

COMPARISON OF SELECTION INDICES BASED ON PER CENT RELATIVE EFFICIENCY IN FINGER MILLET CROP

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ABSTRACT

The data on different biometrical characters of 40 genotypes of finger millet were collected from a P. G. student research work of AAU, Anand for present study. The experiment was carried out in randomised block design with three replications at the Genetics and Plant Breeding Farm, AAU, Anand during *kharif* 2020. Six distinct biometrical characteristics of forty genotypes of finger millet were used in the experiment: days to maturity, main ear length (cm), plant height (cm), test weight (g), productive tillers per plant and grain yield per plant (g). To investigate the crop improvement the selection index technique was used by assigning different weights to each biometric characters. Selection indices for individual characters, combinations of two characters, combinations of three characters, and so forth were computed. The combination that produced the highest relative efficiency was selected. Between yield and yield-attributing traits, the basic correlation coefficient, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated. Six biometric characters were used to calculate the selection indices, which were then built using all potential character combinations. Using the simple correlation coefficient [W_1], GCV [W_2] and PCV [W_3] as weights for each character, a total of 63 selection indices were created. Different indicators' predicted genetic advance and percent relative efficiency (PRE) were determined. The findings showed that, across all index combinations PRE with standard deviation as its weight was generally greater than the other weights. The selection index I_{2456} in GCV weight method was found the best.

Keywords : Finger millet, selection index, GCV, PCV and PRE

INTRODUCTION

Ragi or finger millet is one of the significant minor millets. According to Upadhyay *et al.* (2007), finger millet is produced on a global scale fourth after sorghum, pearl millet and foxtail millet, while in India it is the sixth largest produce after wheat, maize, sorghum, bajra, and rice (Chandra *et al.*, 2016). India is leading country in production

of ragi in the world with occupancy of 1.004 million ha, average production of 1.755 million tones and productivity of 1747 kg/ha in 2019-20 (Indiastatagri, 2020). In Gujarat, finger millet occupies an area of 11610 ha with an average production of 10010 tones and productivity of 862 kg/ha in 2019-20 (Indiastatagri, 2020).

The current study used six biometrical characteristics from 40 finger millet

RELATIVE EFFICIENCY IN FINGER MILLET CROP

genotypes to compare several selection indices based on different weights. The data was collected from the experiment conducted by the P.G. student during *kharif* 2020. The Genetics and Plant Breeding Farm, B. A. College of Agriculture, AAU, Anand was the site of the randomised block design experiment, which had 3 replications. Six of the 9 significant characters - main ear length (cm), plant height (cm), test weight (g), days to maturity, productive tillers per plant, and grain yield per plant (g) were used to create selection indices with various weights viz., simple correlation coefficient [W_1], Genotypic Coefficient of Variance [W_2] and Phenotypic Coefficient of Variance [W_3]. ANOVA, simple correlation, GCV, PCV, mean performance of genotypes and selection index technique utilising different weights was applied to the data on six characters.

MATERIALS AND METHODS

It is possible to compute the selection index for an individual character, a combination of two characters, a combination of three characters, and so on. The combination that has the highest relative efficiency is being selected. Using the following formulas, genetic advance and PRE were determined. The selection index for an individual character or set of characters that yields the highest PRE was selected. The expected genetic advance was calculated by following (Dabholkar, 1992)

$$GA = \frac{Z}{P} \left(\frac{\sum \sum a_i b_i G_{ij}}{\sqrt{\sum \sum b_i b_j P_{ij}}} \right)$$

where,

Z/P = Selection intensity i.e., 2.06 at 5% level of significance

G_{ij} = Genotypic variance and covariance of the component characters

P_{ij} = Phenotypic variance and covariance of the component characters

a_i = Equal weight assigned to i^{th} character

b_i = Coefficients of i^{th} character

b_j = Transpose of b_i

$i=j$ = 1, 2, 3, ..., p character

The gain of grain yield was used as the standard to compute each index's percent relative efficiency. It was computed as follows:

Relative Efficiency (%) =

$$\frac{\text{Genetic gain of selection index}}{\text{Genetic gain of grain yield}} \times 100$$

The selection score value, which was computed as follows, was used to assess the genotype's worth.

$$\text{Selection score (I)} = \sum_{i=1}^n b_i X_i$$

where,

n = 1, 2, ..., 6 characters

X_i = Value of i^{th} character

b_i = Coefficient of i^{th} character

Based on the greatest score value across all approaches, the top five genotypes were chosen, and the rank correlation between various ways was used to assess how similar or distinct the methods were.

Spearman rank correlation

Selection score (I) was calculated for all genotypes using all selection indices in all six methods. Method wise ranking was done on the basis of selection score to identify the

genotypes with their merit. The ranking of all genotypes in all six methods was subjected to spearman rank correlation analysis to find out degree of association between different methods (weights) employed in the study. Spearman rank correlation was worked out as under.

$$r_s = 1 - \frac{6 \sum d_i^2}{n(n^2 - 1)}$$

where,

r_s = Spearman correlation coefficient.

d = Deviation square of ranks of genotypes by two different methods

n = Number of genotypes.

The test of significance of 'r' was done as under

$$t = \frac{r_s \sqrt{n-2}}{\sqrt{1-r^2}}$$

The t value was compared with table t at (n-2) degree of freedom at 5% and 1% level of significance.

Simple correlation coefficient [W_1]

Correlation coefficient was calculated between grain yield and different biometrical characters using Pearson's formula (Pearson, 1896).

$$r = \frac{\sum xy}{\sqrt{\sum x^2 \sum y^2}}$$

where,

r = correlation coefficient

This value was used to assign weights in selection indices.

Genotypic coefficient of variation (GCV) [W_2]

Genotypic coefficient of variation was computed using the following formula given by Burton (1952).

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

where,

GCV = Genotypic coefficient of variation

$\bar{X}$ = General mean of the character

σ_g^2 = Expected genetic variance

Phenotypic coefficient of variation (PCV) [W_3]

Phenotypic coefficient of variation was computed using the following formula given by Burton (1952).

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

where,

PCV = Phenotypic coefficient of variation

$\bar{X}$ = General mean of the character

σ_p^2 = Expected phenotypic variance

RESULTS AND DISCUSSION

Mean, range and coefficient of variation

The genotypic variation for different characters was found to be significant. Table 1 displays the mean performance results. Genotype WN 594 had the highest grain yield per plant (32.73 g) and maximum number of productive tillers per plant (6.13), genotype KOPN 1230 had maximum test weight (3.07), genotype VL149 had the least number of days to maturity (93.00), the highest main ear length (11.39 cm) was found for genotype KMR 340 and the highest plant height (121.00 cm) was for genotype KOPN 1228.

Simple correlation coefficients

The simple correlation coefficient results (Table 2) showed that there was a positive

and significant correlation of grain yield per plant with number of productive tillers per plant (0.6541), test weight (0.4620), days to maturity (0.3723), main ear length (0.3292) and plant height (0.3193) (Keerthana *et al.* 2019, Lad *et al.* 2020). Additionally, productive tillers per plant and main ear length had significant and positive correlations with test weight (0.3317) and plant height (0.5257), respectively, as well as days to maturity (0.5693) and plant height (0.4901), respectively.

Genotypic and phenotypic coefficient of variation

PCV was found to be higher than GCV based on current research on GCV and PCV (Jyothsana *et al.* 2016, Anuradha and Patro, 2019, Abhilash *et al.* 2020, Shashibhushan *et al.* 2022). The small variation between GCV and PCV for each character (Table 3) indicates a reduced environmental impact. Grain yield per plant (20.92, 23.28%), productive tillers per plant (16.36, 19.33%) and main ear length (10.03, 11.38%) showed the highest variability of GCV and PCV, while days to maturity, test weight and plant height showed the lowest variability of GCV and PCV. Therefore, it is possible to increase grain yield in finger millet by utilising productive tillers per plant and main ear length.

Selection indices using different weights

All potential combinations of the six biometrical characters were taken into consideration while creating the selection indices. By assigning basic correlation coefficient (W_1), GCV (W_2) and PCV (W_3) as weights for each character, a total of 63 selection indices were created.

Expected genetic gain and relative efficiency (%) for individual character

The expected genetic advance and PRE of different indices were worked out (Table 4). In both single and combination characters, the genetic advance of grain yield (7.9927) with equal weight was taken into consideration as a base. In light of this, the efficiency was calculated for every selection index using various weights. For every weight approach (W_1 , W_2 , and W_3), a total of six selection indices were created, along with information on each one's genetic advance and percentage of relative efficiency. For W_1 , W_2 and W_3 , the corresponding PREs for the selection index of biometrical characters were 1.98 to 100.00, 7.74 to 2243.33 and 9.14 to 2328.00 percent.

Expected genetic gain and relative efficiency (%) for two characters

Using various weight algorithms, all feasible combinations of 2 characters were used to create the selection indices (W_1 to W_3). In all, 15 selection indices were created for each weight method, together with their genetic advance and percentage relative efficiency (Table 5). The single character genetic advance for grain yield (7.9927) with equal weight technique was taken as the starting point, and the effectiveness of all selection indices of all conceivable combinations of six characters for various weights was calculated. In the genotypic and phenotypic coefficient of variation weight techniques, as well as the simple correlation coefficient, the highest PRE was noted for the grain yield per plant and days to maturity combination (I_{14}). The lowest PRE was that of test weight and main ear length combination (I_{35}) in simple correlation coefficient, genotypic and phenotypic coefficient of variance weight methods.

Expected genetic gain and relative efficiency (%) for three characters

To create selection indices using each weight method, all possible combinations of 3 of the 6 biometrical traits were taken one at a time. A total of 20 selection indices with various character combinations were created (Table 6). For every weight technique, the selection indices were computed together with their projected genetic advance and percentage relative efficiency. The combination of test weight, days to maturity (I_{134}), and grain yield per plant showed the highest percentage relative efficiency among all feasible combinations in all weight techniques. On the other hand, across all weight techniques, the combination of productive tillers per plant, test weight, and main ear length (I_{235}) showed the lowest PRE.

Expected genetic gain and relative efficiency (%) for four characters

Total 15 different combinations of selection indices along with genetic advance and percent relative efficiency were constructed for each weight method using 4 biometrical characters (Table 7). The highest PRE was of index I_{1456} in phenotypic coefficient of variance as weight (5486.21%) and index I_{2456} in simple correlation coefficient (433.99%) and genotypic coefficient of variance (10931.39%) weight methods.

Expected genetic gain and relative efficiency (%) for five characters

To create the selection indices for each weight technique, every potential combination of 5 distinct characteristics, out of a total of six, was taken into account. There were 6 selection indices created for every weight method (Table 8). For every weight technique, the selection indices were computed together with their genetic

advance and PRE. Comparing various combinations of biometrical characters within each weight method, the highest PRE was found in the selection index (I_{12456}), which included days to maturity, main ear length, plant height, productive tillers per plant, and grain yield per plant across all weight methods. However, the selection index (I_{12345}), which includes test weight, days to maturity, main ear length, productive tillers per plant, and grain yield per plant, showed the lowest PRE among all the weight methods.

Expected genetic gain and relative efficiency (%) for six characters

Using various weights, combinations of the 6 biometrical features were utilised to create selection indices. The genetic advance and PRE of the selection indices were computed (Table 9). The per cent relative efficiencies were 215.52, 5069.78 and 5648.84 per cent for simple correlation coefficient, GCV and PCV weight methods, respectively.

Among all methods, the highest PRE was observed in GCV (10931.39%) followed by PCV (8960.31%) and simple correlation coefficient (433.99%) weight methods among all the combinations.

The highest percent relative efficiency was observed with index I_{2456} consisting of productive tillers per plant, days to maturity, main ear length and plant height with GCV (10931.39) and simple correlation coefficient (433.99) weight method and by index I_{12456} consisting of grain yield per plant, productive tillers per plant, days to maturity, main ear length and plant height in the PCV (8960.31) weight method. In order to obtain greater genetic gain, selection indices can be constructed using the GCV of the variables. Given its better relative efficiency, the selection index (I_{2456}) using the GCV weight

method which includes productive tillers per plant, days to maturity, main ear length, and plant height was thought to be more reliable.

For each genotype, the index score values were calculated using the three weight techniques, taking into account the highest PRE indicated by various character combinations (Table 10). The findings showed that, across all index combinations, PRE with GCV was generally greater than the other weights. There was agreement with all approaches as indicated by the positive and extremely significant rank correlation among the various methods for the selection score values. Overall, the results showed that the selection index with GCV had the highest PRE as well. The rank correlation (Table 11) between the PCV weight technique and the GCV weight method with simple correlation coefficient was positive and very significant ($r_s > 0.8$). As a result, the following index, which is based on GCV as weight is superior to all others.

$$I = 582.988X_2 + 11.104X_4 + 7.931X_5 + 3.533X_6$$

Where,

X_2 = productive tillers per plant

X_4 = days to maturity

X_5 = main ear length (cm)

X_6 = plant height (cm)

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Table 1: Mean performance of forty genotypes for yield and yield attributing characters of finger millet

Parameters	Grain Yield per Plant (g)	Productive Tillers per Plant	Test Weight (g)	Days to Maturity	Main Ear Length (cm)	Plant Height (cm)
Mean	20.63	3.49	2.67	111.11	9.17	93.78
Range	12.93- 32.73	2.27- 6.13	2.04- 3.07	93.00- 142.67	7.33- 11.39	77.67- 121.00
S. Em. $\pm$	1.22	0.21	0.11	1.35	0.29	3.38
C.D. at 5%	3.43	0.58	0.31	3.81	0.81	9.51
CV %	10.22	10.29	7.15	2.11	5.46	6.24

Table 2: Simple correlation coefficients between different characters of finger millet

Characters	GY	PT	TW	DM	MEL	PH
GY	1.0000	0.6541**	0.4620**	0.3723*	0.3292*	0.3193*
PT	-	1.0000	0.3317*	0.0564	0.0967	0.1707
TW	-	-	1.0000	0.2252	-0.0119	0.2956
DM	-	-	-	1.0000	0.5693**	0.4901**
MEL	-	-	-	-	1.0000	0.5257**
PH	-	-	-	-	-	1.0000

*, ** significant at 5 and 1 per cent level of significance, respectively

GY: Grain Yield per Plant, PT: Productive Tillers per Plant, TW: Test Weight, DM: Days to Maturity, MEL: Main Ear Length, PH: Plant Height

Table 3 : Genotypic and phenotypic coefficients of variation for different characters of finger millet

Characters	Coefficient of Variation (%)	
	Genotypic	Phenotypic
Grain yield per plant	20.92	23.28
Productive tillers per plant	16.36	19.33
Test weight	8.72	11.28
Days to maturity	8.97	9.22
Main ear length	10.03	11.38
Plant height	8.45	10.50

Table 4 : Selection indices, expected genetic advance and Per cent Relative Efficiency (PRE) for individual character by using different weight methods

Sr. No.	Equations	Genetic Advance	PRE
1	Simple Correlation Coefficient taken as Weights (W_1)		
I_1	$I=0.808X_1$	7.9927	100.00
I_2	$I=0.480X_2$	0.6629	8.29
I_3	$I=0.257X_3$	0.1586	1.98
I_4	$I=0.353X_4$	7.4420	93.11
I_5	$I=0.257X_5$	0.5521	6.91
I_6	$I=0.207X_6$	2.0600	25.77
2	Genotypic Coefficient of Variation (GCV) taken as Weights (W_2)		
I_1	$I=16.896X_1$	167.2079	2092.00
I_2	$I=0.017X_2$	0.6185	7.74
I_3	$I=4.844X_3$	2.9939	37.46
I_4	$I=8.500X_4$	179.3037	2243.33
I_5	$I=7.822X_5$	16.8219	210.46
I_6	$I=5.470X_6$	111.0003	1388.77

Sr. No.	Equations	Genetic Advance	PRE
3	Phenotypic coefficient of variation (PCV) taken as Weights (W_3)		
I_1	$I=18.802X_1$	186.0708	2328.00
I_2	$I=0.020X_2$	0.7308	9.14
I_3	$I=6.267X_3$	3.8728	48.45
I_4	$I=8.736X_4$	184.3010	2305.86
I_5	$I=8.874X_5$	19.0860	238.79
I_6	$I=6.803X_6$	138.0607	1727.33

Where, $I_1, I_2, I_3, I_4, I_5, I_6$ are selection indices and X_1 =Grain yield per Plant;
 X_2 = Productive Tillers per Plant; X_3 = Test Weight; X_4 = Days to Maturity; X_5 = Main Ear Length
and X_6 = Plant Height

Table 5 : Selection indices, expected genetic advance and Per cent Relative Efficiency (PRE) for possible combinations of two characters by using different weight methods

Sr. No.	Equations	Genetic Advance	PRE
1	Simple Correlation Coefficient taken as Weights (W_1)		
I_{12}	$I=0.774X_1+0.996X_2$	8.5445	106.90
I_{13}	$I=0.789X_1+1.212X_3$	8.1253	101.66
I_{14}	$I=0.804X_1+0.388X_4$	13.1960	165.10
I_{15}	$I=0.795X_1+0.533X_5$	8.2679	103.44
I_{16}	$I=0.844X_1+0.205X_6$	10.3637	129.66
I_{23}	$I=0.493X_2+0.346X_3$	0.7625	9.54
I_{24}	$I=0.382X_2+0.353X_4$	7.4987	93.82
I_{25}	$I=0.494X_2+0.270X_5$	0.9269	11.60
I_{26}	$I=0.950X_2+0.208X_6$	4.5293	56.67
I_{34}	$I=0.787X_3+0.352X_4$	7.5140	94.01
I_{35}	$I=0.192X_3+0.251X_5$	0.5558	6.95
I_{36}	$I=-0.765X_3+0.217X_6$	4.2597	53.29
I_{45}	$I=0.350X_4+0.395X_5$	7.8435	98.13
I_{46}	$I=0.408X_4+0.211X_6$	11.0025	137.66
I_{56}	$I=0.590X_5+0.191X_6$	4.6093	57.67

Sr. No.	Equations	Genetic Advance	PRE
2	Genotypic Coefficient of Variation (GCV) taken as Weights (W_2)		
I_{12}	$I=16.241X_1+22.561X_2$	180.9546	2263.99
I_{13}	$I=16.499X_1+24.889X_3$	169.7487	2123.79
I_{14}	$I=16.904X_1+9.230X_4$	296.1867	3705.70
I_{15}	$I=16.684X_1+13.531X_5$	175.5906	2196.88
I_{16}	$I=17.870X_1+5.398X_6$	233.7825	2924.94
I_{23}	$I=12.169X_2+7.173X_3$	18.4252	230.52
I_{24}	$I=9.651X_2+8.505X_4$	180.7489	2261.42
I_{25}	$I=12.429X_2+8.152X_5$	25.4043	317.84
I_{26}	$I=24.439X_2+5.499X_6$	119.3956	1493.80
I_{34}	$I=17.677X_3+8.464X_4$	180.6951	2260.74
I_{35}	$I=2.873X_3+7.715X_5$	16.7441	209.49
I_{36}	$I=-22.26X_3+5.755X_6$	112.5356	1407.97
I_{45}	$I=8.457X_4+10.978X_5$	191.5773	2396.89
I_{46}	$I=9.992X_4+5.501X_6$	274.2518	3431.26
I_{56}	$I=16.61X_5+5.06X_6$	123.5303	1545.53
3	Phenotypic Coefficient of Variation (PCV) taken as Weights (W_3)		
I_{12}	$I=18.096X_1+25.832X_2$	202.2980	2531.02
I_{13}	$I=18.377X_1+28.468X_3$	189.2857	2368.22
I_{14}	$I=18.760X_1+9.558X_4$	316.5475	3960.44
I_{15}	$I=18.570X_1+15.224X_5$	195.5861	2447.05
I_{16}	$I=20.019X_1+6.704X_6$	271.2821	3394.11
I_{23}	$I=14.430X_2+8.989X_3$	21.9893	275.12
I_{24}	$I=11.764X_2+8.742X_4$	186.1371	2328.83
I_{25}	$I=14.663X_2+9.266X_5$	29.4169	368.05
I_{26}	$I=29.658X_2+6.833X_6$	148.0066	1851.76
I_{34}	$I=19.414X_3+8.708X_4$	186.0618	2327.89
I_{35}	$I=4.032X_3+8.734X_5$	19.0271	238.06

Sr. No.	Equations	Genetic Advance	PRE
I ₃₆	$I = -27.436X_3 + 7.157X_6$	139.9936	1751.51
I ₄₅	$I = 8.710X_4 + 12.030X_5$	198.2548	2480.44
I ₄₆	$I = 10.653X_4 + 6.680X_6$	304.3131	3807.37
I ₅₆	$I = 19.821X_5 + 6.290X_6$	152.3545	1906.16

Table 6 : Selection indices, expected genetic advance and Per cent Relative Efficiency (PRE) for possible combinations of three characters by using different weight methods

Sr. No.	Equation	Genetic Advance	PRE
1	Simple Correlation Coefficient taken as Weights (W_1)		
I ₁₂₃	$I = 0.755X_1 + 0.988X_2 + 1.233X_3$	8.677	108.56
I ₁₂₄	$I = 0.784X_1 + 0.821X_2 + 0.390X_4$	13.544	169.46
I ₁₂₅	$I = 0.753X_1 + 1.063X_2 + 0.575X_5$	8.815	110.28
I ₁₂₆	$I = 0.762X_1 + 1.508X_2 + 0.214X_6$	10.937	136.83
I ₁₃₄	$I = -4.313X_1 + 229.839X_3 - 0.101X_4$	91.564	1145.59
I ₁₃₅	$I = 0.777X_1 + 1.191X_3 + 0.542X_5$	8.392	105.00
I ₁₃₆	$I = 0.856X_1 - 0.083X_3 + 0.206X_6$	10.464	130.92
I ₁₄₅	$I = 0.799X_1 + 0.380X_4 + 0.515X_5$	13.579	169.90
I ₁₄₆	$I = 1.030X_1 + 0.008X_4 + 0.351X_6$	14.108	176.51
I ₁₅₆	$I = 0.827X_1 + 0.888X_5 + 0.177X_6$	10.767	134.71
I ₂₃₄	$I = 0.327X_2 + 0.971X_3 + 0.351X_4$	7.582	94.86
I ₂₃₅	$I = 0.516X_2 + 0.268X_3 + 0.262X_5$	0.988	12.36
I ₂₃₆	$I = 1.209X_2 + 0.510X_3 + 0.002X_6$	1.886	23.60
I ₂₄₅	$I = 0.384X_2 + 0.349X_4 + 0.418X_5$	7.906	98.91
I ₂₄₆	$I = 0.794X_2 + 0.405X_4 + 0.214X_6$	11.142	139.40
I ₂₅₆	$I = 0.949X_2 + 0.572X_5 + 0.193X_6$	4.926	61.64
I ₃₄₅	$I = 0.722X_3 + 0.349X_4 + 0.386X_5$	7.908	98.94
I ₃₄₆	$I = -0.579X_3 + 0.411X_4 + 0.218X_6$	11.068	138.48
I ₃₅₆	$I = -0.697X_3 + 0.537X_5 + 0.203X_6$	4.660	58.30
I ₄₅₆	$I = 0.408X_4 + 0.367X_5 + 0.206X_6$	11.415	142.82

RELATIVE EFFICIENCY IN FINGER MILLET CROP

Sr. No.	Equation	Genetic Advance	PRE
2	Genotypic Coefficient of Variation (GCV) taken as Weights (W_2)		
I ₁₂₃	$I=15.843X_1+22.377X_2+25.552X_3$	183.493	2295.75
I ₁₂₄	$I=16.626X_1+17.871X_2+9.246X_4$	304.383	3808.25
I ₁₂₅	$I=15.866X_1+23.887X_2+14.402X_5$	189.072	2365.55
I ₁₂₆	$I=15.96X_1+36.022X_2+5.631X_6$	247.806	3100.39
I ₁₃₄	$I=-89.159X_1+4803.761X_3-2.274X_4$	1914.779	23956.50
I ₁₃₅	$I=16.312X_1+23.394X_3+13.722X_5$	177.893	2225.68
I ₁₃₆	$I=18.242X_1-9.738X_3+5.491X_6$	235.691	2948.81
I ₁₄₅	$I=16.811X_1+9.075X_4+13.416X_5$	308.025	3853.81
I ₁₄₆	$I=22.327X_1+0.154X_4+8.772X_6$	323.359	4045.66
I ₁₅₆	$I=17.491X_1+22.679X_5+4.741X_6$	246.098	3079.02
I ₂₃₄	$I=8.194X_2+22.274X_3+8.454X_4$	182.390	2281.95
I ₂₃₅	$I=12.884X_2+4.772X_3+8.007X_5$	26.370	329.92
I ₂₃₆	$I=30.928X_2+13.449X_3+0.056X_6$	48.322	604.57
I ₂₄₅	$I=9.774X_2+8.432X_4+11.556X_5$	193.181	2416.96
I ₂₄₆	$I=20.632X_2+9.922X_4+5.581X_6$	277.902	3476.93
I ₂₅₆	$I=24.480X_2+16.160X_5+5.112X_6$	131.437	1644.46
I ₃₄₅	$I=15.501X_3+8.439X_4+10.845X_5$	192.786	2412.01
I ₃₄₆	$I=-17.935X_3+10.05X_4+5.714X_6$	275.594	3448.06
I ₃₅₆	$I=-20.827X_3+15.227X_5+5.398X_6$	124.712	1560.32
I ₄₅₆	$I=10.018X_4+10.479X_5+5.385X_6$	286.868	3589.11
3	Phenotypic Coefficient of Variation (PCV) taken as Weights (W_3)		
I ₁₂₃	$I=17.667X_1+25.651X_2+29.297X_3$	205.512	2571.24
I ₁₂₄	$I=18.42X_1+21.248X_2+9.578X_4$	326.614	4086.39
I ₁₂₅	$I=17.683X_1+27.302X_2+16.191X_5$	211.487	2645.99
I ₁₂₆	$I=17.766X_1+42.527X_2+6.980X_6$	287.693	3599.43
I ₁₃₄	$I=-99.903X_1+5349.553X_3+-2.435X_4$	2131.672	26670.14
I ₁₃₅	$I=18.177X_1+26.715X_3+15.387X_5$	198.500	2483.51
I ₁₃₆	$I=20.540X_1-14.722X_3+6.843X_6$	273.760	3425.11

Sr. No.	Equation	Genetic Advance	PRE
I ₁₄₅	$I=18.667X_1+9.403X_4+14.771X_5$	329.873	4127.17
I ₁₄₆	$I=24.349X_1+0.646X_4+10.011X_6$	364.188	4556.48
I ₁₅₆	$I=19.563X_1+26.491X_5+5.925X_6$	285.535	3572.44
I ₂₃₄	$I=10.342X_2+24.485X_3+8.694X_4$	188.224	2354.93
I ₂₃₅	$I=15.241X_2+6.265X_3+9.078X_5$	30.722	384.38
I ₂₃₆	$I=37.771X_2+16.715X_3+0.070X_6$	59.210	740.80
I ₂₄₅	$I=11.929X_2+8.680X_4+12.700X_5$	200.283	2505.81
I ₂₄₆	$I=25.584X_2+10.568X_4+6.769X_6$	309.047	3866.60
I ₂₅₆	$I=29.660X_2+19.272X_5+6.347X_6$	161.750	2023.71
I ₃₄₅	$I=16.848X_3+8.706X_4+11.791X_5$	199.775	2499.46
I ₃₄₆	$I=-23.382X_3+10.728X_4+6.959X_6$	306.094	3829.65
I ₃₅₆	$I=-25.349X_3+18.113X_5+6.705X_6$	153.840	1924.75
I ₄₅₆	$I=10.682X_4+11.926X_5+6.547X_6$	318.632	3986.52

Table 7 : Selection indices, expected genetic advance and Per cent Relative Efficiency (PRE) for possible combinations of four characters by using different weight methods

Sr. No.	Equations	Genetic Advance	PRE
1	Simple Correlation Coefficient taken as Weights (W_1)		
I ₁₂₃₄	$I=0.757X_1+0.803X_2+1.645X_3+0.389X_4$	13.677	171.11
I ₁₂₃₅	$I=0.734X_1+1.057X_2+1.221X_3+0.584X_5$	8.939	111.84
I ₁₂₃₆	$I=1.479X_1-1.180X_2+12.359X_3-1.071X_6$	5.023	62.84
I ₁₂₄₅	$I=0.775X_1+0.849X_2+0.381X_4+0.539X_5$	13.925	174.22
I ₁₂₄₆	$I=0.714X_1+1.525X_2+0.455X_4+0.206X_6$	16.731	209.32
I ₁₂₅₆	$I=0.735X_1+1.600X_2+0.933X_5+0.185X_6$	11.333	141.80
I ₁₃₄₅	$I=0.771X_1+1.610X_3+0.377X_4+0.543X_5$	13.703	171.45
I ₁₃₄₆	$I=0.824X_1+1.369X_3+0.485X_4+0.081X_6$	16.061	200.94
I ₁₃₅₆	$I=0.831X_1+0.299X_3+0.882X_5+0.175X_6$	10.859	135.87
I ₁₄₅₆	$I=0.799X_1+0.442X_4+0.550X_5+0.188X_6$	16.760	209.69
I ₂₃₄₅	$I=0.336X_2+0.906X_3+0.347X_4+0.415X_5$	7.981	99.86

Sr. No.	Equations	Genetic Advance	PRE
I ₂₃₄₆	$I=0.917X_2-0.765X_3+0.408X_4+0.223X_6$	11.218	140.36
I ₂₃₅₆	$I=1.100X_2-1.008X_3+0.500X_5+0.209X_6$	5.008	62.66
I ₂₄₅₆	$I=23.132X_2+0.452X_4+0.269X_5+0.133X_6$	34.688	433.99
I ₃₄₅₆	$I=-0.649X_3+0.414X_4+0.293X_5+0.217X_6$	11.480	143.64
2	Genotypic Coefficient of Variation (GCV) taken as Weights (W ₂)		
I ₁₂₃₄	$I=16.025X_1+17.444X_2+35.735X_3+9.219X_4$	306.907	3839.83
I ₁₂₃₅	$I=15.482X_1+23.770X_2+24.250X_3+14.606X_5$	191.393	2394.59
I ₁₂₃₆	$I=16.420X_1+39.316X_2-19.462X_3+6.823X_6$	265.809	3325.63
I ₁₂₄₅	$I=16.459X_1+18.533X_2+9.072X_4+13.938X_5$	316.091	3954.73
I ₁₂₄₆	$I=14.809X_1+36.464X_2+10.975X_4+5.426X_6$	391.167	4894.04
I ₁₂₅₆	$I=15.361X_1+38.156X_2+23.716X_5+4.942X_6$	259.818	3250.67
I ₁₃₄₅	$I=16.201X_1+33.701X_3+9.023X_4+14.084X_5$	310.315	3882.47
I ₁₃₄₆	$I=17.824X_1+44.642X_3+12.335X_4+0.367X_6$	372.642	4662.26
I ₁₃₅₆	$I=17.740X_1-2.002X_3+22.038X_5+4.799X_6$	247.751	3099.71
I ₁₄₅₆	$I=16.805X_1+10.713X_4+14.256X_5+4.997X_6$	394.708	4938.34
I ₂₃₄₅	$I=8.557X_2+20.035X_3+8.390X_4+11.559X_5$	194.603	2434.75
I ₂₃₄₆	$I=23.786X_2-23.066X_3+9.978X_4+5.833X_6$	279.473	3496.59
I ₂₃₅₆	$I=28.337X_2-29.099X_3+14.262X_5+5.543X_6$	133.344	1668.32
I ₂₄₅₆	$I=582.988X_2+11.104X_4+7.931X_5+3.533X_6$	873.717	10931.39
I ₃₄₅₆	$I=-20.283X_3+10.154X_4+8.559X_5+5.688X_6$	288.178	3605.50
3	Phenotypic Coefficient of Variation (PCV) taken as weights (W ₃)		
I ₁₂₃₄	$I=17.782X_1+20.827X_2+39.634X_3+9.552X_4$	329.807	4126.34
I ₁₂₃₅	$I=17.274X_1+27.187X_2+27.76X_3+16.371X_5$	214.427	2682.77
I ₁₂₃₆	$I=18.322X_1+44.870X_2-21.771X_3+7.740X_6$	299.230	3743.77
I ₁₂₄₅	$I=18.245X_1+21.965X_2+9.400X_4+15.390X_5$	339.763	4250.90
I ₁₂₄₆	$I=16.223X_1+44.242X_2+11.769X_4+6.616X_6$	435.294	5446.12
I ₁₂₅₆	$I=17.048X_1+45.066X_2+27.716X_5+6.162X_6$	301.598	3773.40
I ₁₃₄₅	$I=18.034X_1+37.072X_3+9.355X_4+15.391X_5$	332.762	4163.31

Sr. No.	Equations	Genetic Advance	PRE
I ₁₃₄₆	I=20.565X1+80.408X3+14.410X4-2.783X6	410.273	5133.08
I ₁₃₅₆	I=19.949X1-5.583X3+25.455X5+6.034X6	287.655	3598.95
I ₁₄₅₆	I=18.688X1+11.456X4+16.135X5+6.117X6	438.498	5486.21
I ₂₃₄₅	I=10.798X2+21.823X3+8.649X4+12.603X5	202.080	2528.30
I ₂₃₄₆	I=29.712X2-30.339X3+10.640X4+7.100X6	311.173	3893.20
I ₂₃₅₆	I=34.454X2-35.694X3+16.920X5+6.880X6	164.150	2053.74
I ₂₄₅₆	I=649.357X2+12.021X4+9.663X5+4.536X6	974.397	12191.03
I ₃₄₅₆	I=-26.204X3+10.858X4+9.445X5+6.940X6	320.370	4008.27

Table 8 : Selection indices, expected genetic advance and Per cent Relative Efficiency (PRE) for possible combinations of five characters by using different weight methods

Sr. No.	Equations	Genetic Advance	PRE
1	Simple Correlation Coefficient taken as Weights (W_1)		
I ₁₂₃₄₅	I=0.748X1+0.834X2+1.647X3+0.378X4+0.568X5	14.051	175.79
I ₁₂₃₄₆	I=0.719X1+1.534X2+0.219X3+0.457X4+0.205X6	16.827	210.53
I ₁₂₃₅₆	I=0.741X1+1.605X2+0.205X3+0.921X5+0.185X6	11.427	142.96
I ₁₂₄₅₆	I=0.710X1+1.545X2+0.447X4+0.570X5+0.195X6	17.134	214.37
I ₁₃₄₅₆	I=0.801X1+0.422X3+0.444X4+0.545X5+0.185X6	16.851	210.83
I ₂₃₄₅₆	I=0.938X2-0.858X3+0.412X4+0.274X5+0.222X6	11.630	145.51
2	Genotypic Coefficient of Variation (GCV) taken as Weights (W_2)		
I ₁₂₃₄₅	I=15.854X1+18.181X2+34.795X3+9.013X4+14.637X5	318.446	3984.20
I ₁₂₃₄₆	I=13.689X1+42.474X2-47.257X3+9.576X4+10.317X6	403.198	5044.56
I ₁₂₃₅₆	I=15.633X1+38.412X2-4.173X3+22.938X5+5.026X6	261.516	3271.92
I ₁₂₄₅₆	I=14.733X1+36.942X2+10.841X4+14.741X5+5.172X6	403.537	5048.79
I ₁₃₄₅₆	I=16.976X1+0.870X3+10.758X4+13.640X5+5.015X6	396.337	4958.71
I ₂₃₄₅₆	I=24.454X2-26.099X3+10.103X4+8.030X5+5.829X6	292.078	3654.29

Sr. No.	Equations	Genetic Advance	PRE
3	Phenotypic Coefficient of Variation (PCV) taken as Weights(W_3)		
I_{12345}	$I=17.612X_1+21.623X_2+38.355X_3+9.346X_4+16.049X_5$	342.735	4288.08
I_{12346}	$I=16.535X_1+44.821X_2+-6.860X_3+11.791X_4+6.686X_6$	437.592	5474.88
I_{12356}	$I=17.453X_1+45.458X_2+-8.155X_3+26.522X_5+6.302X_6$	303.785	3800.77
I_{12456}	$I=16.136X_1+44.785X_2+11.616X_4+16.73X_5+6.327X_6$	716.174	8960.31
I_{13456}	$I=19.000X_1-3.253X_3+11.520X_4+15.015X_5+6.189X_6$	440.607	5512.59
I_{23456}	$I=30.506X_2+-34.026X_3+10.797X_4+8.728X_5+7.111X_6$	325.461	4071.96

Table 9 : Selection indices, expected genetic advance and Per cent Relative Efficiency (PRE) for combinations of all six characters by using different weight methods

Sr. No.	Equations	Genetic Advance	PRE
1	Simple Correlation Coefficient taken as Weights (W_1)		
I_{123456}	$I=0.713X_1+1.550X_2+0.325X_3+0.450X_4+0.558X_5+0.193X_6$	17.2263	215.52
2	Genotypic Coefficient of Variation (GCV) taken as Weights (W_2)		
I_{123456}	$I=14.923X_1+37.239X_2-1.370X_3+10.892X_4+13.965X_5+5.216X_6$	405.2140	5069.78
3	Phenotypic Coefficient of Variation (PCV) taken as Weights (W_3)		
I_{123456}	$I=16.460X_1+45.276X_2-6.035X_3+11.688X_4+15.414X_5+6.432X_6$	451.4970	5648.84

Table 10 : Top three ranking selection indices in different weight methods including finger millet grain yield per plant

Combinations	Rank	Simple Correlation (W_1)	GCV (W_2)	PCV (W_3)
Combinations of two characters	1	$I_{14}(165.10)$	$I_{14}(3705.70)$	$I_{14}(3960.44)$
	2	$I_{46}(137.66)$	$I_{46}(3431.26)$	$I_{46}(3807.37)$
	3	$I_{16}(129.66)$	$I_{16}(2924.94)$	$I_{16}(3394.11)$
Combinations of three characters	1	$I_{134}(1145.59)$	$I_{134}(23956.50)$	$I_{134}(26670.14)$
	2	$I_{146}(176.51)$	$I_{146}(4045.66)$	$I_{146}(4556.48)$
	3	$I_{145}(169.90)$	$I_{145}(3853.81)$	$I_{145}(4127.17)$

Combinations		Rank	Simple Correlation (W1)	GCV (W2)	PCV (W3)
Combinations of four characters		1	$I_{2456}(433.99)$	$I_{2456}(10931.39)$	$I_{1456}(5486.21)$
		2	$I_{1456}(209.69)$	$I_{1236}(4938.34)$	$I_{1246}(5446.12)$
		3	$I_{1246}(209.32)$	$I_{1246}(4894.04)$	$I_{1346}(5133.08)$
Combinations of five characters		1	$I_{12456}(214.37)$	$I_{12356}(109.53)$	$I_{12456}(8960.31)$
		2	$I_{13456}(210.83)$	$I_{12345}(108.01)$	$I_{13456}(5512.59)$
		3	$I_{12346}(210.53)$	$I_{12346}(4958.71)$	$I_{12346}(5474.88)$

Parenthesis value indicates Per cent Relative Efficiency (PRE)

Table 11 : Rank correlations between different weight methods based on the best selection index of respective weight methods including finger millet grain yield per plant

Weight	Correlation Wt.	GCV Wt.	PCV Wt.
Correlation Wt.	1.000	0.998**	0.788**
GCV Wt.	-	1.000	0.804**
PCV Wt.	-	-	1.000

** significant at 1 per cent level of significance, respectively; n = 40