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Study of genetic divergence for forage yield and biochemical traits in sorghum [*Sorghum bicolor* L. Moench] germplasm

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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 2018 and 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 biochemical 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 highest number of genotypes was grouped into cluster-VIII (75) whereas cluster-XI exhibited only single genotype. The maximum intra-cluster distance was exhibited by cluster-II (58.202) whereas minimum intra-cluster distance was exhibited by cluster-XI (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. The highest inter-cluster distance was observed between clusters-V and XI (341.437) 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 the lowest inter-cluster distance was observed between clusters-VIII and IX (53.27) 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

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) [32]. 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) [5].
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.

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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) [3]. Genetic improvement of yield especially in self-pollinated crops depends on nature and amount of genetic diversity (Joshi and Dhawan, 1966) [16].

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) [26]. 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) [24].

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) [14]. It aids plant breeders to characterize and classify accessions into heterotic groups (Menz et al., 2004) [20]. 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) [25]. 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) [17]. The higher genetic diversity between parents, the higher heterosis in progeny can be observed (Joshi and Dhawan, 1966) [16]. 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.

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*, 2018 and 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. The experiment was carried out in an Augmented Block Design (Federer, 1956,

1961, and Federer & Raghavrao, 1975) [10, 11] with each block containing 35 test entries and 6 checks which were randomly allocated in 8 blocks. All genotypes were sown during *Kharif* 2018 and *Kharif* 2019 on 23rd July 2018 and 27th July 2019 respectively 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) [30], shoot fly (*Atherigona soccata*) incidence (Dead hearts %), dry matter (%), brix %, HCN content (ppm) (Hogg and Ahlagreen, 1942) [13] and Gilchrist *et al*. (1967) [12], protein content (%) (Jeckson, 1973) [15], in-vitro dry matter disappearance (IVDMD) % (Erwin and Ellinston, 1959) [7], neutral detergent fiber (Van Soest, 1991) [33], acid detergent fiber (%) and cellulose (%) (Van Soest, 1991) [33], acid detergent lignin (%), cellulose (%) and silica (%) (Van Soest, 1991) [33]. The data obtained from both years was pooled for diversity analysis. 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:

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

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) [2]. The statistical analysis was performed by Indostat Hyderabad.

Results 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) [22]. 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. 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) [27]. The genotypes were grouped into XI distinct non-overlapping clusters. The highest number of genotypes were grouped into cluster-VIII (75) followed by cluster-II (39), cluster-IV (35), cluster-VII (35), cluster-III (26), cluster-I (21), cluster-IX (20), cluster-VI (16), cluster-X (15), cluster-V (3) whereas cluster-XI exhibited only single genotype.

Cluster-I: This cluster consisted of twenty one genotypes *viz.*, E2-2, Malwan, IS-3318, SSG-222, PC-23, IS-23586, EJ-25, IS-25733, SSG-225, SSG-212, HJ-513, IS-20703-1, GP-2011-471, SPV-1752, GP-2011-44-1, IS-1219, SSG-260, SSG-263, SSG-234, SSG-611 and SMC-14. This cluster mean had high cluster mean for panicle length, panicle width, hydrocyanic acid content, cellulose content, lignin content and silica content.

Cluster-II: This cluster had thirty nine genotypes *viz.*, SEVS-1, IS-4726-2, IS-21021, IS-1478, IS-23988, IS-25419-2, SMC-5, IS-25419-1, 1910(08-BZL-01-32-4), 1946(08-RLD-01-7-2), 1941(08-RLD-01-32-4), R-72 (09R-AGR-23), IS-5434-1, IS-6045, IS-7002, IS-14278-1, IS-6953, JJ-1041, CS-3541-1, IS-21622, IS-15008-1, SEVS-2, B-437(09B-RUS04), IS-2363, IS-21461, Pant Chari-5, HC-171, SMC-2, Nizamabad, EJN-37, EJN-54, SMC-6, (SDSL-92101 x IS-3359) x Pant Chari-5, UTMC-531,ESRK-7, SSG-227, CSV-14, IS-3237-2 and EG-11. This cluster had high cluster mean for leaf area, leaf: stem ratio, total soluble solids, silica content, zonate leaf spot.

Cluster-III: This cluster was marked with twenty six genotypes *viz.*, IS-9162, IS-607, ICSV-111, SPV-1725, IS-6090, 9533-1, PC-1001, IS-9722, EJN-40, UTFS-42, PC-1002, EJN-46, UTMC-523, CSV-10, 1890(08-BZL-01-14-1), EJN-58, PSSV-61, UPFS-38 x UPFS-36, SPV-1749, RS-673, RAJ-32, EP-122, E-7, E-28, ESRK-4 and EJN-39. This cluster mean had high cluster mean for leaf width, flag leaf width, stem girth, 1000-grains weight, grain yield per plant, protein percent, in-vitro dry matter disappearance, acid detergent fiber, cellulose content, silica content, anthracnose, zonate leaf spot and shoot fly incidence.

Cluster-IV: This cluster exhibited thirty five genotypes *viz.*, IS-20740, SPV-1750, SPV-1616, IS-20782, IS-23948-1, GMS-1422, SPV-1252, IS-29794, GGUB-55, UP Chari-1, SSG-59-3, SRF-286, SL-44, SPV-1754, PC-121, SPV-462,

UPFS-40, SMC-7, EJN-51, GP-2011-18-2, EJN-43, SST-4, SPV-1753, SRF-285, R-74(09R-AGR-26), R-77(09R-AGR-26), UPFS-39, RAJ-21, R-72(09-AGR-23), R-73(09R-AGR-24), R-255(09R-SS-26), UP Chari-2, UPFS-38, IS-3359 and Pant Chari-3. This cluster mean had high cluster mean for leaf width, leaf area, flag leaf length, flag leaf width, stem girth, 1000-grains weight, grain yield per plant, hydrocyanic acid content., in-vitro dry matter disappearance and neutral detergent fiber,.

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

Cluster-VI: This cluster was marked with sixteen genotypes *viz.*, EJ-3, RAJ-9-1, EJ-42, C-43, RAJ-15, IS-313, Pant Chari-6, EJ-19, EJ-26, EJ-27, EJ-40, IS-23992, EJ-30, IS-4925 and IS-33096. This cluster had high cluster mean for inter-nodal length, leaf: stem ratio, dry matter percent and total soluble solids.

Cluster-VII: This cluster had thirty five genotypes *viz.*, IS-21577, EJN-45, GGUB-27, EJN-47, EJN-52, GP-2011-372, EJ-30, EJ-24, EJN-48-1, EJN-63, EJN-64, E-25, EJN-59, E-105, GGUB-36, EJN-56, IS-699, IS-12956, EJ-19, EJ-15, EJN-48-2, EJN-62, EJN-57, EJN-60, IS-14816, EJ-30, EP-135, EP-124, ICSV-702, IS-12743, GP-2011-110-1, IS-29314, E-1, ESRK-10 and HC-260. This cluster mean had high cluster mean for stem girth, hydrocyanic acid content and zonate leaf spot.

Cluster-VIII: This cluster consisted of seventy five genotypes *viz.*,RAJ-20, Pant Chari-5 x UPMC-512, SSV-74, SSG-304, IS-4307, SMC-12, IS-29691, IS-31861, SSG-225, SMC-10, ESRK-26, IS-3359, ICSV-95119-1-2, 77113, IS-639, IS-3199, GM-1378-1, IS-6193, IS-21602-1, IS-22241, PSSV-49, GMS-1338, IS-14298-1, NSSV-259, IS-14333-1, IS-18008-2, UTMC-532, IS-3314, IS-3345, IS-3145, EA-11, SSG-221, Ramkel, MP Chari, EJN-38, ART-1008, UPFS-38 x IS-7002, SSG-219, SSG-256-1, UPFS-38 x SSG-59-3, IS-3313, PC-23 x (SDSL-92101 x UPFS-23), IS-20399, SSG-244, UPFS-37 x UPMC-6, Rajasthan Local, GGUB-25, UTFS-49, SMC-11, HC-171, IS-15680, UPFS-36 x Pant Chari-6, IS-3821, SMC-18, SSG-236, ESRK-27, SSG-241, SSG-250, SSG-245, UPMC-503 x (SDSL-92101 x UPFS-23), ESRK-29, EJN-67, UPMC-504 x UPMC-8, SMC-17, UTFS-48, SSG-224, SSG-226-1, SSG-256-2, SMC-3, SSG-227, SSG-226-2, SSG-253, SSG-243, SSG-248 and SSG-234-1. This cluster mean had high cluster mean for plant height, internodal length, panicle length and zonate leaf spot.

Cluster-IX: This cluster had twenty genotypes *viz.*,IS-2549-3, ICSR-93023, EJN-73, SMC-9, RS-29, UPFS-35, UPFS-36(Pant Chari-7), ESRK-12, ESRK-16, SSG-223, PM-98019-2, GD-68718-1, UPFS-34, IS-14756, HC-136, CSV-21F, RAJ-16, EJN-49, EJN-68 and IS-3821. This cluster mean had high cluster mean for days to flowering, days to maturity, number of leaves, grain yield per plant, neutral

detergent fiber, hemicelluloses content and shoot fly incidence.

Cluster-X: This cluster was marked with fifteen genotypes *viz.*, CO (FS)-29, IS-18850, SSG-21, IS-30117, IS-3353, E-159, IS-14357, IS-12735, IS-13566, IS-18927, IS-18844, IS-18933, SMC-8, SMC-13 and IS-28313. This cluster mean had high cluster mean for days to flowering, days to maturity, number of leaves, number of nodes, leaf length, flag leaf length, green fodder yield per plant, dry fodder yield per plant, protein percent and lignin content.

Cluster-XI: This cluster had only single genotype IS-14241. This cluster mean had highest cluster mean for days to flowering, days to maturity, number of leaves, number of nodes and leaf length.

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) [19].

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) [18]. 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**.**

Intra-cluster distance: The maximum intra-cluster distance was exhibited by cluster-II (58.202) followed by cluster-III (54.572), cluster-VII (49.145), cluster-X (48.898), cluster-VI (47.994), cluster-IX (45.248), cluster-I (44.766), cluster-IV (43.784), cluster-VIII (43.133), cluster-V (32.891) whereas minimum intra-cluster distance was exhibited by cluster-XI (0.000).

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-V and XI (341.437) 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-VI and XI (307.299), clusters-III and XI (299.023), clusters-I and XI (297.763), clusters-VII and XI (285.332), clusters-II and XI (274.878), clusters-IV and XI (262.448), clusters-VIII and XI (257.255), clusters-IX and XI (253.061), clusters-X and XI (222.757), clusters-V and X (167.507), clusters-I and V (132.1256), clusters-V and VI (132.038), clusters-V and VII (131.258), clusters-V and VIII (119.958), clusters-V and IX (109.524), clusters-III and V (109.5), clusters-II and V (103.667), clusters-IV and V (93.48), clusters-VI and X (91.111), clusters-III and X (89.107), clusters-III and VI

(87.636), clusters-IV and X (85.208), clusters-VII and X (84.015), clusters-II and VI (82.463), clusters-IV and VI (79.67), clusters-I and IX (79.647), clusters-II and X (79.103), clusters-VI and IX (78.084), clusters-IX and X (77.787), clusters-I and VI (75.161), clusters-III and IX (74.579), clusters-II and VII (72.74), clusters-I and VII (70.804), clusters-III and VIII (70.665), clusters-III and VII (70.541), clusters-I and IV (69.915), clusters-I and X (67.73), clusters-IV and VII (67.564), clusters-II and IX (66.38), clusters-I and II (66.28), clusters-II and III (66.07), clusters-VIII and X (64.412), clusters-VI and VIII (64.156), clusters-I and III (63.284), clusters-III and IV (62.945), clusters-VI and VII (62.906), clusters-VII and IX (62.01), clusters-II and VIII (61.21), clusters-VII and VIII (60.408), clusters-II and IV (59.712), clusters-I and VIII (58.578), clusters-IV and IX (56.649), clusters-IV and VIII (55.105) whereas the lowest inter-cluster distance was observed between clusters-VIII and IX (53.27) 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.

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 highest cluster mean for days to flowering was exhibited by cluster-XI (83.600), cluster-X (77.600), cluster-IX (73.100), cluster-II (69.900), cluster-III (67.000), cluster-VII (63.700), cluster-V (62.900), cluster-VIII (62.000), cluster-I (61.400), cluster-VI (59.000) whereas lowest cluster mean for days to flowering was exhibited by cluster-IV (57.700). The maximum cluster mean for days to maturity was observed in cluster-XI (145.000) followed by cluster-X (140.000), cluster-IX (137.000), cluster-II (133.000), cluster-V (132.000), cluster-III (130.000), cluster-VII (129.000), cluster-I (126.000), cluster-VIII (126.000), cluster-VI (125.000) whereas minimum by cluster-IV (120.000).

The highest cluster mean for number of leaves was exhibited by cluster-XI (20.000), cluster-X (18.000), cluster-IX (17.000), cluster-V (17.000), cluster-IV (16.000), cluster-VIII (16.000), cluster-II (16.000), cluster-III (16.000), cluster-I (16.000), cluster-VII (16.000) whereas lowest cluster mean for number of leaves was exhibited by cluster-VI (12.000). The maximum cluster mean for number of nodes was observed in cluster-XI (18.100) followed by cluster-V (17.400), cluster-X (16.500), cluster-IX (16.100), cluster-IV (15.100), cluster-II (14.900), cluster-VIII (14.800), cluster-III (14.300), cluster-I (14.300), cluster-VII (14.100) whereas minimum by cluster-VI (11.800).

The highest cluster mean for plant height was exhibited by cluster-X (409.000), cluster-IX (393.000), cluster-VIII (390.000), cluster-I (378.000), cluster-XI (366.000), cluster-II (362.000), cluster-III (350.000), cluster-IV (350.000),

cluster-VII (333.000), cluster-VI (291.000) whereas lowest cluster mean for plant height was exhibited by cluster-V (290.000). The maximum cluster mean for leaf length was observed in cluster-XI (98.430) followed by cluster-X (92.540), cluster-IV (92.260), cluster-II (90.180), cluster-III (83.960), cluster-V (83.760), cluster-I (82.720), cluster-IX (81.010), cluster-VIII (80.630), cluster-VII (72.870) whereas minimum by cluster-VI (69.250).

The highest cluster mean for leaf width was exhibited by cluster-V (11.200), cluster-IV (9.160), cluster-III (8.890), cluster-II (8.780), cluster-IX (7.970), cluster-VII (7.490), cluster-VIII (7.290), cluster-I (7.220), cluster-VI (7.160), cluster-X (5.080) whereas lowest cluster mean for leaf width was exhibited by cluster-XI (4.590). The maximum cluster mean for leaf area was observed in cluster-V (732.000) followed by cluster-IV (549.000), cluster-II (531.000), cluster-III (501.000), cluster-IX (436.000), cluster-VIII (398.000), cluster-I (397.000), cluster-VII (368.000), cluster-VI (331.000), cluster-XI (327.000) whereas minimum by cluster-X (304.000).

The highest cluster mean for flag leaf length was exhibited by cluster-XI (51.100), cluster-IV (46.800), cluster-X (46.500), cluster-II (45.400), cluster-III (42.900), cluster-V (42.700), cluster-I (41.500), cluster-IX (40.900), cluster-VIII (40.700), cluster-VII (36.900) whereas lowest cluster mean for flag leaf length was exhibited by cluster-VI (34.600). The maximum cluster mean for flag leaf width was observed in cluster-V (9.000) followed by cluster-III (5.000), cluster-IV (5.000), cluster-II (4.000), cluster-IX (4.000), cluster-VII (4.000), cluster-VI (4.000), cluster-VIII (4.000), cluster-I (4.000), cluster-XI (3.000) whereas minimum by cluster-X (2.000).

The highest cluster mean for stem girth was exhibited by cluster-IX (2.658), cluster-III (26.636), cluster-IV (2.595), cluster-VII (2.539), cluster-II (2.471), cluster-I (2.465), cluster-VIII (2.438), cluster-V (2.303), cluster-VI (2.217), cluster-X (2.020) whereas lowest cluster mean for stem girth was exhibited by cluster-XI (2.017). The maximum cluster mean for inter-nodal length was observed in cluster-V (36.000) followed by cluster-VI (31.000), cluster-VIII (30.500), cluster-I (29.700), cluster-II (28.200), cluster-IV (27.000), cluster-IX (27.000), cluster-VII (26.900), cluster-X (26.600), cluster-III (26.300) whereas minimum by cluster-XI (19.200).

The highest cluster mean for panicle length was exhibited by cluster-XI (37.000), cluster-VIII (27.000), cluster-I (27.000), cluster-X (26.000), cluster-IV (24.000), cluster-IX (23.000), cluster-II (22.000), cluster-V (20.000), cluster-III (19.000), cluster-VI (17.000) whereas lowest cluster mean for panicle length was exhibited by cluster-VII (14.000). The maximum cluster mean for panicle width was observed in cluster-XI (20.000) followed by cluster-I (15.000), cluster-X (15.000), cluster-VIII (15.000), cluster-V (12.000), cluster-IX (11.000), cluster-II (10.000), cluster-IV (10.000), cluster-III (8.000), cluster-VI (7.000) whereas minimum by cluster-VII (7.000).

The highest cluster mean for leaf:stem ratio was exhibited by cluster-V (0.440), cluster-VI (0.38), cluster-II (0.330), cluster-I (0.320), cluster-VIII (0.310), cluster-VII (0.310), cluster-III (0.300), cluster-IX (0.300), cluster-X (0.300), cluster-XI (0.300) whereas lowest cluster mean for leaf:stem ratio was exhibited by cluster-IV (0.290). The maximum cluster mean for 1000-grains weight was observed in cluster-V (40.000) followed by cluster-III (28.000), cluster-

IV (27.000), cluster-IX (27.000), cluster-II (22.000), cluster-VIII (21.000), cluster-VII (20.000), cluster-I (20.000), cluster-VI (15.000), cluster-XI (13.000) whereas minimum by cluster-X (12.000).

The highest cluster mean for grain yield per plant was exhibited by cluster-III (108.100), cluster-IV (107.800), cluster-IX (106.400), cluster-V (103.400), cluster-II (87.890), cluster-VIII (83.240), cluster-VII (79.440), cluster-I (78.210), cluster-VI (57.600), cluster-XI (48.340) whereas lowest cluster mean for grain yield per plant was exhibited by cluster-X (47.830). The maximum cluster mean for green fodder yield per plant was observed in cluster-XI (940.000) followed by cluster-V (445.000), cluster-X (378.000), cluster-IV (366.000), cluster-II (344.000), cluster-III (336.000), cluster-IX (335.000), cluster-VIII (301.000), cluster-VII (301.000), cluster-VI (260.000) whereas minimum by cluster-I (259.000).

The highest cluster mean for dry fodder yield per plant was exhibited by cluster-XI (426.000), cluster-V (182.000), cluster-X (140.000), cluster-IV (133.000), cluster-III (122.000), cluster-II (119.000), cluster-IX (118.000), cluster-VII (111.000), cluster-VIII (107.000), cluster-VI (99.300) whereas lowest cluster mean for dry fodder yield per plant was exhibited by cluster-I (95.100). The maximum cluster mean for dry matter percent was observed in cluster-V (42.500) followed by cluster-III (38.200), cluster-VI (37.500), cluster-I (37.500), cluster-IV (37.500), cluster-X (37.100), cluster-IX (37.100), cluster-VII (36.800), cluster-VIII (36.100), cluster-II (34.600) whereas minimum by cluster-XI (34.400).

The highest cluster mean for total soluble solids was exhibited by cluster-V (13.000), cluster-II (9.000), cluster-VI (9.000), cluster-IV (8.000), cluster-IX (7.000), cluster-VIII (7.000), cluster-XI (7.000), cluster-III (6.000), cluster-X (6.000), cluster-I (5.000) whereas lowest cluster mean for total soluble solids was exhibited by cluster-VII (5.000). The maximum cluster mean for hydrocyanic content was observed in cluster-XI (110.000) followed by cluster-I (94.48), cluster-IV (93.320), cluster-VII (92.370), cluster-VIII (87.500), cluster-VI (87.230), cluster-III (87.170), cluster-X (85.470), cluster-II (84.200), cluster-IX (83.260) whereas minimum by cluster-V (72.930).

The highest cluster mean for protein content was exhibited by cluster-XI (16.200), cluster-III (12.900), cluster-X (12.400), cluster-VIII (11.800), cluster-II (11.700), cluster-I (11.100), cluster-VII (10.900), cluster-IV (10.800), cluster-IX (10.600), cluster-VI (9.640) whereas lowest cluster mean for protein content was exhibited by cluster-V (7.170). The maximum cluster mean for in-vitro dry matter disappearance per cent (IVDMD) was observed in cluster-III (59.000) followed by cluster-V (59.000), cluster-IV (58.000), cluster-VI (57.000), cluster-IX (57.000), cluster-X (56.000), cluster-XI (56.000), cluster-VIII (55.000), cluster-VII (54.000), cluster-I (54.000) whereas minimum by cluster-II (53.000).

The highest cluster mean for neutral detergent fiber was exhibited by cluster-XI (60.000), cluster-IX (57.000), cluster-IV (56.000), cluster-VIII (56.000), cluster-VI (56.000), cluster-VII (56.000), cluster-X (55.000), cluster-II (55.000), cluster-III (55.000), cluster-I (54.000) whereas lowest cluster mean for neutral detergent fiber was exhibited by cluster-V (52.000). The maximum cluster mean for acid detergent fiber was observed in cluster-III (38.800) followed by cluster-I (38.600), cluster-V (37.500), cluster-X (36.800),

cluster-II (36.300), cluster-IV (35.100), cluster-VII (35.000), cluster-VIII (34.700), cluster-VI (34.400), cluster-IX(33.200) whereas minimum by cluster-XI (32.300).

The highest cluster mean for cellulose content was exhibited by cluster-III (31.000), cluster-I (30.000), cluster-X (30.000), cluster-II (30.000), cluster-IV (29.000), cluster-VIII (29.000), cluster-VII (29.000), cluster-VI (29.000), cluster-V (28.000), cluster-IX (28.000) whereas lowest cluster mean for cellulose content was exhibited by cluster-XI (28.000). The maximum cluster mean for lignin content was observed in cluster-I (6.890) followed by cluster-III (6.275), cluster-X (5.684), cluster-II (5.585), cluster-VI (5.566), cluster-VII (5.389), cluster-IV (5.056), cluster-VIII (5.011), cluster-V (5.005), cluster-XI (4.931) whereas minimum by cluster-IX (4.917).

The highest cluster mean for silica content was exhibited by cluster-I (2.640), cluster-II (2.420), cluster-III (2.370), cluster-V (2.130), cluster-X (2.070), cluster-IV (2.040), cluster-VII (2.010), cluster-VIII (1.920), cluster-VI (1.860), cluster-IX (1.710) whereas lowest cluster mean for silica content was exhibited by cluster-XI (1.230). The maximum cluster mean for hemicelluloses content was observed in cluster-XI (29.300) followed by cluster-IX (26.500), cluster-V (24.800), cluster-VIII (23.600), cluster-IV (23.600), cluster-VII (23.500), cluster-VII (23.100), cluster-X (21.200), cluster-II (29.900), cluster-III (17.900) whereas minimum by cluster-I (16.700).

The highest cluster mean for anthracnose was exhibited by cluster-VII (53.700), cluster-III (29.500), cluster-XI (27.700), cluster-I (24.800), cluster-IV (22.500), cluster-IX (20.000), cluster-VI (18.400), cluster-VIII (18.400), cluster-X (15.300), cluster-II (13.300) whereas lowest cluster mean for anthracnose was exhibited by cluster-V (8.160). The maximum cluster mean for zonate leaf spot was observed in cluster-II (12.000) followed by cluster-III (9.000), cluster-IV (8.000), cluster-VII (8.000), cluster-V (8.000), cluster-I (7.000), cluster-IV (7.000), cluster-IX (7.000), cluster-VI (5.000), cluster-X (4.000) whereas minimum by cluster-XI (2.000).

The highest cluster mean for shoot fly incidence was exhibited by cluster-VII (38.620), cluster-IX (32.350), cluster-III (30.380), cluster-II (21.070), cluster-V (17.570), cluster-IV (17.450), cluster-VI (16.780), cluster-VIII (14.260), cluster-I (10.710), cluster-X (9.718) whereas lowest cluster mean for shoot fly incidence was exhibited by cluster-XI (4.906).

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) [4], (Ahalawat *et al*., 2018) [1] and (Rohila *et al*., 2022)] [24]. 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) [31] and (Deep *et al.,* 2020) [6]. 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 [28, 1, 24, 23].

Table 1: Distribution of genotypes into different clusters.

Sl. No.	Cluster	Number of genotypes	Members
1.	Cluster-I	21	E2-2, Malwan, IS-3318, SSG-222, PC-23, IS-23586, EJ-25, IS-25733, SSG-225, SSG-212, HJ-513, IS-20703-1, GP-2011-471, SPV-1752, GP-2011-44-1, IS-1219, SSG-260, SSG-263, SSG-234, SSG-611 and SMC-14
2.	Cluster-II	39	SEVS-1, IS-4726-2, IS-21021, IS-1478, IS-23988, IS-25419-2, SMC-5, IS-25419-1, 1910(08-BZL-01-32-4), 1946(08-RLD-01-7-2), 1941(08-RLD-01-32-4), R-72 (09R-AGR-23), IS-5434-1, IS-6045, IS-7002, IS-14278-1, IS-6953, JJ-1041, CS-3541-1, IS-21622, IS-15008-1, SEVS-2, B-437(09B-RUS04), IS-2363, IS-21461, Pant Chari-5, HC-171, SMC-2, Nizamabad, EJN-37, EJN-54, SMC-6, (SDSL-92101 x IS-3359) x Pant Chari-5, UTMC-531,ESRK-7, SSG-227, CSV-14, IS-3237-2 and EG-11
3.	Cluster-III	26	IS-9162, IS-607, ICSV-111, SPV-1725, IS-6090, 9533-1, PC-1001, IS-9722, EJN-40, UTFS-42, PC-1002, EJN-46, UTMC-523, CSV-10, 1890(08-BZL-01-14-1), EJN-58, PSSV-61, UPFS-38 x UPFS-36, SPV-1749, RS-673, RAJ-32, EP-122, E-7, E-28, ESRK-4 and EJN-39
4.	Cluster-IV	35	IS-20740, SPV-1750, SPV-1616, IS-20782, IS-23948-1, GMS-1422, SPV-1252, IS-29794, GGUB-55, UP Chari-1, SSG-59-3, SRF-286, SL-44, SPV-1754, PC-121, SPV-462, UPFS-40, SMC-7, EJN-51, GP-2011-18-2, EJN-43, SST-4, SPV-1753, SRF-285, R-74(09R-AGR-26), R-77(09R-AGR-26), UPFS-39, RAJ-21, R-72(09-AGR-23), R-73(09R-AGR-24), R-255(09R-SS-26), UP Chari-2, UPFS-38, IS-3359 and Pant Chari-3
5.	Cluster-V	3	CHS-22-SS, CSV-24-SS and CSV-19
6.	Cluster-VI	16	EJ-3, RAJ-9-1, EJ-42, C-43, RAJ-15, IS-313, Pant Chari-6, EJ-19, EJ-26, EJ-27, EJ-40, IS-23992, EJ-30, IS-4925 and IS-33096
7.	Cluster-VII	35	IS-21577, EJN-45, GGUB-27, EJN-47, EJN-52, GP-2011-372, EJ-30, EJ-24, EJN-48-1, EJN-63, EJN-64, E-25, EJN-59, E-105, GGUB-36, EJN-56, IS-699, IS-12956, EJ-19, EJ-15, EJN-48-2, EJN-62, EJN-57, EJN-60, IS-14816, EJ-30, EP-135, EP-124, ICSV-702, IS-12743, GP-2011-110-1, IS-29314, E-1, ESRK-10 and HC-260
8.	Cluster-VIII	75	RAJ-20, Pant Chari-5 x UPMC-512, SSV-74, SSG-304, IS-4307, SMC-12, IS-29691, IS-31861, SSG-225, SMC-10, ESRK-26, IS-3359, ICSV-95119-1-2, 77113, IS-639, IS-3199, GM-1378-1, IS-6193, IS-21602-1, IS-22241, PSSV-49, GMS-1338, IS-14298-1, NSSV-259, IS-14333-1, IS-18008-2, UTMC-532, IS-3314, IS-3345, IS-3145, EA-11, SSG-221, Ramkel, MP Chari, EJN-38, ART-1008, UPFS-38 x IS-7002, SSG-219, SSG-256-1, UPFS-38 x SSG-59-3, IS-3313, PC-23 x (SDSL-92101 x UPFS-23), IS-20399, SSG-244, UPFS-37 x UPMC-6, Rajasthan Local, GGUB-25, UTFS-49, SMC-11, HC-171, IS-15680, UPFS-36 x Pant Chari-6, IS-3821, SMC-18, SSG-236, ESRK-27, SSG-241, SSG-250, SSG-245, UPMC-503 x (SDSL-92101 x UPFS-23), ESRK-29, EJN-67, UPMC-504 x UPMC-8, SMC-17, UTFS-48, SSG-224, SSG-226-1, SSG-256-2, SMC-3, SSG-227, SSG-226-2, SSG-253, SSG-243, SSG-248 and SSG-234-1
9.	Cluster-IX	20	IS-2549-3, ICSR-93023, EJN-73, SMC-9, RS-29, UPFS-35, UPFS-36(Pant Chari-7), ESRK-12, ESRK-16, SSG-223, PM-98019-2, GD-68718-1, UPFS-34, IS-14756, HC-136, CSV-21F, RAJ-16, EJN-49, EJN-68 and IS-3821
10.	Cluster-X	15	CO (FS)-29, IS-18850, SSG-21, IS-30117, IS-3353, E-159, IS-14357, IS-12735, IS-13566, IS-18927, IS-18844, IS-18933, SMC-8, SMC-13 and IS-28313
11.	Cluster-XI	1	IS-14241

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

	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster-VI	Cluster-VII	Cluster-VIII	Cluster-IX	Cluster-X	Cluster-XI
Cluster-I	44.766	66.28	63.284	69.915	132.156	75.161	70.804	58.578	79.647	67.73	297.763
Cluster-II		58.202	66.07	59.712	103.667	82.463	72.74	61.21	66.38	79.103	274.878
Cluster-III			54.572	62.945	109.5	87.636	70.541	70.665	74.579	89.107	299.023
Cluster-IV				43.784	93.48	79.67	67.564	55.105	56.649	85.208	262.448
Cluster-V					32.891	132.038	131.258	119.958	109.524	167.507	341.437
Cluster-VI						47.994	62.906	64.156	78.084	91.111	307.299
Cluster-VII							49.145	60.408	62.01	84.015	285.332
Cluster-VIII								43.133	53.27	64.412	257.255
Cluster-IX									45.248	77.787	253.061
Cluster-X										48.898	222.757
Cluster-XI											0

Table 3: Cluster means for different characters in sorghum germplasm.

	DF	DM	NL	NN	PH	LL	LW	LA	FLL	FLW	SG
Cluster-I	61.387	125.905	15.691	14.276	378.333	82.717	7.221	396.662	41.465	3.503	2.465
Cluster-II	69.865	132.615	16.198	14.931	362.109	90.182	8.778	531.431	45.425	4.403	2.471
Cluster-III	66.971	129.962	15.735	14.312	349.911	83.956	8.885	500.705	42.91	4.548	2.636
Cluster-IV	57.721	119.971	16.298	15.059	349.891	92.255	9.164	548.887	46.838	4.522	2.595
Cluster-V	62.875	132.333	17.324	17.425	290.4	83.761	11.223	731.538	42.742	8.696	2.303
Cluster-VI	59.039	124.688	12.077	11.808	290.506	69.247	7.158	330.781	34.592	3.713	2.217
Cluster-VII	63.654	128.714	15.645	14.119	332.727	72.872	7.49	368.402	36.891	3.847	2.539
Cluster-VIII	62.038	125.553	16.236	14.777	389.573	80.625	7.29	397.692	40.742	3.624	2.438
Cluster-IX	73.119	137.275	17.386	16.144	393.324	81.008	7.973	435.987	40.933	4.038	2.658
Cluster-X	77.558	139.567	17.798	16.467	409.274	92.538	5.079	303.867	46.47	2.468	2.02
Cluster-XI	83.625	145	19.658	18.064	366.059	98.431	4.591	326.658	51.119	2.691	2.017

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).

	INL	PL	PW	L:S	TGW	GYP	GFY	DFY	DM%	TSS%	HCN
Cluster-I	29.672	26.968	15.219	0.322	19.671	78.211	259.028	95.13	37.489	5.479	94.48
Cluster-II	28.242	22.201	10.358	0.33	22.229	87.891	344.107	118.671	34.577	9.048	84.195
Cluster-III	26.3	19.247	8.316	0.303	27.506	108.059	336.452	122.125	38.185	5.889	87.168
Cluster-IV	27.002	23.57	10.032	0.285	27.359	107.807	365.881	133.347	37.476	7.594	93.324
Cluster-V	35.96	20.423	11.635	0.435	39.53	103.424	445.213	182.319	42.545	12.855	72.928
Cluster-VI	30.95	16.831	7.36	0.377	14.838	57.6	260.165	99.251	37.507	8.805	87.232
Cluster-VII	26.872	13.844	6.657	0.312	20.27	79.44	300.851	111.401	36.807	5.004	92.372
Cluster-VIII	30.54	27.401	14.744	0.313	20.963	83.239	301.125	107.172	36.083	6.98	87.497
Cluster-IX	26.958	23.395	11.118	0.303	27.19	106.413	335.376	118.212	37.057	7.142	83.263
Cluster-X	26.612	25.77	15.062	0.300	12.168	47.83	378.493	139.671	37.116	5.815	85.469
Cluster-XI	19.194	36.886	20.351	0.300	12.784	48.344	940.373	426.333	34.384	6.754	110.021

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)

	PP	IVDMD	NDF	ADF	C	L	S	HC	A	ZLS	SFI
Cluster-I	11.097	53.91	53.683	38.636	30.383	6.89	2.637	16.697	24.768	7.44	10.705
Cluster-II	11.698	53.172	55.045	36.328	29.649	5.585	2.415	20.892	13.275	12.093	21.07
Cluster-III	12.864	58.827	54.737	38.795	31.469	6.275	2.372	17.92	29.513	9.1	30.381
Cluster-IV	10.841	57.549	56.476	35.062	29.128	5.056	2.039	23.578	22.523	7.001	17.447
Cluster-V	7.174	58.725	51.922	37.495	28.255	5.005	2.131	24.815	8.156	7.955	17.573
Cluster-VI	9.636	57.073	56.161	34.413	28.748	5.566	1.864	23.457	18.422	4.662	16.781
Cluster-VII	10.877	54.065	55.971	34.993	28.82	5.389	2.013	23.056	53.713	8.154	38.616
Cluster-VIII	11.817	55.165	56.393	34.669	29.004	5.011	1.922	23.649	18.385	8.163	14.259
Cluster-IX	10.556	57.028	57.216	33.17	27.78	4.917	1.708	26.534	19.988	6.917	32.345
Cluster-X	12.416	56.084	55.093	36.846	29.85	5.684	2.074	21.168	15.25	4.339	9.718
Cluster-XI	16.153	55.725	59.575	32.259	27.611	4.917	1.227	29.321	27.656	1.688	4.906

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 (%)

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 eleven 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 highest number of genotypes was grouped into

cluster-VIII (75) whereas cluster-XI exhibited only single genotype. The maximum intra-cluster distance was exhibited by cluster-II (58.202) whereas minimum intra-cluster distance was exhibited by cluster-XI (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-V and XI (341.437) 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 the lowest inter-cluster distance was observed between clusters-VIII and IX (53.27) 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.

Competing interests
Authors have declared that no competing interests exist.

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