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Pure line selection for performance evaluation of Sorghum Breeding Lines for Grain Yield and Its Related Traits

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ABSTRACT

Sorghum is an important cereal crop grown in arid and semi-arid regions for food and feed purposes. Considering its potential use as a carbohydrate source in animal feed, a breeding program was launched at Universiti Putra Malaysia (UPM) to develop local grain sorghum varieties. The research aims to evaluate the performance of selected breeding lines in terms of growth and grain yield traits. The breeding lines include 12 sorghum pure lines, together with two advanced forage sorghum genotypes, Putra SB1 and Putra SB2, as controls. The experiment was conducted in a Randomised Complete Block Design at Field 10 UPM. Traits with high heritability and positive correlation to grain yield were the selection criteria. Results suggest that line V7 (5-3-6) recorded the highest grain yield (1785 kg/ha), while V10 produced the lowest yield (541 kg/ha), and was also the earliest to reach flowering (64 days). The longest height was achieved by V6 (2-36-3), at 294.4 cm, whereas V12 (Upms) recorded the least mean height (166.2 cm). There was moderate intra-population homogeneity observed for growth and yield characteristics, with coefficient of variation values ranging from 2.3% to 33.7%, because the population was still segregating. The results indicate that V7 demonstrated significant yield potential among the pure lines, highlighting their suitability for developing high-yielding grain sorghum cultivars from the existing population that are adapted to the local climatic conditions of Malaysia. However, further assessment is recommended to purify the evaluated population.

Keywords: Genetic variation, grain yield, pure line selection, sorghum

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INTRODUCTION

Sorghum (*Sorghum bicolour* L. Moench) belongs to the Poaceae family and is cultivated in warm climates worldwide (Xin et al., 2021). It has been the staple and traditional food of the African continent since ancient times (Widowati & Luna, 2022). Sorghum ranks fifth among cereal crops, with a worldwide production of 86.2 million tonnes in 2020 (Bakari et al., 2023). The importance of sorghum lies in its diverse range of utilisation, from human consumption, animal feed, and in industries as well, for the production of bio-composite and biofuel (Silva et al., 2024). The varietal development of grain sorghum has various nutritional benefits, including sufficient fibre content, a low glycemic index, and gluten-free (Bazié et al., 2023). The consumption of sorghum grains includes 55% as food, whereas 33 % of it is consumed as animal feed (Kumar et al., 2013). The main constituents of sorghum grain are starch, proteins, and non-starch polysaccharides. The key features of grain sorghum varieties include a height ranging from three to six feet and a bulky panicle head. These are mainly utilised as a food source for humans or as feed for livestock (Dexuan et al., 2022).

In breeding programs for self-pollinated crops such as rice and beans, the pure line selection strategy has been widely used. (De Oliveira Amaral et al., 2019). Across decades, breeders have opted for a diverse range of techniques for varietal development, but have found pure line selection to be the most suitable for self-pollinated crops. (Rakshit & Bellundagi, 2018). In individual plant selection, the base population is genetically variable but homogenous, and the progeny of selected individual plants are evaluated to identify superior pure lines (Visarada, 2018). Evaluation is usually based on growth and yield-related traits (Vom Brocke et al., 2010). A line is considered a cultivar by its ability to adapt, react, and withstand a particular environment. (Aruna & Cheruku, 2019).

Yield is the most complex among the traits, as it depends upon multiple components. It is a quantitative trait of utmost importance and is immensely influenced by environmental factors. The heritability of yield is very low, and selection entirely based on it is not preferable (Xin et al., 2021). Therefore, parameters contributing to grain yield, such as the number of grains per panicle and 1000-grain weight, are also considered and optimised (Von Pinho et al., 2022). Grains per panicle is a crucial trait in sorghum breeding programs. Plant breeders aim to develop sorghum varieties with higher grain yield potential; therefore, the yield components are also an essential criterion for selecting promising breeding lines. The goal is to breed varieties that produce more grains per plant (Dembele et al., 2021). For practical purposes in agriculture, farmers and growers can use grain per panicle data to select sorghum varieties with potential for higher grain yields (Kovtunov & Kovtunova, 2021). The selection of pure lines also depends on the morphological traits that help determine and differentiate a grain sorghum variety (Bernardeli et al., 2022). Plant height plays a vital role in accepting varieties in a breeding experiment when developing a grain sorghum variety (Derese et al., 2018). A pure line having a plant height ranging from 3 to 6 feet is considered a grain sorghum variety (Dexuan et al., 2022). A vital quality trait that needs to be addressed while developing a grain sorghum pure line for animal feed is grain colour (Ratnavathi, 2018). The darker-coloured grains in sorghum contain a phenolic compound called tannin, which makes sorghum taste bitter and less desirable (Pan et al., 2019). It negatively affects the overall nutrition and can hinder the digestibility of proteins and carbohydrates. Thus, it will result in the disruption of nutrient metabolism and a decrease in appetite for feed. Therefore, the selection is also based on the colour of the seed coat as well (Farahat et al., 2020).

Heritability is a vital phenomenon for the selection of traits that contribute to and correlate with grain yield. Heritability is a genetic parameter that allows for measuring the genetic influence on traits. It shows the extent to which genetic diversity contributes to phenotypic diversity within a population. The research focuses on heritability estimates to assess the genetic variation in sorghum breeding lines for the proper execution of selection (Herawati et al., 2025).

The current study is part of a breeding program aimed to identify an adapted grain sorghum pure line that is adaptable to the tropical climate of Malaysia. The current breeding program will serve the purpose of germplasm expansion needs, enabling the farmers to cultivate locally adapted sorghum cultivars. It is important to evaluate the genetic diversity in sorghum and the linkages among quantitative traits for the possibility of joint selection of two or more traits. This study will pave the way for considering the inclusion of a new crop, which will be a move towards self-sustainability due to its broad spectrum of utilisation. The deployment of sorghum in Malaysia would primarily focus on grain for feed as an alternative food source with potential energy for animals. (Naharudin et al., 2021).

The current study aims to identify high-yielding grain sorghum pure lines that are adapted to the local climatic conditions of Malaysia. Furthermore, the study aims to assess and purify the existing germplasm to produce locally adapted grain sorghum pure lines that yield adequately to meet local feed requirements. The current findings form part of a comprehensive breeding program that will ultimately lead to the development of a potent grain sorghum variety suitable for local cultivation.

MATERIALS AND METHODS

Planting Materials and Experimental Location

The germplasm was obtained from the Agrogene Bank, Department of Crop Science, Faculty of Agriculture, Universiti Putra Malaysia (UPM). The plant materials include 14 sorghum lines from grain and forage types (Table 1). Nine lines (V1-V9) had undergone two selection cycles, and three lines (V10-V12) were commercial varieties that have not been evaluated, and two forage sorghum advanced lines that have undergone 5 cycles (V13 and V14) were included as controls.

Table 1
List of sorghum genotypes and their breeding development status

Label	Accession Number	Type	Number of Selections
V1	1-1-1	Grain	2
V2	1-2-1	Grain	2
V3	1-3-1	Grain	2
V4	1-4-1	Grain	2
V5	1-4-4	Grain	2
V6	2-36-3	Forage	2
V7	5-3-6	Grain	2
V8	6-31-1	Forage	2
V9	6-34-7	Forage	2
V10	White	Grain	0
V11	Sabah	Forage	0
V12	Upms	Grain	0
V13	Putra SB1	Forage	5 (Control)
V14	Putra SB2	Forage	5 (Control)

The study was conducted at Field 10, Universiti Putra Malaysia, Selangor, Malaysia, at coordinates 2.991321088220838° N latitude, 101.71457207742054° E longitude. The soil was sandy loam, with a pH of 5.8. The average temperature was 35 °C, whereas the area received 227.5 mm of average rainfall during the study period.

Experimental Design and Agronomic Practices

Planting began in February, and harvesting was completed by June 2023. The sorghum lines were assigned to rows following a Randomised Complete Block Design (RCBD) with three replications. The inter-plant distance was 25 cm, and the distance between rows was set at 150 cm apart to avoid cross-pollination among the genotypes. A total of 30 plants per genotype was planted and evaluated across replicates. Silver shine was installed to prevent weed growth in this experiment. To ensure uniform growth, sorghum seeds were germinated using Jiffy peat pellets and later were transplanted to the field at 9-10 days after sowing. A basal dose of NPK (15:15:15) was applied 4 days after transplanting, and NPK (12:12:17) was applied 28 days after transplanting, at a rate of 120 kg/ha, to promote vegetative and reproductive growth, respectively. Upon flowering, the panicles were covered with pollination nets to prevent cross-pollination. (Chakravarthi et al., 2018).

Data Collection

The development of sorghum lines was carried out through pure line selection, which continued into the third cycle of selection cycle. Therefore, growth and yield traits were recorded for each individual plant, and the mean performance of each line was used to represent the overall population performance. Plants were harvested at physiological maturity to reduce the effect of biotic factors. This approach helped prevent potential fungal infections caused by rainfall and reduced the risk of bird predation, thus avoiding the depletion of the grains. Each harvested panicle was kept in a separate paper bag and was labelled accordingly. The harvested panicles were kept in a hot air oven for four days at 35°C until the grains reached 8% storage moisture. Data collection was done on phenological, growth, and yield parameters. Phenological parameters, including 50% flowering and 50% physiological maturity, were recorded when the plant reached the desired stage. For the growth parameters, a measuring tape was utilised to determine the plant height, while the number of leaves was counted manually. Yield parameters, including the panicle length and weight, number of grains per panicle, 1000 grain weight, and overall grain yield, were measured post harvest.

Grain yield was determined using the formula:

$$\text{Grain yield (kg/ha)} = \frac{\text{Grain yield (kg) / subplot}}{\text{Area/subplot}} \times 1000 \qquad [1]$$

(Shahzad et al., 2002)

Data Analysis

Analysis of variance (ANOVA) was used to analyse the mean differences between the populations in RStudio (version 2025.09.2). The mean comparison was done using the least significant difference (LSD) method ($p<0.05$). Genetic variability analysis was performed using the variability package in RStudio. Correlation between the traits was also measured using the Pearson correlation method ($p<0.05$). Principal component analysis was performed to observe the percentage-wise contribution of traits to total genetic variation (Bartzialis et al., 2020).

RESULTS AND DISCUSSION

Performance of Morphological Traits and Yield among Sorghum Breeding Lines

The descriptive statistics provided with ANOVA (mean, genetic variance, and coefficient of variation) exemplify all measured traits of 14 sorghum genotypes represented in Table 2.

Table 2
Descriptive statistics and genetic variability parameters for agronomic traits of sorghum genotypes

Genotypes	Trait								
	Days to flowering (days)	**Days to physiological maturity (days)**	**Plant height (cm)**	**Number of leaves (leaves)**	**Panicle length (cm)**	**Panicle weight (g)**	**Number of grains per panicle (grains)**	**1000 grain weight (g)**	**Grain yield (kg/ha)**
V1	76.7	105.7	202.1	11.5	20.7	20.6	708.3	23.3	962.3
V2	70.0	103.3	198.4	9.7	21.9	16.2	453.0	26.0	586.4
V3	70.3	103.3	226.9	10.3	18.1	24.6	818.2	22.0	714.3
V4	68.7	108.3	253.1	10.8	20.1	34.8	1129.2	23.6	1452.0
V5	74.3	104.3	228.6	11.8	22.8	13.5	394.2	25.3	596.0
V6	68.7	110.0	294.4	11.6	26.8	30.9	1132.6	22.4	1325.6
V7	68.0	106.0	231.3	9.8	21.1	29.9	786.6	31.8	1785.0
V8	72.0	112.3	261.3	11.3	23.4	33.3	1515.0	18.4	1637.2
V9	72.0	104.3	281.5	11.4	24.5	24.3	968.4	19.4	1058.2
V10	64.3	108.3	238.3	10.5	36.2	18.3	452.9	19.6	541.2
V11	74.3	109.7	228.5	11.1	20.5	24.2	750.6	20.7	849.9
V12	67.0	99.7	166.4	10.1	24.4	36.6	1065.0	29.8	1592.4
V13	80.0	116.0	205.9	12.7	22.1	23.8	922.2	20.7	1066.7
V14	77.0	115.3	253.4	13.1	26.3	15.4	650.0	18.7	799.3
Mean	71.7	107.6	233.6	11.1	23.5	24.7	839.0	23.0	1069.0
Range	15.7	16.3	128.0	3.5	18.2	23.1	1120.9	13.4	1243.8
Genotypic variance	13.1**	20.41***	1034.0***	-0.0045	18.3***	40.8**	70278.6**	14.8***	172525.4***
Heritability	0.4	0.8	0.7	-0.0015	0.9	0.5	0.5	0.7	0.9
CV (%)	5.9	2.3	8.6	15.8	7.4	27.1	33.7	3.8	12.1

Note. CV: Coefficient of variation * significant at p<0.05, ** significant at p<0.01, *** significant at p<0.001, ns non-significant

Table 2 presents significant genetic differences among sorghum genotypes ($p < 0.05$). The overall coefficient of variation (CV) ranged from 2.3-33.7% for the agronomic traits, show substantial variability among lines. The high CV for the number of leaves, panicle weight, and number of grains per panicle indicates adequate environmental impact, which influenced the expression of these traits. Moreover, panicle weight and the number of grains per panicle can be substantially influenced by rust and bird predation (Tsegau & Tegegn, 2020). Furthermore, the ANOVA results also deduced considerable genetic variability for plant height, number of grains per panicle, and grain yield. The genetic variability can provide insight into the genetic improvement of genotypes. It also affirms that these variations have contributed to overall variability. Panicle length, plant height, days to physiological maturity, 1000-grain weight, and grain yield showed high heritability, ranging between 0.7-0.9. Traits with moderate heritability include days to reach 50% flowering, panicle weight, and number of grains per panicle (0.4-0.5) (Table 2). Characters with high heritability also have a lower coefficient of variation, showing less variability, making the selection appropriate. Traits with higher heritability are considered for the selection of genotypes for the next generation (Yaqoob et al., 2015).

Phenological Parameters

A significant difference was observed among the pure lines in the number of days to reach 50% flowering (Figure 1a). The genotype with the earliest flowering was V10 (64.3 days), followed by V4 and V6 (68 days). The line that took the highest days to flower was the control genotypes V13 (80 days) and V14 (77 days). Phenological traits are essential indicators that can help predict crop maturity. The lines that flower early can possibly mature earlier than others; hence, they can be prevented from any biotic and abiotic threats in the field (Mwamahonje & Maseta, 2018).

Significant variations have been observed between genotypes regarding the number of days needed to reach 50% physiological maturity. The genotype that took the fewest days to reach physiological maturity is V12 (99.7 days), followed by V3 and V2 (103.3 days). Control genotypes V13 (116 days) and V14 (115.3 days) took the longest to mature (Figure 1b). A study conducted by Baloch et al. (2023) found that phenological parameters can assist in predicting the optimal timing to prevent pollination and plan the season based on the environmental stresses of a particular location (Baloch et al., 2023). The early maturing lines are the focus of most breeding programs for producing new varieties (Suza & Lamkey, 2024).

Growth Parameters

A significant difference was observed in plant height among the populations. The genotype with the tallest plant height was V6 (294.4 cm), followed by V9 (281.5 cm). However, for grain sorghum, a dwarf phenotype is preferred. The shortest plant among the evaluated populations was V12, reaching a mean height of 166.2 cm, followed by V2 (198.4 cm) (Figure 2a). Results by Mwamahonje and Maseta (2018) affirmed that to be recognised as a grain sorghum variety, it must be less than 2 meters in height (Mwamahonje & Maseta, 2018). Breeding experiments conducted in tropical regions with high winds and rain have specific challenges. If the plant is taller in size, it will ultimately lodge, leading to significant yield reduction. On the management side, a lower plant height will facilitate the harvesting process (Yan et al., 2023).

Significant and substantial differences were observed between the populations in terms of leaf number. The control genotypes V14 (13.1 leaves) and V13 (12.7 leaves) produced the highest mean number of leaves. The lowest number of leaves was found in V2 (9.7 leaves) (Figure 2b). Kamal and Ahmad (2022) also observed similar variations among the leaves of different sorghum cultivars. They concluded that leaves are the leading site for photosynthesis, which positively influences the grain yield of sorghum. Therefore, an optimum number of leaves will enable the plant to photosynthesise actively by providing more surface area, generating considerable biomass and grain (Kamal & Ahmad, 2022).

Yield Parameters

The longest panicle was produced by genotype V10, with a mean length of 36.2 cm. It was followed by V6 (26.8 cm) and the control genotype, V14 (26.3). V3 produced the smallest panicles with a mean length of 18.1 cm (Figure 3a). A larger panicle can help deduce a good number of grains that may ultimately contribute to increasing grain yield. Studies have also shown a negative correlation between panicle length and grain yield. This is due to the loose and lax nature of the panicle despite having a considerable length (Mamo et al., 2023). The heaviest panicle-producing genotype was V12, with a panicle weighing 36.6 g, followed by V4, with a mean panicle weight of 34.8 g. The value for the lightest panicle was V5, with a mean weight of 13.5 g (Figure 3b). A heavy panicle is a testament to producing more grain yield, but it also depends on factors such as grain size. Panicle weight is an indicator of adaptability and a measure of resource allocation. The weight also depends on the photosynthetic activity of the plant, which eventually facilitates grain filling. (Lin & Guo, 2020).

The genotype producing the highest number of grains per panicle was V8 (1515 grains), while V5 was the least yielding genotype with 394.2 grains (Figure 4a). In a breeding experiment, it is essential to select plants with a desirable seed weight (Surpam et al., 2019). The genotype yielded the highest 1000-grain weight, V7, with a mean weight of 31.8 g. V8 produced the lowest 1000-grain weight with a mean weight of 18.4 g (Figure 4b). Parameters such as panicle length, panicle weight, and 1000-grain weight all contribute to the calculation of grain yield. The grain weight depends on the grain size, and it is the

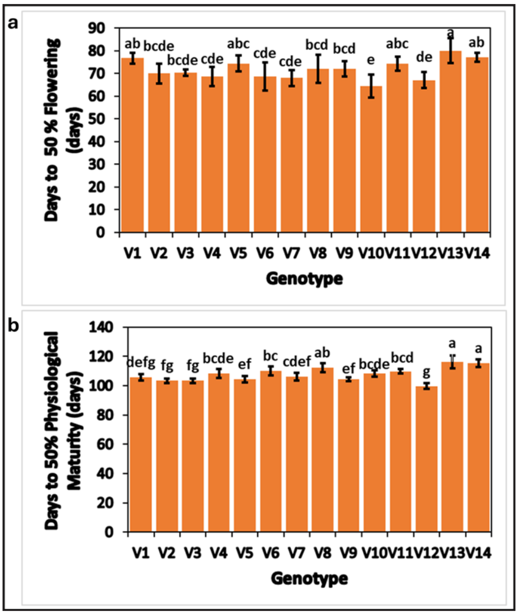

Figure 1. Number of days taken by sorghum pure lines to reach phenological stages: (a) 50% days to flowering and (b) 50% days to physiological maturity. Values are expressed as mean ± standard deviation (SD), where SD is represented by error bars. Small letters indicate significant differences among genotypes at $p < 0.05$, based on the LSD test

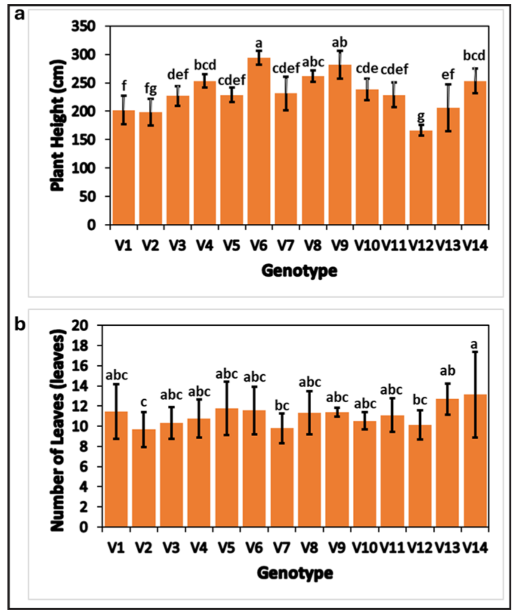

Figure 2. Variation in growth parameters among sorghum pure lines: (a) plant height (cm) and (b) number of leaves. Error bars represent the standard deviation (SD). Small letters indicate significant differences among genotypes at $p < 0.05$, based on LSD

main contributing trait that allows the calculation of grain yield. Grain yield is the ultimate breeding objective for an experiment based on developing a cultivar. (Tao et al., 2018). The genotype producing the highest grain yield was V7 (1785 kg/ha), followed by V8 (1637.15 kg/ha) and V12 (1592.23 kg/ha). The lowest-performing genotype in terms of grain yield was V10, which yielded 541.1 kg/ha (Figure 4c). In a breeding experiment aligned with developing a grain sorghum cultivar, grain yield is the deciding factor. Developing a variety that produces an adequate annual yield is a global necessity to address the alarming issue of food security (Albahri et al., 2023). Improving the crop yield will help address the issue of food security and reduce the environmental impact raised due to the use of chemical fertilisers in such experiments (Dewi et al., 2023).

Correlation Study of Yield and Agronomic Parameters

The analysis of phenotypic correlation measured between the traits on 14 genotypes is presented in Table 3.

Traits related to yield, specifically grain yield and 1000 grain weight, showed a positive correlation ($r = 0.34$; $p<0.05$). These findings align with those of Tao et al. (2018), who

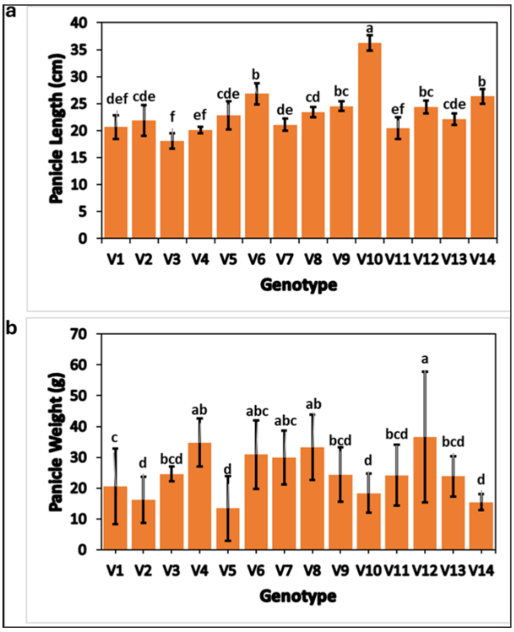

Figure 3. Variation in yield components among sorghum genotypes: (a) panicle length (cm) and (b) panicle weight (g). Error bars represent the standard deviation (SD). Small letters indicate significant differences among genotypes at p < 0.05, based on LSD

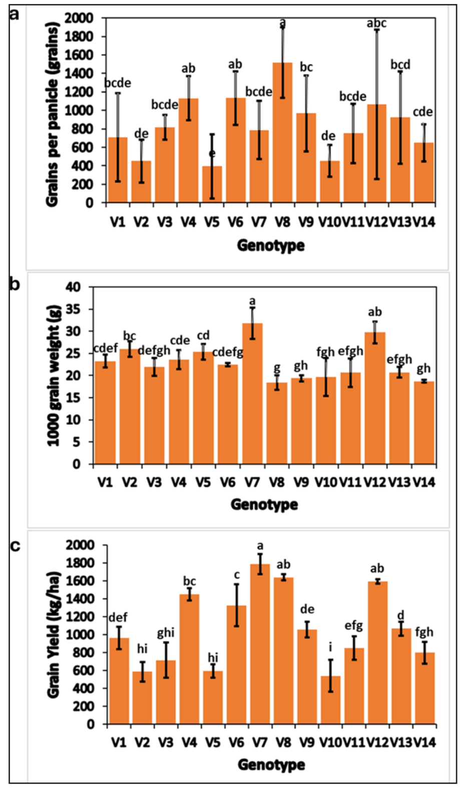

Figure 4. Variation in yield parameters among sorghum genotypes: (a) 1000-grain weight (g), (b) grains per panicle, and (c) grain yield (kg ha^{-1}). Error bars represent the standard deviation (SD). Small letters indicate significant differences among genotypes at p < 0.05, based on LSD

found that the grain yield of the genotypes showed a high correlation with total grain weight, as 1000-grain weight is indicative of grain size and quality. Therefore, a larger grain size can contribute to greater grain yield (Baye et al., 2022). The number of grains per panicle and panicle weight showed a robust positive correlation ($r = 0.90$; $p<0.001$). Parida et al. (2022) also reported similar results, where grains per panicle and panicle weight were strongly correlated, as panicle weight is the major contributing factor; hence, a heavier panicle would bear a greater number of grains (Parida et al., 2022). Panicle length had a negative correlation with grain yield and 1000-grain weight ($r = -0.39$; $p<0.05$), as enormous panicles bear more branches possessing a higher number of grains per panicle, making the grain size smaller and lighter in weight, hence reducing the grain yield. (Asungre et al., 2021).

Among the phenological traits, days to flowering and days to physiological maturity showed a positive correlation ($r = 0.52$; $p < 0.001$). Days to physiological maturity were also positively correlated with the number of leaves ($r = 0.38$; $p< 0.05$). The correlation in the phenological traits is due to the influence of genetic and environmental factors, combined with plant growth rate mainly influenced by nutrient unavailability (Borrell et al., 2020). Days to physiological maturity were negatively correlated with 1000-grain weight ($r = -0.54$; $p < 0.001$). In a study conducted by Wang et al. (2020), the phenological traits were found to be negatively correlated with grain yield because of the absence of adequate moisture (Wang et al., 2020). The negative correlation can also be due to the presence of early flowering genotypes that lead to a reduction in biomass accumulation, hence provoking a negative impact on grain yield (Ostmeyer et al., 2022).

Table 3
Correlation analysis among agronomic and yield traits

	NOL	PH	PL	DPM	DF	GPP	PW	GY
PH	0.29ns							
PL	0.11ns	0.24 ns						
DPM	0.38 *	0.27 ns	0.16 ns					
DF	0.12 ns	-0.20 ns	-0.34 *	0.52 ***				
GPP	-0.18 ns	-0.29 ns	-0.11 ns	0.08 ns	-0.10 ns			
PW	-0.39 *	0.12 ns	-0.11 ns	-0.08 ns	-0.21ns	0.90 ***		
GY	-0.08ns	0.11 ns	-0.21 ns	0.00 ns	-0.18 ns	0.57 ***	-0.60 ***	
1000GW	-0.27ns	-0.39*	-0.23 ns	-0.54 ***	-0.28 ns	-0.09 ns	0.17 ns	0.34 *

*Not*e. PH: plant height (cm), PL: panicle length (cm), GPP: grains per panicle (grains), PW: panicle weight (g), DPM: days to physiological maturity (days), DF: days to flowering, NOL: number of leaves (leaves), 1000GW: 1000 grain weight (g), GY: grain yield (kg/ha)
*Significant at p<0.05, ** significant at p<0.01, *** significant at p<0.001, ns not significant.

Principal Component Analysis of Sorghum Genotypes based on Yield and Morphological Traits

The principal component analysis (PCA) is an important tool for extracting significant data from a large data set. The total number of components in PCA is based on the number of variables being analysed (Sinha & Kumaravadivel, 2016). In this case, the results from the cumulative variance suggest that principal component 1 (PC1) and principal component 2 (PC2) contribute 37.1% and 29.8%, respectively, making it 66.9% of the overall cumulative proportion. The scree plot reflects the variation percentage of each principal component (Figure 4) (Elenen et al., 2019). A biplot is the visual representation of the loading values of the first two principal components. It is constructed based on the loading values for the traits in their respective principal components. Only the higher value from PC1 and PC2 in a biplot is selected because the more considerable loading value indicates a stronger relationship between the variable and its subsequent principal component (Ndiaye et al., 2019) (Figure 5)

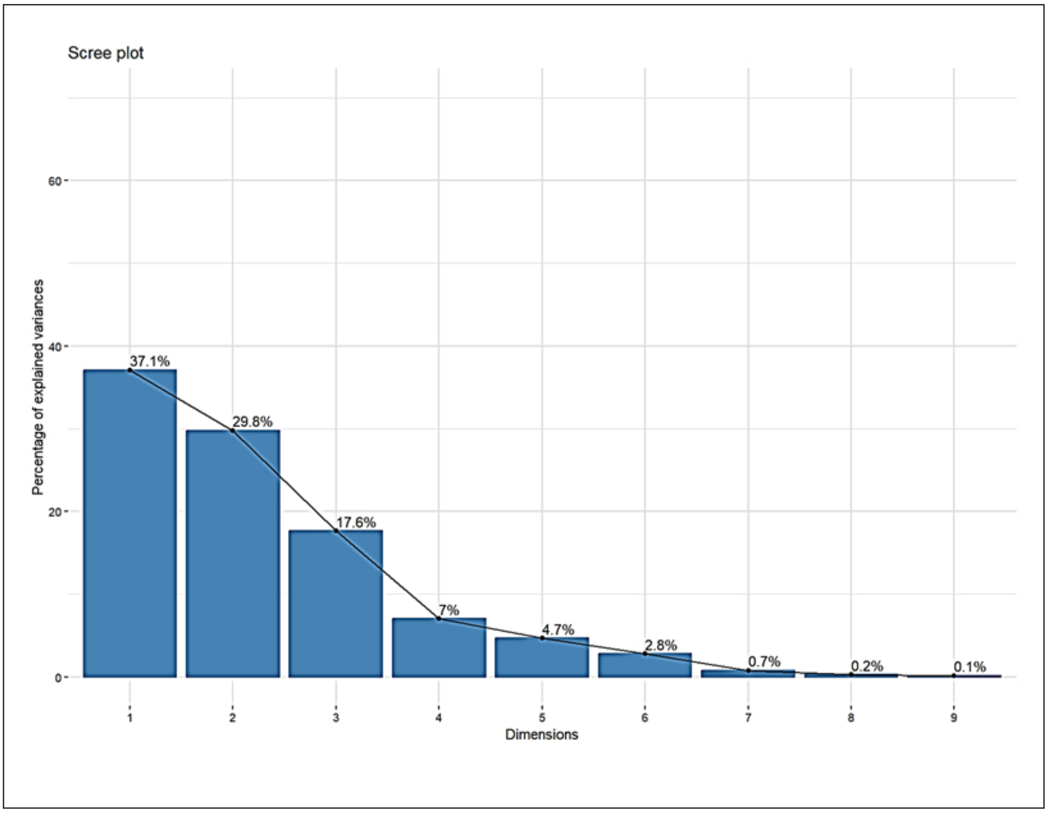

Figure 5. Principal component analysis of agronomic parameters of sorghum genotypes. Scree plot showing the variance percentage of different components

Results from the PCA biplot indicate that V7 and V12 were the most distinctive genotypes, producing the highest grain yield and exhibiting the shortest plant height. Moreover, genotypes V6 and V9 exhibited the highest plant height but yielded minimal grain. The control genotypes took the longest to reach flowering and physiological maturity, resulting in inadequate grain yield (Figure 6).

Similar results have been reported by Kavithamani et al. (2019), where the percentage of cumulative variances of PC1 and PC2 were higher than other components based on agronomic parameters of sorghum cultivars. Usually, the two first components contribute to a large amount of total variance (Kavithamani et al., 2019). Subramanian et al. (2019) presented that data from eight agronomic traits were grouped into three major components accounting for 77 % of total variation, with significant variation confined to the first two components. PCA was able to recognise the key parameters that were responsible for making the population variable (Subramanian et al., 2019)

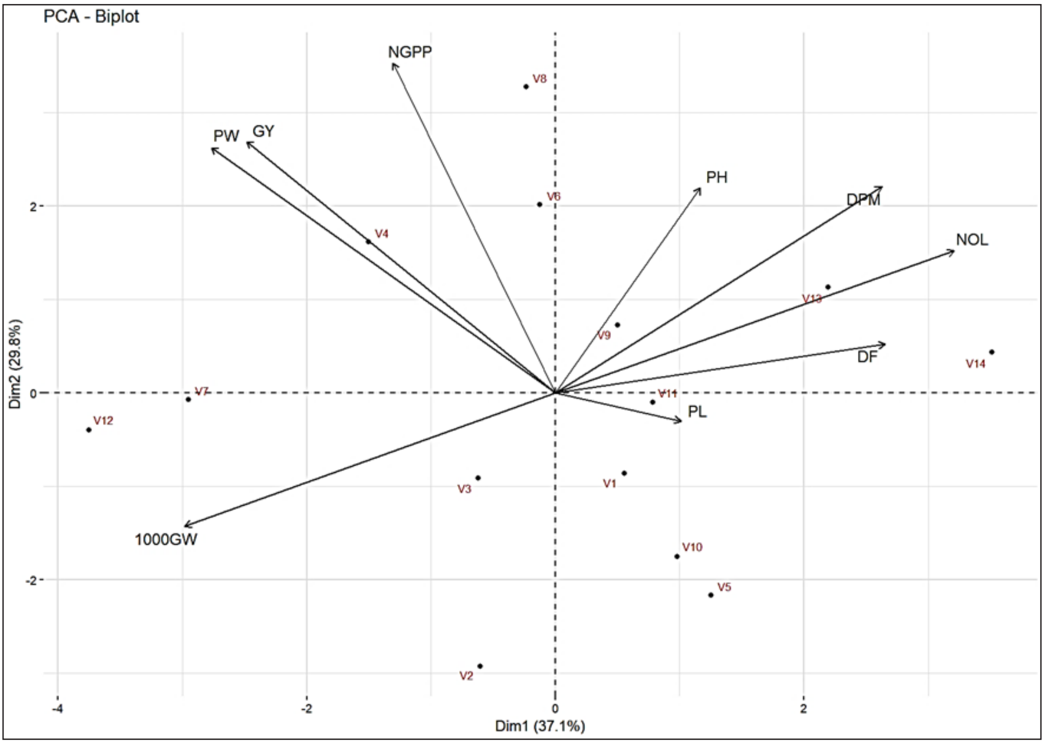

Figure 6. Principal component analysis of agronomic parameters of sorghum pure lines. PCA biplot for the distribution of sorghum genotypes for the first two principal components based on nine quantitative traits. *Note*. PH, plant height (cm); NOL: Number of leaves (leaves); PL: Panicle length (cm); PW: Panicle weight (g); NGPP: Number of grains per panicle (grains); DF: Days to reach 50% flowering (days); DPM: Days to reach 50 % physiological maturity (days); 1000GW: 1000 grain weight (g); GY: Grain yield (kg/ha)

CONCLUSION

The selection study concluded that Genotype 7 produced the highest 1000-grain weight and grain yield. It was also the earliest to reach flowering and physiological maturity, only second to Genotype 12. Genotype 12 recorded the shortest plant, while Genotype 1 produced the highest number of leaves among the evaluated lines. The results based on grain yield as selection criteria decipher adequate potential in the genotypes observed. The decisions made based on heritability estimates suggest that further selection is recommended to purify the existing coterie to develop grain sorghum pure line varieties for animal feed utilisation.

DECLARATION OF INTEREST STATEMENT

The authors do not have any conflict of interest related to the design, data collection, analyses, interpretation or writing of the manuscript.

DECLARATION ON THE USE OF ARTIFICIAL INTELLIGENCE TOOLS

The authors declare that no AI tools were used while preparing the manuscript. The entire work from abstract to conclusion was completed by the authors.

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