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RESEARCH COMMUNICATION

Multivariate analysis for seed yield and its contributing traits in sesame (*Sesamum indicum* L.)

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Abstract

Sesame is one of the important oilseed crops. The present investigation evaluated sixty sesame (*Sesamum indicum* L.) genotypes for seven yield and yield-contributing traits to identify key selection criteria for yield improvement. Significant genetic variability was detected, with number of capsules per plant (range: 32–78), number of branches per plant (2.1–6.3) and seed yield per plant (3.8–9.7 g) exhibiting high heritability (> 70 %) and high genetic advance (> 20 % of the mean), indicating substantial scope for effective selection. Principal component analysis revealed that the first three components explained 82.3 % of the total variation, mainly influenced by branching pattern, capsule traits and phenological attributes. Correlation analysis showed that number of capsules per plant (r = 0.72) and number of branches per plant (r = 0.61) were positively associated with seed yield, whereas days to maturity (r = -0.38) displayed a negative association. Path coefficient analysis identified strong positive direct effects for number of capsules per plant (2.01) and days to maturity (1.36) on seed yield, while plant height (-1.81) and number of branches per plant (-0.63) exerted negative direct effects. Cluster analysis grouped the genotypes into eight clusters, demonstrating substantial genetic divergence. The wide variation among clusters suggests that crossing genotypes from distant clusters, particularly clusters III, VI and VIII, would generate broad segregation and enhance the probability of isolating high-yielding recombinants. These findings provide numerically supported trait priorities and hybridization strategies for designing efficient sesame improvement programmes.

Keywords: correlation; path analysis; principal component analysis; sesame; variability

Introduction

Sesame (*Sesamum indicum* L.), belonging to the Pedaliaceae family, has a diploid chromosome count of 2n = 26. It ranks as one of the most significant oilseed crops in tropical and subtropical regions. In India, it is the third most important oilseed crop, following mustard and groundnut. Sudan, India and Myanmar collectively produce 77.4 % of the world's sesame seeds, making them the leading producers globally, followed by China and Nigeria (1). Rajasthan is the leading sesame-producing state in 2023–24, contributing around 401000 tonnes (2). Sesame breeding is constrained by a narrow genetic base, yield stagnation and limited availability of well-characterized genetic resources. Despite its economic importance, structured diversity studies integrating morphological and molecular data remain insufficient, hindering the effective use of germplasm in improvement programmes. Knowledge gaps in the inheritance of key quantitative traits, along with a lack of robust markers for stress tolerance and yield enhancement, further slow genetic progress. These challenges highlight the need for expanded genetic resources, comprehensive diversity assessment and genomics-assisted breeding to accelerate sesame improvement.

Sesame is often dubbed the "queen of oil seed crops" due to its high oil content (50–60 %), distinctive antioxidants and nutritional and medicinal benefits (3). The seeds are a vital source of oil (44–57 %), proteins (18–25 %), carbohydrates (13.5 %) and ash (5 %) and they also possess medicinal and nutritional value (4). Sesame oil is highly stable, thanks to natural antioxidants like sesamolin, sesamin and sesamol (5). Its chemical composition is marked by a low level of saturated fatty acids (SFAs) (< 15 %). Various studies also highlight the therapeutic potential of its oil, showing anti-cancer, anti-oxidative, anti-hypertensive and immune regulatory properties (6). Despite its proven advantages, sesame remains an under-researched "orphan crop" with limited scientific focus (7).

The variability and genetic diversity present in base population are a prerequisite for the successful breeding programme. Variability studies help to understand the genetic makeup, the influence of the environment on traits, thereby identifying the selection criteria status of the trait in genetic improvement programme. The principal component analysis identifies the indispensable traits that influence seed yield. The cluster analysis reveals the genetic diversity in the base population.

The study aimed to quantify phenotypic and genotypic variability, identify major sources of variation through multivariate analyses, select superior and genetically divergent parents, determine the relative importance of yield-related traits and formulate a trait-based selection strategy for enhancing seed yield in sesame. However, despite several variability and diversity studies in sesame, most existing work has either focused on limited trait groups or narrow genetic backgrounds, providing insufficient integration of variability, multivariate analyses and trait-based selection indices within a single comprehensive framework. Therefore, there remains a need for a holistic assessment combining variability parameters, principal component analysis (PCA), genetic divergence and trait-association analyses to strengthen parent selection and yield improvement strategies in sesame.

Materials and Methods

The study was conducted at the experimental farm of Regional Research Station, Tamil Nadu Agricultural University, Vriddhachalam, Tamil Nadu, during December 2023 to March 2024. The experimental material consisted of 60 sesame genotypes, including 53 advanced lines and seven released varieties. The experiment was laid out in a randomized completely block design (RCBD) with two replications. Each genotype was raised with plot size of 4 m × 3 m. Rows were maintained at 5 m length with a spacing of 30 × 30 cm. The soil was red sandy loam with pH of 6.5, medium Nitrogen (N) and Potassium (K) status and low Phosphorus (P) content. Recommended crop production practices were followed to raise a good crop.

Observations recorded

The quantitative traits such as days to 50 % flowering (DFF), plant height (cm) (PH), number of branches per plant (NBP), number of capsules per plant (NCP), capsule length (mm) (CL), days to maturity (DTM) and seed yield per plant (g) (SY) were studied in this experiment. Data for all traits were recorded on five randomly selected plants and the mean was used for statistical analysis.

Statistical analysis

The variability, correlation and path analysis were analysed using TNAUSTAT software (8). The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) estimates were categorised < 10 % as low, 10-20 % as moderate and > 20 % as high (9). Heritability per cent values were categorized as low (< 30 %), medium (30-60 %) and high (> 60 %) (10). Genetic advance as a per cent of mean values were categorized as low (< 10), moderate (10-20) and high (> 20). Principal component analysis (PCA) was performed using GRAPES software (11). Cluster analysis based on Ward's method using squared Euclidean distance of the standardised variables, was carried out to group the genotypes.

Results and Discussion

Variability analysis

The trait days to 50 % flowering showed low PCV (8.57) and low GCV (5.61) indicating that genotypes had less variability for this trait (Table 1). The heritability of this trait was moderate (42.86) but low genetic advance as mean (GAM)(7.57) suggesting that expression of days to 50 % flowering is highly influenced by the environment. Plant height trait exhibited moderate PCV (13.17) and low GCV (8.86). The heritability of plant height was moderate (45.26) but low GAM (12.28), indicated considerable environment influence on the expression of this trait. The number of branches per plant showed higher PCV (30.61) and GCV (24.33) indicating that this trait had more variation. The number of branches per plant had high heritability (63.19) and high GAM (39.84), demonstrating strong genetic control and good potential for selection.

The number of capsules per plant had high PCV (29.33) and high GCV (21.11) representing that studied sesame genotypes had substantial variance. This trait showed moderate heritability (51.82) and high GAM (31.31), suggesting the potential of this trait for selection. Capsule length had moderate PCV (11.16) and low GCV (8.92) indicating less variability among genotypes. It has high heritability (63.86) with moderate GAM (14.68), indicating the potential for selection. Days to maturity showed low PCV (4.24), low GCV (2.91), moderate h^2 (47.01) and low GAM (4.11) confirming the presence of low variability for this trait and low potential for selection. Seed yield per plant trait expressed moderate PCV (14.65), moderate GCV (13.03), high h^2 (79.10) and high GAM (23.87). It indicated the potential of this trait with high variability and suitability for selection. Traits showing high heritability with low GAM indicated that phenotypic expression is largely governed by environmental effects rather than additive genetic variance. Similar findings of low PCV, GCV for days to 50 % flowering, plant height, days to maturity and related traits have been reported by several researchers (12-14). Comparable observations for heritability and GAM have also been documented by other scientists (15).

Principal component analysis

Principal component analysis is a dimension reduction technique that identifies potential traits responsible for the total variability. The PCA revealed that the first three principal components accounted for 82.3 % of the total variation, indicating that a few key trait groups effectively captured the diversity among genotypes (Table 2; Fig 1.). PC1 (38.7 %) was primarily influenced by days to 50 % flowering, plant height, number of branches, number of capsules per plant and days to maturity, representing a phenology architecture axis where vigorous, late-maturing plants tend to possess greater yield potential. PC2 (28.8 %) was driven by seed yield and capsule number, reflecting reproductive efficiency and distinguished high-yielding, capsule-rich genotypes from longer-duration types. PC3 (14.8 %) was dominated by capsule length and plant height,

Table 1. Analysis of genetic variability, heritability and GAM for various traits in sesame

Characters	Mean	PCV (%)	GCV (%)	h^2 (%)	GAM (%)
Days to 50 % flowering (DFF)	37.39	8.57	5.61	42.86	7.57
Plant height (cm) (PH)	120.53	13.17	8.86	45.26	12.28
Number of branches per plant (NBP)	5.79	30.61	24.33	63.19	39.84
Number of capsules per plant (NCP)	78.83	29.33	21.11	51.82	31.31
Capsule length (mm) (CL)	2.98	11.16	8.92	63.86	14.68
Days to maturity (DTM)	78.42	4.24	2.91	47.01	4.11
Seed yield per plant (g) (SY)	867.61	14.65	13.03	79.10	23.87

Table 2. Principal components with eigen value, variance and loading values of various traits in sesame

Particulars	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7
Eigenvalue	2.71	2.02	1.03	0.63	0.34	0.25	0.02
Variance (%)	38.7	28.8	14.8	9.0	4.8	3.6	0.3
Cumulative variance (%)	38.7	67.5	82.3	91.3	96.1	99.7	100
DFF	**-0.50**	0.33	-0.11	0.36	-0.07	-0.14	-0.69
PH	**-0.43**	0.14	0.47	-0.45	0.53	0.32	-0.06
NBP	**-0.44**	-0.34	-0.14	-0.17	-0.60	0.53	0.05
NCP	-0.33	**-0.45**	0.41	-0.11	-0.18	-0.70	0.06
CL	0.26	0.21	0.76	0.33	-0.39	0.23	-0.04
DTM	**-0.43**	**0.47**	-0.06	0.28	-0.05	-0.10	0.71
SY	-0.13	-0.54	0.05	0.67	0.42	0.24	0.08

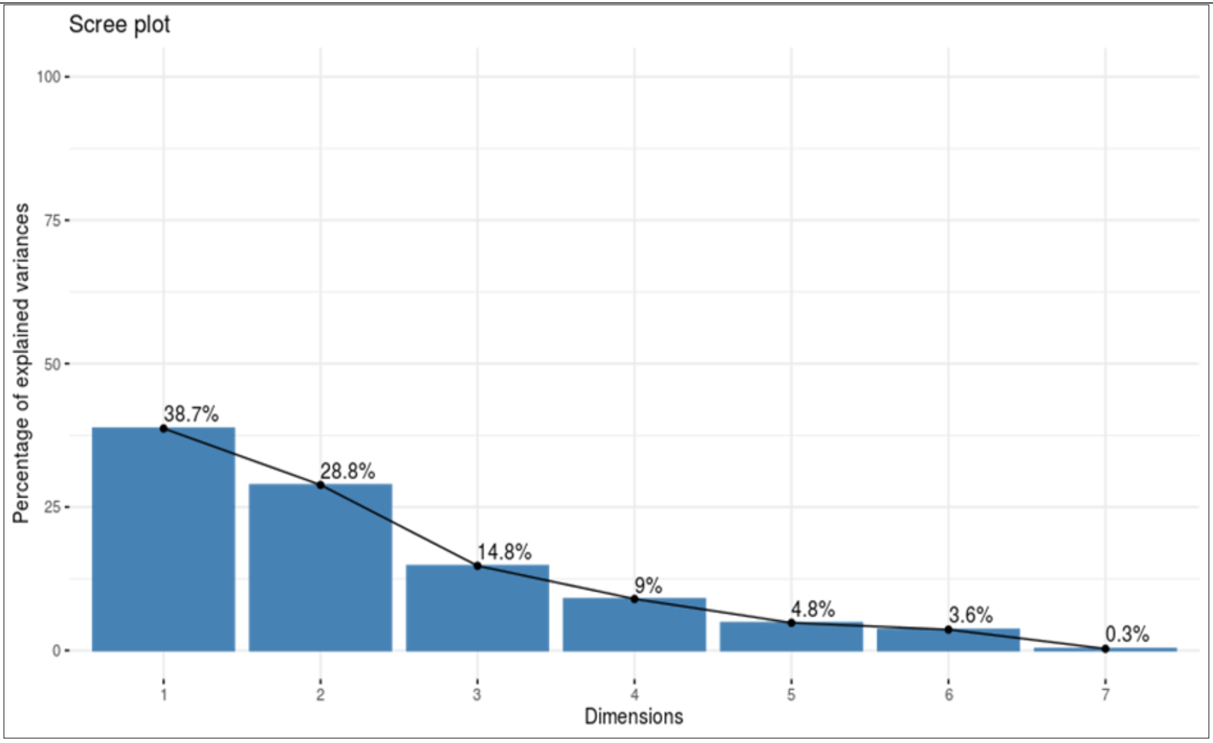

Fig. 1. Scree plot of PCA for eight characters in sesame.

describing the contribution of capsule morphology and structural traits to seed yield.

PC4 (9.0 %) highlighted the role of flowering synchrony and moderate plant height in stabilizing yield, while PC5 (4.8 %) captured a trade-off between branching intensity and plant height affecting capsule distribution. PC6 (3.6 %) reflected variation in capsule arrangement across branches and PC7 (0.3 %) represented minor differences related to maturity duration. Overall, the PCA indicated that vigorous plant architecture, efficient capsule production and favourable capsule morphology are the major determinants driving yield improvement in sesame. The first four components accounted most of the variation with eigenvalues > 1 (16). The first three components explaining 78 % of total variability by studying 45 sesame genotypes (15). According to the loadings in PC1, four traits, such as DFF, PH, NBP and DTM contributed more to variations in PC1, whereas two traits, DTM and NCP contributed more variations in PC2.

The PCA variable plot represents the interaction between the traits and the length of each trait vector indicates its contribution to total divergence (Fig. 2). The character DFF, DTM showed longest vector length, suggesting more contribution to overall divergence, followed by NBP, NCP, SY, PH and CL. Additionally, the angle formed by the traits vector reflects the correlation between traits. Out of seven attributes, NBP, NCP and PH showed positive correlation with SY, whereas CL, DFF and DTM showed negative association with SY. The number of capsules per plant, number of branches per plant and plant height had positive association with seed yield in sesame (17).

PCA biplots reduce competing variations and integrate variables and genotypes into two measures, hence facilitating the identification of principal traits within the analysed datasets. The genetic material is placed within the precise quadrant as the trait vectors present the enhanced performance for those particular traits. Accordingly, the genotypes VS 17-016, VS 20-004, VS 19-014, VS 19-018, TMV 7, VS 20-017, VS 19-005, VRI 3, VS 19-065, VS 19-064, VS 20-031, VS 20-016, VS 20-005 and VS 20-007 demonstrated superiority for the traits SY, NCP and NBP shown in the first quadrant (Fig. 2).

Genotypes VS 20-009, VS 19-063, VS 19-061, VS 19-082, VS 20-019, VS 19-048, VS 19-073, VS 19-078, VS 19-050, VS 19-040 and VS 18-007 showed supremacy for PH, DFF and DTM traits shown in the second quadrant. The genetic material VS 20-013, VS 19-032, VS 20-022, VS 20-026, VS 19-029, VS 20-008, VS 19-023, VS 20-023, VS 20-025, VS 19-054, VS 19-067, VS 19-071 and VS 20-027 exhibited superior

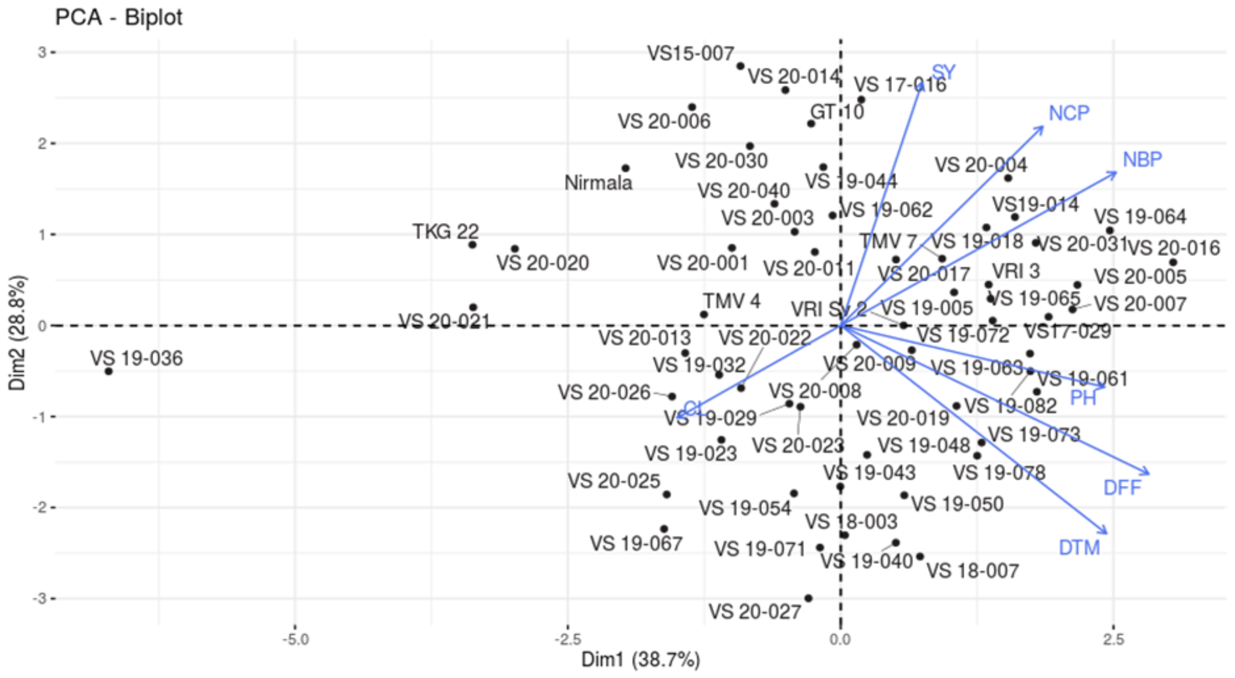

Fig. 2. PCA biplot, traits pattern and variance represented via biplot for PC1 vs PC2.

performance for the CL shown in the third quadrant. Similarly, the biplots based on PCA study were utilised to find the best genotypes for specific traits in sesame by various workers (13, 18, 19).

Correlation analysis

The trait association analysis via correlation efficient at genotypic and phenotypic levels for seven biometrical traits were presented in the Table 3. Seed yield had significant and positive correlation with NBP ($r_p = 0.327$, $r_g = 0.510$) and NCP ($r_p = 0.327$, $r_g = 0.645$) at both in phenotypic and genotypic correlation (Table 4). The attributes *viz.,* CL ($r_g = -0.217$) had significant and negative correlation with seed yield at genotypic level only. The trait DTM ($r_p = -0.188$, $r_g = -0.372$) exhibited significant and negative correlation with seed yield at both phenotypic and genotypic levels. This correlation study indicated that seed yield can be improved through increased number of branches and number of capsules per plant while selecting for earliness.

The trait DFF had positive and significant inter correlation with PH ($r_p = 0.361$, $r_g = 0.775$), NBP ($r_p = 0.267$, $r_g = 0.482$) and DTM ($r_p = 0.965$, $r_g = 0.924$) both at phenotypic and genotypic levels. The trait PH showed positive and significant inter correlation with NBP ($r_p = 0.319$, $r_g = 0.355$), NCP ($r_p = 0.362$, $r_g = 0.456$) and DTM ($r_p = 0.375$, $r_g = 0.772$) at both phenotypic and genotypic levels. The trait NBP showed positive and significant inter correlation with NCP ($r_p = 0.533$, $r_g = 0.700$) while it had negative and significant correlation with CL ($r_p = -0.445$, $r_g = -0.580$) at both phenotypic and genotypic levels. The inter correlation suggested that the traits DFF, CL and PH also need consideration during selection process. Similar findings, where

Table 3. Correlation coefficients among various traits in sesame

Traits	DFF	PH	NBP	NCP	CL	DTM	SY
DFF	1	0.775**	0.482**	0.156	-0.340**	0.924**	-0.121
PH	0.361**	1	0.355**	0.456**	-0.066	0.772**	-0.080
NBP	0.267**	0.319**	1	0.700**	-0.580**	0.224*	0.510**
NCP	0.071	0.362**	0.533**	1	-0.182*	-0.091	0.645**
CL	-0.164	0.006	-0.445**	-0.115	1	-0.149	-0.217*
DTM	0.965**	0.375**	0.138	-0.048	-0.068	1	-0.372**
SY	-0.031	-0.062	0.327**	0.434**	-0.161	-0.188*	1

Note: phenotypic (below diagonal) and genotypic (above diagonal) correlation coefficients.

Table 4. Direct and indirect effects of various traits on seed yield

Traits	DFF	PH	NBP	NCP	CL	DTM	Genotypic correlation with SY
DFF	**-0.040**	-1.401	-0.303	0.314	0.049	1.260	-0.121
PH	-0.031	**-1.807**	-0.223	0.918	0.010	1.053	-0.080
NBP	-0.019	-0.641	**-0.628**	1.409	0.084	0.306	0.510**
NCP	-0.006	-0.824	-0.440	**2.013**	0.026	-0.124	0.645**
CL	0.014	0.119	0.364	-0.366	**-0.145**	-0.203	-0.217*
DTM	-0.0374	-1.396	-0.141	-0.183	0.022	**1.364**	-0.372**
Residual effect	0.347						

number of branches per plant and number of capsules per plant positively associated with seed yield have been reported by several researchers (20-23).

Path co-efficient analysis

The path co-efficient analysis explained cause and effect of yield contributing traits on seed yield. The residual effect was 0.3465, indicating that the studied seven traits were responsible for explaining approximately 66.45 % variability in seed yield studied in path analysis. The attributes *viz.,* NCP (2.0128) and DTM (1.3636) had high direct positive effects on seed yield (Table 4). In contrast, PH (-1.8071) and NBP (-0.6279) showed high negative direct effects on seed yield. All these traits also had high indirect effects among themselves. These negative contributions may reflect biological constraints such as increased susceptibility to lodging in overly tall plants, inefficient canopy structure, or resource competition among excessive branches that diverts assimilates away from capsule filling. Despite these negative direct effects, PH and NBP also influenced seed yield indirectly through favourable interactions with other traits, highlighting the complexity of their contribution to productivity. Overall, the traits NCP, DTM, PH and NBP emerged as key selection indices for improving seed yield in sesame, consistent with earlier reports (23-25).

Cluster analysis

The cluster analysis grouped the 60 genotypes into eight clusters (Fig. 3). The cluster I had nine genotypes, cluster II had two genotypes, cluster III had six genotypes, cluster IV had eight genotypes, cluster V had seven genotypes, cluster VI had nine genotypes, cluster VII had eight genotypes and cluster VIII had comprised 11 genotypes. The presence of multiple, clearly separated clusters indicates substantial genetic divergence and implies ample scope for parent selection in breeding programmes.

Crossing genotypes from genetically distant clusters is expected to generate broader segregation and enhance the probability of obtaining superior recombinants in subsequent generations. Therefore, selecting parents from clusters showing maximum inter-cluster divergence rather than within the same cluster will help broaden the genetic base and facilitate the development of high-yielding and agronomically improved sesame varieties. This strategic use of divergent clusters supports heterotic expression, complementary trait recombination and greater genetic gains in breeding programmes (13, 22, 24).

Conclusion

The study revealed substantial genetic variability among the 60 sesame genotypes, providing strong scope for genetic improvement. The high heritability and high genetic advance observed for number of branches per plant, number of capsules per plant and seed yield per plant indicate that selection would be highly effective for improving these traits. The combined evidence from correlation and path analyses identifies number of capsules per plant, days to maturity, plant height and number of branches per plant as key selection indices for yield enhancement.

In addition, the PCA and cluster analysis highlighted the presence of wide genetic divergence, suggesting that strategic hybridization between genetically distant clusters (e.g., clusters with contrasting architecture and maturity behaviour) will maximize heterosis and promote broad transgressive segregation. From a breeding perspective, these findings support the adoption of multi-

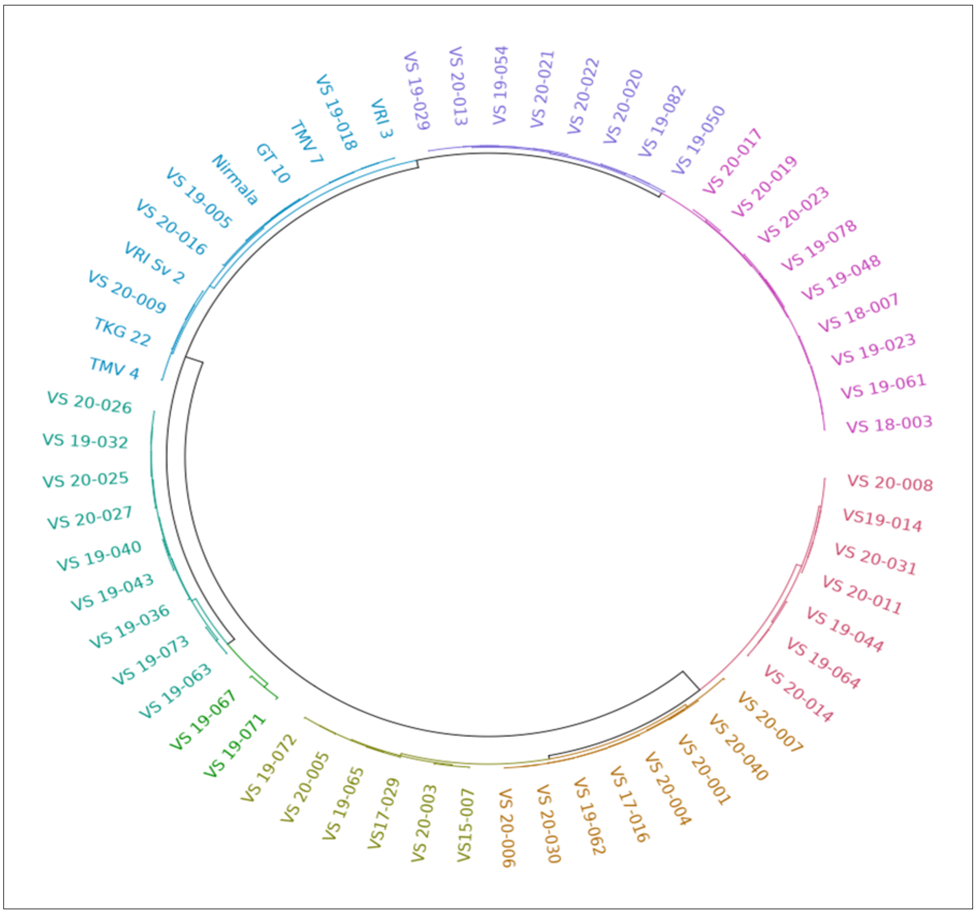

Fig. 3. Dendrogram showing eight clusters of sesame genotypes.

parent crossing schemes, recurrent selection and bi-parental mating among cluster-divergent parents to accumulate favourable alleles for capsule number, optimal plant stature and efficient reproductive duration.

Incorporation of these trait-based indices into marker-assisted selection (MAS) or genomic selection (GS) pipelines could further accelerate genetic gain in sesame. Additionally, targeted development of ideotypes moderately tall, well-branched plants with high capsule load and optimal maturity will contribute to stable yield improvement across environments. At the policy level, strengthening public breeding programmes, promoting on-farm conservation of diverse landraces and enhancing seed delivery systems for newly developed high-yielding varieties are essential. Investments in phenotyping infrastructure, molecular breeding tools and farmer–researcher participatory networks can substantially improve the efficiency of sesame improvement programs. Overall, the results of this study provide a clear direction for designing diversity-based, trait-focused breeding strategies and policy interventions aimed at developing high-yielding, resilient sesame varieties for sustainable production.

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Authors' contributions

SR drafted the manuscript, NM and MA supervised and worked on the manuscript. SK, SG and JK were involved in planning and provided critical feedback on manuscript. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None

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