Journal of Genetics, Genomics & Plant Breeding **4(1) 9-19 (January, 2020)**
ISSN (Online): 2581-3293

RESEARCH ARTICLE

Variability and association studies among the sorghum genotypes for seed yield and yield related traits under rainfed condition of Ethiopia

Ambachew Tefera

Sirinka Agricultural Research Centre, P.O. Box 74, Weldia, Ethiopia

Present working address: Bahirdar University, P.O.Box, 5501, Zenzelma, Ethiopia

Corresponding authors email Id: ambachewtefera@gmail.com

Manuscript received: November, 7, 2019; Decision on manuscript, November 26, 2019; Manuscript accepted :December 9, 2019

Abstract

The experiment was conducted under rain fed condition at Cheffa testing site of Sirinka Agricultural Research Centre in South Wello, Ethiopia with 49 sorghum [*Sorghum bicolor* (L.) Moench] genotypes during 2018 using simple lattice design with two replications to assess the association, direct and indirect effect of different characters on yield. There were statistically significant differences among the genotypes. Grain yield had highly significant positive phenotypic and genotypic correlation with thousand seeds weight, grain filling period and harvest index. Path coefficient analysis showed that among the eight independent traits: thousand seeds weight, head yield per plant, grain filling period, plant height and harvest index had positive direct effects on grain yield at both genotypic and phenotypic levels. Generally, correlation coupled with path coefficient analysis revealed that thousand seeds weight, grain filling period and harvest index had a direct relationship with seed yield and were found to be important yield components that can be used to improve the yield potential of sorghum.

Key words: Correlation, phenotypic, genotypic, seed yield, sorghum

Introduction

Sorghum (*Sorghum bicolor (L.)* Moench) 2n =2x =20 belongs to the genus Sorghum, tribe Andropogoneae, and family Poaceae.The species *Sorghum bicolor* includes all cultivated sorghums as well as a group of semi wild and wild plants regarded as weeds (Mutegi *et al.*, 2011). Based on the morphological features of the inflorescence, grain and glumes, cultivated sorghum has been classified into five races: bicolor, caudatum, durra, guinea and kafir (Harlan and De Wet, 1972). Very high levels of diversity exist among and within the races (House, 1985). The diversity in sorghum ensued mainly by practising disruptive selection and isolation, recombination in the extremely varied habitats and movement of people carrying one or more cultivars of the species (Doggett *et. al.*, 1970). A balance of farmer selection for cultivated traits and natural selection for wild characteristics has generated improved sorghum types, wild types and intermediate types (Doggett *et. al.*, 1970).

Sorghum is a principal source of energy, proteins, vitamins and minerals for people in the semi-arid tropics (Duodu *et. al.*, 2003). It is a good energy source because it is about 70% starch. Proteins are the main constituents of sorghum after starch, making up to 12% dry weight of sorghum grain (Ng'uni *et. al.*, 2012). The essential amino acid profile of sorghum protein differs 3-12% range between varieties, soil and growing conditions. The digestibility of sorghum protein has also been found to vary between varieties, ranging from 30 to 70%. Sorghum's nutritional profile includes several minerals, though unevenly distributed and more concentrated in the germ and seed coat. Sorghum is a good source of the β-complex vitamins and some varieties contain B carotene which can be converted to vitamin A by the human body. Some fat-soluble vitamins like D, E and K have also been detected, though not in sufficient amount.

Genetic variability is essential in plant breeding programs to develop crop cultivars with improved genetic constitution to serve diverse human needs. Genetic diversity encompasses variations in nucleotides, genes, chromosomes or whole genomes of individuals. The most common sources of genetic diversity include landraces, modern cultivars, obsolete or primitive cultivars, wild or semi-wild related species. Genetic analyses help to determine the variations present among individuals, populations or groups of genetic resources for breeding and strategic conservation.

The improvement in sorghum productivity is the result of a combination of improved varieties and improved management practices. The use of hybrid cultivars as well as improved management practices has been instrumental in the yield increases that have been achieved in many developed and a few developing countries (Kumar *et. al.*, 2011).

The low productivity in sorghum is due to frequent moisture stresses encountered during crop growth, as crop being grown mainly on residual soil moisture. Further this crop is generally grown with almost no inputs and unavailability of improved, high yielding sorghum varieties suitable for both grain and fodder. In addition, the food and feed demand of the country is increasing due to the rapidly growing human population and change in standards of living. In order to address the increasing grain demand and to overcome climate change related risks there is an increasing demand for improved varieties which can enhance sorghum productivity while addressing farmers preferred and end use quality trait.

Study of yield and yield components provides a basic framework for selecting useful characters in sorghum improvement programs. Seed yield is an important character that is polygenic in nature and significantly influenced by environmental conditions (Singh *et. al.*, 2014). Most of plant breeders are interested in maximizing selection efficiency that supports the identification of best genotypes. Estimation of correlation coefficient is useful in planning future breeding and provides a measure of association among traits, which could be useful as a selection guide. The path coefficient analysis enables to determine the direct and indirect contribution of various traits toward yield. Correlation analysis provides information of associations among yield components. Path coefficient analysis permits the separation of the correlation coefficient into component of direct and indirect effects and to measure the relative importance of each (Singh and Chaudhary, 1977; Sharma, 1998).

Therefore, the objective of this study was to determine the association of different characters with seed yield, direct and indirect influence of characters towards yield using correlation and path coefficient analysis at both phenotypic and genotypic levels.

Materials and methods

Description of experimental site

The experiment was conducted under rain fed condition at Cheffa testing site of Sirinka Agricultural Research Centre in South Wello, Ethiopia. The site is located at 11^0 0'1.04"N latitude and $39^0$45'27.1 "E longitude. It has an altitude of 1761.98 meters above sea level with average annual rain fall about 938.82 mm. The average annual minimum and maximum temperature, are 13.18^0c and 29.9^0c, respectively. The soil type is generally characterized as eutric vertisol. Rainfall distribution is erratic and usually unpredictable having uni-modal rainfall pattern, which starts in the first week of July and stops at the end of August. Delayed onset (during sowing time), early cessation (during grain filling period), and torrential rainfall is the major and common problems of this area (Taye Tadesse, 2004)

Experimental materials and design

A total of 49 sorghum genotypes were kindly availed by Melkassa Agricultural Research Centre (MARC) and evaluated for the presence of genetic variability, associations, direct and indirect influences among yield and yield related traits. The trial was laid-down using 7 x 7 simple lattice designs in two replications. Each genotype was planted on a plot size of (3m*2m) = $6m^2$with inter and intra row spacing of 75cm and 15cm respectively. Seed rate was adjusted based on the national recommendation rate as 5-10 kg/ha. Urea and DAP fertilizers were applied at the rate of 100 kg/ha each. Full amount of DAP was applied at sowing time while Urea was applied in split, in which the first half was applied at sowing time along with DAP, and the second half was top-dressed at knee- height stage of the plant. All cultural management practices were applied uniformly as per the recommendation. There was no chemical application.

Data collection

The data of morphological, phenological, and agronomical traits were collected during the growth period of the crop. The data of days to 50% heading, days to 95% maturity, Plant height, 1000 seeds weight, head yield per plant, grain filling period, seed yield, biomass yield and harvest index were collected

Analysis of variance

Analysis of variance (ANOVA) was performed for the quantitative data using SAS software computer program (9.2 version) as per the following linear model for simple lattice design.
Yijk = μ + Ri+ Bij+ Ti + eij:where, μ = the grand mean of trait Y; Ri = the effect of replicate I; Bij = effect of block j within replicate I; Ti = effect of treatment i ; eij = random error

Phenotypic and genotypic correlation coefficients

Phenotypic and genotypic correlation were estimated using the formula suggested by Miller et al. (1958)

Phenotypic correlation coefficient ($r_{p_{xy}}$) =

$$\frac{\sigma_{p_{XY}}}{\left[\sqrt{\sigma^2_{p_X} * \sigma^2_{p_Y}}\right]}$$

Where, $r_{p_{xy}}$ = phenotypic correlation coefficients between Character X and Y

$\sigma^2 px$ =Phenotypic variance for character x

$\sigma^2 py$= phenotypic variance for character y

Genotypic correlation coefficient ($r_{g_{xy}}$)

$$= \frac{\sigma_{g_{XY}}}{\left[\sqrt{\sigma^2 g_x * \sigma^2 g_y}\right]}$$

Where, $r_{g_{xy}}$ = genotypic correlation coefficients between character X and Y

$\sigma^2 gx$= genotypic variance for character x

$\sigma^2 gy$= genotypic variance for character y

Significance of phenotypic correlation coefficients will be tested using the following formula (Sharma, 1998).

$$t = \frac{r}{\sqrt{\frac{1-r^2}{n-2}}}$$

The calculated 't' value was compared with the tabulated 't' value at n-2 degree of freedom at 5 % and 1 % level of significance (where n is the number of genotypes).

Genotypic correlation coefficient will be tested with the following formula forwarded by Robertson (1959). $t = \frac{r_{g_{xy}}}{SE r_{g_{xy}}}$ Where,

$$SEr_{g_{xy}} = \sqrt{\frac{\left(1-r^2_{g_{xy}}\right)}{2h^2_x * h^2_y}}$$

$SEr_{g_{xy}}$ = Standard error of genotypic correlation coefficient between character X and Y

h^2_x = broad sense heritability for character X and

h^2_y = broad sense heritability for character Y

Path coefficient analysis

Associations of yield with its components were determined by the application of correlation and path analysis. The use of path analysis requires a cause and effect situation among the variables. Path coefficient analysis was calculated using the formula suggested by Dewey and Lu (1959) to assess direct and indirect effects of different traits on grain yield as:

$r_{ij} = p_{ij} + \sum r_{ik} p_{kj}$ Where,

r_{ij} = mutual association between the independent characters (i) and dependent character, grain yield (j) as measured by the correlation coefficients.

P_{ij} = components of direct effects of the independent character (i) on the dependent variable (j) as measured by the path coefficients and

$\sum r_{ik} p_{kj}$ = Summation of components of indirect effects of a given independent character (i) on a given dependent character (j) *via* all other independent characters (k).

The contribution of the remaining unknown factors is measured as the residual factor (P_R), which is calculated as: $P_R = \sqrt{\left(1-\sum r_{ij}\ p_{ij}\right)}$ the magnitude of P_R indicates how best the causal factors account for the variability of the dependent factor (Singh and Chaudhary, 1999). That is, if P_R value is small (for instance, nearly zero) the dependent character considered (grain yield) is fully explained by the variability in the independent characters, whereas higher P_R value indicates that some other factors which have not been considered, need to be included in the analysis to account fully for the variation in the dependent character (seed yield).

Results and discussion

Analysis of variance

The results of analysis of variance of nine quantitative characters for the 49 sorghum genotypes are presented in Table 1. Mean squares of most of the characters studied showed highly significant difference ($p < 0.01$) among the tested genotypes indicating the presence of adequate variability which can be exploited through selection which is consistent with the findings of Reddy *et. al*., (2007) observed highly significant genotypic differences for most traits in sorghum. The result showed that the magnitudes of the genotypic correlation coefficient values were higher than the corresponding phenotypic correlation coefficient values for most of growth traits which is true in accordance with Singh (2008) who reported that genotypic correlation coefficients were higher in magnitude than the corresponding phenotypic correlation coefficients in case of sorghum.

Table 1: Analysis of variance for yield and yield related traits

Traits	Replication (1)	Genotype (48)	Error (36)	CV
DH	25.51	58.42**	7.74	3.71
GFP	13.22	56.89**	8.59	5.49
DM	0.37	61.79**	8.56	2.22
PH	339.83	7498.67**	256.71	7.73
HYPP	0.89	795.81**	101.25	18.19
TSW	3.38	65.39**	3.97	6.14
GY	0.09	3.41**	0.24	11.93
BY	1.72	81.54**	4.29	10.02
HI	0.85	149.04**	5.00	10.14

Where: ** and ns, significant at 1% probability level and non-significant, respectively. DH=days to heading, GFP=grain filling period, DM=days to maturity, PH=plant height, HYPP=head yield per plant, TSW= thousand seeds weight, GY= grain yield, BY= biomass yield and HI= harvest index.

The magnitude of mean squares due to genotypes was high for plant height, head yield per plant and harvest index while low genotype means square values exhibited for number of productive heads and grain yield (Table 1). This low magnitude of mean squares indicated the traits were relatively sensitive to environmental effects.

Correlation coefficient is the measure of degree of symmetrical association between two characters and helps us in understanding the nature and magnitude of association among yield and yield components. Association between any two traits or among various traits is very important to make desired selection of combination of traits (Ahmed *et. al.,* 2003). Grain yield is the most complex trait and it is influenced by many factors (known and unknown) that determine productivity. Breeders always look for genetic variation among traits to select desirable types. Some of these characters are highly associated among themselves and with seed yield.

The analysis of the relationship among these characters and their association with seed yield is essential to establish desired selection of combination of traits (Singh *et. al.,* 2014). Thus, estimation of the magnitudes of genotypic and phenotypic correlations of grain yield and its component among yield related traits are highly crucial to utilize the existing variability through selection. Estimates of phenotypic and genotypic correlation coefficients between each pair of characters are presented in Table 2.

Association of grain yield with other traits

Seed yield had a highly significant and positive phenotypic correlation with thousand seeds weight (r=0.26), head yield per plant (r=0.24), grain filling period (r=0.35) and harvest index(r=o.35). from this seed yield showed a remarkable relationship with yield contributing traits. Therefore, any improvement of these characters would result a substantial increment on seed yield. Days to maturity (r=-0.21) and plant height (r=-0.38) had negative and highly significant phenotypic correlation with grain yield. Seed yield also showed negative and significant phenotypic association with only days to heading(r=-0.19) (Table 2) that days to heading does not influence seed yield as the plant crop was able to obtain ample amount of moisture during the growing periods.

Seed yield had positive and highly significant genotypic correlation with thousand seeds weight (0.39), grain filling period (r=0.61) and harvest index (r= 0.49) which agrees with the findings of Dabholkar *et. al.* (1992), that grain yield/ha had highly significant positive correlation with thousand seeds weight. It was also correlated positively and significantly with head yield per plant (r=0.25), days to maturity (0.28). and days to heading (0.30) that agrees with the study conducted by Patel *et al.* (1980) stated as positive and significant association of seed yield with thousand seeds weight, days to heading and maturity, Similarly, any improvement of these characters would result in an increment on seed yield. On the other hand, seed yield showed negative and highly significant genotypic correlation with plant height (r=-0.34) (Table 2).

From the correlation analysis, it can be concluded that thousand seeds weight, grain filling period, and head yield per plant were found to be important yield components This result was also confirmed by the findings of (Muhammad *et. al.*, 2003). Knowledge of association between yield and its component traits and among the component parameters themselves can improve the efficiency of selection in plant breeding the same is true for sorghum genotypes under study which agrees with the findings of Dogget (1970) reported that higher thousand seed weight and head yield per plant generally are the most important yield component associated with increased in yield of sorghum which is in aggrement with the present investigation.

Associations among other traits

Days to maturity had positive and highly significant phenotypic correlation with days to heading, grain filling period, plant height and biomass yield that means as heading and grain filling periods became shorter the plant crop matured within the same condition. But it exhibited negative and highly significant association with harvest index. Biomass yield exhibited positive and highly significant association with days to maturity, thousand seeds weight and plant height. That means the total above ground biomass yield was compensated as the plant height of the crop increased even if negatively affected by harvest index.

Grain filling period had negative and significant phenotypic correlation with harvest index but highly significant negative correlation with days to heading and head yield per plant. Grain filling period showed positive and highly significant genotypic correlation with days to heading and maturity that means it is confined with both days as conditions are favorable. Days to maturity had positive and highly significant genotypic association with days to heading, plant height and grain filling period, and also the same for in between plant height and biomass yield.

Thousand seeds weight had positive and highly significant genotypic correlation with days to heading. It also showed positive significant genotypic association with harvest index this indicated that the final product seed yield is the cumulative effect of these thousand seeds weight led to have higher yield of sorghum genotypes under study Harvest index exhibited negative and highly significant genotypic correlation with days to maturity, grain filling period, plant height and biomass yield and also it had negative and significant correlation with thousand seeds weight. Head yield per plant had showed positive and highly significant genotypic correlation with days to heading but negative with grain filling period and plant height. Plant height exhibited highly significant positive genotypic association with days to maturity and biomass yield but it had negative highly significant association with harvest index.

Generally, positive and significant association of pairs of characters at phenotypic and genotypic level justified the possibility of correlated response to selection. The negative correlations prohibit the simultaneous improvement of those traits for further study as they are interacted counter balance

Table 2: Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients

Traits Variable	DH	DM	PH	TSW	HYPP	GFP	GY	BY	HI
DH	1	0.48**	0.17ns	0.049ns	0.03ns	-0.46**	-0.19*	0.12ns	-0.24*
DM	0.50**	1	0.35**	0.08ns	-0.27*	0.54**	-0.21**	0.44**	-0.40**
PH	0.16ns	0.38**	1	0.32**	-0.03ns	0.22ns	-0.38**	0.67**	-0.68**
TSW	0.33**	0.09ns	0.33*	1	0.13ns	0.03ns	0.26**	0.27**	-0.18ns
HYPP	0.35**	-0.04ns	-0.24*	0.11ns	1	-0.42**	0.24**	-0.03ns	0.21*
GFP	0.42**	0.54**	0.27*	0.05ns	-0.27*	1	0.35**	0.33**	-0.21*
GY	0.30*	0.28*	-0.34**	0.39**	0.25*	0.61**	1	0.14ns	0.35**
BY	0.15ns	0.41*.	0.69**	0.23*	-0.05ns	0.36**	0.10ns	1	-0.73**
HI	0.22ns	-0.42**	-0.71**	0.39*	0.20ns	-0.32**	0.49**	-0.74**	1

Where: *, ** and ns, significant at 5%, 1% probability level and non-significant, respectively. DH=days to heading, GFP=grain filling period, DM=days to maturity, PH=plant height, TSW = thousand seeds weight, HYPP= head yield per plant, GY = grain yield, BY = biomass yield and HI = harvest index

Path coefficient analysis

Seed yield is the final products of various characters and here it was considered to be the resultant variable while the rest of the variables were casual variables. When more characters are involved in correlation study, it becomes difficult to ascertain the characters which really contribute to yield. The path coefficient analysis under such situations helps to determine the direct contribution of these characters and their indirect contributions via other characters. In the present study, only 8 out of the 9 characters that are believed to have direct relationship with seed yield were included in the path analysis (Dewey and Lu, 1959). The phenotypic and genotypic correlations were partitioned in to direct and indirect effects using seed yield as a dependent variable.

Grain yield is the product of interaction of component traits. Apart from correlation studies, path coefficient analysis is important to obtain information about different ways in which the component characters influence grain yield. Direct effect of any component characters on grain yield gives an idea about reliability of indirect selection to be made through that character to bring about improvement in grain yield. High values of direct effects suggest that the true relationship and direct selection for these traits may also increase and give better response for improvement of grain yield (Ali, 2012). If both correlation coefficient and the direct effect are high and positive then correlation explains its true relationship and a selection for that character will be effective. If the correlation coefficient is positive, but the direct effect is negative or negligible, in such relations the indirect causal factors are to be considered simultaneously for selection, when correlation coefficient is negative but the direct effect is positive and high in such cases direct selection for such traits should be practiced to reduce the undesirable indirect effect.

The estimated residual effect of path analysis was low (0.065), which indicated that about 93.5 % of the variability in grain yield was contributed by the traits studied. This residual effect towards grain yield in the present study might be due to other characters or environmental factors and, or sampling errors (Sengupta and Kataria, 1971).

Phenotypic path analysis of seed yield with other characters

The phenotypic direct and indirect effect of different characters on seed yield is presented in Table 3. Direct positive and negative phenotypic effect on seed yield were ranged from 0.08 (BY) to 0.71(TSW) and 0.38 for DH respectively. Characters such as thousand seeds weight (0.71) followed by plant height (0.59), days to maturity (o.48), head yield per plant (0.23), harvest index (0.14) and biomass yield (0.08) had exerted positive direct phenotypic effect on seed yield that above all thousand seeds weight has contributed more in the case of yield increment which agrees with the findings of Reddy *et. al*., (1981) that thousand seeds weight is the most important yield component in grain sorghum.

High values of positive direct effects suggest that these characters have true relationship and direct selection for these traits may also increase and give better response for improvement of grain yield and can be major selection criteria in sorghum breeding programs which agrees with the findings of Dewey and Lu (1959) that stated high values of positive direct effects contributed for increment of yield /ha.

Days to heading had attributed positive indirect effect on seed yield through grain filling period. Days to maturity had more positive indirect phenotypic effect on seed yield via days to heading, grain filling period and biomass yield. Plant height exerted positive indirect effect on seed yield through both days to maturity and biomass yield.

In addition, thousand seeds weight had exerted positive indirect phenotypic effect on seed yield via plant height and biomass yield. Grain filling period had also contributed positively and indirectly on seed yield through days to heading and head yield per plant. Genetic improvement in grain yield can be accelerated if yield contributing traits are used as selection criteria. For this purpose, it is necessary not only identify indirect linkage to gain yield potential, but also to improve the understanding of the genetic bases controlling this trait for easy handling (Garcia *et. al*., 2011).

Genotypic path analysis of seed yield with other characters

The genotypic direct and indirect effect of different characters on seed yield is presented in Table 3. Both days to heading and maturity had exhibited negative direct genotypic effect on seed yield. Plant height, thousand seeds weight, grain filling period, harvest index, head yield per plant and biomass yield had showed positive direct genotypic effect on seed yield so that they can be used as direct selection criteria for an increment of seed yield.

On the other hand, both days to heading and maturity showed positive indirect effect on seed yield through harvest index. Plant height had exerted substantial positive indirect effect on seed yield via days to maturity, thousand seeds weight, grain filling period and biomass yield. Grain filling period had also the same effect on seed yield via days to heading and maturity, and biomass yield. On the other hand, days to heading had more exhibited indirect negative genotypic effect on seed yield through days to maturity, thousand seeds weight, head yield per plant, grain filling period and biomass yield. Days to maturity also showed negative indirect effect on seed yield via days to heading, plant height, grain filling period and biomass yield.

The genotypic direct and indirect effect of different characters on seed yield is presented in Table 3. Both days to heading and maturity had exhibited negative direct genotypic effect on seed yield. Plant height, thousand seeds weight, grain filling period, harvest index, head yield per plant and biomass yield had showed positive direct genotypic effect on seed yield so that they can be used as direct selection criteria for an increment of seed yield. On the other hand, both days to heading and maturity showed positive indirect effect on seed yield through harvest index. Plant height had exerted substantial positive indirect effect on seed yield via days to maturity, thousand seeds weight, grain filling period and biomass yield. Grain filling period had also the same effect on seed yield via days to heading and maturity, and biomass yield. On the other hand, days to heading had more exhibited indirect negative genotypic effect on seed yield through days to maturity, thousand seeds weight, head yield per plant, grain filling period and biomass yield. Days to maturity also showed negative indirect effect on seed yield via days to heading, plant height, grain filling period and biomass yield. Earlier in sorghum Sengupta and Kataria (1971) reported similar results.

Table 3: Estimates of direct (bold diagonal) and indirect effect (off diagonal) phenotypic (P) and genotypic (G) level for different characters

Variable	DH	DM	PH	TSW	HYPP	GFP	BY	HI
P	**-0.38**	0.2304	0.1003	0.0348	0.0069	0.2484	0.0096	-0.034
G	**-0.49**	-0.21	0.072	0.0693	0.021	0.0756	0.006	-0.0198
P	-0.182	**0.48**	0.2065	0.0568	-0.062	-0.292	0.0352	-0.056
G	-0.245	**-0.42**	0.171	0.0189	-0.0024	0.0918	0.0164	-0.0378
P	-0.065	0.168	**0.59**	0.2272	-0.007	-0.119	0.0536	-0.095
G	-0.0784	-0.1596	**0.45**	0.0693	-0.0144	0.0486	0.0276	-0.0639
P	-0.019	0.0384	0.1888	**0.71**	0.0299	-0.016	0.0216	-0.025
G	-0.1617	-0.0378	0.1485	**0.21**	0.0066	0.009	0.0092	-0.0351
P	-0.011	-0.13	-0.018	0.0923	**0.23**	0.2268	-0.002	0.0294
G	-0.1715	0.0168	-0.108	0.0231	**0.06**	-0.0486	-0.002	0.018
P	0.175	0.2592	0.1298	0.0213	-0.097	**0.54**	0.0264	-0.029
G	-0.2058	-0.2142	0.1215	0.0105	-0.0162	**0.18**	0.0144	-0.0288
P	-0.046	0.2112	0.3953	0.1917	-0.007	-0.178	**0.08**	-0.102
G	-0.0735	-0.1722	0.3105	0.0483	-0.003	0.0648	**0.04**	-0.0666
P	0.091	-0.192	-0.401	-0.128	0.0483	0.1134	-0.058	**0.14**
G	0.1078	0.1764	-0.3195	-0.0819	0.012	-0.0576	-0.0296	**0.09**

Residual effect for phenotypic and genotypic level = 0.065; 0.061

Where: DH=days to heading, DM=days to maturity, PH=plant height, TSW= thousand seeds weight, HYPP=head yield per plant, GFP=grain filling period, BY= biological yield and HI= harvest index.

Acknowledgements

First of all, the author deepest gratitude and acknowledge goes to Amhara Agricultural Research Institute for providing research budget and facilitate to conduct the research. I would like also to express sincere thanks to Cheffa Agricultural Research Sub-Centre staff members for contributing their greatest effort for the successful accomplishment of the experiment.

References

1. Ahmed, H. M., Khan, B. M., Khan, S., Kissana, N. S. .and Laghari, S. 2003. Path coefficient analysis in bread wheat. Asian J. Plant Sci., 2(6): 491-494.
2. Ali, H. 2012. Heritability, variability, genetic correlation and path analysis for quantitative traits in durum and bread wheat under dry farming conditions. Mesopotamia J. Agricul., 40(4): 27-39.
3. Dabholkar, A. R. 1992. Element of Biometrical Genetics. Concept Publishing Company, New Delhi, pp. 431.
4. Dewey, D.R. and Lu K.H. 1959. A correlation and path coefficient analysis of crested wheat grass seed production. Argon. J., 51:515-518.
5. Doggett, H., Starks, K. and Eberhart ,S. 1970. Breeding for resistance to the sorghum shoot fly Crop Sci., 10(5): 528-531.
6. Duodu, K., Taylor, J., Belton, P. and Hamaker B. 2003. Factors affecting sorghum protein digestibility. J. Cereal Sci., 38(2): 117-131.
7. García ,G .A., Serrago ,R ..A., Appendino, M..L., Lombardo, L. A., Vanzetti, L. S., Helguera, M. and Miralles, D. J. 2011. Variability of duration of pre-anthesis phases as strategy increasing wheat grain yield. Field Crops Res.,124(3): 408-416
8. Harlan, J. and De Wet, J. 1972. A simplified classification of cultivated sorghum. Crop Sci.,12(2): 172-176.
9. House, L.R. 1985. A guide to sorghum breeding. 2nd. Edn. Patancheru, India: International Crops Research Institute for the Semi-Arid Tropics, Hyderabad, India.
10. Kumar, I. and Saini, S. S.2011. Path analysis in short statured rice varieties. Indian J. Genet, 33: 13-15.
11. Miller, P. A., Williams, J. C., Robinson, H . F..and Comstock, R. E. 1958. Estimates of Genotypic and environmental variances and covariances in upland cotton and their implications in selection. Agron. J., 50(3): 126-131.
12. Mohammadi, S. A. and Prasanna, B. M. 2003. Analysis of genetic diversity in crop plants salient statistical tools and considerations. Crop Sci., 43(4): 1235-1248.
13. Mutegi, E., Sagnard .F., Semagn, K., Deu M., Muraya, M., Kanyenji, B., De Villiers S., Kiambi, D., Herselman, L. and Labuschagne M. 2011. Genetic structure and relationships within and between cultivated and wild sorghum (*Sorghum bicolor* (L.) Moench) in Kenya as revealed by microsatellite markers. Theor. Applied Genet., 122(5): 989-1004.
14. Ng'uni, D., Hofvander, P., Fatih, M..and Bryngelsson T. 2012. Comparative genetic diversity and nutritional quality variation among some important southern African sorghum accessions [*Sorghum bicolor* (L.) Moench]. Australian J. Crop Sci., 6(1): 56-64.

15. Patel, R. H., Desai, K .B., Kukadia, M.U. and Desai, D.T. 1980. Component analysis in sorghum. Sorghum Newsl., 23: 23-24
16. Reddy, K.N.N. and Nagur, T. 1981. Correlation studies between yield and yield components in sorghum. Sorghum Newsl., 24 (1): 18.
17. Reddy, B.V. S., Ramaia B., Kumar A A. and Reddy, P. S. 2007. Evaluation of sorghum genotypes for the stay-green trait and grain yield. J. SAT Agril. Res. ,3(1): 1-4.
18. Robertson, G. E. 1959. The sampling variance of genetic correlation coefficient. Biometrics, 15, 469-485.
19. Sengupta, K. and Kataria, A. S. 1971 .Path coefficient analysis for some characters in soybean. Indian J. Genet., 31, 290-295.
20. Sharma, J. R.1998. Statistical and biometrical techniques in plant breeding. New Age International Publication. New Delhi, India, pp. 432.
21. Singh, R.. K. and Chaudhary. 1977. Biometrical methods in quantitative genetic analysis. Kalyani Publisher, New Delhi, Ludhiana, India.
22. Singh, R. K. and Choudhury, B. D. 1990. Biometrical method in quantitative genetic analysis. Kalyani Publishers, Ludhiana, New Delhi, India, pp. 54-57.
23. Singh, R.. K. and Chaudhary, B. D. 1999. Biometrical Methods in Quantitative genetics analysis, Kalyani Publishers, New Delhi, India, pp. 73.
24. Singh, Sukhchain, Karnail. 2008. Association analysis among vegetative traits in forage sorghum (*Sorghum bicolor*). Range Managemnt. Agroforest., 29(2): 147-148.
25. Singh, J. L., Prasad, C., Madakemohekar, A. H. and Bornare, S. S. 2014. Genetic variability and character association in diverse genotypes of barley (*Hordeum vulgare* L.). The Bioscan (Supplement on Genetics and Plant Breeding), 9(2), 759-761.