Correlation and Path Coefficient Studies on Selected Agronomic Traits of Bread wheat (*Triticum aestivum* L.) genotypes at Korem, Northern Ethiopia

ABSTRACT

Comment [D1]: Design Blocks Randomized Complete

Correlations between quantitatively inherited plant characters and their direct and indirect effects on yield are decisive in plant breeding. To generate such information, a field study was conducted in 2014 cropping season at Ofla District, Northern Ethiopia. Twenty six bread wheat genotypes were planted using RCB design in three replications. Analysis of variance and genetic analyses were done for twelve quantitative traits. There were significant differences (P<0.05) among genotypes for 10 quantitative traits including yield. Yield ranged from 2.96 (Digalu) to 6.35 t ha^{-1}*(ETBW7888). Yield was positively correlated with number of productive tillers, number of kernels per spike and biomass. Biomass had strong and positive direct effect on yield, but number of tillers per plant and number of kernels per spike had low direct effect. Positive and strong genotypic and phenotypic indirect effect on yield via biomass suggested that selection on biomass would lead to increased of yield directly and selection on number of tillers per plant and number of kernels per spike indirectly via biomass. Conformation of this result is important as the result is from one year and one location.*

Keywords: Bread wheat, Correlation, Path Coefficient, Agronomic characters, Ethiopia.

INTRODUCTION

Comment [D2]: The summary needs to be brief and mention the superior numbers in the results and discussion .

Wheat (*Triticum* spp L.) is one of the small cereals used extensively in many parts of the world for the production of bread and many bakery products (1).

During 2013, wheat stands 4th both for area of production and total production next to maize, Sorghum and tef. Total area production and national average productivity during 2013 cropping season were 1627647 hectares and 2.10 tons ha $^{-1}$ respectively (2). Wheat import in Ethiopia is rising at an average of 9% annually while production is increasing at an average of 7% in the last decade (2). Thus, there is a need to balance the gap between the two by improving the productivity of the crop and this can be achieved through varietal development. Studying genetic variability for the characters of interest is the primary precondition for development of varieties (3).

Because of its complex nature selection for high yield is difficult. Yield is the end product of components of several polygenic inherited traits which are highly influenced by environment. Because of this, direct selection for yield resulted little progress. Hence, indirect selection through yield components is the best method and effective way of selection. Selection for yield based on highly correlated characters becomes easy if the contribution of different characters to yield is quantified using path coefficient analysis (4). Therefore, this study was initiated to estimate association of traits and the direct and indirect contribution of traits to yield.

Comment [D3]: source

2. METHODOLOGY

Study Site

An experiment was conducted at Ofla district, Awliegara research station, Souther Tigray, Ethiopia. Awliegara (39^{o}33'E and 12 ^{o}31'N) is located 160km South of Mekele and 620km North of Addis Ababa at an altitude of 2490 meters above sea level. The site receives 450-1200mm annual rain fall at main cropping season and 180-250mm at Belg (winter season). The mean annual temperature is 22^{o}C with minimum and maximum temperature of 6^{o}C and 30^{o}C, respectively. The soil type of the study site is clay (5). The genotypes were planted on the last week of July 2014.

Genotypes used for Experiment

Twenty three bread wheat genotypes which were under preliminary variety trial via: ETBW7870, ETBW7884, ETBW7862, ETBW7888, ETBW7881, ETBW7879, ETBW7868, ETBW7866, ETBW7889, ETBW7864, ETBW7891, ETBW7867, ETBW7875, ETBW7869, ETBW7874, ETBW7892, ETBW7887, ETBW7877, ETBW7880, ETBW7890, ETBW7873, ETBW7882 and three released variety (Hidase, Danda'a and Digalu) were included in the experiment.

Design of the experiment

The RCB design with 3 replications was used. A seed rate of 45gm plot^{-1} based on the national seed rate recommendation of 150kg ha^{-1} was used for each genotype. Plot size was 2.5m length with 1.2m width. 20cm was a space used between rows. The spacing between plots and replications were 0.5m and 1.5m, respectively. The source of P_2O_5 and N were DAP and Urea respectively with application rate of 100kgha^{-1} for both.

Data Collection and Analysis

Data collection was made both from plot basis and plant basis. Analysis of variance was made using the procedures outlined by (6). The RCBD analysis of variance was also used to derive variance components as presented by (7).

Estimation of genotypic and phenotypic correlation coefficients was done based on the procedure of (8). The calculated phenotypic correlation values were tested for statistical significance using the students' t-test (9). The coefficients of correlations at genotypic levels were also tested for statistical significance by the formula described by (10). The path coefficient analysis was computed using the formula of (4) and with statistical package developed by (11). The residual factor (P^2R) was also estimated as described in (4).

RESULTS AND DISCUSSION

Analysis of Variance

There was significant ($P<0.01$) differences among genotypes for all characters considered except for plant height and number of spikelets per plant (table 1).

It is suggested from the result that the genotypes tested had significance variations for ten of twelve traits studied. The result also showed presence of ample scope of selection for different quantitative characters for the improvement of the crop and the need to undertake further genetic analysis on the genotypes.

Table 1. Mean squares of 12 parameters of 26 bread wheat genotypes tested at Korem in 2014

Parameters	Replication (2)	Genotype (25)	Error (50)	CV (%)
Days to heading	7.54^{**}	38.27^{**}	1.45	2.10
Days to maturity	26.32^{ns}	135.02^{**}	8.61	2.57
Grain filling period (days)	5.86^{**}	52.45^{**}	7.05	4.65
Tillers per plant	0.32^{ns}	0.55**	0.48	31.68
Plant height (cm)	34.44ns	53.68ns	47.83	7.97
Spike length (cm)	0.20^{ns}	1.08^{**}	0.28	7.22
Number of spikelets per spike	6.61^{**}	3.82^{ns}	0.95	7.17
Number of seeds per spike	17.80^{ns}	54.68^{**}	17.98	10.60
Thousand seed weight (g)	57.64^{ns}	223.94^{**}	67.70	10.25
Biomass(t ha^{-1})	1.99^{ns}	17.47^{**}	7.72	27.06
Yield (t ha^{-1})	0.97^{ns}	2.23^{*}	1.08	24.44
Harvest index (%)	14^{ns}	36.27^{**}	9.67	7.38

*, **= significant ($P<0.05$) and highly significant ($P<0.01$), respectively. ns = no significant difference at $P<0.05$. Numbers in bracket refers to degrees of freedom.

Genotypic and Phenotypic Correlation Coefficients

Correlation coefficient of yield with other Parameters

Yield showed positive and highly significant ($P<0.01$) genotypic correlation with biomass ($r_g=0.90$). Therefore, any improvement of this character would result in a substantial increase in yield. This result is substantiated with those of (12) and (13) who reported positive and highly significant genotypic correlation of yield with biomass. Besides, yield had positive and non-significant genotypic correlation ($r_g=0.1$ to 0.34) with grain filling period, number of tillers per plant, spike length, number of kernels per spike and thousand kernel weight. This suggested that improvement of these traits would not affect the increment of yield. This is in agreement with the report by (13).

Yield showed positive and highly signifcant ($P<0.01$) phenotypic association with number of tillers per plant ($r = 0.46$) and biomass ($= 0.91$). It had significant ($P<0.05$) and positive phenotypic correlation with spike length, number of kernels per spike and days to heading with correlation coefficient in the range between 0.25 and 0.26. This suggests that these traits should be given prime importance regarding its contribution to yield. Other authors also reported positive and signifcant phenotypic association of yield with number of tillers per plant, spike length and number of kernels per spike (14; 15; 16).

Yield and days to heading showed negative and significant correlation. The negative association of the traits may be due to late set of rainfall, which was a month later than the usual in the study area. This indicated that selection of genotypes for delayed days to heading might reduce yield. (13) also revealed negative phenotypic correlation of yield with days to heading for bread wheat genotypes tested in moisture deficit condition. This result contradicts with the result reported by (17). This might be attributed to the optimum area of the study site, where late heading genotypes might have been favored for yield.

Correlation coefficient of biomass with other traits

Biomass had negative and high significant genotypic correlation with harvest index (r_g=-0.52) (Table 2), suggesting that selection of genotypes for high biomass might lower harvest index. The rest of other traits had weak genotypic correlation with biomass and their correlations were not significant. This is consistence with finding by (18) indicated insignificant genotypic correlation of biomass with days to heading and days to maturity.

At phenotypic level, biomass correlation coefficients were positive and highly significant with number of fertile titters per plant (r=0.47) and spike length (=0.31) (Table 2). Genotypes which had high biomass also had high number of fertile tillers per plant and longer spike length. These correlation coefficient results re-emphasizes suggested the importance of these traits to biomass. Similarly, (13) reported positive and significant phenotypic correlation of biomass with spike length. (12) also indicated highly significant and positive phenotypic correlation of biomass with number of fertile tillers per plant and with spike length.

Estimates of correlation coefficients among other agronomic characters

Days to heading had positive and significant genotypic association with days to maturity and with grain filling period. Similarly, days to maturity exhibited positive and significant association with grain filling period. Both days to maturity and grain filling period had positive but no significant association with other traits except with spike length, days to maturity, and harvest index where these traits exhibited negative correlations. Spike length and harvest index each other and both with number of kernels per spike showed positive non-significant genotypic associations (Table 2). The result justifies that, early heading genotypes had a probable short grain filling period and mature early without affecting most of growth traits except that with the probability of reduction spike length and harvest index. Similar results were also reported by (19; 20; 18) where days to heading with days to maturity on bread wheat were significantly associated.

Table 2. Estimate of Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients estimation for 10 traits of bread wheat genotypes grown at Korem in 2014

Traits	DH	DM	GFP	NT	SL	NKS	TSW	BY	HI	GY
DH	1	0.84**	0.49*	-0.13	0.07	0.02	0.01	-0.13	-0.33	-0.33
DM	0.80**	1	0.89**	0.17	-0.05	0.08	0.05	0.02	-0.18	-0.11
GFP	0.43**	0.88**	1	0.38	-0.13	0.1	0.07	0.14	0.00	0.11
NT	-0.04	0.13	0.24*	1	-0.07	-0.24	-0.27	0.38	-0.12	0.34
SL	0.05	0.01	-0.03	0.20	1	0.26	0.29	0.12	-0.1	0.1
NKS	-0.04	0.02	0.06	0.03	0.2	1	0.99**	0.16	0.03	0.19
TSW	-0.04	0.00	0.03	0.01	0.09	0.98**	1	0.12	0.02	0.14
BY	-0.12	0.06	0.18	0.47**	0.03	0.22	0.18	1	-0.52**	0.90**
HI	-0.26*	-0.16	-0.04	-0.07	0.47	-0.01	0.00	-0.45**	1	-0.11
GY	-0.26*	-0.04	0.15	0.47**	0.01	0.25*	0.21	0.91**	-0.07	1

*, **= significant ($P<0.05$) and highly significant ($P<0.001$), respectively computed using standard linear Pearson correlation, DH=Number of days to heading, DM= Number of days to maturity, GFP= Number of days for grain filling, NT=Number of tillers per plant, SL=Spike length(cm), NKS= number of kernels per spike, TKW=Thousand kernel weight(g), BY=biomass (tone per hectare), GY=yield (tone per hectare), HI=Harvest index.

(21) Indicated weak genotypic correlation for tillers per plant with spike length, number of kernels per spike, harvest index and 1000 kernel weight. This is in agreement with this result. The genotypic correlation of 1000 kernel weight with number of kernels per spike is positive and highly significant which is in agreement with the result of (16). On the other hand, (21) showed no significant correlation of 1000 kernel weight with number of kernels per spike and no significant genotypic correlation for 1000 kernel weight with the rest of the other studied traits.

At phenotypic level, days to heading, days to maturity and grain filling period had positive and significant correlation with each other. Coefficient of correlation for days to heading with harvest index was significant and negative. Harvest index also showed insignificant and negative correlation with days to maturity and grain filling period. i.e., early heading genotypes had higher harvest index than the late heading genotypes.

For grain filling period, phenotypic correlation with number of fertile tillers per plant was positive and significant. This indicates genotypes with high grain filling period had higher number of tillers and vice verse. Phenotypic correlation coefficients of spike length with number of kernels per spike, harvest index, 1000 kernel weight, and number of tillers per plant are positive and non significant. This is partially in agreement with (21) who reported no significant positive correlation of spike length with number of kernels per spike, 1000 kernel weight, but negative and significant correlation with number of fertile tillers per plant.

Path-coefficient Analysis

Phenotypic path coefficient analysis of yield with other traits

Biomass exerted highest and positive direct effect on yield with positive and high significant phenotypic correlation. The indirect effects were negligible (Table 3). This showed that the correlation with yield was largely due to the direct effect. Therefore, direct selection through this trait will improve yield. This result is substantiated by the study on bread wheat by (12). In addition, (22) and (23) also reported similar findings on durum wheat, where high phenotypic correlation coefficient of biomass was exerted by its direct effect.

Days to heading correlated significantly and negatively with yield and exerted negative direct effect and it has also negative indirect effects through biomass and harvest index. Therefore, the phenotypic correlation of this trait with yield was due to both the direct effect and the indirect effect through biomass and harvest index. Therefore, whenever selection is made for improving yield, days to heading accompanied by biomass and harvest index should be considered.(24) also reported negative correlation of days to heading with yield resulted from both the direct and indirect negative effects.

Number of tillers per plant and number of kernels per spike exerted positive, but negligible phenotypic direct effect on yield. On the other hand, they exerted positive and high indirect effect on yield through biomass. Therefore, the observed highly significant phenotypic correlations of these traits with yield were due to the indirect effects through biomass. This suggested that selection of genotypes for high performance of number of fertile tillers per plant and number of kernels per spike may improve yield of bread wheat through the increased biomass, but these traits themselves cannot be regarded as a reliable source of getting high yield in bread wheat. Therefore, selection for high number of tillers per plant and number of kernels per spike cannot guarantee for high yield. Similarly (12) showed weak direct effect of number of fertile tillers per plant on yield, but high indirect effect through biomass.

Table 3 Direct (underlined diagonal) and indirect (off diagonal) effects of traits on yield at phenotypic level in 26 bread wheat genotypes tested at Korem (2014)

Traits	DH	DM	GFP	NT	SL	NKS	TSW	BY	HI	r_p
DH	**-0.13**	0.20	-0.09	0.00	0.00	-0.00	0.00	-0.13	-0.11	-0.26*
DM	-0.10	**0.25**	-0.17	-0.00	0.00	0.00	0.00	0.05	-0.07	-0.04
GFP	-0.05	0.22	**-0.20**	-0.01	-0.00	0.01	-0.00	0.20	-0.02	0.15
NT	0.01	0.03	-0.05	**-0.04**	0.00	0.00	-0.00	0.51	-0.03	0.47**
SL	-0.01	0.00	0.01	-0.01	**0.02**	0.02	-0.02	0.34	-0.07	0.01
NKS	0.01	0.01	-0.01	-0.00	0.01	**0.08**	-0.07	0.24	-0.00	0.25*

TSW	0.01	0.00	-0.01	0.00	0.01	0.08	**-0.07**	0.20	0.00	0.21
BY	0.02	0.01	-0.04	-0.02	0.01	0.02	-0.01	**1.09**	-0.20	0.91**
HI	0.03	-0.04	0.01	0.00	-0.00	-0.00	0.00	-0.49	**0.44**	-0.07

Residual = 0.056, r_p=phenotypic coefficient of correlation.

Days to maturity and harvest index exerted positively high direct effect on yield, while their indirect effect through grain filling period and biomass respectively were negatively high. So their direct effects were counter balanced by the indirect effects. Hence, the correlation of these traits remained non significant. This suggested that selection of late mature genotypes may not result to increased yield since they increase for biomass and harvest index which were negatively correlated with yield.

Grain filling period and thousand kernel weight had negative direct effect on yield. On the other hand, their coefficient of correlation was positive and non significant. This is because the direct effects were counter balanced by the indirect effects through days to maturity and biomass for grain filling period and through biomass for thousand kernel weight. When selection is made in favor of these traits, yield is disfavored directly. On the other hand, days to maturity favored and biomass disfavored which had positive association with yield are favored. So that, the negative direct effect is counterbalanced. However, the results of the current study contradicted with the findings of (16).

Residual effect in the present study was 0.056 (Table 3), showing that 94.4% of the variability in yield was explained by the component factors. The remaining 5.6% is explained by other traits not considered in this study. This further elucidated that yield attributing traits chosen for the study of the bread wheat genotypes were good.

Genotypic path coefficient analysis of yield with other traits

The results of genotypic path coefficient analysis of yield with other traits were presented in Ttable 4. The maximum positive genotypic direct effect on yield t ha^{-1} was exerted by biomass ha^{-1} (1.17) followed by harvest index (0.54), days to maturity (0.13). Traits with highly negative direct effects on yield were grain filling period (-0.16), days to heading (-0.05) and number of tillers per plant (-0.04). Other traits' direct effects were insignificant.

Biomass that had positive and highly significant ($P<0.01$) genotypic correlation coefficient with yield ($r = 0.91$) had the highest direct effect on yield. It had also negative indirect effect via harvest index. The result suggested that selection of genotypes with high biomass will lead to improvement of yield, but its negative indirect effect via harvest index need to be handled wisely. This result is in line with the finding of (23) on durum wheat. Harvest index and days to maturity exerted high and positive direct effect on yield. On the other hand, they had negative indirect effect via biomass and grain filling period respectively. Therefore, the genotypic correlations they had was negative and non significant because of the counter balancing of the direct effects with indirect effect. This result is in opposite to the finding of (18) who stated the negative direct effect and negligible indirect effect through biomass on yield by harvest index and days to maturity. The result suggested that selection of genotypes for high performance of these traits might not effective when the breeding objective is selection of genotypes for higher yield.

Residual effects from genotypic path analysis was 0.116 (Table 4), indicating that all the traits included in the study explained high percentage of variation in yield t ha^{-1} (88.6%); other factors not included in the study can explain only 11.4%. so that, yield components used were good.

Table 4 Direct (underlined and diagonal) and indirect (off diagonal) effects of traits on yield at genotypic level in 26 bread wheat genotypes tested at Korem (2014)

Traits	**DH**	**DM**	**GFP**	**NT**	**SL**	**NKS**	**TSW**	**BY**	**HI**	**r_g**
DH	**-0.05**	0.11	-0.08	0.01	0.00	0.00	0.00	-0.15	-0.18	-0.33
DM	-0.04	**0.13**	-0.14	-0.01	-0.00	-0.00	-0.00	0.02	-0.10	-0.11
GFP	-0.02	0.12	**-0.16**	-0.02	-0.00	-0.00	-0.00	0.16	0.00	0.11
NT	0.01	0.02	-0.06	**-0.04**	-0.00	0.00	0.01	0.45	-0.06	0.34
SL	-0.00	-0.01	0.01	0.00	**0.02**	-0.00	-0.01	0.14	-0.05	0.10
NKS	-0.00	0.01	-0.02	0.01	0.01	**-0.01**	-0.03	0.19	0.02	0.19
TSW	0.00	0.01	-0.01	0.01	0.01	-0.01	**-0.03**	0.14	0.01	0.14
BY	0.01	0.00	-0.02	-0.02	0.00	-0.00	-0.00	**1.17**	-0.28	0.90**
HI	0.02	-0.02	0.00	0.01	-0.00	0.00	-0.00	-0.61	**0.54**	-0.11

Residual = 0.116, r_g=genotypic coefficient of correlation.

CONCLUSION AND RECOMMENDATIONS

Twenty six bread wheat genotypes were tested in RCBD at Ofla district, South Tigray, Ethiopia in 2014. Among the tested genotypes there was no significant difference only for two of the twelve traits considered. Yield showed positive and signifcant correlation with biomass both at genotypic and phenotypic levels and negative significant correlation with days to heading. The glance of the correlation coefficient results indicated the prime importance of considering these traits and selection based on these.

Phenotypic path coefficient analysis showed posetive direct effect of biomass, harvest index and days to maturity on yield. However, grain filling period and days to heading had negative direct effect on yield. The remaining traits had neither direct nor indirect effects on yield at phenotypic level.

Biomass and days to maturity had positive and high significant phenotypic correlation with yield exerted by direct effect. Days to heading had negative and high significant phenotypic correlation exerted by the direct effect. Thus, Direct selection through biomass and days to heading will be effective for yield improvement, but number of tillers per plant, thousand kernel weight and plant height had high significant correlation exerted by the indirect effect through biomass. Therefore, indirect selection for those traits through biomass is recommended. At phenotypic level, spike length and number of kernels per spike had positive indirect effects on yield mainly through biomass. Therefore, spike length and number of kernels per spike together with biomass should be considered simultaneously in breeding programme designed to improve yield. While negative indirect effects can be reduced by using careful breeding strategies. Biomass had positive and highly significant genotypic correlation with yield due to its direct effect. Thus, selection of genotypes for yield based on biomass is effective.

REFERENCES

1. Fincher, G. B. and Stone, B. A. 1986. Cell wall and their components in cereal gain technologies pp. 207-295. In Pomeranz, Y. Advances in cereal science and technology. St. Paul, MN: American Association of cereal chemists.
2. Central Statistical Agency (CSA), 2013. Agricultural sample Sample survey 2013. Report on crop and livestock product utilization. Statistical bulletin. Addis Ababa, Ethiopia.
3. Scossiroli, R. E., Ferrari, A. and Haussmann, G. 1963. Genetic variability for quantitative characters in Alfalfa. pp.597-608.
4. Dewey, D. R. and Lu, K.H. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*, 51: 515-518.
5. Teklay Abebe, Kiros Meles, Yemane Nega, Hadas Beyene and Abrha Kebede. 2013. Interaction between broomrape (*Orobanche crenata*) and resistance faba bean genotypes (*Vicia faba* L.) in Tigray region of Ethiopia. *Canadian Journal of Plant Protection*. 1 (3):104-109.
6. 6. Gomez, K.A. and Gomez, 1984. Statistical Procedures for Agricultural Research 2nd ed. John Wiley & Sons. New York, p680.
7. Cochran, W. G. and Cox, M. 1957. *Experimental designs*. John Wiley and Sons, Inc, New York. p611.
8. Dabholkar, A.R., 1992. *Elements of biometrical genetics*. Concept Publishing Company, New Delhi, India, p431.
9. Sharma, J. R. 1998. *Statistical and biometrical techniques in plant breeding*. New Age International (P) limited, publishers. New Delhi. P432.
10. Robertson, G.E., 1959. The sampling variance of the genetic correlation coefficient. *Biometrics*. 15: 469-485.
11. Doshi, S.P. 1991. Statistical Package for Agricultural Research SPAR. IASRI, New Delhi.
12. Bagrei, B., and Bybordi, B. 2015. Yield and yield components in bread wheat (*Triticum aestivum* L.) under non-stress and drought stress conditions. *International Journal of Biosciences*, 6(3):338-348.

13. Ahmadi, M., Farshadfar, E. and Veisi, S. 2012. Evaluation of Genetic Diversity in Land races of Bread Wheat under Irrigated and Rain fed Conditions. *International Journal of Agriculture and Crop Sciences*, 4(21):1627-1636.
14. Kalimullah, Khan,S., Irfaq, M. and Rahman, H. U. 2012. Gentetic variability, correlation and diversity studies in bread wheat (*Triticum aestivum* L.) germplasm. *The Journal of Animal & Plant Sciences*, 22(2): 330-333.
15. Mohsin, T., Khan, N. and Nasir, N. F. 2009. Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. *Journal of Food, Agriculture & Environment.*7 (3):278-282.
16. Iftikhar, R., Khaliq, I., Ijaz, M., and Abdul, M. R. R. 2012. American-*Eurasian Journal of Agriculture and environmental Science*, 12 (3): 389-392.
17. Subuhan, G.M., and Chewdrhy, M.A. 2000. Correlation and path coefficient analysis in bread wheat under drought stress and normal condition. *Pakistan Journal of Biological Science*, 3(1): 72-77
18. Kumar, B., Singh, C. M., Jaiswal, K. K. 2013. Genetic variability, association and diversity Studies in Bread Wheat (*Triticum aestivum* L.). *The bios can*, 8(1): 143-147
19. Degewione and Alamerew. 2013. Genetic Diversity in Bread Wheat (Triticum aestivum L.) Genotypes. *Pakistan Journal of Biological Science*, DOI:10,3923/pjbs.2013
20. Ali, S., Mehar, S.A., Hassnain, A., Shah, Z., and Munir, I. 2007. Genotypic Variation for Yield and Morphological Traits in Wheat. *Sarhad Journal of Agriculture*, 23(4):943-946
21. Hafiz, K.M., and Nayeem, D. A., 2010. Correlation and Path Coefficient Analysis of Some Quantitative Traits in Wheat. *African Crop Science Journal*, 18(1):9 – 14
22. Dawit Tsegaye, Tadesse Dessalegn, Yigzaw Dessalegn and Getnet Share. 2012. Genetic variability, correlation and path analysis in durum wheat germplasm (*Triticum durum* Desf). *Wudpecker Research Journals*, 1(4): 107 – 112
23. Abderrahmane, H., Zine, F. E., Hamenna, B. and Ammar, B. 2013. Correlation, Path Analysis and Stepwise Regression in Durum wheat (*Triticum durum* Desf.) under Rainfed Conditions. *Journal of Agriculture and Sustainability*, 3(2): 122-131.
24. Mohammadi, M., Sharif, P., Karimizadehi, R., Shefazadeh, K. 2012. Relationships between Yield and Yield Components in Bread Wheat under Different Water Availability. *Horticulture Agro-botany*, 40(1):195-200