Original Research Article

Genetic Diversity Analysis for Forage Yield and Quality Traits in Sorghum [*Sorghum Bicolor* L. Moench] Germplasm

ABSTRACT

The present investigation was carried out with two hundred eighty sorghum germplasm lines in augmented block design at GBPUAT, Pantnagar under normal sown condition during the K*harif* season 2019. The observations were recorded on different yield contributing traits such as days to flowering, plant height, number of leaves; stem girth etc., quality traits such as protein content, total soluble solids, in vivo dry matter digestibility etc., and quality traits like cellulose content, silica content, and hemicelluloses etc. The statistical analysis for genetic diversity was done using hierarchical cluster analysis. The hierarchical cluster analysis revealed that significant amount of genetic diversity was present in sorghum germplasm with respect to different yield related traits, quality traits and biochemical traits. The 280 germplasm lines were grouped into XI distinct non-overlapping clusters. The cluster-VIII (50) consisted of highest number of genotypes whereas lowest numbers of genotypes were grouped into cluster-III (1). The maximum intra-cluster distance was observed in cluster-IV (54.652) suggesting highest genetic diversity among genotypes of this cluster in comparison to other clusters whereas minimum intra-cluster distance was observed in cluster-III (0.000). The highest inter-cluster distance was observed between clusters-III and VI (334.554) suggested distant relationship between members of these two clusters and upon crossing the members of these two clusters will give more genetic diversity in segregating generation whereas minimum inter-cluster distance was observed between clusters-VIII and IX (52.512) suggested a closer relationship between these two clusters and low degree of genetic diversity among the genotypes. . Presence of substantial genetic diversity among the genotypes screened in the present study indicated that this material may serve as a good source for selecting the diverse parents for hybridization programme. In order to increase the possibility of isolating good trangressive segregants in the segregating generations it would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster distances.

Keywords: Germplasm, Cluster, Genetic Diversity, Intra and Inter- cluster distance.

1. Introduction:

Sorghum is one of the most important and widely grown crops in the world having the area of 41.14 million hectare with the production of about 58.72 million tonnes globally whereas 5.00 million hectare and 4.50 million tonnes grain production in India **(USDA Foreign Agricultural Services, 2019).** Sorghum is known by various names in Africa, such that *guinea-corn, dawa* or *sorgho* in West Africa, *durra* in the Sudan, *mshelia* in Ethiopia and Eritrea, *mtama* in East Africa, *kaffir corn* in South Africa and *amabele* or *mabele* in several countries in Southern Africa. In the Indian sub-continent, it is known as *jowar* (Hindi), *cholam* (Tamil Nadu), *jonna* (Andhra Pradesh) and *jola* (Karnataka). Five basic races of cultivated sorghum are recognized as *Bicolor, Guinea, Kafir, Durra* and *Caudatum* **(Harlan and De Wet, 1972)**.

It has extensive variability of usage such as forage sorghum, grain sorghum and sweet sorghum, providing food, fodder, feed, fuel and fiber. The crop is mainly grown in tropical and subtropical areas because of its drought tolerance capacity, and quick growing habit, good palatability where agro-climatic conditions such as rainfall, temperature and soil are variable. Much of the crop is grown in the stress-prone and marginal areas of the semi-arid tropics, mainly on small holdings. In Northern Western India, it is grown for meeting the major fodder requirement of *kharif* and summer seasons. Precise information on nature and degree of genetic variability helps the plant breeder in selecting the genetically diverse parents for the purposeful hybridization. **(Arunachalam, 1981)**.Genetic improvement of yield especially in self-pollinated crops depends on nature and amount of genetic diversity **(Joshi and Dhawan, 1966)**.

Nutritionally, among the *kharif* fodders, sorghum is a crop *par excellence* with starch (63-68%), potential of high digestibility (50-60%), dry matter (20-35%), sugars (8-17%), crude protein (7.5-10.0%), calcium (0.53%), phosphorus (0.24%), and crude fiber (30-32%) **(Sheoran *et. al.*, 2000)**. Beside the higher content of carbohydrates, it has iron (Fe) and vitamin B_3 contents which are higher than maize and rice**.** It is a major staple food of many countries in Asia and Africa, sorghum is now a major feed crop in the United States, Argentina, Mexico, South Africa, and Australia **(Miller and Kebede, 1984)**.

Genetic diversity and relationship among different individuals is a prerequisite for any successful breeding programme. Genetic diversity among accessions provides opportunities for improvement of agronomic and nutritional quality traits in crops **(Huang, 2004).** It aids plant breeders to characterize and classify accessions into heterotic groups **(Menz et al., 2004).** Genetic diversity of plants determines their potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced forage production. Genetic diversity explains the genetic differences between different populations within a species or between species. The parents having more genetic diversity result into higher heterotic expression in F_1 and greater amount of genetic variability in segregating populations **(Shekhawat *et al*., 2001).** One of the important approaches to sorghum breeding is hybridization and subsequent selection. Parents' choice is the first step in plant breeding program through hybridization. In order to obtain transgressive segregants, genetic diversity between parents is necessary **(Joshi *et al*., 2004)**. The higher genetic diversity between parents, the higher heterosis in progeny can be observed **(Joshi and Dhawan, 1966).** Estimation of genetic diversity is one of appropriate tools for parental selection in sorghum hybridization programs. Appropriate selection of the parents is essential to be used in crossing nurseries to enhance the genetic recombination for potential yield increase. In view of the above, there is need to screen the diversity of sorghum germplasm based on yield and quality parameters to find out their suitability in different breeding programmes. There is a need to make genuine efforts to assess available diversity. Hence the present investigation was conducted to estimate the magnitude of genetic diversity present among the elite sorghum genotypes.

2. Materials and Methods:

The initial research related to germplasm screening was carried out in the experimental area of Instructional Dairy Farm, Nagla, G.B. Pant University of Agriculture and Technology. Pantnagar, District U. S. Nagar, Uttarakhand during *Kharif*, 2019. The experimental material for this experiment consisted of two hundreds and eighty diverse germplasm lines of sorghum along with six checks *viz*., SSG 59-3, Pant Chari- 5, Pant Chari- 6, CSV-21 F, CSH-22S, and CSV-24SS. The germplasm lines were evaluated in Augmented Block Design during *Kharif* season of 2019. The experiment was carried out in an Augmented Block Design **(Federer, 1956, 1961, and Federer & Raghavrao, 1975)** with each block containing 35 test entries and 6 checks which were randomly allocated in 8 blocks. All genotypes were sown on 27th July 2019 in single row of 5 meter length with a row spacing of 45 cm. All the recommended package of practices for sorghum was followed to raise a healthy crop. The observations were recorded on days to 50% flowering, days to maturity, number of leaves per plant, number of nodes, plant height (cm), leaf length (cm), leaf width (cm), leaf area (cm^2), flag leaf length (cm), flag leaf width (cm), stem girth (cm), internodal length (cm), panicle length (cm), panicle width (cm), leaf:stem ratio, 1000-grains weight (gm), grain yield per plant (gm), green fodder yield per plant (gm), dry fodder yield per plant (gm), foliar diseases zonate leaf spot and anthracnose **(Thakur *et al*., 2010)**, shoot fly (*Atherigona soccata*) incidence (Dead hearts %), dry matter (%), brix %, HCN content (ppm) (**Hogg and Ahlagreen, 1942)** and **Gilchrist *et al*. (1967) ,** protein content (%) **(Jeckson, 1973),** in-vitro dry matter disappearance (IVDMD) % **(Erwin and Ellinston, 1959),** neutral detergent fiber **(Van Soest, 1991),** acid detergent fiber (%) and cellulose (%) **(Van Soest, 1991),** acid detergent lignin (%), cellulose (%) and silica (%) **(Van Soest, 1991).** Hierarchical cluster analysis was performed on the basis of Euclidean distance between the genotypes. Euclidean distance was calculated by using the following method:

Euclidean distance: The Euclidean distance between ith and kth accession is:

$$D_{ik} = \left[E_{j=1}^{n}\left(A_{ij} - A_{kj}\right)^{2}\right]^{1\!/\!2}$$

Where,

D_{ik} = Euclidean distance between ith and kth accession
A_{ij}= performance of ith accession for jth character.
A_{kj} = performance of kth accession for jthcharacter.
m = number of accessions (I or k = 1, 2… m)
n = number of characters (j =1, 2…n)

When the similarity matrix is computed from distance function, the hierarchical clustering method begins by finding the link between the two closest genotypes **(Anderberg, 1973).** The statistical analysis was performed by **Indostat Hyderabad.**

3. Result and Discussion:

Knowledge about genetic diversity of parents in hybridization programme is essential as the crosses involving genetically diverse parents who are likely to produce not only high heterotic effects, but it also produce desirable transgressive segregants in the later segregating generations. The hierarchial cluster analysis discriminates genotypes in a different cluster on the basis of genetic diversity among the genotypes and thus enable breeder to select more genetically diverse parents for their crossing programme to recover desirable seggregants. The genotypes included in the same cluster may have different generations of time, different parental combinations or different generations of the same parental combinations. This proved that geographical diversity need not necessarily be related sown conditioned to the genetic diversity.

The hierarchial cluster analysis had been found to be a potent tool in quantifying the degree of divergence in germplasm .This analysis provides a measurement of relative contribution of different components on diversity both in inter cluster and intra cluster level and genotypes drawn from widely divergent clusters are likely to produce heterotic combinations and wide variability in segregating generation **(Rao, 1952).** Among the different approaches of selecting parents, selection based on diversity has its own merit.

3.1 Distribution of genotypes into different clusters: The clustering pattern of genotypes on the basis of Hierarchial cluster analysis has been presented in **Table 1** during *Kharif* 2019**.** The genotypes were grouped into XI distinct non-overlapping clusters suggesting considerable amount of genetic diversity prsesent in the experimental material. The cluster pattern of the genotypes showed non-parallelism between geographic and genetic diversity **(Singh et al., 2009).** The genotypes were grouped into XI distinct non-overlapping clusters. The cluster-VIII (50) consisted of highest number of genotypes followed by cluster-IX (46), cluster-I (39), cluster-VII (36), cluster- V (35), cluster- IV (27), cluster- XI (24), cluster- II (14), cluster- X (11), cluster-VI (3) and lowest number of genotypes were grouped into cluster-III (1).

Cluster-I: This cluster consisted of thirty nine genotypes viz., E2-2, Malwan, SSG-212, HJ-513, IS-23586, HC-171, IS-3318, SSG-222, PC-23, ICSV-702, IS-12743, CSV-10, 1890 (08BZL-01-43-1), IS-20703-1, GP-2011-471, SSG-260, SSG-263, SSG-234, IS-1219, 9533-1, PC-1001, SPV-1752, UTFS-42, IS-9722, EJN-40, PC-1002, EJN-46, SSG-611, SMC-14, SEVS-2, B-437 (09B-RUS-04), IS-2363, IS-9162, IS-607, ICSV-111, SPV-1725, IS-6090, PSSV-61, UPFS-38 x UPFS-36. This cluster had highest cluster mean for acid detergent fiber, cellulose content, lignin content and silica content.

Cluster-II: This cluster exhibited fourteen genotypes viz., CO (FS)-29, IS-18850, SSG-21, IS-30117, IS-3353, E-159, IS-14357, IS-13566, IS-18927, IS-18844, IS-18933, SMC-8, SMC-13, and IS-28313. This cluster had high cluster mean for days to flowering, number of leaves, panicle width, green fodder yield per plant, dry fodder yield per plant, protein percent, acid detergent fiber, cellulose content and lignin content.

Cluster-III: This cluster consisted lowest number of genotype (1) i.e. IS-14241. This cluster had highest cluster mean for days to flowering, days to maturity, number of leaves, number of nodes, leaf length, flag leaf length, panicle length, panicle width, green fodder yield per plant, dry fodder yield per plant, hydrocyanic acid content, protein percent, neutral detergent fiber and hemicelluloses content.

Cluster-IV: This cluster consisted of twenty seven genotypes viz., SEVS-1, IS-4726-2, IS-2101, IS-25419-2, SMC-5, IS-25419-1, IS-1478, IS-23988, IS-5434-1, IS-6045, IS-14278-1, IS-6953, IS-7002, IS-21977, UTMC-523, IS-15008-1, CS-3541-1, RS-673, IS-20740, IS-20782, IS-23948-1, IS-20399, JJ-1041, Pant Chari-5, IS-21622, IS-21461, and SSG-59-3. . This cluster had high cluster mean for leaf width, leaf area, flag leaf width, leaf: stem ratio, total soluble solids, protein percent, cellulose content and shoot fly incidence.

Cluster-V: This cluster had thirty five genotypes viz., UTMC-531, ESRK-7, SSG-227, CSV-14, SPV-1749, UPChari-1, EJN-37, EJN-54, SMC-2, SMC-6, Nizamabad, (SDSL-92101 x IS-3359) x Pant Chari-5, UP Chari-2, UPFS-38, IS-3359, PC-121, Pant Chari-3, IS-3199, GM-1378-1, IS-29794, GGUV-55, GMC-1422, SPV-1252, SPV-1616, SPV-1750, SST-4, SPV-1753, SRF-285, R-74(09R-AGR-26), R-77 (09R-AGR-26), RAJ-21, R-72(09R-AGR-23), UPFS-39, R-73 (09-AGR-24), and R-255 (09R-SS-26). This cluster had high cluster mean for number of leaves, leaf length, leaf width, leaf area, flag leaf length, flag leaf width, stem girth, 1000-grains weight, grain yield per plant, dry matter percent, in-vitro dry matter disappearance, silica content and zonate leaf spot.

Cluster-VI: This cluster had only three genotypes viz., CSV-19, CSV-24SS, and CHS-22SS. This cluster had high cluster mean for number of nodes, leaf width, leaf area, flag leaf width, internodal length, leaf: stem ratio, 1000-grains weight, green fodder yield, dry fodder yield per plant, total soluble solids, in-vitro dry matter disappearance, acid detergent fiber and hemicelluloses content.

Cluster-VII: This cluster consisted of thirty six genotypes viz., IS-2549-3, ICSR-93023, EJN-73, SMC-9, HC-260, GP-2011-372, E-1, ESRK-10, UPFS-35, E-25, E-105, EJN-59, ESRK-12, ESRK-16, SSG-223, 1910(08BZL-01-32-4), 1946 (08RLD-01-5-3), 1941(08RLD-01-5-3), R-72 (09R-AGR-23), EJN-58, PM-98019-2, GD-68717-1, UPFS-34, IS-14756, RAJ-16, EJN-49, EJN-68, IS-3821, HC-136, RAJ-32, EP-122, E-7, E-28, ESRK-4, EJN-39, and IS-12735. . This cluster had high cluster mean for days to flowering, days to maturity, plant height, stem girth, 1000-grains weight, grain yield per plant and anthracnose.

Cluster-VIII: This cluster was marked with highest number of genotypes (50) viz., ART-1008, UPFS-38 x IS-7002, SSG-219, SSG-256, IS-3313, SSG-244, UPFS-37 x UPMC-6, Rajasthan Local, GGUB-25, PC-23 x (SDSL-92101 x UPFS-23), EG-11, SRF-286, SL-44, SPV-462, UPFS-40, SMC-7, EJN-51, SPV-1754, UPMC-504 x UPMC-8, UTFS-48, GP-2011-44-1, UTFS-49, SMC-11, IS-15680, UPFS-36 x Pant Chari-6, IS-3821, SMC-18, HC-171, SMC-17, SSG-245, UPMC-503 x (SDSL-92101 x UPFS-23), ESRK-29, EJN-67, SSG-221, Ramkel, MP Chari, EJN-38, SSG-236, ESRK-27, SSG-241, SSG-250, SSG-224, SSG-256, SMC-3, SSG-227, SSG-243, SSG-248, SSG-234-1, SSG-253, and SSG-226. This cluster had high cluster mean for plant height, stem girth, internodal length, panicle length, panicle width and neutral detergent fiber.

Cluster-IX: This cluster had forty six genotypes viz., EJ-3, RAJ-9-1, EJ-42, C-43, RAJ-15, IS-313, Pant Chari-6, RS-29, UPFS-36(Pant Chari-7), UTMC-532, IS-3314, IS-3345, IS-3145, EA-11, IS-12956, GGUB-27, IS-699, RAJ-20, Pant Chari-5 x UPMC-512 , CSV-21F, SSV-74, SSG-304, IS-4307, SMC-12, ICSV-95119-1-2, 77113, IS-639, IS-29691, SMC-10, IS-31861, ESRK-26, IS-3359, SSG-226, SSG-225-1, UPFS-38 x SSG-59-3, SSG-225-2, IS-6193, IS-21602-1, IS-3237-2, IS-14298-1, NSSV-259, IS-14333-1, IS-18008-2, IS-22241, PSSV-49, and GMS-1338. This cluster had high cluster mean for internodal length, neutral detergent fiber, hemicelluloses content and zonate leaf spot.

Cluster-X: This cluster consisted of eleven genotypes viz., EJ-19, EJ-26, EJ-27, EJ-40, EJ-25, IS-25733, EJ-30, IS-4925, IS-33096, CSV-17, and IS-23992. This cluster had high cluster mean for leaf: stem ratio, dry matter percent, hydrocyanic acid content, total soluble solids, in-vitro dry matter disappearance and lignin content.

Cluster-XI: This cluster had twenty four genotypes viz., EJ-19, EJ-15, EJ-48-1, EJN-62, IS-14816, EJN-57, EJN-56, EJN-60, EJN-63, EJN-64, GGUB-36, IS-29314, GP-2011-110-1, EJ-30, EP-135, EP-124, EJ-24, EJN-48-2, EJ-30, EJN-43, EJN-45, GP-2011-18-2, EJN-47, and EJN-52. This cluster had highest cluster mean for hydrocyanic acid content.

The pattern of distribution of genotypes in different cluster exhibited that geographical diversity was not related to genetic diversity as genotypes of same geographical region were grouped into different clusters and vice-versa **(Kumar *et al.*, 2009, and Rahman *et al.*, 2015).**

3.2 Average intra and inter cluster distances: The intra-cluster and inter-cluster distances were calculated to determine the genetic relationship between members of different clusters and among the individuals within a cluster. The intra-cluster and inter-cluster distances has been represented in **Table 2.** Inter-cluster distance is the main criterion for the selection of genotypes **(Khare *et al.*, 2015)**. The genotypes belonging to those clusters having maximum inter-cluster distance are genetically more divergent and hybridization between these genotypes of different clusters is likely to produce wide range of variability with desirable individuals in segregating generations**.**

3.2.1 Intra-cluster distance: The maximum intra-cluster distance was observed in cluster-IV (54.652) suggesting highest genetic diversity among genotypes of this cluster in comparison to other clusters followed by cluster-VII (52.193), cluster-V (50.732), cluster-I (50.481), cluster-IX (49.583), cluster-XI (46.631), cluster-II (46.316), cluster-X (40.065), cluster-VIII (38.591), cluster-VI (30.366) whereas minimum intra-cluster distance was observed in cluster-III (0.000).

3.2.2 Inter-cluster distance: The genotypes belonging to those clusters having maximum inter-cluster distance are genetically more divergent and hybridization between these genotypes of different clusters is likely to produce wide variability with desirable individuals. The highest inter-cluster distance was observed between clusters-III and VI (334.554) suggested distant relationship between members of these two clusters and upon crossing the members of these two clusters will give more genetic diversity in segregating generation followed by clusters-III and X (321.316), clusters-III and XI (291.861), clusters-I and III (289.659), clusters-III and IV (280.335), clusters-III and IX (270.152), clusters-III and V (267.593), clusters-III and VII (260.334), clusters-III and VIII (245.298), clusters-II and III (218.755), clusters-II and VI (161.43), clusters-VI and X (137.992), clusters-VI and XI (125.337), clusters-VI and IX (116.215), clusters-I and VI (112.814), clusters-VI and VII (110.712), clusters-VI and VIII (108.318), clusters-IV and VI (95.978), clusters-II and X (92.231), clusters-V and X (91.74), clusters-VII and X (90.572), clusters-II and XI (88.733), clusters-V and VI (88.182), clusters-II and V (86.633), clusters-II and IV (84.875), clusters-II and VII (78.683), clusters-VIII and X (76.258), clusters-I and X (74.436), clusters-V and XI (74.418), clusters-I and II (74.38), clusters-II and IX (74.378), clusters-I and

XI (73.742), clusters-IV and X (73.702), clusters-I and VII (72.079), clusters-III and XI (71.454), clusters-I and IX (71.197), clusters-V and IX (69.247), clusters-VII and IX (66.597), clusters-IV and VII (66.407), clusters-I and V (65.409), clusters-I and IV (64.572), clusters-X and XI (64.481), clusters-VII and XI (64.078), clusters-IV and IX (63.058), clusters-II and VIII (62.93), clusters-V and VII (62.632), clusters-VIII and XI (62.178), clusters-IX and X (62.109), clusters-IV and V (61.652), clusters-I and VIII (61.239), clusters-IX and XI (61.224), clusters-IV and VIII (58.536), clusters-VII and VIII (54.901**),** clusters V and VIII (53.071) whereas lowest inter-cluster distance was observed between clusters-VIII and IX (52.512) suggested a closer relationship between these two clusters and low degree of genetic diversity among the genotypes. Presence of substantial genetic diversity among the genotypes screened in the present study indicated that this material may serve as a good source for selecting the diverse parents for hybridization programme. In order to increase the possibility of isolating good trangressive segregants in the segregating generations it would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster distances.

3.3 Cluster mean for different characters: Cluster means were calculated for all the yield and quality traits along with some biochemical traits which exhibited considerable differences among the clusters. The mean performance of the clusters was used to select genetically diverse and agronomically superior genotypes under present study.

The maximum cluster mean for days to flowering was observed in cluster-III (85.100) followed by cluster-II (78.400), cluster-VII (76.900), cluster-IV (67.200), cluster-I (66.700), cluster-VIII (63.300), cluster-VI (63.200), cluster-IX (63.200), cluster-XI (61.500), cluster-V (60.900) whereas minimum by cluster-X (55.000). The highest cluster mean for days to maturity was exhibited by cluster-III (147.000), cluster-VII (142.000), cluster-II (141.000), cluster-VI (133.000), cluster-IV (129.000), cluster-I (129.000), cluster-VIII (129.000), cluster-XI (126.000), cluster-IX (125.000), cluster-V (123.000) whereas lowest cluster mean for days to maturity was exhibited by cluster-X (121.000).

The maximum cluster mean for number of leaves was observed in cluster-III (20.000) followed by cluster-II (19.000), cluster-V (18.000), cluster-VII (18.000), cluster-VIII (18.000), cluster-VI (18.000), cluster-I (16.000), cluster-IX (16.000), cluster-XI (16.000), cluster-IV (15.000) whereas minimum by cluster-X (11.000). The highest cluster mean for number of nodes was exhibited by cluster-III (18.640), cluster-VI (17.620), cluster-II (17.370), cluster-V (16.560), cluster-VII (16.260), cluster-VIII (15.820), cluster-I (15.100), cluster-IX (14.890), cluster-XI (14.200), cluster-IV (14.100) whereas lowest cluster mean for number of nodes was exhibited by cluster-X (10.860).

The maximum cluster mean for plant height was observed in cluster-II (414.000) followed by cluster-VIII (405.000), cluster-VII (385.100), cluster-III (368.000), cluster-V (362.000), cluster-I (358.000), cluster-IV (350.000), cluster-IX (347.000), cluster-XI (340.000), cluster-X (298.000) whereas minimum by cluster-VI (291.000). The highest cluster mean for leaf length was exhibited by cluster-III (99.700), cluster-V (93.390), cluster-II (92.620), cluster-IV (88.020), cluster-III (86.040), cluster-I (85.370), cluster-VII (84.310), cluster-VI (84.300), cluster-IX (75.620), cluster-XI (73.790) whereas lowest cluster mean for leaf length was exhibited by cluster-X (72.170).

The maximum cluster mean for leaf width was observed in cluster-VI (11.300) followed by cluster-V (9.721), cluster-IV (9.255), cluster-VII (8.669), cluster-I (8.487), cluster-VIII (8.372), cluster-XI (7.960), cluster-IX (7.494), cluster-X (7.005), cluster-II (5.478) whereas minimum by cluster-III (4.881). The highest cluster mean for leaf area was exhibited by cluster-VI (733.000), cluster-V (559.000), cluster-IV (526.000), cluster-VII (463.000), cluster-I (457.000), cluster-VIII (455.000), cluster-XI (379.000), cluster-IX (357.000), cluster-III (333.000), cluster-X (315.000) whereas lowest cluster mean for leaf area was exhibited by cluster-II (308.000).

The maximum cluster mean for flag leaf length was observed in cluster-III (51.990) followed by cluster-V (47.970), cluster-II (46.970), cluster-IV (44.890), cluster-VIII (44.030), cluster-I (43.780), cluster-VI (43.180), cluster-VII (43.110), cluster-IX (38.220), cluster-XI (38.030) whereas minimum by cluster-X (36.740). The highest cluster mean for flag leaf width was exhibited by cluster-VI (9.000), cluster-V (5.000), cluster-IV (5.000), cluster-VII (4.000), cluster-I (4.000), cluster-XI (4.000), cluster-VIII (4.000), cluster-IX (4.000), cluster-X (4.000), cluster-III (3.000) whereas lowest cluster mean for flag leaf width was exhibited by cluster-II (3.000).

The maximum cluster mean for stem girth was observed in cluster-VII (2.821) followed by cluster-VIII (2.739), cluster-V (2.667), cluster-XI (2.656), cluster-I (2.525), cluster-IV (2.403), cluster-VI (2.323), cluster-IX (2.247), cluster-X (2.220), cluster-II (2.105) whereas minimum by cluster-III (2.082). The highest cluster mean for inter-nodal length was exhibited by cluster-VI (36.300), cluster-IX (32.100), cluster-VIII (30.700), cluster-X (30.300), cluster-IV (30.300), cluster-I (29.600), cluster-XI (29.400), cluster-II (27.600), cluster-V (27.500), cluster-VII (25.600) whereas lowest cluster mean for intermodal length was exhibited by cluster-III (20.100).

The maximum cluster mean for panicle length was observed in cluster-III (38.000) followed by cluster-VIII (30.000), cluster-II (27.000), cluster-I (26.000), cluster-V (25.000), cluster-IX (24.000), cluster-IV (22.000), cluster-VI (21.000), cluster-VII (20.000), cluster-X (17.000) whereas minimum by cluster-XI (13.000). The highest cluster mean for panicle width was exhibited by cluster-III (21.000), cluster-II (16.000), cluster-VIII (16.000), cluster-I (13.000), cluster-IX (13.000), cluster-VI (12.000), cluster-V (11.000), cluster-VII (11.000), cluster-IV (11.000), cluster-X (7.000) whereas lowest cluster mean for panicle width was exhibited by cluster-XI (6.000).

The maximum cluster mean for leaf:stem ratio was observed in cluster-VI (0.448) followed by cluster-X (0.369), cluster-IV (0.352), cluster-IX (0.351), cluster-VIII (0.337), cluster-XI (0.337), cluster-I (0.332), cluster-VII (0.330), cluster-II (0.329), cluster-III (0.325) whereas minimum by cluster-V (0.324). The highest cluster mean for 1000-grains weight was exhibited by cluster-VI (39.700), cluster-V (28.300), cluster-VII (26.500), cluster-IV (23.600), cluster-I (23.400), cluster-IX (21.900), cluster-VIII (21.200), cluster-XI (20.700), cluster-X (15.600), cluster-III (13.700) whereas lowest cluster mean for 1000-grains weight was exhibited by cluster-II (11.300).

The maximum cluster mean for grain yield per plant was observed in cluster-V (111.2) followed by cluster-VI (103.900), cluster-VII (103.500), cluster-IV (91.530), cluster-I (91.250), cluster-IX (85.400), cluster-VIII (83.290), cluster-XI (79.550), cluster-X (60.500), cluster-III (49.770) whereas minimum by cluster-II (43.250). The highest cluster mean for green fodder yield per plant was exhibited by cluster-III (917.717), cluster-VI (447.300), cluster-II (385.700), cluster-V (367.000), cluster-VIII (334.900), cluster-IV (331.400), cluster-VII (326.100), cluster-I (320.300), cluster-XI (301.900), cluster-IX (296.700) whereas lowest cluster mean for green fodder yield per plant was exhibited by cluster-X (241.800).

The maximum cluster mean for dry fodder yield was observed in cluster-III (472.000) followed by cluster-VI (183.000), cluster-II (144.000), cluster-V (133.000), cluster-VIII (119.000), cluster-VII (118.000), cluster-I (117.000), cluster-IV (117.000), cluster-XI (110.000), cluster-IX (107.000) whereas minimum by cluster-X (94.800). The highest cluster mean for dry matter percent was exhibited by cluster-VI (42.950), cluster-X (39.140), cluster-V (38.890), cluster-I (38.680), cluster-XI (38.460), cluster-II (38.380), cluster-VII (37.790), cluster-VIII (37.570), cluster-IX (37.000), cluster-IV (35.910) whereas lowest cluster mean for dry matter percent was exhibited by cluster-III (25.360).

The maximum cluster mean for total soluble solids was observed in cluster-VI (13.000) followed by cluster-IV (12.000), cluster-X (9.000), cluster-IX (9.000), cluster-III (7.000), cluster-V (7.000), cluster-I (7.000), cluster-II (6.000), cluster-VII (6.000), cluster-VIII (6.000) whereas minimum by cluster-XI (5.000). The highest cluster mean for hydrocyanic acid content was exhibited by cluster-III (112.850), cluster-X (101.110), cluster-XI (95.928), cluster-VIII (92.714), cluster-I (91.898), cluster-VII (91.683), cluster-IV (91.101), cluster-II (88.498), cluster-V (87.628), cluster-IX (85.540) whereas lowest cluster mean for hydrocyanic acid content was exhibited by cluster-VI (73.570).

The maximum cluster mean for protein percent was observed in cluster-III (16.400) followed by cluster-II (12.800), cluster-IV (12.400), cluster-I (12.200), cluster-VIII (12.000), cluster-VII (11.900), cluster-IX (11.400), cluster-V (11.400), cluster-XI (11.100), cluster-X (10.000) whereas minimum by cluster-VI (7.250). The highest cluster mean for in-vivo dry matter digestibility was exhibited by cluster-VI (59.000), cluster-X (58.000), cluster-V (58.000), cluster-I (58.000), cluster-II (57.000), cluster-III (57.000), cluster-VIII (57.000), cluster-VII (56.000), cluster-IX (56.000), cluster-XI (56.000) whereas lowest cluster mean for in-vivo dry matter digestibility was exhibited by cluster-IV (54.000).

The maximum cluster mean for neutral detergent fiber was observed in cluster-III (60.000) followed by cluster-VIII (57.000), cluster-IX (57.000), cluster-VII (57.000), cluster-XI (56.000), cluster-V (56.000), cluster-IV (56.000), cluster-II (56.000), cluster-X (56.000), cluster-I (54.000) whereas minimum by cluster-VI (52.000). The highest cluster mean for acid detergent fiber was exhibited by cluster-I (39.730), cluster-VI (37.690), cluster-II (37.590), cluster-X (36.500), cluster-IV (36.500), cluster-V (36.280), cluster-VIII (35.660), cluster-XI (35.480), cluster-VII (35.350), cluster-IX (35.090) whereas lowest cluster mean for acid detergent fiber was exhibited by cluster-III (32.780).

The maximum cluster mean for cellulose content was observed in cluster-I (31.300) followed by cluster-II (30.400), cluster-IV (30.100), cluster-IX (29.700), cluster-VIII (29.700), cluster-V (29.700), cluster-XI (29.400), cluster-IX (29.300), cluster-VII (29.300), cluster-VI (28.400) whereas minimum by cluster-III (28.100). The highest cluster mean for lignin content was exhibited by cluster-I (7.204), cluster-X (6.484), cluster-II (6.000), cluster-IV (5.810), cluster-IX (5.498), cluster-V (5.474), cluster-XI (5.429), cluster-VII (5.370), cluster-III (5.206), cluster-VIII (5.171) whereas lowest cluster mean for lignin content was exhibited by cluster-VI (5.063).

The maximum cluster mean for silica content was observed in cluster-I (2.615) followed by cluster-IV (2.321), cluster-V (2.307), cluster-X (2.183), cluster-II (2.180), cluster-VI (2.156), cluster-XI (2.060), cluster-VIII (2.048), cluster-VII (1.968), cluster-IX (1.817) whereas minimum by cluster-III (1.303). The highest cluster mean for hemicelluloses content was exhibited by cluster-III (30.100), cluster-IX (25.400), cluster-VI (25.100), cluster-VII (24.700), cluster-VIII (24.600), cluster-XI (24.000), cluster-V (23.200), cluster-IV (22.600), cluster-II (22.000), cluster-X (21.900) whereas lowest cluster mean for hemicelluloses content was exhibited by cluster-I (17.800).

The maximum cluster mean for anthracnose was observed in cluster-XI (65.56) followed by cluster-III (27.910), cluster-VII (27.250), cluster-I (24.060), cluster-VIII (21.870), cluster-IX (20.300), cluster-V (17.430), cluster-IV (15.140), cluster-II (15.020), cluster-X (14.680) whereas minimum by cluster-VI (8.406). The highest cluster mean for zonate leaf spot was exhibited by cluster-IV (11.000), cluster-V (11.000), cluster-IX (10.000), cluster-XI (8.000), cluster-VI (8.000), cluster-VII (8.000), cluster-VIII (7.000), cluster-I (7.000), cluster-II (4.000), cluster-X (10.300) whereas lowest cluster mean for zonate leaf spot was exhibited by cluster-III (2.000). The maximum cluster mean for shoot fly incidence was observed in cluster-XI (36.169) followed by cluster-VII (35.928), cluster-IV (23.360), cluster-I (21.052), cluster-V (18.010), cluster-VI (17.823), cluster-X (17.543), cluster-IX (16.746), cluster-VIII (15.240), cluster-II (11.199) whereas minimum by cluster-III (5.656).

Classification of the germplasm in to divergent groups based on inter cluster distances, per se performance and selection of parents from diverse clusters was reported in several studies [(**Damor *et al*., 2017), (Ahalawat *et al*., 2018) and (Rohila *et al*., 2022)].** Crosses suggesting parents belonging to most divergent clusters would be expected to manifest maximum heterosis and also wide variability of genetic architecture [(**Thant *et al.*, 2020) and (Deep *et al.*, 2020).** These results of our present study areare somewhat in accordance with the findings of**, Tesfaye, 2017; Ahalawat *et al*., 2018; Rohila *et al*., 2022 and Rathod *et al.*, 2023.**

4. Summary and Conclusion:

It can be summarized and concluded from the above discussion that there is a presence of huge amount of genetic variability in the material under investigation as seven different clusters were obtained and intra cluster distance were found to be lesser than the inter cluster distances. The genotypes were grouped into XI distinct non-overlapping clusters. The cluster-VIII (50) consisted of highest number of genotypes whereas lowest numbers of genotypes were grouped into cluster-III (1). The maximum intra-cluster distance was observed in cluster-IV (54.652) suggesting highest genetic diversity among genotypes of this cluster in comparison to other clusters whereas minimum intra-cluster distance was observed in cluster-III (0.000). The clusters with high intra-cluster distances suggested that genotypes in these clusters were more genetic diverse than the genotypes in other clusters with low intra-cluster distances. Low intra-cluster distance suggested a closer relationship between these two clusters and low degree of genetic diversity among the genotypes whereas high intra cluster distance represented high amount of genetic diversity among members of same cluster. The highest inter-cluster distance was observed between clusters-III and VI (334.554) suggested distant relationship between members of these two clusters and upon crossing the members of these two clusters will give more genetic diversity in segregating generation whereas minimum inter-cluster distance was observed between clusters-VIII and IX (52.512) suggested a closer relationship between these two clusters and low degree of genetic diversity among the genotypes. Presence of substantial genetic diversity among the genotypes screened in the present study indicated that this material may serve as a good source for selecting the diverse parents for hybridization programme. In order to increase the possibility of isolating good trangressive segregants in the segregating generations it would be logical to attempt crosses between the diverse genotypes belonging to clusters separated by large inter-cluster distances.

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Table 1: Distribution of genotypes into different clusters during *Kharif* 2019.

SI. No.	Cluster	Number of genotypes	Members
1.	**Cluster-I**	**39**	E2-2, Malwan, SSG-212, HJ-513, IS-23586, HC-171, IS-3318, SSG-222, PC-23, ICSV-702, IS-12743, CSV-10, 1890 (08BZL-01-43-1), IS-20703-1, GP-2011-471, SSG-260, SSG-263, SSG-234, IS-1219, 9533-1, PC-1001, SPV-1752, UTFS-42, IS-9722, EJN-40, PC-1002, EJN-46, SSG-611, SMC-14, SEVS-2, B-437 (09B-RUS-04), IS-2363, IS-9162, IS-607, ICSV-111, SPV-1725, IS-6090, PSSV-61, UPFS-38 x UPFS-36
2.	**Cluster-II**	**14**	CO (FS)-29, IS-18850, SSG-21, IS-30117, IS-3353, E-159, IS-14357, IS-13566, IS-18927, IS-18844, IS-18933, SMC-8, SMC-13, and IS-28313
3.	**Cluster-III**	**1**	IS-14241
4.	**Cluster-IV**	**27**	SEVS-1, IS-4726-2, IS-2101, IS-25419-2, SMC-5, IS-25419-1, IS-1478, IS-23988, IS-5434-1, IS-6045, IS-14278-1, IS-6953, IS-7002, IS-21977, UTMC-523, IS-15008-1, CS-3541-1, RS-673, IS-20740, IS-20782, IS-23948-1, IS-20399, JJ-1041, Pant Chari-5, IS-21622, IS-21461, and SSG-59-3.
5.	**Cluster-V**	**35**	UTMC-531, ESRK-7, SSG-227, CSV-14, SPV-1749, UPChari-1, EJN-37, EJN-54, SMC-2, SMC-6, Nizamabad, (SDSL-92101 x IS-3359) x Pant Chari-5, UP Chari-2, UPFS-38, IS-3359, PC-121, Pant Chari-3, IS-3199, GM-1378-1, IS-29794, GGUV-55, GMC-1422, SPV-1252, SPV-1616, SPV-1750, SST-4, SPV-1753, SRF-285, R-74(09R-AGR-26), R-77 (09R-AGR-26), RAJ-21, R-72(09R-AGR-23), UPFS-39, R-73 (09-AGR-24), and R-255 (09R-SS-26)
6.	**Cluster-VI**	**3**	CSV-19, CSV-24SS, and CHS-22SS
7.	**Cluster-VII**	**36**	IS-2549-3, ICSR-93023, EJN-73, SMC-9, HC-260, GP-2011-372, E-1, ESRK-10, UPFS-35, E-25, E-105, EJN-59, ESRK-12, ESRK-16, SSG-223, 1910(08BZL-01-32-4), 1946 (08RLD-01-5-3), 1941(08RLD-01-5-3), R-72 (09R-AGR-23), EJN-58, PM-98019-2, GD-68717-1, UPFS-34, IS-14756, RAJ-16, EJN-49, EJN-68, IS-3821, HC-136, RAJ-32, EP-122, E-7, E-28, ESRK-4, EJN-39, and IS-12735
8.	**Cluster-VIII**	**50**	ART-1008, UPFS-38 x IS-7002, SSG-219, SSG-256, IS-3313, SSG-244, UPFS-37 x UPMC-6, Rajasthan Local, GGUB-25, PC-23 x (SDSL-92101 x UPFS-23), EG-11, SRF-286, SL-44, SPV-462, UPFS-40, SMC-7, EJN-51, SPV-1754, UPMC-504 x UPMC-8, UTFS-48, GP-2011-44-1, UTFS-49, SMC-11, IS-15680, UPFS-36 x Pant Chari-6, IS-3821, SMC-18, HC-171, SMC-17, SSG-245, UPMC-503 x (SDSL-92101 x UPFS-23), ESRK-29, EJN-67, SSG-221, Ramkel, MP Chari, EJN-38, SSG-236, ESRK-27, SSG-241, SSG-250, SSG-224, SSG-256, SMC-3, SSG-227, SSG-243, SSG-248, SSG-234-1, SSG-253, and SSG-226
9.	**Cluster-IX**	**46**	EJ-3, RAJ-9-1, EJ-42, C-43, RAJ-15, IS-313, Pant Chari-6, RS-29, UPFS-36(Pant Chari-7), UTMC-532, IS-3314, IS-3345, IS-3145, EA-11, IS-12956, GGUB-27, IS-699, RAJ-20, Pant Chari-5 x UPMC-512 , CSV-21F, SSV-74, SSG-304, IS-4307, SMC-12, ICSV-95119-1-2, 77113, IS-639, IS-29691, SMC-10, IS-31861, ESRK-26, IS-3359, SSG-226, SSG-225-1, UPFS-38 x SSG-59-3, SSG-225-2, IS-6193, IS-21602-1, IS-3237-2, IS-14298-1, NSSV-259, IS-14333-1, IS-18008-2, IS-22241, PSSV-49, and GMS-1338
10.	**Cluster-X**	**11**	EJ-19, EJ-26, EJ-27, EJ-40, EJ-25, IS-25733, EJ-30, IS-4925, IS-33096, CSV-17, and IS-23992
11.	**Cluster-XI**	**24**	EJ-19, EJ-15, EJ-48-1, EJN-62, IS-14816, EJN-57, EJN-56, EJN-60, EJN-63, EJN-64, GGUB-36, IS-29314, GP-2011-110-1, EJ-30, EP-135, EP-124, EJ-24, EJN-48-2, EJ-30, EJN-43, EJN-45, GP-2011-18-2, EJN-47, and EJN-52

Table 2: Intra and inter cluster distances between the clusters based on hierarchical cluster analysis of sorghum germplasm during *Kharif* 2019.

	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster-VI	Cluster-VII	Cluster-VIII	Cluster-IX	Cluster-X	Cluster-XI
Cluster-I	**50.481**	74.38	289.659	64.572	65.409	112.814	72.079	61.239	71.197	74.436	73.742
Cluster-II		**46.316**	218.755	84.875	86.633	161.43	78.683	62.93	74.378	92.231	88.733
Cluster-III			**0**	280.335	267.593	334.554	260.334	245.298	270.152	321.316	291.861
Cluster-IV				**54.652**	61.562	95.978	66.407	58.536	63.058	73.702	71.454
Cluster-V					**50.732**	88.182	62.632	53.071	69.247	91.74	74.418
Cluster-VI						**30.336**	110.712	108.318	116.215	137.992	125.337
Cluster-VII							**52.193**	54.901	66.597	90.572	64.078
Cluster-VIII								**38.591**	52.512	76.258	62.178
Cluster-IX									**49.583**	62.109	61.224
Cluster-X										**40.065**	64.481
Cluster-XI											**46.631**

Table 3: Cluster means for different characters in sorghum germplasm during *Kharif* 2019.

	DF	DM	NL	NN	PH	LL	LW	LA	FLL	FLW	SG
Cluster-I	66.048	128.692	16.403	15.098	358.247	85.372	8.487	457.166	43.775	4.28	2.525
Cluster-II	78.411	140.5	18.769	17.365	414.266	92.62	5.478	307.823	46.972	2.736	2.105
Cluster-III	85.125	147	20.208	18.639	368.139	99.731	4.881	333.283	51.994	2.916	2.082
Cluster-IV	67.245	129.13	15.381	14.101	349.978	88.015	9.255	526.387	44.893	4.712	2.403
Cluster-V	60.882	123.414	17.824	16.557	361.825	93.394	9.721	559.292	47.971	4.808	2.667
Cluster-VI	63.208	132.667	17.524	17.615	291.009	84.295	11.298	733.08	43.184	8.776	2.323
Cluster-VII	76.903	141.611	17.791	16.263	385.223	84.312	8.669	462.588	43.108	4.358	2.821

Cluster-VIII	63.325	128.64	17.603	15.823	405.176	86.04	8.372	455.307	44.034	4.07	2.739
Cluster-IX	63.19	125.174	16.043	14.886	347.396	75.62	7.494	357.163	38.217	3.793	2.247
Cluster-X	55.034	120.909	11.249	10.859	298.178	72.168	7.005	315.142	36.735	3.657	2.22
Cluster-XI	61.5	126.333	15.958	14.203	340.13	73.791	7.96	379.005	38.03	4.077	2.656

DF= Days to 50% flowering, DM= Days to maturity, NL= Number of leaves per plant, NN= Number of nodes, PH= Plant height (cm), LL= Leaf length (cm), LW= Leaf width (cm), LA= Leaf area (cm^2), FLL= Flag leaf length (cm), FLW= Flag leaf width (cm), SG= Stem girth (cm).

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	INL	**PL**	**PW**	**L:S**	**TGW**	**GYP**	**GFY**	**DFY**	**DM%**	**TSS%**	**HCN**
Cluster-I	29.581	25.906	13.021	0.332	23.401	91.245	320.271	116.739	38.683	6.721	91.898
Cluster-II	27.588	26.765	16.242	0.329	11.329	43.226	385.67	143.558	38.382	6.316	88.498
Cluster-III	20.064	37.761	21.026	0.325	13.674	49.769	917.729	472.253	35.359	7.129	112.846
Cluster-IV	30.309	21.904	10.593	0.352	23.57	91.528	331.357	116.663	35.908	12.027	91.101
Cluster-V	27.477	25.156	11.383	0.324	28.323	111.204	367.003	133.47	38.888	6.976	87.628
Cluster-VI	36.314	20.648	11.91	0.448	39.71	103.899	447.29	183.378	42.945	12.969	73.57
Cluster-VII	25.632	19.782	11.05	0.33	26.537	103.512	326.097	118.397	37.792	5.987	91.683
Cluster-VIII	30.675	29.685	15.984	0.337	21.235	83.287	334.915	118.615	37.568	5.75	92.714
Cluster-IX	32.079	24.37	12.701	0.351	21.928	85.401	296.728	106.556	37.002	9.05	85.54
Cluster-X	30.349	16.725	6.892	0.369	15.568	60.496	241.79	94.781	39.143	9.472	101.112
Cluster-XI	29.364	13.242	6.333	0.337	20.727	79.548	301.921	109.743	38.462	4.828	95.928

INL= Internodal length (cm), PL= Panicle length (cm), PW= Panicle width (cm), L:S= Leaf:stem ratio, TGW= 1000-grains weight (gm), GYP= Grain yield per plant (gm), GFY= Green fodder yield per plant (gm), DFY= Dry fodder yield per plant (gm), DM= Dry matter (%), TSS= Total soluble solids (%), HCN= HCN content (ppm)

Continued……..

	PP	**IVDMD**	**NDF**	**ADF**	**C**	**L**	**S**	**HC**	**A**	**ZLS**	**SFI**
Cluster-I	12.242	57.576	54.478	39.727	31.317	7.204	2.615	17.803	24.064	6.709	21.052
Cluster-II	12.822	57.23	55.734	37.593	30.431	6	2.18	21.956	15.021	4.438	11.199

Cluster-III	16.427	57.015	60	32.784	28.136	5.206	1.303	30.146	27.906	1.808	5.656
Cluster-IV	12.394	54.119	56.004	36.497	30.072	5.81	2.321	22.56	15.143	11.125	23.36
Cluster-V	11.43	58.368	56.182	36.281	29.666	5.474	2.307	23.229	17.426	10.832	18.011
Cluster-VI	7.254	59.075	52.047	37.687	28.43	5.063	2.156	25.106	8.406	7.995	17.823
Cluster-VII	11.876	56.421	57.051	35.348	29.288	5.37	1.968	24.729	27.245	7.599	35.928
Cluster-VIII	12.03	56.78	57.384	35.659	29.68	5.171	2.048	24.604	21.87	7.464	15.24
Cluster-IX	11.438	56.293	57.157	35.087	29.311	5.498	1.817	25.386	20.303	10.145	16.746
Cluster-X	10.037	58.377	55.57	36.502	29.74	6.484	2.183	21.935	14.679	3.376	17.543
Cluster-XI	11.113	56.212	56.398	35.482	29.381	5.429	2.06	23.98	65.556	8.294	36.169

PP= Protein content (%)**,** IVDMD= Iin-vitro dry matter disappearance (IVDMD)**,** NDF= Neutral detergent fiber**,** ADF= Acid detergent fiber (%), C= Cellulose (%)**,** L= Lignin (%), S= Silica (%), HC= Hemicellulose, A= Anthracnose (%), ZLS= Zonate Leaf Spot, SFI= Shoot Fly Index (%)