

# Genetic Variability, Correlation and Path Coefficient Analysis of Bread Wheat (*Triticum aestivum* L.) Genotypes under Irrigation in Raya Azebo District, South Tigray

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DOI: <https://doi.org/10.5281/zenodo.10074538>

Published Date: 06-November-2023

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**Abstract:** Ethiopia has started to expand wheat production in the lowlands under irrigation to substitute wheat import, achieve wheat self-sufficiency and create jobs along the wheat value chain. The experiment was laid out in random complete block design with three replications to evaluate 20 bread wheat genotypes. A field experiment was undertaken to analyze the genetic variability, correlation and path coefficient analysis of yield and its contributing traits under irrigation. Analysis of variance showed highly significant differences ( $\leq 0.01$ ) among the genotypes for all the traits considered, which indicate the presence of adequate variability among the genotypes. The highest estimates of phenotypic coefficient of variation and genotypic coefficient of variation were observed for total tillers and effective tillers. Moderate phenotypic coefficient of variation and genotypic coefficient of variation were observed for grain yield, grain filling period and heading. High heritability values were recorded for days to heading and days to maturity, which indicating that the traits were least influenced by environmental factors. Among the traits higher values of genetic advance as percent of means were observed for total tillers, effective tillers and grain yield. Grain yield had positive genotypic and phenotypic correlation with number of kernels per spike and spike length, indicating that selection of genotypes based on high mean values for these traits could be used to improve wheat yield rather than selecting based on yield alone. Genotypic path coefficient analysis revealed that number of kernels per spike, total tillers and number of spikelets per spike had the highest positive contribution towards grain yield. Over all the results indicates that any genetic improvement on those traits might improve grain yield.

**Keywords:** Coefficients of Variance, Correlation, Genetic Advance as Percent of Mean, Heritability, Path Coefficient Analysis.

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## 1. INTRODUCTION

Wheat belongs to cereal grass Gramineae (Poaceae) family and the genus *Triticum*. Bread wheat (*Triticum aestivum* L.) is believed to be one of the first of the grains domesticated by humans since the Neolithic period ~ 10,000 years B.C., and to date it counts one of the most important cereal grain feeding the increasing world population and grows on more land area than any other commercial crops. It is grown in about 220.83 million hectares with annual production around 769.31 million tones (USDA, 2019). Bread wheat is widely cultivated in Ethiopia mainly under Rainfed conditions. Besides Ethiopia has a potential of 5.3 million hectares of land suitable for irrigated agriculture, however only less than 2% has been utilized to-date. Now a days the government of Ethiopia has started to expand wheat production in the lowlands using irrigation to substitute wheat import, achieve wheat self-sufficiency and create jobs along the wheat value chain. Hence, the productivity in irrigated conditions can be enhanced by the development of cultivars that are well adapted to irrigated conditions.

The magnitude of genetic variability present in a population is essential for effective genetic improvement. For genetic manipulation of grain yield, there is a need to examine the nature of genetic variability for the yield related trait. Various studies reported the existence of variability, heritability and genetic advance in bread wheat varieties (Donga *et al.*, 2022 and Garome *et al.*, 2022). Correlation and path coefficient analysis provide a better understanding of the association of different traits with grain yield. 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 (Majumder *et al.*, 2008). The grain yield was positively correlated with number of grains per spike, spike length, peduncle length, 1000 grains weight, biological yield per plot (Donga *et al.*, 2022). Tafesse (2022) found positive direct effect of days to maturity, plant height, thousand kernel weight and Hectoliter weight on grain yield. So far, few improved varieties and agronomic practices have been developed and promoted in the irrigated areas of the country. However, the importance of the crop in the irrigated areas is increasing as the area covered by wheat is increasing year after year. Thus, the study was aimed to determine the extent of genetic variability, heritability, genetic advance, genotypic and phenotypic associations among traits and to determine the direct and indirect effects of yield related traits on grain yield under irrigation.

## 2. MATERIALS AND METHODS

### Experimental Site, Plant Materials and Experimental Design

The study was conducted at southern Tigray at Mehoni Agricultural Research Center Fachagama testing site, which is 668 km from Addis Ababa, Ethiopia during off-season (2014). The testing site is located between 12°41' 50" to 12°41' 67" N latitude and 39° 42'08" to 39° 42'26" E longitude with an altitude of 1578 m.a.s.l. The soil types in the testing site are dominantly Vertisols and Fluvisols. The plant materials used in this study comprised of 20 bread wheat genotypes obtained from Worer Agricultural Research Center (Table1). The experiment was laid out in Random Complete Block Design with three replications and each experimental plot had six rows of 3m long spaced 30 cm apart with a plot area of 1.8 m x 3 m (5.4 m<sup>2</sup>) under Furrow irrigation at an interval of 10-15 days in early stages and 15-20 days in later stages. Seeds were drilled on the rows manually at a rate of 100 kg ha<sup>-1</sup>. Plants were fertilized with phosphorus 50 kg ha<sup>-1</sup> in the form of DAP and nitrogen 100kg /ha in the form of Urea. The DAP fertilizer was applied once at sowing time whereas the Urea was applied in split (half at sowing time and the remaining 50% at booting stages).

**Table 1: List of 20 bread wheat genotypes**

No	Genotypes	No	Genotypes
1	ADEL-6	11	QAFZAH-33/FLORKWA-2
2	SABA/FLAG-1	12	NABUR-6
3	NEJMAH-6	13	GA'AMBO
4	NEJMAH-14	14	UTIQUE 96/FLAG-1
5	GONGLASE-4	15	CROW,S,/BOW,S,-3-1994/95//TEVEE,S/TADINIA
6	SAAMID-3	16	DOUKKALA-4
7	ZAIN-6	17	SISABAN-3
8	MOONTIJ-3	18	DOUKKALA-35
9	SHABILL-2	19	GIZA- 168//SHUHA,S/DOBU,S,C,
10	NOUHA-4	20	SANDALL-3u

### Data Collected

Data were collected from the middle four central rows in each plot on plant and plot basis. Data were collected on Days to heading (DH), Maturity date (MD), Grain filling period (GFP) and Grain yield (YLD) at 12.5% moisture on plot basis, whereas Plant height (PH), Spike length (SL), Number of spikelets per spike (NSS), Number of kernels per spike (NKS), Total tillers (TT) Effective tillers(ET):were collected from 10 randomly selected plants.

### Data Analyses

Data of the 20 bread wheat genotypes were subjected to Analysis of variance using Proc GLM procedures of SAS 9.2 software. The expected mean squares from the analysis of variance were used to estimate the phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV), heritability (H<sup>2</sup>) and genetic advance (GAM) using Micro Soft Excel 2010 program. Genotypic and phenotypic correlation analysis was carried out using META-R software version 4. Path coefficient analysis was carried out using SAS 9.2 software.

### 3. RESULTS AND DISCUSSION

#### Analysis of variance and performance of genotypes

The analysis of variance (Table 3) exhibited highly significant ( $p \leq 0.01$ ) differences among the genotypes for all of the measured traits. This indicated the presence of considerable amount of variation in the genotypes which can help for further improvement in these traits.. Significant range of variation were observed among the genotypes, This suggested that sufficient level of genetic variability existed among the genotypes for set of traits studied and would respond positively to selection (Table 3). Grain yield ranged from (2.13–3.9 ton ha<sup>-1</sup>) with the mean value of 2.71 ton ha<sup>-1</sup>. Days to heading and maturity date ranged from 46-73 and 90-112 days respectively with a mean of 63 for days to heading and 102 for maturity date. Grain filling period ranged from 28-47 days with a mean of 39 days. Plant height and spike length ranged from 39-67cm and 5-8cm respectively with a mean of 51cm for plant height and 7cm for spike length. Total tillers and effective tillers ranged from 8-5 and 7-14 respectively with a mean of 11 for total tillers and 10 for effective tillers. Number of number of spikelets per spike and number of kernels per spike ranged from 10-16 and 2-3 respectively with a mean 13 for number of number of spikelets per spike and 2.4 for number of Kernels per spike. Such variations are very essential to develop varieties fitting to various agro-ecologies and cropping systems.

**Table 2: Means of genotypes for grain yield and its components**

No	Genotypes	GYL	HD	MD	GFP	PHT	TT	ET	SL	NSS	NKS
1	ADEL-6	2.53e-i	50.33h	91.00g	40.67b-e	47.33e-h	14.00abc	13.67a	5.13d	10.00f	2.67ab
2	SABA/FLAG-1	3.10bc	69.00bc	106.33bcd	37.33d-g	38.67h	11.00def	9.67d-g	8.33a	12.67b-f	2.00b
3	NEJMAH-6	2.77c-f	62.00e	90.33g	28.33h	50.00d-g	12.33b-e	11.00bcd	6.93bc	14.33abc	2.33ab
4	NEJMAH-14	2.70c-g	61.00ef	94.67fg	33.67fgh	46.00e-h	13.67abc	12.67ab	7.60abc	14.00a-d	2.67ab
5	GONGLASE-4	2.63d-h	57.00g	98.67ef	41.67a-d	48.33e-h	7.67h	7.00hi	7.07bc	11.67c-f	2.33ab
6	SAAMID-3	2.53e-i	64.00de	105.33bcd	41.33a-e	59.67a-d	9.67fgh	7.67f-i	8.00ab	13.33a-e	2.00b
7	ZAIN-6	2.30ghi	46.00i	92.67g	46.67a	45.00fgh	12.00b-f	9.67d-g	7.00bc	11.67c-f	2.67ab
8	MOONTIJ-3	2.83cde	61.00ef	106.00bcd	45.00abc	63.67ab	12.67a-d	10.67b-e	8.00ab	14.33abc	3.00a
9	SHABILL-2	3.90a	60.33efg	102.33de	42.00a-d	55.33b-e	13.00a-d	11.00bcd	8.00ab	12.67b-f	3.00a
10	NOUHA-4	2.33f-i	47.00hi	93.00fg	46.00ab	44.00gh	11.67c-f	9.00d-i	6.73c	11.33def	2.00b
11	QAFZAH-33/FLORKWA-2	2.40e-i	71ab	106.67a-d	35.67efg	45.00fgh	10.67d-g	10.00c-f	7.33abc	11.33def	2.00b
12	NABUR-6	3.60a	66.00cd	106.33bcd	40.33b-e	45.00fgh	10.00e-h	9.33d-h	7.67abc	15.00ab	2.67ab
13	GA'AMBO	3.47ab	64.00de	106.00bcd	42.00a-d	66.00a	13.67abc	12.33abc	8.00ab	15.00ab	3.00a
14	UTIQUE 96/FLAG-1	2.37f-i	58.00fg	91.33g	33.33gh	45.67e-h	8.00h	7.33ghi	8.00ab	12.00c-f	2.33ab
15	CROW,S,/BOW,S,-3-1994/95//TEVEE,S/TADINIA	2.40e-i	69.33abc	106.33bcd	37.00d-g	52.67c-g	7.67h	6.67i	7.67abc	13.33a-e	2.00b
16	DOUKKALA-4	2.20hi	73a	111.00ab	38.00d-g	60.33abc	15.00a	13.67a	7.00bc	13.33b-e	2.00b
17	SISABAN-3	2.13i	70.00ab	112.33a	42.33a-d	54.33b-f	14.33ab	13.00ab	7.67abc	14.33abc	2.33ab
18	DOUKKALA-35	2.57e-i	70.33ab	109.67abc	39.33c-f	66.67a	15.00a	13.00ab	8.00ab	16.00a	2.67ab
19	GIZA- 168//SHUHA,S/DOBU,S,C,	3.07bcd	66.00cd	105.33bcd	39.33c-f	47.00e-h	8.33gh	7.67fghi	7.00bc	11.00ef	2.00b
20	SANDALL-3u	2.33f-i	67.33bcd	104.67cd	37.33d-g	45.00fgh	8.33gh	8.33e-i	8.00ab	14.00a-d	2.67ab

#### Coefficient of Variances, Heritability and Genetic Advance

The estimates of coefficient of variances, heritability and genetic advance are presented in Table 3. The phenotypic coefficient of variance (PCV) values were higher than genotypic coefficient of variance (GCV) values for all the traits studied, that reflects the influence of environment on the expression of all the traits. The GCV and PCV were categorized as low (0-10%), moderate (10-20%) and high (> 20%) (Burton and devane1953) In this study, the values for PCV ranged from 7.6 % for maturity date to 25.63 % for effective tillers. GCV ranged from 6.8 % for maturity date to 21.21 % for effective tillers. High PCV and GCV values were observed for effective tillers (25.63 %, 21.21%), total tillers (24.72%, 20.61%) respectively, indicating better opportunity for improvement in these traits through selection. However grain yield (19.85%), plant height (18.43%), number of number of spikelets per spike (16.33%), grain filling period (13.46%), heading date (12.82%) and spike length (12.12%) had moderate PCV values. Besides GCV had moderate values for number of kernels per spike (18.67%), grain yield (17.02%), plant height (14.44%), heading date (12.31%) and grain filing period (10.24%).

Heritability and genetic advance are determining the success of selection in breeding programs. Singh (2001) classified heritability values as high (>80%), moderate (40-80%) and low (<40%). In view of that, heritability was high for heading date (92%) and maturity date (80%). High heritability indicated that the characters were least influenced by environmental factors. The results were in agreement with the findings of Sugandh *et al.* (2022) for heading date and Garome *et al.* (2022) for maturity date. Moderate heritability value was observed for grain yield (73%). It has been emphasized that without genetic advance, the heritability values would not be of practical importance in selection based on phenotypic appearance. So, genetic advance should be considered along with heritability in coherent selection breeding program. Genetic advance as percent of mean (GAM) was categorized as low (0-10%), moderate (10-20%) and high >20% (Johnson *et al.*, 1955). Among the traits higher values of genetic advance as percent of means were observed for total tillers (59.64%), effective tillers (36.22%) and grain yield (30, 99 %). Moderate values of genetic advance as percent of means were observed for grain filling period (18.70%), plant height (18.21%), kernel per spike (14.43%) and spike length (11.61%). Moderate heritability values coupled with high genetic advance was recorded for grain yield, which indicated that these characters can be considered as favourable for improvement through selection.

**Table 3. Mean square, heritability, coefficient of variances and genetic advance of 20 bread wheat genotypes**

Traits	MST	range	MEAN	PCV (%)	GCV (%)	H <sup>2</sup> (%)	GA	GAM
YLD	0.71**	2.13-3.90	2.71	19.85	17.02	73	0.84	30.99
HD	183.40**	46.00-73.00	62.63	12.82	12.31	92	5.81	9.27
MD	156.32**	90.33-112.33	102.00	7.60	6.80	80	9.61	9.43
GFP	60.56**	28.33-46.67	39.37	13.46	10.24	58	7.36	18.70
PH	198.99**	38.67-66.67	51.28	18.43	14.44	61	9.34	18.21
TT	19.09**	7.67-15.00	11.43	24.72	20.61	69	6.82	59.64
ET	16.09**	7.00-13.67	10.17	25.63	21.21	69	3.68	36.22
SL	1.58**	5.13-8.33	7.46	12.12	8.26	46	0.87	11.61
NSS	7.55**	10.00-16.00	13.05	16.33	9.41	33	0.37	2.82
NKS	0.42**	2.00-3.00	2.42	20.62	18.67	34	0.35	14.43

\*\*=Significant 1%, MST=Mean square of Treatment, GCV=genotypic coefficient of variance, PCV=phenotypic coefficient of variance, H<sup>2</sup>=heritability GAM=genetic advance as % of mean, YLD= Grain yield, DH =Days to heading, DM =Maturity date, GFP= Grain-filling period, PH =Plant height, SL= Spike length, NSS =Number of number of spikelets per spike, NKS Number of Kernels per spike, TT=Total tillers and ET= Effective tillers.

### Genotypic and Phenotypic Correlations of Yield and Its Components

The information regarding correlation among various traits is an important aspect for the initiation of any breeding program as it provides an opportunity for the selection of desirable genotypes having desirable traits. The phenotypic and genotypic correlation for all the characters is presented in Table 4. Grain yield had positive genotypic and phenotypic correlation with number of kernels per spike and spike length, indicating that selection of genotypes based on high mean values for these traits could be used to improve wheat yield rather than selecting based on yield alone. Sugandh *et al.* (2022) for number of kernels per spike and spike length and Tamiru (2022) for grain yield with spike length were reported which supports the present studies. Days to heading was positively correlated with maturity date, number of spikelets per spike, spike length and plant height, while it was negatively correlated with grain filling period and number of Kernels per spike at both genotypic and phenotypic level. Maturity date was positively correlated with days to heading, number of spikelets per spike, spike length and plant height at genotypic level. It was positively correlated with days to heading, plant height, number of spikelets per spike, spike length, effective tillers and total tillers at phenotypic level. The grain filling period exhibited negative genotypic and phenotypic correlation with days to heading, whereas it exhibited positive correlation with number of Kernels per spike and plant height. Plant height was positively correlated with all traits except for grain yield at genotypic and phenotypic levels. Total traits and effective traits were positively correlated with each other and with plant height, number of Kernels per spike and number of spikelets per spike at genotypic and phenotypic levels.

The highest genotypic correlation found between spike length and number of spikelets per spike followed by the genotypic correlation between days to heading and maturity date, grain yield and number of Kernels per spike and number of spikelets per spike with plant height Spike length was positively correlated with grain yield, plant height, number of Kernels per spike, days to heading, maturity date and number of spikelets per spike, whereas it was negatively correlated with total tillers and effective tillers at genotypic and phenotypic levels. Number of spikelets per spike had positive genotypic and phenotypic correlations with spike length, days to heading, maturity date, total tillers, effective tillers and number of Kernels per spike. These results were in agreement with the finding of (Tarkeshwar *et al.*, 2020) reported for spike length and number of kernels per spike. Number of kernels per spike had positive correlation with grain yield, number of spikelets per spike, plant height, total tillers, grain filling period, plant height, total tillers, effective tillers, spike length and number of spikelets per spike, whereas it had negative correlation with days to heading at both phenotypic and genotypic levels.

**Table 4. Genotypic (below diagonal) and Phenotypic (above diagonal) Correlation coefficients on traits in bread wheat**

Traits	GY	HD	MD	GFP	PHT	TT	ET	SL	NSS	NKS
GY	1	0.02	0.07	0.07	0.07	0.04	0.05	0.32	0.18	0.47
HD	0.05	1	0.80	-0.40	0.28	0.11	0.28	0.38	0.41	-0.20
MD	0.13	0.85	1	0.21	0.46	0.22	0.29	0.39	0.36	-0.05
GFP	0.14	-0.44	0.09	1	0.23	0.14	-0.02	-0.04	-0.13	0.25
PHT	0.03	0.32	0.54	0.32	1	0.52	0.47	0.26	0.57	0.38
TT	0.00	0.01	0.10	0.16	0.46	1	0.96	0.02	0.47	0.36
ET	0.00	0.12	0.13	0.00	0.37	0.97	1	0.05	0.53	0.37
SL	0.23	0.61	0.63	-0.09	0.27	-0.25	-0.33	1	0.50	0.39
NSS	0.16	0.68	0.65	-0.18	0.68	0.28	0.25	0.91	1	0.53
NKS	0.68	-0.29	-0.12	0.35	0.56	0.51	0.50	0.26	0.67	1

**Path Coefficient Analysis**

Plant breeders are able to divide direct and indirect effect attributable via path Coefficient analysis by partitioning the correlations. Estimates of direct and indirect effect are presented in Table 5 and 6. Number of kernels per spike exhibited the highest positive direct effect on grain yield followed by total tillers and number of spikelets per spike at genotypic path analysis level. These results were in agreement with the finding of Donga *et al* (2022), Tarkeshwar *et al* (2020) and Shahnawaz and Shailesh (2016) for number of kernels per spike. These results provided that those traits must be given preference in selection to superior genotypes. Effective tillers, plant height and spike length exhibited highest negative direct effect on grain at genotypic path analysis level. Total tillers, effective tillers and number of spikelets per spike exhibited the highest positive indirect effect on grain yield via effective tillers, total tillers and number of kernels per spike respectively (Table 5).

**Table 5. Direct effect (bold values) and indirect (off-diagonal) effects of traits on grain yield at genotypic level**

Traits	PHT	TT	ET	SL	NSS	NKS
Plant height	<b>-0.617</b>	0.458	0.595	0.145	0.252	0.68
Total tillers	-0.283	<b>1.00</b>	1.583	0.134	0.104	0.626
Effective tillers	-0.226	0.972	<b>-1.628</b>	0.175	0.09	0.614
Spike length	-0.169	-0.254	0.537	<b>-0.529</b>	0.333	0.317
Number of spikelets per spike	-0.423	0.285	-0.401	-0.48	<b>0.367</b>	0.815
Number of kernels per spike	-0.343	0.511	-0.817	-0.137	0.244	<b>1.224</b>

According to phenotypic path analysis, number of kernels per spike had the highest positive direct effect on grain yield. Indicating that, by phenotypically selecting number of kernels per spike it is possible to improve grain yield. Total tillers and spike length had also positive direct effect on grain yield, whereas number of spikelets per spike, effective tillers and plant height had negative direct effect on grain yield. All the studied traits at phenotypic path analysis had positive indirect effect on grain yield via number of kernels per spike (Table 6).

**International Journal of Novel Research in Interdisciplinary Studies**

 Vol. 10, Issue 6, pp: (1-6), Month: November – December 2023, Available at: [www.noveltyjournals.com](http://www.noveltyjournals.com)
**Table 6. Direct effect (bold values) and indirect (off-diagonal) effects of traits on grain yield at phenotypic level**

Traits	PHT	TT	ET	SL	NSS	NKS
Plant height	<b>-0.098</b>	0.034	-0.053	0.054	-0.057	0.190
Total tillers	-0.051	<b>0.066</b>	-0.107	0.004	-0.048	0.180
Effective tillers	-0.047	0.064	<b>-0.111</b>	0.011	-0.053	0.185
Spike length	-0.026	0.001	-0.006	<b>0.205</b>	-0.050	0.195
Number of spikelets per spike	-0.056	0.031	-0.059	0.101	<b>-0.100</b>	0.267
Number of kernels per spike	-0.037	0.024	-0.041	0.080	-0.053	<b>0.501</b>

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