*Frontiers in Crop Improvement, Vol. 7 (1) : 52-58 (2019)*
*Print ISSN : 2393-8234, Online ISSN : 2454-6011*
*ASTHA FOUNDATION*
*Meerut (U.P.) INDIA*

# GENETIC DIVERSITY IN FINGER MILLET GERMPLASM AS REVEALED THROUGH HIERARCHICAL CLUSTER ANALYSIS

**Anchal Bish and A.S. Jeena**
*Department of Genetics and Plant Breeding, G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand*

## ABSTRACT

The finger millet germplasm (112 accessions) collected from different district of Uttarakhand, were evaluated along with 5 checks in augmented block design. The adjusted mean of genotypes were subjected to Hierarchical Cluster Analysis (HCA) and the genotypes were grouped in different clusters based the dendrogram. All the genotypes including checks were grouped in seven clusters based on hierarchical cluster analysis. The grouping pattern of accessions indicates no parallelism between geographical diversity and genetic diversity. Highest inter-cluster distance was observed between cluster I and V followed by cluster I and cluster VI. Accessions namely GP-2012-61 (III), GP-2011-579 (V), GP-2011-294 (IV), GP-2011-583 (V), GP-2012-47 (III), GP-2012-37 (II), GP-2012-41 (II), GP-2012-68 (II ), MSKS-2 (II), GP-2011-322 (IV), GP-2011-43 (VII), PCPGR-8047 (VI), GP-2011-455( II) were identified to be promising for productive tillers , finger length, spikelet density per centimetre, 1000 grain weight. These accessions possessing yield contributing characters could be used as donors for yield improvementby the breeders in order to enhance the production of finger millet.

***Key words*** **:** *Finger millet, eleusine coracana, germplasm, genetic diversity, yield.*

Finger millet (*Eleusinecoracana* (L.) Gaertn) commonly known as 'ragi', is an important cereal crop among the small millets and third most important millet in India as per area and production after sorghum and pearl millet.It is cultivated mostly as rainfed crop in India for its valued food grains and its adaptability to wide range of geographical areas and agro-ecological diversity. India is major producer of finger millet in Asia. Genetic diversity gives species, the ability to adapt to changing environments, including new pests and diseases and new climatic conditions. Plant genetic resources, that component of genetic diversity is of actual or potential use to humanity, provides the raw material for breeding new varieties of crops. These, in turn, provide a basis for more productive and resilient production systems that are better able to cope with biotic and abiotic stresses. Knowledge about genetic diversity is a prerequisite of any breeding programme. Inclusion of diverse parents in hybridization programmes serves the purpose of combining desirable genes in new recombinents. Several studies on degree of divergence based on phenotypic observations in different crops shown that accessions from the same geographical region may differ genetically as well as phenotypically and also in adaptability.

There are several method of studying genetic diversity which includes morphometric, biochemical and molecular methods.Hirarchical cluster analysis is a morphometric method and a powerful tool in quantifying the divergence at genotypic level.The ultimate aim of breeding programme is to evolve superior accessions which can be exploited as cultivar. The success of any crop improvement programme is dependent on the magnitude of variability present in the crop. For this reason, there is renewed interest in germplasm as a source of genetic variation. The knowledge of genetic divergence has been successfully utilized in different crop species for the selection of suitable parents for varying conditions as the concept of 'Genetic Divergence' has been vital utility in differentiating well defined populations. The more diverse the parents, the greater will be the chance of obtaining heterotic combinations and broad spectrum of variability in segregating generations (1).

In the past Mahalanobis $D^2$ statistic has been used as a statistical tool for estimating genetic divergence for use in plant breeding programme. The use of Mahalanobis $D^2$ statistic becomes limited in application when a large number of entries are to be objectively evaluated in a breeding programme. Under these conditions the Hierarchical Euclidean cluster analysis (2) a method of numerical taxonomy has been found successful as a tool for estimation of genetic divergence. Therefore, in the present study Hierarchical cluster analysis (HCA) based on Euclidean distances was employed for characterizing the genetic divergence among finger millet germplasm and the results obtained are presented hereunder. Regardless of the vast materials available and the urgent need to improve finger millet unit productivity through genetic manipulation, little is known about their variability, major characters and the potential usefulness of the individual accessions stored in the bank. Therefore, investigating and identifying plants for the genetic variation available in the breeding materials is the first step of plant breeding and so vital for successful crop improvement program.

**Table-1 :** List ofgermplasm accessions of finger milletcollected from uttarakhand**.**

| Sl. | Entry | Sl. | Entry | Sl. | Entry | Sl. | Entry | Sl. | Entry |
|---|---|---|---|---|---|---|---|---|---|
| | Checks | 23 | GP-2011-454 | 47 | GP-2012-66 | 71 | PCPGR-8059 | 95 | PCPGR-8131 |
| 1 | VL 315 | 24 | GP-2011-455 | 48 | GP-2012-68 | 72 | PCPGR-8061 | 96 | PCPGR-8138 |
| 2 | VL 149 | 25 | GP-2011-460 | 49 | GP-2012-71 | 73 | PCPGR-8064 | 97 | PGR-1407 |
| 3 | VL 324 | 26 | GP-2011-473 | 50 | GP-2012-74 | 74 | PCPGR-8065 | 98 | PGR-1507 |
| 4 | PRM 1 | 27 | GP-2011-532 | 51 | GP-2012-78 | 75 | PCPGR-8066 | 99 | PGR-1707 |
| 5 | PRM 2 | 28 | GP-2011-578 | 52 | GP-2012-82 | 76 | PCPGR-8067 | 100 | PGR-1807 |
| | Germplasm | 29 | GP-2011-579 | 53 | MDS-1 | 77 | PCPGR-8110 | 101 | PGR-1907 |
| 6 | GP-2011-109 | 30 | GP-2011-580 | 54 | MSKS-2 | 78 | PCPGR-8111 | 102 | PGR-20.7 |
| 7 | GP-2011-123 | 31 | GP-2011-582 | 55 | MWS-1 | 79 | PCPGR-8112 | 103 | PGR-21.07 |
| 8 | GP-2011-156 | 32 | GP-2011-583 | 56 | PCPGR-3139 | 80 | PCPGR-8113 | 104 | PGR-22.07 |
| 9 | GP-2011-166 | 33 | GP-2011-75 | 57 | PCPGR-7605 | 81 | PCPGR-8114 | 105 | PGR-24.07 |
| 10 | GP-2011-19 | 34 | GP-2011-78 | 58 | PCPGR-7675 | 82 | PCPGR-8115 | 106 | PGR-25.07 |
| 11 | GP-2011-203 | 35 | GP-2011-79 | 59 | PCPGR-8045 | 83 | PCPGR-8116 | 107 | PGR-26.07 |
| 12 | GP-2011-215 | 36 | GP-2012-25 | 60 | PCPGR-8046 | 84 | PCPGR-8117 | 108 | PGR-32.07 |
| 13 | GP-2011-236 | 37 | GP-2012-36 | 61 | PCPGR-8047 | 85 | PCPGR-8118 | 109 | PGR-34.07 |
| 14 | GP-2011-294 | 38 | GP-2012-37 | 62 | PCPGR-8048 | 86 | PCPGR-8119 | 110 | PGR-35.07 |
| 15 | GP-2011-322 | 39 | GP-2012-41 | 63 | PCPGR-8049 | 87 | PCPGR-8123 | 111 | PGR-36.07 |
| 16 | GP-2011-366 | 40 | GP-2012-44 | 64 | PCPGR-8050 | 88 | PCPGR-8124 | 112 | PGR-37.07 |
| 17 | GP-2011-367 | 41 | GP-2012-47 | 65 | PCPGR-8051 | 89 | PCPGR-8125 | 113 | PGR-38.07 |
| 18 | GP-2011-381 | 42 | GP-2012-51 | 66 | PCPGR-8052 | 90 | PCPGR-8126 | 114 | PGR-907 |
| 19 | GP-2011-42 | 43 | GP-2012-54 | 67 | PCPGR-8053 | 91 | PCPGR-8127 | 115 | PGR-MA-23-07 |
| 20 | GP-2011-420 | 44 | GP-2012-58 | 68 | PCPGR-8054 | 92 | PCPGR-8128 | 116 | PGR-MA-6-07 |
| 21 | GP-2011-43 | 45 | GP-2012-61 | 69 | PCPGR-8055 | 93 | PCPGR-8129 | 117 | PGR-MA-7-07 |
| 22 | GP-2011-431 | 46 | GP-2012-63 | 70 | PCPGR-8056 | 94 | PCPGR-8130 | | |

## MATERIALS AND METHODS

The present investigation was carried out at Pantnagar Centre for Plant Genetic Resource, G.B Pant University of Agriculture and Technology, Pantnagar with 112 accessions of finger millets germplasm alongwith 5 standard checks namely VL 315, VL 149 and VL 324 (Almora), PRM 1 and PRM 2 (Teheri).The list is given in Table 1.

The accessions were collected from various blocks and districts from all over Uttarakhand. The present study inclues two accessions from Bageshwar, four from Nainital, five from Almora, fifteen form Chamoli, eighteen from Champawat, twenty-four from Pithoragarh district and rest fourty-four from Tehri garhwal district.The experiment was laid out in augmented block design with four blocks, each consisted of thirty-three rows interviened by the five checks placed randomly within each block. Augmented design incorporates the provision of accommodating single replication of all treatments by spreading it over all the blocks (b), while a set of checks (c), numbering three or more are replicated in each block. Randomization is done in such a way that all the checks (c) and a part of test genotypes fall only once in each block. Equal number of test genotypes was planted in each block to facilitate statistical analysis.Twenty eight accessions were sown in each block in a single row plot of 3m length spaced at 30 cm row to row distance. Data was recorded for fifteen characters out of which three were gradial including plant pigmentation, ear shape and grain colour while twelve were non-gradial which includes plant height, number of productive tillers, days to fifty percent flowering, finger number and number of grains per spikelet, finger length, spikelet density per centimeter,1000 grain weight, grain yield per plant, fodder yield per plant, harvest index, biological yield.

## RESULT AND DISCUSSION

In the present investigation, significant differences among accessionswere recorded for all the characters studied except for days to 50% floweringand plant height. Analysis of variances was revealed that there were significant differences among checks varieties for days to 50% flowering, number of grains per spikelet and 1000 grain weight. The variances for productive tillers, finger number, finger length, grain yield per plant, fodder yield

**Table-2 :** Distribution of finger millet accessions in different clusters based on Hierarchical Cluster Analysis.

| Clusters | No. of Entries | Entry Number (See Table 1 for entry name) |
|---|---|---|
| Cluster I | 2 | 46, 89 |
| Cluster II | 32 | 3, 8, 9, 11, 17, 22, 23, 24, 26, 27, 36, 37, 38, 39, 40, 42, 48, 50, 51, 52, 54, 55, 59, 64, 65, 70, 75, 81, 92, 93, 101, 117 |
| Cluster III | 22 | 7, 10, 28, 30, 31, 33, 41, 45, 49, 71, 73, 76, 77, 78, 79, 87, 94, 95, 106, 108, 110, 112 |
| Cluster IV | 47 | 2, 4, 5, 12, 13, 14, 15, 16, 18, 19, 20, 25, 34, 35, 43, 44, 47, 57, 66, 67, 68, 69, 72, 74, 80, 82, 83, 84, 85, 88, 90, 96, 97, 98, 99, 100, 102, 103, 104, 105, 107, 109, 111, 113, 114, 115, 116 |
| Cluster V | 2 | 29, 32 |
| Cluster VI | 2 | 6, 61 |
| Cluster VII | 10 | 1, 21, 53, 56, 58, 60, 62, 63, 86, 91 |

**Table-3 :** Intra (diagonal) and Inter- cluster (Off-diagonal) distances between the clusters based on Hierarchical Cluster Analysis of finger millet germplasm.

| Cluster | I | II | III | IV | V | VI | VII |
|---|---|---|---|---|---|---|---|
| I | 20.47 | 145.74 | 62.17 | 98.34 | 266.32 | 244.76 | 206.95 |
| II | | 27.35 | 90.60 | 56.86 | 124.90 | 102.55 | 66.98 |
| III | | | 32.58 | 48.44 | 209.80 | 188.50 | 150.59 |
| IV | | | | 28.27 | 171.37 | 153.27 | 113.54 |
| V | | | | | 32.34 | 52.63 | 63.90 |
| VI | | | | | | 29.78 | 52.09 |
| VII | | | | | | | 31.91 |

**Table-4 :** Cluster means for different characters studied on finger millet germplasm.

| Characters | I | II | III | IV | V | VI | VII |
|---|---|---|---|---|---|---|---|
| Days to 50 percent flowering | 80.60 | 77.24 | 73.25 | 67.77 | 71.30 | 82.60 | 73.95 |
| Productive tillers | 3.37 | 3.42 | 3.43 | 3.26 | 4.08 | 3.41 | 3.40 |
| Finger number | 7.00 | 6.84 | 7.71 | 7.14 | 8.8 | 6.30 | 7.00 |
| Finger length | 7.28 | 6.97 | 7.19 | 6.60 | 6.66 | 8.76 | 7.08 |
| Spikelet density per centimetre | 10.31 | 11.87 | 9.82 | 10.50 | 11.44 | 10.29 | 10.83 |
| Number of grains per spikelet | 6.30 | 6.74 | 6.70 | 6.99 | 9.00 | 6.50 | 7.22 |
| 1000 grain weight | 2.50 | 2.57 | 2.50 | 2.54 | 2.45 | 2.69 | 2.49 |
| Plant height | 107.95 | 115.44 | 110.72 | 100.77 | 96.37 | 135.07 | 110.1 |
| Grain yield per plant | 3.75 | 16.00 | 10.16 | 13.05 | 35.98 | 23.16 | 26.95 |
| Fodder yield per plant | 24.23 | 119.25 | 60.77 | 86.27 | 193.49 | 185.12 | 156.58 |
| Biological yield | 27.48 | 135.26 | 71.20 | 99.32 | 229.47 | 208.28 | 183.54 |
| Harvest index | 13.36 | 11.82 | 14.86 | 13.20 | 15.69 | 11.2 | 14.63 |

per plantand biological yield were found to be highly significant, however non significant differences were observed for plant height, spikelet density per centimetre and harvest index.The analysis of variance revealed that there are highly significant differences among all hundred and seventeen genotypes for all the twelve characters studied. It means the genotypes studied permits greater scope for selection.

**Cluster formation based on HCA :** The adjusted mean of genotypes were subjected to Hierarchical Cluster Analysis (HCA) and the genotypes were grouped in different clusters based on 40 % dissimilarity level in the dendrogram prepared after the HCA (Fig. 1).The 117 genotypes including 5 checks were grouped in 7 clusters based on hierarchical cluster analysis (Table 2). Cluster IV had the highest number of genotypes (47) belonging to various districts viz., Teheri (25), Chamoli (9), Champawat (5), Pithoragarh (5), Bageshwar (1) and Almora (2), followed by Cluster II with (32) accessions from Pithoragarh (11), Teheri (7) Chamoli (6), Almora (3), Champawat (3) and Nainital (2), ClusterIII with (22) accessions fromTeheri (10), Pithoragarh (5), Champawat (5) Nainital (1) and Bageshwar (1) and Cluster VII with (10) genotypes from Teheri (3), Chapawat(2), Chamoli (1), Nainital (1), Almora (2) and Pithoragarh (1). Cluster I, V and VI each had 2 accessions collected from Pithoragarh, Teheri and Champawat.

The critical analyses of distribution pattern of accessions from various districts to different clusters indicated that accessions from different locations are clustered together in one cluster and also accessions from the same region are grouped under different

**Table-5 :** List of suitable donors for different traits identified in finger millet germplasm.

| S. No. | Characters | Donors |
|---|---|---|
| 1. | Days to flowering | PGR-MA-18-07(IV), PGR-MA-20-7 (IV), PRG-MA-22-07 (IV), PGR-MA-25-07(III), PGR-MA-32-07 (III) |
| 2. | Productive tillers | GP-2012-61 (III), GP-2011-579 (V) |
| 3. | Finger number | GP-2011-294 (IV), GP-2011-583 (V) |
| 4. | Finger length | GP-2011-156 (II), GP-2012-47 (III), MSKS-2 (II), PGR-MA-35-07 (III), GP-2011-236 (IV) |
| 5. | Spikelet density per centimetre | GP-2012-47 (III), GP-2012-37 (II), GP-2012-41 (II), GP-2012-68 (II ), MSKS-2 (II) |
| 6. | Number of grains per spikelet | GP-2012-51 (II), PCPGR-8130 (III), PGR-MA-1907 (II), GP-2011-294 (IV), GP-2011-583 (V) |
| 7. | 1000 grain weight | GP-2011-166 (II), GP-2011-322 (IV), GP-2011-43 (VII), PCPGR-8047 (VI), GP-2011-455( II) |
| 8. | Plant height | PCPGR-8112 (III), PCPGR-8113(IV), PCPGR-8116 (IV), PGR-MA-17-07(IV), GP-2011-460(IV) |
| 9. | Grain yield per plant | GP-2011-583 (V), PCPGR-8048 (VII) , PCPGR-8049 (VII), PCPGR-8046 (VII) , GP-2011-579 (V) |
| 10. | Fodder yield per plant | PCPGR-8049 (VII), PCPGR-8047(VI), GP-2011-579 (V), GP-2011-109 ( VI), GP-2011-583 (V) |
| 11. | Biological yield | PCPGR-8047 (VI), PCPGR-8049 (VII), GP-2011-109 (VI), GP-2011-579 (V), GP-2011-583 (V) |
| 12. | Harvest index | PGR-MA-32-07 (III), PCPGR-8061 (IV), GP-2011-78 (IV), GP-2011-580 (III) , GP-2011-582 (III) |

clusters. It suggests that there is no parallelism between geographical diversity and genetic diversity. Similar observations were also reported by (3). Further, there were accessions from the same district, distributed in different clusters indicated that farmers are still conserving the diversity in their growing forms. Accessions included in one cluster were closely related to each other hence lead to narrow down the variability.

**Inter and intra-cluster distance :** The number of clusters represents the number of groups in which a population can be classified. The distance between two clusters is the measure of the degree of diversification. The greater the distance between two clusters the greater the divergence and vice-versa. The genotypes falling in the same cluster are more likely to be related than those belonging to another cluster. In other words the genotypes grouped in one cluster are less divergent than those which are placed in different cluster. The intra and inter cluster distances calculated for different clusters have been presented in Table 3.The lowest intra-cluster distance was observed for cluster I (20.47) followed by cluster II (27.35), cluster IV (28.27), cluster VI (29.78). Highest intra-cluster distance was recorded for cluster III (32.58) followed by cluster V (32.34) and cluster VII (31.91).Cluster III had genotypes with high intra-cluster distance. More distance among its members means there is wide range of variabilitystill present for the concerned character. Ifwe lower down the dissimilarity level there will be further breakdown of the existing cluster. On the other hand clusters with less intra-cluster distance imply that there accessions are closely related and less variability present among its member genotypes with respect to their mean values. These accessions their mean values close to the cluster mean so the extraction of donors from these clusters will be easier.

The inter-cluster distance was highest between cluster I and cluster V (266.32) then followed by cluster I and cluster VI (244.76) on the other hand narrow distance was estimated between cluster VI and cluster VII (52.09) thereafter by cluster V and cluster VI (52.63). There was more distance observed between cluster I and cluster V, these two clusters are distinctly related and so are the member genotypes present within each cluster. More the distance more will be the diversity between the accessions, in turn we may be able to select a number of donors to carry out hybridization programmes for the improvement of desirable trait in the finger millet.

We can proceed with the hybridization programme by making cross between the two distinctly related genotypes with desired traits in order to get more number of transgressive segregants, out of which may undergo selection for desirable ones. (4) also suggested that more variability in genetic makeup of genotypes included in distinct clusters and crossing the genotypes from those clusters would generate wide spectrum variability for yield improvement in finger millet. Similar findings were also reported by (5), who studied 150 finger millet germplasm and found that considerable amount of genetic diversity

was present among the entries for yield and yield attributes. They suggested that inter-crossing between genotypes of diverse clusters would generate a broad spectrum of variability for effective selection in the segregating generations for the development of high yielding cultivars.

**Cluster Mean for Different Clusters :** The cluster mean for different character under study was computed and presented in Table 4. The perusal of the table revealed that the clusters are exhibiting differences for various morpho-agronomic characters. This indicates that there is option available for identification of donors for different traits to be proposed for inclusion in hybridization programme.

For days to 50% flowering highest mean value was recorded for VI cluster (82.6) and lowest value for cluster IV (67.77) and other clusters had mean values of 71.3, 73.25, 73.95, 77.24 and 80.6, respectively for cluster V, Cluster III, Cluster VII, Cluster II, Cluster I.Highest Mean value for productive tillers was observed in cluster V (4.08) followed by cluster III (3.43), Cluster II (3.42), Cluster VI (3.41), Cluster VII (3.40), Cluster I (3.37) and lowest value of 3.26 in cluster IV. Among the seven clusters, highest value was recorded as 8.8 (cluster V) for the finger number while cluster VI recorded the least number of fingers(6.3). Cluster II hadmean finger number as 6.84 and Cluster I and VII with 7 finger number each. Cluster IV and Cluster III had 7.14 and 7.71 mean value respectively.For the finger length cluster VI (8.76 cm) has the highest mean and lowest mean value was observed in cluster IV (6.60 cm). Cluster V, Cluster II, Cluster VII, Cluster III, Cluster I had mean values of 6.66, 6.97, 7.08, 7.19, 7.28 cm, respectively.

Out of the seven clusters the highest value for spikelet density per centimetre was recorded in cluster II (11.87) and lowest in III (9.82). Cluster VI, Cluster I, Cluster IV, Cluster VII, Cluster V exhibited 10.29, 10.31, 10.50, 10.83, 11.44, 11.44 values of cluster means, respectively.Cluster V recorded the highest mean value (9.0) for number of grains per spikelet followed by cluster VII (7.22), Cluster IV (6.99), Cluster II (6.74), Cluster III (6.70), Cluster VI (6.5) and cluster I recorded the lowest value as 6.3 grains per spikelet.For 1000 grain weight cluster mean value was recorded highest for cluster VI (2.69g) and lowest for cluster IV (2.45g). Rest of the clusters showed mean values as 2.49g (Cluster VII), 2.50g (Cluster I and IIIboth), 2.54g (Cluster IV) and 2.57g (Cluster II). Lowest mean values for the plant height was observed in cluster V (96.37cm), followed by cluster IV (100.77cm), Cluster VII (110.1cm), Cluster III (110.72cm), Cluster I (107.95cm) and Cluster II(115.4cm) reaching a highest mean value for cluster VI (135.07cm).

The mean value for grain yield per plant was recorded highest for cluster V (35.98g) and lowest for clusterI (3.75g). Mean values for other clusterswere observed as 10.16g (cluster III), 13.05g (cluster IV), 16.00g (cluster II), 23.16g (cluster VI) and 26.95g (cluster VII).Cluster V (193.49g) exhibited highest mean value for fodder yield per plant followed by Cluster VI(185.12g), Cluster VII (156.58g), Cluster II (119.25g), Cluster IV (86.25g), Cluster III (60.77g) and cluster I (24.23g) having the least mean value.For biological yield per plant highest mean was recorded in cluster V (229.47g) followed by cluster VI (208.28g), cluster VII (183.54g), cluster II (135.26g), cluster IV (99.32g), cluster III (71.20g) and cluster I with the lowest mean value of 27.48g.For Harvest index cluster V recorded the highest mean value of 15.59% and lowest mean value was found for cluster VI (11.2%).The mean values in other clusters were observed as 11.2% (Cluster VI), 11.82% (Cluster II), 13.20% (Cluster IV), 13.36% (Cluster I) and 14.63% (Cluster VII).

Cluster IV was reported to have the genotypes with earliness in flowering so accessions from this cluster can be included in the breeding program as donor for earliness. Cluster V included most of the accessions having high mean values for yield contributing characters like number of productive tillers, finger length, finger number, number of grains per spikelet, grain yield per plant, fodder yield per plant, biological yield per plant. It also comprised of accessions with short plantheight, which could be used as donors to bred dwarf varieties. Cluster VI on the other hand had accessions having more of 1000 grain weight, while Cluster II composed of accessions exhibited more spikelet density per centimetre.

Among all the clusters, cluster V showed highest cluster mean across the maximum number of trait followed by cluster II, cluster IV and cluster VI,indicating presence of most promising genotypes in them. Selection of parents for hybridization could be made from these clusters to get desirable recombinants in order to improve the yield of finger millet. Similar findings were also reported by (6).

**Identification of Suitable donors for different traits :** Yield is the multiplicative product of several yield component characters. To develop any successful breeding programme it is not only desirable to select parents based on their yield performance and combining abilities but the identification of principal yield components. There may not be genes for yield *per se* but for their components, the multiplicative interaction of which results in ultimate yield. The improved genetic donors may be employed for combining additional

desirable characters in an otherwise good variety. Germplasm may serve as a valuable genetic donor for which a careful screening and evaluation is a must.The critical analysis of means, variability and genetic diversity in the present investigation revealed that some of the germplasm accessions of finger millet, particularly the accessions better than the best check could be utilized as donor (Table 5) for different yield components in order to breed for high yielding varieties.

PGR-MA-18-07(IV), PGR-MA-20-7 (IV), PGR-MA-22-7(IV), PGR-MA-25-07(III), PGR-MA-32-07 (III) were early maturing types as their means for days to 50% flowering were found at par with the best check (VL-149). Moreover the cluster means of the clusters having these accessions were also estimated low for this character. These accessions could be incorporated in breeding programme for developing early maturing varieties for finger millet.For productive tillers accessions GP-2012-61 (III) and GP-2011-579 (V) had more productive tillers per plant and their mean values were also found superior to the best available check (VL-315). The high cluster means of clusters III and V along with high inter cluster distance between them suggests that hybridization of these accessions will be fruitfully utilized to get transgressive segregant for this character.

However, Cluster V, III and IV exhibited high cluster mean values for finger number, the accessions GP-2011-583 (V) and GP-2011-294 (IV) only showed higher mean values superior over the best check (PRM-2) and could be used as donors for this character. Finger length was observed high for accessions GP-2011-156, MSKS-2 from cluster II, GP-2012-47, PGR-MA-35-07 from cluster III and GP-2011-236 from cluster IV. Although the cluster means for all these clusters showed intermediate values for finger length but the mean values for these accessions were found superior over the best check (VL-149), hence these accessions could be the donor for finger length.Highest mean value for spikelet density per centimetre was recorded for GP-2012-47 (III) followed by GP-2012-37 (II), GP-2012-41 (II), GP-2012-68 (II) and MSKS-2 (II) with cluster mean values of 9.82 (cluster III) and 11.87 (cluster II). The mean values of these accessions were also found higher than the best check (VL-315). The inter-cluster distance between cluster II and III was estimated as moderate indicating similarity between genotypes, so these accessions could be crossed to accessions of the other distinct clusters in order invoke variability for this character.

Members of cluster II, III, IV, V comprised of accessions which had more number of grains per spikelet such as GP-2012-5, PGR-MA-1907 from cluster II, PCPGR-8130 from cluster III, GP-2011-294 in cluster IV and GP-2011-583 from cluster V. All these accessions showed higher mean for number of grains per spikelet superior than the best check (VL-324) and represented the clusters which had higher cluster mean for the character in concern. As the inter-cluster distance between cluster II and V is high thus inter-crossing between genotypes of these diverse clusters would generate variability in the segregating generations for the development of high yielding cultivars.

For character like 1000 grain weight, remarkable diversity was seen as the accessions showing the higher mean values for the trait were distributed in different clusters. The cluster mean values for cluster II, IV, VI and VII were higher for 1000 grain weight which included genotypes GP-2011-166 (II), GP-2011-455 (II), GP-2011-322 (IV), PCPGR-8047 (VI) and GP-2011-43 (VII) with higher mean *per se*. The cluster distances between these clusters were of moderate range but these accessions could be utilized in hybridization to get better segregants. Most of the dwarf accessions were accommodated in cluster IV which included PCPGR-8113, PCPGR-8116, PGR-MA-17-07, GP-2011-460 but the most superior accession over the best dwarf check (PRM 1) was PCPGR-8112 which was included in cluster III with the cluster mean value of 110.72, however, the mean value for this shortest accession was observed as 83.48. Since all the above mentioned accessions were shorter in height therefore they could be utilized in breeding finger millet varieties for short height.

Two of the accessions present in cluster V (GP-2011-583, GP-2011-579) and three accessions from cluster VII (PCPGR-8048, PCPGR-8049, PCPGR-8046) showed highest cluster mean value for grain yield per plant with 35.98g and 26.95g mean yield per plant for cluster V and cluster VII, respectively. All the five accessions had mean values superior to the best check (VL-315). For fodder yield per plant two genotypes from cluster V (GP-2011-579, GP-2011-583), two from cluster VI (PCPGR-8047, GP-2011-109 ) and one from cluster VII (PCPGR-8049) showed higher mean values for fodder yield per plant. Out of these accessions PCPGR-8047, GP-2011-109 had the higher fodder yield per plant over the highest fodder yielding check (VL-315).Biological yield was observed higher for PCPGR-8047 (VI) followed by PCPGR-8049 (VII), GP-2011-109 (VI), GP-2011-579 (V) and GP-2011-583 (V). The cluster means for all these clusters were also found higher. All these accessions also exhibited higher mean values for fodder as well as for grain yield. Hence these accessions as such could be improved through selection to get high yielding varieties or could be utilized in hybridization to throw transgressive segregants.

Three genotypes from cluster III (PGR-MA-32-07, GP-2011-580, GP-2011-582), and two from cluster IV (PCPGR-8061, GP-2011-78) showed higher mean value for harvest index among all the genotypes under study and were superior than the best check (VL315).These accessions could be used for improving harvest index of the finger millet through hybridization. Accessions from Teheri were suitable for earliness and shorter plant height. These could be used for development of early maturing and short statured finger millet genotypes. The accessions from the region of Pithoragarh and Champawat (GP-2011-583, PCPGR-8048, PCPGR-8049, PCPGR-8046, GP-2011-579) contributed more towards the more productive tillers, finger length, finger number, spikelet density per centimetre, number of grains per spikelet, grain yield per plant, fodder yield per plant, biological yield per plant, harvest index. These traits comprised of the yield contributing characters thus they can be included in the breeding programme for the enhancement of yield. Furthermore, accessions from the regions of Chamoli and Nainital had more finger length and high 1000 grain weight, can also be utilised for increasing the yield of finger millet.

The present investigation revealed the variability and genetic diversity for different yield and contributing characters along with an attempt to characterize the accessions on the basis of morphological markers. A combination of such morphological markers differentiated the accessions from each other and grouped them in different groups but more morphological characters can be included in order to differentiate the individual accessions. Genetic diversity analyses grouped the accessions on the basis of the characters studied but higher intra cluster distances of some of the clusters indicated need of inclusion of more number of characters to achieve highly diverse grouping of the accessions.

## REFERENCES

1. Arunachalam, V. (1981). Genetic distance in plant. *Indian J. Genet. Plant Breed. 41:* 226-236.
2. Ward, J. H., Jr. (1963). Hierarchical Grouping to Optimize an Objective Function. *Journal of the American Statistical Assosiation. 58:* 236–244.
3. Kandam, D.D. (2007). Genetic architecture on finger millet [*Elusine corcana* (L.) Gaertn]. *International Journal of Agricultural Sciences. 3(2):* 104-107.
4. Kadam, D.D. (2008). Genetic divergence in finger millet (Nachani/Ragi/Nagali/Eluesine coracana). *Journal of Soils and Crops, 18(1):* 138-142.
5. Prabhu, D.A., Selvi, B. and Govindaraj, M. (2008). Genetic variability and multivariate analysis in finger millet (*Eleusine coracana*) germplasm for yield characters. *Crop-Research-Hisar. 36(1/3):* 218-223.
6. Satish, D., Shanthakumar, G., Salimath, P.M., Prasad, S.G. (2007). Genetic diversity for productivity traits in finger millet. Dept.of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad (Karnataka), India. *International-Journal-of-Plant-Sciences-Muzaffarnagar. 2(2):* 34-37.

Received : December-2018; Revised : January-2018; Accepted : January-2019