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Genetic Parameters Assessment of Yield Attributing Traits in Finger Millet Germplasm Collected from Uttarakhand Hills

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Abstract

Genetic parameters could assist plant breeders in determining breeding methods and selection criteria. The aim of this study was to estimate the components of variance, heritability, and genetic advance for grain yield and related traits in diverse germplasm lines of finger millet collected from highlands of Uttarakhand. The research was conducted at Pantnagar center for Plant Genetic Resources (PCPGR), G.B. Pant University of Agriculture and Technology, Pantnagar in *Kharif* 2020 season. Experimental material consisted of fifty-two germplasm lines along with seven standard checks. All germplasm accessions were laid out in a randomized complete block design with three replicates. The results showed significant genetic variability for all fourteen quantitative traits. Phenotypic coefficient of variation varied from 7.17 to 31.40. Genotypic coefficient of variation ranged from 4.21 to 29.35. It was highest for grain yield per plot followed by biological yield per plot. Moderate GCV was recorded for 1000 grain weight and finger length. Broad sense heritability varied from 21.00 % to 98.15%. High heritability values were obtained for 1000 grain weight, Grain Yield per Plot, Biological Yield per Plot, Days to Maturity, Finger Length and Flag leaf blade length. Whereas, moderate broad sense heritability was recorded for Days to 50% flowering, Plant Height, Ear Head length, Finger Number on Main Ear, Peduncle length, Flag leaf blade width and Finger width. High genetic advance was predicted upon selection for the grain yield per plot, biological yield per plot, 1000 grain weight and finger length. High heritability was accompanied by high genetic advance for 1000 grain weight, grain yield per plot, biological yield per plot and finger length indicating effectiveness of selection for these traits from this experiment population.

Key words : *Coefficient of variation, finger millet, genetic parameters, genetic advance, heritability.*

Introduction

Finger Millet *(Eleusine coracana)* is a highly productive crop that can be cultivated under varied of stressed environmental conditions. It is adaptable for low fertility soils and is not dependent on the use of chemical fertilizers, hence, is popular in vast arid and semi-arid regions of Asia and Africa (1). Finger millet is native to the Ethiopian highlands in Africa (2). Earliest report of finger millet in India was approximately in 2300 BC (3). It is one of the oldest crops domesticated in India, known by various vernacular names, most commonly *Mandua* and *Ragi*. India is the world's largest producer of finger millet. In 2019-20 it was cultivated over 0.99 million hectares with production of 1.74 million tones and an average productivity of 1761 kg per hectare (4). The cultivated *E. coracana* is an allotetraploid (2n=4X=36) and exhibits morphological similarity to *E. indica* (2n=18) and *E. Africana* (2n=36). Cultivated finger millet is highly variable in Africa (primary centre of origin) and Indian sub-continent (secondary centre). The secondary genepool of this crop consist of diploid wild species *E. indica*, *E. floccifolia* and *E. tristachya* further tertiary genepool consist of *E. semisterlis*, *E. gaegeri*, *E. kigeziensis, E. multiflora* and *E. intermedia.* In the recent years the value of finger millet has increased this increment corresponds to its modest growth and productivity under minimal resources, compatibility with cultural organic practices and also for its high nutraceutical profile (5). Finger millet is seen as a "Future crop" having the potential to mitigate multiple challenges of humanity like malnutrition, food insecurity and climate change. India is gifted with the vast diversity of finger millet especially in Himalayas harboring the immense morphological and genetic diversity among finger millet accessions (6). Genetic diversity refers to the diversity found within different genotypes of the same species. It is of immense value for a breeder to improve the crop for different agronomical traits mainly grain yield. The variability present in the germplasm can be resolved using genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) further effective selection can be determined by studying heritability and genetic advances estimates.

Materials and Methods

The current study was conducted at the Pantnagar Center for Plant Genetic Resources (PCPGR), Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Udham Singh Nagar, Uttarakhand, during the kharif 2020. The plant material for the study comprised of 52 germplasm accessions with seven checks *viz.* PRM-1, VL-352, VL-324, VL-325, VL-347, VL-315 and VL-149. These germplasms/landraces were collected from hills of

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Table-1 : Estimates of genetic parameters for quantitative traits in finger millet germpasm.

Trait	Mean	Range	GCV	PCV	Heritability	Genetic advance	GAM
Days to 50% flowering	86.19	66.67 - 99.00	9.89	13.00	57.88	13.36	15.50
Days to Maturity	116.32	89.00 - 131.00	8.70	10.35	70.71	17.54	15.08
Flag leaf blade length	32.29	24.80 - 38.80	7.77	9.93	61.17	4.04	12.51
Flag leaf blade width	0.92	0.80 - 1.10	5.33	9.17	33.78	0.06	6.38
Peduncle length	19.58	17.13 - 22.33	4.21	7.17	34.46	1.00	5.09
Ear Head length	10.64	8.73 - 15.80	9.95	15.16	43.06	1.43	13.45
No. of Productive Tillers/plant	2.31	2.07 - 2.87	5.08	11.06	21.06	0.11	4.80
Finger Number on Main ear	7.56	6.47 - 9.33	7.62	11.62	43.02	0.78	10.30
Finger Length	8.73	7.40 - 12.93	12.93	15.50	69.53	1.94	22.20
Finger width	0.8	0.70 - 0.96	6.20	11.04	31.58	0.06	7.18
Plant Height	110.78	83.17 - 125.13	4.96	7.28	46.49	7.72	6.97
1000 grains weight	2.16	1.25 - 2.84	15.62	15.71	98.95	0.69	32.02
Grain Yield per Plot	68.08	34.80 - 137.07	29.35	31.40	87.36	38.48	56.51
Biological Yield per Plot	526.55	266.67 - 783.33	24.22	27.29	78.78	233.22	44.29

Uttarakhand. The experiment was laid in Randomized Complete Block Design with three replications. Each entry was allotted to a single row plot measuring 2 meter long and plot to plot spacing was kept to 30 centimeter. The experimental population was studied for 14 quantitative traits viz. days to 50% flowering, flag leaf blade length, flag leaf blade width, peduncle length, ear head length, number of productive tillers per plant, finger number on main ear, finger length, finger width, plant height, day to maturity, 1000 grain weight, biological yield per plot and grain yield per plot. Analysis of variance of conducted followed by computation of phenotypic and genotypic coefficients of variation (PCV and GCV) as suggested by (6). The estimates of PCV and GCV were classified as high >20%, moderate 10-20% and low <10% (7). Heritability in broad sense and genetic advance for each character was estimated following formulae by (8) and (9) for respective parameter. Heritability and genetic advance as percent of mean were further categorized into low, medium and high as per (9).

Results and Discussion

Genetic variability studies forms the basis for any crop improvement program in plant breeding. It aids to decipher the main components of variation in the base population. This infsormation further indicates towards the extent of sensitivity towards environment and transform ability to the next generation. The analysis of variance revealed a wide range of variation and significant differences for all the fourteen traits undertaken for study, indicating the presence of adequate variability in the base population for further improvement under selection. The estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance and genetic advance as percent of mean (GAM) for all fourteen traits are furnished in Table-1.

Overall, the estimates of PCV were higher than GCV for all the yield attributing traits under study. The values for phenotypic coefficient of variation varied from 7.17 to 31.40 per cent corresponding to trait peduncle length and grain yield per plot respectively. PCV estimates were low for peduncle length, plant height, flag leaf blade width and flag leaf blade length, it was moderate for days to maturity, finger width, number of productive tiller per plant, finger number on main ear, days to 50% flowering, ear head length, finger length and 1000 grains weight. PCV estimates for high for biological yield per plot and grain yield per plot. The values for genotypic coefficients of variation ranged from 4.21 for peduncle length to 29.35 percent for grain yield per plot. GCV estimates for categorized low for peduncle length, plant height, number of productive tiller per plant, flag leaf blade width, finger width, finger number on main ear, flag leaf blade length, days to maturity, days to 50% flowering and ear head length it was moderate for finger length and 1000 grains weight. GCV estimates were high for biological yield per plot and grain yield per plot. Overall, together PCV and GCV estimates were high for biological yield per plot and grain yield per plot, moderate for finger length and 1000 grains weight and low for peduncle length, plant height, flag leaf blade width and flag leaf blade length. Therefore, it is indicated that variability is high for grain yield per plot and biological yield per plot. These findings corroborate with earlier studies of (11) for finger length, (12) for 1000 grains weight and (13,14,15) for grain yield.

Broad sense heritability estimates varied from 21.00 % to 98.15%. 1000 grains weight (98.15 %) exhibited the maximum value for heritability followed by grain yield per plot (87.36 %), biological yield per plot (78.78 %), days to maturity (70.71 %), finger length (69.53 %) and flag leaf blade length (61.17 %) showed high estimates for heritability. [13] reported high heritability for grain yield per plot and finger length. [10, 16] had similar findings for finger length and biological yield per plot respectively. Heritable portion of variance is a good index for transfer of characters from parents to offspring but heritability estimates are influenced by environment, thereby the information on heritability alone is not sufficient for effective selection. Meanwhile, the heritability estimates in coupled with values of the genetic advance as percent of mean could resolve the picture of genetic makeup and help to improve the efficiency of selection.

Genetic advance as percent of mean ranged from 4.80 to 56.51 percent. Grain yield per plot (56.51%) registered the highest GAM followed by biological yield per plot (44.29%), 1000 grains weight (32.02%) and finger length (22.20%) also showed high GAM estimates. Similar results were reported for 1000 grains weight by [17] and for Grain yield per plot by [13]. High GAM reflects that these traits may be governed by additive genes. Moderate values of GAM was found for finger number on main ear (10.30%), flag leaf blade length (12.51%), ear head length (13.45%), days to maturity (15/08%) and days to 50% flowering (15.50%). Overall four traits namely grain yield per plot, biological yield per plot, and 1000 grains weight and finger length exhibited high broad sense heritability coupled with high genetic advance as percent mean. Therefore selection of base population based on these four traits is expected to give modest response to selection in the current experiment trial. Meanwhile, three traits *viz.* flag leaf blade width, plant height and finger width have low heritability and low genetic advance therefore selection will be ineffective for these traits.

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