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Genetic Diversity Studies in Coloured Pericarp Sorghum Genotypes (*Sorghum bicolor* L. Moench)

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Abstract

A total of 81 genotypes were evaluated to estimate genetic diversity using Mahalanobis D² statistics and Tocher's clustering method for morphological and shoot fly tolerance traits. Based on the D² analysis, the genotypes were grouped into eight clusters for morphological traits and six clusters for shoot fly-related traits, indicating substantial genetic divergence among the material studied. Among the 13 morphological characters, the highest contribution to total genetic diversity was recorded for glume colour (39.10%), grain color (32.75%), plant height (11.33%), and number of primaries per panicle (10.96%). For the six shoot fly tolerance traits, adaxial (69.23%) and abaxial (24.69%) trichome density, followed by shoot fly dead hearts (4.72%) and seedling glossiness (0.51%), contributed most to the observed variability. The maximum inter-cluster distance was recorded between clusters V and VII (D=57.91) for morphological traits and between clusters V and II (D=80.81) for shoot fly traits, suggesting that genotypes in these clusters are genetically most distant and offer high potential for hybridization to obtain desirable recombinants. Cluster mean analysis revealed considerable variation particularly for plant height, days to 50% flowering, trichome density, and dead heart percentage at 28 DAS. These traits may serve as effective selection criteria for further breeding and for developing transgressive segregants with enhanced shoot fly tolerance and improved agronomic performance.

1.INTRODUCTION

Sorghum (Sorghum bicolor (L.) Moench) is one of the most ancient and resilient cereal crops cultivated by humankind and has been described as indispensable for human survival due to its adaptability and wide utility (Harlan, 1971). Commonly known as the "Great Millet," sorghum is considered the "king of millets" owing to its large grain size, vast cultivation range, and superior environmental adaptability. It occupies the fifth position among global cereal crops after wheat, maize, rice, and barley (FAO, 2018). The name sorghum originates from the Latin word sorgo, meaning "to rise," reflecting the tall stature of the crop. In India, sorghum is popularly known as "jowar." Sorghum originated in East-Central Africa, particularly in Ethiopia and Sudan, and has since spread to tropical and subtropical regions of the world (Doggett, 1988). It is a C4 photosynthetic species, well adapted to hot and dry environments, and predominantly cross-pollinated with a chromosome number of 2n=20. Taxonomically, sorghum belongs to the family Poaceae, subfamily Panicoideae, tribe Andropogoneae and genus Sorghum. India is one of the major producers of sorghum and the crop plays an important role in food, feed, and fodder systems. Sorghum is cultivated on 4.10 million ha in the country with an annual production of 4.49 million tonnes and productivity of 1018 kg/ha (Government of India, 2019–20). Maharashtra is the leading state in sorghum cultivation, followed by Karnataka, Tamil Nadu, Andhra Pradesh, Rajasthan, and Madhya Pradesh. Both kharif and rabi sorghum are cultivated, with kharif sorghum largely used for feed and rabi sorghum serving grain and fodder purposes. The rabi season accounts for nearly 64% of total sorghum area in India. Nutritionally, sorghum is a gluten-free cereal rich in fiber, proteins, phenolic acids, and flavonoids, making it increasingly valuable for health-focused food systems (Awika & Rooney, 2004). Significant variation in grain color among sorghum landraces—from white to pink, orange, red, and brown—is largely governed by pigments such as anthocyanins and

flavan-4-ols present in the pericarp (Dykes et al., 2005). This natural variation reflects the wide genetic diversity available in global sorghum germplasm. The assessment and utilization of this genetic diversity is critical for the development of improved cultivars, particularly in regions facing biotic and abiotic stresses. Characterization of diverse genotypes provides breeders with the opportunity to identify superior parents, broaden the genetic base, and develop high-yielding, resilient sorghum varieties. Therefore, systematic evaluation of sorghum germplasm for morphological, physiological, and stress-adaptive traits remains a major priority in crop improvement programs.

2. Materials and Methods

The field experiment "Genetic Diversity studies in Coloured Pericarp Sorghum (Sorghum bicolor (L.) Moench)" was conducted during Rabi 2019-20 at the Sorghum Research Station, VNMKV, Parbhani (19.27°N, 76.78°E; 347 m above mean sea level). A total of 81 sorghum genotypes, including 76 germplasm lines and 5 checks, obtained from ICRISAT Hyderabad, IIMR Rajendranagar, and VNMKV Parbhani, were evaluated. The crop was sown on 16 November 2019 in a Randomized Block Design (RBD) with two replications, using a single-row plot of 3.0 m length and a spacing of 45 cm × 15 cm. The crop received the recommended fertilizer dose of 80:40:40 NPK kg/ha, and standard cultivation practices were adopted. Two hand weedings were done at 30 and 45 days after sowing to maintain a healthy crop. Data were recorded on five randomly selected and tagged plants from each genotype in both replications. A comprehensive set of quantitative, qualitative, and shoot fly resistance parameters was measured, including days to 50% flowering, plant height, panicle traits, 100-seed weight, grain yield, fodder yield, seedling vigour, glossiness, dead heart percentage, trichome density, leaf angle, grain colour, and glume colour. Standard procedures were followed for specialized observations such as trichome density, which was examined microscopically at 10× magnification after tissue clearing. The data collected were subjected to statistical analysis using standard biometrical procedures. Analysis of variance (ANOVA) was conducted as per Panse and Sukhatme (1985) to test the significance among genotypes. Genetic variability parameters, including PCV, GCV, heritability, and genetic advance, were estimated following Burton (1952) and Johnson et al. (1955). Phenotypic and genotypic correlations were calculated to determine interrelationships among traits, and path coefficient analysis was carried out as per Dewey and Lu (1959) to partition direct and indirect effects on grain yield. Genetic divergence among genotypes was estimated using Mahalanobis' D^2 statistics (Mahalanobis 1936; Rao 1952) to classify genotypes and assess trait contribution toward diversity.

3. RESULTS

3.1 Genetic Divergence Analysis

Evaluation of 81 coloured pericarp sorghum genotypes for thirteen morphological and seven shoot fly tolerance traits revealed highly significant differences among genotypes, indicating wide genetic variability. The multivariate Wilk's λ test was significant for both yield-related traits (x^2 = 2542.589, df = 560) and shoot fly tolerance traits (x^2 = 3990.510, df = 1040), justifying further computation of genetic divergence statistics.
Genetic divergence among genotypes was quantified using Mahalanobis D^2 statistics as proposed by Rao (1952). Since the original variables were correlated, pivotal condensation was applied to generate uncorrelated components, enabling accurate calculation of pairwise D^2 distances. The distribution of genotypes based on aggregated distance matrices showed substantial diversity, confirming suitability for selection and hybridization breeding.

3.2 Cluster Formation Based on Morphological Traits

Tocher's method grouped the 81 genotypes into eight distinct clusters (Table 1), with Cluster I having the largest number of entries (30 genotypes), followed by Clusters II (15) and III (12). The presence of single-genotype clusters (VI, VII, VIII) indicates genetically isolated types possibly developed through restricted gene flow, selection pressure, or unique adaptation complexes. According to Rao (1952) and supported by Murthy & Arunachalam (1966), crosses among genotypes from widely separated clusters are more likely to generate desirable heterosis and broader variability.

These results also reveal that genotypes from similar geographic origin did not always fall within the same cluster, proving that genetic divergence is not strictly associated with geographic diversity. Similar observations have been reported by Singh et al. (2001), Umakanth et al. (2002), and Jhansi Rani et al. (2012).

Table 3.1. Cluster composition based on grain yield and related traits

Cluster No.	No. of Strains	Genotypes included in the cluster
I	30	RIL40395-2, RIL32919-2, ISSVT108, RIL40853-1, ISSVT346, GP564, IS-23891, RIL40261-2, RIL41056-1, GP2843, GP2028, GP2375, ISSVT104, GD-, ICRISAT409, GP1539, ISSVT109, ISSVT714, RIL40261-2, GP716, B-35, YPT-1007, ISSVT324, RIL40158-2, GP3104, ISSVT223, GP40053-1-2, GP595, YPT-1030, GP 2017-5 (Red-7, White-3, Yellow-6, Pearly-14)
II	15	ISSVT 325,627(ICSB), YPT1021, ISSVT108, GP576, ISSVT306, GP93, DJ6514, IC-9108, GP2016-1, GP75, Parbhani Moti, GD-62417, ISSVT102, GP520 (Red-11, White-1, Yellow-2, Pearly-1)

III	12	ICSR-93036, ICSR-93026, GP211, RIL40679-1-2, GP587, RIL40141-1, GP920, ICRISAT109, RIL40369-1, ISSVT710, ISSVT 712, GP 374 (Red-9, Yellow-2, Pearly- 1)
IV	14	GP44, Udgir local, RIL40679-1-1, GP3138, IS-15466, YPT-1412, IS11189, RIL40818-3-1, CSV22R, GP55690, RIL32919-1, RIL 40276-1-1, IS18551, IS-23143 (White-8, Yellow-2, Pearly- 4)
V	7	Bajra type, RIL 40679-1-, RIL 32919-2, BT×623, YPT-1014, RIL40274-2, YPT-1015 (Yellow-7, Pearly-6)
VI	1	GP1673(Red)
VII	1	RII40679-3-1 (Red)
VIII	1	GP53 (Red)

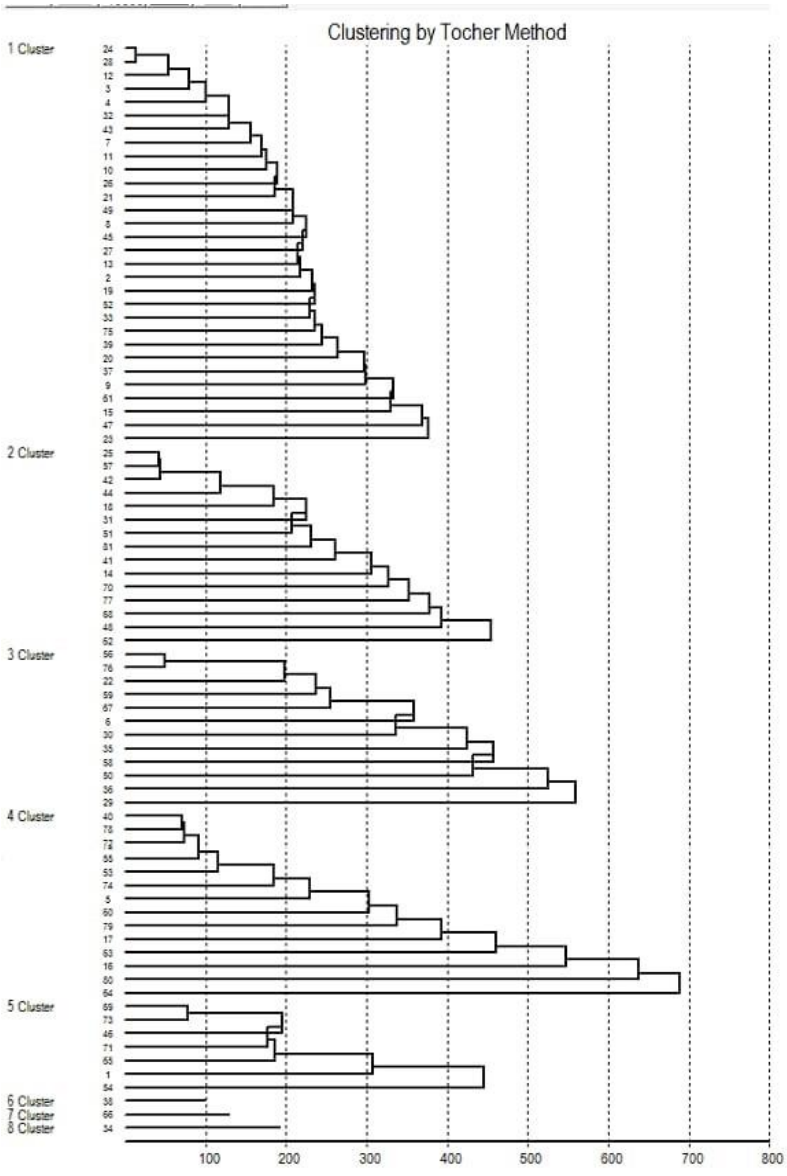

Fig.1 Clustering of genotypes by Tocher's method for grain yield & it's attributing traits in coloured pericarp sorghum

3.3 Cluster Formation Based on Shoot Fly Tolerance Traits

Clustering based on seven traits associated with shoot fly resistance grouped the 81 genotypes into six clusters, of which Cluster III contained the maximum number of genotypes (36), followed by Cluster II (16) and Cluster IV (10) (Table 2). Genotypes in Clusters II and III exhibited desirable resistance features such as higher trichome density, greater leaf glossiness and lower shoot fly dead hearts, making them superior candidates for developing tolerant high-yielding lines. High trichome density and seedling glossiness have been recognized as reliable resistance mechanisms due to physical restriction imposed on larvae (Mote, 1986), and as consistent visual selection criteria (Agarwal & House, 1982; Maiti & Gibson, 1983).

Table 3.2 Cluster composition based on shoot fly tolerance traits

Cluster No.	No. of Strains	Genotypes included in the cluster
I	9	ISSVT223, GP75, ISSVT306, DJ6514, ISSVT324, GP2843, ICSR-93026, GP 576, GP 716 (Red-5, White-2, Pearly- 9)
II	16	GP2028, YPT-1412, GP564, GP3104, RIL40679-1-2, GP595, YPT-1021, IS-23143, GP53, GP920, YPT1014, GP1539, IS-23891, B-35, IC-9108, IS-15466 (Red-5, White-2, Yellow-1, Pearly-8)
III	36	ISSVT 714, GD-, YPT-1030, RIL 40261-2, RIL 40158-2, 627(ICSB), ICSR-93036, RIL41056-1, GP211, RIL32919-1, GP 374, RIL40395-2, ISSVT346, YPT-1030, RIL40853-1, RII 40679-3-1, RIL40818-3-1, ISSVT108, GP587, RIL40274-2, BT×623, GD-62417, YPT-1007, RIL 40274-2, GP 2375, ICRISAT109, Parbhani Moti, ISSVT712, GP93, GP3138, RIL40369-1, Udgir local, ISSVT-710, GP40053-1-2, ICRISAT409, RIL40679- 1-1 (Red-13, White-3, Yellow-8, Pearly-12)
IV	10	RIL40141-1, GP2016-1, ISSVT 109, GP55690, RIL40261-2, YPT-1015, RIL40276-1-1, RIL32919-2, Bajra type, GP 1673 (Red-4, White-1, Yellow-2, Pearly-3)
V	4	GP2017-5, IS18551, ISSVT108, ISSVT325 (Red-1, White-1, Yellow-2)
VI	6	RIL32919-2, GP520, IS11189, CSV22R, GP44, ISSVT104 (Red-1, White-3, Pearly- 2)

3.4 Intra- and inter-cluster distances

In grain-yield related traits, intra-cluster distances ranged from 0.00 (Clusters VI–VIII) to 21.91 (Cluster IV), indicating moderate to low within-cluster diversity. Inter-cluster distances ranged from 15.08 to 57.91, with the greatest separation recorded between Cluster V and VII, followed by Cluster V and VIII (Table 3). According to standard genetic principles, such wide divergence suggests that hybridization among these clusters may result in maximum heterotic expression (Swamy et al., 2018).

Table 3.3 Average intra- and inter-cluster D^2 values for grain yield traits

Clusters	I	II	III	IV	V	VI	VII	VIII
I	15.47	25.58	23.16	24.08	37.25	24.39	25.67	22.9
II		18.69	29.57	39.14	31.27	34.22	41.81	40.27
III			21.91	33.54	43.41	25	27.31	25.34

IV				21.71	36.67	36.06	36.04	29.94
V					18.6	52.49	57.91	52.55
VI						0	15.91	19.04
VII							0	15.08
VIII								0

For shoot fly resistance traits, intra-cluster distances ranged from 8.77 (Cluster V) to 22.98 (Cluster VI), while the widest inter-cluster divergence was observed between Cluster V and II (D = 80.81), followed by Cluster II and I (D = 66.29) (Table 4). Similar divergence patterns in shoot fly resistance have been previously reported by Dhillon et al. (2006).

Table 3.4 Average intra- and inter-cluster D^2 values for shoot fly tolerance traits

Clusters	I	II	III	IV	V	VI
I	11.19	66.29	31.13	32.34	23.22	49.21
II		11.26	43.01	65.17	80.81	26.12
III			15.06	27.97	40.66	31.92
IV				11.37	26.88	53.22
V					8.77	64.74
VI						22.98

3.5 Cluster Means and Trait Performance

Cluster means were computed to identify potential donor genotypes for individual traits. For yield-related traits, Cluster III recorded the highest grain yield (34.03 g/plant) along with high fodder yield and plant height. Early flowering was recorded in Cluster VII, while 100-seed weight was highest in Cluster IV (Table 5). Such information is valuable for targeted donor selection in line improvement breeding programs.

Table 3.5 Mean performance of clusters for grain yield and related traits

	Char. 1	Char. 2	Char. 3	Char. 4	Char. 5	Char. 6	Char. 7	Char. 8	Char. 9	Char. 10	Char. 11	Char. 12	Char. 13
Group. 1	74.80	176.12	58.26	5.70	27.17	5.62	121.60	3.25	2.68	4.34	83.31	27.21	2.44
Group. 2	74.80	173.95	48.70	7.00	27.21	5.15	119.73	4.50	5.30	3.96	81.58	24.42	2.28
Group. 3	77.42	200.53	62.04	6.00	29.89	6.19	124.75	4.63	2.88	4.02	85.97	34.03	2.63
Group. 4	76.68	189.10	58.35	5.88	27.54	5.23	121.71	1.43	1.93	4.65	83.29	27.07	2.56
Group. 5	74.57	174.09	58.33	5.06	27.26	6.11	123.57	1.71	5.86	4.33	83.68	28.24	2.39
Group. 6	72.50	168.50	41.67	9.00	25.50	5.50	118.00	5.00	2.00	3.96	77.75	17.41	2.50
Group. 7	71.00	171.00	61.49	5.00	25.00	4.66	131.00	5.00	1.00	4.51	81.13	21.83	2.35
Group. 8	77.00	185.00	70.66	9.00	26.33	6.33	118.00	4.00	1.00	3.98	85.75	32.23	2.60

(Char.1- days to 50 percent flowering, Char.2- plant height, Char.3- number of primaries per panicle, Char.4- panicle type, Char.5- panicle length, Char.6- panicle width, Char.7- days to physiological maturity, Char.8- grain color, Char.9- glume color, Char.10- 100-seed weight, Cahr.11-threshability, Char.12-grainyieldperplant, Char 13-fodderyield per plant)

For shoot fly tolerance, Cluster III and IV outperformed others for major resistance traits including lower dead heart percentage, higher glossiness and greater trichome density, confirming their breeding value as resistance donors. (Table 3.6)

3.6 Trait Contribution to Genetic Divergence

Trait contribution analysis revealed that among yield-related traits, glume colour (39.10%) and grain colour (32.75%) contributed maximum to divergence, followed by plant height and number of primaries per panicle. Similar patterns of dominant contribution of grain and glume characteristics were also reported by Swamy et al. (2018).

In shoot fly tolerance traits, adaxial trichome density contributed the largest share (69.23%), followed by abaxial trichomes (24.69%), confirming the role of leaf surface characteristics as major determinants of resistance. These results align with earlier observations by Omori (1988).

4. CONCLUSION

The diversity analysis clearly demonstrated substantial genetic variability among sorghum genotypes for both morphological and shoots fly tolerance traits. Genotypes drawn from widely separated clusters—specifically Clusters V, VII, III, and II—offer the best potential for hybridization to generate high-yielding and shoot fly tolerant segregants. The study further highlighted the importance of phenotypic traits such as trichome density, glossiness, and grain characteristics as major contributors to genetic divergence, making them valuable criteria for selection in coloured pericarp sorghum improvement programs.

Table 3.6. Mean cluster performance for shoot fly tolerance traits

Group/ Character	Char.1	Char.2	Char. 3	Char. 4	Char. 5	Char.6	Char.7
Group 1	2.67	2.94	34.53	9.00	72.53	100.61	172.50
Group 2	2.33	2.72	42.03	10.26	73.75	16.59	0.75
Group 3	2.83	2.75	44.26	9.51	73.56	145.46	55.32
Group 4	2.55	3.00	42.26	10.85	74.25	225.75	22.85
Group 5	2.13	1.50	37.08	9.25	75.56	255.75	135.25
Group 6	2.26	2.83	42.39	9.76	73.76	69.08	70.00

(Char.1- seedling vigor, Char.2- seedling glossiness, Char.3- shoot fly dead hearts percent @ 28 DAS, Char.4- shoot fly eggs @ 21 DAS, Char.5-trichomes (Adaxial at 10X magnification) Char.6 (Abaxial at 10X magnification) Char.7-leafangle)

Table 3.7 Percent contribution of different grain yield and it's attributing characters to genetic diversity in coloured pericarp sorghum

Sr. No.	Source	Times Ranked 1st	Contribution%
1	Days to 50% flowering	2	0.06%
2	Plant height(cm)	367	11.33%
3	Number of primaries per panicle	355	10.96%
4	Panicle type (1-9score)	151	4.66%
5	Panicle length (cm)	0	0.00%
6	Panicle width (cm)	5	0.15%
7	Days to physiological maturity	0	0.00%
8	Grain color (1-5 score)	1061	32.75%
9	Glume color (1-6 score)	1267	39.10%
10	100-seed weight (g)	1	0.03%
11	Threshability (%)	0	0.00%
12	Grain yield per plant(g)	29	0.90%
13	Fodder yield per plant(g)	2	0.06%

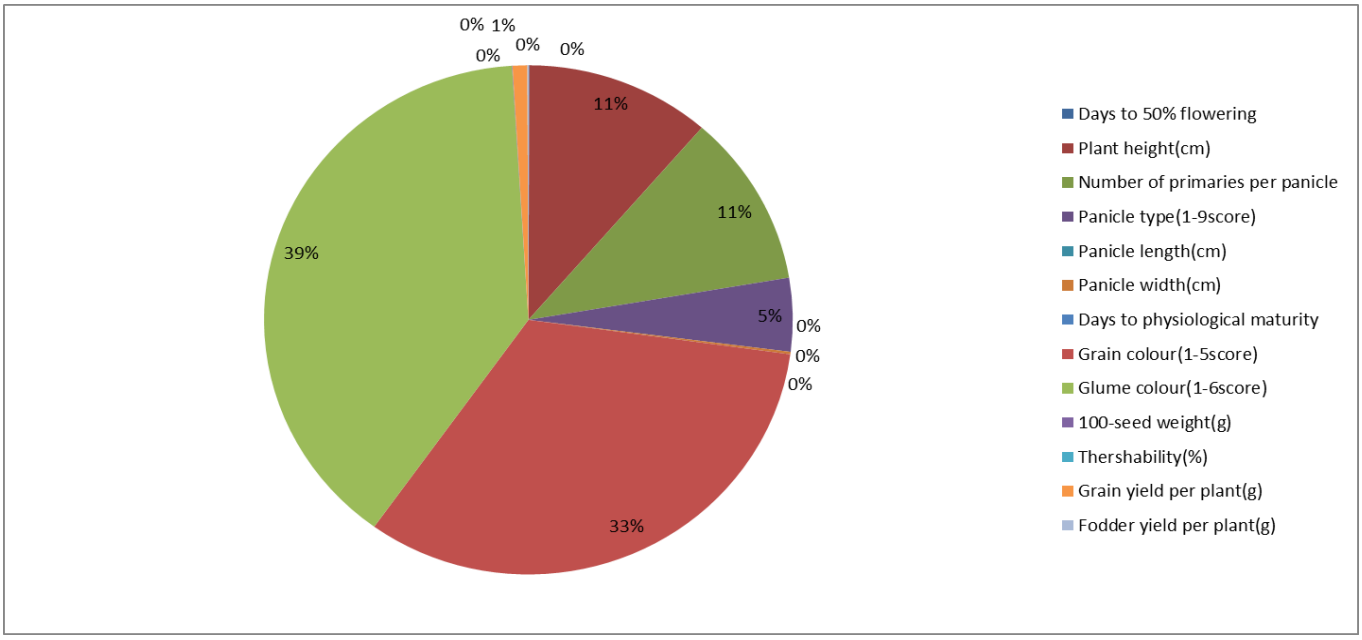

Fig.3 Percent contribution of grain yield & it's attributing characters to genetic diversity in coloured pericarp sorghum

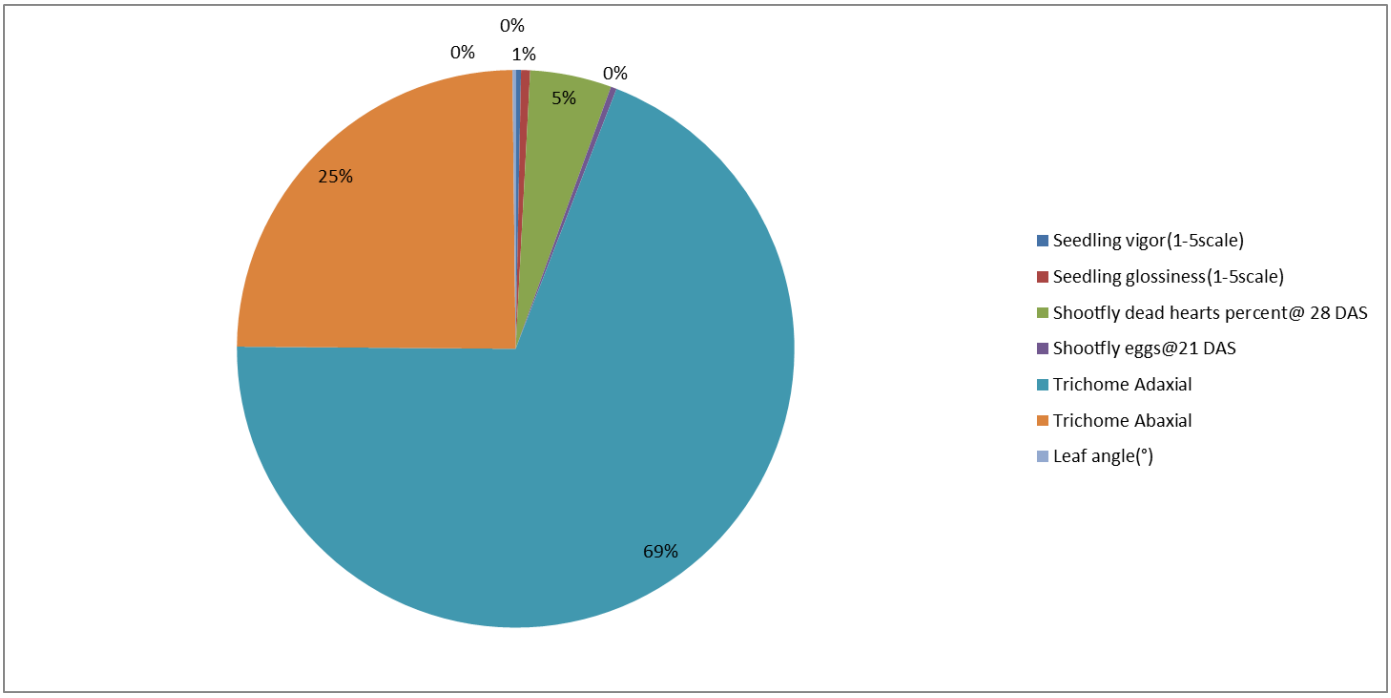

Fig.4 Percent contribution of different traits related to shoofly tolerance to genetic diversity in coloured pericarp sorghum

Table 3.8 Percent contribution of traits related to shoot fly tolerance in coloured pericarp sorghum

Sr. No.	Source	Times Ranked 1st	Contribution%
1	Seedling vigor (1-5scale)	10	0.31%
2	Seedling glossiness (1-5scale)	17	0.52%

3	Shoofly dead hearts percent@ 28 DAS	153	4.72%
4	Shoofly eggs@21 DAS	11	0.34%
5	Trichome (adaxial at 10X magnification)	2243	69.23%
6	Trichome (abaxial at 10X magnification)	800	24.69%
7	Leaf angle (°)	6	0.19%

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