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Exploiting genetic variability and D² statistics for divergence-based classification of genotypes in sorghum [*Sorghum bicolor* (L.) Moench]

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Abstract

Sorghum [*Sorghum bicolor* (L.) Moench] is one of the most significant dry land cereals of the semi-arid tropics. Still, its improvement has not been as rapid as that of other major cereals due to limited genetic diversity used in traditional breeding programmes. Twenty-two diverse sorghum genotypes were evaluated in a Randomised Complete Block Design with three replications during rabi 2025-26 at the Research Farm, School of Agricultural Sciences, G. H. Raison University, Saikheda, Madhya Pradesh, India (21.51° N, 78.76° E), to characterise genetic variability, heritability and genetic advance for eleven yield-attributing traits, and to resolve the genetic divergence among them through Mahalanobis's D² statistic and Tocher's clustering. Analysis of variance revealed highly significant ($p < 0.01$) genotypic mean squares for all eleven traits, with plant height and biological yield per plant recording the highest genotypic mean squares. Grain yield per plant varied from 45.27 g (774-B) to 78.03 g (CSH-17), with a grand mean of 66.20 g. High heritability was followed by high genetic advance as percentage of mean for grain yield per plant, with the rest of the ten traits showing high heritability followed by low to moderate genetic advance indicating that non-additive gene effects were more prominent for those traits. Tocher's clustering separated the 22 genotypes into six clusters with widely variable sizes from a large and heterogeneous Cluster I (12 genotypes) to two single clusters, RSLG-2438 (Cluster V) and SSG-59-3 (Cluster VI). Inter-cluster distances consistently and substantially exceeded intra-cluster distances, with the maximum divergence recorded between Cluster IV (B-35, 774-B) and Cluster VI (SSG-59-3) ($D^2 = 3490.45$), and the minimum between Cluster III and Cluster V ($D^2 = 236.23$). Cluster mean analysis identified RSLG-2438 (Cluster V) and the genotypes of Cluster III (SPV-2831, CSV-10, PR-105) as combining superior grain and biological yield with wide genetic divergence from Clusters IV and VI. The most rational way for genetic improvement in grain yield in sorghum is a dual breeding strategy involving direct phenotypic selection for grain yield within superior clusters and planned hybridisation between genetically divergent, high yielding genotypes, specifically RSLG-2438 and the Cluster IV and Cluster VI genotypes.

Keywords: *Sorghum bicolor*; genetic variability; heritability; genetic advance; Mahalanobis's D²; Tocher's clustering; genetic divergence; grain yield

Introduction

Sorghum [*Sorghum bicolor* (L.) Moench], commonly known as jowar, is a diploid ($2n = 2x = 20$), often cross-pollinated cereal of the family Poaceae. It is a C₄ plant with high photosynthetic efficiency and strong tolerance to abiotic stress, and hence performs well under drought and marginal input conditions, where maize and other crops that can be grown under such conditions fail^[1]. Sorghum ranks as the fifth most important cereal crop in the world after wheat, rice, maize and barley, and serves as a dietary staple for millions of people across the semi-arid tropics of Africa and Asia, as well as a major source of fodder and industrial raw materials^[2]. Harlan and de Wet^[3] classified cultivated sorghum into five primary races - bicolor, caudatum, durra, guinea and kafir - and ten intermediate races arising from their combinations, a classification that continues to underpin sorghum germplasm characterisation today.

In India, an estimated 44 lakh tonnes of sorghum were produced on 3.97 million hectares in 2023-24, following the 3rd Advance Estimates of the Government of India^[4] that estimated it at 47.42 lakh tonnes. India, however, continues to be one of the major sorghum-producing countries, with

a national productivity of around 1 t/ha, which remains behind that of the United States, China, and European Union countries, which achieve 4-5 t/ha and are the top producers [4]. In India, kharif sorghum is concentrated in Rajasthan, Uttar Pradesh, Haryana and Madhya Pradesh, while rabi sorghum is dominated by Maharashtra, Karnataka, Tamil Nadu and Andhra Pradesh [4]. The contribution of Madhya Pradesh is nearly one-tenth of the kharif sorghum area of the country. In the past few years, it has been producing approximately 1.6 lakh tonnes of sorghum on about 87,000-1.4 lakh hectares with less than its potential productivity due to its use of the poor cultivars [4, 5]. This underscores the scope for genetic improvement through systematic evaluation of germplasm under state-specific agro-climatic conditions, such as those prevailing at G. H. Rasoni University, Saikheda, Madhya Pradesh, where the present investigation was carried out.

The foundation of any crop improvement programme rests on the existence and precise quantification of genetic variability in the available breeding material. Since grain yield is a complex, polygenically controlled trait strongly influenced by environmental fluctuations, an evaluation based on yield alone is often unreliable for selection purposes [6]. Partitioning the observed phenotypic variability into its genotypic and environmental components, through estimation of the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance, enables breeders to assess both the extent of variability present and the extent to which it is heritable and amenable to improvement through selection [7]. High heritability combined with a high genetic advance per cent of the mean typically indicates that additive gene effects are dominant and that direct phenotypic selection is more reliable. In contrast, high heritability and low genetic advance per cent of the mean typically suggest non-additive gene actions or effects and therefore warrant resorting to alternative breeding methods [6].

Variability parameters are important for indicating the extent of intraspecific variability, but not for assessing genetic distances or relatedness between individual genotypes, which is essential for selecting parents for hybridisation. This difference is overcome by multivariate analysis of genetic divergence, usually by calculating Mahalanobis's generalised distance (D^2) [8] between pairs of genotypes, which also accounts for the correlated effects of multiple quantitative traits [9]. Genotypes are then grouped into relatively homogenous clusters by Tocher's method; the intra-cluster distance (similarity within a cluster) and inter-cluster distance (dissimilarity between clusters) together give a quantitative basis for the identification of relatively genetically diverse, genetically unrelated parental combinations which will most likely lead to high heterotic expression and useful transgressive segregants in the progeny [9]. Selection from widely separated clusters with good mean performance in yield contributing traits has repeatedly proven to be more effective than selection based on geographic origin or phenotypic similarity alone for genetic improvement [9].

Several recent studies on sorghum across diverse agro-ecologies have reaffirmed the coexistence of substantial genetic variability, differential heritability and pronounced divergence patterns among quantitative traits, findings that have consistently guided the identification of superior and diverse genotypes for further breeding use (7, 10-13). However, information of this nature remains comparatively limited for sorghum genotypes evaluated under the specific agro-climatic and soil conditions of the Saikheda region of Madhya Pradesh. Generating such location-specific data on genetic variability, heritability, genetic advance,

and D^2 -based divergence, including cluster mean performance and inter- and intra-cluster distances, is therefore essential for the meaningful selection of genetically distant and agronomically superior parents for future sorghum hybridisation and varietal development programmes suited to this region.

Keeping these considerations in view, the present investigation was undertaken on 22 sorghum genotypes with the following objectives: (i) to evaluate the extent of genetic variability, heritability and genetic advance for yield and yield-contributing traits; (ii) to assess genetic divergence among the genotypes through Mahalanobis's D^2 analysis and Tocher's clustering, including estimation of inter- and intra-cluster distances; and (iii) to identify genetically diverse and high-yielding genotypes, based on cluster mean performance, for use as potential parents in future sorghum breeding programmes.

Materials and Methods

Experimental site and plant material

The present investigation was carried out during the rabi season of 2025-26 at the Research Farm, School of Agricultural Sciences, G. H. Rasoni University, Saikheda, Madhya Pradesh, India, situated at 21.514862° N latitude and 78.76364° E longitude. The experimental material comprised 22 sorghum genotypes from diverse sources, namely SPV-2831, SPV-2048, SPV-1830, SPV-1626, RSV-458, RSLG-2438, B-35, 774-B, PJ-1430, PJ-2510, PC-1080, RC-2, SSG-59-3, CSV-10, CSV-23, CSH-17, SU-1557, SU-1570, SU-1708, PR-105, SSV-74 and SSV-84.

Experimental design and crop management

The 22 genotypes were tested in a Randomised Block Design (RBD) replicated three times, resulting in 66 single row plots. The experimental area was laid out in plots, the dimensions of which were 2.0 m x 0.45 m (row length 2.0 m; row-to-row spacing 45 cm; plant-to-plant spacing 15 cm; 13 plants per row), leaving 59.4 m² excluding borders and paths. The crop was fertilised with the recommended dose of 80:40:40 kg N:P₂O₅:K₂O ha⁻¹, and the standard agronomic package of practices for the rabi sorghum region was followed across all plots. The meteorological observations recorded on weekly basis during crop growing period (Standard Meteorological Weeks 46 of 2025 to 13 of 2026) revealed that rainfall ranged from 0.0 to 5.0 mm, with the maximum temperature ranged from 24.8 to 35.0 °C and minimum temperature ranged from 11.2 to 21.2 °C, and relative humidity ranged from 30 to 52%, signifying that the crop was produced under typical dry, cool to warm weather conditions of the rabi season with no significant weather aberration.

Observations recorded

Observations were recorded on five randomly selected and tagged plants in each plot of every replication for eleven quantitative, yield-attributing traits, viz., days to 50 per cent flowering (DF50), days to maturity (DM), plant height (PH, cm), stem girth (SG, cm), leaf length (LL, cm), leaf width (LW, cm), panicle length (PaL, cm), panicle width (PaW, cm), grain yield per plant (GY, g), biological yield per plant (BY, g) and harvest index (HI, %), following [24, 25]. Days to 50 per cent flowering and days to maturity were recorded on a plot basis, while the remaining nine traits were recorded on the five tagged plants and averaged to obtain the plot mean.

Statistical analysis

All of the data for the 11 quantitative traits were collected and

statistically analysed by R software (Version 4.5.1). Analysis of variance for the Randomised Block Design, along with estimation of the genotypic and phenotypic coefficients of variation, broad-sense heritability, and genetic advance (both as an absolute value and as a percentage of the mean, worked out at 5% selection intensity), was carried out using the R package 'variability', which partitions the observed phenotypic variance into its genotypic, environmental and error components and derives the associated genetic parameters directly from the fitted model. GCV and PCV were categorised as low, moderate or high following Burton and Devane, and Vivek *et al.* [14, 24], broad-sense heritability was categorised following Johnson *et al.* [15], and genetic advance as a percentage of the mean was likewise categorised following Johnson *et al.* [15].

Genetic divergence among the 22 genotypes was worked out using Mahalanobis's [8] D^2 statistic, and the resulting distances were used to group the genotypes by Tocher's method; both these steps, together with the computation of average inter- and intra-cluster distances and cluster mean performance for each trait, were carried out in R using the package 'biotools', following the procedure outlined by Rao [16] and Singh and Chaudhary [17]. The relative contribution of individual characters towards total divergence was likewise obtained from this analysis. All graphs, including the dendrogram depicting the clustering pattern and the bar and line plots comparing GCV, PCV, heritability and genetic advance across traits, were prepared using the 'ggplot2' package in R.

Results and Discussion

Analysis of variance

The mean sum of squares due to replications was not significant for all eleven traits studied, and the mean sum of squares due to genotypes was highly significant ($p < 0.01$) for all traits, indicating that the field was reasonably homogeneous and that the experimental layout effectively controlled field heterogeneity. Genotypic mean squares were highest for plant height (1457.06**) and biological yield per plant (1678.46**), with grain yield per plant (216.91**) being the next most significant, indicating a high potential to improve plant architecture, biomass, and yield in this material. This trend of large and significant genotypic differences across almost all agro-morphological and yield attributes, as demonstrated in the recent literature on sorghum improvement (7, 10-13), is characteristic and well-confirmed evidence of genetic differentiation for such traits in sorghum breeding programs. The genotypic mean square for height was the second-highest of all the evaluated traits, the upward variability being similar to what was reported by Izge and Adam [10] and Niyibigira *et al.* [11], where more or less tall varieties/trials had higher biomass production among the measured traits above ground. Grain yield per plant, which is a complex, polygenically inherited character and is related to several component characters, was the second-highest genotypic mean square as has been reported in practically all sorghum varietal evaluation studies [12, 13] reporting highly significant genotypic variance for this character.

Table 1: Analysis of variance (mean squares) for eleven quantitative traits in 22 sorghum genotypes

Trait	Replication (df = 2)	Genotype (df = 21)	Error (df = 42)
Days to 50% flowering	1.697	58.650**	1.141
Days to maturity	0.0455	17.897**	1.2518
Plant height (cm)	25.780	1457.060**	11.780
Stem girth (cm)	0.000192	0.047122**	0.001370
Leaf length (cm)	2.783	85.916**	2.136
Leaf width (cm)	0.00243	0.77909**	0.01681
Panicle length (cm)	0.036	4.2629**	0.0987
Panicle width (cm)	0.0197	0.33905**	0.00951
Grain yield per plant (g)	1.992	216.910**	4.251
Biological yield per plant (g)	49.130	1678.460**	85.270
Harvest index (%)	0.0151	7.3525**	0.3867

** Significant at $p < 0.01$.

Genetic variability, heritability and genetic advance

The total phenotypic variability observed in a population comprises both heritable (genotypic) and non-heritable (environmental) components; unless these are properly partitioned, phenotypic performance alone cannot reliably guide selection. The estimates of PCV, GCV, broad-sense heritability, genetic advance (GA) and genetic advance as a percentage of the mean (GAM) for the eleven traits are presented in Table 2.

Following the classification of Sivasubramanian and Menon [18], the PCV estimates ranged from 2.26% (days to maturity) to 13.09% (grain yield per plant), and the corresponding GCV estimates ranged from 2.04% to 12.72% for the same two traits. Low PCV and GCV values were recorded for days to 50% flowering, days to maturity, plant height, stem girth, leaf length, leaf width, panicle length, panicle width, biological yield per plant and harvest index. In contrast, grain yield per plant alone recorded moderate PCV and GCV. In every case, the PCV was only slightly higher than the corresponding GCV, indicating that genotype had a relatively greater effect on phenotypic expression and that environmental effects were relatively small; a narrow PCV-GCV difference suggests that phenotypic selection would be reasonably good for the traits in the present material. This close

correspondence between PCV and GCV, together with the comparatively larger coefficients of variability for grain yield relative to other traits, is consistent with recent reports in sorghum [12, 19, 20, 24].

For all 11 traits, a high broad sense heritability (between 81.59% and 97.61%) suggested that the phenotypic variation for all traits was primarily genetic and had low environmental effect. This consistently high heritability of morphological and yield-attributing characters in sorghum has been reported in many studies [2, 7, 11]. Heritability estimated in the broad sense, however, is composed of additive and non-additive components of genetic variance and high heritability alone does not necessarily mean good responsiveness to phenotypic selection; it has to be evaluated in relation to the genetic advance.

Following Johnson *et al.* [15], GAM was low only for days to maturity (3.79%), moderate for days to 50% flowering, plant height, stem girth, leaf length, leaf width, panicle length, panicle width, biological yield per plant and harvest index (11.47-18.56%), and high only for grain yield per plant (25.45%). Grain yield per plant was thus the only trait combining high heritability (94.34%) with high GAM (25.45%), a combination strongly indicative of the preponderance of additive gene action and,

consequently, of good responsiveness to simple, direct phenotypic selection for this economically vital trait. Despite their consistently high heritability values, the remaining 10 traits had low to moderate GAM, indicating that selection alone will not be sufficient to improve their inheritance and that hybridisation-based breeding strategies will be a better approach. This high heritability in combination with moderate to high genetic advance

achieved only for grain yield found in the majority of the component traits, indicates that the pattern of independent evaluation of sorghum and other Poaceae under the present circumstances is in accord with that reported by Jafar *et al.* ^[12], Yali and Nepir ^[13], and Vivek *et al.* ^[24] in separate evaluations, giving confidence to the validity of the present estimates.

Table 2: Estimates of genetic variability parameters for eleven agro-morphological traits in 22 sorghum genotypes

Trait	PCV (%)	GCV (%)	h ² b (Broad sense) (%)	GA	GAM (%)
Days to 50% flowering	7.04	6.84	94.38	8.76	13.69
Days to maturity	2.26	2.04	81.59	4.38	3.79
Plant height (cm)	9.23	9.12	97.61	44.67	18.56
Stem girth (cm)	7.85	7.51	91.62	0.24	14.81
Leaf length (cm)	7.58	7.30	92.90	10.49	14.50
Leaf width (cm)	8.08	7.82	93.80	1.01	15.61
Panicle length (cm)	6.69	6.47	93.36	2.35	12.87
Panicle width (cm)	6.05	5.80	92.04	0.65	11.47
Grain yield per plant (g)	13.09	12.72	94.34	16.85	25.45
Biological yield per plant (g)	6.58	6.11	86.17	44.07	11.68
Harvest index (%)	9.40	8.71	85.72	2.91	16.61

PCV = phenotypic coefficient of variation; GCV = genotypic coefficient of variation; h²b = broad-sense heritability; GA = genetic advance; GAM = genetic advance as a percentage of the mean.

Genetic divergence: D² analysis and Tocher's clustering

Application of Tocher's method to the Mahalanobis D² values computed among the 22 genotypes resolved the germplasm into six clusters of markedly unequal size (Table 3 and Fig 1). Cluster I was the largest, comprising twelve genotypes (SPV-2048, SPV-1830, SPV-1626, RSV-458, PC-1080, RC-2, CSV-23, CSH-17, SU-1557, SU-1708, SSV-74 and SSV-84); Clusters II and III each comprised three genotypes (PJ-1430, PJ-2510 and SU-1570 in Cluster II; SPV-2831, CSV-10 and PR-105 in Cluster III); Cluster IV comprised two genotypes, B-35 and 774-B; while Clusters V

and VI were solitary, mono-genotypic clusters represented by RSLG-2438 and SSG-59-3, respectively. This arrangement of one large, heterogeneous cluster and a few small or solitary highly divergent clusters, has been regularly described in the literature of sorghum divergence ^[9, 22, 23], and generally is a consequence of the narrow genetic base resulting from the frequent use of a restricted number of elite parents in breeding programmes, with a few highly divergent, but genetically unassimilated with the majority of material, genotypes interspersed in between.

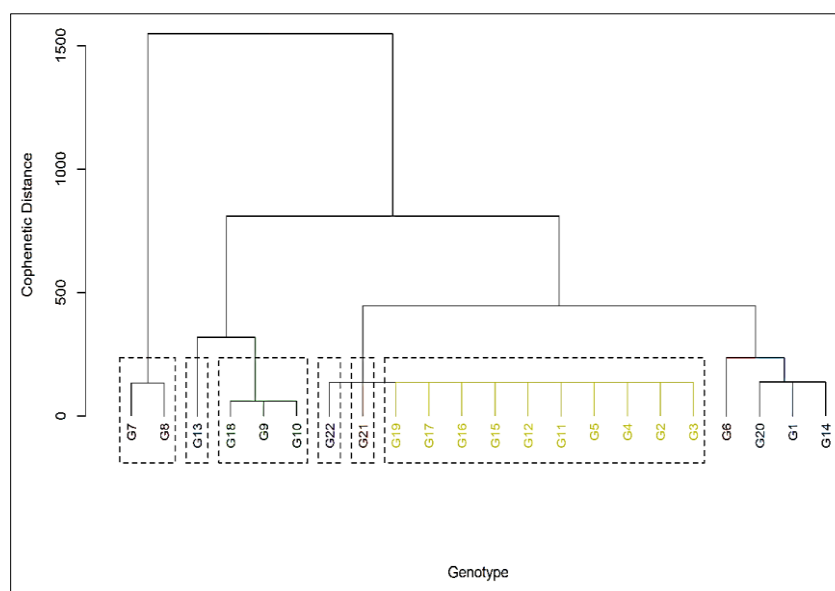


Fig 1: Dendrogram showing clustering pattern of 22 sorghum genotypes based on D² (Mahalanobis) statistics.

Table 3: Grouping of 22 sorghum genotypes into six clusters based on D² (Mahalanobis) statistics

Cluster	No. of genotypes	Genotypes included
I	12	SPV-2048, SPV-1830, SPV-1626, RSV-458, PC-1080, RC-2, CSV-23, CSH-17, SU-1557, SU-1708, SSV-74, SSV-84
II	3	PJ-1430, PJ-2510, SU-1570
III	3	SPV-2831, CSV-10, PR-105
IV	2	B-35, 774-B
V	1	RSLG-2438
VI	1	SSG-59-3

Inter- and intra-cluster distances

The averages of intra- and inter-cluster D² distances among the six clusters are shown in Table 4. The intra-cluster distances correlated with the clusters of multiple members. Cluster III (137.66) showed the maximum distance. In contrast, Cluster II (60.58) showed the minimum distance, indicating a higher level of genetic proximity among the three genotypes within Cluster II than among the other clusters. For the two clusters that were left out in the centre, V and VI, the intra-cluster distance was recorded as zero, as expected.

Table 4: Average intra- (diagonal) and inter-cluster (off-diagonal) D² values among six clusters of 22 sorghum genotypes

Cluster	I	II	III	IV	V	VI
I	135.80	375.48	435.11	1336.32	479.88	1087.38
II	375.48	60.58	1278.22	2471.95	1247.97	318.36
III	435.11	1278.22	137.66	876.90	236.23	2532.42
IV	1336.32	2471.95	876.90	132.29	1378.11	3490.45
V	479.88	1247.97	236.23	1378.11	0.00	2400.75
VI	1087.38	318.36	2532.42	3490.45	2400.75	0.00

Diagonal values (in bold in the original analysis) represent average intra-cluster D² distance; off-diagonal values represent average inter-cluster D² distance. Clusters V and VI show zero intra-cluster distance as each comprises a single genotype.

The most genetically distant pair of genotype-groups in the entire study was found to be: B-35/774-B (Cluster IV) and SSG-59-3 (Cluster VI) with a maximum inter-cluster distance of D² = 3490.45, followed by B-35/774-B (Cluster IV) and SSG-59-3 (Cluster VI) with a maximum inter-cluster distance of D² = 2532.42, while B-35/774-B (Cluster IV) and B-44/774-B (Cluster II) and SSG-59-3 (Cluster VI) and B-28/774-B (Cluster V) were also the most distant pairs with D² = 2471.95 and 2400.75 respectively. In contrast, the minimum inter-cluster distance was observed between Cluster III and Cluster V (D² = 236.23), Cluster II and Cluster VI (D² = 318.36) and Cluster I and Cluster II (D² = 375.48), which showed that Cluster III and Cluster V, Cluster II and Cluster VI and Cluster I and Cluster II, respectively, are genetically close to each other. In all cases, the inter-cluster distances were significantly larger than the intra-cluster distances, indicating that the clustering obtained using Tocher's method was statistically valid and biologically meaningful. This overall situation, where inter-cluster distances were found to be considerably larger than the intra-cluster distances, was a general

rule in all divergence studies of Poaceae on D² [22, 23, 24] and gave external validity to the present result, showing that the crossing of IV and VI Cluster genotypes should be expected to produce the broadest possible recombinant gene pool relating to the traits studied.

Cluster mean performance

Cluster mean values for the eleven quantitative traits are presented in Table 5. Cluster VI (SSG-59-3) recorded the lowest mean values for days to 50% flowering (57.33 days), days to maturity (110.00 days) and plant height (196.15 cm), confirming its status as the earliest-flowering, earliest-maturing and most dwarf group. However, its grain yield (55.04 g) and biological yield (338.07 g) remained comparatively modest. Cluster II combined early flowering (59.56 days) and short stature (214.97 cm) with the second-highest harvest index (18.45%) among all clusters, indicating an agronomically efficient, early-duration group.

Cluster III (SPV-2831, CSV-10, PR-105) and Cluster V (RSLG-2438) emerged as the two most promising clusters from a yield standpoint, recording the highest mean grain yield (73.06 g and 77.27 g, respectively) coupled with the highest biological yield (400.33 g and 429.80 g) and the largest panicle dimensions, indicating that genotypes of these two clusters combine superior source (biomass) and sink (grain-filling) capacity. Cluster I, the largest and most heterogeneous cluster, recorded near-average performance for practically all traits, consistent with its broad genetic base. In sharp contrast, Cluster IV (B-35, 774-B), despite recording the tallest plant stature (284.93 cm), the longest leaves (81.37 cm) and among the highest biological yield (352.97 g), recorded the lowest grain yield (46.45 g) and lowest harvest index (13.17%) of all clusters, reflecting poor partitioning efficiency despite substantial vegetative vigour, and rendering it more suitable as a source of biomass or lodging-resistance donor material than as a direct grain-yield-improving parent.

Both the identification of high-yielding clusters separate from low-yielding clusters and the suggestion to choose parents with wide inter-cluster distance and good mean yield rather than size only have been repeated in recent sorghum divergence studies [9, 22, 23] and other Poaceae family [24]. In the current experiment, the single genotype (RSLG-2438) of Cluster V outperformed the twelve genotypes of Cluster I. Also, it showed higher biological yield, indicating that biological yield is not directly correlated with cluster size.

Table 5: Cluster mean values for yield and yield-attributing traits in 22 sorghum genotypes

Cluster	N	DF50	DM	PH	SG	LL	LW	PaL	PaW	GY	BY	HI
I	12	63.58	115.25	237.42	1.63	71.92	6.36	18.29	5.77	67.96	380.20	17.86
II	3	59.56	113.44	214.97	1.49	65.49	5.81	17.67	5.53	65.55	355.36	18.45
III	3	67.44	118.44	260.24	1.74	76.82	6.96	19.57	6.08	73.06	400.33	18.26
IV	2	72.67	118.83	284.93	1.88	81.37	7.36	16.16	5.10	46.45	352.97	13.17
V	1	61.67	114.67	255.90	1.80	77.83	6.95	20.84	6.28	77.27	429.80	17.98
VI	1	57.33	110.00	196.15	1.43	61.21	5.49	16.55	5.11	55.04	338.07	16.28

N = number of genotypes in the cluster. DF50 = days to 50% flowering; DM = days to maturity; PH = plant height (cm); SG = stem girth (cm); LL = leaf length (cm); LW = leaf width (cm); PaL = panicle length (cm); PaW = panicle width (cm); GY = grain yield per plant (g); BY = biological yield per plant (g); HI = harvest index (%).

Identification of genetically diverse and high-yielding genotypes

The effectiveness of hybridisation for crop improvement depends on the selection of parents that possess excellent per se yield and also a high degree of genetic divergence to provide broad recombination and, if applicable, heterotic vigour. Synthesising the evidence generated from the genotypic mean squares (Table 1), the variability parameters (Table 2) and the divergence

analysis (Tables 3-5), the genotype RSLG-2438 was identified as the single most valuable genotype among the material evaluated, on account of its combination of the highest biological yield, near-highest grain yield, and membership of a genetically distinct, solitary cluster (Cluster V) well separated from the bulk of the germplasm housed in Cluster I. The high-yielding genotypes of Cluster III (SPV-2831, CSV-10, PR-105), together with CSH-17 of Cluster I, were similarly identified as promising parents. In

contrast, the genetically most divergent genotypes, B-35, 774-B (Cluster IV) and SSG-59-3 (Cluster VI), were recognised as valuable sources of complementary variation, biomass and plant stature in the case of the former pair, and earliness and dwarf stature in the case of the latter, for exploitation in future hybridisation programmes.

In recent years, the literature on sorghum divergence consistently recommends selecting the genotype with both the best cluster/genotype mean yield and the maximum inter-cluster genetic distance, rather than the largest cluster or the best cluster mean yield [9, 22, 23, 24]. Crossover combinations in which the RSLG-2438 genotype served as one parent, and the other parent came from the genetically most distant Cluster IV and Cluster VI, would be likely to have a good amount of genetic recombination and a fair chance of transgressive segregation in earliness and biomass potential, respectively.

Taken together, since grain yield per plant was the only trait combining high heritability with high genetic advance as a percentage of the mean, direct phenotypic mass selection for grain yield within the high-mean-performing Cluster III and Cluster V genotypes is expected to be immediately rewarding. Future generations of superior transgressive segregants are most likely to be recovered. Undesirable trait linkages such as the tall and low harvest index combination seen in Cluster IV can be broken, by using a hybridisation approach involving the crossing of RSLG-2438 or the high-yielding genotypes of Cluster III with the genetically distant genotypes of Cluster IV and Cluster VI, where the genetic advance for the remaining ten traits was relatively low, although high heritability is observed. The genotypes RSLG-2438, CSH-17, SPV-2831, CSV-23, PR-105, B-35, 774-B and SSG-59-3 are accordingly recommended as priority parental material for future sorghum improvement programmes based on the present set of genotypes.

Conclusion

A significant and exploitable genetic variability was found in 11 yield and yield-contributing traits among 22 sorghum genotypes tested during the present investigation where highly significant genotypic differences were recorded for all the traits studied. Grain yield showed most high heritability and also highest genetic advance as% of mean of all characters indicating unquestionably favourable additive gene action. In contrast, the rest had had better heritability level which were predominant by non-additive type of gene action in favor of hybridisation-based improvement programme. Mahalanobis's D^2 analysis and the clustering of Tocher separated the germplasm into six genetically distinct clusters, with the inter-cluster distances always significantly larger than the intra-cluster distances, validating the presence of exploitable real genetic differences between the clusters. The identification of the tall, late-maturing, low-yielding genotypes B-35 and 774-B as the most divergent from the dwarf, early-maturing genotype SSG-59-3, together with the recognition of RSLG-2438 as a uniquely high-yielding and genetically distinct genotype, provided clear, practically useful guidance for parental selection. Therefore, a combination of direct phenotypic selection for grain yield of superior clusters and planned hybridisation among genetically divergent high-yielding clusters (Cluster IV & Cluster VI) provides the most logical route for genetic improvement of grain yield and its component traits in sorghum. The data on genetic parameters, cluster composition and inter/intra-cluster distances should prove useful as a reference for sorghum plant breeders involved in the selection of complementary parental combinations for use in their hybridisation and varietal-improvement programmes of sorghum

as a dryland crop.

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Authors' contributions

All authors contributed equally.

Compliance with ethical standards

Conflict of interest: The authors declare no conflicts of interest.

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