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# Studies on genetic diversity for yield and nutritional components in foxtail millet genotypes

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**Abstract**
The Agricultural Research Station in Buldhana was the location where this study was conducted during the Kharif 2018 and Kharif 2019 seasons. Foxtail millet, (*Setaria italica* (L.) P. Beauv) was used as the experimental material, and there were 52 different accessions altogether. The purpose of this study was to collect data on twelve quantitative factors to determine the degree of genetic divergence that exists between yield and the attributes that contribute to yield. Within the scope of this inquiry, the $D^2$ statistic illuminated the genetic differences that existed between the genotypes that were being investigated. On the basis of the genetic distances between the 52 genotypes, six groups were constructed between them. Cluster I has the top 41 genotypes, whereas Cluster II, which is another significant cluster, contains seven genotypes derived from a variety of sources. Clusters III–VI, which collectively contain a single genotype, are referred to be monogenic. The relationships with the largest distances were those between clusters II and III ($D^2$ = 2864.39), clusters II and IV ($D^2$ = 2201.49), and clusters IV and VI. Cluster V had the highest average grain yield (18.21), followed by cluster IV with a yield of 20.86, and cluster VI with the lowest yield (11.91). Using genotypes from a separate cluster (IV and II) might be a viable option for a hybridization program aiming to increase millet yield, according to the $D^2$ research.

**Keywords:** Foxtail millet, genetic divergence, clusters, inter-cluster, intra-cluster, yield

## Introduction
Foxtail millet, scientifically named *Setaria italica* (L.) P. Beauv., is also referred to as Italian, German, Chinese, and Hungarian millet. Navane from the Kannad area, Korralu from the Telgu language, Tenai from Tamil, Kangini from Gujrathi and Hindi, and Kang and Rala from Marathi are among the most common names in India. The cultivation of this ancient crop began with grazing, and later expanded to include hay and grain for human use. The primary variation center for this crop is situated in East Asia, which encompasses both Japan and China, as stated by Vavilov (1926) [18]. According to recent archeological findings, millet was the earliest crop ever cultivated, having a history of 8,700 years in China (Lu *et al.*, 2009) [8]. So, the oldest crop you can cultivate is millet. This grain crop is grown in several sections of southern Europe, tropical and subtropical Asia, and some areas of Asia overall. China, India, and Japan are the three main millet-growing nations in the globe. "Foxtail millet can only be grown in the Indian states of Andhra Pradesh, Karnataka, Tamil Nadu, and a tiny portion of Maharashtra. In many parts of the world, including Asia, Africa, Europe, North America, and Australia, foxtail millet is still widely farmed as a grain crop or animal feed, despite its progressive reduction in importance over the previous eight decades due to the rapid growth of maize and other crops (Austin, 2006) [3]. It would be absurd to suppose that foxtail millet yields are low. The primary problem isn't a lack of superior cultivars; rather, it's because the crop is frequently grown in conditions that aren't ideal for plant development-rainfed fields. China has produced yields that range from 1,500 kg ha$^{-1}$ to 2,250 kg ha$^{-1}$, according to Jiaju (1986) [5]."According to the ICAR-AICRP on Small Millets, Annual Progress Report, 2021–2022, this crop is currently grown on a 4.58 lakh hectares in a number of locations throughout the states of Andhra Pradesh, Karnataka, Tamil Nadu, Maharashtra, Rajasthan, Madhya Pradesh, Uttar Pradesh, and the North Eastern states." This crop yields 804 kg ha$^{-1}$ and produces 3.70 lakh tons annually.

**Materials and Methods:** In the experiment, there were a total of 52 different genotypes of foxtail millet that were utilized.

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These genotypes were collected from various locations across India. For the purpose of determining the extent of the genetic variation, twelve characteristics that contribute to yield were assessed. During the 2018 and 2019 Kharif seasons, these genotypes were experimentally planted in the field of the Agriculture Research Station in Buldhana (MH) using a randomized block design with three replications. "Every plant was separated from the others by 10 cm, and there were three meters each row. There was a thirty-centimeter space between each row. Plant height, total tillers per plant, productive tillers per plant, panicle length, panicle girth, grain yield per plant, straw yield per plant, and thousand grain weight were assessed for five randomly selected plants from each genotype in each replication. On plot basis, we monitored the days to 50% flowering and the days to maturity. A statistical study was performed on the means of five plants, and the genetic divergence was determined by the utilization of multivariate analysis and the $D^2$ statistic developed by Mahalanobis (1936) [9], as Rao (1952) [13] demonstrated." Tocher's method, which was developed by Rao (1952) [13], was utilized to categorize genotypes into separate clusters for the purpose of determining $D^2$ values.

**Results and Discussion**
Studies on genetic diversity offer fundamental knowledge about the genotypes' genetic characteristics, which is used to build breeding strategies for future crop development. Understanding the type and degree of variation that may be linked to many causes, crop sensitivity to environment and genetic divergence is another benefit of this research.

Mahalanobis initially proposed the idea of $D^2$ statistics in 1936; since then, plant breeders have used it to classify genotypes into different groups according to the degree of genetic diversity between them.

With a total of 42.31%, grain yield per plant was the most significant factor in the total genetic divergence. Next came the straw yield per plant (34.54% of the total) and the panicle length (8.07% of the total) and. Other characters' contributions were quite minor, as seen in Table 2.

Six clusters were formed from all the genotypes as a result of the clustering pattern. The biggest cluster, with 41 genotypes from different parts of the world, was Cluster I. Cluster II included a grand total of seven genotypes. There is just one genotype in each of the other four clusters (III, IV, V, and VI), as shown in Figure 1 and Table 1. We say that these clusters are monogenic.

The intra- and inter-cluster $D^2$ values were computed using the $D^2$ values obtained from the divergence analysis. The average $D^2$ values of the cluster members were used to calculate all distances, both within and across clusters. The intra-cluster $D^2$ values varied widely from 143.46 to nil. Cluster II had the longest intra-cluster distance ($D^2$ = 143.76), whereas Cluster I had the second-largest distance (91.01). The cluster had a single genotype shows zero intra cluster distance. The largest inter-cluster distance was found between cluster IV and cluster VI ($D^2$ = 3174.20), followed

by cluster II and cluster III ($D^2$ = 2864.39) cluster II and cluster IV ($D^2$ = 2201.49). The largest distance of cluster I was found with cluster VI ($D^2$ =454.54, then cluster II ($D^2$ =448.17), cluster IV ($D^2$ =445.21) and cluster V ($D^2$ =339.90). The cluster II has the longest inter-cluster distance between cluster III ($D^2$ =2864.39) after that cluster IV ($D^2$ =2201.49) and cluster V ($D^2$ =1572.92). Third cluster was most distant from cluster VI ($D^2$ =1297.37) then, cluster V ($D^2$ =379.04) and cluster IV ($D^2$ =276.65). The cluster IV showed the highest inter-cluster distance with cluster VI ($D^2$ =3174.20) followed by cluster V ($D^2$ =129.28). The cluster V found longest inter cluster distance with cluster VI ($D^2$ =1336.63) (Table 3) (Fig.2).

When looking at the number of days till 50% flowering, cluster VI had the highest cluster mean at 67.67 and cluster IV had the lowest at 55.00. Cluster I had the highest cluster mean for days to maturity (99.00 days), cluster IV had the shortest (87.50 days). The cluster II (5.29) had the highest cluster mean for total number of tillers, while cluster V (3.52) had the lowest. For the quantity of productive tillers, cluster II had the greatest cluster mean (4.23), whilst cluster V had the lowest (2.52). In terms of cluster mean, Cluster II was at the top. Cluster V had the greatest mean values (161.83) for plant height, while Cluster VI had the lowest (126.00). Cluster VI had the shortest panicle length (16.43), in contrast to cluster IV longest panicle length (22.60). Cluster VI has the lowest mean (4.28) for panicle girth compared to the other clusters, whereas cluster V has the largest mean (7.12). Cluster IV had the highest cluster mean grain yield per plant (20.86), followed by cluster V (18.21) and cluster VI (11.91) found to be lowest. "The average amount of straw yield per plant was the lowest in Cluster VI (20.03), while it was the highest in Cluster IV (34.90). Cluster IV had the greatest cluster mean (3.02) for thousand grains weight, whereas Cluster III exhibited the lowest value (2.42). The grain Fe content was highest in Cluster IV (52.12) and lowest in Cluster VI (15.57). The cluster mean was greatest in Cluster III (55.98) for Zn concentration while it was lowest in Cluster II (21.81) compared to Cluster the cluster with the highest mean. (Table 4).

Grain yield per plant was highest in the cluster IV genotype group, which was strongly connected with more panicle length, straw yield per plant, thousand grain weight, and grain iron content. Furthermore, both the days to maturity and the number of days to 50% flowering were low in this cluster. Members of the genotype group located in cluster V had tall plants with large panicles." Cluster II genotypes had an high total tillers as well as a very high productive tiller per plant. Cluster III genotypes were shown to have high zinc concentrations in their grain.

Considering the information given before Intercrossing genotypes from different clusters can increase diversity, which in turn can increase yield, tillers, and nutritional value through selection. The scientists who disclosed these findings are Sheriff (1992) [16], Maloo and Bhattacharjee (1999) [10], Satish (2003) [14], Shanmuganathan et al. (2006) [15], Bedis et al. (2007) [4], Nirmalakumari and Vetriventhan (2010) [12], Kumuda et al. (2011) [7], Yogeesh et al. (2015) [19], Amarnath et al. (2019) [1], and Karvar et al. (2022) [6].

**Table 1:** Clustering pattern of foxtail millet genotypes

| Clusters | Total no. of genotypes | Genotypes included in the clusters | | |
|---|---|---|---|---|
| I | 41 | IC-120148 | IC-97195 | IC-97107 |
| | | IC-120204 | IC-97167 | IC-97114 |
| | | IC-120177 | IC-333258 | IC-97188 |
| | | IC-120237 | IC-97105 | IC-97185 |
| | | IC-120195 | IC-97191 | IC-97196 |
| | | IC-120166 | IC-120236 | IC-97194 |
| | | IC-120247 | IC-120406 | IC-97189 |
| | | IC-120208 | IC-28471 | IC-120201 |
| | | IC-120167 | IC-120243 | IC-120200 |
| | | IC-97296 | IC-120183 | IC-97293 |
| | | IC- 356779 | IC-120228 | IC-97177 |
| | | IC-120255 | IC-120221 | IC-120192 |
| | | IC-97109 | IC-326751 | IC-120150 |
| | | IC-120182 | PS4 | |
| II | 7 | IC-120408 | IC-97130 | IC-120234 |
| | | Lepakshi | IC-97111 | |
| | | IC-97116 | IC-120244 | |
| III | 1 | IC-120213 | | |
| IV | 1 | IC-120235 | | |
| V | 1 | IC-120149 | | |
| VI | 1 | IC-97172 | | |

**Table 2:** Contribution of each character towards Total genetic divergence

| Sr. No. | Character | % Contribution | Times ranked 1st |
|---|---|---|---|
| 1 | Days to 50% flowering | 0.53 | 7 |
| 2 | Days to maturity | 0.13 | 2 |
| 3 | Total No. of tillers | 1.58 | 21 |
| 4 | No. of productive tillers | 0.83 | 11 |
| 5 | Plant height (cm) | 1.51 | 20 |
| 6 | Panicle length (cm) | 8.07 | 107 |
| 7 | Panicle girth (cm) | 2.41 | 32 |
| 8 | Grain yield / plant (gm) | 42.31 | 561 |
| 9 | Straw yield / plant (gm) | 34.54 | 458 |
| 10 | 1000 grain weight (gm) | 5.30 | 70 |
| 11 | Grain Fe Content (mg/kg) | 2.64 | 35 |
| 12 | Grain Zn Content (mg/kg) | 0.15 | 2 |

**Table 3:** Average intra and inter clusters distance in Foxtail millet

| Clusters | I | II | III | IV | V | VI |
|---|---|---|---|---|---|---|
| I | 9.54 (91.01) | 21.17 (448.17) | 17.93 (321.48) | 21.1 (445.21) | 18.42 (339.90) | 21.32 (454.54) |
| II | | 11.99 (143.76) | 53.52 (2864.39) | 46.92 (2201.49) | 39.66 (1572.92) | 25.93 (672.36) |
| III | | | 0.00 (0.00) | 16.63 (276.65) | 19.47 (379.04) | 36.02 (1297.37) |
| IV | | | | 0.00 | 11.37 (129.28) | 56.34 (3174.20) |
| V | | | | | 0.00 (0.00) | 36.56 (1336.63) |
| VI | | | | | | 0.00 (0.00) |

**Table 4:** Cluster mean performance for 12 characters in Foxtail millet

| Sr. No. | Character | Clusters | | | | | |
|---|---|---|---|---|---|---|---|
| | | I | II | III | IV | V | VI |
| 1 | Days to 50% flowering | 57.33 | 57.62 | 57.50 | 55.00 | 66.17 | 67.67 |
| 2 | Days to maturity | 88.41 | 88.57 | 89.00 | 87.50 | 97.00 | 99.00 |
| 3 | Total No. of tillers | 4.68 | 5.29 | 4.35 | 4.62 | 3.52 | 4.85 |
| 4 | No. of productive tillers | 3.65 | 4.23 | 3.42 | 3.55 | 2.52 | 3.92 |
| 5 | Plant height (cm) | 130.94 | 127.69 | 128.83 | 139.50 | 161.83 | 126.00 |
| 6 | Panicle length (cm) | 17.37 | 17.41 | 17.10 | 22.60 | 21.02 | 16.43 |
| 7 | Panicle girth (cm) | 4.97 | 4.81 | 4.62 | 5.47 | 7.12 | 4.28 |
| 8 | Grain yield / plant (gm) | 13.40 | 12.62 | 15.82 | 20.86 | 18.61 | 11.91 |
| 9 | Straw yield / plant (gm) | 23.66 | 22.56 | 28.72 | 34.90 | 33.06 | 20.03 |
| 10 | 1000 grain weight (gm) | 2.52 | 2.47 | 2.42 | 3.02 | 2.88 | 2.48 |
| 11 | Grain Fe Content (mg/kg) | 34.18 | 25.17 | 44.17 | 52.12 | 45.52 | 15.57 |
| 12 | Grain Zn Content (mg/kg) | 38.30 | 21.81 | 55.98 | 41.72 | 39.82 | 40.65 |
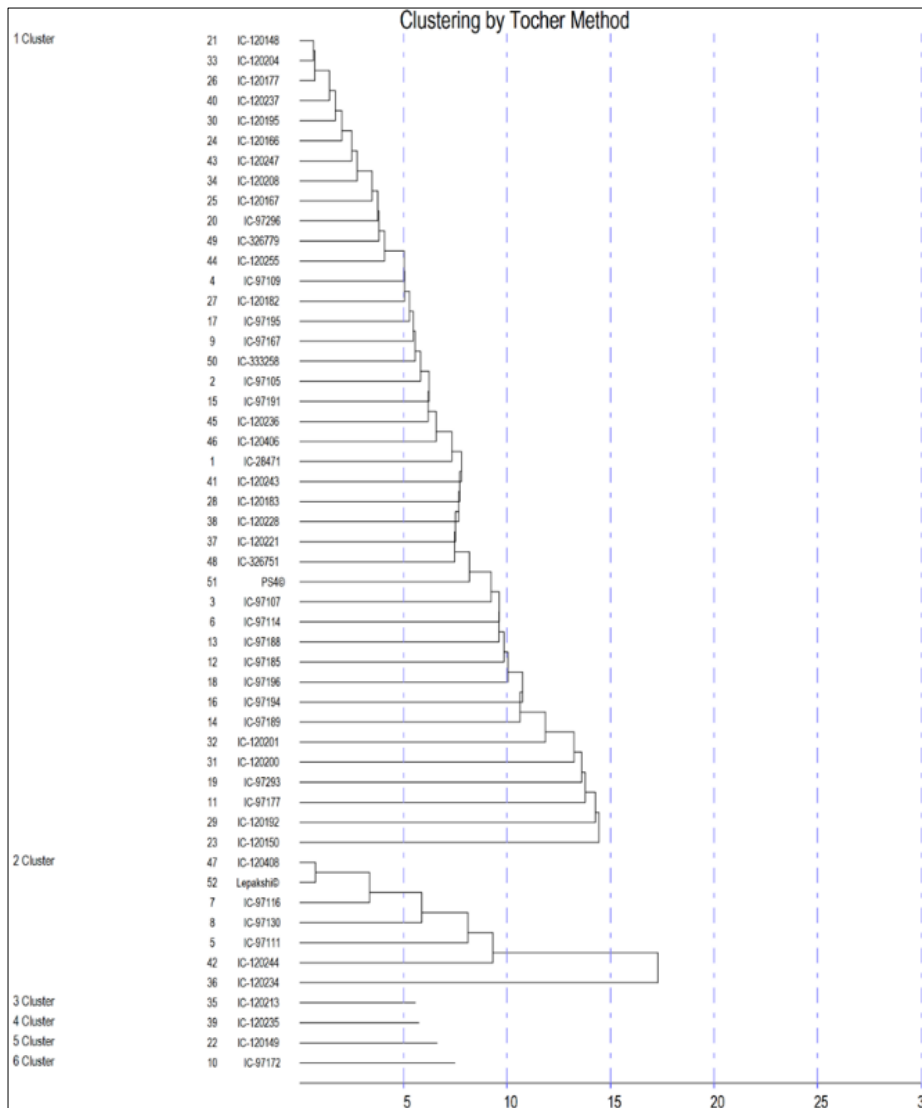
**Fig 1:** Clustering pattern of 52 genotypes foxtail millet (Tocher`s method)
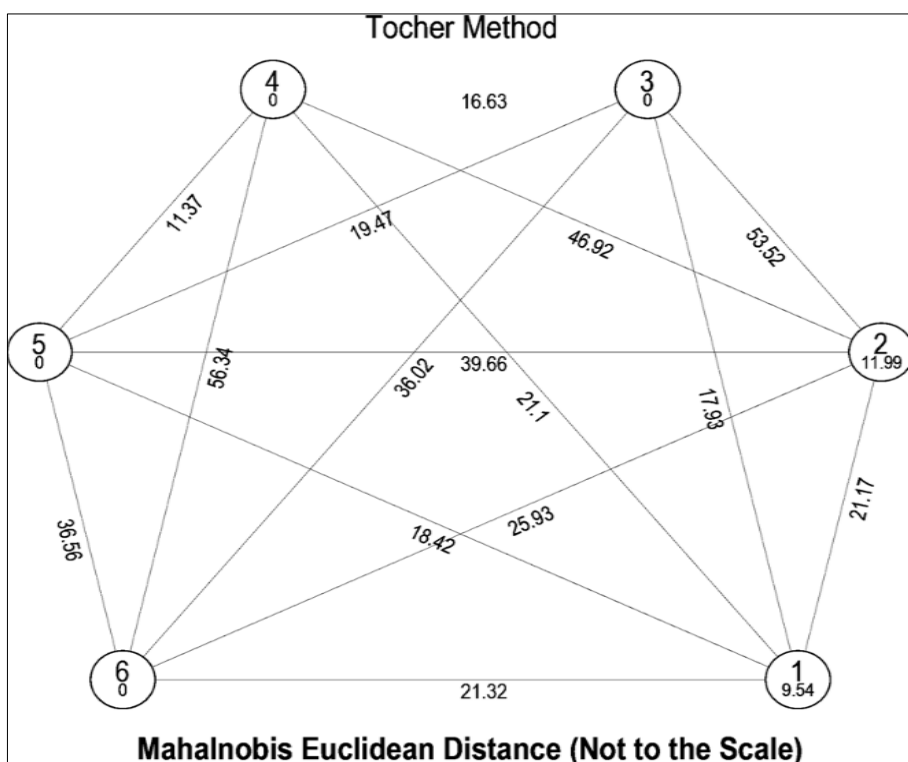


**Fig 2:** Intra and inter cluster distances among six clusters in foxtail millet

## Conclusion

For this reason, we are able to assert that the genotypes from clusters IV and V were the most dissimilar of all the clusters. In order to obtain a wide range of variation among the sergeants, a hybridization method may use the genotypes from the different cluster (IV and II). This would be done in order to acquire the desired results.

## Future Scope

The creation of high-yielding foxtail millet cultivars might be aided by further research on critical traits such as the length of the panicle, the number of days to fifty percent flowering, the amount of iron and zinc in the grain, and the amount of grain produced per plant. It is possible that more research into the genes and genetic process that lie under the surface may give meaningful insights into the character.

## Acknowledgements

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