia brings more areas under wheat production in irrigation agriculture. The wheat research program objectively works by targeting different wheat-producing agro ecology in the country to solve wheat production and productivity challenges. The national wheat research program introduced the 19th high-temperature wheat yield trial (19HTWYT) from the International Maize and wheat improvement center (CIMMYT), Mexico, in 2021.A total of fifty genotypes were tested at two locations. The design was alpha laticce design with two replications. Broad sense heritability (H^2) and correlation ware computed. High heritability: For DTM H2= 0.94; For DTM= H2= 0.88; for HLW H2= 0.89; and for GYLD H2= 0.96 observed in the result and moderate heritability obtained for PHT H2= 0.77and for TKW H2= 0.77on tested bread wheat genotypes at Kulumsa. But, for a trial conducted at Melkasa heritability were low for some traits: for DTM H2= 0.52; for PHT H2= 0.16; for TKW H2= 0.12; and for GYLD H2= 0.47(Table 2).Grain yield had a negative non-significant genotypic correlation r=-0.15 with date of heading; Non-significant positive correlation r= 0.11 with date of maturity; Highly significant positive correlations r= 0.61*** with Plant height; Highly significant positive correlation r=0.96*** with Thousand kernel weight; and postive significant correlation r=0.54 with Hectoliter weight at Kulumsa (Table 4). Selection for traits of interest is one of the major activities in the generating bread wheat varieties for different wheat-producing areas. The application of noble evaluation technics on genotypes selection leads to exploiting the best of the genetic potential for the trait intended.

Key words: CIMMYT, genotypic, Heritability, correlation

1. INTRODUCTION

Wheat (Triticum aestivum) is one of the world's major staple crops, and billions of people depend on it for food. Wheat production in the world for 2021/2022 was

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778.6 million metric tons. Its production is mainly for cash crops; its trade is higher than all other crops combined [1, 2]. Ethiopia is one of the high wheat-producing countries in Africa. Wheat production in Ethiopia is mainly by subsistence farmers under rain-fed agriculture. Its production in 2021/2022 was about 5.52 million tonnes [3]. Production has increased over the years, but the country imports about 25 % of its internal consumption. To be wheat self-sufficient, the government of Ethiopia brings more areas under wheat production in irrigation agriculture.

The National wheat research program targeted different wheat-producing agroecology and set trials accordingly. Likewise, the crossing of parent varieties in the program aimed to exploit merits from parents to meet the requirement for a wide range of environments. Priority traits identified by the program as Wheat rust resistance, drought tolerance, high grain yield, and wheat quality outlined as breeding objectives. Hence, breeding wheat in Ethiopia works around the mentioned benefits for the target environments. In addition to crossing wheat for different goals, the National wheat Research program introduces wheat trials from outside. CIMMYT and ICARDA. The wheat breeding program uses different breeding methods to improve the existing bread wheat varieties for grain yield and wheat rust disease resistance. The introduction of wheat trials is one of the breeding methods that the National wheat research program of Ethiopia uses besides its crossings blocks [8]. Introduction of different genotypes from other countries, mainly from the International Maize and wheat improvement center (CIMMYT) and International Center for Agricultural Research in the Dry Areas (ICARDA) is one of a source for germplasms. Introduced genotypes from CGIAR centers and genotypes from the national wheat research breeding program, placed together in the early stage of breeding pipelines, Observation nursery yield trial. Then, the program evaluates and select under different breeding stages: Observation nurseries yield trial, Preliminary variety trial, national variety trial, and variety verification trial before being released as a new variety.

Although Ethiopia has potential for wheat production, wheat productivity retard by different problems. Some of the major are wheat rust diseases, pests, drought, management practices, and water lodging [9].The wheat research program objectively works by targeting different wheat-producing agroecology in the country to solve wheat production and productivity challenges.

2. MATERIAL AND METHOD

Material, location, and Design

The national wheat research program introduced the 19th high-temperature wheat yield trial (19HTWYT) from the International Maize and wheat improvement center (CIMMYT), Mexico, in 2021. The experiment had 49 genotypes and one empty room for a local check. Durst, a bread wheat variety released in 2020 for moisture stress areas of Ethiopia added as a local check.

A total of fifty genotypes were tested at two locations: Melkasa Agricultural Research Center (MARC) and Kulumsa Agricultural Research Center (KARC). MARC is at 8°24′N 39°12′E latitude and longitude with an Altitude of 550 m.a.s.l. The minimum and maximum temperatures are 14oc and 280c. The area received an annual rainfall of about 763mm. KARK is at 8°02′N 39°10′E latitude and longitude with an Altitude of 2200 m.a.s.l. The minimum and maximum temperatures are 100c and 220c. Annual rainfall in kulumsa is about 840mm.

The design was alpha laticce design with two replications. A rep or a block had five sub-blocks; each sub-block had five entries. The plot size was 1.2m in width by 2.5m in length at both locations. The total area of the plot was 3m2. The distance between the sub-lock and the block was 1m and 1.5m. A plot had six rows 20cm apart. The seed rate is about 45g/3m2 and, Urea and NPS fertilizers are applied based on the area’s recommendation.

Data Collection and Analysis

The date of heading (DTH) obtained from the difference between the sowing date and the time when the flag leaf emerged by half on more than half of the plot. The date of maturity (DTM) calculated from the difference between the sowing date and physiological maturity. Data from thousand kernel weight, Hectoliter weight, and Grain yield electronically collected in Kulumsa wheat breeding Lab. Broad sense heritability (H^2) computed using a formula outlined by [5]

$$H^2 = \frac{Vg}{Vg + \frac{Ve}{r}}$$

Wherein Vg = genetic variance
Ve = environmental variance and
r = number of replications
All statistics computed using META- R statistical software [4]

Wheat stem rust and yellow rust data were collected but they were not used for this paper. Moreover, all agronomic practices implemented during growing season of the trail.

3. RESULTS AND DISCUSSION

The selection of genotypes for the development of varieties for different wheat-producing agroecology needs to examine traits from different breeding approaches to make an efficient selection. Selection for traits depends on the heritability of the characters. High heritability means the trait has a high response for selection. High heritability: For DTM H2= 0.94; For DTM= H2= 0.88; for HLW H2= 0.89; and for GYLD H2= 0.96 observed in the result and moderate heritability obtained for PHT H2= 0.77and for TKW H2= 0.77on tested bread wheat genotypes at Kulumsa (Table 1). The same result was reported by [7, 8]. But, for a trial conducted at Melkasa heritability were low for some traits: for DTM H2= 0.52; for PHT H2= 0.16; for TKW H2= 0.12; and for GYLD H2= 0.47(Table 2). The result for grain yield supported by [14]. These showed that the environmental impact on the phenotypical appearance of the trait is higher at Melkasa than at Kulumsa. Or the test population can express the genetic potential for traits at Kulumsa. Overall, the pressure of wheat stem rust disease at Melkasa was very high on the trial in the test year. Those susceptibly genotypes are highly devastated by wheat rust, while resistant genotypes resist the pressure. Thus, the magnitude of the environmental variation became large, which result in low heritability (Table 2).

Table 1. Broad sense heritability, Genotypic and residual variance, grand mean, LSD, CV, and level of genotypic significance for Different wheat traits tested at Kulumsa

Trait	**DTH**	**DTM**	**PHT**	**TKW**	**HLW**	**GYLD**
Heritability	0.94	0.88	0.77	0.77	0.89	0.96
Genotype variance	14.73	4.71	27.01	18.58	11.23	168437.20
Residual variance (environmental variance)	1.95	1.28	15.77	11.29	2.66	13791.13
Grand mean	69.50	124.56	89.20	27.28	64.19	1246.53
LSD	2.85	2.22	7.30	5.95	NA	248.50
CV	2.01	0.91	4.45	12.32	2.54	9.42
Genotype significance level	***	***	***	***	***	***

DTH=Date of heading; DTM=Date of maturity; PHT=plant height; TKW= thousand kernel weight; HLW=Hectoliter weight; GYLD= Grain yield; Genotype significance for the traits at: ns =non significance, *,**, and *** significant 5%, 1%, and 0.1% level of significance, consecutively.

Table 2. Broad sense heritability, Genotypic and residual variance, grand mean, LSD, CV, and level of genotypic significance for Different wheat traits tested at Melkasa

Trait	**DTH**	**DTM**	**PHT**	**TKW**	**HLW**	**GYLD**
Heritability	0.89	0.52	0.16	0.12	0.81	0.47
Genotype variance	12.62	1.31	2.47	1.87	4.29	18928.86
Residual variance	3.24	2.44	26.71	27.35	2.00	42422.60
Grand mean	52.02	91.26	78.20	31.64	63.58	1097.25
LSD	3.42	2.27	4.12	3.66	2.57	285.80
CV						
Genotype significance level	***	*	ns	ns	***	*

DTH=Date of heading; DTM=Date of maturity; PHT=plant height; TKW= thousand kernel weight; HLW=Hectoliter weight; GYLD= Grain yield; Genotype significance for the traits at: ns =non significance, *, **, and *** significant 5%, 1%, and 0.1% level of significance, consecutively.

Genotype variation in the population is one of the good opportunities for the breeder for selection among his materials. Genotypes selected from introduced trial from abroad interred into the observation nursery trials with genotypes from the crossing block of the national wheat research program. Observation nursery trial in the early stages for variety development that genotypes selected here passes through preliminary variety trial for one year and national variety trial for two years before selected as candidate variety to release. But sometimes, the program uses fast track variety development strategy where noble, elite genotypes are directly tested in a national variety trial from one year test as an introduction trial without testing in observation nursery trials and preliminary variety trials. Yield is a primary trait in selection genotypes besides disease resistance at nursery stages of trial in breeding pipelines. It is better to study the yield component traits in a population for indirect selection of yield. Therefore, variation among introduced genotypes for yield and yield components is a key to deciding the fate of the genotypes either to discard or to select and put in breeding trials of the program.

Higher genotype variation at Kulumsa obtained for: Date of heading 14.73, Date of maturity 4.71, Plant height 27.01, thousand kernel weight 18.58, Hectoliter weight 11.23, And grain yield 168437.20 (Table 1) compared to Melkasa (Table 2).Higher genotype variation made the heritability of the trait high. Because, the genotype variation is a numerator in heritability formula; and they are directly proportionals. Increase in genotype variance or decrease in residual/ environmental variance, increases the heritability. The trait has a chance to express itself phenotypically. Variation in heritability for the trait between the test locations was due to environmental variation between the two sites. Mainly, the moisture and the wheat stem rust affect the genotypic variance from potentially express at Melkasa compared to Kulumsa. Therefore, selection on Kulumsa's data is more reliable to exploit the real genetic potential of the population.

Table 3. Genotypic and phenotypic correlation between tested sites for different bread wheat traits

Traits	**DTH**	**DTM**	**PHT**	**TKW**	**HLW**	**GYLD**
Genotypic correlation	**0.95^{ns}**	**-0.54^{ns}**	**0.32^{ns}**	**0.84^{ns}**	**0.20^{ns}**	**-0.06^{ns}**
Phenotypic correlation	**0.87*****	**-0.37****	**0.11^{ns}**	**0.26^{ns}**	**0.17^{ns}**	**$-0,04^{ns}$**

DTH=Date of heading; DTM=Date of maturity; PHT=plant height; TKW= thousand kernel weight; HLW=Hectoliter weight; GYLD= Grain yield; ns =non significance, *,**, and *** significant 5%, 1%, and 0.1% level of significance, consecutively.

There was no significant genotypic correlation between Kulumsa and Melkasa for tested bread wheat traits in the population (Table 3). The two sites had a positive genotypic correlation for all traits, but Date of Maturity r=-0.54. Highly significant positive phenotypic correlation, was gained for the Date of heading r=0.87*** (Table 3). A negative and high significant phenotypic correlation r=-0.37** was found for the Date of maturity between the sites (Table 3). Although the two locations had no significant correlations for most of the traits there is a possibility to select both agroecology from this kind of introduced materials. The trial is in the early stages of breeding pipelines. So, the selection at both locations enables to group and further test the introduced genotypes to appropriate agroecology in advanced trials.

Table 4. Genotypic correlations below diagonal and phenotypic correlation above diagonal for wheat grain yield and yield components at Kulumsa

Traits	DTH	DTM	PHT	TKW	HLW	GYLD
DTH	1.00	0.56***	0.10	-0.17	-0.04	-0.18
DTM	0.65***	1.00	0.17	0.07	0.11	0.09
PHT	0.13	0.25	1.00	0.38**	0.19	0.51***
TKW	-0.16	0.11	0.56***	1.00	0.79***	0.86***
HLW	0.03	0.14	0.11	0.59***	1.00	0.84***
GYLD	-0.15	0.11	0.61***	0.96***	0.54***	1.00

DTH=Date of heading; DTM=Date of maturity; PHT=plant height; TKW= thousand kernel weight; HLW=Hectoliter weight; GYLD= Grain yield**;** *,**, and *** significant 5%, 1%, and 0.1% level of significance, consecutively.

The national bread wheat research program has an objective to improve wheat variety for yield, wheat rust disease resistance, and wheat quality. Genotype selection for grain yield can achived through directly selection for the trait or indirectly selection for its components. To do so, needs to study the correlation between grain yield and the yeild components. Grain yield had a negative non-significant genotypic correlation r=-0.15 with date of heading; Non-significant positive correlation r= 0.11 with date of maturity; highly significant positive correlations r= 0.61*** with Plant height; highly significant positive correlation r=0.96*** with Thousand kernel weight; and positive significant correlation r=0.54 with Hectoliter weight at Kulumsa (Table 4). The same results reported by different studies [11.12. and13]. These highly significant positive correlations told us the possibility of indirect selection for grain yield by selecting for the traits. The grain yield showed phenotypic correlation the same as genotypic correlations, a negative non-significant with date of heading and very highly significant with Plant height, thousand kernel weight, and Hectoliter weight (Table 4).

Table 5. Genotypic correlations below diagonal and phenotypic correlation above diagonal for wheat grain yield and yield components at Melkasa

Traits	DTH	DTM	PHT	TKW	HLW	GYLD
DTH	1.00	-0.42**	0.23	-0.22	-0.30*	-0.05
DTM	-0.51***	1.00	-0.45**	-0.24	-0.23	-0.48***
PHT	0.32*	-0.53***	1.00	0.26	0.33*	0.57***
TKW	-0.74***	-0.63***	0.99***	1.00	0.43**	0.50***
HLW	-0.42**	-0.10	0.52***	0.92***	1.00	0.68***
GYLD	-0.17	-0.33*	0.72***	0.99***	0.72***	1.00

DTH=Date of heading; DTM=Date of maturity; PHT=plant height; TKW= thousand kernel weight; HLW=Hectoliter weight; GYLD= Grain yield; *,**, and *** significant 5%, 1%, and 0.1% level of significance, consecutively.

Grain yield were negatively correlated phenotypically with the date of heading and date of maturity at Melkasa. The correlation values were: r= -0.17 between grain yield and date of heading and a significant correlation r=-0.33* between grain yield and date of maturity (Table 4) [10]. It showed that selection for late-maturing genotype is not acceptable if grain yield is our primary target in areas like Melkasa and moisture stress areas. Since Melissa is a drought-prone area, those genotypes with an early maturity group can escape the environmental influence that can come during the late growing period of the crop. Like Kulumsa, highly significant positive genotypic correlations r=0.72***, 0.99***, and 0.72*** were found between grain yield and plant height, between grain yield and thousand kernel weight, and grain yield and hectoliter weight successively. In addition, Grain yield had a very high significant positive correlation with: Plant height r=0.57***, thousand kernel weight r=0.50***, and hectoliter weight r= 0.68*** at Melkasa (table 5).

4. CONCLUSION

Selection for traits of interest is one of the major activities in the generating bread wheat varieties for different wheat-producing areas. The application of noble evaluation technics on genotypes selection leads to exploiting the best of the genetic potential for the trait intended. Grain yield have highly significant genotypic correlations with: Plant height, Hectoliter weight, and thousand kernel weights at both locations. Therefore, grain yield can improve through selection for these traits. The date of maturity had significant negative correlations and moderate heritability in the drought-prone area, Melkasa. Thus, looking for early maturing types of genotypes is essential in the development of variety for moisture stress areas.

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Conflicts of interests

The authors declare that there are no conflicts of interests.

Data and materials availability

All data associated with this study are present in the paper.

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