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## Genetic divergence studies for shoot fly tolerance in post rainy sorghum (*Sorghum bicolor* (L.) Moench)

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**Abstract**

**Aims:** The present study was carried out on a diverse array of sorghum genotypes to assess the genetic diversity in 116 sorghum accessions for shoot fly tolerance traits and grain yield. The germplasm lines along with four checks (One resistant check IS-18851, one susceptible check DJ-6514 and two varietal checks SPV-1411 and PVK-801) were planted in randomized block design with two replications during *rabi* 2015-16 at Sorghum Research Station, Vasanttrao Naik Marathwada Krishi Vidyapeeth, Parbhani. Observations were recorded on five randomly selected plants in each plot and replication for grain yield, yield contributing traits and following shoot fly tolerant associated traits from each replication. 120 genotypes including 4 checks were grouped into sixteen clusters with variable number of entries revealing the presence of considerable amount of genetic diversity in the material. Among the sixteen clusters, Cluster III was the largest involving 40 genotypes. Out of the 18 characters studied, trichome density (adaxial and abaxial) contributed maximum (43.42%) and (39.06%) towards genetic diversity, respectively. The relative contributions of different traits towards genetic divergence was plant height (8.03%), leaf angle (2.98%), chlorophyll content (1.50%), days to 50% flowering (1.29%), leaf length (0.90%) and grain yield per plant (0.64%). Cluster II, VI, IX and X exhibiting shoot fly tolerant sources as high mean for shoot fly resistant parameters has good scope for future breeding programme. Genotypes IS 17757, IS 33770, IS 33746, PVR 658 and IS 40269 with less dead heart per cent and shoot fly resistant parameters may be used as promising sources for breeding shoot fly resistant genotypes.

**Keywords:** Sorghum, genetic diversity, shoot fly, trichome density, D<sup>2</sup> statistics

**Introduction**

Sorghum plays an important role in Indian economy, but there are many factors affecting its productivity and insect pest is the most important one. About 150 insect species have been recorded in sorghum out of which 31 species are economically important. In India, 20 insect species have been recorded to infest sorghum. Among these, shoot fly (*Atherigona soccata* Rond.) assumed the most important pest. Status in the states in general and *rabi* in particular indicates that, the losses due to this pest have been estimated to reach as high as 86 per cent of grain and 46 per cent of fodder yield <sup>[1]</sup>. Shoot fly incidence is high in late sown *kharif* (rainy season), early sown *rabi* season (post rainy season) sorghum crops. The level of infestation even may go up to 99-100%.

Adoption of chemical methods for insect control in staple food crops is not economically feasible for resource poor farmers of the semi-arid tropics (SAT). Therefore host plant resistance combined with timely sowing is the most realistic approach to minimize grain and store yield losses due to insect pests such as sorghum shoot fly. Genetic variability for shoot fly resistance in plant exists in sorghum germplasm. Many of the germplasm sources for resistance to this pest have poor agronomic features and grain yield potential and sources with high levels of resistance are not available in the cultivated species. Germplasm accessions with absolute resistance have been found in wild relatives of sorghum (*Sorghum purpursericeum*, *S. nitidum*, *S. versicolor* and *S. australiense*) <sup>[2, 3]</sup>; however their utilization in sorghum breeding programs is hindered by crossing barriers. Therefore, the present study was carried out on a diverse array of sorghum genotypes to assess the genetic diversity in sorghum accessions for shoot fly tolerance traits and grain yield.

**Materials and Methods**

The experimental material consisted of 116 genotypes and four checks, one resistant check

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(IS-18551), one susceptible check (DJ-6514) and two varietal checks (SPV-1411 and PVK-801) of sorghum collected from Directorate of Sorghum Research, Hyderabad and Sorghum Research Station, VNMKV, Parbhani, which were utilized to elucidate information on genetic divergence for eighteen qualitative and quantitative characters including seed yield.

The germplasm lines were planted in randomized block design with two replications. The observations were recorded on five randomly selected plants for grain yield and shoot fly characters from each replication. The genetic divergence was estimated by D2 statistics for 18 quantitative characters [4]. Grouping of the genotypes into cluster was done by using tocher's method [5]. The average intra and inter cluster D2 was calculated by the formula  $\Sigma D2i/n$ . With the help of D2 value between and within clusters, cluster diagram showing the relationship between different populations was drawn.

## Results and Discussion

Analysis of variance showed significant differences among the genotypes for all the 18 characters studied. Based on D<sup>2</sup> statistics and Tocher's method, 120 genotypes including 4 checks were grouped into sixteen clusters with variable number of entries revealing the presence of considerable amount of genetic diversity in the material. Among the sixteen clusters, Cluster III was the largest involving 40 genotypes. The next largest cluster was cluster IV consisting 28 genotypes which had shoot fly tolerant genotypes IS-33874, IS-30974, Pop and Sorg. 51. Cluster II consist of 17 genotypes with some resistant germplasm lines; Pop. Sorg. 15, IS-4496, IS-5375 and resistant check IS-18551. Clusters I and V having 15 and 9 genotypes, respectively. The cluster VI, VII, VIII, IX, X, XI, XII, XIII, XIV, XV and XVI had one genotype each. Cluster VIII included the varietal check SPV-1411 and the cluster XVI included the susceptible check DJ-6514 (Table 1). Based on the deadheart incidence, morphological, nutritional and biochemical traits of the sorghum genotypes, principle component analysis placed the test genotypes into three clusters. The genotypes showing susceptible reaction to shoot fly were placed in cluster C (Swarna, CK 60B, ICSV 745, 296B, and ICSV 112), while those with moderate levels of resistance to shoot fly were placed in clusters A and those with high and/or stable resistance to shoot fly were placed in cluster B [6]. Sorghum genotypes were also clustered in different groups based on genetic divergence studies by using Mahalanobis D2 statistic earlier for grain yield and its contributing traits [7, 8] for shoot fly tolerant traits [9, 10].

Results from table 2 revealed that average intra and inter cluster distances for sixteen clusters of sorghum Germplasm. The pattern of distribution of genotypes into various clusters was ranged from 0.00 to 19.62 for intra cluster. Maximum difference among the genotypes within the same cluster (intra cluster) was shown by Cluster IV (19.62) followed by cluster

V (17.08), cluster III (16.20), cluster II (15.31) and cluster I (14.23) and remaining two clusters have their zero intra cluster distance. The results were in accordance with the research findings of [11].

Diversity among the clusters varied with inter cluster values of 12.88 to 66.25. The average inter cluster distance was showed maximum between clusters XVI and VII (66.25), followed by clusters III and VII (63.37), clusters XIII and V (60.80), clusters VI and XVI (60.09), clusters III and VI (57.20), cluster III and IX (54.09) followed by cluster V and XII (51.95) and cluster II and XVI (51.81). Genotypes for hybridization should be selected from the more distant clusters as chances are more to obtain heterotic combinations as compared to combinations involving genotypes from the same cluster. Crosses between accessions of these different clusters could give heterotic responses and better segregants after hybridization [8, 12].

In the present study, it was observed that out of the 18 characters studied, trichome density (adaxial and abaxial) contributed maximum (43.42%) and (39.06%) towards genetic diversity, respectively (Table 3). The relative contributions of different traits towards genetic divergence was plant height (8.03%), Leaf angle (2.98%), Chlorophyll content (1.50%), Days to 50% flowering (1.29%), Leaf length (0.90%), Grain yield per plant (0.64%), Plumule and leaf sheath pigmentation (0.56%), Leaf breadth (0.42%), Dead heart % at 28 DAE (0.38), 100 seed weight (0.32), Leaf glossiness (0.24%), Days to maturity (0.17%), Seedling vigour (0.06%) and dead heart % at 14 DAE (00.01%). However, the traits like leaf wetness and number of tillers had not contributed towards diversity. Days to maturity, number of tiller/plant and 1000 grain weight showed maximum contribution towards the total divergence [13]. Traits contributing maximum towards the D2 value need to be given more emphasis for deciding the cluster to be taken for further selection and choice of parents for hybridization programme [7, 14].

The Cluster means of 18 characters showed an interesting picture of nature of genetic diversity. Cluster VI recorded high mean performance for six characters viz., plant height, leaf length, no. of tillers, chlorophyll content, days to 50% flowering and days to maturity. While the clusters II has recorded low mean performance for maximum characters like dead heart % at 14 DAE, dead heart % at 28 DAE, leaf glossiness (non-glossy), seedling vigour (non-vigorous), leaf wetness, chlorophyll content, plant height, days to 50% flowering, days to maturity, yield per plant. This indicates that genotypes in cluster II exhibited desirable shoot fly tolerance parameter and may be used in future breeding programme. Based upon hierarchical clustering considering parameters viz., shoot fly oviposition shoot fly deadhearts and stem borer induced deadhearts, the entries were classified in to resistant, moderately resistant and susceptible [9].

**Table 1:** Grouping constellation of sorghum germplasm based on divergence analysis

Cluster No.	No. of breeding lines included	Breeding lines
I	15	IS 17665, Pop. S. 151, Pop. S. 145, IS 4739, IS 4482, Pop. Srg. 141, IS 2272, IS 5221, IS 36077, Pop. Sorg. 115, IS 13721, IS 4479, IS 2122, IS 40838, PVR 660.
II	17	Pop. Sorg. 15, IS 4496, IS 5375, IS 33824, Kagimote Jola, SPV 1641, Pop. Sorg. 43, Pop. Sg. 187, IS 5148, IS 40283, IS 35733, 204 B, Tandur-2, SPV 1709, PVR 658, IS 5873, IS-18851.
III	40	IS 5047, Pbn Ent. 1, IS 36079, IS 26998, Balagnur, IS 18353, IS 5595, IS 5136, SPV 570, IS 18378, Pop. Sorg. 35, IS 25450, IS 25260, IS 4803, PVK-801, IS 26752, Bidar Local, IS 5089, IS 31164, PVR 617, IS 23611, IS 5132, IS 25540, IS 25028, IS 31175, IS 2187, IS 27238, Pop.Sorg.15, IS 31202, IS 26620, IS 17788, IS 26307, Pbn Ent.4, Pbn Ent.3, IS 25481, IS 17771, Pbn Ent. 2, IS 26838, IS 26402, IS 31420.

IV	28	IS 33874, IS 30974, Pop. Sorg. 51, IS 40290, Pop. Sorg. 164, IS 2511, IS 33815, IS 40675, DVR 637, IS 40793, IS 4577, PVR 623, IS 24878, Solapur Dagde, PVR 638, Pop. Sorg 138, IS 18053, IS 33743, IS 40704, Pop. Sorg. 19, MH Jola, IS 40199, Chittapur Local, IS 4883, IS 40915, IS 33890, IS 3962, ICSD 37 B.
V	9	IS 8315, EP 55, IS 4132, IS 17948, IS 5423, Pop. Sorg. 1, Pbn Ent.5, IS 4763, IS 4882.
VI	1	IS 17757
VII	1	PVP 657
VIII	1	SPV-1411
IX	1	IS 33770
X	1	IS 33746
XI	1	IS 25473
XII	1	Surgaon L.
XIII	1	Pop. sorg. 118
XIV	1	IS 17666
XV	1	IS 40269
XVI	1	DJ-6514

**Table 2:** Average intra and inter clusters distances for sixteen clusters of sorghum germplasm

	Gr. 1	Gr. 2	Gr. 3	Gr. 4	Gr. 5	Gr. 6	Gr. 7	Gr. 8	Gr. 9	Gr. 10	Gr. 11	Gr. 12	Gr. 13	Gr. 14	Gr. 15	Gr. 16
Group. 1	14.23	40.88	25.09	24.17	24.63	46.73	51.75	35.87	38.87	33.64	35.64	38.55	47.4	30.19	35.32	25.2
Group. 2	40.88	15.31	52.63	27.41	44.41	19.9	21.66	19.27	21.04	26.11	19.24	29.23	34.86	42.85	36.6	51.81
Group. 3	25.09	52.63	16.2	36.49	40.72	57.2	63.37	43.26	54.09	37.74	49.27	39.8	45.89	24	32.52	22.79
Group. 4	24.17	27.41	36.49	19.62	29.83	33.8	38.35	24.88	26.66	25.91	23.4	31.2	39.36	33.31	32.36	35.07
Group. 5	24.63	44.41	40.72	29.83	17.08	50.43	54.98	45.39	37.6	45.5	35.58	51.95	60.8	48.12	50.26	34.61
Group. 6	46.73	19.9	57.2	33.8	50.43	0	12.88	25.95	32.32	34.29	25.82	32.68	36.86	46.61	39.69	60.09
Group. 7	51.75	21.66	63.37	38.35	54.98	12.88	0	27.83	32.4	37.38	29.52	36.29	40.78	51.84	45.58	66.25
Group. 8	35.87	19.27	43.26	24.88	45.39	25.95	27.83	0	25.97	13.47	24.46	17.12	22.76	30.75	25.43	44.6
Group. 9	38.87	21.04	54.09	26.66	37.6	32.32	32.4	25.97	0	30.12	18.91	38.81	44.55	48.46	43.64	49.06
Group. 10	33.64	26.11	37.74	25.91	45.5	34.29	37.38	13.47	30.12	0	27.99	13.7	19.83	25.58	19.14	37.78
Group. 11	35.64	19.24	49.27	23.4	35.58	25.82	29.52	24.46	18.91	27.99	0	33.22	41.26	44.86	38.37	45.41
Group. 12	38.55	29.23	39.8	31.2	51.95	32.68	36.29	17.12	38.81	13.7	33.22	0	13.98	23.8	15.43	43.93
Group. 13	47.4	34.86	45.89	39.36	60.8	36.86	40.78	22.76	44.55	19.83	41.26	13.98	0	28.17	19.95	50.03
Group. 14	30.19	42.85	24	33.31	48.12	46.61	51.84	30.75	48.46	25.58	44.86	23.8	28.17	0	17.89	33.21
Group. 15	35.32	36.6	32.52	32.36	50.26	39.69	45.58	25.43	43.64	19.14	38.37	15.43	19.95	17.89	0	37.61
Group. 16	25.2	51.81	22.79	35.07	34.61	60.09	66.25	44.6	49.06	37.78	45.41	43.93	50.03	33.21	37.61	0

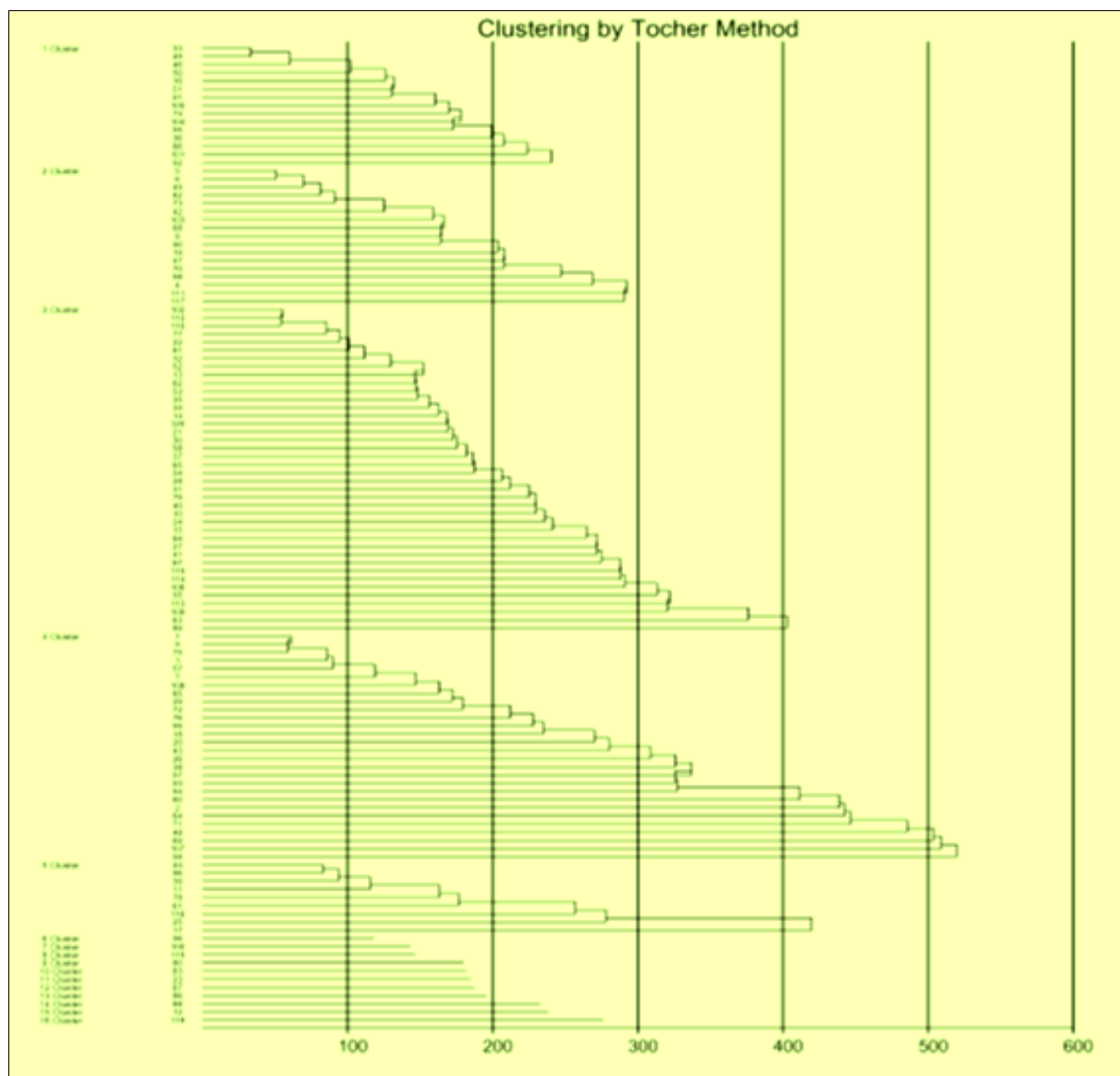
**Table 3:** Contribution of characters towards genetic divergence

Source	Times ranked 1st	Contribution %
Deadheart 14 DAE	1	0.01%
Deadheart 28 DAE	27	0.38%
Trichome density US	2789	39.06%
Trichome density LS	3100	43.42%
Leaf Glossiness	17	0.24%
Seedling Vigor	4	0.06%
Leaf Wetness	0	0.00%
Plumule Leaf pigmnt.	40	0.56%
Plant Height	573	8.03%
Leaf length	64	0.90%
Leaf breadth	30	0.42%
No of Tillers	0	0.00%
Leaf angle	213	2.98%
Chlorophyll content	107	1.50%
Days to 50% flowering	92	1.29%
Days to maturity	12	0.17%
Seed Weight 100	23	0.32%
Grain yield plant	46	0.64%

**Table 4:** Cluster means for sixteen clusters of *Sorghum germplasm*

	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	Char. 14	Char. 15	Char. 16	Char. 17	Char. 18	Char. 19	Char. 20
Group. 1	37.73	34.80	24.27	42.78	136.07	16.60	2.90	2.88	2.92	1.93	138.83	54.90	5.61	1.19	56.60	42.06	74.73	124.27	2.33	22.33
Group. 2	35.50	31.82	13.99	24.28	207.79	156.68	2.29	2.72	2.79	1.79	135.12	56.10	5.49	1.34	55.03	41.24	77.38	122.32	2.44	19.37
Group. 3	36.06	32.50	27.47	51.28	16.20	1.96	3.49	3.58	3.51	1.94	126.84	54.06	5.42	1.46	56.93	47.73	76.84	124.06	2.39	19.49
Group. 4	36.48	33.09	19.69	32.61	174.18	78.64	2.79	2.95	3.12	1.88	128.48	54.98	5.54	1.49	56.91	45.31	77.21	122.82	2.61	22.31
Group. 5	36.83	32.89	27.60	48.23	242.61	9.94	3.47	3.50	3.44	2.56	133.56	52.52	5.20	1.13	52.00	49.58	78.44	122.67	2.46	18.45
Group. 6	37.50	33.50	16.05	23.75	188.00	182.50	2.50	2.25	3.00	1.25	189.50	59.65	6.40	1.70	39.00	53.10	94.50	132.00	2.50	10.75

Group. 7	36.00	32.50	15.25	22.70	213.50	194.00	1.75	3.00	3.00	2.50	198.00	62.10	7.80	1.00	50.50	41.30	81.50	127.00	2.75	24.00
Group. 8	38.50	34.50	21.35	38.60	137.00	139.00	2.75	2.25	2.25	1.50	122.50	58.60	6.70	0.90	71.00	39.20	76.50	121.50	3.20	32.85
Group. 9	35.00	32.00	10.20	17.90	277.50	121.00	2.50	3.00	2.75	2.75	101.50	54.40	4.40	1.00	78.00	32.55	83.00	126.00	2.35	34.50
Group. 10	35.50	32.50	13.85	33.15	92.00	117.00	3.00	3.25	2.75	3.00	101.50	49.15	5.05	1.00	64.00	37.15	78.00	127.00	1.85	49.80
Group. 11	29.00	26.50	19.15	23.95	228.50	120.50	2.50	2.75	2.25	2.50	106.50	54.40	7.15	1.80	42.50	55.20	88.00	138.00	1.85	22.75
Group. 12	37.50	35.00	17.95	26.35	42.50	136.00	2.25	2.50	3.00	3.00	125.50	48.55	6.25	1.10	49.00	40.15	74.00	124.00	3.00	32.20
Group. 13	37.50	35.00	14.55	26.05	10.00	164.00	2.50	3.00	3.00	2.75	119.50	46.70	5.00	1.00	68.50	43.30	84.50	125.50	2.65	25.75
Group. 14	38.00	36.50	14.70	27.30	0.00	64.50	2.00	2.25	3.00	1.00	140.00	46.90	5.35	1.80	64.00	39.90	66.50	110.50	2.35	20.55
Group. 15	32.50	28.00	16.40	22.40	15.00	98.50	2.25	2.25	2.75	3.00	121.50	50.00	5.00	1.65	46.50	36.95	90.00	118.00	2.20	21.95
Group. 16	35.00	30.50	36.35	65.50	80.00	0.00	4.00	3.50	3.50	3.00	67.50	38.95	4.25	1.70	61.50	47.40	75.00	118.50	1.55	10.80



**Fig 1:** Clustering pattern of 110 sorghum germplasm lines drawn according to Tocher method

## Conclusion

Cluster II, VI, IX and X exhibiting shootfly tolerant sources as high mean for shootfly resistant parameters may be utilized in future breeding programme. Genotypes IS 17757, IS 33770, IS 33746, PVR 658 and IS 40269 with less dead heart per cent and shoot fly resistant parameters may be used as promising sources for breeding shoot fly resistant genotypes.

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