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GENETIC VARIABILITY AND DIVERGENCE STUDIES FOR PRODUCTIVITY TRAITS IN RABI SORGHUM (*SORGHUM BICOLOR* L. MOENCH)

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ABSTRACT

Fourty nine sorghum genotypes were evaluated for different quantitative traits to assess the genetic variability and diversity during *Summer* 2024 for yield and its associating traits. Analysis of variance revealed significant differences among genotypes for most of the traits studied indicating substantial genetic variability. Less difference between the estimates of GCV and PCV implying the minimal influence of environmental agencies and importantly, improvement through selection seems feasible. High phenotypic coefficient of variance, genetic coefficient of variance, heritability and GAM were recorded for almost all of the traits except hundred seed weight, where moderate GCV was observed. High heritability and genetic advance were recorded for traits such as seed yield per plant, panicle width, and number of leaves per plant, suggesting the predominance of additive gene action. Cluster analysis revealed five genetically diverse groups, and maximum divergence was observed between Clusters II and V. Promising genotypes identified from this study can serve as potential parents in future hybridization programs to enhance yield and adaptability. This indicates the scope for improvement of these characters through selection.

Keywords**:** *Rabi* sorghum, productivity traits, genetic variability, diversity.

Introduction

Sorghum is an important staple food for more than 300 million people and feed for cattle living in Asia and Africa. Sorghum is being cultivated in both the *kharif* and *Rabi* seasons. *Rabi* sorghum is highly valued because of its excellent grain and fodder quality. The most important factor affecting the utilization of *rabi* sorghum is its low productivity, this is mainly because of the varieties developed and released did not become popular because of yield advantage was not substantial over M 35-1 and the hybrids released were susceptible to shoot fly and hence leads to poor grain quality.

Progress in plant breeding depends on the extent of genetic variability and diversity present in a population. Therefore, the first step in any plant breeding program is to assess the magnitude of genetic variability and diversity present in the population. The genetic facts are inferred from phenotypic observations, which are the results of interactions of genotype and the environment. The variability available in breeding material is the prime requirement for the improvement and selection of elite genotypes. However, the quantitative characters are influenced by environment and necessitate the partitioning of overall variances as heritable and non-heritable components. The present investigation was carried out with the objective to estimate the extent of variability, heritability, genetic advance and diversity (D^2) analysis.

Materials and Methods

The present investigation was carried out during *summer* season 2024 at University of Agricultural Sciences, Dharwad (Karnataka, India). The design adopted was Randomized Block Design with two replications, with a spacing of 60 × 15 cm. Recommended package of practices were followed, and the crop growth was satisfactory. Three competitive plants were selected randomly from each row in each replication for recording the observations on various yield and component characters except for the characters days to 50 per cent flowering and days to physiological maturity which were recorded on plot basis.

The data was subjected to statistical analysis using R Studio software to estimate mean, range, ANOVA, variability parameters and diversity.

Results and Discussion

The mean sum of squares of different characters pertaining to yield and yield components were highly significant for all the 10 characters studied indicating the presence of sufficient amount of variability of these characters which provides ample scope for selection of superior and desirable genotypes for plant breeder for further genetic improvement (Table 1).

Mean performance of sorghum genotypes

The performance of the fourty nine sorghum genotypes was recorded for 10 quantitative traits (Table 3). For the most of the studied, all genotypes exhibited significant variation. Among grain and its component characters, the mean performance for days to fifty per cent flowering range from lowest 43.50 in genotype IS 29733 to highest146.50 in genotype IS 5301, whereas mean range for days to maturity range from minimum 84.00 (IS 29733) to maximum 184.00(IS 5301). Plant height (cm) showed mean range from 107.50 to 482.50 in genotype IS 3158 and IS 22986, respectively. Mean values for panicle length (cm) and panicle width (cm) lies 38.00 (IS 30417) to 13.00 (SMJ-1) and 17.50 (IS 30417) to 4.11 (SMJ-1), respectively. Mean values for Number of primary branches per panicle lies between 35.98 to 106.70 in genotypes SMJ-1and IS 30417, respectively. Likewise Hundred seed weight mean performance ranged from highest in genotype 11473(4.23) to lowest in IS 22609(1.63). The mean values for economic part i.e. Panicle weight is ranged from maximum 93.28 (BRJ 204) to minimum 25.00 (IS 12706), whereas, for Seed yield per plant it's ranged from 84.60 (BRJ 204) to minimum 12.64 (IS 12706).

This shows that these characters were responsible for wide variation in grain yield of various genotypes. These results also indicating that these genotypes are useful as genetic source in sorghum improvement program. Similar results obtained from the study of Kisua *et al.* (2015), Kinfe and Tesfaye (2018), Mengistu *et al.* (2020) which concurred partial results from our study.

Genotypic and Phenotypic variation

The present investigation indicated wide range of values for all the characters studied (Table 2), the phenotypic coefficient of variation (PCV) was though higher than genotypic coefficient of variation (GCV) for all the characters under study but the narrow range of difference indicated that most of the characters were least influenced by the environment. Similar result was also reported by Elangovan *et al.* (2009). These finding suggested that selection can be effective on the basis of phenotype along with equal probability of genotypic values. High values of GCV and PCV were obtained for most of the characters like plant height (31.02 and 31.20%), number of leaves (33.03 and 33.32%), days to fifty percent flowering (%), days to maturity (%), panicle length (23.48 and 26.72%), panicle width (36.36 and 36.75%), number of primary branches per plant (23.41 and 26.68%), panicle weight (33.58 and 37.10%), seed yield per plant (51.23 and 54.09%) indicating variation for these characters contributed markedly to the total variability. Similar, results were reported by Biradar *et al.* (1996), Reddy *et al.* (1996), Godbharle *et al.* (2010) and Seetharam and Ganesamurthy (2013).

Moderate GCV values were recorded for hundred seed weight (17.82%). This result was in accordance with findings of Ranjith *et al.* (2016) and Zinzala *et al.* (2018) for grain yield per plant; Kavipriya *et al.* (2020) for yield per plant; Nyadanu and Dikera (2014) for dry fodder yield per plan and harvest index; Tiwari *et al.* (2003) and Negash *et al.* (2005) for plant height; Prabhakar (2001), Veerabadhiran and Kennedy (2001); Seetharam and Ganesamurthy (2013) for days to 50 per cent flowering.

Heritability and Genetic Advance

High magnitude of heritability coupled with high magnitude of genetic advance over mean (Table 2) was obtained for the characters *viz.,* plant height (98.87 and 63.54%), number of leaves(98.30 and 67.47%), days to fifty percent flowering (97.26 and 62.99%), days to maturity (96.18 and 42.33%), panicle length (77.20 and 42.49%), panicle width (97.89 and 74.10%), number of primary branches per plant (76.97 and 42.31%), hundred seed weight (70.36 and 30.78%), panicle weight (81.93 and 62.61%), seed yield per plant (89.72 and 99.97%). Hence, selection made through these characters would be effective as they are more predominantly controlled by additive gene effect and thus while expecting genetic variability, due emphasis should be given to these characters. These results are in confirmation with the results of Seetharam and Ganesamurthy (2013), Negash *et al.* (2005), Bello *et al.* (2007) and Deepalakshmi and Ganesamurthy.

Similar kind of high estimate of heritability were reported by Shreenivasa *et al.* (2000) for plant height, total number of leaves; Umadevi and Kumaravadivel (2009) for plant height, panicle length, and grain yield per plant; Bello *et al.* (2007), Deepalakshmi and Ganesamurthy (2007), Prabhakar (2001) for days to 50 % flowering, plant height, panicle length and total number of leaves; Kumar *et al.* (2011) for plant height, grain yield per plant, days to maturity; Shinde *et al.* (2011), Anup and Vijayakumar (2000) for total number of leaves and panicle width; Bhagasara *et al.* (2017) and Swamy *et al.* (2018) for grain yield per plant.

Diversity Studies

Genetic divergence among 49 genotypes was assessed using D^2 analysis for ten quantitative traits. The character, Seed yield per plant (25.04%) was the highest contributor towards diversity followed by Panicle weight (23.39%), Number of primary branches per plant (18.44%) and Days to 50 per cent flowering (10.24%) (Table 4). These traits contributed over 77% of total genetic divergence, suggesting that these should be the primary selection criteria for choosing divergent parents in hybridization programs. The traits exhibiting high contribution towards genetic divergence help in selection of genotypes for improvement of that trait (Nirmala *et al.,* 2004). Traits like hundred seed weight and number of leaves per plant showed minimal contribution (<0.5%), indicating less variability and limited scope for improvement through direct selection.

The Mahalanobis D^2 analysis grouped the 49 genotypes into five distinct clusters using Tocher's method (Rao, 1952), indicating substantial genetic divergence among the sorghum accessions evaluated (Table 5). Among the five clusters, Cluster IV was the largest cluster containing 13 genotypes followed by cluster I and III each having 12 genotypes. The intra-cluster distances were smaller compared to inter-cluster distances**,** confirming that genotypes within a cluster are more genetically similar, whereas genotypes in different clusters are more divergent. The maximum inter-cluster distance was recorded between Cluster II and Cluster V ($D^2 = 38.370$)**,** followed by Cluster II and Cluster III (35.877) (Table 7). This suggests that hybridization between genotypes from these clusters could yield maximum heterosis and transgressive segregants (Griffing and Lindstrom, 1954). Minimum inter-cluster distance was found between Cluster I and Cluster III ($D^2 = 5.394$), suggesting close genetic relationships. The lowest intra-cluster distance was in Cluster I ($D^2 = 8.863$) and Cluster III ($D^2 = 5.916$)**,** indicating that the genotypes within these clusters are genetically more homogeneous. Cluster V also showed moderate intra-cluster distance ($D^2 = 6.167$), suggesting a good mix of variation but still with a level of homogeneity.

An analysis of cluster mean values for 10 agronomic traits (Table 6) revealed considerable variation across clusters. Cluster V had the highest seed yield per plant (71.11 g), along with the highest panicle weight (81.86 g)**,** indicating that this cluster contains elite genotypes with superior yield potential. Cluster II exhibited the highest values for plant height (426.53 cm)**,** days to 50% flowering (131.44 days), and days to maturity (170.71 days), suggesting tall and late-maturing genotypes. Cluster III recorded earliest flowering and maturity and shorter plant height, making it suitable for early maturing and short-duration sorghum breeding programs. Crosses between genotypes from Cluster II and Cluster V, or Cluster II and Cluster III**,** are expected to produce maximum heterosis due to greater genetic distance. Genotypes in Cluster V (e.g., BJV44, BRJ204, SPV2217) should be prioritized as donors for high yield and panicle weight, while those in Cluster III may be used for early maturity and compact growth habit. The dendrogram (Figure 1) confirmed the clustering results from Mahalanobis D^2, where genotypes grouped into similar clusters had closer branch lengths, affirming reliable genetic grouping based on multivariate phenotypic traits.

The present study revealed substantial genetic variability and divergence among 49 sorghum genotypes. Traits such as seed yield per plant, panicle width, and number of leaves exhibited high heritability and genetic advance, indicating the efficacy of direct selection. Crosses involving genetically divergent genotypes, especially between clusters II and V, can lead to the development of high-yielding, heterotic hybrids. This study provides a valuable genetic base for improving sorghum productivity under diverse agro-climatic conditions. Traits like seed yield, panicle weight, and flowering time playing significant roles in genetic divergence. The identified genetically diverse parents and trait-specific clusters offer substantial potential for improvement in sorghum breeding programs aimed at enhancing yield, earliness, and adaptability.

Table 1: Analysis of variance of different characters in sorghum

Source of variation	**df**	**Plant height**	**Number of leaves per plant**	**Days to 50 per cent flowering**	**Days to maturity**	**Panicle length**	**Panicle width**	**Number of primary branches per plant**	**Hundred seed weight**	**Panicle weight**	**Seed yield per plant**
Replication	1	14.40	0.39	21.16	32.11	0.53	0.09	3.02	0.01	15.24	10.91
Genotype	48	14826.70**	20.93**	1306.67**	1321.12**	61.93**	17.50**	486.89**	0.66**	634.37**	609.66**
Error	48	84.50	0.18	18.17	25.70	7.97	0.19	63.36	0.11	63.02	33.04

Table 2: Estimation of genetic variability parameters

Traits	**Plant height**	**Number of leaves per plant**	**Days to 50 per cent flowering**	**Days to maturity**	**Panicle length**	**Panicle width**	**Number of primary branches per plant**	**Hundred seed weight**	**Panicle weight**	**Seed yield per plant**
GCV	31.02	33.03	31.01	20.95	23.48	36.36	23.41	17.82	33.58	51.23
PCV	31.2	33.32	31.44	21.36	26.72	36.75	26.68	21.24	37.1	54.09
h2 (BS) %	98.87	98.3	97.26	96.18	77.2	97.89	76.97	70.36	81.93	89.72
GA% mean	63.54	67.47	62.99	42.33	42.49	74.1	42.31	30.78	62.61	99.97

Table 3: Mean performance of sorghum genotypes for yield and its component traits

Genotypes	**PH**	**NL**	**DFF**	**DM**	**PL**	**PW**	**NPP**	**HSW**	**PWT**	**SYP**
IS 608	212.50	9.00	56.00	95.00	29.63	7.25	83.18	1.63	26.50	15.29
IS 2397	177.50	5.66	60.00	99.50	22.50	5.50	63.18	2.59	32.50	22.25
IS 3158	107.50	3.43	63.50	102.00	24.25	8.25	68.09	3.36	32.50	16.43
IS 5301	447.50	14.28	146.50	184.00	23.25	14.00	65.29	2.39	27.75	13.73
IS 5386	205.00	6.54	68.50	111.50	14.00	6.25	39.31	2.52	33.50	19.56
IS 5919	382.50	12.20	103.00	141.00	22.75	12.25	63.88	3.06	44.50	22.00
IS 6351	372.50	11.88	116.00	157.50	21.50	5.00	60.37	2.92	72.25	35.70
IS 6354	317.50	10.13	121.00	164.00	22.75	6.50	63.88	2.96	76.25	35.48
IS 7310	422.50	13.48	131.00	172.00	30.50	8.50	85.64	3.04	60.25	35.30
IS 7987	437.50	13.96	140.50	176.50	36.25	11.50	101.79	3.94	42.50	27.56
IS 8348	217.50	6.94	60.50	100.00	20.00	10.75	56.16	2.68	52.50	34.07
IS 8774	177.50	5.66	57.00	99.00	23.75	8.75	66.69	2.54	58.00	38.67
IS 10302	332.50	10.61	84.50	122.50	25.00	9.60	70.20	3.28	66.25	36.46
IS 11473	205.00	6.54	96.50	133.50	19.50	9.75	54.76	4.23	54.50	29.40
IS 12302	297.50	9.49	70.00	111.00	20.50	5.70	57.56	3.56	77.50	56.89
IS 12447	172.50	5.50	68.50	106.00	22.50	6.75	63.18	4.00	52.50	27.80
IS 12706	247.50	7.90	56.00	95.00	23.25	10.70	65.29	2.57	25.00	12.64
IS 13919	202.50	6.46	62.50	103.00	21.00	7.75	58.97	2.72	52.25	27.83
IS 15170	417.50	13.32	113.50	152.50	19.00	4.80	53.35	3.81	33.25	21.24
IS 19389	327.50	10.45	64.00	101.00	25.25	13.60	70.90	2.82	41.25	25.16
IS 22239	212.50	6.78	61.00	97.50	27.00	9.65	75.82	2.87	37.50	24.04
IS 22609	402.50	12.84	119.50	160.00	13.00	6.15	36.50	1.63	33.50	21.31
IS 22986	482.50	15.39	125.00	168.75	14.00	8.80	39.31	2.46	45.25	27.99
IS 23216	422.50	13.48	123.50	162.00	29.50	10.60	82.83	2.23	55.50	32.14
IS 23521	252.50	8.06	76.50	116.50	27.75	11.55	77.92	2.77	48.00	27.28
IS 23586	322.50	10.29	74.50	113.00	21.50	7.75	60.37	3.59	52.75	23.44
IS 24348	212.50	6.78	59.50	103.00	23.25	7.60	65.29	2.96	36.00	17.96
IS 24462	142.50	4.55	52.50	91.00	21.25	5.10	59.67	2.77	31.50	17.63
IS 25732	322.50	10.29	109.50	149.00	17.50	6.75	49.14	3.15	33.00	16.60
IS 26701	182.50	5.82	59.50	102.50	16.75	6.60	47.03	2.11	49.50	28.79

IS 27557	292.50	9.33	97.50	139.50	22.25	15.60	62.48	2.29	37.50	25.08
IS 29187	252.50	8.06	61.00	98.50	25.25	7.00	70.90	2.51	45.00	40.41
IS 29314	267.50	8.53	67.50	109.00	26.25	8.75	73.71	2.33	69.00	37.35
IS 29568	282.50	9.01	67.00	109.50	29.00	7.75	81.43	2.68	47.75	30.55
IS 29733	273.50	8.73	43.50	84.00	25.50	5.25	71.60	2.38	46.25	25.32
IS 29950	238.00	7.59	81.00	122.50	21.75	7.25	61.07	3.03	35.75	28.86
IS 30079	301.00	9.60	93.00	135.50	20.25	7.25	56.86	2.78	39.50	26.59
IS 30092	252.50	8.06	66.50	102.00	21.50	8.75	60.37	3.19	33.00	18.23
IS 30400	264.00	8.42	61.00	103.00	20.50	8.20	57.56	2.82	58.50	33.67
IS 30417	281.50	8.98	61.00	101.00	38.00	17.50	106.70	2.53	42.50	23.05
IS 30572	342.50	10.93	97.00	141.00	29.00	8.25	81.43	3.06	28.00	16.83
BJV 44	246.92	13.09	79.83	117.00	17.65	5.26	47.86	3.43	88.82	84.60
BRJ 204	227.76	13.73	80.51	122.00	16.96	5.65	46.74	4.02	93.28	75.01
SMJ-1	236.87	12.42	82.00	115.00	13.00	4.11	35.98	2.88	65.69	54.57
AKJ 1	265.34	15.88	74.20	109.50	15.46	5.16	43.09	2.88	55.06	49.56
DSMR 8	264.16	14.98	67.94	116.30	14.65	5.45	44.16	3.74	89.92	73.00
PDVK Kartiki	167.56	6.29	77.50	113.50	17.02	5.37	51.18	3.45	61.95	57.53
M35-1 (check-1)	227.07	9.89	73.77	111.00	16.06	4.96	45.12	2.98	59.63	53.48
SPV 2217 (check-2)	243.44	13.57	79.37	112.50	15.51	5.36	42.01	3.31	85.24	79.58
Mean	276.78	9.75	81.86	121.47	22.13	8.09	62.16	2.93	50.33	33.14
Max	482.50	15.39	146.50	184.00	38.00	17.50	106.70	4.23	93.28	84.60
Min	107.50	3.43	43.50	84.00	13.00	4.11	35.98	1.63	25.00	12.64
SEm(±)	6.50	0.30	3.01	3.58	2.00	0.31	5.63	0.24	5.61	4.06
CD (5%)	18.48	0.85	8.57	10.19	5.68	0.87	16.00	0.68	15.96	11.56
CV(%)	31.20	33.32	31.44	21.36	26.72	36.75	26.68	21.24	37.10	54.09

PH- Plant height
NL- Number of leaves per plant
DFF- Days to 50 per cent flowering
DM- Days to maturity
PL- Panicle length
PW- Panicle width
NPP- Number of primary branches per plant
HSW- Hundred seed weight
PWT- Panicle weight
SYP- Seed yield per plant

Table 4: Per cent contribution of different characters towards genetic divergence in sorghum

Trait	Percent Contribution (%)	Rank
Plant height (cm)	9.2	5
Number of leaves per plant	0.38	9
Days to 50 per cent flowering (%)	10.24	4
Days to maturity (%)	8.11	6
Panicle length (cm)	0.02	10
Panicle width (cm)	0.54	8
Number of primary branches per plant	18.44	3
Hundred seed weight	4.65	7
Panicle weight (g)	23.39	2
Seed yield per plant (g)	25.04	1

Table 5: Classification of genotypes with good per se values represented in different clusters

Cluster	Number of genotypes	Genotypes
I	12	IS 608, IS 8774, IS 12706, IS 19389, IS 22239, IS 23521, IS 27557, IS 29187, IS29314, IS29568, IS 29733, IS 30417
II	3	IS 7310, IS 7987, IS23216
III	12	IS 2397, IS 3158, IS 5386, IS 8348, IS 12447, IS 13919, IS 24348, IS 24462, IS 26701, IS 29950, IS 30092, IS 30400
IV	13	IS 5301, IS 5919, IS 6351, IS 6354, IS 10302, IS 11473, IS 15170, IS 22609, IS 22986, IS 23586, IS 25732, IS 30079, IS 30572
V	9	IS 12302, BJV44, BRJ 204, SMJ 1, AKJ 1, DSMR 8, PDVK Kartiki, M 35-1, SPV 2217

Table 6: Cluster mean of characters among five clusters in sorghum

	Plant height	**Number of leaves per plant**	**Days to 50 per cent flowering**	**Days to maturity**	**Panicle length**	**Panicle width**	**Number of primary branches per plant**	**Hundred seed weight**	**Panicle weight**	**Seed yield per plant**
1	258.19	8.37	65.59	106.83	2.43	10.28	68.01	28.23	41.91	26.16
2	426.53	13.64	131.44	170.71	3.16	10.20	73.70	35.06	49.89	30.89
3	199.56	6.31	63.83	104.09	2.90	7.40	53.15	19.63	42.49	24.99
4	355.99	11.41	107.83	148.48	3.05	8.22	53.46	19.51	46.55	24.63
5	244.97	12.48	76.19	114.38	3.33	5.22	41.35	16.49	81.86	71.11

Table 7: Average intra and inter cluster distances (D^2) for five clusters of sorghum

	1	2	3	4	5
1	8.863	22.315	5.394	12.125	22.676
2		7.216	35.877	11.491	38.370
3			5.916	12.236	15.015
4				13.307	15.688
5					6.167

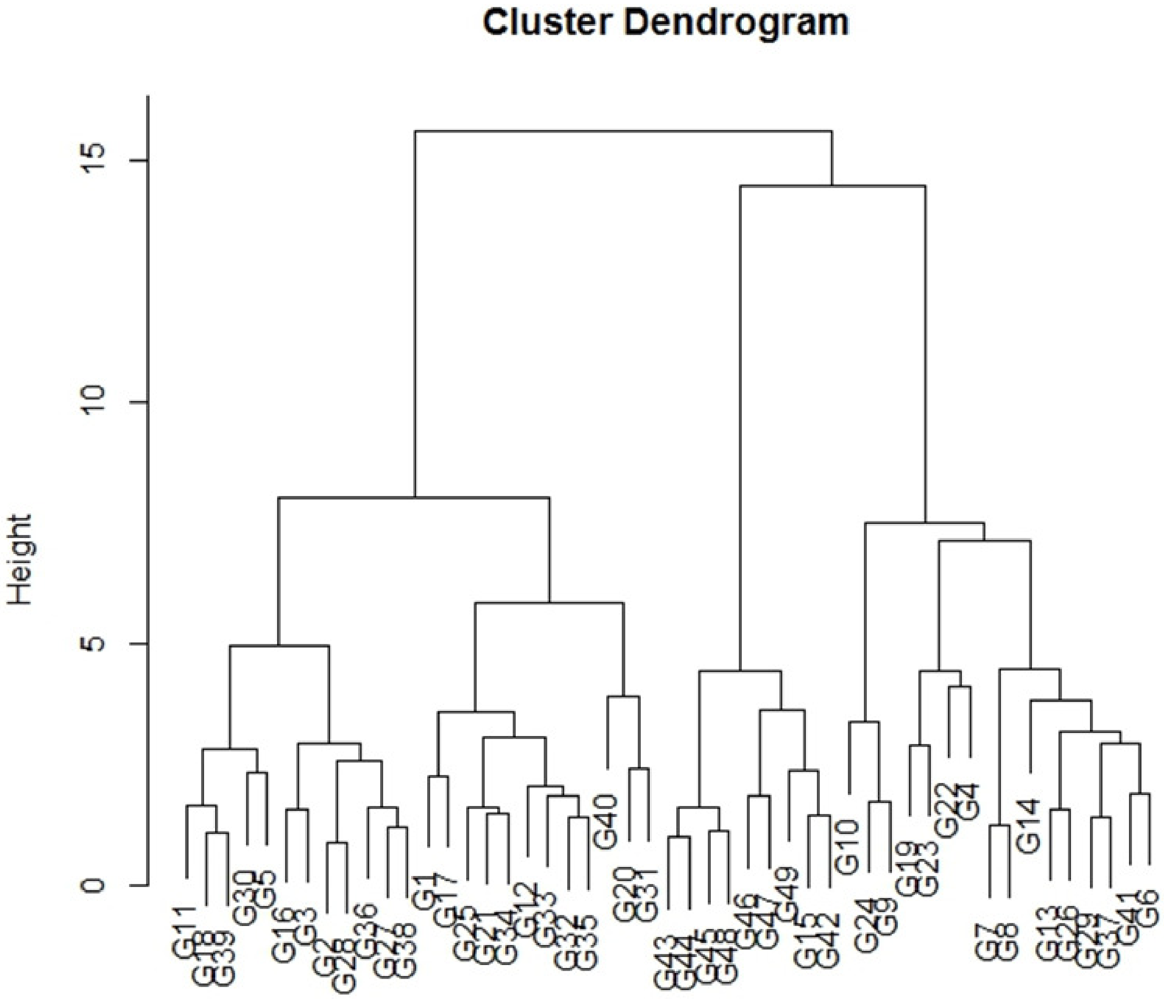
Cluster Dendrogram

Fig. 1 : Dendrogram of sorghum germplasm based on phenotypic data

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