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Exploiting Genetic Divergence in Italian Millet (*Setaria italica* (L.) P. Beauv) Elite Germplasm Lines : A Neglected and Underutilized Crop

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Abstract One of the orphan crops Italian millet (*Setaria italica* (L.) P. Beauv) known for its drought tolerance and as an indispensable crop in vast rain fed areas in semi-arid regions of India has been adopted for divergence analysis using Mahalanobis D^2 statistic in 40 clite germplasm accessions in RBD worked out by 15 characters including morphological and biochemical traits contributing to divergence. The accessions were collected from diverge eco-geographical regions of India and Abroad. Apparent diversity was noticed in 40 germplasm accessions which diverged into 5 clusters. Cluster 1 was the largest comprising of 32 genotypes followed by Chuster II with 5 genotypes, Cluster III, IV, V were monogenotypic clusters. The maximum inter-cluster distance occurred between cluster II and III. Among the characters studied protein content, carbohydrate content, days to 50% flowering, seed yield/plant contributed maximum towards divergence. The cluster III and highest cluster means for protein content, cluster IV for carbohydrate content, followed by cluster I requires less time for days to 50% bloom, highest means for seed yield/plant and basal tillers respectively, cluster V had highest means for ear length.

Keywords Italian millet, Genetic divergence, D^2 statistics.

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Introduction

Italian millet (*Setaria italica* (L.) P. Beauv) also known as Foxtail millet, Giant setaria, German millet, Chinese millet, Hungarian millet belongs to family. Poaceae with chromosome number 2n=18. It is varied by different names in local languages. It is one of the world's oldest cultivated crops with its domestication and cultivation estimated to have occurred about 4,000 years ago. It is known for its drought tolerance and as an indispensable crop in vast rainfed areas in semi-arid regions of India. It is also grown in nutrient deficient soils and possess tolerance to pests and diseases. The grain is a good source of protein (12.3%) and β-Carotene [1]. It can be cooked whole, made into meal or into alcoholic beverage. The straw can also make a useful hay or Silage.

In any crop improvement program, study of genetic diversity is an essential prerequisite for hybridization. Inclusion of genetically diverse parents in hybridization program helps in isolation of superior recombinants. Genetic diversity can be worked out with the help of D^2 analysis which was given by Mahalanobis [2]. For the first time use of this technique for assessing the genetic variability in plants was suggested by Rao [3]. It is a very potent technique of measuring genetic divergence. In present investigation an effort has been made to study the genetic diversity among 40 genotypes of Italian millet (*Setaria italica* L. P. Beauv) for fifteen characters. Keeping in view that it will provide systematic approach and basic information on which the success of breeding program rests.

Materials and Methods

A field experiment to investigate the genetic diversity in 40 genotypes of Italian millet (*Setaria italica* (L.) P. Beauv) was laid out in a randomized block design (RBI) with three replications, during *kharif* 2015, at Regional station, National Bureau of Plant Genetic replication, during *kharif* 2015, at Regional station, National Bureau of Plant Genetic Resources, Rajendranagar, Hyderabad. The elite germplasm material evaluated here were procured from different location of India (majority), Switzerland, Turkey. Each entry in each replication was sown in rows of 3 meters each spaced at 60 cm spart and inter-plant distance of 15 cm was followed. All the recommended agronomical practices were carried out timely and appropriately. Quantitative and qualitative characters are recorded using descriptor developed by DUS guidelines. Five randomly selected plants were used for recording the observations on fifteen characters viz., plant height (cm), no. of basal tillers, no. of culm branches, flag leaf length (cm), flag leaf width (cm), poduncle length (cm), panicle exertion (cm), ear length (cm), ear width (cm), 1000 seed weight (gm), seed yield/plant (gm), straw yield/plant (gm), days to 50% flowering, protein content (%), carbohydrate content (%). Genetic divergence was estimated by Mahalonobis's D^2 statistics method and genotypes were clustered into different groups on the basis of generalized distance using Tocher's method.

Table 1. Cluster classification of Italian millet germplasm accessions (Tocher's method).

Clusters	No. of genotypes	Germplasm
I	32	SK-13963, PS-4, PRASAD, SIA-2829, IC-308966, KP/SC-1579, ISE-1629, ISE-200, IC-426581, IC-413272, BS-9293, IC-598145, KP/SC-1483, SRILAKSHMI, KP/SC-1452, KP/SC-1532, IC-308861, ISE-237, IC-308981, RJR-608, LEPAKSHI, IC-28910, IC-308939, IC-283911, ISE-1511, IC-610532, SK-13933, IC-413275, NARACHIMARYA, RJR-643, SIA-2871, ISE-1286.
I	5	KRISHNADEVARAYA, IC-436885, ISE-663, KP/SC-1580, KP/SC-1482
III	1	KP/SC-1484
IV	I	KP/SC-1505
V	1	AR-13

Results and Discussion

The analysis of variances for genetic divergence showed highly significant differences among the genotypes for all the thirteen growth characters studied, indicating appreciable amount of variability among the genotypes. Forty genotypes were grouped into five clusters based on D^2 values using Tocher's method such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of genotypes into various clusters is shown in (Table 1). Out of five clusters, cluster I was the largest comprising of thirty two genotypes followed by cluster II with five genotypes, cluster III, IV and V with single genotype each indicating high degree of heterogeneity among the genotypes. The checks Krishnadevaraya. Lepakshi, Narashimarya, Prasad, Sia-2871, Sia-2829, Srilakshmi were included in the cluster I and II respectively indicating their distinctness from the germplasm accessions with respect to traits studied. These reports were in agreement with the earlier reports of [4] in Sunflower.

Intra cluster D^2 values ranged from zero (cluster III, IV, V) to 100.20 (cluster I). Maximum intra cluster distance was observed in cluster I (100-201) followed by cluster II (77.616) . The intra cluster distance varied from 100.201 for cluster I to minimum 77.616 for

Table 2. Intra and inter cluster D and D^2 values and extent of diversity among the clusters.

ClusterS	I	II	III	IV	V
I	10.01 (100.201)	14.02 (196.560)	13.77 (189.612)	14.78 (218.448)	18.42 (339.296)
II		8.81 (77.616)	22.75 (517.562)	19.61 (384.552)	21.41 (502.208)
III			0.00 (0.00)	14.35 (205.922)	21.47 (460.960)
IV				0.00 (0.00)	16.29 (265.364)
V					0.00 (0.00)

cluster II having five genotypes though it was zero for solitary clusters (III, IV, V) (Table 2). This reveals that genotypes occupying the same cluster have low level of diversity and selection of parents with in the cluster may not be considered promising as has been reported by Kumar et al. [5].

From the inter cluser D^2 values of five clusters, it can be seen that highest divergence occurred between cluster II and III (517.562), followed by cluster II and V (502.208), cluster III and V (460.960), cluster II and IV (384.552), cluster I and V (339.246), cluster IV and V (265.364), cluster I and IV (218.448), cluster III and IV (205.922), cluster I and II (196.560), cluster I and III (189.612).

The inter-cluster D^2 values ranged widely with minimum value of 189.612 between cluster I and III and maximum value of 517.562 between clusters II and III indicating high diversity among the genotypes of these clusters. The maximum amount of heterosis is expected from the crosses with parents belonging to the most divergent clusters as reported by Kadam [6]. Hence, it is desirable to select the genotypes from the cluster showing high inter-cluster distance in breeding program for obtaining the desirable segregants.

The intercluster distances were higher than the intra-cluster distances indicating the presence of wider genetic diversity between the clusters than within the clusters. The cluster means for plant height, flag leaf length, ear length, days to 50% flowering were highest in cluster V. No. of basal tillers, no. of culm branches means were highest in cluster II. Peduncle length, panicle exertion, protein content means were highest in cluster III. 1000 seed weight, straw yield/ plant means were highest in cluster I. Seed yield/plant, width, flag leaf width and carbohydrate content recorded highest means in cluster IV. (Table 3). The promising germplasms from these clusters with high means values for different traits may be directly used for adaptation. Hence intercrossing the genotypes of these clusters may result in enlarged variability and

Table 3. Mean values of clusters for 15 characters in 40 Italian millet germplasm accessions (Tocher's method). Bold values : Highest and lowest mean values, PH=Plant height (cm), NBT=no. of basal tillers, NCB=no. of culm branches, FLL=flag leaf length (cm), FLW=flag leaf width (cm), PL=peduncle length (cm), PE=panicle exertion (cm), EL=ear length (cm), ER=ear width (cm), 1000 SW=1000 seed weight (g), STV/P=straw yield/plant (g), DAF 50%= days to 50% flowering, PC%=protein content, CC%=carbohydrate content, SEY/P=seed yield /plant (g).

Clusters	PH	NBT	NCB	FLLL	FLW	PL	PE	EL	FW	1000 SW	SEV/P	STW/P	DAF 50%	PC%	CC%
I	145.81	7.66	1.15	31.31	2.21	30.99	16.12	18.55	1.84	2.92	33.32	31.27	54.55	10.95	66.91
II	136.73	8.60	1.40	31.32	2.23	32.79	18.93	17.06	1.83	2.43	29.03	29.03	53.93	8.40	66.57
III	145.17	1.00	1.00	28.50	2.23	37.67	23.67	15.73	2.00	2.23	16.58	13.48	48.87	13.50	70.70
IV	160.33	3.00	2.00	30.40	2.33	37.33	12.13	23.53	2.27	2.10	48.87	27.30	50.67	11.40	79.80
V	170.20	4.00	0.00	33.89	2.09	34.93	16.50	28.61	1.01	1.64	22.59	22.59	77.00	10.47	77.38

Table 4. Contribution of 15 characters to the divergence.

Sl. No.	Characters	Times ranked	Contribution %
1	Plant height	2	0.26%
2	No. of basal tillers	4	0.51%
3	No. of culm branches	8	1.03%
4	Flag leaf length	1	0.13%
5	Flag leaf width	0	0.00%
6	Peduncle length	2	0.26%
7	Panicle exertion	2	0.26%
8	Ear length	7	0.90%
9	Ear width	1	0.13%
10	1000 seed weight	4	0.51%
11	Seed yield/plant	30	3.85%
12	Straw yield/plant	38	4.87%
13	Days to 50% flowering	78	10.00%
14	Protein content%	367	47.05%
15	Carbohydrate content%	236	30.26%

selection for these traits could result in higher yield combined with earliness. These results were in accordance with earlier workers.

It is observed that no cluster contained at least one genotype with all the desirable traits, which ruled out the possibility of selecting one genotype directly for immediate use. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

The number of times that each of the 15 characters appeared in first rank and its respective percent contribution towards genetic divergence is presented in (Table 4). Among the 13 quantitative and two biochemical characters studied the most important character contributing to the divergence was protein content, carbohydrate content, days to 50% flowering, straw yield/plant, seed yield/plant, no. of culm branches, ear length, 1000 seed weight, no. of basal tillers, plant height, peduncle length, panicle exertion, ear width, flag leaf length, flag leaf width. These results are having conformity with the findings of earlier breeders [7].

From present study it can be concluded that there is presence of wide range of genetic diversity in Italian millet genotypes. The maximum inter-cluster distance occurred between cluster II and III. Greater the distance between two clusters, wider the genetic diversity among the genotypes of these clusters. Hence, crosses can be made between the genotypes of these clusters during hybridization program for obtaining heterotic recombinants. While the cluster contributing maximum divergence were gived major emphasis for deciding the type of cluster for the purpose of further selection in hybridization program.

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