RESEARCH ARTICLE

# EXTENT OF RELATEDNESS AMONG PRE-RELEASED AND RELEASED VARIETIES OF FINGER MILLET (*ELEUSINE CORACANA* L. GAERTN)

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**Abstract:** A field study was conducted at Research cum Instructional Farm, S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur, IGKV, Raipur (C.G.),in *Kharif* -2019, in a Randomized Block Design with 3 replications to evaluate 11 accessions of finger millet (*Eleusine coracana* L. Gaertn). The observations of 13 qualitative and 13 quantitative characters were recorded at different stages of plant growth from flowering stage to harvest, according to the Guidelines for the test of DUS on Finger millet by PPV& FRA, Government of India. Genotypes were grouped into three clusters based on the $D^2$ values irrespective of geographical diversities, among which maximum inter-cluster distance was found between cluster II and cluster I, followed by cluster III and cluster II and cluster III and cluster I, which indicates that the use of genotypes from these clusters can serve as potential parents for hybridization. In view of cluster mean and genetic distance, the crossing of entries of cluster I with entries of cluster III would be fruitful for obtaining transgressive segregants for developing high yielding and better quality finger millet varieties.

**Keywords:** $D^2$ statistics, Finger millet, Genetic closeness, Heterotic parents

## INTRODUCTION

Finger millet (*Eleusine coracana* L. Gaertn), also known as Ragi, Birds foot millet or African millet, is an annual robust, tufted, tillering annual grass, mainly grown as a grain cereal in the semi-arid tropics and subtropics of the world, particularly in India, Africa and South Asia, under rain fed conditions. The usually cultivated finger millet is an allotetraploid species with 36 chromosomes (2n= 4x= 36) and is derived from its wild ancestor *E. coracana* subsp. *Africana*and its wideadaptability to diverse environments andcultural conditions makes it a potential foodcrop. The grain is readily digestible, highly nutritious and versatile, and can be cooked like rice, ground to make porridge or flour, or used to make cakes and is advisable for infants as well as elderly people. Finger millet is also used to make liquor and beer, which yields by-products used for livestock feeding, but is of lesser quality for livestock than maize, sorghum and pearl millet (Rao, 2017).

Techniques that measure the genetic relationship without any influence of environmental factors can be made used along with required phenotypic characteristics for the breeding programme.Genetic improvement through conventional breeding approaches depends mainly on the availability of the diverse germplasm and the amount of genetic variability present in the population(Arun*et al.*, 2008). An attempt was made to estimate the extent of variation for yield contributing traits in 11 fingermillet genotypes by studying thegenetic parameters like phenotypic coefficient of variation (PCV), genotypic coefficient ofvariation (GCV), heritability and genetic advance, which may contribute to formulation ofsuitable selection indices for improvement in this crop.Also, the use of, $D^2$ statistics, a concept developed by Mahalanobis (1936), which is an important tool to plant breeder to classify the genotypes into different groups based on genetic divergence between them. The intra and iter-clusture distances between genotypes serves as index for selection of parents with diverse origin (Negi*et al*., 2017). The current study was undertaken to assess the nature and magnitude of genetic divergence for yield and its component in finger millet and also to identify divergent parents from distantly related clusters for suitable hybridization through genetic divergence analysis.

## MATERIALS AND METHODS

The study was conducted during *Kharif* **-**2019 at Research cum Instructional farm, S. G. College of Agriculture and Research station, Kumhrawand, Jagdalpur, Bastar, under IGKV, Raipur (C.G.). Eleven distinct genotypes were sown on 24th July 2019 with Randomized Block Design (RBD) as the experimental design in three replications.The seeds were directly line sown with a spacing of 22.5 cm within rows and 10 cm between the plants and a recommended dose of 40 kg N/ha and 25 kg DAP/ha was applied at the time of sowing. Recommended package of cultural practices were followed throughout crop growth period to raise a good crop.Two varieties *viz.* Indira Ragi 01 and Chhattisgarh Ragi 02 were grown as local check varieties and others were pre- released genotypes from different geographical locations of the sub-continent, all provided uniform cultural practices. The quantitative characters are recorded by calculating the averages of five randomly selected

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plants from each plots, except for Days to 50% flowering. The stages and methods for observation are accordingto the Guidelines for the conduct of test for Distinctiveness, Uniformity and Stability (DUS) on finger millets (*Eleusine coracana* (L.) Gaertn.) byProtection of Plant Varieties and Farmers' Rights Authority(PPV & FRA). Thirteen quantitative characters were observed namely, days to 50% flowering, flag leaf blade length, flag leaf blade width, peduncle length, ear head length, finger length, finger width, number of finger on main ear, number of productive tillers per plant, plant height at maturity, 1000 grain weight, fodder yield per plot and grain yield per plot, during different stages of plant growth. The mean data of all three replications of all quantitative characters were used for statistical and genetic analysis. The genetic divergence was computed using Mahalanobis' $D^2$ statistics among all the eleven genotypes and based on genetic distance, all the genotypes were grouped into different clusters. Relative contributions of each quantitative character towards genetic divergence were also taken into consideration for establishing diversity among genotypes.

## RESULTS AND DISCUSSION

$D^2$statistics is a concept developed by Mahalanobis (1936), which is used as a prime tool by plant breeder to classify the genotypes into different groups based on genetic divergence between them. The basic idea behind formation of clusters is to get the intra and inter-cluster distances, which serves as index for selection of parents with diverse origin. Clustering of genotypes were done according to Tocher's method as described by Rao (1952) (Negi *et al*. 2017). The eleven genotypes of finger millet were grouped into three different non-overlapping clusters as shown in Table 1. Cluster III had maximum number of genotypes i.e. five genotypes, cluster I and cluster II had three genotypes each. Intra and inter cluster $D^2$ values were worked out to establish divergence among the genotypes as shown in Table 2 and Figure 1**.** Cluster III showed maximum intra- cluster distance (2.815), followed by cluster I (2.755) and cluster II (2.552). This implies that these clusters have the genotypes with varied genetic architecture. High intra-cluster genetic distance in cluster III was because of heterogeneous composition of that cluster. Collaborative results have also been given by Bedis *et al.*, 2007, Das *et al.*, (2013),Wolie *et al.*, (2013) and Negi *et al.*, (2017). Maximum inter-cluster distance was observed between cluster I and cluster II (4.292). High inter-cluster distances were also found between cluster II and cluster III (3.629) and least inter-cluster distance was observed between cluster I and cluster III (3.322). The clusters with higher inter-cluster distances indicates that the genotypes grouped in those clusters showed high genetic variation and hybridization between genotypes of these clusters may result in heterotic hybrids because of convergence of diverse genes scattered in parents to progeny. The clusters with low inter-cluster distances indicated that genotypes present in these cluster pairs were genetically close to each other and the crosses between genotypes belonging to these clusters are likely to throw promising recombinants in the segregating generations. Complementary results were recorded by Kumar *et al.*, (2010), Sahu *et al.*, (2012), Harti *et al.*, (2013), Negi *et al.*, (2017)

Cluster I, with three genotypes showed highest cluster mean values for peduncle length, number of productive tillers per plant and plant height at maturity. Genotypes included in cluster I showed high values for characters controlling vegetative growth and therefore it can be used for the improvement of vegetative parameters when used for breeding programme. Cluster II, with three genotypes exhibited highest cluster mean values for days to 50% flowering, flag leaf blade width, ear-head length, finger length, number of finger on main ear, fodder yield per plot and grain yield per plot. Genotypes of cluster II showed high cluster mean values mainly for pre yield and yield parameters, thus genotypes including in this cluster can be used for improvement of a large number of seed yield and yield contributing characters, at the same time. Cluster III having three genotypes, showed highest cluster means for flag leaf blade length and 1000 grain weight. The genotypes in cluster III can be used to improve grain filling as they show high values for flag leaf blade length and 1000 grain weight. Cluster means of finger millet genotypes for different quantitative traits are shown in Table 3. Characters with high cluster means in respective clusters when used as criteria for hybridisation in genotypes of that clusters, will give better results.

Highest percentage contribution towards genetic divergence was shown by flag leaf blade length (11.91%), followed by flag leaf blade width (11.63%) and plant height at maturity (10.45%). Lowest percentage contribution towards genetic divergence was shown by finger number on main ear (3.38%), followed by grain yield per plot (4.52%), days to 50% flowering (4.76%) and number of productive tillers per plant (4.86%). Characters which show high contribution towards divergence tends to exhibit low variations among genotypes. Also these characters are not inherited to the next generation in a commendable amount and its expression is also reduced. Characters contributing less towards genetic divergence seem to show high variations among the genotypes. These characters are passed on and expressed well in the next generation. The latter trend is observed in characters like number of productive tillers per plant, finger number on main ear, grain yield per plot, finger length and days to 50% flowering. Percentage contributions towards genetic divergence of thirteen quantitative characters of finger millet are given in Table 4. The observation is complementary to the studies by Bedis *et al.,* 2007, Shinde *et al.*, 2014 and Negi *et al.*, 2017.

## CONCLUSION

The study revealed significant diversities among the 11 finger millet accessions in terms of quantitative characters and genetic parameters. High coefficients of variability are found in number of productive tillers per plant and finger length, indicating that these characters are more variable among the germplasms. High heritability coupled with high genetic advance was observed for days to 50% flowering, suggested that it may be successfully used as selection criteria in improving grain yield. Diversity among the genotypes were predominantly assessed through $D^2$ distances between them, when grouped into different clusters. Maximum inter-cluster distance is found between cluster I and cluster II, which proves that genotypes under these two clusters shows wide variability among each other.Genotypes in cluster II were showing lowest intra-cluster distances, hence those genotypes are most closely related ones. Low contribution towards genetic divergence was shown by finger number on main ear, number of productive tillers per plant and days to 50% flowering, which indicates that it is inherited and expressed in a good amount from generation to generation, hence can be used as a viable criterion for breeding programmes. This study will serve as a reference for agro-morphological characterization studies and genetic diversity studies on finger millet under rainfed conditions in future.

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**Table 1.** Clustering pattern of 11 finger millet genotypes based on genetic divergence

| **Cluster** | **Genotypes** |
|---|---|
| Cluster I | BR-9, BR-14-28, BR-14-1 |
| Cluster II | BR-14-17, Indira Ragi -01, GPU-67 |
| Cluster III | BR-14-27, BR-14-3, BR-14-2, CG Ragi -02, GPU-28 |

**Table 2.** Average intra and inter-cluster $D^2$ values among 11 finger millet genotypes

| **Cluster** | Cluster I | Cluster II | Cluster III |
|---|---|---|---|
| Cluster I | **2.755** | | |
| Cluster II | 4.292 | **2.552** | |
| Cluster III | 3.322 | 3.629 | **2.815** |

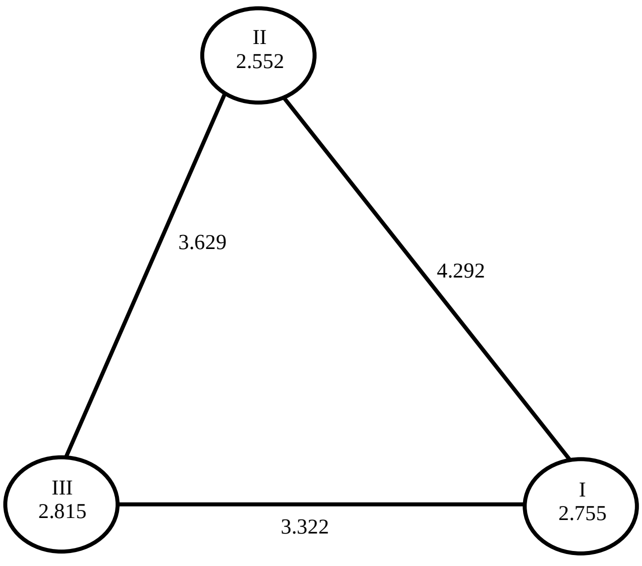


**Figure 1.** Intra and inter cluster distances among 3 clusters of 11 finger millet genotypes

**Table 3.** Cluster means of components of 3 clusters of 11 finger millet genotypes

| Sl. No. | Characters | Cluster I | Cluster II | Cluster III |
|---|---|---|---|---|
| 1. | Days to 50% flowering | 59.11 | 85.11 | 75.47 |
| 2. | Flag Leaf Blade Length (cm) | 30.44 | 30.54 | 34.33 |
| 3. | Flag Leaf Blade Width (cm) | 1.00 | 1.04 | 1.02 |
| 4. | Peduncle length (cm) | 21.61 | 20.99 | 19.23 |
| 5. | Ear-head length (cm) | 7.67 | 10.13 | 7.46 |
| 6. | Finger: Length (cm) | 5.78 | 9.62 | 7.75 |
| 7. | Finger: Width (cm) | 1.02 | 1.05 | 0.94 |
| 8. | Finger: No. on main ear | 7.20 | 8.27 | 7.68 |
| 9. | Number of productive tillers per plant | 1.98 | 1.49 | 1.89 |
| 10. | Plant: Height at maturity (cm) | 101.56 | 100.20 | 89.35 |
| 11. | 1000 Grain weight (g) | 2.86 | 3.15 | 3.28 |
| 12. | Fodder yield in kg/plot | 2.91 | 4.04 | 3.41 |
| 13. | Grain yield in kg/plot | 1.24 | 1.76 | 1.25 |

**Table 4.** Percentage contribution of 13 quantitative characters towards genetic divergence

| Sl. No. | Characters | Mean | % Contribution |
|---|---|---|---|
| 1. | Flag Leaf: Blade Length (cm) | 32.24 | 11.91 |
| 2. | Flag Leaf: Blade Width (cm) | 1.02 | 11.63 |
| 3. | Plant: Height at maturity (cm) | 95.64 | 10.45 |
| 4. | Finger: Width (cm) | 0.99 | 9.75 |
| 5. | Peduncle length (cm) | 20.36 | 9.37 |
| 6. | Ear-head length (cm) | 8.25 | 8.73 |
| 7. | 1000 Grain weight (g) | 3.13 | 8.21 |
| 8. | Fodder yield in kg/plot | 3.45 | 7.07 |
| 9. | Finger: Length (cm) | 7.72 | 5.37 |
| 10. | Number of productive tillers per plant | 1.81 | 4.86 |
| 11. | Days to 50% flowering | 73.64 | 4.76 |
| 12. | Grain yield in kg/plot | 1.39 | 4.52 |
| 13. | Finger: No. on main ear | 7.71 | 3.38 |

## REFERENCES

**Arun Prabhu, D., Selvi, B. and Govindaraj, M.** (2008). Genetic variability and multivariate analysis in finger millet (*Eleusine coracana*) germplasm for yield characters. *Crop Res*., 36 (1, 2 & 3): 218-223.

**Bedis, M.R., Patil, H.S., Jangle, G.D. and Patil, V.S.** (2007). Correlation and path coefficient analysis in finger millet(*Eleusine coracana* (L.) Gaertn.). *Crop Res*., 31 (2): 264-266.

**Das, R., Sujatha, M., Pandravada, S.R. and Sivasankar, A.** (2013). Trait relationship and path coefficient analysis in finger millet (*Eleusine coracana*L.). Journal of Progressive Agriculture, 4(1): 81-84

**Gowda, M.V.C., Ravishankar, P. and Patro, T.S.S.K**. (2001). Guidelines for the conduct of test for Distinctiveness, Uniformity and Stability onFinger millet (*Eleusine coracana* (L.) Gaertn.) Protection of Plant Varieties and Farmers' Rights Authority. Government of India.

**Haradari, I.C., Ugalat, J. and Nagabhushan** (2012). A study on character association, geneticvariability and yield components of finger millet (*Eleusine coracana* L.). *J. of Crop and Weed*.8(2):32-35.

**Harti, M., Gowda, J., Mallikarjun, K., Basavaraja, T. and Vijayakumar, L**. (2013). Genetic diversity assessment for yield and its attributes characters of white seeded accession in finger millet (*Eleusine coracana* (L.) Gaertn). *Environ. and Eco.* 31(2): 740-744.

**John, S. and Kumar, P**. (2018). Character Association among Vegetative, Pre-yield and Yield Parameters in Finger Millet (*Eleusine coracana* L.), *Int. J. Pure App. Biosci*. 6(2): 156-161.

**Kumar, D., Tyagi, V., Ramesh, B. and Pal, S**. (2010). Genetic diversity in finger millet (*Eleusine coracana* (L.) Gaertn). *Crop Imp.* 37(1):25-28.

**Mahalanobis, P.C.** (1936). On the generalized distances in statistics. *Proc. Nat. Inst. Sci., India.* 2(1): 49-55.

**Negi, S., Kumar, V. and Bhatt, A**. (2017). Genetic Diversity among Finger Millet [*Eleusine coracana*(L.) Gaertn] Genotypes for Yield and Its Contributing Traits. *Int. J. Curr. Microbiol. App. Sci.,* 6(8): 3332-3337.

**Rao, C.R.** (1952). Advance statistical methods in biometric research. *Wiley and Sons, New York*.pp.390.

**Rao, B. D., Bhaskarachary, K., Christina, G.D., Devi, S.G. and Tonapi, V.A**. (2017). Nutritional and Health benefits of Millets., ICAR, Indian Institute of Millets Research (IIMR), 1: 15-17, 5: 65-68.

**Sahu, S., and Pradhan, K.** (2012). Genetic divergence in finger millet (*Eleusine coracana* (L.) Gaertn). *Environ. and Eco.,*30(2): 291-294.

**Shinde, S.R., Desai, S.V. and Pawar, R.M.** (2014). Genetic variability and character association in finger millet [*Eleusine coracana* (L.) Gaertn]. *Int. J. Plant Sci.*, 9 (1): 13-16.

**Wolie, A. and Belete, K.** (2013). Genetic divergence and variability studies in some Ethiopian finger millet germplasm collections. Scholarly *J. of Agric. Sci*., 3(4): 110-116.