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# CHARACTER ASSOCIATION AND PATH ANALYSIS OF SORGHUM (*Sorghum bicolour* L. Moench) GENOTYPES FOR *STRIGA* RESISTANCE

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## Abstract

Association and path analysis of yield related traits is essential for breeders. The objectives of this study was to investigate the relationship among yield, yield related traits and *Striga* parameters using forty nine sorghum genotypes including resistance and susceptible checks to *Striga hermonthica*. The experiment was conducted at Kobo research sub-center, Northeastern Ethiopia in 2018 main cropping season in simple lattice design. Data on 13 traits were collected and analyzed. Differences among the genotypes were significant ($p < 0.05$). Phenotypically positively significant traits were head weight (0.79), head number (0.45), panicle width (0.29), and panicle length (0.26). Whereas, phenotypically and genotypically negative significant ($p < 0.05$) for days to flowering (DF) ($r_p$ = -0.28, $r_g$ = -0.32), days to maturity (DM) ($r_p$ = -0.27, $r_g$ = -0.28) and *Striga* count per meter square (Stm-2)($r_p$ = -0.36, $r_g$ = -0.61), *Striga vigourisity* (SV)($r_p$ = -0.48, $r_g$ = -0.73) and *Striga* severity (SSV) ($r_p$ = -0.37, $r_g$ =-0.69 ), respectively. Generally, positive and significant genotypic correlation in grain yield (kg $ha^{-1}$) showed with head weight, panicle width, above ground biomass and thousand kernel weight.

**Keywords:** Correlation, Path analysis, Significance

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## 1. Introduction

Sorghum [*Sorghum bicolor* (L.) Moench; 2n = 2x =20] is the fifth most important cereal crop in the world after maize, rice, wheat and barley (FAOSTAT, 2017). Sorghum serves as staple food crop for millions of people in the semi-arid and arid regions of Asia, Africa and Central America. Its grain and stalk is also used as animal feed, for bio-ethanol production and as industrial raw materials (FAOSTAT, 2015). The greatest variability of the crop is found in the Ethio-Sudan region of Africa, an area recognized as the center for sorghum origin (Doggett, 1988). It seems that sorghum moved into other parts of eastern Africa around or before 200 AD. It was adopted and carried to the savannah countries of eastern and southern Africa by the Bantu people, who used the grain mainly to make beer. Sorghum is consumed into a wide variety of foods, such as baked products, tortillas, couscous, gruel, steam-cooked products semi-leavened breads, popped form, porridges, fermented alcoholic and non-fermented non-alcoholic beverages. Moreover, grain sorghum has great potential to be used in different industrial applications and processed into starch, flour, grits and flakes as well as malted products. A more recent use is as a source of ethanol and by-products from the ethanol production are also finding a place in the market. In eastern Africa, more than 70% of sorghum is cultivated in the dry and hot lowlands where soil fertility low, poor stand establishment, in addition to serious water deficit are among the major production constraints (Orr et al., 2016).

In Ethiopia, sorghum is a major staple food crop, ranking second after maize in total production. It ranks third after wheat and maize in productivity per hectare, and after tef and maize in area cultivated. It is grown in almost all regions, covering a total land area of 1.84 million ha (CSA, 2018). Drought and *Striga* weed have been found to be the most important constraints in the northern and north-eastern parts of the country (Gebretsadik et al., 2014). *Striga* is major biotic constraint and a serious threat to subsistence cereal crops (sorghum, Pearl millet, finger millet, maize and upland rice) grown in sub-Saharan Africa and India (Rispail et al., 2007). A report on sorghum production survey in the Northeastern part of the country (South Wollo, North Wollo, and Waghmera) indicated that sorghum coverage decreased because of various negative factors: increasingly erratic rainfall, poor soil fertility, *Striga*, and stalk borer infestations (Amelework et al., 2016).

Yield is a polygenic character highly influenced by the seasonal fluctuation (environment). Hence selection of plants based directly on yield would not be very reliable. Study of agronomic, yield and yield related traits provide a fundamental framework for selecting potentially useful characters in sorghum improvement programs. Most plant breeders are interested in maximizing selection efficiency that facilitates the identification of best genotypes. Correlation coefficient is the measure of the degree for linear association between two variables (Gomez and Gomez, 1984). Breeders are interested in the relationship that may exist between characters. When more characters are involved in correlation study, it becomes difficult to determine the characters that really contribute to yield because of the presence of some amount of interdependence. Under such complex circumstances, path coefficient analysis provides more effective means of separating direct and indirect factors; permitting a critical examination of the specific forces acting to produce a given correlation and measuring the relative importance of the causal factors. The path coefficient analysis under such situations helps to determine the direct contribution of these characters and their indirect contributions via other characters (Tesfaye et al., 2014). Information on correlation among yield and yield related traits in relation to *Striga* resistance traits is fundamental for direct or indirect selection and development of improved resistance and/or tolerance varieties. Path coefficient analysis measures the direct influence of one variable upon the other and permits separation of correlation coefficients in to component of direct and indirect components. Hence, the objective of this study is to determine the traits having greater interrelationship with grain yield utilizing the correlation and path analysis.

## 2. Materials and Methods

### 2.1. Description of the Experimental Site

The experiment was carried out at Kobo research substation under artificially *Striga* infested field (sick plot), in Raya Kobo district, North Wollo Zone in 2018 cropping season. Kobo is located 567 km from the capital Addis Ababa. Geographically the experimental site is located at 12°8.41′′ N latitude and 39° 38.45′ E longitude and at an altitude of 1468 meter above sea level (m. a. s. l). The site receives 692.82 mm annual rain fall with an average maximum and minimum temperature of 30.4 °C and 22.0 °C, respectively. The soil is *Euratic fluvi* sol having loam textural classes. The major cultivated crops in the study area are sorghum and tef.

### 2.2. Experimental Materials and Design

Forty nine sorghum genotypes brought from Melkasa Agricultural Research Center (MARC) including resistance check (Gobye) and local or susceptible checks (Jigurty) were tested (Table 1). The genotypes are crosses of *Striga* resistant varieties as male parent and pure lines and /or early maturing varieties as a female. The experiment was executed during 2018 main cropping season using 7 x 7 simple lattice design. Each genotype were sown in two rows at 0.75m, 0.15m, 1m spacing between rows, plants and plots respectively; with 2m row length, separated from the neighboring entry by one empty row. The seed rate was 10 kg/ha. Fertilizer was applied at the rate of 23/46/8 kg $ha^{-1}$ N, $P_2O_5$ and S, respectively. No split application of nitrogen and no hoeing were done to avoid negative effect of *Striga* attachment or emergence.

### 2.3. Data Collection

Data was taken from two rows for days to flowering and days to maturity, plant height, panicle length, panicle count, head/panicle weight, 1000 kernel weight and grain yield following recommendations by International Board for Plant Genetic Resources (IBPGR) and ICRISAT descriptor list for sorghum (IBPGR/ICRISAT, 1993).

### 2.4. Data Analysis

Data on phenological parameters, growth parameters, yield, yield components, grain parameters and *Striga* parameters were subjected to analysis of variance (ANOVA). Analysis of variance was done using the help of SAS Computer Statistical Package version 9.0 (SAS, 2004).

**Table 1.** Sorghum genotypes

| Genotype Number | Genotype |
|---|---|
| 1 | ETSC_14181-5-4 |
| 2 | ETSC_14184-8-3 |
| 3 | ETSC_14214-7-3 |
| 4 | ETSC_14018-1-2 |
| 5 | ETSC_14154-8-3 |
| 6 | ETSC_14019-14-2 |
| 7 | ETSC_14214-6-1 |
| 8 | ETSC_14124-6-1 |
| 9 | ETSC_14153-7-1 |
| 10 | ETSC_14149-6-3 |
| 11 | ETSC_14018-1-3 |
| 12 | ETSC_14018-4-1 |
| 13 | ETSC_14020-4-2 |
| 14 | ETSC_14214-6-2 |
| 15 | ETSC_14118-2-1 |
| 16 | ETSC_14199-8-2 |
| 17 | ETSC_14209-2-1 |
| 18 | ETSC_14209-3-2 |
| 19 | ETSC_14124-4-2 |
| 20 | ETSC_14190-20-2 |
| 21 | ETSC_14194-5-1 |
| 22 | ETSC_14217-10-1 |
| 23 | ETSC_14216-11-2 |
| 24 | ETSC_14124-8-3 |
| 25 | ETSC_14127-1-1 |
| 26 | ETSC_14128-6-1 |
| 27 | ETSC_14199-18-1 |
| 28 | ETSC_14019-9-1 |
| 29 | ETSC_14121-4-4 |
| 30 | ETSC_14217-11-2 |
| 31 | ETSC_14121-4-3 |
| 32 | ETSC_14149-6-1 |
| 33 | ETSC_14018-3-1 |
| 34 | ETSC_14209-3-1 |
| 35 | ETSC_14179-1-2 |
| 36 | ETSC_14125-10-1 |
| 37 | ETSC_14019-1-2 |
| 38 | ETSC_14209-5-3 |
| 39 | ETSC_14220-1-4 |
| 40 | ETSC_14195-1-2 |
| 41 | ETSC_14220-1-3 |
| 42 | ETSC_14127-1-3 |
| 43 | ETSC_14126-5-2 |
| 44 | ETSC_14017-1-1 |
| 45 | ETSC_14196-1-3 |
| 46 | ETSC_14181-5-2 |
| 47 | ETSC_14214-2-3 |
| 48 | Susceptible check (Jigurty) |
| 49 | Resistance check (Gobye) |

### 2.5. Correlation Coefficients ($r$)

Phenotypic correlation, the observable correlation between two variables, which includes both genotypic and environmental components between two variables, was estimated using the formula suggested by Miller et al. (1958).

$$r_{pxy} = \frac{\sigma^2_{pxy}}{\sqrt{(\sigma^2_{px})(\sigma^2_{py})}}$$

Genotypic correlations were computed as;

$$r_{gxy} = \frac{\sigma^2_{gxy}}{\sqrt{(\sigma^2_{gx})(\sigma^2_{gy})}}$$

where, $r_{pxy}$ is phenotypic correlation coefficient and $r_{gxy}$ is genotypic correlation coefficient between characters $x$ and $y$; $\sigma^2_{pxy}$ and $\sigma^2_{gxy}$ are phenotypic covariance and genotypic covariance between characters $x$ and $y$, respectively. $\sigma^2_{px}$ and $\sigma^2_{gx}$ are phenotypic and genotypic variances for character $x$ and $\sigma^2_{py}$ and $\sigma^2_{gy}$ are phenotypic and genotypic variances for character $y$.

Covariance analysis between all pairs of characters was calculated by the following formula;

$Cov_{gxy} = (MSP_g - MSP_e)/r$

$Cov_{pxy} = COV_{gxy} + Cov_{exy}$

where, $Cov_{gxy}$= genotypic covariance between traits $x$ and $y$

$Cov_{pxy}$ = phenotypic covariance between traits $x$ and $y$

$MSP_g$= Genotypic mean sum product of traits $x$ and $y$

$MSP_e$ = Environmental mean sum product of traits $x$ and $y$

$r$ = Number of replication

### 2.6. Path Coefficient Analysis

Path coefficient technique involves a method of partitioning correlation coefficients in to direct effect and indirect effects through alternative pathways [Pathway ($P$) x correlation coefficient ($r$)] (Aryeetey and Laing, 1973). The path coefficients were obtained by solution of simultaneous equation through the method of least square as shown by Dewey and Lu (1959). The use of the method of "path coefficients" is illustrated as a means of analyzing correlation coefficients.

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

Where, $\mathbf{r_{ij}}$ = Mutual association between the independent character ($i$) and dependent character ($j$) as measured by the genotypic correlation coefficient, $P_{ij}$ = 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 character ($k$). The residual effect, which determines how best the causal factors account for the variability of the dependent factor yield, was computed using the formula;

$$1 = p^2R + \sum p_{ij} r_{ij}$$

where, $p^2R$ is the residual effect, $p_{ij}r_{ij}$ = the product of direct effect of any variable and its correlation coefficient with dependent trait. The residual effect ($p^2R$) was estimated using $\sqrt{1\text{-}R^2}$. Where, $R^2 = \Sigma p_{ij} r_{ij}$ $p^2R = \sqrt{1 - \Sigma\, p_{ij} r_{ij}}$.

## 3. Results and Discussion

### 3.1. Estimation of Correlation Coefficient of Yield and Yield Related Traits

Correlation coefficient helps in determining the direction of selection and the characters to be considered in improving the grain yield. Estimates of the phenotype ($r_p$) and genotype ($r_g$) among each pair of studied traits (association among *Striga* related and *Striga* and yield related traits) are presented (Table 2). Genotypic correlation coefficients were relatively higher in magnitude than that of phenotypic correlation coefficients, which indicates the presence of inherent association among various traits. These finding is in agreement with previous findings Khandelwal et al. (2015) in sorghum. Positive and significant genotypic correlation in grain yield (kg $ha^{-1}$) showed with head weight ($r_g$=0.80**), panicle width ($r_g$=0.69**), above ground biomass ($r_g$=0.54**) and thousand kernel weight ($r_g$=0.10*). Therefore, selection of sorghum genotypes with better above ground biomass, panicle width which would lead to better head weight and thousand kernel weight would enhance grain yield. This finding is in line agreement with Temesgen (2018) reported both genotypically and phenotypically positive significant of head weight and panicle width with grain yield. Whereas grain yield was genotypically negatively significant ($p < 0.05$) correlated with days to flowering ($r_g$=-0.32), days to maturity ($r_g$ =-0.28), *Striga* count $m^2$ ($r_g$=-0.61), *Striga vigourisity* ($r_g$=-0.73) and *Striga* severity ($r_g$=-0.69), respectively. Abate (2016) reported the same result for days to flowering and days to maturity which were negatively correlated to grain yield in sorghum.

Phenotypically, grain yield ($kgha^{-1}$) showed positive and significant ($p < 0.05$) correlation with panicle/head weight ($r_p$=0.79), head number ($r_p$=0.45), panicle width ($r_p$=0.29), panicle length ($r_p$=0.26) and biomass ($r_p$=0.30). Whereas phenotypically negative significant ($p < 0.05$) for $Stm^{-2}$($r_p$=-0.36), SV ($r_p$=-0.49), SSV ($r_p$=-0.37), DF ($r_p$=-0.29,) and DM ($r_p$=-0.28), respectively. These results were similar with Mesfin (2016) and Temesgen (2018) where most *Striga* related traits and days to flowering and days to maturity were negatively significant for grain yield in sorghum genotypes.Correlations among yield components and other quantitate traits help in understanding the interrelation of traits. In this study plant height showed positively significantly ($p < 0.05$) correlated to thousand kernel weight ($r_p$=0.47) and above ground biomass ($r_p$=0.21). Days to maturity showed phenotypically highly significant ($p < 0.01$) correlation to days to flowering ($r_p$=0.91) and positive significant ($p < 0.05$) correlation to *Striga* count ($r_p$=0.17), *Striga* vigourisity ($r_p$=0.18) and *Striga* severity ($r_p$=0.16).Positive significant correlation showed between thousand kernel weight ($r_g$=0.51), days to flowering ($r_g$=0.25) and days to maturity ($r_g$=0.27) with plant height. Panicle width showed positive significant ($p < 0.05$) correlation with head weight ($r_g$=0.71) and panicle length ($r_g$=0.60). Genotypic negative correlations also existed between head weight and days to flowering ($r_g$=-0.41) and days to maturity ($r_g$=-0.32).

Positive significant ($p < 0.05$) correlations showed between *Striga* related parameters and days to flowering ($r_g$=0.43) for *Striga* count per square meter ($Stm^{-2}$) and ($r_g$=0.43) for *Striga* severity and days to maturity ($r_g$=0.37) for *Striga* counts, days to maturity ($r_g$=0.37) for *Striga* severity, plant height ($r_g$=0.19) for *Striga* counts, plant height ($r_g$=0.25) for *Striga* severity, respectively. So improving these traits (days to flowering and days to maturity) would increase resistance and/or tolerance to *Striga* for sorghum genotypes. Generally, the *Striga* parameters (*Striga* count, *Striga* vigourisity and *Striga* severity) showed negative correlation for most yield and yield related traits except for plant height, days to flowering and days to maturity.

### 3.2. Estimation of Phenotypic Direct and Indirect Effects on Grain Yield

Separation of the total correlation into direct and indirect effects provides actual information on contribution of characters and thus forms the bases for selection to improve yield. The result of phenotypic path analysis is presented (Table 3) and out of thirteen characters, five characters revealed positive direct effect on grain yield.Head weight (0.74) shown the highest positive direct effect on grain yield followed by days to maturity (0.033), head number (0.021), panicle length (0.017) and above ground biomass (0.012). Similar results were reported by Temesgen (2018) for days to maturity, head number and panicle length. In significant negative direct effect on grain yield was showed by the characters, Days to flowering (-0.019), plant height (-0.003), panicle width (-0.074), *Striga* count (-0.046), *Striga* vigourisity (-0.314) and *Striga* severity (-0.16).

Independent traits exhibiting direct effect have indirect effect on grain yield through other independent traits. Days to maturity, head weight and panicle length were traits which showed both direct and indirect effects on grain yield and are important traits that could be considered under improvement. Plant height had negative indirect effect through days to flowering and panicle width but had positive indirect effect through days to maturity, head weight, panicle length and above ground biomass on grain yield. The negative indirect effects come largely through days to flowering, head weight and *Striga* vigourisity. Head/panicle weight which had the highest positive direct effect (0.74) had also considerable negative indirect effect via panicle width (-0.031) and thousand kernel weight (-0.014). Panicle length had positive indirect effect via head weight (0.253) and negative indirect effect through panicle width (-0.023). Thousand kernel weight in addition to its negative direct effect had also considerable positive indirect effect via head weight (0.233).

**Table 2.** Sorghum Genotypic (**above diagonal**) and phenotypic (**below diagonal**) correlation coefficients of major traits of sorghum evaluated for *Striga* at Kobo, 2018

| Traits | DF | PH | DM | HN | HW | Pcl | Pcw | BM | GY | TKW | Stm-2 | SV | SSV |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DF | 1 | 0.25* | 0.89** | -0.65* | -0.41* | -0.21ns | -0.12ns | 0.03ns | -0.32* | -0.04ns | 0.43* | 0.41* | 0.43* |
| PH | 0.18* | 1 | 0.28* | -0.38ns | -0.06ns | 0.05ns | -0.01ns | -0.34* | 0.03* | 0.51* | 0.19* | 0.16* | 0.25* |
| DM | 0.91** | 0.19* | 1 | -0.64* | -0.32* | -0.21* | -0.10ns | 0.05ns | -0.28* | -0.01ns | 0.37* | 0.33* | 0.37* |
| HN | -0.46* | -0.14ns | -0.44* | 1 | -0.12ns | -0.09ns | 0.30ns | -0.32* | 0.23* | -0.01ns | -0.90* | -0.92* | -0.85* |
| HW | -0.36* | 0.15ns | -0.35* | 0.50* | 1 | -0.38* | 0.71* | 0.05ns | 0.80** | 0.22* | -0.57* | -0.80* | -0.81* |
| Pcl | -0.28ns | 0.13* | -0.26* | 0.17ns | 0.34* | 1 | 0.60* | 0.06ns | 0.08ns | 0.10* | 0.15ns | -0.19* | 0.03ns |
| Pcw | -0.18ns | 0.14ns | -0.17* | 0.13ns | 0.42* | 0.31* | 1 | -0.03ns | 0.69** | 0.59* | -0.24* | -0.90* | -0.34* |
| BM | 0.02ns | 0.21* | 0.05ns | 0.18ns | 0.40* | 0.03* | 0.14ns | 1 | 0.54** | 0.63* | -0.54* | -0.43* | -0.33* |
| GY | -0.29* | 0.08ns | -0.28* | 0.45* | 0.79* | 0.26* | 0.29* | 0.31* | 1 | 0.10* | -0.61* | -0.73* | -0.69* |
| TKW | -0.15* | 0.48* | -0.14* | -0.02ns | 0.31* | 0.27* | 0.07* | 0.21* | 0.19* | 1 | -0.15* | -0.15* | -0.14* |
| Stm-2 | 0.16* | -0.02ns | 0.17* | -0.24* | -0.32* | -0.07* | -0.21* | -0.09ns | -0.36* | -0.11* | 1 | 0.98** | 0.95** |
| SV | 0.17* | -0.01ns | 0.18* | -0.30* | -0.39* | -0.12* | -0.23* | -0.09ns | -0.49* | -0.05ns | 0.82** | 1 | 0.92** |
| SSV | 0.15* | 0.16ns | 0.16* | -0.23* | -0.32* | -0.08ns | -0.20* | -0.10* | -0.37* | -0.08ns | 0.92** | 0.86** | 1 |

Where: DF: days to 50% flowering, PH: plant height (cm), DM: days to 95% maturity, HN: head count, HW: panicle/head weight, Pcl: panicle length (cm), Pcw: panicle width (cm), BM: above ground biomass ($kgha^{-1}$), TKW: 1000 kernel weight, $Stm^{-2}$: (Striga count per square meter), SV: *Striga* vigourisity(0-9score), SSV: *Striga* severity.

**Table 3.** Path coefficient analysis of direct (**diagonal**) and indirect (**off diagonal**) effects at phenotypic level of thirteen traits on grain yield of sorghum genotypes evaluated for *Striga* hermonthica at Kobo, 2018

| Traits | DF | PH | DM | HN | HW | Pcl | Pcw | BM | TKW | Stm-2 | SV | SSV | $r_p$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DF | -0.019 | -0.001 | 0.033 | -0.010 | -0.268 | -0.005 | 0.014 | 0.001 | 0.007 | 0.159 | -0.054 | 0.146 | -0.29 |
| PH | -0.003 | -0.004 | 0.007 | -0.003 | 0.108 | 0.002 | -0.010 | 0.003 | -0.021 | 0.001 | 0.004 | 0.000 | 0.08 |
| DM | -0.019 | -0.001 | 0.034 | -0.009 | -0.258 | -0.004 | 0.012 | 0.001 | 0.006 | -0.008 | -0.055 | -0.025 | -0.28 |
| HN | 0.009 | 0.001 | -0.015 | 0.021 | 0.371 | 0.003 | -0.009 | 0.002 | 0.001 | 0.011 | 0.095 | 0.036 | 0.45 |
| HW | 0.007 | -0.001 | -0.012 | 0.011 | 0.742 | 0.006 | -0.031 | 0.005 | -0.014 | 0.015 | 0.122 | 0.051 | 0.80 |
| Pcl | 0.005 | 0.001 | -0.009 | 0.004 | 0.253 | 0.017 | -0.023 | 0.001 | -0.012 | 0.003 | 0.039 | 0.012 | 0.26 |
| Pcw | 0.004 | -0.001 | -0.006 | 0.003 | 0.312 | 0.005 | -0.075 | 0.002 | -0.003 | 0.010 | 0.073 | 0.032 | 0.29 |
| BM | 0.001 | -0.001 | 0.002 | 0.004 | 0.294 | 0.001 | -0.011 | 0.013 | 0.205 | 0.004 | 0.028 | 0.016 | 0.31 |
| TKW | 0.003 | 0.001 | -0.005 | -0.001 | 0.233 | 0.005 | -0.005 | 0.003 | -0.045 | 0.005 | 0.015 | 0.013 | 0.19 |
| Stm-2 | -0.003 | -0.002 | 0.006 | -0.005 | -0.234 | -0.001 | 0.015 | -0.001 | 0.005 | -0.047 | -0.258 | -0.155 | -0.36 |
| SV | -0.003 | 0.001 | 0.006 | -0.006 | -0.289 | -0.002 | 0.017 | -0.001 | 0.002 | -0.038 | -0.314 | -0.138 | -0.49 |
| SSV | -0.003 | 0.001 | 0.005 | -0.005 | -0.238 | -0.001 | 0.015 | -0.099 | 0.004 | -0.045 | 0.860 | -0.160 | -0.37 |

Where: DF: days to 50% flowering, PH: plant height (cm), DM: days to 95% maturity, HN: head count, HW: panicle/head weight, Pcl: panicle length (cm), Pcw: panicle width (cm), BM: above ground biomass ($kgha^{-1}$), TKW: 1000 kernel weight, $Stm^{-2}$: (Striga count per square meter), SV: *Striga* vigourisity (0-9score), SSV: *Striga* severity.

Residual=0.33, $r_p$ Phenotypic correlation with grain yield.

The Striga related parameters in addition to their considerable direct negative effect; Striga count per square meter (-0.234), Striga vigourisity (-0.289) and Striga severity (-0.238) showed negative indirect effect through head weight. Therefore, these traits can be taken as an indicator of selection indices for Striga resistance and/or tolerance sorghum genotypes development. The phenotypic residual value (0.33) indicated that the traits included in the phenotypic path analysis explained (67%) of the variation for grain yield.

### 3.3. Estimation of Genotypic Direct and Indirect Effects of Various Traits on Grain Yield

Estimates of genotypic direct and indirect effects of the selected traits on grain yield are presented (Table 4). Thousand kernel weight showed the highest positive direct effect (0.911) followed by panicle width (0.504), days to flowering (0.294) and head weight (0.169) and insignificant positive direct effect to head number. This result is in line with Chittapur and Biradar (2015) for direct positive correlation of thousand kernel weight. Thousand kernel weight had positive direct effect and the genotypic correlation with grain yield was positive and significant. Its indirect effect through panicle width and panicle length was positive therefore, the positive correlation with grain yield was mainly due to its direct and indirect effects. Panicle width had positive direct effect and negative indirect effect through panicle length (0.303) and thousand kernel weight (-0.298). Head weight had positive direct effect and the genotypic correlation was positive and significant with grain yield. Its indirect positive effect through panicle width (0.35), panicle length (0.22), and thousand seed weight (0.20) given considerable correlation to grain yield.

The highest negative direct effect was showed by *Striga* parameters [Striga count per square meter (-0.44), *Striga* vigourisity (-0.85) and *Striga* severity (-0.87)]. The *Striga* related traits exerted also negative indirect effects via most traits with grain yield. Panicle length (-0.58), days to maturity (-0.44) and plant height (-0.56) also had direct negative effect with grain yield. The genotypic residual value (0.27) indicated that the traits used in the genetic path analysis explained (73%) of the variation for grain yield.

**Table 4.** Path coefficient analysis of direct (**diagonal**) and indirect (**off diagonal**) effects at genotypic level of thirteen traits on grain yield of sorghum genotypes evaluated for *Striga hermonthica* at Kobo, 2018

| Traits | DF | PH | DM | HN | HW | Pcl | Pcw | BM | TKW | Stm-2 | SV | SSV | $r_g$ |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DF | 0.294 | -0.143 | -0.443 | -0.011 | -0.070 | 0.125 | -0.060 | -0.006 | -0.038 | -0.188 | -0.344 | -0.376 | -0.322 |
| PH | 0.074 | -0.568 | -0.124 | -0.033 | -0.011 | -0.031 | -0.008 | 0.064 | 0.465 | -0.086 | -0.139 | -0.215 | -0.034 |
| DM | 0.294 | -0.159 | -0.443 | -0.056 | -0.055 | 0.126 | -0.051 | -0.009 | -0.010 | -0.165 | -0.284 | -0.325 | -0.284 |
| HN | -0.192 | 0.216 | -0.639 | 0.087 | -0.021 | 0.051 | 0.149 | 0.061 | -0.087 | 0.545 | 0.833 | 0.870 | 0.232 |
| HW | -0.121 | 0.036 | -0.324 | -0.011 | 0.169 | 0.221 | 0.359 | -0.009 | 0.202 | 0.253 | 0.850 | 0.706 | 0.980 |
| Pcl | -0.063 | -0.030 | 0.095 | -0.008 | -0.064 | -0.587 | 0.303 | -0.011 | 0.096 | -0.069 | 0.161 | -0.027 | -0.084 |
| Pcw | -0.214 | 0.008 | 0.045 | 0.026 | 0.121 | -0.353 | 0.504 | 0.006 | -0.539 | 0.107 | 0.860 | 0.298 | 0.697 |
| BM | -0.035 | 0.193 | -0.022 | -0.028 | 0.008 | -0.035 | -0.015 | -0.190 | 0.902 | 0.239 | 0.366 | 0.287 | 0.870 |
| TKW | 0.009 | -0.290 | 0.005 | -0.008 | 0.037 | -0.062 | -0.298 | -0.169 | 0.911 | 0.066 | 0.124 | 0.118 | 0.098 |
| Stm-2 | -0.012 | -0.111 | -0.165 | -0.107 | -0.097 | -0.092 | -0.121 | 0.102 | -0.135 | -0.443 | -0.840 | -0.868 | -0.615 |
| SV | 0.125 | -0.093 | -0.148 | -0.086 | -0.193 | 0.111 | -0.640 | 0.756 | -0.133 | -0.488 | -0.850 | -0.972 | -0.740 |
| SSV | 0.127 | -0.140 | -0.165 | -0.087 | -0.137 | -0.018 | -0.342 | 0.063 | -0.123 | -0.442 | 0.85 | -0.870 | -0.698 |

Where: DF: days to 50% flowering, PH: plant height (cm), DM: days to 95% maturity, HN: head count, HW: panicle/head weight, Pcl: panicle length (cm), Pcw: panicle width (cm), BM: above ground biomass ($kgha^{-1}$), TKW: 1000 kernel weight, $Stm^{-2}$: (Striga count per square meter), SV: *Striga* vigourisity (0-9score), SSV: *Striga* severity.

Residual=0.27 $r_g$=Genotypic correlation with grain yield.

## 4. Conclusion

Grain yield in a given crop is a complex character affected directly or indirectly by every gene present in plant. Selection on the basis of grain yield character alone is usually not very effective and efficient. Knowing the association between yield and yield traits and cause and effect contributes to yield has great advantage in plant breeding. Grain yield was genotypically positively significantly correlated to head/panicle weight (0.80), panicle width (0.69) and above ground biomass (0.54). Days to flowering ($r_p$=-0.29) and days to maturity ($r_p$=-0.28) and *Striga* parameters (*Striga* count m$^2$, $r_p$=-0. 36), *Striga* vigourisity ($r_p$=-0.49) and *Striga* severity ($r_p$=-0.37) significantly negatively correlated to grain yield.

Head weight (0.74) shown the highest positive direct effect on grain yield and the highest negative direct effect was showed by *Striga* parameters (*Striga* count per square meter (-0.44), *Striga* vigourisity (-0.85) and *Striga* severity (-0.87). Panicle length, days to maturity and plant height also had direct negative effect with grain yield. The present study indicated that these traits are important characters for grain yield improvement. The remaining independent traits showed negative/positive direct effect had indirect effect on grain yield. For instance, thousand kernel weights had positive direct effect and the genotypic correlation with grain yield was positive and significant. Its indirect effect through panicle width and panicle length was positive therefore, the positive correlation with grain yield was mainly due to its direct and indirect effects.

**Conflict of interest**

The authors declare that there is no conflict of interest.

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