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Genetic variability in agronomic traits and associations in sorghum [*(Sorghum bicolor (L.) Moench)*] genotypes at intermediate agro-ecology sorghum growing areas of Ethiopia

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The present study consists of 14 sorghum genotypes evaluated at Bako, Jimma and Mechara research centers to study genetic variability and interrelationships of traits with grain yield. The experiment was conducted by using randomized complete block design (RCBD) with three replications during 2014 and 2015 main rainy season. Data on important agronomic traits were collected. The combined analysis of variance (ANOVA) across years and locations showed highly significant differences among genotypes for all traits, indicating the presence of sufficient variability among the genotypes. Environmental coefficients of variation (ECV), genotypic coefficients of variation (GCV) and Phenotypic coefficient of variation (PCV) ranges of the study are days to 50% maturity (DM, 0.49) to number of seeds per panicle (NSPP, 6.11); DM (0.31) to PAS (16.99) and DM (1.12) to GY (20.86) in the same order. High h^2_{BS} values were observed in hundred seed weight (HSW, 76%), DS (70%), plant height (PH, 65%) and PAS (63). High value of genetic advance as a percentage of mean ($GA\% \mu$) was recorded by PAS (27.42%), PH (26.29%) and DS (20.65%) and moderate amount of $GA\% \mu$ was recorded by HSW (11.78%) and HW (11.08%). High h^2_{BS} coupled with high to moderate $GA\% \mu$ was reported for PH (65 and 26.29%); HSW (76 and 11.78%); PAS (63 and 27.42%) and DS (70 and 20.65%) indicating PH and HSW are controlled by additive gene action. GY had strong positive genotypic association with HW (0.99) followed by NSPP (0.96). These results suggested that any positive increase in such traits will increase the grain yield. The genotypic path analysis also showed that head weight per plot (HW, 1.96) and PH (0.55), had high and very high positive direct effect, respectively on GY indicating that these traits are the most important yield component traits. Hence, due consideration should be given to these traits while selecting promising lines.

Key words: Correlation coefficient, genetic advance, heritability, path coefficient, sorghum.

INTRODUCTION

Sorghum [*Sorghum bicolor (L.) Moench*] is the third (area coverage) and fourth (production) most important food crop of the Ethiopia (CSA, 2014). Intermediate agro-

ecology sorghum growing areas of the country are characterized by intermediate altitude (1600 to 1900 masl), high annual rain fall (~1000 mm), temperature and

humidity which support the development of several biotic stresses such as leaf and grain diseases. The efficiency of selection in crop improvement depends on the extent and nature of phenotypic and genotypic variability present in different agronomic traits of populations (Arora, 1991). Research work so far done on sorghum in intermediate altitude sorghum growing agro-ecology did not bring significant increase in the yield crop efficiency. Yield, being quantitative in nature is a complex trait with low heritability and depends upon several other components with high heritability (Grafius, 1959). Hence, selection of plants based directly on yield would not be very reliable. Association of characters was also used to determine the strength relationship among variables. Path analysis was made to assess the direct and indirect effects of each trait on grain yield (Dewey and Lu, 1959). The understanding of association between yield and yield related traits allows the breeders to plan the breeding program accordingly. The present study was conducted to study genetic variability and the interrelationships of traits with grain yield.

MATERIALS AND METHODS

A total of 14 sorghum genotypes which were previously developed by pedigree breeding method were used for this experiment. The experiment was conducted at three locations which represented the intermediate agro ecology, namely: Bako, Jimma and Mechara Agricultural Research Centers in 2014 and 2015 main rainy seasons. The experiment was carried out by using a randomized complete block design (RCBD) with three replications. A plot size of 3 rows with 5 m row length and 0.75 m row width was also used to conduct the experiment at national variety trial stage. Sowing was conducted manually, and the seeds were drilled and spaced 0.75 m apart and latter thinned to a spacing of 20 cm between plants. The trial received Di-ammonium Phosphate (DAP) and urea fertilizers at planting and approximately at 35 to 40 days after emergency, respectively on basis of 100 kg ha⁻¹. Data on days to 50% flowering, plant height (cm), days to maturity, grain yield (tones/ha), hundred seed weight (g), head weight per plot (kg), disease score (1-5 scale, where 1=resistance and 5=susceptible), number of seeds per panicle by following the procedures of (Adugna and Bekele, 2013) and overall agronomic aspect (1-5 scale, where 1=excellent and 5=poor), were recorded.

Data analysis

The General Linear Model procedure (PROC GLM) of SAS (SAS, 2008) was used to determine the variations of genotypes. In this analysis, genotypes, locations and years were fitted as a random effect. The data recorded on the aforementioned parameters across locations and years were analyzed using the following linear additive model as outlined by Snedecor and Cochran (1980) and Annicchiarico (2002). Format of combined analysis of variance across location and year is shown in Table 1. The linear statistical model for the combined analysis of experiments laid out in a

randomized complete block design is:

$$X_{ijkl} = \mu + G_i + R_{jkl} + L_k + Y_l + GL_{ik} + GY_{il} + LY_{kl} + GLY_{ikl} + E_{ijkl}$$

where X_{ijkl} = observed value, μ = overall mean, G_i = effect of genotype, R_{jkl} = effect of replication, L_k = effect of location, Y_l = effect of year, $GL_{ik} + GY_{il} + LY_{kl} + GLY_{ikl}$ = effects of Genotype×Location, Genotype×Year, Location×Year, and Genotype×Location×Year interactions, respectively. E_{ijkl} = residual effects or experimental error. Additionally, $g, r, l,$ and y are numbers of genotypes, replications, locations and years, in the same order and $g = 14, r = 3, l = 3$ and $y = 2$.

Components of variance, estimation of heritability and genetic advance

The phenotypic and genotypic variances for the combined data across year and location were computed according to the method suggested by Annicchiarico (2002).

$$\sigma^2_g = M5 - M3 - M4 + M2/rl$$

where σ^2_g = variance of genotypes.

$$\sigma^2_{gl} = M3 - M2/ry$$

where σ^2_{gl} = variance of genotypes by locations interactions.

$$\sigma^2_{gy} = M4 - M2/rl$$

where σ^2_{gy} = variance of genotypes by years interactions.

$$\sigma^2_{gly} = M2 - M1/r$$

where σ^2_{gyl} = variance of genotypes by location and years interactions.

Phenotypic, genotypic and environmental coefficients of variation

Phenotypic coefficient of variation (PCV), genotypic coefficients of variation (GCV) and environmental coefficients of variation (ECV) were calculated according to Burton (1952) using combined data across the three locations and two years.

$$GCV = \sqrt{(\sigma^2_g/\mu)} \times 100$$

$$PCV = \sqrt{(\sigma^2_p/\mu)} \times 100$$

$$ECV = \sqrt{(\sigma^2_e/\mu)} \times 100$$

Broad sense heritability (h^2_{BS}) for the combined data across year and location was estimated according to Gordon et al. (1972), and it was grouped as low (below 30%), medium (30-60%) and high (above 60%) as suggested by Johnson et al. (1955).

$$h^2_{BS} = \sigma^2_g / (\sigma^2_g + \sigma^2_{gy}/y + \sigma^2_{gl}/l + \sigma^2_{gyl}/ly + \sigma^2_{ryl})$$

where r, y and l denote the number of replicates, years and

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Table 1. Format of combined ANOVA across years and locations used in the present study.

Source of variations	Degree of freedom	Mean squares	Expected mean squares
Locations (L)	l-1	M9	$\sigma^2 + \gamma\sigma^2_{\rho} + \rho\sigma^2_{\gamma\lambda\psi} + \rho\psi\sigma^2_{\gamma\lambda} + \rho\gamma\sigma^2_{\lambda\psi} + \rho\gamma\psi\sigma^2_{\lambda}$
Year (Y)	y-1	M8	$\sigma^2 + \gamma\sigma^2_{\rho} + \rho\sigma^2_{\gamma\lambda\psi} + \rho\lambda\sigma^2_{\gamma\psi} + \rho\gamma\sigma^2_{\lambda\psi} + \rho\gamma\lambda\sigma^2_{\psi}$
YxL	(y-1)(l-1)	M7	$\sigma^2 + \gamma\sigma^2_{\rho} + \rho\sigma^2_{\gamma\lambda\psi} + \rho\gamma\sigma^2_{\lambda\psi}$
Replications (r)	r-1	M6	$\sigma^2 + \gamma\sigma^2_{\rho}$
Genotypes (G)	g-1	M5	$\sigma^2 + \rho\sigma^2_{\gamma\lambda\psi} + \rho\lambda\sigma^2_{\gamma\psi} + \rho\psi\sigma^2_{\gamma\psi} + \rho\lambda\psi\sigma^2_{\gamma}$
GxY	(g-1)(y-1)	M4	$\sigma^2 + \rho\sigma^2_{\gamma\lambda\psi} + \rho\lambda\sigma^2_{\gamma\psi}$
GxL	(g-1)(l-1)	M3	$\sigma^2 + \rho\sigma^2_{\gamma\lambda\psi} + \rho\psi\sigma^2_{\gamma\lambda}$
GxLxY	(g-1)(l-1)(y-1)	M2	$\sigma^2 + \rho\sigma^2_{\gamma\lambda\psi}$
Error	(g-1)(r-1)ly	M1	σ^2

locations, respectively.

Genetic advance (GA) was computed by following the procedure suggested by Johanson et al. (1955).

$$GA = K \times h^2BS \times \sqrt{\sigma^2_p}$$

where K= the selection intensity at 5% (2.06).

Genetic advance as percent of mean [GA (% mean)] computed as follows and it was further sorted out as low (0-10%), moderate (10-20%) and high ($\geq 20\%$) as given by Johnson et al. (1955) and Falconer and Mackay (1996).

$$GA (\% \text{ of mean}) = GA/\mu \times 100$$

Correlation and path coefficient analyses

Correlation coefficient was computed from variance and covariance components as suggested by Burton (1952), Wright (1968) and Singh and Chaundhary (1985). The correlation coefficient was further partitioned into direct and indirect causes according to Dewey and Lu (1959), Wright (1960) and Singh and Chaundhary (1985).

RESULTS AND DISCUSSION

The combined analysis of variance across years and locations showed highly significant differences among the genotypes (G) for all traits, which indicates the presence of variability among the genotypes being evaluated and the possibility of ample scope of improvement by selection (Table 2). The GxL interactions of genotypes were significant for all traits except for days to maturity. The significant difference of GxL interactions indicates that genotypes respond differently across location for these traits and this requires testing of genotypes over a range of locations. A highly significant GxLxY interaction was also observed for most of the traits, showing that genotypes were inconsistent in their performance when tested across locations and years. Similar finding was reported by Phuke et al. (2017). They reported highly significant variation of G and GxYxL interaction for days to 50% flowering, plant height, hundred seed weight and grain yield on sorghum. Highly significant yield differences between genotypes, locations, year and their

interactions show the need to develop genotypes that are adapted to specific environmental conditions and the need to identify genotypes that are exceptionally stable across environments. A large yield and agronomic traits variation explained by genotypes indicated that the genotypes were diverse, with large differences between locations means causing most of the variation of traits.

Insignificant GxLxY interaction for days to 50% flowering, days to maturity and hundred seed weight indicating genotypes performed similarly across year and locations with respect to these traits. For all traits in the present study, the mean square values of GxLxY interactions were lower than genotypic value (Table 2), signifying that the traits are mainly under genetic control. Similar finding was reported by Nida et al. (2016) on grain yield of sorghum. GxL interactions were non-significant for days to maturity, significant ($p < 0.05$) for hundred seed weight and highly significant ($p < 0.01$) for the rest of traits. The significant difference of GxL interactions indicates that genotypes respond differently across location for these traits and this requires testing of genotypes over a range of locations to identify stable genotypes. These results are supported by Khan et al. (2013) who found significant variation of G, GxL and LxY interactions for plant height in sunflower. Highly significant GxL interactions for days to 50% flowering, plant height and grain yield was also reported by Tadesse et al. (2008) on sorghum parental lines.

Estimates of variance components, heritability and genetic advance

The present results on variance component showed that the phenotypic variances were slightly higher than the genotypic variance for days to 50% flowering, plant height, hundred seed weight, disease score and overall agronomic aspect, signifying the influence of environment on these traits was very low. ECV, GCV and PCV ranges of this study are days to maturity (0.49) to number of seeds per panicle (6.11), days to maturity (0.31) to overall agronomic aspect (16.99) and days to maturity

Table 2. Mean square for agronomic traits of sorghum genotypes tested at Mechara, Bako & Jimma in 2014 & 2015 main rainy seasons.

Source of variation	Degree of freedom	Days to 50% flowering	Plant height (cm)	Days to 50% maturity	Gain yield (tons ha ⁻¹)	Hundred seed weight (g)	Head weight per plot (kg)	Disease score (1-5)	Number of seeds per panicle	Overall agronomic aspect (1-5)
Locations (L)	2	3619.8**	58259.1**	9468.6**	4.5**	4.5**	105.9**	6.9**	4561187001.0**	6.9**
Year (Y)	1	24702.5**	212628.6**	20773.6**	421.7**	1.9**	1499.9**	6.8**	7996833.0 ^{ns}	14.0**
Y×L	2	1781.0**	49162.5**	21.8 ^{ns}	67.3**	0.5*	101.9**	8.2**	1974642669.0**	3.1**
Replications	2	80.3 ^{ns}	557.9 ^{ns}	18.5 ^{ns}	0.1 ^{ns}	0.3 ^{ns}	3.0 ^{ns}	2.9**	628374733.0**	0.3 ^{ns}
Genotypes (G)	13	183.0**	22047.5**	64.2**	9.3**	0.6**	13.1**	1.7**	634475393.0**	6.0**
G×Y	26	313.4**	6240.6**	60.7**	9.6**	0.1 ^{ns}	10.7**	0.2 ^{ns}	557218242.0**	1.9**
G×L	26	86.8**	1550.6**	26.3 ^{ns}	2.0**	0.2*	2.9**	0.6**	325777153.0**	1.2**
G×L×Y	13	37.7 ^{ns}	2642.8**	17.7 ^{ns}	2.6**	0.1 ^{ns}	8.4**	0.3*	217382942.0**	0.9**
Error	166	32.0	458.1	13.0	0.2	0.2	1.3	0.2	85887800.0	0.4
CV (%)	-	5.0	11.1	2	12.2	16.7	18.3	21.8	25.9	21.7
Mean	-	114.18	193.49	172.38	4.01	2.29	6.35	2.08	35759.40	2.76
LSD	-	3.7	14.1	2.4	0.3	0.3	0.8	0.3	6099.0	0.42

*, **, ^{ns}Significant at 0.05, 0.01 and non significant, respectively; LSD: The least significant difference value; CV(%): coefficient of variation in percentage.

Table 3. Genetic parameters for agronomic traits of combined data of sorghum lines tested at Mechara, Bako and Jimma in 2014 and 2015 main rainy season.

Genetic parameter	Days to 50% flowering	Plant height (cm)	Days to 50% maturity	Gain yield (tons ha ⁻¹)	Hundred seed weight (g)	Head weight plot ⁻¹ (kg)	Disease score (1-5)	Number of seeds per panicle	Overall agronomic aspect (1-5)
PV	28.75	1443.56	3.72	0.70	0.03	1.66	0.09	41507133.3	0.34
GV	9.97	938.84	0.29	0.02	0.02	0.44	0.06	1729836.7	0.22
EV	1.78	25.45	0.72	0.01	0.01	0.08	0.01	4771544.0	0.02
PCV%	4.70	19.64	1.12	20.86	7.56	20.29	14.42	18.02	21.13
GCV%	2.77	15.84	0.31	3.53	6.18	10.45	11.78	3.68	16.99
ECV%	1.17	2.61	0.49	2.49	4.37	4.45	4.81	6.11	5.12
h ² BS (%)	35	65	8	2	76	27	70	4	63
GA	3.83	50.87	0.31	0.04	0.27	0.70	0.43	557.41	0.76
GA%μ	3.36	26.29	0.18	0.95	11.78	11.08	20.65	1.56	27.42
Mean(μ)	114.18	193.49	172.38	4.01	2.29	6.35	2.08	35759.40	2.76

GV: Genotypic variance, EV: environmental variance, PV: phenotypic variance.

(1.12) to grain yield (20.86), in the same order (Table 3). Based on the classification of Sivasubramanian and Madhavamenon (1973),

high PCV values were observed in grain yield, head weight and overall agronomic aspect and moderate PCV value were observed in plant

height, disease score and number of seeds per plant. Moderate amount of GCV were observed in plant height, head weight, disease score and

overall agronomic aspect. PCV value of genotypes was much higher than GCV for grain yield showing the environments were diverse as a result of this, the response of genotypes were significantly different in each environment. The difference between PCV and GCV was maximum for grain yield followed by number of seeds per panicle, indicating that these traits are more influenced by the environment. The highest PCV and GCV value for plant height is in accordance with the report of Abraha et al. (2015). Tomar et al. (2012) and Godbharle et al. (2010) also reported low PCV and GCV on days to 50% flowering and Warkad et al. (2008) and Abraha et al. (2015) also reported low PCV and GCV on days to maturity. Similarly, moderate value of PCV and GCV on plant height reported by Warkad et al. (2008) agrees with present research report.

The GCV is only an indication of the presence of high degree of genetic variation; however, the amount of heritable portion of variation can only be determined with the help of estimates of heritability and genetic advance. Broad heritability (h^2_{BS}) for the combined data across year and location was estimated according to Gordon et al. (1972) and it was further grouped as low (below 30%), medium (30-60%) and high (above 60%) as suggested by Johnson et al. (1955). Based on the aforementioned classification, high heritability values were observed in hundred seed weight (76%), disease score (70%), plant height (65%) and over all agronomic aspect (63) and moderate value of heritability was observed in days to 50% flowering (35%). High heritability of the traits indicates that they are less influenced by environment in their phenotypic expression. Therefore, the breeders could get chance to select promising genotypes based on the phenotypic performance of these traits. Agreeing with the present study, high heritability estimates for overall agronomic aspect were reported by Abraha et al. (2015). High heritability estimates for plant height was also reported by Tomar et al. (2012), Godbharle et al. (2010) and Bhagasara et al. (2017) which is in accordance with the present findings. Like the present study, high heritability estimates for hundred seed weight was also reported by Bhagasara et al. (2017).

On the other hand, low heritability was observed for days to maturity (8%), grain yield (2%), head weight (27%) and number of seed per panicle (4%) indicating that these traits would not respond to phenotypic selection. Low heritability for grain yield were also reported by Bello et al. (2001), Bello et al. (2007), Naim et al. (2012) and Abraha et al. (2015) which is in agreement with the present study. Furthermore, in the present finding, Naim et al. (2012) reported low heritability for head weight and number of seed per panicle.

The heritability values alone provide no indication of the amount of genetic progress that would result in selecting the best individual, but heritability estimates along with the genetic advance are more useful (Johnson et al.,

1955). Genetic advance as percent mean [GA (% mean)] sorted out as low (0-10%), moderate (10-20%) and high ($\geq 20\%$) as given by Johnson et al. (1955) and Falconer and Mackay (1996). Thus, in the present study high value of GA% μ was recorded by overall agronomic aspect (27.42%), plant height (26.29%) and disease score (20.65%) and moderate amount of GA% μ was recorded by hundred seed weight (11.78%) and head weight (11.08%). On the other hand, low amount of GA% μ was recorded by days to maturity (0.18%), grain yield (0.95%) and number of seed per panicle (1.56%) and days to 50% flowering (3.36%) in the same order. High heritability coupled with high to moderate genetic advance as percent of mean was reported for plant height (65 and 26.29%), hundred seed weight (76 and 11.78%), overall agronomic aspect (63 and 27.42%) and disease score (70 and 20.65%) in the same order. These indicate that plant height and hundred seed weight are controlled by additive gene action. Therefore, the phenotypic selection based on these traits would result in the improvement of the genotypes. Similar finding of high heritability coupled with high to moderate genetic advance as percent of mean was reported by Sharma et al. (2006) and Ranjith et al. (2017) for hundred seed weight; Arunkumar et al. (2004), Godbharle et al. (2010), Tomar et al. (2012), Kour and Pradhan, (2016), and Ranjith et al. (2017) for plant height. On the other hand, moderate value of heritability along with low genetic advance as percent of mean was observed for days to 50% flowering indicating that variability is mainly due to the non-additive gene effects and hence heterosis breeding can be successfully exploited in improving this character.

Phenotypic, genotypic and environmental correlation coefficients

The results of genotypic correlation coefficient were higher than those of phenotypic and environmental correlation coefficients for all the characters except the genotypic association of days to 50% flowering with grain yield and disease score which revealed that there was a greater contribution of genetic factors in the expression of these traits in relation to the environmental factor (Table 4). Grain yield had strong positive genotypic association with head weight (0.99) followed by number of seeds per panicle (0.96). These results suggested that any positive increase in such traits will increase the grain yield. Similar findings of strong positive grain yield association with number of seeds per panicle and head weight were reported by Turchi and Rezai (1997), by Tesso et al. (2011) with head weight and by Yang and Yang (1995) with number of seeds per panicle. The genotypic association also showed that hundred seed weight had strong positive association with disease score (0.72), indicating that small seeded genotypes are more resistance to disease reaction that is why during data

Table 4. Phenotypic (r_p), genotypic (r_g) and environmental (r_e) correlation coefficients of various traits for the combined data.

Correlation		PH	DM	GY	HSW	HW	DS	NSPP	PAS
DF	r_p	0.49*	0.60**	-0.36*	-0.20 ^{NS}	-0.42*	-0.07 ^{NS}	-0.06 ^{NS}	0.20 ^{NS}
	r_g	0.73**	0.65**	-0.36*	-0.28 ^{NS}	-0.78**	-0.05 ^{NS}	0.12 ^{NS}	0.43*
	r_e	0.16 ^{NS}	0.22 ^{NS}	-0.23 ^{NS}	-0.10 ^{NS}	-0.10 ^{NS}	-0.03 ^{NS}	-0.09 ^{NS}	-0.08 ^{NS}
PH	r_p	1	0.55**	-0.43*	0.01 ^{NS}	-0.57**	0.21 ^{NS}	-0.26 ^{NS}	0.59**
	r_g	1	0.75**	-0.64**	0.03 ^{NS}	-0.91**	0.28 ^{NS}	-0.44*	0.72**
	r_e	1	0.17 ^{NS}	-0.04 ^{NS}	0.10 ^{NS}	0.03 ^{NS}	0.06 ^{NS}	-0.11 ^{NS}	0.07 ^{NS}
DM	r_p		1	-0.41*	0.28 ^{NS}	-0.35*	0.31 ^{NS}	-0.52**	0.61**
	r_g		1	-0.49*	0.63**	-0.46*	0.54**	-0.92**	0.89**
	r_e		1	-0.32*	0.01 ^{NS}	-0.16 ^{NS}	-0.02 ^{NS}	-0.20 ^{NS}	0.10 ^{NS}
GY	r_p			1	0.02 ^{NS}	0.93**	-0.61**	0.78**	-0.80**
	r_g			1	-0.27 ^{NS}	0.99**	-0.97**	0.96**	-0.99**
	r_e			1	0.08 ^{NS}	0.64**	0.05 ^{NS}	0.52**	-0.25 ^{NS}
HSW	r_p				1	0.21 ^{NS}	0.51*	-0.48*	0.31 ^{NS}
	r_g				1	0.15 ^{NS}	0.72**	-0.70**	0.50*
	r_e				1	0.03 ^{NS}	-0.03 ^{NS}	-0.35*	0.05 ^{NS}
HW	r_p					1	-0.45*	0.58**	-0.74**
	r_g					1	-0.81**	0.77**	-0.99**
	r_e					1	0.09 ^{NS}	0.26 ^{NS}	-0.24 ^{NS}
DS	r_p						1	-0.77**	0.81**
	r_g						1	-0.99**	0.99**
	r_e						1	0.08 ^{NS}	0.10 ^{NS}
NSPP	r_p							1	-0.80**
	r_g							1	-0.99**
	r_e							1	-0.13 ^{NS}

^{NS}, *, ** and are no significant, significant at 0.05 and 0.01 probability level, respectively.

collection, 1 is assigned for resistance and 5 is for susceptible genotypes. In the present study, plant height had positive significant genotypic association with days to flowering (0.73) showing that late blooming genotypes are taller than early blooming ones. This result agrees with research findings of Murray et al. (2008), Bunphan et al. (2014), and Abraha et al. (2015). In the present study, days to 50% flowering has also positive significant genotypic association with overall agronomic aspect (0.43) showing that early blooming genotypes were preferred by sorghum breeder during evaluation.

On the other hand, the genotypic association showed that the overall agronomic aspect and disease score had strong negative association with grain yield, indicating that disease resistance genotypes and genotypes with excellent in overall agronomic aspect gave better yield that is why during data collection, 1 is assigned for excellent genotypes and 5 is for poor genotypes.

Similarly, overall agronomic aspect had the strongest negative genotypic association with grain yield (-0.99), head weight (-0.99) and number of seeds per panicle (-0.99), showing that high yielding along with big panicle and high number of seeds per panicle are a good parameter to select a genotype of excellent in agronomic desirability (Table 4).

Path coefficient analysis

In crop improvement, information on the association between two traits is necessary to improve the simultaneous selection of traits. However, evaluating and interpreting the amount an association can lead to mistakes in the selection strategy due to pleiotropism. As a result of this reason, investigating the cause and effect of the relationships into direct and indirect effects of a

Table 5. Genotypic path coefficient analysis direct effects on main diagonal (bold & diagonal) and indirect effects (off diagonal) of different agronomic traits on grain yield of sorghum genotypes.

Correlation	DF	PH	DM	HSW	HW	NSPP	r _g
DF	-0.70	0.38	0.99	0.50	-1.53	-0.01	-0.36
PH	-0.51	0.53	1.15	-0.05	-1.78	0.04	-0.64
DM	-0.46	0.39	1.53	-1.14	-0.90	0.08	-0.49
HSW	0.19	0.02	0.96	-1.80	0.29	0.06	-0.27
HW	0.55	-0.48	-0.70	-0.27	1.96	-0.07	0.99
NSPP	-0.08	-0.23	-1.41	1.26	1.51	-0.09	0.96

DF: Days to 50% flowering, PH: Plant height in cm, DM: days to 50% maturity, GY: grain yield in ton/ha, HSW: hundred seed weight (g), HW: head weight per plot (kg), NSPP: Number of seeds per panicle, r_g: genotypic correlation coefficients with grain yield.

group of traits over the dependent variable by path analysis is very important (Cruz et al., 2004).

Path coefficients were classified as suggested by Lenka and Mishra (1973), where, 0.00-0.09 is negligible association effects, 0.10-0.19 is low, 0.20-0.29 is moderate, 0.30-0.99 is high and >1.0 is very high. Accordingly, the genotypic direct effect of plant height on grain yield was high and positive (0.55) but their genotypic correlation coefficient was negative (-0.64) and it was mostly due to very high positive indirect effects via days to maturity (1.13). Similarly, genotypic direct effect of days to maturity on grain yield was very high and positive (1.53) but their genotypic correlation coefficient was negative (-0.49) this is due to very high negative indirect effects via hundred seed weight (-1.14), and high negative indirect effects via head weight (-0.90) and days to 50% flowering (-0.46). The genotypic path analysis (Table 5) also showed that head weight had very high positive direct effect on grain yield (1.96) indicating the importance of head weight as one of the most important yield component traits. Hence, due consideration should be given to traits like head weight and plant height, while planning a breeding strategy for increased grain yield and promising lines could be selected based on these traits. High and positive direct effect of head weight on grain yield was reported by Ezeaku and Mohammed (2006).

Conclusions

The present study showed that plant height (PH) and hundred seed weight (HSW) are controlled by additive gene action; thus, the phenotypic selection based on these traits would result in the improvement of the genotypes. On the other hand, low heritability traits like grain yield (GY) are greatly influenced by the environment and are suggested either to be tested over a wide range of environments or could be selected using molecular markers linked to QTLs for the target traits that enables individuals to be scored based on their genetic makeup and their phenotypic performance. The present studies also showed that the GY of sorghum genotypes can be increased by selecting head weight (HW) and

number of seeds per panicle jointly. It could also be concluded that selection of short plants will favor a higher yield (negative correlation). The genotypic path analysis also showed that plant height and head weight had high positive direct effect on grain yield indicating these traits are the most important yield component traits. Hence, due consideration should be given to these traits while selecting promising lines.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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