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Genetic diversity studies in finger millet: *Eleusine coracana* L. Gaertn

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Abstract
The present investigation was conducted to examine the genetic diversity among 34 genotypes of finger millet, during Kharif-2019 in Randomized Block Design with three replications. The data were recorded on fifteen quantitative characters to study variability, heritability, genetic advance and genetic divergence. Analysis of Variance showed significant differences among 34 finger millet genotypes for all the characters under study at 1% level of significance. Thus, indicating that a good amount of variability thus revealed that these genotypes have been developed from different genetic background. On the basis of per se performance for different quantitative traits, genotype IE3473 was found to be the best genotype in Prayagraj agro-climatic conditions. High estimates of GCV and PCV were observed for harvest index. High heritability coupled with high genetic advance was recorded for harvest index, followed by biological yield per plant, test weight, days to 50% flowering, indicating the predominance of additive gene effects and the possibilities of effective selection for the improvement of these characters. Based on the relative magnitude of D2 value, the genotypes were grouped into seven clusters by Euclidean method of divergence study. Cluster I constituted maximum number genotypes with 18 genotypes. Maximum inter- cluster distance (D2) was observed between cluster VII and VI, suggesting that the genotypes from these clusters can be selected to yield superior segregants and further genetic improvement. Grain yield appeared to be the most important trait contributing maximum towards genetic divergence. This indicated that this attributes should form the criteria for selection of parents for hybridization programme.

Keywords: Genetic diversity, heritability, genetic advance and finger millet (*E. coracana* (L.) Gaertn.)

Introduction
Finger millet (*Eleusine coracana* (L.) Gaertn.) Is popularly known as „nagali" or „ragi", is a minor cereal in world food grain production but is one of the most important crop belonging to family Poaceae and subfamily Chloridoidae. Finger millet is self-pollinated tetraploid with chromosome number 2n=4x=36.Annual cereal millet crop that includes two distinct subspecies: subsp. Coracana (cultivated finger millet or Ragi) and subsp. Africana (wild finger millet) so known as African millet.

Based on morphological, cytogenetic, and molecular evidence, it is believed that modern finger millet (Eleucine coracana subsp. coracana) is domesticated from wild finger millet (Eleusine coracaca subsp. africana) populations. It was originally cultivated from cool climate of Ethiopian highlands (Hilu *et al*., 1977) [2].

Finger millet is extensively cultivated in India, Africa, Ceylon, Malaysia, China and Japan. In India it is cultivated over an area of 1.19 million ha. Withan average production of about 1.98 million tonnes with an average productivity of 1661 kg/ha. In Uttar Pradesh area under finger millet is 8 thousand hectares and production 5.0 tonnes, productivity is 625(kg/ha).

Finger millet crop requires day temperatures of 30 ^{0}C to 34 ^{0}C and 22 ^{0}C to 25 ^{0}C night temperatures for optimal growth along with good sunshine. It thrives best in the areas where annual rainfall is about 100 cm. It can be grown on a wide range of soils from rich loam to poor shallow upland soils with good organic matter. This crop thrives best in soils with a pH of 5.0 to 8.2.

The achievement in plant breeding programme largely depend upon the genetic variability available in breeding population and the efficiency of selection technique. Genotypic and phenotypic association reveals the degree of association between different characters and thus, aids in selection to improve the yield and yield attributing characters.

Heritability measures the relative amount of the heritable portion of variation while the genetic advance helps to measure the amount of progress that could be expected with selection in a character.

The importance of genetic diversity in plant breeding is obvious from results obtained in different crops. The recognition and measurement of such diversity, its nature and magnitude are beneficial, perhaps crucial to any breeding programme. This is particularly important in a crop like finger millet where hybridization is difficult, there being limited scope for making large number of crosses by random mating and hence, the information regarding the nature of genetic diversity of the parents to be used in the hybridization, is of per amount importance to finger millet breeder.

Genetic diversity plays an important role in plant breeding either to exploit heterosis or to generate productive recombinants. The choice of parents is of greater importance in the breeding program. Assessment of germplasm for genetic diversity is of immense importance in the selection of diverse genotypes for hybridization program. The use of D2 statistic (Mahalanobis, 1936) [7] is one of the most important biometrical techniques for estimating genetic divergences. This helps to measure the genetic distance among the breeding lines and to identify characters responsible for divergence. Mahalanobis D2statistic, Principal component analysis are few powerful tools for quantifying genetic divergence among germplasm collections.

Materials and Methods

The present investigation was carried out at the Field Experimentation Center of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj, (U.P) during Kharif 2019. The university is situated on the left side of Prayagraj-Rewa National Highway, about 5km from Prayagraj city. All types of facilities necessary for the cultivation of successful crop including field preparation inputs, irrigation facilities were provided from the Department of Genetic and Plant Breeding, Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj (U.P).

The experiment was conducted in randomized block design with 34 genotypes the genotypes were replicated 3 times. Genotypes were randomly arranged in each replication divided into 102 plots. The row to row spacing was 30 cm and plant to plant distance was 10 cm. The 5 competitive plants from each of the replication were tagged and observations were taken from these tagged plants at various stages of the crop plant growth. Data were recorded from 15 characters *viz*, Days to 50% flowering, days to maturity, plant height (cm), number of leaves, flag leaf length (cm), flag leaf width (cm), no of productive tillers per plant, finger length (cm) finger width (cm), no. fingers per ear, ear head length (cm), biological yield, harvest index (%), test weight (1000 gm) grain yield per plant (gm).mean values were computed data were analyzed for analysis of variance and coefficient of variances as well as heritability (in broad sense), as suggested by Burton and Devane (1953) [1]. The estimates of genetic advance were obtained by the formula suggested by Lush (1949) [6] and Johnson *et al*. (1955) [3] and Genetic divergence (Mahalanobis, 1936) [7].

Results and Discussion

The present investigation entitled “Genetic divergence studies of finger millet (*Eleusine coracana* (L.) Garten.)” was carried out in order to study the nature and amount of variability, heritability, genetic advance and genetic diversity analysis for 15 quantitative characters *viz*., days to 50% flowering, days to maturity, plant height (cm), number of leaves, flag leaf length (cm), flag leaf width (cm), ear head length(cm), finger length(cm), finger width(cm), number of fingers per panicle, number of productive tillers, biological yield per plant (g), harvest index (%), test weight (g), grain yield per plant (g).

Analysis of Variance showed significant differences among 34 finger millet genotypes for all the characters under study at 1% level of significance. Thus, indicating that a good amount of variability was present in the experimental material, and offer ample scope for selection of promising lines from the present gene pool for yield and quality improvement.

On the basis of per se performance for grain yield per plant, best high yielding genotype identified was IE 3473, IE 4759, IE 2568, IE 2960, IE 5302 for grain yield per plant and its component characters.

The Phenotypic Coefficient of Variation were higher in magnitude than the Genotypic Coefficient of Variation for all the characters and the difference between PCV and GCV was low for most of the characters, indicates less influence of environment in the expression of these characters in finger millet germplasm. The maximum PCV was observed in Test weight (20.84), harvest index (19.84%), number of productive tillers per plant (18.83%), biological yield per plant (16.01%), flag leaf length (15.77%), ear head length (15.38%), number of leaves (14.57%), flag leaf length (13.36%), plant height (13.30%), days to 50% flowering (12.96%), finger width (12.27%), finger length (11.48%), grain yield per plant (10.48%).

High heritability coupled with high genetic advance as per cent mean (>20) in the present set of genotypes were recorded for harvest index (87% and 35.82%), biological yield per plant (94% and 31.29%), test weight (66% and 28.39%), days to 50% flowering (97% and 25.90%), number of productive tillers per plant(51% and 20.12%), indicating a predominance of additive gene effects and the possibilities of effective selection for the improvement of these characters. Similar findings were reported by Kumari and Singh (2015) [5] for harvest index, 1000 grain weight and days to 50% flowering.

High heritability coupled with moderate genetic advance (>10 to <20) was recorded for ear head length (63% and 19.95%), number of leaves (58% and 17.54%), plant height (61% and 16.72%), finger length (68% and 16.23%), days to maturity (95% and 15.60%), number of finger per panicle(75% and 15.09%), grain yield per plant (67% and 14.64%), and finger width (42% and 10.62%),suggesting the greater role of both additive and non-additive gene action in their inheritance. Similar findings were reported by Ulaganathan and Nirmalakumari (2011) [8] and Karad and Patil (2013) [4].

Low heritability coupled with low genetic advance (<10) was recorded for flag leaf width (29% and 9.41%), flag leaf length (32% and 8.90%), It is indicative of non-additive gene action. The low heritability is being exhibited due to the favourable influence of environment rather than genotype and selection for such traits may not be rewarding.

On the basis of Mahalanobis D2 statistics, the 34 finger millet genotypes were grouped into 7 clusters. The cluster I was with 18 genotypes emerged as the largest cluster. The cluster II with 8 genotypes, cluster IV with 4 genotypes, Cluster III, Cluster V, VI and cluster VII are mono genotypic indicating wide diversity from the rest and cluster with 1 genotype each.

The maximum intra cluster distance was observed for cluster IV (40.66) followed by cluster II and minimum intra cluster distance was observed in cluster IV (25). The clusters IV, V, IV and VII were mono genotypic and showed no intra cluster distances.

The highest contribution in the manifestation of genetic divergence was exhibited by Grain yield per plant (40.82%), biological yield (32.44%) followed by number of fingers per panicle (8.38%), harvest index (3.92%), flag leaf length (2.67%), test weight (2.14%), finger length (2.14%), number of productive tillers (2.14%). days to maturity (1.78), plant height (1.6%), ear head length (0.89%), days to 50% flowering (0.53%), finger width (0.36%), flag leaf width (0.18), contributed least among all the character towards genetic diversity.

Therefore, grain yield per plant, biological yield, number of fingers per panicle, harvest index, flag leaf length, test weight, finger length, Number of productive tillers contributing 94.65% to the total divergence need to be focused in the selection of these traits for hybridization program.

Table 1: Mean performance of 34 genotypes of finger millet for 15 quantitative characters during Kharif-2019

Genotypes	Days to 50% flowering	Days to maturity	Plant height	No of leaves	Flag leaf length	Flag leaf width	Ear head length	Finger length	Finger width	No of finger per panicle	No of productive tillers	Biological yield per plant	Harvest index	Test weight	Grain yield per plant
IE 5736	58.00	88.07	104.40	11.87	47.04	0.58	6.39	4.94	0.48	5.54	1.67	19.84	11.64	0.85	2.30
IE 5965	75.54	104.54	127.98	15.20	41.54	0.72	6.48	5.18	0.49	5.87	1.47	23.79	11.28	0.74	2.68
IE 6013	59.47	90.40	91.79	13.40	36.05	0.72	7.37	5.88	0.46	5.87	1.27	24.20	11.76	0.84	2.85
IE 6154	78.14	106.34	104.20	15.00	38.68	0.66	7.36	5.68	0.48	5.67	1.07	20.74	12.85	0.70	2.66
IE 6890	67.00	97.87	129.73	16.80	34.22	0.62	6.24	5.74	0.51	5.07	1.60	20.36	12.63	0.66	2.58
IE 7386	61.54	92.54	143.13	14.40	41.92	0.68	6.39	5.82	0.51	5.40	1.60	26.77	9.09	0.86	2.44
IE 7407	76.60	106.60	125.62	14.87	34.84	0.64	4.10	3.86	0.52	4.67	1.14	17.36	15.16	0.60	2.62
IE 7508	62.80	94.74	114.30	9.67	45.18	0.68	6.92	5.75	0.51	5.07	1.20	19.29	15.40	0.64	2.96
IE 3788	77.94	106.94	117.36	13.27	31.18	0.62	6.98	6.02	0.49	4.40	1.00	22.46	11.53	0.62	2.59
IE 3952	82.34	109.80	122.10	15.54	41.76	0.50	6.00	5.40	0.50	5.27	1.47	19.82	12.74	0.59	2.53
IE 4443	57.34	89.34	114.28	10.47	42.75	0.70	7.89	6.29	0.45	4.94	1.54	18.58	14.40	0.72	2.67
IE 4759	55.87	87.87	94.18	11.67	32.30	0.60	4.80	4.48	0.45	4.47	1.34	16.45	19.41	0.56	3.20
IE 5057	77.00	105.00	108.13	14.67	37.10	0.56	5.95	5.59	0.49	4.27	1.40	18.77	15.06	0.62	2.83
IE 5066	79.47	107.14	142.90	14.60	38.17	0.52	6.12	5.25	0.52	5.47	1.14	24.40	11.21	0.54	2.73
IE 5179	79.80	107.80	130.53	12.87	44.53	0.62	7.66	6.12	0.56	5.27	1.47	17.62	15.38	0.63	2.70
IE 5291	78.87	107.07	103.77	10.14	35.58	0.64	6.89	5.40	0.49	5.14	1.00	17.42	14.84	0.64	2.58
IE 5302	79.74	106.54	124.44	15.07	41.28	0.76	5.72	5.23	0.59	5.20	1.40	17.54	16.74	0.78	2.92
IE 2606	79.00	106.00	128.52	13.40	37.63	0.67	6.55	5.76	0.51	4.40	1.20	21.21	11.95	0.44	2.53
IE 2789	78.34	106.34	109.98	12.27	38.70	0.70	7.34	5.08	0.50	5.14	1.40	21.91	11.48	0.64	2.49
IE 2957	58.40	89.40	86.64	11.14	36.32	0.79	7.43	5.44	0.52	4.60	1.47	17.13	13.93	0.60	2.39
IE 3130	79.20	104.27	109.42	13.20	35.72	0.64	7.58	7.03	0.57	4.60	1.67	17.96	12.26	0.46	2.20
IE 3132	81.00	106.67	117.04	15.20	42.34	0.74	7.28	5.62	0.65	5.54	1.14	22.67	10.98	0.54	2.49
IE 3280	76.00	106.00	127.16	15.74	32.23	0.53	7.44	6.04	0.54	5.40	1.40	23.02	10.96	0.66	2.52
IE 3399	76.27	106.27	106.10	13.74	37.46	0.76	7.72	5.85	0.56	5.47	1.74	22.58	11.10	0.56	2.51
IE 3473	82.60	109.94	108.36	14.27	40.18	0.66	7.92	5.38	0.56	5.00	1.60	21.92	15.42	0.36	3.33
IE 2039	75.27	102.27	107.54	14.87	39.21	0.62	7.61	5.86	0.56	5.34	1.60	17.94	14.39	0.45	2.57
IE 2288	75.34	101.34	123.44	12.94	40.08	0.66	6.01	5.02	0.64	5.07	1.54	27.77	9.30	0.73	2.60
IE 2322	55.00	85.00	111.03	14.34	34.90	0.78	6.60	5.52	0.62	5.00	1.40	24.06	10.70	0.64	2.48
IE 2568	80.40	108.67	113.72	13.54	41.32	0.64	7.54	5.23	0.52	5.20	1.60	23.36	13.48	0.62	3.13
IE 9	73.54	103.54	113.20	15.67	43.06	0.76	7.37	5.35	0.60	4.60	1.80	23.65	10.65	0.66	2.52
IE 96	62.20	94.20	116.06	13.54	42.96	0.73	7.03	5.13	0.56	4.87	1.67	25.46	11.18	0.72	2.85
IE 501	72.80	100.94	128.03	14.87	40.88	0.60	7.88	5.28	0.55	4.07	1.67	25.18	10.18	0.65	2.42
IE 588	63.67	94.67	99.90	12.94	37.62	0.76	5.56	4.78	0.56	4.94	1.67	29.03	9.44	0.49	2.74
IE 2030	58.67	86.67	109.72	14.54	40.70	0.70	7.57	5.14	0.58	5.00	1.67	26.68	9.34	0.59	2.49
Mean	71.62	100.61	115.14	13.70	38.98	0.670	6.82	5.48	0.53	5.06	1.44	21.68	12.59	0.63	2.65
C.D. 5%	2.63	2.75	15.58	2.10	6.98	0.15	1.04	0.58	0.09	0.40	0.31	1.28	1.43	0.13	0.26
Range Lowest	55.00	85.00	86.64	9.67	31.18	0.50	4.10	3.86	0.45	4.07	1.00	16.45	9.09	0.36	2.20
Range Highest	82.60	109.94	143.13	16.80	47.04	0.79	7.92	7.03	0.65	5.87	1.80	29.03	19.41	0.86	3.33

Table 2: Genetic parameters for 15 quantitative characters in 34 finger millet genotypes

Sl. No.	Characters	General mean	Range		$\sigma^2 g$	$\sigma^2 p$	Coefficient of variance (%)		(h^2) %	Genetic advance As 5%	G.A as a per cent of mean
							GCV (%)	PCV (%)			
1	Days to 50% flowering	71.62	55.00	82.60	83.55	86.14	12.77	12.96	97.00	18.55	25.90
2	Days to maturity	100.61	85.00	109.94	60.70	63.53	7.75	7.93	95.50	15.69	15.60
3	Plant height (cm)	115.14	86.64	143.13	142.98	234.30	10.39	13.30	61.00	19.25	16.72
4	Number of leaves (cm)	13.70	9.67	16.80	2.33	3.98	11.14	14.57	58.50	2.41	17.54
5	Leaf length (cm)	38.98	31.18	47.04	8.77	27.09	7.60	13.36	32.40	3.47	8.90
6	Leaf width (cm)	0.67	0.50	0.79	0.01	0.02	8.49	15.77	29.00	0.07	9.41
7	Ear head length (cm)	6.82	4.10	7.92	0.70	1.10	12.21	15.38	63.00	1.36	19.95
8	Finger length (cm)	5.48	3.86	7.03	0.28	0.40	9.51	11.48	68.70	0.89	16.23
9	Finger width (cm)	0.53	0.45	0.65	0.01	0.01	7.95	12.27	42.00	0.06	10.62

10	Number of fingers per panicle	5.06	4.07	5.87	0.19	0.24	8.42	9.67	75.80	0.77	15.09
11	Number of Productive tillers	1.44	1.00	1.80	0.04	0.08	13.56	18.83	51.90	0.29	20.12
12	Biological yield per plant	21.68	16.45	29.03	11.42	12.03	15.59	16.01	94.90	6.78	31.29
13	Harvest Index (%)	12.59	9.09	19.41	5.46	6.23	18.57	19.84	87.70	4.51	35.82
14	Test weight (g)	0.63	0.36	0.86	0.02	0.02	16.95	20.84	66.10	0.18	28.39
15	Grain yield per plant (g)	2.65	2.20	3.33	0.06	0.08	8.63	10.48	67.80	0.39	14.64

Conclusion

It is concluded that based on per se performance for different quantitative traits, the best high yielding genotype identified was IE 3473 followed by IE 4759, IE 2568, IE 2960, IE 5302.

In the present study, the characters, days to 50% flowering followed by days to maturity, biological yield per plant had high heritability coupled with high genetic advance as percent mean indicating the predominance of additive gene effects and the possibilities of effective selection for the improvement of these characters.

The cluster VII and VI and cluster VII and IV were found more diverse to each other. Genotypes present in these clusters are supposed to provide a broad spectrum of variability for grain yield upon hybridization. Therefore, it will be desirable to use these divergent parents for future hybridization program in order to obtained new transgressive segregants.

Grain yield appeared to be the most important trait contributing maximum towards genetic divergence. This indicated that this attributes should form the criteria for selection of parents for hybridization programme.

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