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Comparison of selection indices using equal weight, standard deviation and heritability weight methods in finger millet

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Abstract

The data of forty genotypes of finger millet were used for the present study. The experiment was conducted in a Randomized Block Design with three replications at the Genetics and Plant Breeding Farm, Anand Agricultural University, Anand during *khariif* 2020. The experimental material comprised of six different biometrical characters *viz.* grain yield per plant, productive tillers per plant, test weight, days to maturity, main ear length and plant height of forty genotypes of finger millet. The selection index technique was employed to study the crop improvement using different characters giving different weights to each character. Selection index for individual character, combination of two characters, three characters and so on was calculated and the combination which provided the higher relative efficiency was selected. The standard deviation and heritability were worked out between yield and yield attributing characters. Selection indices were worked out taking six biometrical characters and were constructed taking all possible combinations of the characters. Total sixty-three selection indices were constructed using equal weight (W_1), standard deviation (W_2) and heritability (W_3) as weights for all the characters. The expected genetic advance and Per cent Relative Efficiency (PRE) of different indices were calculated. The results indicated that in general PRE with standard deviation as weight was higher than rest of the weights in all combinations of indices. The selection index I_{2456} in standard deviation weight method was found the best and the genotype WN 594 ranked first thus, can be used for future breeding programmes.

Keywords: Finger millet, per cent relative efficiency, selection index, selection score

1. Introduction

Finger millet *also* known as ragi is one of the important minor millets. Finger millet ranks fourth among millets on a global scale of production next to sorghum, pearl millet and foxtail millet (Upadhyay *et al.*, 2007) ^[9], while in India it is the sixth largest produce after wheat, maize, sorghum, bajra, and rice (Chandra *et al.*, 2016) ^[1]. India is in the lead in production of ragi in the world, and occupies an area of 1.004 million ha with an average production of 1.755 million tones and productivity of 1747 kg/ha in 2019-20 (Indiastatagri, 2020) ^[13]. 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) ^[13].

The present investigation entitled was carried out to compare different selection indices based on different weights using six biometrical characters of forty genotypes of finger millet. The data was collected from the experiment conducted by the P.G. student during *khariif* 2020. The experiment was conducted in randomized block design with three replications at the Genetics and Plant Breeding Farm, B. A. College of Agriculture, AAU, Anand. Among the nine characters six important characters *viz.* grain yield per plant (g), productive tillers per plant, test weight (g), days to maturity, main ear length (cm) and plant height (cm) were utilized to construct selection indices using different weights *viz.*, equal weight [W_1], standard deviation [W_2] and heritability [W_3]. The data on six characters were subjected to mean performance of genotypes, ANOVA, simple correlation, standard deviation, heritability, genotypic coefficient of variation, phenotypic coefficient of variation and selection indices technique using different weights of the characters.

2. Materials and Methods

Selection index for individual character, combination of two characters, three characters and so on can be calculated and the combination which provides the higher relative efficiency is selected. Genetic advance and percent relative efficiency (PRE) were calculated by using the following formulae. Selection index for single or combination of characters which provides the high PRE was selected.

The expected genetic advance was calculated by following (Dabholkar, 1992) [10].

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

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 ith character

b_i= Coefficients of ith character

b_j = Transpose of b_i

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

The per cent relative efficiency of each index was calculated using gain of grain yield as standard. It was calculated as under

$$\text{Relative Efficiency (\%)} = \frac{\text{Genetic gain of selection indices}}{\text{Genetic gain of grain yield}} \times 100$$

The merit of the genotype was measured using selection score value which was calculated as under.

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

Where,

n = 1, 2, 3, 6 character

X_i = value of ith character

b_i = coefficient of ith character

The first five best genotypes were selected on the bases of the highest score value in all methods and the similarity/dissimilarity of the methods were judged on the bases of rank correlation among different methods.

In equal weight, a value of 1 was assigned for all characters to construct selection indices.

$$a_1 = a_2 = a_3 = \dots = a_6 = 1$$

Standard deviation was calculated by using the method given by Karl Pearson (1896) [12].

$$s = \sqrt{\frac{\sum (X - \bar{X})^2}{n - 1}}$$

Where,

s = Standard deviation

\bar{X} = General mean of characters

n = Number of observations

The broad sense heritability as the ratio of genetic variance to phenotypic variance was calculated for all characters and used as weight (Lush, 1949) [11].

$$h_b^2 = \frac{\sigma_g^2}{\sigma_p^2}$$

Where,

h_b^2 = Heritability

σ_g^2 = Genetic variance

σ_p^2 = Phenotypic variance

3. Results and Discussions

The variation among genotypes for different characters was found significant. The results of mean performance, standard deviation and heritability are given in Table 1. Genotype WN 594 had the highest grain yield per plant (32.73) and maximum number of productive tillers per plant (6.13), genotype KOPN 1230 had maximum test weight (3.07), maximum number of days to maturity (128.67) were of genotype KOPN 235 while, genotype VL149 had the least number of days to maturity (93.00), the highest main ear length (11.39) was found for genotype KMR 340 and the highest plant height (121.00) was that of genotype KOPN 1228. The results of standard deviation exhibited that days to maturity had the highest deviation (10.06) followed by plant height (8.61), grain yield per plant (4.49), main ear length (0.96), productive tillers per plant (0.60) and test weight (0.26). The broad sense heritability (h_b^2 %) was the highest (94.76) for days to maturity, (Sao *et al.* 2016) [7], (Udamala *et al.* 2020) [8] and (Rani *et al.* 2021) [6] followed by grain yield per plant (80.76), main ear length (77.75), productive tillers per plant (71.64), plant height (64.73) and test weight (59.79).

Table 1: Mean performance, standard deviation and heritability of forty genotypes for yield and yield attributing characters of finger millet

	Grain Yield per Plant (g)	Productive Tillers per Plant	Test Weight (g)	Days to Maturity	Main Ear Length (cm)	Plant Height (cm)
General Mean	20.63	3.49	2.67	111.11	9.17	93.78
Standard Deviation	4.49	0.60	0.26	10.06	0.96	8.61
H ² (Broad Sense)	80.76	71.64	59.79	94.76	77.75	64.73

The selection indices were constructed taking all possible combinations of the six biometrical characters. Total sixty-three selection indices were constructed using equal weight (W₁), standard deviation (W₂) and heritability (W₃) as weights for all the characters. The expected genetic advance and percent relative efficiency (PRE) of different indices were worked out. The genetic advance of grain yield (7.9927) with equal weight was considered as a base in all single as well as combinations of characters. Relative to this, the efficiency

was worked out for all selection index with different weights. Total six selection indices were constructed for each weight method (W₁, W₂ and W₃) along with their genetic advance and per cent relative efficiency. The PRE for selection index of biometrical characters ranged from 4.30 to 250.09, 1.11 to 2516.14 and 2.58 to 237.59 per cent for W₁, W₂ and W₃, respectively. The highest PRE was observed for days to maturity (Patil *et al.* 2018) [5] whereas, the lowest PRE was observed for test weight in all the three weight methods.

The selection indices were constructed using all possible combinations of two characters using different weight methods (W_1 to W_3). Total fifteen selection indices were constructed in each weight method with their genetic advance and per cent relative efficiency. The genetic advance for grain yield (single character) with equal weight method (7.9927) was considered as base and the efficiency was worked out for all selection indices of all possible combinations of six characters for different weights. The highest PRE was observed for days to maturity and plant height combination (I_{46}) in equal weight (391.38%) and heritability (326.72%) weight methods and for grain yield per plant and plant height combination (I_{16}) in standard deviation (10497.90%) weight method. The lowest PRE was observed for productive tillers per plant and test weight combination (I_{23}) in the three weight methods.

Among the six biometrical characters all possible combinations of three characters were taken at a time to construct selection indices using each weight method. Total twenty selection indices consisting different combinations of characters were constructed along with their expected genetic advance and per cent relative efficiency for each weight method. The highest per cent relative efficiency was observed for combination of grain yield per plant, test weight and days to maturity (I_{134}) in standard deviation and heritability weight methods (Kour *et al.* 2018) ^[4] whereas, combination of grain yield per plant, days to maturity and plant height (I_{146}) for equal weight method. The lowest PRE was observed for combination of productive tillers per plant, test weight and main ear length (I_{235}) in all the weight methods.

Total fifteen different combinations of selection indices were constructed for each weight method using four biometrical characters. The genetic advance and percent relative efficiency of these combinations were calculated. The highest PRE was of index I_{1456} in equal weight (462.76%) and heritability (383.94%) and index I_{2456} in standard deviation (33834%).

Out of six characters all possible combinations of five different characters were considered to construct the selection indices using each weight method. Six selection indices were constructed for each weight method along with their genetic advance and per cent relative efficiency. The highest PRE was observed in the selection index (I_{12456}) consisting grain yield per plant, productive tillers per plant, days to maturity, main ear length and plant height in all the weight methods as compared to different combinations of biometrical characters within the respective weight method. While, the lowest PRE was observed in selection index (I_{12356}) consisting grain yield per plant, productive tillers per plant, test weight, main ear length and plant height in all the weight methods.

Combinations of all six biometrical characters were used to construct selection indices using different weights and their genetic advance and per cent relative efficiency were calculated. The per cent relative efficiencies were 470.17%, 3973.16% and 388.42% for equal weight, standard deviation and heritability weight methods, respectively.

Among all methods (Table 2), the highest percent relative efficiency was observed in standard deviation (33834.00%) followed by equal weight (467.90%) and heritability (387.14%) weight methods among all the combinations.

Table 2: Top three ranking selection indices in different weight methods including finger millet grain yield per plant

Combinations	Rank	Equal Weight	Standard Deviation	Heritability
Combinations of two characters	1	I_{46} (391.38)	I_{16} (497.90)	I_{46} (326.72)
	2	I_{14} (309.22)	I_{46} (3717.90)	I_{45} (249.48)
	3	I_{45} (265.38)	I_{45} (2532.40)	I_{34} (238.86)
Combinations of three characters	1	I_{146} (452.69)	I_{134} (5160.54)	I_{134} (928.86)
	2	I_{456} (407.09)	I_{456} (3733.61)	I_{456} (338.93)
	3	I_{246} (394.27)	I_{246} (3722.15)	I_{246} (328.38)
Combinations of four characters	1	I_{1456} (462.76)	I_{2456} (33834.00)	I_{1456} (383.94)
	2	I_{1246} (452.01)	I_{1456} (31909.99)	I_{1246} (374.76)
	3	I_{1346} (426.07)	I_{1246} (31831.13)	I_{1346} (356.67)
Combinations of five characters	1	I_{12456} (467.90)	I_{12456} (3969.85)	I_{12456} (387.14)
	2	I_{13456} (464.93)	I_{13456} (3966.31)	I_{13456} (385.18)
	3	I_{12346} (454.38)	I_{12346} (3957.57)	I_{12346} (376.11)

Parenthesis value indicates Per cent Relative Efficiency (PRE)

Results presented in Table 2 indicated that the highest percent relative efficiency was observed with index I_{2456} (33834.00) consisting of productive tillers per plant, days to maturity, main ear length and plant height with standard deviation weight method whereas, the highest PRE was observed with the index I_{12456} consisting of grain yield per plant, productive tillers per plant, days to maturity, main ear length and plant height in the equal weight and heritability weight methods. Therefore, one can use standard deviation of variables for construction of selection indices to achieve higher genetic gain. The selection index consisting of productive tillers per plant, days to maturity, main ear length and plant height (I_{2456}) with standard deviation weight method was considered more reliable as it was commonly having higher relative efficiency.

The comparison of top three ranking selection indices for combinations of different characters in each weight method based on per cent relative efficiency were also reported by Kalola *et al.* (2018) ^[3] in pearl millet crop and Kour *et al.* (2018) ^[4] in forage sorghum.

The index score values were worked out for all three weight methods for all genotypes in respect of the highest PRE given by different combination of characters (Table 3). The results indicated that in general PRE with standard deviation was higher than rest of the weights in all combinations of indices. Ranking of genotypes based on selection score value for different weights were also noted by Chaudhary *et al.* (2017) ^[2] in rice crop and Kour *et al.* (2018) ^[4] in forage sorghum.

Table 3: Selection score values and ranks of finger millet genotypes based on best selection index for respective weight methods

Genotypes	Equal Wt. [W ₁]	Std. Dev. Wt. [W ₂]	Heri. Wt. [W ₄]
KOPN 1204	91.83 (28)	1059.88 (26)	63.90 (29)
KOPN 1211	86.97 (34)	994.18 (37)	61.11(34)
KOPN 1213	92.51 (26)	1082.09 (21)	64.52 (27)
KOPN 1214	94.72 (22)	1141.34 (11)	65.97 (23)
KOPN 1227	98.10 (18)	1066.83 (25)	68.43 (18)
KOPN 1228	107.39 (9)	1239.95 (4)	75.20 (9)
KOPN 1230	104.95 (10)	1252.39 (2)	73.35 (10)
Phule Kesari	96.86 (19)	1116.67 (15)	67.77 (19)
GPU 45	86.88 (35)	1006.04 (34)	60.81 (36)
GPU 67	92.71 (25)	1051.30 (27)	65.09 (26)
VL 352	85.48 (39)	1000.19 (35)	60.36 (38)
VL 315	93.27 (24)	1048.79 (28)	65.65 (24)
VL 149	88.28 (31)	971.81 (40)	61.19 (33)
VL 324	92.33 (27)	1041.80 (30)	65.53 (25)
VL 376	86.83 (36)	1021.88 (32)	61.30 (32)
VL 314	91.49 (29)	1010.43 (33)	64.21 (28)
KOPN 235	109.93 (3)	1243.13 (3)	77.65 (3)
KOPN 942	107.82 (7)	1180.07 (8)	75.95 (8)
Phule Nachani	99.47 (15)	1142.15 (10)	69.84 (14)
VR 708	85.73 (38)	977.64 (39)	59.62 (39)
VR 847	101.65 (12)	1085.59 (20)	71.82 (12)
VR 936	94.97 (21)	1105.29 (17)	66.78 (21)
PR 202	96.59 (20)	1075.55 (24)	67.27 (20)
GPU 66	107.81 (8)	1282.90 (1)	75.98 (7)
GPU 28	101.18 (13)	1109.49 (16)	71.17 (13)
MR 6	108.11 (5)	1216.01 (5)	76.32 (6)
KMR 340	108.08 (6)	1188.57 (7)	76.38 (5)
KMR 204	91.33 (30)	1078.09 (23)	63.84 (30)
KMR 603	82.25 (40)	982.32 (38)	57.03 (40)
OEB 532	93.85 (23)	1081.45 (22)	66.00 (22)
Indira Ragi 1	86.09 (37)	1044.72 (29)	60.73 (37)
Chhattisgarh Ragi 2	99.60 (14)	1086.58 (19)	69.83 (15)
RAU 8	98.37 (17)	1123.43 (14)	69.46 (17)
GN 1	87.43 (33)	1039.76 (31)	61.71 (31)
GNN 6	99.28 (16)	1092.54 (18)	69.70 (16)
GNN 7	102.05 (11)	1138.66 (12)	71.99 (11)
GN 8	87.73 (32)	995.52 (36)	61.10 (35)
WN 587	110.21 (2)	1124.89 (13)	78.38 (2)
WN 593	109.61 (4)	1198.88 (6)	76.44 (4)
WN 594	114.60 (1)	1147.86 (9)	79.79 (1)

Value in parenthesis are ranks of genotypes in different weight methods.

The rank correlation (Table 4) among different methods for selection score values were positive and highly significant indicating agreement with all methods. Kour *et al.* (2018) ^[4] also stated all correlation coefficients among different weight methods were more than 0.60 in forage sorghum which is similar to our findings in finger millet crop.

Table 4: Rank correlations between different weight methods based on the best selection index of respective weight methods including finger millet grain yield per plant

	Equal Weight	Standard Deviation	Heritability
Equal Weight	1.000	0.900**	0.995**
Standard Deviation		1.000	0.906**
Heritability			1.000

** significant at 0.01 level of probability, respectively; n = 40

Looking to the overall results it was observed that selection index with standard deviation had the highest PRE also, the rank correlation of standard deviation weight method with

equal weight and heritability weight methods was positive and highly significant ($r_s \geq 0.9$). Therefore, the following index based on standard deviation taken as weight is considered better than all other indices.

$$I_{2456} = 20.062X_2 + 10.936X_4 + 4.333X_5 + 5.498X_6$$

Where,

X₂ = productive tillers per plant

X₄ = days to maturity

X₅ = main ear length (cm)

X₆ = plant height (cm)

The combined selection score and rank of forty genotypes were worked out (Table 5) to find the best genotype irrespective of the weights. The genotype WN 594 ranked first among the forty genotypes under study (Table 5) and can be used for future breeding programmes.

Table 5: Combined selection score and rank of forty finger millet genotypes

Sr. No.	Genotypes	Selection Score	Rank
1	KOPN 1204	9.64752	39
2	KOPN 1211	12.46536	32
3	KOPN 1213	12.70416	31
4	KOPN 1214	11.17584	34
5	KOPN 1227	12.8952	30
6	KOPN 1228	9.88632	38
7	KOPN 1230	14.71008	20
8	Phule Kesari	13.56384	28
9	GPU 45	10.746	35.5
10	GPU 67	13.99368	25
11	VL 352	14.71008	19
12	VL 315	15.90408	13
13	VL 149	10.5072	37
14	VL 324	15.9996	12
15	VL 376	13.89816	26
16	VL 314	14.99664	18
17	KOPN 235	17.33688	9
18	KOPN 942	18.29208	6
19	Phule Nachani	14.61456	22
20	VR 708	11.36688	33
21	VR 847	19.05624	3
22	VR 936	15.18768	16
23	PR 202	14.28024	23
24	GPU 66	18.10104	7
25	GPU 28	16.19064	11
26	MR 6	16.57272	10
27	KMR 340	18.48312	5
28	KMR 204	13.70712	27
29	KMR 603	9.26544	40
30	OEB 532	15.0444	17
31	Indira Ragi 1	12.99072	29
32	Chhattisgarh Ragi 2	15.7608	14
33	RAU 8	15.66528	15
34	GN 1	14.13696	24
35	GNN 6	14.61456	21
36	GNN 7	17.71896	8
37	GN 8	10.746	35.5
38	WN 587	22.11288	2
39	WN 593	18.76968	4
40	WN 594	23.45016	1

Conclusion

In a nutshell the equal weight, standard deviation and heritability weight methods showed similar results. Considering the ease of calculation, the selection index I₂₄₅₆

calculated using standard deviation as weight was found to be the best. $I_{2456} = 20.062X_2 + 10.936X_4 + 4.333X_5 + 5.498X_6$, where, X_2 = productive tillers per plant, X_4 = days to maturity, X_5 = main ear length (cm), X_6 = plant height (cm). The genotype GPU 66 was selected as the top-ranking genotype followed by genotypes KOPN 1228, KOPN 235 and KOPN 1230 among all three weight methods. The results of equal weight and heritability as weight method are almost similar based on the PRE values hence, either of them can be taken as weight. The genotype GPU 66 can be used for plant breeding improvement programmes in finger millet crop.

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