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Potential traits for aiding selection for high grain yield based on trait association and path analysis in sorghum

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Background: Simultaneous breeding of grain yield and desirable agronomic traits are effective when the traits are positively correlated and heritability is high. Knowledge of the magnitude of trait contribution is essential in hastening crop breeding progress.

Aim: This study aimed to investigate the correlations and path analysis of yield traits in grain sorghum.

Setting: The experiment was conducted in three different agro-ecological regions in Zimbabwe.

Methods: A total of 20 experimental sorghum genotypes were evaluated during the 2021–2022 and 2022–2023 cropping seasons across five sites representing primary sorghum production areas in Zimbabwe. A randomised complete block design replicated thrice was used. Correlation and path analysis were performed.

Results: Correlation analysis showed significant ($p \leq 0.05$) and positive correlation between grain yield and days to 50% flowering (phenotypic correlation [rp] = 0.48; genotypic correlation [rg] = 0.53), days to 95% physiological maturity (rp = 0.59; rg = 0.31) and panicle length (rp = 0.61; rg = 0.57) over the two seasons at both phenotypic and genotypic level. The path analysis revealed that days to 50% flowering (Pp = 0.185; Pg = 0.280), days to 95% physiological maturity (phenotypic path coefficient [Pp] = 0.169; genotypic path coefficient [Pg] = 0.201) and panicle length (Pp = 0.354; Pg = 0.194), had significant ($p \leq 0.05$) positive direct effects on sorghum grain yield at both phenotypic and genotypic level. Days to 50% flowering and panicle length had high heritability of 0.72 and 0.86, respectively.

Conclusion: Breeders are recommended to select high sorghum grain yielding genotypes through days to 50% flowering and panicle length making effective indirect selection for sorghum grain improvement.

Contribution: Identification and use of correlated traits for grain yield saves resources and increases breeding efficiency.

Keywords: correlated traits; drought stress; secondary traits; sorghum breeding; sorghum grain yield.

Introduction

Sorghum (*Sorghum bicolor* [L.] Moench) is the fifth important crop globally after wheat (*Triticum aestivum* L.), rice (*Oryza sativa* L.), barley (*Hordeum vulgare* L.) and maize (*Zea mays* L.) (Mundia et al. 2019). Africa accounts for 61% of total global area under sorghum with 41% output (Mundia et al. 2019). Sorghum productivity averages between 1.5 and 2 t ha^{-1} in Africa (FAO 2023). It is mainly grown for food in the arid and semi-arid regions of Africa, which are characterised by frequent long dry spells and heat stress (Hossain et al. 2022). In Africa, sorghum is considered the second most important crop for food security after maize. Sorghum is used as a source of carbohydrates and has a high nutritional profile that addresses mal-nutrition in Africa (Xiong et al. 2019). Sorghum also has antioxidant and anti-inflammatory capacities that assist in human disease prevention and treatment (Althwab et al. 2015).

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The prevailing effects of climate change that have led to induced drought and heat stresses are anticipated to worsen food insecurity in sub-Saharan Africa (Hadebe, Modi & Mabhaudhi 2017). In Zimbabwe, maize is failing even in high potential areas because of the effects of global warming, including *El Nino* (Mugiyo et al. 2023). During the 2023–2024 cropping season, the country experienced *EI Nino,* which was characterised by a more than 30 days dry spell that led to significant crop failures, with 40% of maize crops classified as 'poor' and 60% considered as total crop failure (UNOCHA 2024). Despite planting the usual ±1 777 540 ha of maize, only (30%) 744 271 metric tonnes were harvested, thereby exposing more than six million people to food insecurity, given that maize is a staple food in Zimbabwe (UNOCHA 2024; Zimbabwe Now 2024).

Sorghum remains undercultivated and underutilised compared to maize, despite its resilience to drought, superior nutritional profile and adaptability, making it an ideal candidate for ensuring food security in the face of climate variability (Phiri et al. 2019). Planting area and output for sorghum remain far below its potential, as maize continues to dominate agricultural landscapes (Phiri et al. 2019). Approximately 67% of farmers in Zimbabwe are located in arid and semi-arid regions, where agriculture is heavily impacted by erratic rainfall and recurrent droughts (FAO 2020). Sorghum, a drought-tolerant crop, is cultivated in these areas but yields remain low, averaging less than 0.4 t ha^{-1} (Phiri et al. 2019). This low productivity is because of various factors including reduced market demand compared to maize, poor agronomic practices and limited access to improved seeds (Nyoni et al. 2023). Despite these limitations, sorghum remains a viable crop for these regions because of its ability to thrive under drought and heat conditions, offering a critical food security option for farmers (Chadalavada, Kumari & Kumar 2021; Hossain et al. 2022; Liaqat et al. 2024; Phiri et al. 2019). It is imperative to prioritise high grain yield, drought resilience and disease resistance to boost sorghum production. Pyramiding these traits into one variety is what farmers expect and most agronomic traits are strongly correlated to final yield (Gasura, Setimela & Souta 2015).

Grain yield is a quantitative trait with low heritability, and it is mostly affected by the environment, which reduces breeding efficiency (Amare, Zeleke & Bultosa 2015; Enyew et al. 2021). In scenarios where heritability is low, indirect selection is inevitable. Traits that are positively and strongly correlated to yield and have high heritability can be used to improve selection efficiency through the use of a selection index (Mukoyi, Gasura & Makunde 2018). Improvement in any of such traits will simultaneously improve yield. It is of paramount importance for breeders to have information on the selection index as it saves both time and money, while maximising genetic gains for traits of interest (Gasura et al. 2015). Studies have reported that sorghum grain yield is strongly associated with traits such as seed size, panicle length, panicle width, plant height, days to 50% flowering and days to 95% physiological maturity (Mengesha et al. 2019; Mukondwa et al. 2020). Much progress occurs in crop breeding programmes when the desired traits are significantly and positively correlated.

Furthermore, the increasing number of secondary traits makes it increasingly challenging for breeders to identify those that significantly contribute to the final grain yield. Phenotypic or genotypic correlation estimates the significant presence, degree and direction of the mutual relationship between grain yield and yield contributing traits without necessarily considering the causality (Jaisi, Thapa & Poudel 2021). Such a short fall has stimulated many studies to focus on correlation and path coefficient analysis (Alnajjar & Dawod 2021; Chauhan & Pandey 2021; Kumar et al. 2023; Rohila, Arya & Kumari 2020). Path analysis is a multiple regression statistical analysis that estimates the magnitude and significance of cause and effect of each variable in order to determine the direct and indirect effects between sets of variables (Dong 2024). Determination of the associations among different traits, their direct and indirect effects on grain yield is a fundamental step in crop improvement, enabling breeders to identify key traits, simplify selection strategies and optimise multi-trait breeding programmes. It is a powerful tool for achieving genetic gains efficiently and effectively. Earlier studies reported that panicle weight, panicle length, panicle width and 100 seed weight had direct effects on grain yield, and that a selection of these traits improve sorghum yield (Khadakabhavi, Girish & Yashoda 2017; Vinoth et al. 2021). Other traits that were found to have positive direct effects on yield were leaf width and stem girth (Akatwijuka, Rubaihayo & Odong 2019; Subalakhshmi et al. 2019). However, information on critical traits that are correlated to grain yield, their direct and indirect effects is limited under combined drought stress and non-stress environments. Hence, this study aims to determine secondary traits associated with the grain yield of sorghum and their relative contributions using correlation and path analysis under combined non-stress, semi-arid and arid regions of Zimbabwe.

Research methods and design

A total of 20 sorghum genotypes collected from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) gene bank in Zimbabwe were used in the study. Five study sites representing sorghum production areas in Zimbabwe were used to conduct multi-environmental trials (Table 1), during the 2021–2022 and 2022–2023 cropping seasons. Zimbabwe has five agro-ecological regions that range from humid to arid (Mugandani et al. 2012). The trial used four of these different climate regions and excluded the high humid region I, which is not suitable for sorghum. The University of Zimbabwe Farm and the Gwebi Research Centre are located in agro-ecological II, while the Kadoma Research Centre is located in agro-ecological IIb. Kwekwe Research Centre and Makoholi Research Centre are located in agro-ecological III and IV, respectively.

TABLE 1: Study sites description.

Site code	City	Name of location	Geographical coordinates	Altitude (m)	Average seasonal rainfall	Mean temperature data
1	Harare	University of Zimbabwe Farm	31° 80'E, 17° 40'S	1490	750 mm – 1000 mm	18° C
2	Harare	Gwebi Research Centre	30° 32'E, 17° 41'S	1448	750 mm – 1000 mm	18° C
3	Kadoma	Kadoma Research Centre	29° 53'E, 18° 19'S	1149	650 mm – 800 mm	27° C
4	Kwekwe	Kwekwe Research Centre	23° 53'E, 18° 19'S	1220	500 mm – 700 mm	19° C
5	Masvingo	Makoholi Research Centre	30° 46'E, 19° 50'S	1204	300 mm – 550 mm	29° C

The study sites are located in different agro-ecologies with different soil characteristics. University of Zimbabwe farm site is characterised by xanthic *Ferralsols* derived from dolerite (FAO 2006). The top 0.2 m has medium textured sandy clay loams with 34% clay and 0.2 m – 0.4 m of the subsoil contains 38% clay content. Dominant soils at Gwebi Research Centre are classified as orthic *Ferralsols* according to Food and Agriculture Organization of United Nations (FAO) classification (FAO 2006). They have 38% clay content and 23% silt content in the top 0.30 m. Clay percentage increases to 41% in 0.2 m – 0.4 m subsoil. Kadoma Research Centre has silty clay loams that are derived from mafic rocks and fall under 5AE.3 Zimbabwe soil classification system (Nyamapfene 1991) which matches to a chromic *Luvisol* FAO classification (FAO 2006). The top 0.30 m is dominated by soils with 50% silt and 27% clay content, which increases to 35% in below 0.5 m depth. Kwekwe Research Centre has sandy loams that contain 15% and 30% clay content in the first 0.2 m layer and 0.2 m – 0.4 m subsoil, respectively. According to FAO classification, these soils are classified as granitic derived abruptic *Lixisols* (FAO 2006). Soils at Makoholi Research Centre are classified as 5G.2 under the Zimbabwe soil classification system (Nyamapfene 1991) which matches closely to a *Ferralic Arenosol* FAO classification (FAO 2006). Soils consist of 94% sand, 3.5% silt and 2.5% clay in the first 0.5 m layer. Clay content continues to increase by 1% resulting in sandy loam subsoils.

Experimental design and crop management

A total of 20 genotypes used as treatments were organised and planted in a randomised complete block design, replicated thrice. The plot consisted of four rows, each measuring five meters in length, with an inter-row spacing of 0.75 m and an in-row spacing of 0.20 m (Chikobvu 2008). Land ploughing was done and later disked before planting to break soil clods ensuring soil seed contact. Compound D (N7:P14:K7) basal fertiliser application was done at planting, using a rate of 200 kg ha^{-1} (Chikobvu 2008). During planting, seeds were drilled into the soil, and 2 weeks after germination, the plots were thinned to retain one plant per planting station. Six weeks post crop emergence, ammonium nitrate 34.5% N was applied at 100 kg ha^{-1} as a top-dressing fertiliser (Chikobvu 2008). Top dressing was applied once in sites with heavy clay soils, while split application at 4 and 7 weeks after germination was done at sites with sandy loam soils. Split application for ammonium nitrate 34.5% N was done in sandy loam soils to reduce nutrient leaching and improve nutrient uptake, issues that are less critical in clay soils (Singh et al. 2024). The trials were raised under rainfed conditions across all the sites. Weeds were controlled manually using hoes at all the sites. Fall armyworm (*Spodoptera frugiperda*) and stalk borers (*Busseola fusca*) were controlled using Belt® and Thionex® insecticides at the rate of 0.1 and 1 l ha^{-1}, respectively (Chikobvu 2008).

Phenotypic data collection

Data were collected from the net plot, consisting of two central rows, while a 0.5 m border at each end of the rows was discarded to eliminate border effects (Xu 2016). Data were collected on days to 50% flowering, which were recorded as number of days from planting to when 50% of the plants in a plot have shade pollen as well as days to 95% physiological maturity, which were recorded as number of days from planting to the date where 95% of the plants matured on which seeds on the lower part of the panicle formed a black layer (IBPGR & ICRISAT 1993). In addition, panicle length, panicle width, plant height, plant count, 100 grain weight per plant and grain yield were also recorded. The presence of northern leaf blight (*Exserohilum turcicum*) and sorghum sooty stripe (*Ramulispora sorghi*) damage was also recorded, which were scored during the grain filling stage using a scale 1–5 with a score of 1 representing very healthy (i.e., disease-free) plants and 5 representing severely diseased plants. Using a ruler, panicle length was measured in centimetres from the base of the panicle to the tip of the panicle, and panicle width was measured in centimetres as the diameter of the head at its widest part after the grain filling stage (IBPGR & ICRISAT 1993). Plant height was measured in centimetres from the base of the stalk at the ground level to the tip of the head. Plant count was recorded as the total number of plants per plot at the harvesting stage. Plant height and plant count were recorded when 95% of the plants in a plot had reached physiological maturity (Wang et al. 2020). The harvested panicles were sundried before being tested for moisture content, which was adjusted to 12.5%. Grain weight per plant was recorded as the weight of dried grain harvested per plant. One hundred grain weight was determined by weighing 100 grains for each genotype, and grain yield was recorded as the weight of dried grain harvested per plot converted to tonnes per hectare (IBPGR & ICRISAT 1993).

Data analysis

Best Linear Unbiased Predictors (BLUPs) were calculated for all traits across five sites over two seasons, as well as for each season, using Multi Environment Trial Analysis with R (META-R) software version 6.0 (Alvarado et al. 2020).

Pearson's correlation coefficients were also generated with the same software. In addition, using R software version 4.3.1, phenotypic and genotypic path analysis was performed based on phenotypic correlations to deduce direct and indirect effects of sorghum grain yield related traits on sorghum yield (Dong 2024; R Core Team 2023).

Ethical considerations

This article followed all ethical standards for research without direct contact with human or animal subjects.

Results and discussion

The phenotypic (P) and genotypic (G) correlation analysis among yield and secondary traits of the studied sorghum genotypes are presented for cropping season 2021–2022 (Table 2), cropping season 2022–2023 (Table 3) and combined seasons (Table 4), where significant ($p < 0.05$) correlations are shown.

The correlation coefficient (|r|) is considered weak, moderate, strong and very strong when |r| is 0.20 to 0.39, 0.40 to 0.59, 0.60 to 0.79 and 0.80 to 1.00, respectively

TABLE 2: Phenotypic and genotypic correlation coefficients between grain yield and secondary traits across all sites in cropping season 2021–2022.

Traits	TOC	GYHa	DF	DMP	ET	RS	PL	PW	PH	HGW
GYHa	P	-	-	-	-	-	-	-	-	-
	G	-	-	-	-	-	-	-	-	-
DF	P	0.55***	-	-	-	-	-	-	-	-
	G	0.53**	-	-	-	-	-	-	-	-
DMP	P	0.60***	0.51***	-	-	-	-	-	-	-
	G	0.32***	0.45***	-	-	-	-	-	-	-
ET	P	0.38**	0.29**	0.51**	-	-	-	-	-	-
	G	0.22NS	0.71NS	-0.13**	-	-	-	-	-	-
RS	P	0.02NS	0.12NS	0.28NS	0.49***	-	-	-	-	-
	G	-0.68NS	-0.56NS	-0.39NS	0.56NS	-	-	-	-	-
PL	P	0.57**	0.52***	0.74*	0.43***	0.39***	-	-	-	-
	G	0.69***	0.61***	0.82***	0.69NS	0.32NS	-	-	-	-
PW	P	0.34***	0.22**	0.41***	0.29**	0.18NS	0.38***	-	-	-
	G	0.20NS	0.33NS	0.29NS	0.51NS	-0.79NS	0.40NS	-	-	-
PH	P	0.31***	0.33***	0.37***	0.14NS	0.01NS	0.34**	0.28**	-	-
	G	0.45NS	0.40NS	0.58NS	0.18NS	-0.33NS	0.53NS	0.35NS	-	-
HGW	P	0.50**	0.28**	0.30**	0.17NS	-0.04NS	0.39**	0.27**	0.51***	-
	G	0.56***	0.13**	0.89**	0.47NS	-0.32NS	0.48NS	0.92NS	0.52NS	-
GWPlant	P	0.89***	0.42***	0.48***	0.32***	-0.03NS	0.45**	0.29**	0.22*	0.42***
	G	0.71*	0.53*	0.46NS	0.17NS	-0.72NS	-0.03NS	0.38NS	0.19NS	0.46NS

TOC, type of correlation; GYHa, grain yield (t ha-1); DF, days to 50% flowering (days); DMP, days to 95% physiological maturity (days); ET, *E. turcicum* (score); RS, *R. sorghi* (score); PL, panicle length (cm); PW, panicle width (cm); PH, plant height (cm); HGW, 100-grain weight (g); GWPlant, grain weight per plant (g); P, phenotypic correlation; G, genotypic correlation; NS, non-significant.
*, ** and *** level of significance at $p \leq 0.05$, $p \leq 0.01$ and $p \leq 0.001$, respectively.

TABLE 3: Phenotypic and genotypic correlation coefficients between grain yield and secondary traits across five sites in cropping season 2022–2023.

Traits	TOC	GYHa	DF	DMP	ET	RS	PL	PW	PH	HGW
GYHa	P	-	-	-	-	-	-	-	-	-
	G	-	-	-	-	-	-	-	-	-
DF	P	0.45***	-	-	-	-	-	-	-	-
	G	0.51*	-	-	-	-	-	-	-	-
DMP	P	0.60***	0.52***	-	-	-	-	-	-	-
	G	0.43**	0.44*	-	-	-	-	-	-	-
ET	P	0.39**	0.26**	0.50**	-	-	-	-	-	-
	G	0.24NS	0.53NS	-0.87NS	-	-	-	-	-	-
RS	P	0.14NS	0.21NS	0.44NS	0.29**	-	-	-	-	-
	G	-0.56NS	-0.37NS	-0.28NS	0.51NS	-	-	-	-	-
PL	P	0.65**	0.54***	0.72***	0.40***	0.46***	-	-	-	-
	G	0.58**	0.41*	0.59**	0.65NS	0.38NS	-	-	-	-
PW	P	0.77***	0.46***	0.69***	0.25**	0.02NS	0.67***	-	-	-
	G	0.16NS	0.27NS	0.25NS	0.32NS	-0.34NS	0.49NS	-	-	-
PH	P	0.35**	0.38***	0.36***	0.03NS	0.05NS	0.34***	0.27**	-	-
	G	0.25NS	0.43NS	0.41NS	0.30NS	-0.32NS	0.29NS	0.39NS	-	-
HGW	P	0.44**	0.22*	0.31***	0.14NS	0.17NS	0.36***	0.29**	0.42***	-
	G	0.42*	0.05*	0.76*	0.28NS	-0.12NS	0.42NS	0.50NS	0.47NS	-
GWPlant	P	0.84***	0.39***	0.49***	0.39***	0.16NS	0.51**	0.73**	0.15NS	0.30**
	G	0.92*	0.41*	0.28NS	0.26NS	-0.99NS	-0.12NS	0.61NS	0.23NS	0.38NS

TOC, type of correlation; GYHa, grain yield (t ha-1); DF, days to 50% flowering (days); DMP, days to 95% physiological maturity (days); ET, *E. turcicum* (score); RS, *R. sorghi* (score); PL, panicle length (cm); PW, panicle width (cm); PH, plant height (cm); HGW, 100-grain weight (g); GWPlant, grain weight per plant (g); P, phenotypic correlation; G, genotypic correlation; NS, non-significant.
*, ** and *** level of significance at $p \leq 0.05$, $p \leq 0.01$ and $p \leq 0.001$, respectively.

(Schober, Boer & Schwarte 2018). Direct (diagonal and bold) and indirect path coefficients at phenotypic and genotypic levels of secondary traits on grain yield across five sites in cropping season 2021–2022 (Table 5), cropping season 2022–2023 (Table 6) and combined seasons (Table 7), are based on phenotypic correlation analyses.

Phenotypic correlation analysis

The existence of positive correlation between some of the secondary traits and grain yield reveals their potential for use in sorghum grain yield improvement programmes as such traits guide selection index (Gasura et al. 2015). In this study, sorghum grain yield was a dependant variable while yield related traits were treated as independent variables. Although correlation studies provide the interrelationships of all the traits under study, generally some correlations between independent variables are not important to breeders. Traits that confirmed same pattern of association in first 2021–2022 season (Table 2), second 2022–2023 season (Table 3) and in combined analysis (Table 4) were discussed in detail.

TABLE 4: Phenotypic and genotypic correlation coefficients between grain yield and secondary traits across all sites during 2021–2022 and 2022–2023 cropping season.

Traits	TOC	GYHa	DF	DMP	ET	RS	PL	PW	PH	HGW
GYHa	P	-	-	-	-	-	-	-	-	-
	G	-	-	-	-	-	-	-	-	-
DF	P	0.48***	-	-	-	-	-	-	-	-
	G	0.53*	-	-	-	-	-	-	-	-
DMP	P	0.59***	0.52***	-	-	-	-	-	-	-
	G	0.31*	0.44**	-	-	-	-	-	-	-
ET	P	0.38**	0.27**	0.51**	-	-	-	-	-	-
	G	0.20NS	0.74NS	-0.13NS	-	-	-	-	-	-
RS	P	0.08NS	0.17*	0.35***	0.4***	-	-	-	-	-
	G	-0.69NS	-0.58NS	-0.37NS	0.60NS	-	-	-	-	-
PL	P	0.61**	0.52***	0.72***	0.41***	0.42***	-	-	-	-
	G	0.57**	0.46*	0.62***	0.55NS	0.31NS	-	-	-	-
PW	P	0.47**	0.30***	0.49***	0.33**	0.18**	0.46***	-	-	-
	G	0.27NS	0.37NS	0.25NS	0.47NS	-0.62NS	0.36NS	-	-	-
PH	P	0.33***	0.34***	0.35***	0.08NS	0.02NS	0.34***	0.26**	-	-
	G	0.20NS	0.38NS	0.46NS	0.14NS	-0.26NS	0.42NS	0.32NS	-	-
HGW	P	0.36**	0.24*	0.30***	0.15**	0.06NS	0.37***	0.26**	0.46***	-
	G	0.45*	0.09NS	0.61*	0.36NS	-0.24NS	0.46NS	0.94NS	0.50NS	-
GWPlant	P	0.85***	0.40***	0.48***	0.35***	0.06NS	0.48**	0.43**	0.18**	0.36**
	G	0.88*	0.36*	0.27*	0.21NS	-0.86*	-0.08*	0.35NS	0.16NS	0.40NS

TOC, type of correlation; GYHa, grain yield (t ha-1); DF, days to 50% flowering (days); DMP, days to 95% physiological maturity (days); ET, *E. turcicum* (score); RS, *R. sorghi* (score); PL, panicle length (cm); PW, panicle width (cm); PH, plant height (cm); HGW, 100-grain weight (g); GWPlant, grain weight per plant (g); P, phenotypic correlation; G, genotypic correlation; NS, non-significant.

*, ** and *** level of significance at $p \leq 0.05$, $p \leq 0.01$ and $p \leq 0.001$, respectively.

TABLE 5: Direct (diagonal and bold) and indirect effect path coefficients at phenotypic and genotypic level of secondary traits on grain yield across five sites in cropping season 2021–2022 based on phenotypic correlation analyses.

Traits	TOC	DF	DMP	ET	RS	PL	PW	PH	HGW	GWPlant	TCGYHa
DF	P	**0.128*****	0.069	0.019	-0.004	0.020	0.009	-0.040	0.039	0.303	**0.55*****
	G	**0.320****	0.147	-0.024	-0.021	0.004	0.005	0.002	0.014	0.094	**0.53****
DMP	P	0.068	**0.130*****	0.030	-0.015	0.027	0.012	-0.045	0.041	0.345	**0.6*****
	G	0.051	**0.154*****	-0.027	0.004	0.121	0.003	0.035	0.014	0.036	**0.32*****
ET	P	0.038	0.066	**0.051****	-0.033	0.015	0.007	-0.017	0.022	0.229	**0.38****
	G	0.029	0.051	**0.032NS**	-0.031	0.004	0.015	0.002	-0.003	0.016	**0.22NS**
RS	P	0.039	0.067	0.052	**-0.032NS**	0.016	0.008	-0.016	0.023	-0.021	**0.02NS**
	G	-0.161	-0.023	-0.110	**0.128NS**	-0.44	0.008	-0.006	0.056	-0.033	**-0.68NS**
PL	P	0.070	0.099	0.028	-0.022	**0.036****	0.013	-0.040	0.053	0.325	**0.57****
	G	0.093	0.112	-0.052	-0.003	**0.296*****	0.017	0.003	0.169	0.055	**0.69*****
PW	P	0.030	0.054	0.017	-0.010	0.014	**0.021*****	-0.035	0.035	0.209	**0.34*****
	G	0.050	0.061	-0.038	-0.004	0.064	**0.037NS**	0.061	0.085	0.002	**0.20NS**
PH	P	0.052	0.058	0.019	0.011	0.022	0.017	**0.124*****	0.073	0.168	**0.31*****
	G	0.069	0.013	0.115	-0.059	0.009	0.016	**0.144NS**	0.153	0.006	**0.45NS**
HGW	P	0.082	0.113	0.036	0.001	0.036	0.038	0.460***	**0.109****	0.227	**0.50****
	G	0.021	0.045	-0.019	-0.001	0.113	0.007	0.010	**0.153*****	0.286	**0.56*****
GWPlant	P	0.135	0.171	0.055	0.013	0.058	0.055	0.180	0.360	**0.545*****	**0.89*****
	G	0.155	0.086	0.149	-0.058	0.062	0.022	0.014	0.156	**0.314***	**0.71***

Note: Bold figures are the path coefficients with direct effects on grain yield. Non bolded figures are path coefficients with indirect effects on grain yield.

TOC, type of correlation; GYHa, grain yield (t ha-1); DF, days to 50% flowering (days); DMP, days to 95% physiological maturity (days); ET, *E. turcicum* (score); RS, *R. sorghi* (score); PL, panicle length (cm); PW, panicle width (cm); PH, plant height (cm); HGW, 100-grain weight (g); GWPlant, grain weight per plant (g); P, phenotypic correlation; G, genotypic correlation; NS, non-significant; TCGYHa, Total correlation to grain yield (t ha-1).

*, ** and *** level of significance at $p \leq 0.05$, $p \leq 0.01$ and $p \leq 0.001$, respectively.

TABLE 6: Direct (diagonal and bold) and indirect effect path coefficients at phenotypic and genotypic level of secondary traits on grain yield across five sites in cropping season 2022–2023 based on phenotypic correlation analyses.

Traits	TOC	DF	DMP	ET	RS	PL	PW	PH	HGW	GWPlant	TCGYHa
DF	P	**-0.001*****	0.062	-0.003	-0.026	0.149	0.053	-0.033	-0.008	0.245	**0.45*****
	G	**0.220***	0.045	-0.004	-0.081	0.001	0.049	0.005	0.016	0.149	**0.51***
DMP	P	0.002	**0.116*****	-0.008	-0.058	0.198	0.078	-0.030	-0.012	0.308	**0.60*****
	G	0.054	**0.254*****	-0.029	0.003	0.119	0.005	0.039	0.017	0.038	**0.43****
ET	P	0.001	0.178	**-0.011****	-0.085	0.347	0.131	-0.064	0.020	0.553	**0.39****
	G	0.027	0.047	**0.021NS**	-0.035	0.001	0.020	0.001	0.002	0.024	**0.24NS**
RS	P	0.003	0.294	0.020	**-0.143NS**	0.546	0.209	-0.094	-0.033	0.861	**0.14NS**
	G	-0.062	-0.019	-0.108	**0.131NS**	-0.380	0.011	-0.002	0.051	-0.290	**-0.56NS**
PL	P	0.001	0.084	-0.007	-0.062	**0.273****	0.075	-0.029	-0.016	0.319	**0.65****
	G	0.087	0.107	-0.057	-0.001	**0.185*****	0.022	0.008	0.174	0.101	**0.58****
PW	P	0.002	0.081	-0.008	-0.025	0.184	**0.110*****	-0.023	-0.012	0.455	**0.77*****
	G	0.044	0.058	-0.030	-0.001	0.063	**0.066NS**	0.041	0.077	0.004	**0.16NS**
PH	P	0.003	0.165	-0.015	-0.087	0.456	0.185	**0.258****	-0.028	0.575	**0.35****
	G	0.032	0.016	0.115	-0.028	0.005	0.011	**0.074NS**	0.080	0.004	**0.25NS**
HGW	P	0.003	0.038	0.000	-0.021	0.101	0.035	-0.037	**0.252****	0.189	**0.44****
	G	0.012	0.045	-0.009	-0.004	0.119	0.028	0.011	**0.133***	0.183	**0.42***
GWPlant	P	-0.002	0.057	-0.008	-0.021	0.139	0.079	-0.013	-0.015	**0.620*****	**0.84*****
	G	0.129	0.104	0.153	-0.052	0.080	0.051	0.064	0.205	**0.361***	**0.92***

Note: Bold figures are the path coefficients with direct effects on grain yield. Non bolded figures are path coefficients with indirect effects on grain yield.

TOC, type of correlation; GYHa, grain yield (t ha-1); DF, days to 50% flowering (days); DMP, days to 95% physiological maturity (days); ET, *E. turcicum* (score); RS, *R. sorghi* (score); PL, panicle length (cm); PW, panicle width (cm); PH, plant height (cm); HGW, 100-grain weight (g); GWPlant, grain weight per plant (g); P, phenotypic correlation; G, genotypic correlation; NS, non-significant; TCGYHa, Total correlation to grain yield (t ha-1).

*, ** and *** level of significance at $p \leq 0.05$, $p \leq 0.01$ and $p \leq 0.001$, respectively.

TABLE 7: Direct (diagonal and bold) and indirect effect path coefficients at phenotypic and genotypic level of secondary traits on grain yield across five sites in cropping seasons 2021–2022 and 2022–2023 based on phenotypic correlation analyses.

Traits	TOC	DF	DMP	ET	RS	PL	PW	PH	HGW	GWPlant	TCGYHa
DF	P	**0.185*****	0.089	-0.002	0.001	-0.025	0.027	-0.036	-0.007	0.146	**0.48*****
	G	**0.280***	0.165	-0.004	-0.028	0.001	0.014	0.001	0.012	0.084	**0.53***
DMP	P	-0.012	**0.169*****	-0.006	0.000	0.255	0.042	-0.037	-0.010	0.175	**0.59*****
	G	0.034	**0.201***	-0.031	0.001	0.109	0.002	0.037	0.015	0.041	**0.31***
ET	P	-0.007	0.086	**-0.015****	-0.002	0.145	0.028	-0.008	-0.005	0.127	**0.38****
	G	0.025	0.038	**0.019NS**	-0.030	0.000	0.016	0.005	0.003	0.026	**0.20NS**
RS	P	-0.004	0.059	-0.006	**-0.005NS**	0.149	0.016	-0.001	-0.001	0.023	**0.08NS**
	G	-0.157	-0.019	-0.102	**0.028NS**	-0.440	0.006	-0.003	0.042	-0.053	**-0.69NS**
PL	P	-0.012	0.122	-0.004	0.000	**0.354****	0.040	-0.036	-0.013	0.175	**0.61****
	G	0.102	0.181	-0.035	-0.006	**0.194****	0.012	0.005	0.158	0.098	**0.57****
PW	P	-0.007	0.083	-0.004	0.000	0.163	**0.083*****	-0.027	-0.009	0.156	**0.47*****
	G	0.014	0.050	-0.070	-0.001	0.143	**0.121NS**	0.061	0.048	0.007	**0.27NS**
PH	P	-0.015	0.209	-0.005	0.004	0.520	0.127	**-0.059*****	-0.018	0.335	**0.33*****
	G	0.022	0.023	0.108	-0.021	0.012	0.015	**0.054NS**	0.060	0.001	**0.20NS**
HGW	P	-0.005	0.052	0.000	0.002	0.132	0.023	-0.049	**-0.038****	0.132	**0.36****
	G	0.037	0.030	-0.005	-0.008	0.094	0.046	0.013	**-0.061**	0.267	**0.45***
GWPlant	P	-0.010	0.081	-0.005	0.000	0.169	0.036	-0.019	-0.014	**0.361*****	**0.85*****
	G	0.109	0.102	0.148	-0.054	0.074	0.045	0.084	0.205	**0.291***	**0.88***

Note: Bold figures are the path coefficients with direct effects on grain yield. Non bolded figures are path coefficients with indirect effects on grain yield.

TOC, type of correlation; GYHa, grain yield (t ha-1); DF, days to 50% flowering (days); DMP, days to 95% physiological maturity (days); ET, *E. turcicum* (score); RS, *R. sorghi* (score); PL, panicle length (cm); PW, panicle width (cm); PH, plant height (cm); HGW, 100-grain weight (g); GWPlant, grain weight per plant (g); P, phenotypic correlation; G, genotypic correlation; NS, non-significant; TCGYHa, Total correlation to grain yield (t ha-1).

*, ** and *** level of significance at $p \leq 0.05$, $p \leq 0.01$ and $p \leq 0.001$, respectively.

This article observed positive and significant ($p \leq 0.01$) phenotypic correlation coefficient (rp) between sorghum grain yield and days to 50% flowering (rp = 0.48) and also days to 95% physiological maturity (rp = 0.59) (Table 4). This association explains prolonged days for the plant to accumulate photosynthates for biomass production which triggers many large sinks, which require more time for grain filling resulting in high yield. These findings corroborate with earlier studies by Jimmy et al. (2017), Senbetay and Belete (2020), and Chauhan and Pandey (2021).

Grain yield was positively and highly significantly ($p \leq 0.05$) correlated with panicle length (rp = 0.61) and panicle width (rp = 0.47) (Table 4). This means that as panicle length increases, grain yield tends to increase as well and as panicle width increases, grain yield increases. This suggests that both panicle length and panicle width are important traits influencing grain yield as they enhance the number of grains per panicle (Zhang, Li & Tong 2018). Plant breeders should offer due consideration to these traits when selecting for sorghum grain yield. El-Raheem and Tag (2020) and Chauhan and Pandey (2021) supported these findings. Moreover, Khandelwal et al. (2015) and Shivaprasad et al. (2019) reported a positive and significant correlation between sorghum grain yield and panicle length while Jimmy et al. (2017) observed a significant association of grain yield and panicle width.

A significant ($p \leq 0.01$) and positive association was found between sorghum grain yield and plant height (rp = 0.31). This result aligns with earlier studies of Amare et al. (2015), Shivaprasad et al. (2019), El-Raheem and Tag (2020), Enyew et al. (2021) and Chauhan and Pandey (2021). The positive and significant relationship for grain yield and plant height, which was observed, is true because plant height affects the number of nodes and leaves that a plant can produce (Zhang et al. 2017). Taller plants tend to yield more nodes and leaves which are responsible for the increases in photosynthetic factories and subsequent numerous bigger flowers and sink sizes (Faralli & Lawson 2020; Wu et al. 2019).

Sorghum grain yield had a positive and significant ($p \leq 0.05$) association with 100 grain weight (rp = 0.36) (Table 4). Previous sorghum studies have reported positive and significant correlations between grain yield and 100 grain weight (Chauhan & Pandey 2021; El-Raheem & Tag 2020; Jimmy et al. 2017; Khandelwal et al. 2015;). A high 100 grain weight translates to superior seed size which promotes germination, plant stand and final yield.

Strong and highly significant ($p \leq 0.001$) correlation between grain yield and grain weight per plant (rp = 0.85) was observed in this present study, further emphasising its importance as a yield component. Earlier findings by Amare et al. (2015) and Senbetay and Belete (2020) supported the present results as the authors reported a positive and significant phenotypic correlation between grain yield and grain weight per plant. Non- significant correlation was noted between grain yield and sorghum sooty stripe in both seasons (Table 2 and Table 3). It indicates that the disease showed non-significant variations in different genotypes for grain yield. The genotypes under study were tolerant to sorghum sooty stripe. Conversely, positive correlations were exhibited between grain yield and northern leaf blight (rp = 0.4). This kind of relationship explains the disease tolerance of the genotypes used in this study. Most fungal diseases thrive in the presence of prolonged high humidity and hot temperatures. The prevailing effects of global warming not limited to random long dry spells are not warranting conducive environment for disease development; hence, sorghum sooty stripe revealed a non-significant correlation with grain yield per season and in combined analysis.

Positive and significant correlations between grain yield and yield components; days to 50% flowering, days to 95% physiological maturity, panicle length panicle width, plant height, 100 grain weight and grain weight per plant over the two seasons across sites paves the way for simultaneous trait improvement (Table 2, Table 3 and Table 4). It also facilitates effective indirect selection saving resources in sorghum grain yield improvement programmes (Gasura et al. 2013).

It is of paramount importance for sorghum breeders to consider genotypic correlations, which are more important than phenotypic correlations. The reliability of genotypic correlations is on the exclusion of environmental and/or genotype by environment interaction effects when being computed (Azimi, Marker & Bhattacharjee 2017). The environmental effects reduce the precision of correlation among traits.

Genotypic correlation analysis

It is crucial for sorghum breeders to consider genotypic associations, which are more important than phenotypic correlations. The reliability of genotypic correlations is on the exclusion of environmental and/or genotype by environment interaction effects, which reduce precision of correlation among traits. In this study, sorghum grain yield had significant ($p \leq 0.05$) and positive genotypic correlation coefficient (rg) with days to 50% flowering (rg = 0.53), days to 95% physiological maturity (rg = 0.31), panicle length (rg = 0.57) and 100-grain weight per plant (rg = 0.45) (Table 2, Table 3 and Table 4). The significant and positive association suggests that simultaneously selecting these traits enhances the efficiency of sorghum yield improvement. An earlier study by Thant et al. (2021) reported a significant and positive genotypic correlation coefficient of days to 50% flowering, days to 95% physiological maturity, panicle length and grain weight per plant which was in agreement with our findings.

Phenotypic path coefficient analysis

Information on the correlation between two traits is important for the concurrent selection of traits, which speeds up progress in crop breeding. The only analysis and interpretation of the association magnitude usually results in a poor selection strategy in the presence of pleiotropism. A genetic phenomenon, pleoitrophy is when a single gene influences multiple unrelated traits, which occurs because the gene produces proteins that are involved in multiple biological pathways (Stearns 2010). Therefore, analysing the cause-and-effect relationships through path analysis to differentiate between the direct and indirect effects of independent (secondary traits) variables on the dependent variable (grain yield) is crucial (Dong 2024). Highly significant ($p \leq 0.01$) positive direct effect on sorghum grain yield was observed on panicle length (Pp = 0.036), 100 grain weight (Pp = 0.109) and grain weight per plant (Pp = 0.545) in 2021–2022 season (Table 5), and the same pattern was observed in 2022–2023 season on panicle length (Pp = 0.354), 100 grain weight (Pp = 0.268) and grain weight per plant (Pp = 0.361) (Table 6). Grain weight per plant had the highest positive direct effect on sorghum grain yield. Northern leaf blight (Pp = −0.015) exhibited significant ($p \leq 0.05$) negative direct effects on grain yield showing that an improvement in any of these traits can directly support sorghum grain yield thereby indicating the efficiency of indirect selection (Table 6).

Lenka and Mishra (1973) classified path coefficients as negligible, low, moderate, high and very high when association effects are 0.00–0.09, 0.10–0.19, 0.20–0.29, 0.30–0.99 and > 1.0, respectively. In order to increase accuracy and precision in sorghum breeding, more emphasis is given to high path coefficients. Accordingly, panicle length had a high positive phenotypic direct effect (Pp = 0.354) on sorghum grain yield (Table 6). Highly positive and direct effects of panicle length on grain yield were also reported by Khandelwal et al. (2015), Shivaprasad et al. (2019) and Senbetay and Belete (2020). Such a relationship indicates that panicle length is one of the most important yield component traits. The phenotypic path analysis showed that grain weight per plant had very high positive direct effect (Pp = 0.361) on sorghum grain yield indicating the importance of grain weight per plant as yield related character that directly increases grain yield potential. This is in agreement with Chauhan and Pandey (2021) who reported a very high positive direct effect on sorghum grain yield by grain weight per plant.

Genotypic path coefficient analysis

Significant ($p \leq 0.05$) positive genotypic direct effects on sorghum grain yield was observed on days to 50% flowering (Pg = 0.280), days to 95% physiological maturity (Pg = 0.201), panicle length (Pg = 0.194) and grain weight per plant (Pg = 0.291) (Table 5, Table 6 and Table 7). These are moderate path coefficients whose traits can be used as selection indices (Lenka & Mishra 1973). Endalamaw, Adugna and Mohammed (2017) reported that days to 50% flowering and panicle length had positive significant ($p \leq 0.05$) direct effects on sorghum grain yield and these findings corroborate with results of this study. Khadakabhavi et al. (2017) reported similar findings, particularly regarding panicle length, which exhibited positive and significant ($p \leq 0.05$) genotypic direct effects on sorghum grain yield. In contrast, 100-grain weight showed negative direct effects on grain yield, as revealed by a cross-site path coefficient analysis, indicating that it is not suitable for indirect selection for yield improvement. Grain weight per plant had significant $p \leq 0.05$) positive genotypic direct effects on sorghum grain yield. However, it cannot be used as a reliable predictor of yield as it is measured only after harvest. In addition, relying on this trait can delay breeding programmes, particularly in seasons with frequent terminal droughts, which hinder grain filling. This challenge is further exacerbated by the ongoing impacts of climate change (Ajeigbe et al. 2018).

Desirable traits that are significantly and positively correlated and exhibit high heritability can be used efficiently as selection indices for grain yield in sorghum breeding (Gasura et al. 2013). Traits with < 30%, 40% – 60% and > 60% heritability are considered to have low, moderate and high heritability, respectively, making their selection easy (Johnson, Robinson & Comstock 1955). Accordingly, days to 50% flowering and panicle length had high heritability of 0.72 and 0.86, respectively (Table 8). Although days to 95% physiological maturity have positive and significant ($p \leq 0.05$) genotypic direct effects on sorghum grain yield, indirect selection for yield is not rewarding because it has a low heritability of 0.25 (Table 8). Moreover, days to 50% flowering and panicle length had a significant ($p \leq 0.05$) and positive correlation at both phenotypic and genotypic level, and it follows that breeders can successfully use either one of the two for indirect selection of sorghum grain yield. In this case, days to 50% flowering is easier, quicker and cheaper to use than panicle length, which requires more time.

TABLE 8: Broad sense heritability of traits under study across 2021–2022 and 2022–2023 seasons.

Traits	Season 1	Season 2	Combined seasons
DF	0.70	0.75	0.72
DMP	0.23	0.28	0.25
ET	0.57	0.37	0.10
RS	0.73	0.24	0.59
PL	0.88	0.84	0.86
PW	0.73	0.79	0.70
PH	0.86	0.85	0.86
HGW	0.91	0.89	0.88
GWPlant	0.94	0.97	0.96
GYHa	0.97	0.83	0.93

GYHa, grain yield (t ha-1); DF, days to 50% flowering (days); DMP, days to 95% physiological maturity (days); ET, *E. turcicum* (score); RS, *R. sorghi* (score); PL, panicle length (cm); PW, panicle width (cm); PH, plant height (cm); HGW, 100-grain weight (g); GWPlant, grain weight per plant (g).

Conclusion

This study showed that sorghum grain yield was positively and significantly correlated with days to 50% flowering, days to 95% physiological maturity, panicle length at both phenotypic and genotypic levels. Days to 50% flowering, days to 95% physiological maturity and panicle length exhibited moderate, positive and significant genotypic direct effects on sorghum grain yield. Days to 50% flowering and panicle length had high heritability, and moderate, positive and significant genotypic direct effects on grain yield. Breeders are recommended to select for high sorghum grain yielding genotypes through days to 50% flowering and panicle length making effective indirect selection for sorghum grain improvement.

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Competing interests

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Authors' contributions

M.K.C. conceptualised and wrote the original draft. E.G. performed data analysis and conceptualised, while C.N.K., S.M. and B.M. critically revised the draft. E.N., A.N., F.M. and P.M. contributed to the project's conceptualisation, supervision of execution and fundraising.

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Data availability

The data that support the findings of this study are available from the corresponding author, E.G., upon reasonable request. The data are not publicly available because of university's private policy.

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