



Assessment of Genetic Divergence for Forage Yield and Biochemical Traits in Sorghum [*Sorghum Bicolor* L. Moench] Germplasm

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

Article Information

DOI: <https://doi.org/10.9734/ijpss/2024/v36i74820>

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/119526>

Original Research Article

Received: 03/05/2024
Accepted: 05/07/2024
Published: 08/07/2024

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 Kharif season 2018. 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

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Cite as: Santosh, and P. K. Pandey. 2024. "Assessment of Genetic Divergence for Forage Yield and Biochemical Traits in Sorghum [*Sorghum Bicolor* L. Moench] Germplasm". *International Journal of Plant & Soil Science* 36 (7):1055-71. <https://doi.org/10.9734/ijpss/2024/v36i74820>.

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-I (52) consisted of highest number of genotypes whereas lowest numbers of genotypes were exhibited by cluster-XI (1). The highest intra-cluster distance was exhibited by cluster-I (52.381) whereas lowest 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 genetically diverse than the genotypes in other clusters with low intra-cluster distances. The maximum inter-cluster distance was observed between clusters-IV and XI (346.854) 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 (46.803) 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 transgressive 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” [1]. “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 *amabeleor 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*” [2].

“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, [3] “Genetic improvement of yield especially in self-pollinated crops depends on nature and amount of genetic diversity” [4].

“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%)” [5]. “Beside the higher content of carbohydrates, it has iron (Fe) and vitamin B₃ 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” [6].

“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” [7]. “It aids plant breeders to characterize and classify accessions into heterotic groups” [8]. “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" [9]. "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 [10]. The higher genetic diversity between parents, the higher heterosis in progeny can be observed" [4]. 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*, 2018. 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 2018. The experiment was carried out in an Augmented Block Design [11-13] with each block containing 35 test entries and 6 checks which were randomly allocated in 8 blocks. All genotypes were sown on 23rd July 2018 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 (cm²), 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 [14] shoot fly (*Atherigona soccata*) incidence (Dead hearts %), dry matter (%), brix %, HCN content (ppm) [15] and Gilchrist et al. [16] protein content (%) [17] *in-vitro* dry matter disappearance (IVDMD) % [18] neutral detergent fiber [19] acid detergent fiber (%) and cellulose (%) [19] acid detergent lignin (%), cellulose (%) and silica (%) [19]. 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 i^{th} and k^{th} accession is:

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

Where,

D_{ik} = Euclidean distance between i^{th} and k^{th} accession

A_{ij} = performance of i^{th} accession for j^{th} character.

A_{kj} = performance of k^{th} accession for j^{th} character.

m = number of accessions (l or $k = 1, 2, \dots, m$)

n = number of characters ($j = 1, 2, \dots, n$)

When the similarity matrix is computed from distance function, the hierarchical clustering method begins by finding the link between the two closest genotypes [20]. The statistical analysis was performed by Indostat Hyderabad (Windostat Version 9.3).

3. RESULTS AND DISCUSSION

Knowledge about genetic diversity of parents in hybridization programme is essential as the crosses involving genetically diverse parents which are likely to produce not only high heterotic effects, but it also produce desirable transgressive segregants in the later segregating generations. The hierarchical 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 segregants. 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 hierarchical 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 [21]. 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 hierarchical cluster analysis has been presented in Table 1 and Fig. 1 during *Kharif* 2018. The genotypes were grouped into XI distinct non-overlapping clusters suggesting considerable amount of genetic diversity present in the experimental material. The cluster pattern of the genotypes showed non-parallelism between geographic and genetic diversity [22]. The cluster-I (52) consisted of highest number of genotypes followed by cluster-VIII (49), cluster-II (48), cluster-IX (33), cluster-VII (30), cluster-V (22), cluster-III (20), cluster-X (15), cluster-VI (13), cluster-IV (3) whereas lowest number of genotypes were exhibited by cluster-XI (1).

Cluster-I: This cluster consisted of highest number of genotypes (52) viz., E2-2, Malwan, IS-3318, SSG-222, PC-23, IS-23586, IS-12743, IS-20703-1, GP-2011-471, SSG-260, SSG-263, SSG-234, SSG-212, HJ-513, ICSV-702, ESRK-10, EJN-58, IS-21461, PC-5, HC-171, SMC-2, Nizamabad, EJN-37, EJN-54, SMC-6, SEVS-2, B-4377 (09B-RUS04), IS-607, IS-2363, IS-9162, PC-1002, ESRK-4, EJN-30N, ICSV-111, SPV-1725, IS-6090, PSSV-61, UPFS-38 x UPFS-36, UTM-523, EJN-46, CSV-10, 1890(08BZL01-14-1), 9533-1, PC-1001, IS-9722, EJN-40, UTFS-42, SPV-1752, GP-2011-44-1, IS-1219, SSG-611, and SMC-14. This cluster had high cluster mean for protein percent, stem girth, acid detergent fiber, cellulose content, lignin content and silica content.

Cluster-II: This cluster exhibited forty eight genotypes viz., IS-6193, IS-21602-1, IS-3237-2, EG-11, UTM-531, ESRK-7, SSG-227, CSV-14, SPV-1749, (SDSL-92101 x IS-3359) x PC-5, RS-673, JJ-1041, CS-3541-1, IS-21622, IS-15008-1, IS-20740, SPV-1750, SPV-1616, IS-20782, IS-23948-1, GMS-1422, SPV-1252, IS-29794,

GGUV-55, UPFS-39, RAJ-21, R-72(09R-AGR-23), R-73(09R-AGR-24), R-255(09R-SS-26), SST-4, SPV-1753, SRF-285, R-74(09R-AGR-26), R-77(09R-AGR-26), GP-2011-18-2, EJN-43, EJN-51, SRF-286, SL-44, SPV-462, PC-121, SPV-1754, UTFS-48, SMC-17, UPMC-503 x (SDSL-92101 x UPFS-23), UPMC-504 x UPMC-8, UP Chari-1, and SSG-59-3. This cluster had high cluster mean for leaf length, leaf width, leaf area, flag leaf length, flag leaf width, 1000-grains weight, grain yield per plant, total soluble solids and in-vitro dry matter disappearance.

Cluster-III: This cluster consisted of twenty genotypes viz., PM-98019-2, GD-68717-1, UPFS-34, IS-14756, RAJ-16, EJN-49, EJN-68, IS-3821, E-7, E-28, 1910(08BZL-01-32-4), 1946(08RLD-01-7-2), 1941 (08RLD-01-5-3), R-72 (09R-AGR-23), UP Chari-2, UPFS-38, IS-3359, Pant Chari-3, RAJ-32, and EP-122. This cluster had high cluster mean for days to flowering, number of leaves, number of nodes, plant height, leaf width, leaf area, flag leaf width, stem girth, 1000-grains weight, dry fodder yield per plant, dry matter percent, hydrocyanic acid content, in-vitro dry matter disappearance, neutral detergent fiber and shoot fly incidence.

Cluster-IV: This cluster had only three genotypes viz., CSH-22SS, CSH-24SS, and CSV-19. This cluster had high cluster mean for number of leaves, number of nodes, 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, silica content, hemicellulose content and zonate leaf spot.

Cluster-V: This cluster consisted of twenty two genotypes viz., EJ-3, RAJ-9-1, C-43, EJ-42, EJ-30, IS-4925, RAJ-15, IS-313, Pant Chari-6, SEVS-1, IS-4726-2, IS-21021, IS-1478, IS-23988, IS-5434-1, IS-6045, IS-14278-1, IS-6953, IS-7002, IS-25419-1, IS-25419-2, and IS-20399. This cluster had high cluster mean for inter-nodal length, leaf:stem ratio, total soluble solids and neutral detergent fiber.

Cluster-VI: This cluster exhibited thirteen genotypes viz., EJ-19, EJ-26, EJ-27, EJ-40, EJ-25, IS-25733, IS-33096, CSV-17, EJ-19, EJ-15, EJ-30, EP-135, and EP-124. This cluster had high cluster mean for leaf:stem ratio, hydrocyanic acid content, cellulose content, lignin content, silica content, anthracnose and shoot fly incidence.

Cluster-VII: This cluster was marked with thirty genotypes viz., IS-21977, EJV-45, GUV-27, EJV-47, EJV-52, EJV-48, EJV-62, IS-699, IS-12956, EJV-30, E-25, EJV-59, E-105, EJV-57, EJV-60, EJV-56, IS-14816, GP-2011-110-1, IS-29314, E-1, EJV-48, GP-2011-372, EJV-73, IS-3345, IS-23992, GMS-1338, EJV-24, EJV-63, EJV-64, and HC-136. This cluster had high cluster mean for dry matter percent.

Cluster-VIII: This cluster exhibited forty nine genotypes viz., RAJ-20, Pant Chari-5-UPMC-512, CSV-21F, IS-29691, SMC-10, IS-31861, SSV-74, SSG-304, IS-4307, SMC-12, IS-14298-1, NSSV-259, IS-14333-1, IS-18008-2, IS-22241, TSSV-49, UTM-532, IS-3314, IS-3145, EA-11, SSG-221, Ramkel, MP Chari, EJV-38, ICSV-9519-1-2, 77113, IS-639, IS-3199, GM-1378-1, ART-1008, UPFS-38 x IS-7002, SSG-219, SSG-256, IS-3313, PC-23 x (SDSL-92101 x UPFS-23), SSG-244, UPFS-37 x UPMC-6, GUV-25, Rajasthan Local, SSG-245, GUV-36, HC-260, SSG-226, SSG-225, UPFS-38 x SSG-59-3, SSG-225, ESRK-26, IS-3359, and SSG-227. This cluster had high cluster mean for internodal length and panicle length.

Cluster-IX: This cluster consisted of thirty three genotypes viz., IS-2549-3, ICSR-93023, UPFS-40, SMC-7, IS-15680, UPFS-36 x Pant Chari-6, IS-3821, SMC-18, ESRK-29, EJV-67, SMC-9, RS-29, UPFS-35, UPFS-36 (Pant Chari-7), ESRK-12, ESRK-16, SSG-223, UTM-49, SMC-11, HC-171, SSG-236, ESRK-27, SSG-241, SSG-250, SSG-224, SMC-5, SMC-3, SSG-256, SSG-243, SSG-248, SSG-234-1, SSG-253, and SSG-226. This cluster had high cluster mean for plant height, stem girth, panicle length, panicle width, hemicelluloses content, anthracnose and zonate leaf spot.

Cluster-X: This cluster was marked with fifteen genotypes viz., CO (FS-29), IS-18850, SSG-21, IS-30117, IS-3353, E-159, IS-14337, IS-12735, IS-13566, IS-18927, IS-18844, IS-18933, SMC-1, SMC-13, and IS-28313. This cluster had high cluster mean for days to flowering, days to maturity, leaf length, flag leaf length, green fodder yield per plant, protein percent, acid detergent fiber, cellulose content and lignin content.

Cluster-XI: This cluster had only single genotype 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 hemicellulose 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 Deep et al. [23] Karadi and Kajjidoni [24] Kavya et al. [25] Thant et al. [26] Umakanth et al. [27] Deep et al. [28] Kanbar et al. [29] Vara prasad and Sridhar [30] Navya et al. [31] Sameera et al. [32] Pal et al. [33] Rohilla et al. [34] and Rathod et al. [35].

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 [36] 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 Damor et al. [37] Prasad et al. [38] Tesfaye [39] Ahlawat et al. [40] More et al. [41] Swamy et al. [42] Deep et al. [23] Karadi and Kajjidoni [24] Kavya et al. [25] Thant et al. [26] Umakanth et al. [27] Deep et al. [28] Kanbar et al. [29] Vara prasad and Sridhar [30].

3.2.1 Intra-cluster distance

The highest intra-cluster distance was exhibited by cluster-I (52.381) followed by cluster-II (52.338), cluster-V (49.798), cluster-X (49.224), cluster-VII (48.959), cluster-VI (47.915), cluster-III (47.013), VIII (42.603), cluster-IX (39.666), cluster-IV (36.974) whereas lowest 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.

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 maximum inter-cluster distance was observed between clusters-IV and XI (346.854) 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 (341.099), clusters-I and XI (290.374), clusters-II and XI (280.925), clusters-VII and XI (277.694), clusters-V and XI (276.841), clusters-VIII and XI (265.397), clusters-III and IX (251.038), clusters-IX and XI (244.736), clusters-X and XI (225.389), clusters-IV and X (174.465), clusters-IV and VI (158.022), clusters-IV and VII (138.218), clusters-IV and VIII (130.215), clusters-IV and IX (123.255), clusters-I and IV (121.206), clusters-IV and V (111.77), clusters-II and IV (106.118), clusters-II and IV (106.109), clusters-III and VI (97.585), clusters-VI and X (97.35), clusters-II and X (86.063), clusters-II and VI (85.398), clusters-VII and X (82.477), clusters-V and X (80.512), clusters-VI and IX (79.855), clusters-III and X (79.458), clusters-I and VI (77.272), clusters-I and X (74.455), clusters-I and VII (73.264), clusters-I and V (70.843), clusters-II and VII (70.293), clusters-I and III (68.249), clusters-V and VI (68.077), clusters-III and V (68.014), clusters-II and V (66.981), clusters-VIII and X (66.297), clusters-I and II (65.662), clusters-III and VIII (65.524), clusters-VI and VIII (65.354), clusters-I and IX (65.277), clusters-IX and X (64.65), clusters-VI and VII (64.431), clusters-III and VII (64.038), clusters-I and VIII (63.069), clusters-V and VII (62.021), clusters-VII and IX (60.744), clusters-II and III (60.062), clusters-II and VIII (59.571), clusters-V and IX (59.235), clusters-VII and VIII (57.481), clusters-III and IX (57.44), clusters-II and IX (57.235), clusters-V and VIII (54.879) whereas minimum inter-cluster distance was observed between clusters-VIII and IX (46.803) 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 transgressive 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 (Table 3, Fig. 2, Fig. 3 and Fig. 4).

The highest cluster mean for days to flowering was exhibited by cluster-XI (82.125) followed by cluster-X (76.392), cluster-III (75.650), cluster-V (67.313), cluster-I (65.113), cluster-VII (64.375), cluster-IX (62.670), cluster-IV (62.542), cluster-VIII (60.429), cluster-II (58.529) whereas lowest cluster mean for days to flowering was exhibited by cluster-VI (47.279). The maximum cluster mean for days to maturity was observed in cluster-XI (143.000) followed by cluster-III (138.975), cluster-X (138.33), cluster-V (132.5), cluster-IV (132.00), cluster-VII (129.483), cluster-I (128.375), cluster-IX (126.97), cluster-VIII (123.551), cluster-II (120.74) while lowest cluster mean was observed in cluster-VI (116.000).

The highest cluster mean for number of leaves was exhibited by cluster-XI (19.108) followed by cluster-III (17.598), cluster-IV (17.124), cluster-X (17.095), cluster-IX (16.431), cluster-II (15.551), cluster-I (15.327), cluster-VIII (15.008), cluster-VII (14.828), cluster-V (13.360) whereas lowest by cluster-VI (11.751). The maximum cluster mean for number of nodes was observed in cluster-XI (17.489), cluster-IV (17.235), cluster-III (16.272), cluster-X (15.855), cluster-IX (14.766), cluster-I (14.702), cluster-II (14.510), cluster-VIII (13.614), cluster-VII (13.491), cluster-V (12.703) whereas minimum by cluster-VI (10.850).

The highest cluster mean for plant height was exhibited by cluster-X (407.560), cluster-IX (403.631), cluster-III (377.219), cluster-VIII (372.848), cluster-I (366.170), cluster-XI (363.979), cluster-II (353.849), cluster-VII (334.455), cluster-V (325.756), cluster-VI (301.675) whereas lowest cluster mean for plant height was exhibited by cluster-IV (289.792). The maximum cluster mean for leaf length was observed in cluster-XI (97.131) followed by cluster-X (91.138), cluster-II (90.805), cluster-III (86.894), cluster-I (84.237), cluster-IX (83.930), cluster-IV (83.228), cluster-V (78.677), cluster-VIII (75.907), cluster-VII (72.303) whereas minimum by cluster-VI (67.239).

Table 1. Distribution of genotypes into different clusters during *Kharif* 2018

Sl. No.	Cluster	Number of genotypes	Members
1.	Cluster-I	52	E2-2, Malwan, IS-3318, SSG-222, PC-23, IS-23586, IS-12743, IS-20703-1, GP-2011-471, SSG-260, SSG-263, SSG-234, SSG-212, HJ-513, ICSV-702, ESRK-10, EJN-58, IS-21461, PC-5, HC-171, SMC-2, Nizamabad, EJN-37, EJN-54, SMC-6, SEVS-2, B-4377 (09B-RUS04), IS-607, IS-2363, IS-9162, PC-1002, ESRK-4, EJN-30N, ICSV-111, SPV-1725, IS-6090, PSSV-61, UPFS-38 x UPFS-36, UTM-523, EJN-46, CSV-10, 1890(08BZL01-14-1), 9533-1, PC-1001, IS-9722, EJN-40, UTFS-42, SPV-1752, GP-2011-44-1, IS-1219, SSG-611, and SMC-14
2.	Cluster-II	48	IS-6193, IS-21602-1, IS-3237-2, EG-11, UTM-531, ESRK-7, SSG-227, CSV-14, SPV-1749, (SDSL-92101 x IS-3359) x PC-5, RS-673, JJ-1041, CS-3541-1, IS-21622, IS-15008-1, IS-20740, SPV-1750, SPV-1616, IS-20782, IS-23948-1, GMS-1422, SPV-1252, IS-29794, GGU-55, UPFS-39, RAJ-21, R-72(09R-AGR-23), R-73(09R-AGR-24), R-255(09R-SS-26), SST-4, SPV-1753, SRF-285, R-74(09R-AGR-26), R-77(09R-AGR-26), GP-2011-18-2, EJN-43, EJN-51, SRF-286, SL-44, SPV-462, PC-121, SPV-1754, UTFS-48, SMC-17, UPMC-503 x (SDSL-92101 x UPFS-23), UPMC-504 x UPMC-8, UP Chari-1, and SSG-59-3
3.	Cluster-III	20	PM-98019-2, GD-68717-1, UPFS-34, IS-14756, RAJ-16, EJN-49, EJN-68, IS-3821, E-7, E-28, 1910(08BZL-01-32-4), 1946(08RLD-01-7-2), 1941 (08RLD-01-5-3), R-72 (09R-AGR-23), UP Chari-2, UPFS-38, IS-3359, Pant Chari-3, RAJ-32, and EP-122.
4.	Cluster-IV	3	CSH-22SS, CSH-24SS, and CSV-19
5.	Cluster-V	22	EJ-3, RAJ-9-1, C-43, EJ-42, EJ-30, IS-4925, RAJ-15, IS-313, Pant Chari-6, SEVS-1, IS-4726-2, IS-21021, IS-1478, IS-23988, IS-5434-1, IS-6045, IS-14278-1, IS-6953, IS-7002, IS-25419-1, IS-25419-2, and IS-20399
6.	Cluster-VI	13	EJ-19, EJ-26, EJ-27, EJ-40, EJ-25, IS-25733, IS-33096, CSV-17, EJ-19, EJ-15, EJ-30, EP-135, and EP-124
7.	Cluster-VII	30	IS-21977, EJN-45, GGU-27, EJN-47, EJN-52, EJN-48, EJN-62, IS-699, IS-12956, EJ-30, E-25, EJN-59, E-105, EJN -57, EJN-60, EJN-56, IS-14816, GP-2011-110-1, IS-29314, E-1, EJN-48, GP-2011-372, EJN-73, IS-3345, IS-23992, GMS-1338, EJ-24, EJN-63, EJN-64, and HC-136
8.	Cluster-VIII	49	RAJ-20, Pant Chari-5-UPMC-512, CSV-21F, IS-29691, SMC-10, IS-31861, SSV-74, SSG-304, IS-4307, SMC-12, IS-14298-1, NSSV-259, IS-14333-1, IS-18008-2, IS-22241, TSSV-49, UTM-532, IS-3314, IS-3145, EA-11, SSG-221, Ramkel, MP Chari, EJN-38, ICSV-9519-1-2, 77113, IS-639, IS-3199, GM-1378-1, ART-1008, UPFS-38 x IS-7002, SSG-219, SSG-256, IS-3313, PC-23 x (SDSL-92101 x UPFS-23), SSG-244, UPFS-37 x UPMC-6, GGU-25, Rajasthan Local, SSG-245, GGU-36, HC-260, SSG-226, SSG-225, UPFS-38 x SSG-59-3, SSG-225, ESRK-26, IS-3359, and SSG-227
9.	Cluster-IX	33	IS-2549-3, ICSR-93023, UPFS-40, SMC-7, IS-15680, UPFS-36 x Pant Chari-6, IS-3821, SMC-18, ESRK-29, EJN-67, SMC-9, RS-29, UPFS-35, UPFS-36 (Pant Chari-7), ESRK-12, ESRK-16, SSG-223, UTFS-49, SMC-11, HC-171, SSG-236, ESRK-27, SSG-241, SSG-250, SSG-224, SMC-5, SMC-3, SSG-256, SSG-243, SSG-248, SSG-234-1, SSG-253, and SSG-226
10.	Cluster-X	15	CO (FS-29), IS-18850, SSG-21, IS-30117, IS-3353, E-159, IS-14337, IS-12735, IS-13566, IS-18927, IS-18844, IS-18933, SMC-1, SMC-13, and IS-28313
11.	Cluster-XI	1	IS-14241

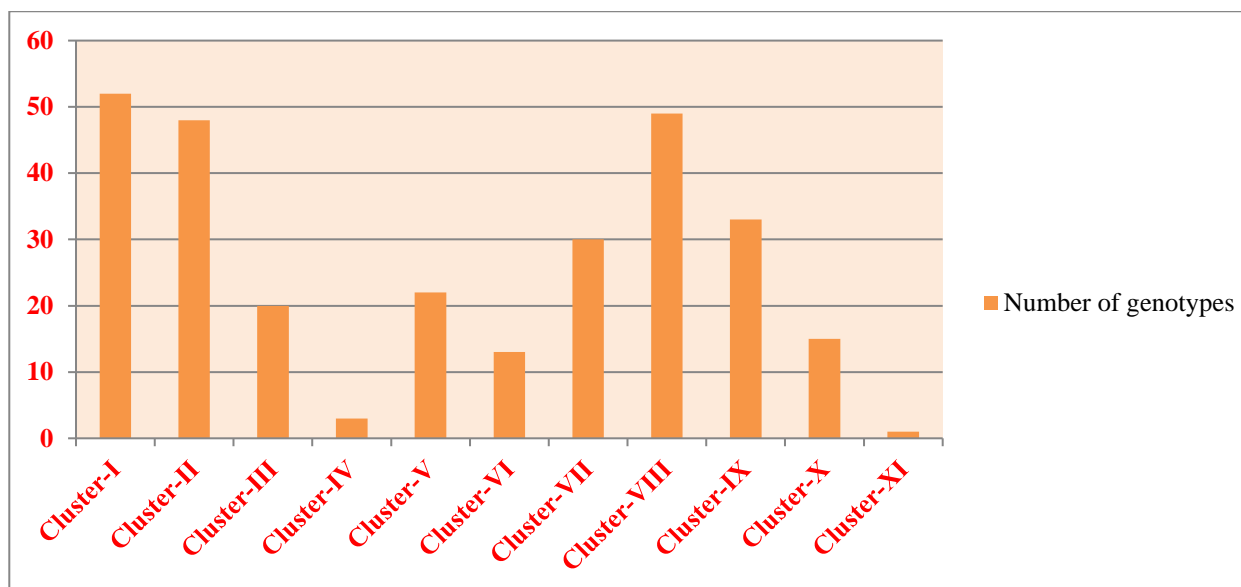


Fig. 1. Distribution of genotypes into different clusters during *Kharif* 2018

Table 2. Intra and inter cluster distances between the clusters based on hierarchical cluster analysis of sorghum germplasm during *Kharif* 2018

	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster-VI	Cluster-VII	Cluster-VIII	Cluster-IX	Cluster-X	Cluster-XI
Cluster-I	52.381	65.662	68.249	121.206	70.843	77.272	73.264	63.069	65.277	74.455	290.374
Cluster-II		52.338	60.062	106.118	66.981	85.398	70.293	59.571	57.235	86.063	280.925
Cluster-III			47.013	106.109	68.014	97.585	64.038	65.524	57.44	79.458	251.038
Cluster-IV				36.974	111.77	158.022	138.218	130.215	123.255	174.465	346.854
Cluster-V					49.798	68.077	62.021	54.879	59.235	80.512	276.841
Cluster-VI						47.915	64.431	65.354	79.855	97.35	341.099
Cluster-VII							48.959	57.481	60.744	82.477	277.694
Cluster-VIII								42.603	46.803	66.297	265.397
Cluster-IX									39.666	64.65	244.736
Cluster-X										49.224	225.389
Cluster-XI											0

Table 3. Cluster means for different characters in sorghum germplasm during Kharif 2018

	DF	DM	NL	NN	PH	LL	LW	LA	FLL	FLW	SG
Cluster-I	65.113	128.375	15.327	14.702	366.170	84.237	7.645	455.798	42.012	3.845	2.487
Cluster-II	58.529	120.74	15.551	14.510	353.849	90.805	8.509	538.348	45.457	4.228	2.461
Cluster-III	75.650	138.975	17.598	16.272	377.219	86.894	8.326	512.688	44.166	4.281	2.761
Cluster-IV	62.542	132.000	17.124	17.235	289.792	83.228	11.148	729.997	42.3	8.616	2.282
Cluster-V	67.313	132.5	13.36	12.703	325.756	78.677	7.826	438.556	39.089	3.983	2.238
Cluster-VI	47.279	116	11.751	10.850	301.675	67.239	6.144	304.522	34.017	3.266	2.292
Cluster-VII	64.375	129.483	14.828	13.491	334.455	72.303	7.081	359.542	36.339	3.573	2.373
Cluster-VIII	60.429	123.551	15.008	13.614	372.848	75.907	6.497	357.966	37.930	3.278	2.278
Cluster-IX	62.670	126.97	16.431	14.766	403.631	83.930	7.350	442.959	41.216	3.559	2.610
Cluster-X	76.392	138.33	17.095	15.855	407.560	91.138	4.695	297.862	45.427	2.230	1.944
Cluster-XI	82.125	143.000	19.108	17.489	363.979	97.131	4.301	320.033	50.244	2.466	1.952

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 (cm²), FLL= Flag leaf length (cm), FLW= Flag leaf width (cm), SG= Stem girth (cm).

Continued.....

	INL	PL	PW	L:S	TGW	GYP	GFY	DFY	DM%	TSS%	HCN
Cluster-I	27.548	23.708	11.709	0.289	22.842	91.243	313.529	112.373	35.819	6.057	87.153
Cluster-II	26.433	22.981	9.910	0.269	25.936	103.276	301.856	107.736	35.637	7.556	88.444
Cluster-III	24.186	17.986	7.925	0.273	25.724	101.801	369.703	138.634	36.262	6.528	90.216
Cluster-IV	35.607	20.198	11.36	0.422	39.350	102.949	443.159	181.261	42.145	12.742	72.286
Cluster-V	31.038	16.731	7.202	0.353	17.920	70.995	332.447	116.722	34.176	9.816	79.688
Cluster-VI	28.278	13.769	4.790	0.317	15.344	61.142	211.527	78.825	36.033	7.195	95.829
Cluster-VII	25.635	13.436	5.544	0.272	21.014	83.599	306.261	114.971	36.538	4.764	87.642
Cluster-VIII	30.142	25.023	12.933	0.287	21.439	86.198	293.830	103.929	34.589	7.058	83.178
Cluster-IX	26.660	27.889	14.768	0.305	18.432	74.084	333.742	114.546	34.450	5.064	82.917
Cluster-X	25.610	24.888	14.102	0.271	11.520	46.342	371.868	136.558	36.028	5.368	82.908
Cluster-XI	18.324	36.011	19.676	0.275	11.894	46.919	962.998	425.000	33.409	6.379	107.196

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	11.520	54.302	53.245	37.83	30.031	6.425	2.556	16.461	24.414	6.45	20.451
Cluster-II	11.207	56.120	55.581	34.753	28.962	4.841	2.050	21.915	19.669	14.341	16.556
Cluster-III	10.988	56.043	56.165	34.451	28.903	4.741	1.993	22.635	23.819	5.554	34.321
Cluster-IV	7.094	58.375	51.797	37.304	28.08	4.946	2.106	24.523	7.906	7.915	17.323
Cluster-V	10.228	53.315	56.214	34.178	29.006	4.832	1.895	22.525	16.279	5.003	15.920
Cluster-VI	9.102	55.922	54.241	35.670	29.079	5.669	2.296	19.244	33.668	6.969	27.499
Cluster-VII	10.588	53.558	55.971	33.834	28.194	5.004	1.728	23.279	51.838	6.814	35.716
Cluster-VIII	11.409	53.528	55.827	34.186	28.714	4.691	1.972	22.564	16.895	7.486	14.249
Cluster-IX	10.653	53.206	55.411	32.849	27.375	4.743	1.726	23.576	16.700	7.504	17.600
Cluster-X	12.105	54.874	54.535	36.244	29.320	5.452	2.013	20.283	14.700	4.222	8.660
Cluster-XI	15.877	54.435	59.150	31.734	27.086	4.656	1.153	28.496	27.406	1.568	4.156

PP= Protein content (%), IVDMD= *in-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 (%)

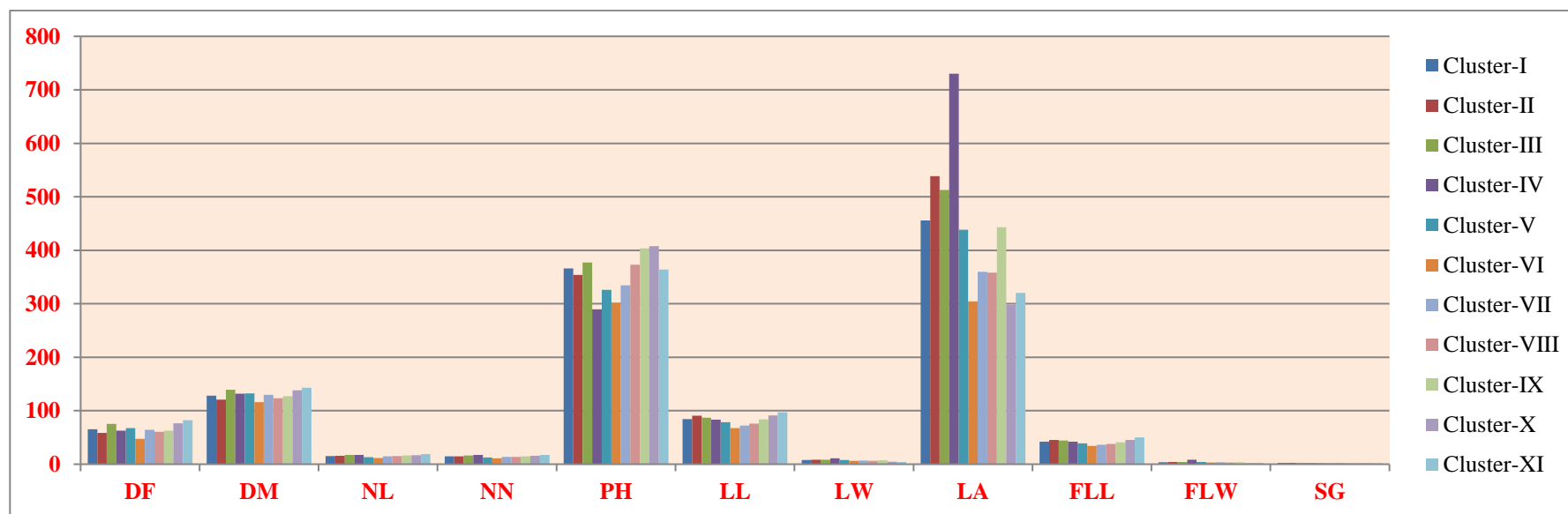


Fig. 2. Cluster means for the characters DF, DM, NL, NN, PH, LL, LW, LA, FLL, FLW, and SG

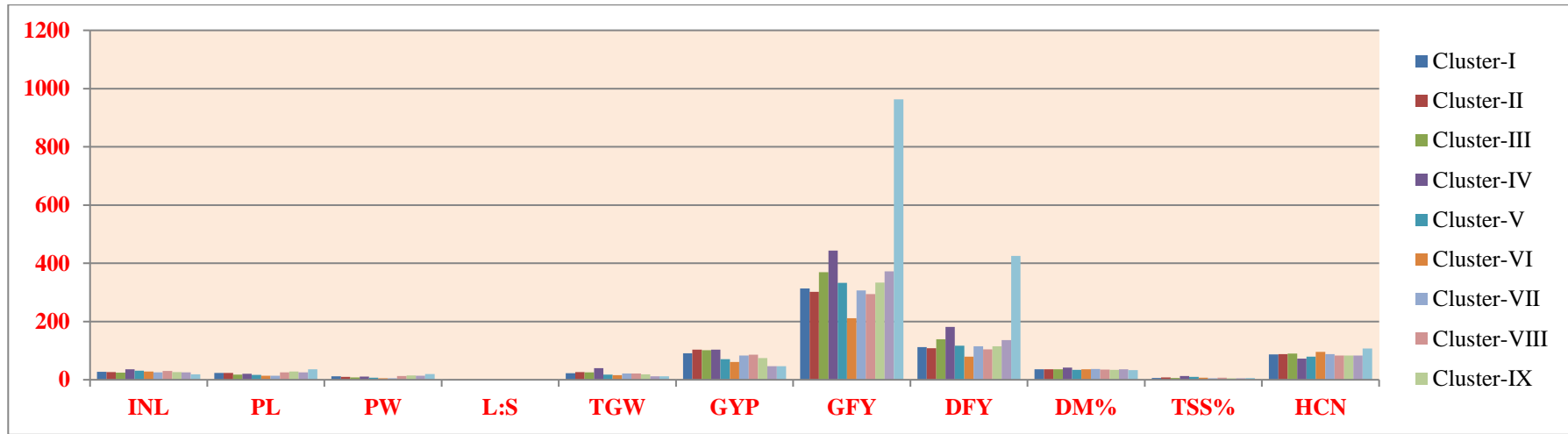


Fig. 3. Cluster means for the characters INL, PL, PW, L:S, TGW, GYP, GFY, DFY, DM (%), TSS (%), and HCN (ppm)

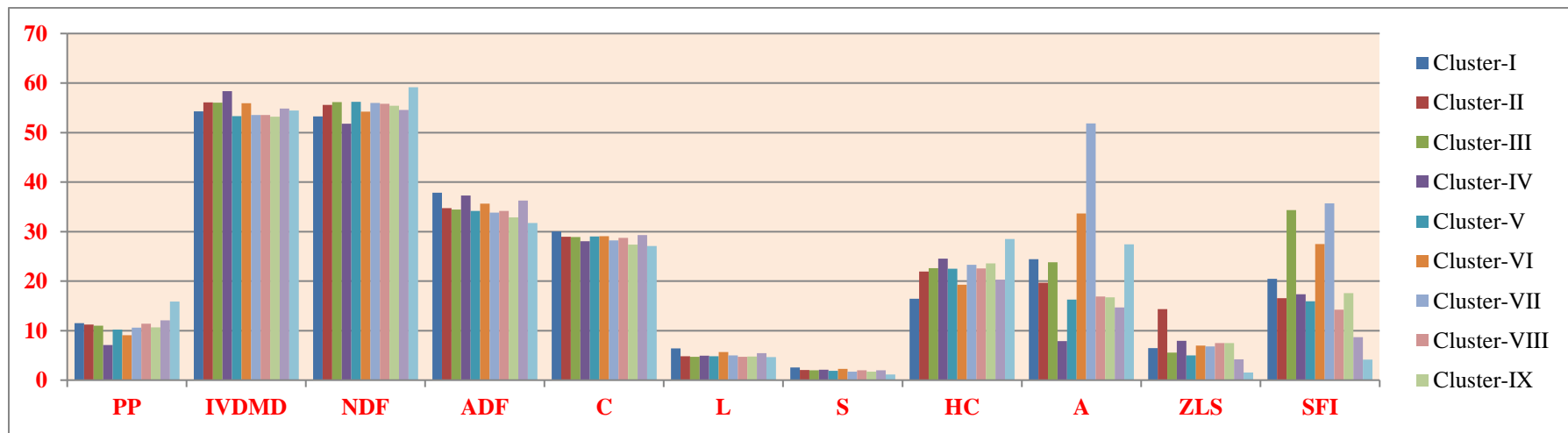


Fig. 4. Cluster means for the characters PP, IVDMD, NDF, ADF, C, L, S, HC, A, ZLS and SFI

The highest cluster mean for leaf length was exhibited by cluster-IV (11.148), cluster-II (8.509), cluster-III (8.326), cluster-V (7.826), cluster-I (7.645), cluster-IX (7.350), cluster-VII (7.081), cluster-VIII (6.497), cluster-VI (6.144), cluster-X (4.695) whereas lowest cluster mean for leaf length was exhibited by cluster-XI (4.301). The maximum cluster mean for leaf area was observed in cluster-IV (729.997) followed by cluster-II (538.348), cluster-III (512.688), cluster-I (455.798), cluster-IX (442.959), cluster-V (438.556), cluster-VII (359.542), cluster-VIII (357.966), cluster-XI (320.033), cluster-VI (304.522) whereas minimum by cluster-X (297.862).

The highest cluster mean for flag leaf length was exhibited by cluster-XI (50.244), cluster-II (45.457), cluster-X (45.427), cluster-III (44.166), cluster-IV (42.300), cluster-I (42.012), cluster-IX (41.216), cluster-V (39.089), cluster-VIII (37.93), cluster-VII (36.339) whereas lowest cluster mean for flag leaf length was exhibited by cluster-VI (34.017). The maximum cluster mean for flag leaf width was observed in cluster-IV (8.616) followed by cluster-III (4.281), cluster-II (4.228), cluster-V (3.983), cluster-I (3.845), cluster-VII (3.573), cluster-IX (3.559), cluster-VIII (3.278), cluster-VI (3.226), cluster-XI (2.466) whereas minimum by cluster-X (2.230).

The highest cluster mean for stem girth was exhibited by cluster-III (2.761), cluster-IX (2.610), cluster-I (2.487), cluster-II (2.461), cluster-VII (2.373), cluster-VI (2.292), cluster-IV (2.282), cluster-VIII (2.278), cluster-V (2.238), cluster-XI (1.952) whereas lowest cluster mean for stem girth was exhibited by cluster-X (1.944). The maximum cluster mean for inter-nodal length was observed in cluster-IV (35.600) followed by cluster-V (31.000), cluster-VIII (30.100), cluster-VI (28.300), cluster-I (27.500), cluster-IX (26.700), cluster-II (26.400), cluster-VII (25.600), cluster-X (25.600), cluster-III (24.200) whereas minimum by cluster-XI (18.300).

The highest cluster mean for panicle length was exhibited by cluster-XI (36.000), cluster-IX (28.000), cluster-VIII (25.000), cluster-X (25.000), cluster-I (24.000), cluster-II (23.000), cluster-IV (20.000), cluster-III (18.000), cluster-V (17.000), cluster-VI (14.000) whereas lowest cluster mean for panicle length was exhibited by cluster-VII (13.000). The maximum cluster mean for panicle width was observed in cluster-XI (20.000) followed by cluster-IX (15.000), cluster-X (14.000), cluster-VIII (13.000), cluster-I (12.000),

cluster-IV (11.000), cluster-II (10.000), cluster-III (8.000), cluster-V (7.000), cluster-VII (6.000) whereas minimum by cluster-VI (5.000).

The highest cluster mean for leaf:stem ratio was exhibited by cluster-IV (0.420), cluster-V (0.350), cluster-VI (0.320), cluster-IX (0.310), cluster-I (0.290), cluster-VIII (0.290), cluster-XI (0.280), cluster-III (0.270), cluster-VII (0.270), cluster-X (0.270) whereas lowest cluster mean for leaf:stem ratio was exhibited by cluster-II (0.270). The maximum cluster mean for 1000-grains weight was observed in cluster-IV (39.000) followed by cluster-II (26.000), cluster-III (26.000), cluster-I (23.000), cluster-VIII (21.000), cluster-VII (21.000), cluster-IX (18.000), cluster-V (18.000), cluster-VI (15.000), cluster-XI (12.000) whereas minimum by cluster-X (12.000).

The highest cluster mean for grain yield per plant was exhibited by cluster-II (103.300), cluster-IV (102.900), cluster-III (101.800), cluster-I (91.240), cluster-VIII (86.200), cluster-VII (83.600), cluster-IX (74.080), cluster-V (71.000), cluster-VI (61.140), cluster-XI (46.920) whereas lowest cluster mean for grain yield per plant was exhibited by cluster-X (46.340). The maximum cluster mean for green fodder yield per plant was observed in cluster-XI (963.000) followed by cluster-IV (443.000), cluster-X (372.000), cluster-III (370.000), cluster-IX (334.000), cluster-V (332.000), cluster-I (314.000), cluster-VII (306.000), cluster-II (302.000), cluster-VIII (294.000) whereas minimum by cluster-VI (212.000).

The highest cluster mean for dry fodder yield per plant was exhibited by cluster-XI (425.000), cluster-IV (181.000), cluster-III (139.000), cluster-X (137.000), cluster-V (117.000), cluster-VII (115.000), cluster-IX (115.000), cluster-I (112.000), cluster-II (108.000), cluster-VIII (104.000) whereas lowest cluster mean for dry fodder yield per plant was exhibited by cluster-VI (78.800). The maximum cluster mean for dry matter percent was observed in cluster-IV (42.100) followed by cluster-VII (36.500), cluster-III (36.300), cluster-VI (36.000), cluster-X (36.000), cluster-I (35.800), cluster-II (35.600), cluster-VIII (34.600), cluster-IX (34.500), cluster-V (34.200) whereas minimum by cluster-IX (33.400).

The highest cluster mean for total soluble solids was exhibited by cluster-IV (13.000), cluster-V (10.000), cluster-II (8.000), cluster-VI (7.000), cluster-VIII (7.000), cluster-III (7.000), cluster-XI

(6.000), cluster-I (6.000), cluster-X (5.000), cluster-IX (5.000) whereas lowest cluster mean for total soluble solids was exhibited by cluster-VII (5.000).The maximum cluster mean for hydrocyanic acid content was observed in cluster-XI (107.200) followed by cluster-VI (95.830), cluster-III (90.220), cluster-II (88.440), cluster-VII (87.640), cluster-I (87.150), cluster-VIII (83.180), cluster-IX (82.920), cluster-X (82.910), cluster-V (79.690) whereas minimum by cluster-IV (72.290).

The highest cluster mean for protein percent was exhibited by cluster-IX (15.900), cluster-X (12.100), cluster-I (11.500), cluster-VIII (11.400), cluster-II (11.200), cluster-III (11.000), cluster-IX (10.700), cluster-VII (10.600), cluster-V (10.200), cluster-VI (9.100) whereas lowest cluster mean for protein percent was exhibited by cluster-IV (7.090).The maximum cluster mean for in-vivo dry matter digestibility was observed in cluster-IV (58.000) followed by cluster-II (56.000), cluster-III (56.000), cluster-VI (56.000), cluster-X (55.000), cluster-XI (54.000), cluster-I (54.000), cluster-VII (54.000), cluster-VIII (54.000), cluster-V (53.000) whereas minimum by cluster-IX (53.000).

The highest cluster mean for neutral detergent fiber was exhibited by cluster-XI (59.000), cluster-V (56.000), cluster-III (56.000), cluster-VII (56.000), cluster-VIII (56.000), cluster-II (56.000), cluster-IX (55.000), cluster-X (55.000), cluster-VI (54.000), cluster-I (53.000) whereas lowest cluster mean for was exhibited by cluster-IV (52.000).The maximum cluster mean for acid detergent fiber was observed in cluster-I (37.800) followed by cluster-IV (37.300), cluster-X (36.200), cluster-VI (35.700), cluster-II (34.800), cluster-III (34.500), cluster-VIII (34.200), cluster-V (34.200), cluster-VII (33.800), cluster-IX (32.800) whereas minimum by cluster-XI (31.700).

The highest cluster mean for cellulose content was exhibited by cluster-I (30.000), cluster-X (29.000), cluster-VI (29.000), cluster-V (29.000), cluster-II (29.000), cluster-III (29.000), cluster-VIII (29.000), cluster-VII (28.000), cluster-IV (28.000), cluster-IX (27.000) whereas lowest cluster mean for cellulose content was exhibited by cluster-XI (27.000).The maximum cluster mean for lignin content was observed in cluster-I (6.425) followed by cluster-VI (5.669), cluster-X (5.452), cluster-VII (5.004), cluster-IV (4.946), cluster-II (4.841), cluster-V (4.832), cluster-IX (4.743), cluster-III (4.741), cluster-VIII (4.691) whereas minimum by cluster-XI (4.656).

The highest cluster mean for silica content was exhibited by cluster-I (2.560), cluster-VI (2.300), cluster-IV (2.110), cluster-II (2.050), cluster-X (2.010), cluster-III (1.990), cluster-VIII (1.970), cluster-V (1.900), cluster-VII (1.730), cluster-IX (1.730) whereas lowest cluster mean for silica content was exhibited by cluster-XI (1.150).The maximum cluster mean for hemicelluloses content was observed in cluster-XI (28.500) followed by cluster-IV (24.500), cluster-IX (23.600), cluster-VII (23.300), cluster-III (22.600), cluster-VIII (22.600), cluster-V (22.500), cluster-II (21.900), cluster-X (20.300), cluster-VI (19.200) whereas minimum by cluster-I (16.500).

The highest cluster mean for anthracnose was exhibited by cluster-VII (51.800), cluster-VI (33.700), cluster-XI (27.400), cluster-I (24.400), cluster-III (23.800), cluster-II (19.700), cluster-VIII (16.900), cluster-IX (16.700), cluster-V (16.300), cluster-X (14.700) whereas lowest cluster mean for anthracnose was exhibited by cluster-IV (7.910).The maximum cluster mean for zonate leaf spot was observed in cluster-II (14.000) followed by cluster-IV (8.000), cluster-IX (8.000), cluster-VIII (7.000), cluster-VI (7.000), cluster-VII (7.000), cluster-I (6.000), cluster-III (6.000), cluster-V (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 (35.720), cluster-III (34.320), cluster-VI (27.500), cluster-I (20.450), cluster-IX (17.600), cluster-IV (17.320), cluster-II (16.560), cluster-V (15.920), cluster-VIII (14.250), cluster-X (8.660) whereas lowest cluster mean for shoot fly incidence was exhibited by cluster-XI (4.156).

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 Kumar et al. [43] Rahman et al. (2015), Usha and Rekha [44] Doijad et al. [45] Jain and Patel [46] Damor et al. [37] Prasad et al. [38] Tesfaye [39] Ahlawat et al. [47] More et al. [41] Swamy et al. [42] Deep et al. [23] Karadi and Kajjidoni [24] Kavya et al. [25] Thant et al. [26]

Crosses suggesting parents belonging to most divergent clusters would be expected to manifest maximum heterosis and also wide variability of genetic architecture Vara prasad and Sridhar [30] Navya et al. [31] Sameera et al. [32] Pal et al. [33] Rohilla et al. [48] and Rathod et al. [49] Raghavendra et al. [50]

These results of our present study are somewhat in accordance with the findings of Kumar et al. [43] Rahman et al. (2015), Usha and Rekha [44] Doijad et al. [45] Jain and Patel [46] Damor et al. [51] Prasad et al. [38] Tesfaye [39] Ahlawat et al. [40] More et al. [41] Swamy et al. [42] Deep et al. [23] Karadi and Kajjidoni [24] Kavya et al. [25] Thant et al. [26] Umakanth et al. [27] Deep et al. (2020), Kanbar et al. [29] Vara prasad and Sridhar [30] Navya et al. [31] Sameera et al. [32] Pal et al. [33] Rohilla et al. [34] Rathod et al. [49] and Raghavendra et al. [50] [52-54].

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-I (52) consisted of highest number of genotypes whereas lowest number of genotypes were exhibited by cluster-XI (1). The highest intra-cluster distance was exhibited by cluster-I (52.381) whereas lowest 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 maximum inter-cluster distance was observed between clusters-IV and XI (346.854) 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 (46.803). 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 transgressive 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.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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