Correlation and Path Coefficient Studies on Advanced Bread Wheat Lines in Ethiopia

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Abstract: Grain yield is a complex quantitative trait which is influenced by a number of yield contributing traits. To improve grain yield in wheat, selection of genotypes should not only be based on grain yield alone, and the other grain yield components should also be considered. Twenty-three advanced bread wheat genotypes from the national wheat research breeding program; two released bread wheat varieties in Ethiopia; a total of twenty-five genotypes used in this study. The experiment was conducted in square lattice design with three replication over five locations for two consecutive years, in 2018 and 2019 main cropping seasons. The total experimental unit was 2.5m x 1.2m = 3m^2. Overall results from correlations showed a higher genotypic correlation than the corresponding phenotypic correlation for most of the traits. The genotypic correlation between Grain yield and Plant height (r_g=0.51**); between grain yield and thousand kernel weight (rg=0.73**); and between grain yield and hectoliter weight (r_g= 0.52**) are highly significant at (P<0.01) (table 3). The highest phenotypic correlation found between thousand kernel weight and grain yield (r_p=0.68**) followed by the phenotypic correlation between hectoliter weight and grain yield (r_p=0.57**) (Table 5). The date of maturity, Plant height, Thousand Kernel Weight, and HectoLiter Weight had a positive direct effect on Grain yield (table 4). In conclusion, to generate a new technology, a variety with improved grain yield, a breeder needs to apply indirect selection for yield components from an early stage, nurseries to sets of advanced yield trials in the breeding program.

Keywords: Wheat, Genotypic Correlation, Phenotypic Correlation, Direct Effect

1. Introduction

Wheat is one of the most important crops in Ethiopia. It is a staple food for millions of people in the country. The production is very high, which puts Ethiopia, the largest wheat producing country in sub-Saharan Africa. Wheat and wheat products represent 14% of the country's total calorie intake, which makes wheat the second-most important food crop in the country [19].

In Ethiopia, about 4.6 million farmers engaged in wheat production on their small-scale lands. In accumulate, around 1.8 hectares of land covered with wheat by these farmers and their production estimated about 5.0 million tons per annum. Despite the potential of the country, the productivity is very low which is lower than the world average 3.3 t/ha. This is mainly because of the productivity constraints, biotic and abiotic stress. Wheat rusts are among the major factors for low productivity of wheat in the country.

Grain yield is a complex quantitative trait which is influenced by a number of yield contributing traits. To improve grain yield in wheat, selection of genotypes should not only be based on grain yield alone, and the other grain yield components should also be considered. It is therefore, very important to know the relationship between grain yield and its component, and among the component themselves.

The relationship among different traits in wheat can be determined using genotypic and phenotypic correlation analysis. It is an effective tool for the enhancement of crop improvement for traits of interest [1-3]. The correlation coefficient among traits shows a complex chain of interacting relationships and the direction of the relationship. Whereas, Path coefficient analysis partitions the components of the correlation coefficient into direct

and indirect effects; and illustrates the relationship in a more meaningful way [5].

Path coefficient analysis provides a measure of the relative importance of each yield component to the estimation of changes in the grain yield. It is a standardized partial regression coefficient and as such measures the direct effect of one trait upon other and puts the separation of correlation coefficient into direct and indirect effects [7, 8]. And also, show the direct influence of independent variable upon dependent variable [9]. Plant breeders have been used path coefficient analysis in identifying noble genotypes for traits of interest through indirect selection for other traits rather than traits of interest itself [1, 7, 10, 11]. Hence, correlation coefficient studies and path analysis, together provide detailed information to identify important characters to be considered in improvement genotypes with traits of interest through selection.

The objective of this study was to look at the possibility of selection for yield components to improve grain yield through indirect selection of yield components in advanced bread wheat.

2. Material and Method

2.1. Materials, Designs, and Description of the Study Areas

Twenty-three advanced bread wheat genotypes from the national wheat research breeding program; two released bread wheat varieties in Ethiopia; a total of twenty-five genotypes used in this study. The two released bread wheat varieties; the checks: Daka, Moderately resistance variety for major wheat rusts; and, Ogolcho, which is recently become a susceptible variety for major wheat rusts used as checks in the experiment. The twenty-five genotypes set as National Variety Trial set II (NVTSETII) by the national wheat research program in 2018. The multi environmental trial was tested across five different research stations in the country. The experiment was conducted in square lattice design with three replication over five locations for two consecutive years, in 2018 and 2019 main cropping seasons. The total experimental unit was 2.5m x 1.2m = 3m². A plot of six rows with spacing of 20cm between rows was used.

Table 1. Agro ecological discerption of the experimental sites: Kulumsa, Arsirobe. Bokoji, Assasa, and Holeta.

Location	Altitude (m)	Representing Agroecology	Soil type	Rainfall	Temp.	
					Max (°C)	Min (°C)
Kulumsa	2200	Mid-altitude	Clay soil (luisols)	820mm	22.8	10.5
Arsi robre	2420	Water logged vertisoil	Heavy clay soil (vertisiol)	890mm	22.1	6.0
Bokoji	2780	Highland/haigh rainfall	Clay siol (nitosols)	1020mm	18.6	7.9
Assasa	2340	Terminal drought prone	Clay loam soil (gleysols)	620mm	23.6	5.8
Holota	2400	M2-5	Nitosols	1144mm	22	6

The distance between sub-blocks was 1m and between blocks was 1.5m. Urea and NPS fertilizers applied per recommendation 150kg/ha and 121 kg/ha respectively. And, Urea was split in two, 50kg/ha at planting and 100kg/ha at tillering stage.

2.2. Statistical Data Analysis

2.2.1. Analysis of Variance and Correlation Studies

The analysis of variance (ANOVA) for square lattice design performed for each variant using R-software version 4.0.1.

Genotypic correlation and phenotypic correlation were computed using R-software version 4.0.1 using the method described in [6] Genotypic and phenotypic variances and co-variances computed from ANOVA and ANCOVA were used to estimate genetic and phenotypic correlations among traits.

The formula used to compute genotypic and phenotypic correlation are

$$r_g = \frac{gcovx-y}{\sqrt{\sigma_{gX}^2 \sigma_{gY}^2}} = \text{and } r_p = \frac{pcovx-y}{\sqrt{\delta2px \cdot \delta2py}}$$

Where rg and rp are genotypic and phenotypic correlation coefficients, respectively; g cov x·y and pcovx · y are genotypic and phenotypic covariances between variables x and y, respectively; δ2gx and δ2px are genotypic and phenotypic variances, respectively, for variable x; and δ2gy and δ2py are genotypic and phenotypic variances, respectively, for variable y.

2.2.2. Path Coefficient Analysis

Path coefficient analysis was computed as suggested by [7] using phenotypic and genotypic correlation coefficients to know the direct and indirect effect of yield components on grain yield. It was obtained by solving the following simultaneous equations, which express the basic relationship between correlation and path coefficient.

$$r_{ij} = P_{ij} + \sum r_{rk}P_{kj}$$

Where r_{ij} represents the mutual relationship between the yield component i and grain yield j as measured by the genotypic correlation coefficients; P_{ij} refers to the components of direct effects of the grain yield component i on the grain yield j as measured by the path coefficients; and $\sum r_{ik}$ P refers to the summation of components of indirect effects of a given grain yield component i on a given grain yield j via all other grain yield components k.

The residual effect, which determines how best the causal factors account for the variability of the dependent factor, was calculated using the following formula.

$$1 = p^2r + \sum p_{iy}.r_{iy}$$

Where, P2r is the residual factor, Piy is the direct effect of yield by ith trait, and riy is the correlation of yield with the ith trait.

3. Result and Discussion

3.1. Analysis of Variance

The combined analysis of variance (ANOVA) revealed the presence of highly significant differences among the evaluated bread wheat genotypes for all parameters. The existence of variability among the genotypes in all parameters is very useful in plant breeding which is a tool for the selection of elite lines.

Table 2. *Genotype (G), environment (E), and GXE means squares for yield and yield components of twenty five bread wheat genotypes tested at optimum areas.*

Source of variation	DF	DTH	DTM	PHT	TKW	HLW	GYLD
Rep	2	36.2^{ns}	$9.2n^s$	88.8^{ns}	7.08^{ns}	3.34^{ns}	1.75^{ns}
Genotype (G)	24	159.9 ***	52.4**	331.4***	443.20***	57.45***	7.89***
environment (E) (Location: Year)	4	331.4***	7283.8***	8795.4***	1897.92 ***	233.58 ***	56.70 ***
Environment: Genotype (GXE)	96	20.8^{ns}	47.2***	40.5***	31.83 ***	7.58 ***	1.76 **
Pooled error	623	20.5	24.8	23.7	11.09	3.00	0.77

ns=nonsignificant; *,**, and *** significant 5%, 1%, and 0.1% level of significance, consecutively.

The analysis of variance (Table 2) showed that Very high significant difference among the genotypes at (P<0.001) for date of heading, Plant height, thousand kernel weight, hectoliter weight, and Grain yield. Also there is high significant differences at (P<0.01) for date of maturity.

Year and location, collectively referred to as environmental effect revealed very high significant differences for all measured traits at (p≤0.001) (Table 2). The very high significant Genotype by the environment, GXE interaction (P<0.001) were found for date of maturity, plant height, thousand kernel weight, and hectoliter weight. However, non-significant interaction was found for replication within the location; this is because all of the tested sites are plane, and no significant soil variation found on land where the experiment was laid. For grain yield, a highly significant difference at (P<0.01) was observed for GXE interaction.

3.2. Genotypic Correlation

The grain yield of wheat is a complex quantitative trait that is dependent on a number of its components. Knowing the inherent genetic relationship of the components enables the breeders to create a strategic plan for selection. Genotypic and phenotypic correlations indicate the relationship among the traits. The significant genotypic effects indicate the genetic variability among the genotypes and the possibility of genetic improvement in most of the traits.

Table 3. *Estimates of correlation coefficients at phenotypic (above diagonal) and genotypic (below diagonal) levels among six traits in advanced bread wheat lines in Ethiopia.*

Traits	DTH	DTM	PHT	TKW	HLW	GYLD
DTH	1.00	0.44**	0.21	0.02	-0.03	-0.28*
DTM	0.94**	1.00	0.29*	0.27*	0.16	-0.02
PHT	0.24	0.53**	1.00	0.47**	-0.02	0.43**
TKW	0.03	0.54**	0.51**	1.00	0.53**	0.68**
HLW	-0.01	0.42**	-0.02	0.52**	1.00	0.57**
GYLD	-0.35**	0.01	0.51**	0.73**	0.52**	1.00

Where;*=Significant at 0.05 probability level; **=Significant at 0.01 probabilitylevel; GYLD = Grain yield (t/ha); DTH = Date of heading, Days to 50% heading; DTM= Date of maturity, Days to 90% maturity; PHT= plant height (cm); TKW = Thousand kernel weight (g) and HLW = Hectoliter weight (kg/hl)

Overall results from correlations showed a higher genotypic correlation than the corresponding phenotypic correlation for most of the traits except between Date of heading and hectoliter weight; Between Hectoliter weight and thousand kernel weight; and between hectoliter weight and grain yield. This indicates that the association was largely due to genetic factors.

Most of the traits exhibited a positive genotypic correlation with grain yield except the date of heading (r_g=-0.35). The negative genotypic correlation between grain yield and days to heading was also reported by [12-15] Moreover, the genotypic correlation for most traits is highly significant which is possible to select the genotypes for grain yield by selecting for these traits. The genotypic correlation between Grain yield and Plant height (r_g=0.51**); between grain yield and thousand kernel weight (rg=0.73**); and between grain yield and hectoliter weight (r_g= 0.52**) are highly significant at (P<0.01) (table 3). The present study agrees with [16].

Generally, genotypic correlations among traits revealed a true association as they exclude the environmental influences. It is possible improvement in bread wheat grain yield through selection based on these correlations. Therefore, understanding the relationship between grain yield and yield components, and knowing the relationship among the yield component themselves, lead to do effective selection in wheat breeding programs.

3.3. Phenotypic Correlation

Like genotypic correlation, more traits resulted in a positive phenotypic correlation with grain yield except for the date of heading (r_p=-0.28) and date of maturity (r_p=-0.02). The highest phenotypic correlation found between thousand kernel weight and grain yield (r_p=0.68**) followed by the phenotypic correlation between hectoliter weight and grain yield (r_p=0.57**). Plant height also has a significant positive correlation (r_p=0.43**) at (p<0.05).

According to the above result, it is possible to improve total traits of interest through improvements of each component trait [18]. Grain yield is a quantitative trait which is governed by many gens. Hence, both phenotypic and genotypic correlations help in making reasonable decisions in

selecting traits controlled by multiple genes. Therefore, effective grain yield improvement depends on simultaneous selection for all yield components. This is because the selection and advancing genotypes based only for their potential in grain yield is not a fruitful strategy in wheat breeding program [15].

3.4. Path Coefficient

Plant breeders are able to divide direct and indirect effect attributable via path Coefficient analysis by partitioning the correlations. Results of path coefficient analysis of all other traits to grain yield at the genotypic level and phenotypic level are given in the table 4 and table 5 respectively. The diagonal and bold value tells us the direct effect of the other traits on the grain yield.

According to the present study: The date of maturity, Plant height, Thousand Kernel Weight, and HectoLiter Weight had a positive direct effect on Grain yield whereas, the Date of Heading had a negative direct effect at the genotypic level (table 4). The highest direct positive effect on grain yield exhibited by Date of Maturity (0.5885) but the genotypic relationship is nonsignificant (0.01) (table 4). In addition, the indirect effects of this trait is high. Hence, it is hard to improve the grain yield of bread wheat through selection for Date of maturity according to the present study.

Table 4. *Estimate of Direct (Diagonal) and indirect effect path coefficient at genotypic level for twenty five bread wheat advanced genotype.*

	DTH	DTM	PHT	TKW	HLW	rg
DTH	-0.9960	0.5547	0.0876	0.0039	-0.0023	-0.35**
DTM	-0.9338	0.5885	0.1915	0.0486	0.0786	0.01ns
PHT	-0.2434	0.3145	0.3583	0.0795	-0.0034	0.51**
TKW	-0.0251	0.3188	0.1824	0.1561	0.0964	0.73**
HLW	0.0124	0.2483	-0.0067	0.0808	0.1862	0.52**

Residual effect=0.251; DTH = Date of heading; DTM= Date of maturity; PHT= plant height; TKW = Thousand kernel weight; HLW = Hectoliter weight; rg=genotypic correlation.

Table 5. *Estimate of Direct (Diagonal) and indirect effect path coefficient at phenotypic level for twenty five bread wheat advanced genotype.*

	DTH	DTM	PHT	TKW	HLW	rp
DTH	-0.2911	-0.0726	0.0837	0.0073	-0.0111	-0.28*
DTM	-0.1288	-0.1641	0.1181	0.0866	0.0696	-0.02
PHT	-0.0603	-0.0479	0.4042	0.1484	-0.0105	0.43**
TKW	-0.0066	-0.0445	0.1880	0.3191	0.2251	0.68**
HLW	0.0076	-0.0268	-0.0100	0.1684	0.4264	0.57**

Residual effect= 0.281; DTH = Date of heading; DTM= Date of maturity; PHT= plant height; TKW = Thousand kernel weight; HLW = Hectoliter weight; rg=genotypic correlation.

The direct effects: for Plant height (0.5383); for thousand kernel weight (0.1561); for hectoliter weight (0.1862) are positive and the genotypic correlation for Plant height (rg=0.51); for thousand kernel weight (rg=0.73); and for hectoliter weight (rg= 0.52) are significant at (P<0.01). Moreover, the indirect effects for these traits; are negative and some are small. Thus, the correlation coefficient of this trait with grain yield was due to the direct effect. All the above results showed us the possibility of improving grain yield through these components. Similar finding reported on most of the trait in present study by [20, 21].

The phenotypic result for direct effects (table 5) revealed positive for Plant height (0.4042), thousand kernel weight (0.3191), and hectoliter weight. Whereas, the negative direct effects found for date of maturity (-0.1641) and date of heading (-0.2911).

The highest positive direct effect at the phenotypic level (0.4264) was observed for thousand kernel weight. The phenotypic correlation for the same trait is (0.57), which is positive and significant at (P<0.01). But, the levels of indirect effects for this trait; are very small positive values, and some are negative values (Table 5). Therefore, phenotypically by selecting for thousand kernel weight, it is possible to improve for grain yield.

The other positive direct effects at the phenotypic level found for Plant height (0.4042) and thousand kernel weight (0.3191). The phenotypic correlation for these traits (r_p=0.43 for plant height; r_p=0.68 for thousand kernel weight) are positive and significant which give wheat breeders confidence in improving grain yield through selecting for these traits.

4. Conclusion

Selecting and advancing genotypes from germplasm in breeding pipelines is a core activity in a wheat breeding program. Thus, a strategic and well-planned selection of these genotypes for traits of interest through indirect selection for its components is essential and a bridge for the success of any wheat breeding program. For this study, grain yield is a trait of interest that is highly linked with its component. It is a complex trait governed by many genes, and a direct selection for this trait is less effective. Thus, through indirect selection for plant height, thousand kernel weight, and hectoliter weight, any wheat breeding program can attain its goal regarding grain yield. Therefore, to generate new technology, a variety with improved grain yield, a breeder needs to apply indirect selection for yield components from an early stage, nurseries to sets of advanced yield trials in the breeding program.

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