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## Research Article

# Assessment of genetic diversity in Indian Italian millet genetic resources [*Setaria Italica* (L.) Beauv]

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**Abstract**
Fifty Italian millet genetic resources were studied to assess the magnitude of genetic diversity for 12 quantitative traits using Mahalanobis $D^2$ Statistic. Based on Tocher's method, the entire genetic resources were partitioned into nine distinct non-overlapping clusters suggesting availabilty of substantial genetic diversity. Cluster I was the largest comprising of large number of accessions (36) followed by cluster II with (7) accessions and the remaining were mono genotypic clusters III, IV, V,VI,VII, VIII and IX containing only single accession each indicating high degree of heterogeneity among the genotypes. Clusters II and IX showed maximum inter-cluster distance between them implying these genetic resources with high degree of genetic diversity may be utilized in inter-varietal hybridization programme. The trait, culm branches followed by 1000 grain weight contributed maximum towards total divergence indicating feasibility of improvement through those characters.

**Key words**
$D^2$ Statistic and Italian millet.

## Introduction

Millet cultivation is overlooked due to the impact of green revolution and is further stepped down to "Orphan cereals". (Brunda *et al.,*2015). However, in the present scenario, more emphasis is being laid on small millet crops owing to their reorientation to the nutritional importance as "Nutri diet". In recent times, rapid expansion of small millets area is chiefly attributed to short duration ability, resilience to erotic climatic situations and heavy demand from health conscious consumers. Among the small millets, Italian millet ranks second in terms of global production next to finger millet. The grains of this millet are an excellent source of quality proteins (leucine and methionine), beta carotene, minerals (Ca, Fe, K, Mg and Zn), antioxidants, dietary fibre, phytochemicals, vitamins (thiamine, riboflavin and niacin) and possess low glycemic index, a requisite for healthy human diet. Despite its economic importance, limited research progress was made to study the genetic resources of Italian millet. In order to identify diverse genetic resources, precise information on the nature and degree of genetic diversity is required which in turn helps the plant breeders in selecting the parents for targeted hybridization (Reddy *et al.* 2015). Thus, genetic divergence studies enable to assess the extent of genetic diversity prevalent in the genetic resources utilized for study.

## Material and Methods

A set of 50 genetic resources of Italian millet were evaluated during *kharif,* 2017 in a randomized block design, replicated thrice at RARS, Nandyal. The datails are given in the annexure I. Each genetic resource was represented by a single row plot of 3 m length with inter and intra-row spacing of 22.5 cm and 10 cm respectively. Data were recorded on five randomly selected competitive plants of each genetic resource / replication for 12 quantitative traits *viz.*, days to 50% flowering, days to maturity, plant height, peduncle length, peduncle exertion, panicle length, flag leaf blade length, flag leaf blade width, culm branches, total number of productive tillers / plant, 1000 grain weight and grain yield / plant. The data was analyzed through software - WINDOWSTAT 9.2 version.

## Results and Discussion

The analysis of variance (Table 1) revealed significant differences among the genetic resources for all the characters studied indicating considerable extent of variability in the germplasm accessions, which could be utilized in further breeding programmes. Based on relative magnitude of $D^2$ values, 50 genetic resources were grouped into nine distinct non-overlapping clusters (Table 2, Fig 1). The distribution pattern of the genetic resources into clusters indicated that

Cluster I was the largest comprising of large number of accessions (36) followed by cluster II with (7) accessions and the remaining were monogenotypic clusters III, IV, V,VI,VII, VIII and IX containing only single accession each indicating high degree of heterogeneity among the genotypes.

The average intra-cluster and inter-cluster $D^2$ values were worked out using $D^2$ values from divergence analysis (Table 3, Fig. 2). The data analysis revealed that the inter cluster distance ranged from 9.96 to 201.50. The inter-cluster distances were higher than the intra-cluster distances implying the presence of wider genetic diversity between the clusters rather than within the clusters. Intra cluster distances ranged from 0 to 17.67. Least intra cluster distance (0) observed in clusters III, IV, V, VI,VII, VIII and IX indicated the close resemblance between the genetic resources present in that cluster. Contrarily, highest intra cluster distance 17.67 in cluster II represented differences in the genetic resources within cluster. Therefore, genetic resources occupying the same cluster have low levels of diversity and selection of parents with in the cluster may not be considered as promising. Inter-cluster distance values varied from 9.96 (cluster III and cluster VI) to 201.50 (cluster II and cluster IX). Hence the genetic resources between cluster II (SiA 3397, SiA 3396, SiA 3384, SiA 3340, SiA 3447, SiA 3347 and SiA 3369) and cluster IX (SiA 3222) possessing maximum inter cluster distance between them had high degree of genetic diversity and thus may be utilized under inter-varietal hybridization programme (transgressive breeding) for obtaining superior segregants. Similar results were reported earlier by Anantharaju and Meenakshiganesan (2008), Kadam (2008) and Mahanthesha *et al* (2017).

A perusal of cluster means for 12 characters per cluster were presented in Table 4. Wide spectrum of variation was observed in clusters for the characters studied implying that the clusters formed were distinct. The cluster I, cluster V and cluster VI reported maximum 1000 grain weight (2.67), maximum peduncle exertion (22.30) and highest flag leaf blade length (36.40), respectively. High culm branches (4.54) and number of productive tillers / plant (2.44) were noticed in cluster II. Cluster IV recorded desired highest means for most of the traits viz., plant height (137.70), peduncle length (35.35), panicle length (21.87) and flag leaf blade width (2.03). Highest grain yield / plant (4.36) and desired lower values for days to 50% flowering (30.67), days to maturity (61.33) *i.e.*, earliness were reported in cluster IX.

The result indicates that selection of genetic resources having desired values for particular trait could be made and utilized in the hybridization programme for improvement of that character. It is observed that no cluster contained at least one genetic resource with all the desirable traits, which ruled out the possibility of selecting directly one genotype for immediate use. Therefore, hybridization between the selected genetic resources from divergent clusters is essential to judiciously combine all the targeted traits. Similar reports were in consonance with findings of Murugan & Nirmalakumari (2006)

Information on the relative contribution of various plant characters towards divergence (Table 5 and Fig 3) has also been reported to aid the breeder in choice of parents for hybridization and effective selections in the advance generations. Among all the characters studied, culm branches contributed maximum (45.39%) towards genetic divergence followed by 1000 grain weight (27.35%) indicating feasibility of genetic improvement through those characters. Similar reports were published by Sirisha (2008) for 1000 grain weight.

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## References

Anantharaju, P. and Meenakshiganesan, N. 2008. Genetic divergence studies in finger millet (*Eleucine coracana* (L.) Gaertn). *Indian Journal of Agricultural Research*.**42**(2): 120-123.

Brunda, S.M., Kamatar, M.Y., Naveenkumar, K.L., Hundekar, R. 2015. Genetic diversity in the foxtail millet (*Setaria italica*) germplasm as determined by phenotypical traits. *The Ecoscan*. **8**: 483-488.

Kadam, D. 2008. Genetic divergence in finger millet (Nachani /Ragi /Nagali /*Eluesine coracana*). *Journal of Soils and Crops*. **18**: 138-142.

Mahanthesha, M., Sujatha, M., Pandravada, S.R. and Meena, A.K. 2017 b. Study of genetic divergence in finger millet (*Eleusine coracana* (L.) Gaertn) germplasm. *International Journal of Pure and Applied Bioscience*. **5**(3): 373-377.

Murugan, R. and Nirmala kumari, A. 2006. Genetic divergence in italian millet. (*Setaria italica* (L.) Beauv). *Indian Journal of Genetics*. **66**(4): 339- 340.

Reddy, C.V.C.M., Pullibai, P., Manjunath, J and Munirathnam, P. 2015. Genetic diversity and genotype by trait analysis for yield and yield attributing traits in italian millet (*Setaria italica* (L.) Beauv). *International journal of agricultural innovations and research.* **3**(6): 1726-1730.

Sirisha, A.B.M., Panduranga Rao, C., Rama Kumar, P.V and Rao, S.V. 2009. Variability, character association and path coefficient analysis in Italian millet [*Setaria italica* (L.)Beauv]. *The Andhra Agricultural Journal*. **56**(4): 441-446.

**Table 1. ANOVA for 12 quantitative traits in 50 Italian millet genetic resources**

| S. No. | Characters | Mean squares<br>Replications (df:2) | Genotypes (df:49) | Error (df:98) |
|---|---|---|---|---|
| 1. | Days to 50% flowering | 3.02 | 35.96** | 2.37 |
| 2. | Days to maturity | 4.53 | 37.07** | 3.09 |
| 3. | Plant height | 104.27 | 275.89** | 69.31 |
| 4. | Peduncle length | 11.61 | 33.63** | 4.83 |
| 5. | Peduncle exertion | 4.61 | 24.15** | 6.15 |
| 6. | Panicle length | 5.30 | 15.09** | 4.97 |
| 7. | Flag leaf blade length | 21.33 | 23.88** | 10.30 |
| 8. | Flag leaf blade width | 0.049 | 0.056** | 0.019 |
| 9. | Culm branches | 0.002 | 2.39** | 0.06 |
| 10. | Number of productive tillers/plant | 0.28 | 0.74** | 0.12 |
| 11. | 1000 grain weight | 0.013 | 0.13** | 0.00 |
| 12 | Grain yield/plant | 0.60 | 1.60** | 0.21 |

**Table 2. Cluster composition of 50 Italian millet genetic resources based on Tocher's method**

| Cluster number | No. of genotypes | Genotypes |
|---|---|---|
| I | 36 | Suryanandi, SiA 3364, SiA 3375, SiA 3376 SiA 3382, Narasimharaya, SiA 3407, SiA 3403, SiA 3390, SiA 3399, SiA 3389, Srilakshmi SiA 3395, SiA 3404, SiA 3367 , SiA 3156, SiA 3383,Prasad, SiA 3378, SiA 3386, SiA 3355, SiA 3327, SiA 3346, SiA 3335, SiA 3354, Krishnadevaraya, SiA 3392, SiA 3377, SiA 3405, SiA 3328, SiA 3318, SiA 3333, SiA 3085, SiA 3363, SiA 3398, SiA 3400. |
| II | 7 | SiA 3397, SiA 3396, SiA 3384, SiA 3340, SiA 3447, SiA 3347, SiA 3369 |
| III | 1 | SiA-3394 |
| IV | 1 | SiA 3401 |
| V | 1 | SiA 3322 |
| VI | 1 | SiA 3393 |
| VII | 1 | ISC 379 |
| VIII | 1 | SiA 3393 |
| IX | 1 | SiA 3222 |

**Table 3. Average intra and inter cluster distances among nine clusters**

| Clusters | I | II | III | IV | V | VI | VII | VIII | IX |
|---|---|---|---|---|---|---|---|---|---|
| **I** | **15.36** | 35.23 | 24.93 | 27.27 | 24.60 | 37.08 | 27.97 | 46.26 | 130.08 |
| **II** | | **17.67** | 68.97 | 82.44 | 34.50 | 85.46 | 16.42 | 63.31 | 201.50 |
| **III** | | | 0.00 | 10.96 | 23.71 | 9.96 | 12.80 | 35.62 | 85.24 |
| **IV** | | | | 0.00 | 43.23 | 17.63 | 22.03 | 54.73 | 78.71 |
| **V** | | | | | 0.00 | 35.23 | 19.16 | 18.86 | 152.05 |
| **VI** | | | | | | 0.00 | 15.73 | 33.96 | 89.10 |
| **VII** | | | | | | | 0.0 | 32.08 | 140.17 |
| **VIII** | | | | | | | | 0.00 | 114.28 |
| **IX** | | | | | | | | | 0.00 |

**Table 4 Cluster means with respect to yield and yield attributes among 50 Italian millet genetic resources**

| Character Cluster | DFF | DAM | PLH | PEL | PEE | PAL | BLL | BLW | CUB | NPT | TGW | GYP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 Cluster | 49.14 | 79.78 | 133.85 | 30.12 | 15.17 | 18.37 | 32.51 | 1.89 | 2.89 | 1.86 | 2.67 | 3.97 |
| 2 Cluster | 51.19 | 81.48 | 129.97 | 28.51 | 13.50 | 17.29 | 31.57 | 1.74 | 4.54 | 2.44 | 2.56 | 3.48 |
| 3 Cluster | 46.67 | 78.67 | 119.43 | 28.53 | 15.53 | 19.97 | 35.80 | 1.71 | 1.60 | 1.00 | 2.50 | 2.82 |
| 4 Cluster | 45.00 | 78.00 | 137.70 | 35.33 | 18.87 | 21.87 | 37.80 | 2.03 | 1.53 | 0.60 | 2.63 | 4.23 |
| 5 Cluster | 53.33 | 83.67 | 131.80 | 4.90 | 12.48 | 21.79 | 32.47 | 1.85 | 2.93 | 1.55 | 2.27 | 3.18 |
| 6 cluster | 48.33 | 77.33 | 122.20 | 33.87 | 19.30 | 15.63 | 36.40 | 1.73 | 1.53 | 0.90 | 2.37 | 1.95 |
| 7 Cluster | 53.00 | 84.67 | 125.90 | 30.60 | 22.30 | 18.83 | 33.97 | 1.85 | 1.53 | 1.17 | 2.47 | 3.23 |
| 8 Cluster | 49.67 | 80.00 | 126.77 | 25.13 | 14.61 | 10.55 | 25.60 | 1.87 | 3.07 | 2.07 | 2.00 | 3.67 |
| 9 Cluster | 30.67 | 61.33 | 101.73 | 27.80 | 16.20 | 12.61 | 26.47 | 1.87 | 2.13 | 1.29 | 2.23 | 4.36 |

DFF- Days to 50% flowering, DAM- Days to maturity, PLH- Plant height, PEL- Peduncle length, PEE- Peduncle exertion, PAL- Panicle length, FBL- Flag leaf blade length, FBW-Flag leaf Blade width, CUB- Culm branches, NPT- Number of productive tillers / plant, TGW- 1000 Grain weight, GYP- Grain yield / plant.

**Table 5. Contribution of yield and its attributes towards total diversity in 50 Italian millet germplasm accessions.**

| S. No. | Character | Times ranked first | Contribution (%) |
|---|---|---|---|
| 1. | Days to 50% flowering | 101 | 8.24 |
| 2. | Days to maturity | 28 | 2.29 |
| 3. | Plant height | 12 | 0.98 |
| 4. | Peduncle length | 85 | 6.94 |
| 5. | Peduncle exertion | 7 | 0.57 |
| 6. | Panicle length | 4 | 0.33 |
| 7. | Flag leaf blade length | 2 | 0.16 |
| 8. | Flag leaf blade width | 14 | 1.14 |
| 9. | Culm branches | 556 | 45.39 |
| 10. | Number of productive tillers / plant | 9 | 0.73 |
| 11. | 1000 grain weight | 335 | 27.35 |
| 12. | Grain yield / plant | 72 | 5.88 |

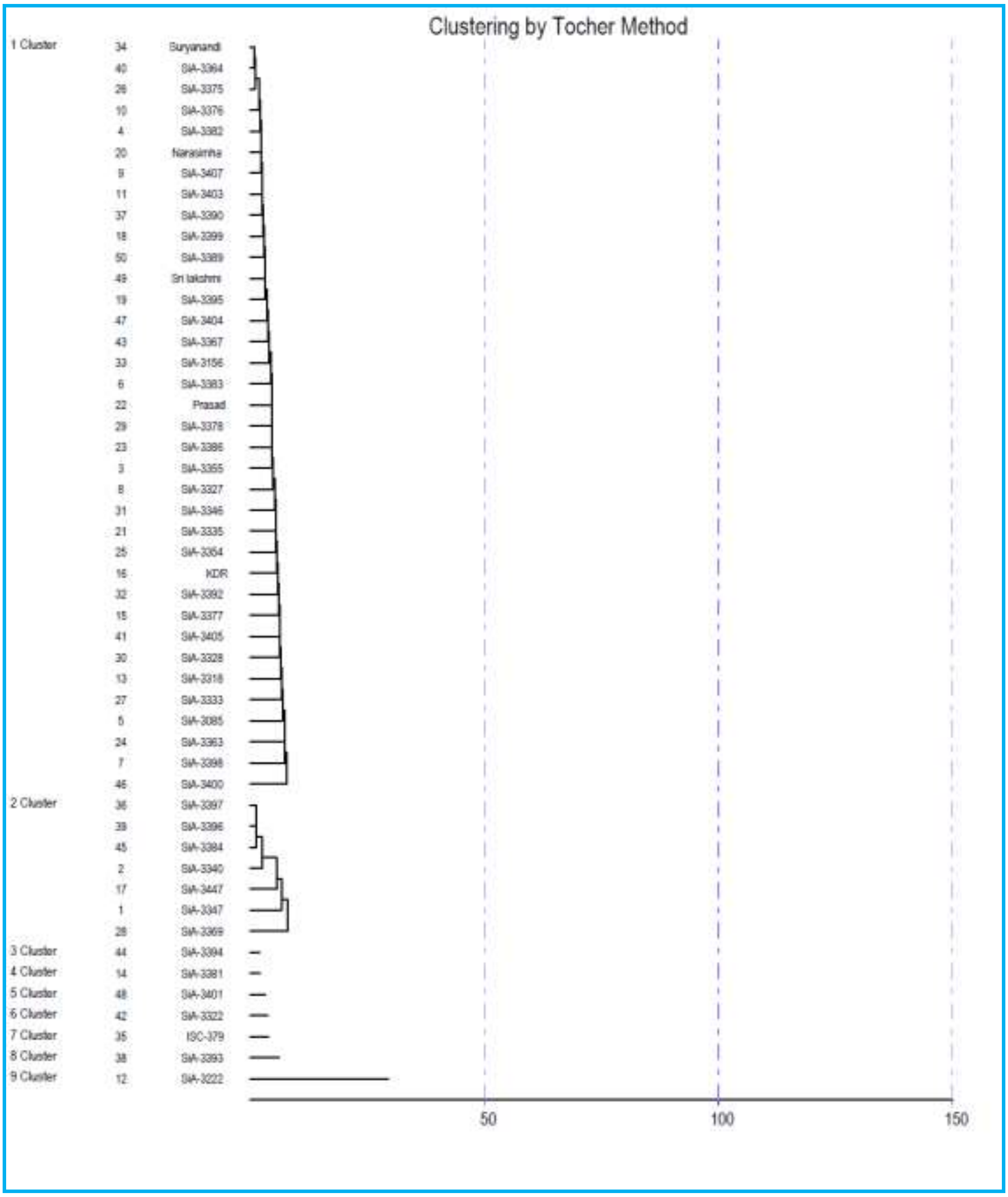

**Fig. 1. Clustering pattern of 50 Italian millet genetic resources by Tochers method**

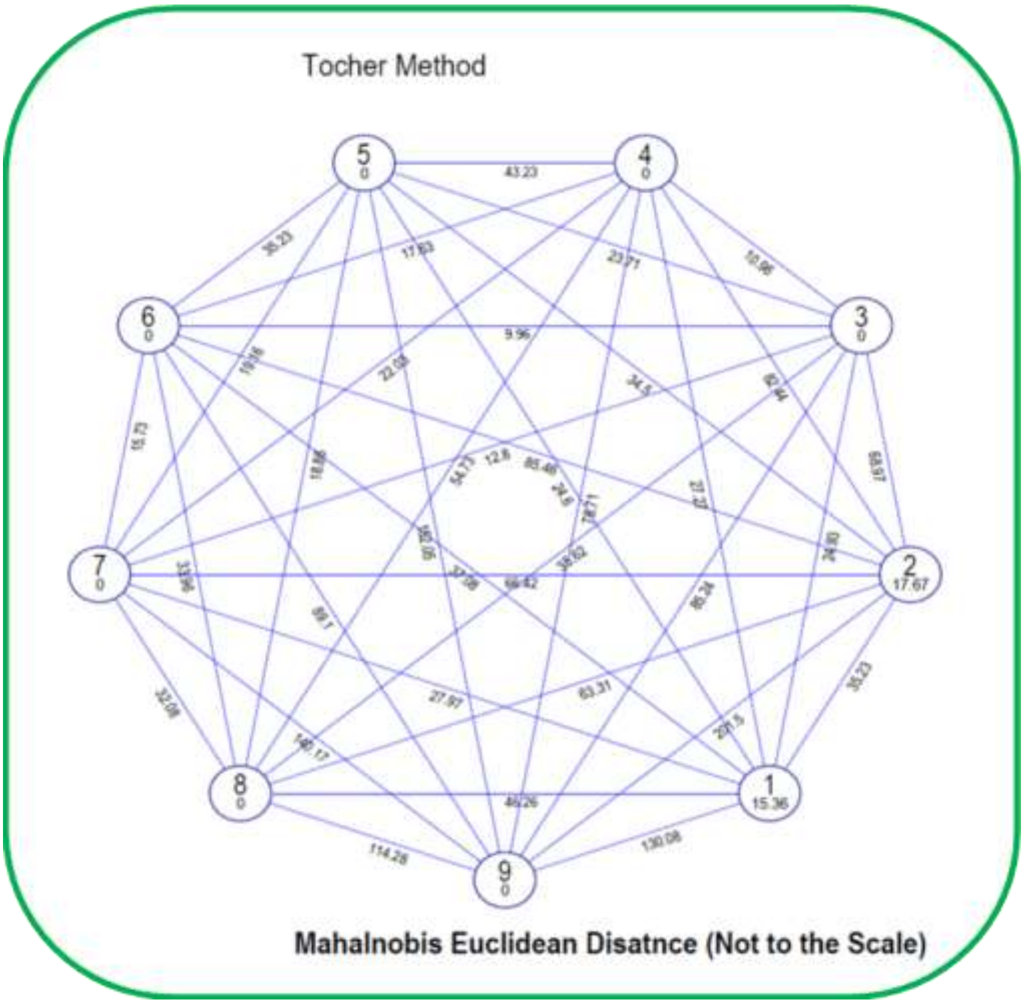

**Fig. 2. Cluster diagram illustrating average intra and inter cluster distances.**

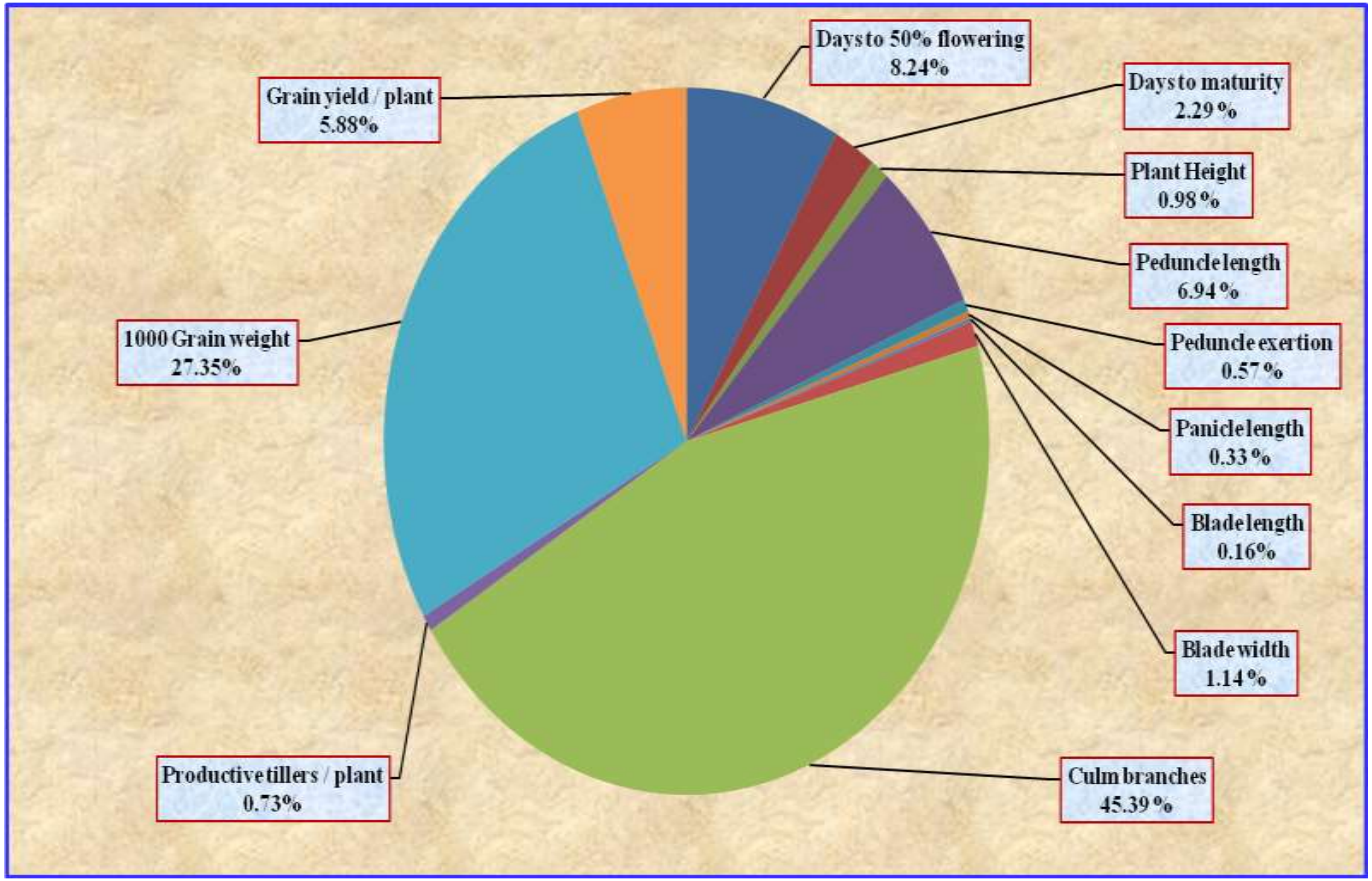

**Fig. 3. Relative contribution of 12 characters to total genetic diversity in 50 Italian millet genetic resources.**

### Annexure I. Details of the 50 Italian millet genetic resources utilized for study

| S. No | Germplasm accession | Parentage |
|---|---|---|
| 1 | SiA 3085 | Selection from SiA 2644 from farmers field |
| 2 | SiA 3156 | Pureline selection from SiA 2871 |
| 3 | SiA 3221 | SiA 3075 x ISC 379 |
| 4 | SiA 3322 | Selection from ISC 1161 |
| 5 | SiA 3327 | Selection from ISC 1076 |
| 6 | SiA 3328 | Selection from ISC 748 |
| 7 | SiA 3333 | Selection from ISC 909 |
| 8 | SiA 3335 | Selection from ISC 745 |
| 9 | SiA 3340 | Selection from ISC 362 |
| 10 | SiA 3346 | Selection from ISC 160 |
| 11 | SiA 3347 | Selection from ISC 1162 |
| 12 | SiA 3354 | Selection from ISC 18 |
| 13 | SiA 3355 | Selection from ISC 869 |
| 14 | SiA 3363 | Selection from ISC 1134 |
| 15 | SiA 3364 | Selection from ISC 267 |
| 16 | SiA 3367 | Selection from ISC 1118 |
| 17 | SiA 3369 | Selection from ISC 1177 |
| 18 | SiA 3375 | Selection from ISC 838 |
| 19 | SiA 3376 | Selection from ISC 796 |
| 20 | SiA 3377 | Selection from ISC 254 |
| 21 | SiA 3378 | Selection from ISC 525 |
| 22 | SiA 3381 | Selection from ISC 398 |
| 23 | SiA 3382 | Selection from ISC 403 |
| 24 | SiA 3383 | Selection from ISC 200 |
| 25 | SiA 3384 | Selection from ISC 480 |
| 26 | SiA 3386 | Selection from ISC 907 |
| 27 | SiA 3389 | Selection from ISC 507 |
| 28 | SiA 3390 | Selection from ISC 828 |
| 29 | SiA 3392 | Selection from ISC 717 |
| 30 | SiA 3393 | Selection from ISC 375 |
| 31 | SiA 3394 | Selection from ISC 792 |
| 32 | SiA 3395 | Selection from ISC 931 |
| 33 | SiA 3396 | Selection from ISC 846 |
| 34 | SiA 3397 | Selection from ISC 917 |
| 35 | SiA 3398 | Selection from ISC 179 |
| 36 | SiA 3399 | Selection from ISC 237 |
| 37 | SiA 3400 | Selection from ISC 388 |
| 38 | SiA 3401 | Selection from ISC 735 |
| 39 | SiA 3403 | Selection from ISC 842 |
| 40 | SiA 3404 | Selection from ISC 195 |
| 41 | SiA 3405 | Selection from ISC 364 |
| 42 | SiA 3407 | Selection from ISC 96 |
| 43 | SiA 3447 | Selection from ISC 1704 |
| 44 | SiA 3381 | Selection from ISC 936 |
| 45 | Srilakshmi | Pureline selection from local |
| 46 | Suryanandi | Pureline selection from SiA 1244 |
| 47 | Prasad | Selection from Dronachalam village |
| 48 | Narasimharaya | SiA 805 x SiA242 |
| 49 | Krishnadevaraya | SiA 326 x SiA242 |
| 50 | ISC 347 | ICRISAT gene bank |

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