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Research Article

Strategy of multiple selection indices for discrimination of potential genotypes and associated traits for yield improvement in pearl millet [*Pennisetum glaucum* (L.) R.Br.]

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Abstract

A study was conducted with 31 genotypes of pearl millet to identify the potential through correlation, path analysis and discriminant function analysis for yield and yield attributing traits at the Department of Millets, Tamil Nadu Agricultural University, Coimbatore during *Kharif* 2019. The top ranking genotypes for single plant yield was Cumbu 2, Kizikuppam local, PT6706, PT6582 and PT6581. High PCV and GCV were recorded for harvest index, single plant yield, biological yield, thousand grain weight, the number of productive tillers and total grains per panicle. The path coefficient analysis revealed that harvest index, biological yield, panicle length and flag leaf length showed a positive high direct effect on grain yield per plant, which can be utilized for the formulation of selection indices. The discriminant function analysis revealed that the maximum genetic gain for grain yield per plant can be obtained by selecting the traits like leaf sheath length, leaf length, flag leaf length, flag leaf width, the number of nodes, panicle length, the number of productive tillers, thousand grain weight, biological yield, harvest index and single plant yield in combination when path direct effect was used as economic weights. Selection criterion score values showed that the genotypes such as Cumbu 2, Kizikuppam local, Nattu Cumbu, PT6705, PT6580, PT6706, Cumbu 1 and PT6067 have outperformed others and can be utilized for further breeding programmes.

Key words: Genetic variability, Path correlation, Discriminant function, Selection index, Pearl millet

INTRODUCTION

Pearl millet [*Pennisetum glaucum* (L.) R.Br.] is one of the most significant nutritious and food-security crops grown by smallholder farmers in semiarid regions around the world. It is one of Sub-Saharan Africa's and tropical India's most widely consumed staple food crops (Fuller *et al.*, 2021). Pearl millet is the sixth most important cereals crop in the world after wheat, rice, maize, barley and

sorghum (FAO, 2020 and Patil *et al.*, 2020) and India is one of the world's largest producers of pearl millet, where pearl millet is the fourth most extensively cultivated crop after rice, wheat and maize.

Pearl millet improvement through different breeding methods and selection is of paramount importance in

achieving higher productivity. Direct selection on yield by *per se* performance is important, whereas selection for component traits is significant and vital since it will result in more genetic gain per generation. The effectiveness of any selection depends upon the genetic variability for a trait and characters with a high coefficient of variation and high heritability coupled with high genetic advance may be governed by additive genes and can be directly selected for improvement through simple plant selection (Singh *et al.*, 2013). To decide the breeding method to improve the complex traits, the association between the yield and yield attributing traits are important (Pujar *et al.*, 2020; Shah *et al.*, 2016). Correlation and path analysis helps in identifying the component traits in a particular breeding population, which may then be used for selection and improvement of the trait by forming selection indices. Selection indices are useful in understanding the extent of improvement that can be affected in yield by the combination of characters. It forms the basis in considering the correlated characters for higher efficiency in selection for yield (Basavaraja and Sheriff, 1992). Simultaneous selection of all component characters along with their relative weights attached to their phenotypic value in such a manner that the correlation between compounded phenotypic score and corresponding compounded genetic score is maximum (Hazel, 1943; Kour *et al.*, 2018). By keeping the above on view, the current study was aimed to explore the genetic variability, the association of yield and yield attributing traits and formulation of selection indices using discriminant function analysis in pearl millet genotypes.

MATERIALS AND METHODS

The experiment was carried out on 31 different genotypes of pearl millet maintained at the Department of Millets, Tamil Nadu Agricultural University, Coimbatore during *Kharif*, 2019 in Randomized Complete Block Design (RCBD) with two replications and adopted 45 x 15 cm spacing. All recommended packages of practices were followed to raise a good crop. Five randomly selected plants in each replication were used for the collection of data and observations were recorded for 16 quantitative traits.

The mean data was subjected to statistical analysis using the software WINDOSTAT ver 7.1. Analysis of variance and summary statistics were calculated as per Panse and Sukathme (1967). Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed as per Burton and Devane (1953). Heritability in a broad sense was computed as per Allard (1960). Genotypic and phenotypic correlations were calculated according to Falconer (1981). Heritability and genetic advancement were categorized into low, medium and high as per Johnson *et al.* (1955). Path coefficient analysis suggested by Wright (1921) and elaborated by Dewey and Lu (1959) was used to calculate the direct and indirect contributions of various traits to yield. Lenka and Mishra (1973) scale were used

to measure the direct and indirect effects. Construction of selection indices was carried out based on Fisher's discriminate function (Fisher, 1936), which was applied to plant improvement by Smith (1936).

Genotypic correlation coefficient with yield and genotypic path direct effect was used as economic weights for construction of selection indices. The genetic advance of individual traits and selection criterion score was obtained by subjected to statistical analysis tool WINDOSTAT ver 7.1. The expected genetic advance and relative efficiency in percentage were computed according to the following formula used by Brim, *et al.* (1959), Pritchard *et al.* (1972) and Robinson and Comstock (1950).

$$\text{Expected genetic advance} = \frac{Z}{P} \sqrt{b_1 G_{1y} + b_2 G_{2y} + \dots + b_n G_{ny}}$$

Where Z/P is the selection differential in standard units. b value is the weights in the selection index and G_{1y} , G_{2y} etc. genotypic covariances of the observed characters with the character being selected. The selection indices were constructed in all possible combinations of traits and respective expected genetic advances were calculated and selected only the highest genetic advance in each set of combinations. Grain yield was considered as the dependant variable with a relative efficiency of 100 per cent to calculate the relative efficiency of other traits and their combinations.

RESULTS AND DISCUSSION

The analysis of variance indicated that a highly significant difference exists among the genotypes for all the studied characters indicated that sufficient variability is present in the experimental material for selection and scope for increasing yield and yield attributing traits for crop improvement (Ram *et al.*, 2014). The mean single plant yield was found to be 48.31 g. The single plant yield ranged from 19.2 g in PT 6059 to 86.17 g in Cumbu 2. Out of 31 genotypes, seven genotypes showed superiority to check Dhanashakti (Table 1). The mean performance of the top five individuals for single plant yield was recorded by Cumbu 2 (86.17), Kizikuppam local (79.02), PT 6706 (74.49), PT 6582 (73.52) and PT 6581 (71.94).

The difference between the PCV and GCV was narrow for most of the traits indicated the least influence of environment on traits and improvement by making selection pressure on these characters at early generation (Dapke *et al.*, 2014; Manga *et al.*, 2013; Rasitha *et al.*, 2019). But single plant yield, biological yield and plant height showed more differences between PCV and GCV revealing the more influence of the environment on these characters indicating that selection at the later generations is promising for these traits.

High PCV and high GCV were observed for most of the traits viz., harvest index, single plant yield, biological yield, thousand grain weight, the number of productive

Table 1. Mean performance of pearl millet genotypes for yield and yield attributing traits

S. No.	Genotypes	DTF	LSL	LL	LW	FL	FW	NN	PL	PD	NT	PH	TGP	TSW	BY	SPY	HI
1	PT 6067	50.00	17.67	65.67	4.60	43.00	4.00	6.67	29.67	2.95	3.00	137.00	2341.73	11.26	88.88	55.23	62.14
2	PT 6674	47.00	17.33	52.67	3.83	40.33	2.80	6.67	16.33	3.14	2.33	127.00	2565.39	9.72	58.74	31.83	53.97
3	PT 6675	51.00	15.00	50.33	3.43	36.67	2.93	7.67	16.00	3.09	2.67	127.00	2948.85	10.59	51.50	39.48	74.98
4	PT 6676	50.00	19.00	64.00	4.77	39.67	4.23	7.00	31.33	3.15	3.33	160.00	4144.95	6.10	109.64	43.12	39.89
5	PT 6677	50.00	17.67	58.33	4.77	42.67	4.70	7.00	25.33	3.16	3.33	146.67	2573.87	9.00	101.50	53.18	52.40
6	PT 6059	56.00	16.00	53.00	4.73	47.33	5.17	4.33	23.67	2.94	1.33	95.00	2713.09	9.89	62.04	19.20	30.94
7	PT 6705	51.00	22.67	54.67	4.43	42.67	3.60	6.00	27.00	2.93	3.33	162.75	2104.83	12.52	69.05	70.03	101.04
8	PT 6706	58.00	20.67	69.00	4.10	49.67	4.57	7.67	27.33	3.51	3.67	188.13	3266.54	13.30	86.52	74.49	87.33
9	PT 6707	54.00	16.33	58.00	3.80	48.67	3.80	6.33	23.00	2.88	3.33	156.00	2622.32	8.05	66.00	38.72	58.66
10	PT 6708	55.00	21.67	60.00	4.27	45.67	4.17	5.67	22.00	3.33	2.67	176.70	2250.20	9.97	116.33	48.56	40.83
11	PT 6709	51.00	19.33	62.67	4.90	49.33	4.87	6.33	34.00	3.13	2.33	178.33	2626.73	10.76	53.30	38.10	69.55
12	PT 6710	54.00	17.67	55.33	4.23	42.33	4.70	5.33	21.00	2.35	3.67	144.00	2799.11	6.69	49.14	37.28	75.54
13	PT 6029	44.00	19.17	37.43	3.67	34.00	4.10	5.33	23.67	2.94	2.33	144.54	2565.20	13.00	60.85	32.86	53.77
14	PT 6580	52.00	20.73	64.67	4.40	53.00	4.27	6.67	25.33	3.04	4.00	198.58	2733.11	11.20	112.05	52.77	47.09
15	PT 6581	50.00	16.17	56.67	3.80	38.33	3.90	6.67	25.33	3.05	3.67	150.33	3702.93	13.60	103.03	71.94	69.82
16	PT 6582	49.00	16.83	57.33	4.57	40.67	4.83	6.67	22.33	3.53	4.33	158.33	2600.79	10.84	92.78	73.52	79.23
17	PT 6583	52.00	23.33	48.33	4.20	43.33	4.50	7.00	31.67	3.04	2.67	177.92	1944.41	9.92	99.77	31.58	31.52
18	ICMB 98222	50.00	15.67	52.33	4.43	39.67	4.13	6.67	19.33	3.55	2.67	139.58	3259.11	7.98	34.44	25.30	73.47
19	ICMB 06111	58.00	14.67	34.00	3.47	25.33	3.50	4.00	15.67	2.68	3.33	83.67	2304.33	7.05	32.73	43.45	132.73
20	ICMB 99222	49.00	17.33	43.67	4.50	39.67	4.70	5.67	18.00	3.72	3.33	128.33	4296.55	10.28	52.22	38.72	74.14
21	Cumbu 1	51.00	19.00	63.50	4.80	51.50	5.05	6.67	24.67	2.51	3.67	184.67	2441.24	11.45	87.69	59.18	66.01
22	Nattu Cumbu	53.00	19.00	62.50	4.70	54.00	5.10	7.00	26.00	2.51	3.33	189.00	2431.23	10.24	47.22	68.82	145.73
23	Cumbu 2	52.00	15.00	65.50	4.50	52.00	4.70	5.67	20.33	3.10	5.00	168.33	2540.91	13.78	128.31	86.17	67.15
24	Kuttu Cumbu 1	42.00	11.50	44.00	3.65	36.00	4.20	7.67	19.67	1.70	5.67	195.33	1522.25	4.76	105.27	35.85	34.97
25	Kuttu Cumbu 2	41.00	12.50	37.50	3.30	22.50	3.10	5.00	20.00	1.63	5.33	161.67	1466.15	5.10	81.95	26.37	32.18
26	Kuttu Cumbu 3	41.00	10.75	43.50	2.45	24.00	2.40	5.00	15.33	1.72	3.67	168.67	1632.55	4.39	64.12	28.91	45.08
27	Kizikuppam local	40.00	16.75	73.00	3.95	53.00	4.50	5.33	25.33	2.93	3.67	170.53	2486.55	12.21	71.50	79.00	110.47
28	Pothu Cumbu	37.00	14.00	55.50	2.95	34.00	3.35	6.00	19.00	1.81	4.67	259.00	1406.84	4.95	57.97	31.39	53.91
29	Uthangarai local	44.00	17.75	60.00	4.35	42.00	4.30	6.67	23.67	2.78	3.33	176.92	2655.85	11.84	68.56	55.14	78.68
30	Shoolagiri local	47.00	16.50	66.50	3.85	48.00	3.80	6.00	23.67	3.17	3.00	171.42	2435.94	11.37	76.44	39.10	50.94
31	Dhanashakti	41.00	15.25	47.00	3.55	34.50	3.45	6.00	22.33	3.04	4.00	163.08	2540.10	13.81	80.04	68.41	83.15
	Mean	49.03	17.19	55.37	4.1	41.73	4.11	6.2	23.16	2.87	3.44	158.02	2578.18	9.86	76.44	48.31	67.01
	Standard Error (±)	0.98	0.53	1.76	0.11	1.49	0.13	0.16	0.85	0.1	0.16	4.81	120.05	0.5	4.47	3.26	4.97
	CD at 5 %	4.5	3.2	12.12	0.49	8.5	0.69	0.89	4.37	0.49	0.96	49.54	803.12	2.02	36.72	19.95	33.99
	Sample Variance	29.5	8.79	96.56	0.35	69.25	0.5	0.84	22.43	0.29	0.84	717.61	446787.55	7.89	619.32	329.87	764.91

DTF - Days to 50% spike emergence , LSL - Leaf sheath length (cm), LL - Leaf length (cm), LW - Leaf width (cm), FL - Flag leaf length (cm), FW - Flag leaf width (cm), NN - Number of nodes , PL - Panicle length (cm), PD - Panicle diameter (cm), NT - Number of productive tillers , PH - plant height (cm), TGP – Total grains per panicle, TSW - Thousand grain weight (g), BY - Biological yield (g), SPY - Single plant yield (g) and HI - Harvest index (%).

tillers and total grains per panicle (**Table 2**). These results were similar to the earlier reports by Annamalai *et al.* (2020) for single plant yield, thousand grain weight, the number of productive tillers, Anuradha *et al.* (2018) and Kumawat *et al.* (2019) for single plant yield and the number of productive tillers, Choudhary *et al.* (2012) for single plant yield, biological yield, thousand grain weight and the number of productive tillers, Dadarwal *et al.* (2020) and Kumar *et al.* (2020) for grain yield per plot and biological yield, Dapke *et al.* (2014) for grain yield per plot, biological yield and harvest index Dhedhi *et al.* (2016) for biological yield, Ram *et al.* (2014) for single plant yield, biological yield number of productive tillers and grains per square centimetre. High PCV and high GCV results indicated the presence of more variation in the population for given traits for further selection and crop improvement (Anuradha *et al.*, 2018).

Heritability is high for almost all the traits concerned except plant height which exhibited moderate heritability. Heritability ranged from 59.01 (plant height) to 98.14 per cent (harvest index) (**Table 2**). The expected genetic advance as a percentage of mean was found to be high for all the traits observed under the study and ranged from 26.01 (plant height) to 83.44 per cent (harvest index).

Along with the heritability estimate, the genetic advance would help a breeder to drive more conclusions than the heritability estimates alone. High heritability coupled with high genetic advance as a percentage of mean were recorded for almost all the characters except plant height, which showed moderate heritability with high genetic advance indicated the additive gene action on the expression of these characters. Similar results were observed by Anuradha *et al.* (2018), Rasitha *et al.* (2019) and Sumathi and Revathi (2017).

Estimates of high heritability and high genetic advance as percentage of mean were observed for harvest index, single plant yield, biological yield, thousand grain weight, panicle length, the number of productive tillers and panicle diameter, which indicated additive genetic variance for these characters. Similar results were reported earlier by Rasitha *et al.* (2019) and Singh *et al.* (2018).

The selection of superior genotypes based on grain yield as such may not be an effective end product of many component traits (Bikash *et al.*, 2013). Correlation of distinct traits provides the knowledge on being inheriting together from one generation to next. It helps in indirect selection for complex traits like yield by other biometrical traits

Table 2. Estimate of important genetic parameters of pearl millet genotypes for yield and yield attributing traits

Traits	Min.	Max.	Kurtosis	Skewness	GV	PV	GCV	PCV	ECV	H	GA	GAM
DTF	37.00	58.00	-0.41	-0.50	27.08	29.50	10.61	11.08	4.49	91.79	10.27	20.94
LSL	10.75	23.33	0.13	-0.04	7.57	8.79	16.00	17.25	9.11	86.06	5.26	30.58
LL	34.00	73.00	-0.40	-0.47	78.96	96.56	16.05	17.75	10.71	81.77	16.55	29.89
LW	2.45	4.90	0.48	-0.85	0.32	0.35	13.88	14.48	5.86	91.81	1.12	27.39
FL	22.50	54.00	0.13	-0.63	60.59	69.26	18.66	19.95	9.98	87.49	15.00	35.95
FW	2.40	5.17	-0.17	-0.63	0.44	0.50	16.19	17.21	8.26	88.47	1.29	31.36
NN	4.00	7.67	-0.01	-0.51	0.77	0.87	14.12	14.95	6.97	89.15	1.71	27.46
PL	15.33	34.00	-0.15	0.32	20.14	22.43	19.38	20.45	9.23	89.81	8.76	37.83
PD	1.63	3.72	0.72	-1.07	0.26	0.29	17.86	18.83	8.44	89.96	1.00	34.90
NT	1.33	5.67	0.84	0.42	0.73	0.84	24.81	26.63	13.69	86.78	1.64	47.61
PH	83.67	198.58	1.18	-1.00	423.43	717.62	13.02	16.95	15.35	59.01	32.56	20.61
TGP	1406.84	4296.55	1.26	0.67	369463.78	446787.94	23.58	25.93	15.25	82.69	1138.65	44.16
TSW	4.39	13.81	-0.66	-0.55	7.40	7.89	27.60	28.49	10.02	93.81	5.43	55.06
BY	32.73	128.31	-0.77	0.23	457.63	619.34	27.99	32.56	23.53	73.89	37.88	49.56
SPY	19.20	86.17	-0.91	0.47	282.11	329.85	34.76	37.59	20.23	85.53	32.00	66.23
HI	30.94	145.73	1.52	1.13	638.48	776.97	37.01	40.82	24.38	82.18	47.19	69.11

DTF - Days to 50% spike emergence, LSL - Leaf sheath length (cm), LL - Leaf length (cm), LW - Leaf width (cm), FL - Flag leaf length (cm), FW - Flag leaf width (cm), NN - Number of nodes, PL - Panicle length (cm), PD - Panicle diameter (cm), NT - Number of productive tillers, PH - plant height (cm), TGP - Total grains per panicle, TSW - Thousand grain weight (g), BY - Biological yield (g), SPY - Single plant yield (g) and HI - Harvest index (%)

GV - Genotypic variance, PV - Phenotypic variance, GCV - Genotypic coefficient of variance, PCV - Phenotypic coefficient of variance, ECV - Environmental coefficient of variance, H - Heritability in broad sense, GA - Genetic advance and GAM - Genetic advance as percent of mean

which are closely and positively associated (Anuradha *et al.*, 2018). This association is due to pleiotropic gene action or linkage or more likely both (Dapke *et al.*, 2014). The phenotypic correlation coefficient is more than the genotypic correlation coefficient for the characters under study (Dhedhi *et al.*, 2016 and Rasitha *et al.*, 2019), which showed the existence of considerable inherent association among the traits (Naveen *et al.*, 2016) (Table 3). Single

plant yield exhibited a positive highly significant genotypic and phenotypic correlation with thousand grain weight, harvest index and leaf length. Similar results were reported in pearl millet by Annamalai *et al.* (2020) and Rasitha *et al.* (2019) for thousand grain weight, Dapke *et al.* (2014) and Mungra *et al.* (2015) for harvest index, Singh *et al.* (2014) for thousand grain weight and leaf length. These traits were important as yield determinant traits due to

Table 3. Genotypic and phenotypic correlation of pearl millet genotypes for yield and yield attributing characters

Traits	DTF	LSL	LL	LW	FL	FW	NN	PL	PD	NT	PH	TGP	TSW	BY	HI	SPY
DTF r_g	1															
r_p	1															
LSL r_g	0.524**	1														
r_p	0.506**	1														
LL r_g	0.250	0.459**	1													
r_p	0.208	0.407*	1													
LW r_g	0.588**	0.650**	0.547**	1												
r_p	0.540**	0.619**	0.529**	1												
FL r_g	0.450*	0.610**	0.983**	0.756**	1											
r_p	0.425*	0.580**	0.831**	0.701**	1											
FW r_g	0.471**	0.524**	0.503**	0.882**	0.758**	1										
r_p	0.433*	0.454*	0.450*	0.822**	0.691**	1										
NN r_g	0.036	0.291	0.516**	0.319	0.369*	0.173	1									
r_p	0.055	0.266	0.405*	0.276	0.331	0.128	1									
PL r_g	0.256	0.769**	0.586**	0.681**	0.604**	0.571**	0.397*	1								
r_p	0.234	0.669**	0.541**	0.615**	0.532**	0.533**	0.351	1								
PD r_g	0.499**	0.611**	0.425*	0.620**	0.506**	0.389*	0.213	0.316	1							
r_p	0.500**	0.558**	0.351	0.573**	0.463**	0.363*	0.226	0.283	1							
NT r_g	-0.455*	-0.485**	-0.082	-0.332	-0.232	-0.129	0.105	-0.238	-0.565**	1						
r_p	-0.425*	-0.454*	-0.056	-0.308	-0.226	-0.116	0.100	-0.231	-0.513**	1						
PH r_g	-0.269	0.466**	0.615**	0.092	0.619**	0.285	0.631**	0.599**	-0.300	0.563**	1					
r_p	-0.261	0.240	0.456*	0.067	0.385*	0.186	0.472**	0.397*	-0.197	0.457**	1					
TGP r_g	0.456**	0.340	0.277	0.538**	0.301	0.396*	0.223	0.182	0.808**	-0.412*	-0.242	1				
r_p	0.401*	0.278	0.237	0.464**	0.267	0.329	0.197	0.178	0.715**	-0.335	-0.253	1				
TSW r_g	0.236	0.550**	0.454*	0.420*	0.593**	0.349	0.189	0.369*	0.715**	-0.295	0.185	0.420*	1			
r_p	0.229	0.506**	0.415*	0.399*	0.540**	0.331	0.172	0.361*	0.639**	-0.263	0.104	0.350	1			
BY r_g	0.028	0.295	0.412*	0.270	0.325	0.144	0.456**	0.359*	0.067	0.503**	0.735**	-0.081	0.262	1		
r_p	0.018	0.197	0.362*	0.221	0.258	0.201	0.319	0.347	0.087	0.391*	0.493**	-0.024	0.214	1		
HI r_g	0.252	0.108	0.141	0.130	0.211	0.226	-0.098	-0.056	0.213	-0.027	-0.206	0.215	0.375*	-0.455*	1	
r_p	0.206	0.111	0.127	0.120	0.166	0.146	-0.049	-0.039	0.164	-0.014	-0.103	0.154	0.317	-0.466**	1	
SPY r_g	0.164	0.321	0.617**	0.323	0.546**	0.348	0.284	0.248	0.346	0.389*	0.442*	0.203	0.753**	0.449*	0.553**	1
r_p	0.121	0.260	0.547**	0.298	0.452*	0.310	0.240	0.270	0.302	0.326	0.349	0.174	0.663**	0.413*	0.551**	1

* Significant at 5% level, **Significant at 1% level

DTF - Days to 50% spike emergence , LSL - Leaf sheath length , LL - Leaf length , LW - Leaf width , FL - Flag leaf length , FW - Flag leaf width , NN - Number of nodes , PL - Panicle length , PD - Panicle diameter , NT - Number of productive tillers , PH - plant height , TGP - Total grains per panicle , TSW - Thousand grain weight , BY - Biological yield , SPY - Single plant yield and HI - Harvest index , r_g - Genotypic correlation, r_p - Phenotypic correlation

their positive and highly significant correlations with grain yield (Annamalai *et al.*, 2020). This signifies that selection for these traits will lead to simultaneous improvement in grain yield. Consequently, the selection of bold seeded plants with long leaves having higher harvest index and biomass would form ideal selection indices for grain yield.

Estimation of correlation alone maybe not sufficient due to mutual cancellation of component traits, so it is necessary to study the path co-efficient analysis, which takes into account, the cause of the relationship in addition to the degree of relationship (Dapke *et al.*, 2014). The cause and effect of the present study were depicted in **Table 4** and the residual effect of 0.095 indicated the adequacy of the traits chosen for path analysis.

Harvest index (0.660), flag leaf length (0.503), biological yield (0.462), panicle diameter (0.458), number of productive tillers (0.321) and panicle length (0.297) showed a high positive direct effect on thousand seed weight (0.219) and showed a moderate positive direct effect on grain yield per plant. A similar positive direct effect was observed by Bikash *et al.* (2013) and Kumar *et al.* (2020) for harvest index, Kumar *et al.* (2020) and Ram *et al.* (2015) for biological yield, Choudhary *et al.* (2012) and Dhakar *et al.* (2013) for panicle diameter, Dehinwal *et al.* (2017), Diz *et al.* (1994) for the number of productive tillers and Annamalai *et al.* (2020) and Subbulakshmi *et al.* (2018) for panicle length. This revealed the true relationship of these characters with

grain yield per plant. Hence, direct selection for these traits could be rewarding for the improvement of grain yield in pearl millet. Flag leaf length showed a highly positive indirect effect via leaf length, leaf width, flag width, panicle length, plant height, thousand grain weight on grain yield per plant indicated the importance of flag leaf length in pearl millet. Panicle diameter also showed the highly positive indirect effect on grain yield per plant via total grains per panicle and thousand grain weight. Biological yield showed positive and high indirect effects via plant height and a moderately positive indirect effect via the number of productive tillers on grain yield per plant. Similar results were recorded by Dapke *et al.* (2014), Ravi *et al.* (2016), Subbulakshmi *et al.* (2018). Days to 50 per cent spike emergence showed negligible positive direct effect (0.09) on grain yield per plant. Similar results of positive direct effect were observed by Choudhary *et al.* (2012) and Dapke *et al.* (2014). Plant height showed a low positive direct effect (0.157) on grain yield per plant. These results corroborate the report of Kumar *et al.* (2020), Pallavi *et al.* (2020) and Ram *et al.* (2015). Days to 50 per cent spike emergence and plant height are mostly considered as the negative traits and its effect on the yield per plant is also less. Path analysis revealed that for increasing the grain yield per plant, direct selection of genotypes with a greater number of tillers having long flag leaf which bears long panicles with more panicle diameter and weighs significant biological yield will be rewarding. These traits were important as component traits for the formulation of the selection index in future.

Table 4. Genotypic path coefficient analyses for yield and yield attributing traits depicting direct and indirect effects in pearl millet genotypes

Traits	DTF	LSL	LL	LW	FL	FW	NN	PL	PD	NT	PH	TGP	TSW	BY	HI
DTF	0.088	0.046	0.022	0.051	0.039	0.041	0.003	0.022	0.044	-0.040	-0.024	0.040	0.021	0.003	0.022
LSL	-0.210	-0.401	-0.184	-0.261	-0.245	-0.210	-0.117	-0.309	-0.245	0.194	-0.187	-0.137	-0.221	-0.118	-0.044
LL	-0.077	-0.141	-0.308	-0.168	-0.303	-0.155	-0.159	-0.181	-0.131	0.025	-0.189	-0.085	-0.140	-0.127	-0.044
LW	-0.128	-0.142	-0.119	-0.218	-0.165	-0.192	-0.069	-0.148	-0.135	0.072	-0.020	-0.117	-0.091	-0.059	-0.028
FL	0.226	0.307	0.494	0.380	0.503	0.381	0.186	0.304	0.254	-0.117	0.311	0.152	0.298	0.164	0.106
FW	-0.065	-0.072	-0.069	-0.121	-0.104	-0.138	-0.024	-0.079	-0.054	0.018	-0.039	-0.055	-0.048	-0.020	-0.031
NN	-0.002	-0.019	-0.034	-0.021	-0.024	-0.011	-0.065	-0.026	-0.014	-0.007	-0.041	-0.015	-0.012	-0.030	0.006
PL	0.076	0.229	0.174	0.203	0.180	0.170	0.118	0.297	0.094	-0.071	0.178	0.054	0.110	0.107	-0.017
PD	0.228	0.280	0.195	0.284	0.231	0.178	0.098	0.145	0.458	-0.259	-0.137	0.370	0.327	0.031	0.098
NT	-0.146	-0.156	-0.026	-0.107	-0.074	-0.042	0.034	-0.077	-0.182	0.321	0.181	-0.132	-0.095	0.162	-0.009
PH	-0.042	0.073	0.097	0.015	0.097	0.045	0.099	0.094	-0.047	0.089	0.157	-0.038	0.029	0.116	-0.032
TGP	-0.014	-0.010	-0.008	-0.016	-0.009	-0.012	-0.007	-0.006	-0.024	0.012	0.007	-0.030	-0.013	0.003	-0.007
TSW	0.052	0.120	0.099	0.092	0.130	0.076	0.041	0.081	0.157	-0.065	0.041	0.092	0.219	0.057	0.082
BY	0.013	0.136	0.190	0.125	0.150	0.067	0.211	0.166	0.031	0.232	0.340	-0.038	0.121	0.462	-0.210
HI	0.166	0.072	0.093	0.086	0.139	0.149	-0.065	-0.037	0.141	-0.018	-0.136	0.142	0.247	-0.300	0.660

Residual effect: 0.0951, Direct effect: Bold diagonal values, Indirect effect: Non diagonal values, DTF - Days to 50% spike emergence, LSL - Leaf sheath length, LL - Leaf length, LW - Leaf width, FL - Flag leaf length, FW - Flag leaf width, NN - Number of nodes, PL - Panicle length, PD - Panicle diameter, NT - Number of productive tillers, PH - plant height, TGP - Total grains per panicle, TSW - Thousand grain weight, BY - Biological yield, SPY - Single plant yield and HI - Harvest index

Selection indices were constructed by discriminant function analysis based on three different economic weights *i.e.*, equal, genotypic correlation coefficient with yield and genotypic path direct effect on yield (**Table 5**) resulted in respective three weighing coefficients. Path direct effect as economic weight showed negative values as compared to the other two economic weights. This indicates that the path direct effect helps in assigning the negative economic weights for yield component traits. The genotypes ICMB 99222, PT 6706, PT 6676, ICMB 98222 and PT 6581 were among the top five when equal economic weights were applied to determine the selection scores. The genotypes ICMB 99222, PT 6706, PT 6581, PT 6676, and ICMB 98222 were among the top five when the correlation coefficient with a yield as economic weights was applied to determine the selection scores. The genotypes Cumbu 2, Kizikuppam local, Nattu Cumbu, PT 6705 and PT 6580 were the top five genotypes when path direct effect on yield as economic weights was applied to determine the selection scores (**Table 6**). The genotypes ICMB 99222, PT 6706, PT 6676, ICMB 98222 and PT 6581 were ranked as top five when allotted equal weights and correlation coefficient with yield, whereas in path direct effect as economic weight replaces all five genotypes. The path direct effect identified the genotypes with more scores for yield component traits and concentrated on the improvement of the combination of yield affected traits. Whereas equal weights as economic weights mislead and gave the importance to improve all the traits. It is also observed that the selection index score is significantly high when economic weights given as equal weights indicated the maximum genetic gain. But

it is failed to identify the genotypes with desirable traits. It is also affected by the negative traits like days to 50 per cent flowering and plant height as it selects the genotypes with late flowering and maximum plant height which are undesirable most of the time. So, the top genotypes recommended for improvement of yield and its attributing traits include Cumbu 2, Kizikuppam local, Nattu Cumbu, PT 6705, PT 6580, PT 6706, PT 6706, PT 6067. Results were in concordance with Kour *et al.* (2018), Prasanna *et al.* (2013) and Singh *et al.* (2013).

Estimates of genetic advance and relative efficiency of selection indices for individual and combination of traits were depicted in the **Table 7** and **Table 8**, respectively. When equal weights was used, high genetic advance were observed for the characters like total grains per panicle (585.48), harvest index (6.39), single plant yield (5.09) and flag leaf length (3.82). The highest genetic advance was observed by the index $I_{1,3,4,9,11,12,13,16}$ (197.62), which consist of eight yield component traits, followed by $I_{1,3,4,6,9,11,12,13,16}$ (197.62), $I_{1,3,4,6,7,9,11,12,13,16}$ (197.42) and $I_{1,3,4,6,7,9,10,11,12,13,16}$ (193.77). When the correlation coefficient with yield was used high genetic advance was observed for the characters like total grains per panicle (555.84), harvest index (8.52), single plant yield (8.34) and flag leaf length (4.64). The highest genetic advance was observed by the index $I_{1,3,4,6,7,9,10,11,12,13,16}$ (90.01) followed by $I_{1,3,4,6,7,9,10,11,12,13,15,16}$ (89.86), $I_{1,3,4,6,9,10,11,12,13,16}$ (89.64) and $I_{1,2,3,4,6,7,9,10,11,12,13,15,16}$ (89.48). Based on the path direct effect it was noticed that high genetic advance for the characters like plant height (17.39), single plant yield (14.60), harvest index (11.76) and biological yield (9.21). The table revealed that

Table 5. Equal, genotypic correlation coefficient with yield and genotypic path direct effect on yield for economic weights and weighing coefficients (b_i) in yield and yield attributing traits of pearl millet genotypes

S. No.	Variables	Economic weights			Weighing coefficients		
		Equal	r_g	Path	Equal	r_g	Path
1	Days to 50% spike emergence (X_1)	1.00	0.16	0.09	25.73	4.83	-0.36
2	Leaf sheath length (X_2)	1.00	0.32	-0.40	-24.53	-1.08	5.47
3	Leaf length (X_3)	1.00	0.62	-0.31	18.68	4.56	1.59
4	Leaf width (X_4)	1.00	0.32	-0.22	274.48	41.90	-16.38
5	Flag leaf length (X_5)	1.00	0.55	0.50	-45.59	-7.56	1.06
6	Flag leaf width (X_6)	1.00	0.35	-0.14	134.16	28.05	1.40
7	Number of nodes (X_7)	1.00	0.28	-0.06	-4.03	3.79	3.63
8	Panicle length (X_8)	1.00	0.25	0.30	-25.63	-4.74	0.24
9	Panicle diameter (X_9)	1.00	0.35	0.46	257.66	42.74	-21.06
10	Number of productive tillers (X_{10})	1.00	0.39	0.32	-60.53	11.44	38.01
11	Plant height (X_{11})	1.00	0.44	0.16	10.05	1.56	-0.80
12	Total grains per panicle (X_{12})	1.00	0.20	-0.03	0.61	0.12	-0.02
13	Thousand grain weight (X_{13})	1.00	0.75	0.22	49.89	15.50	10.29
14	Biological yield (X_{14})	1.00	0.45	0.46	-6.59	-0.99	1.00
15	Harvest index (X_{15})	1.00	0.55	0.66	-2.62	-0.03	1.31
16	Single plant yield (X_{16})	1.00	1.00	1.00	1.67	-0.19	-1.98

the highest genetic advance was observed by the index $I_{2,3,5,6,7,8,10,13,14,15,16}$ (58.43), followed by $I_{1,2,3,5,6,7,8,10,13,14,15,16}$ (58.25), $I_{1,2,3,5,7,10,13,14,15,16}$ (57.88) and $I_{1,2,3,10,13,14,15,16}$ (57.32). Path direct effect as economic weight has exhibited less relative efficiency than equal and correlation coefficient as economic weights. This results in accordance with the reports of Kour *et al.* (2018).

In this study, genetic advance in path direct effect for grain yield was 14.60, whereas with the combination of traits like thousand grain weight, harvest index and single plant yield, the genetic advance was 20.89. This

indicated the usefulness of multi-trait selection for yield over selection based only on a single trait (Choudhary and Joshi, 1996; Shah *et al.*, 2016). The maximum genetic advance and relative efficiency can be achieved by imposing equal economic weights of one over all the characters (Smith, 1983). But this method will consider the maximum weightage to the trait which is expressed in more digits (total number of grains per panicle) and does not considering the negative traits like days to 50 per cent flowering and plant height. The correlation coefficient could not divide the direct and indirect effects of the traits. Even though path direct effect results in less genetic advance

Table 6. Selection criterion score values of pearl millet genotypes estimated for equal, correlation coefficient with yield and path direct effect on yield and yield attributing traits

Genotypes with score values for different weights								
Equal			Correlation coefficient			Path direct effect		
S. No.	Genotypes	Scores	S. No.	Genotypes	Scores	S. No.	Genotypes	Scores
1	ICMB 99222	4678.39	1	ICMB 99222	1219.98	1	Cumbu 2	314.87
2	PT 6706	4313.75	2	PT 6706	1139.10	2	Kizikuppam local	299.45
3	PT 6676	4624.88	3	PT 6581	1190.45	3	Nattu Cumbu	293.95
4	ICMB 98222	4300.86	4	PT 6676	1116.31	4	PT 6705	287.02
5	PT 6581	4699.22	5	ICMB 98222	1205.88	5	PT 6580	284.62
6	PT 6582	5557.56	6	PT 6582	1388.07	6	PT 6706	274.27
7	PT 6709	4695.20	7	Uthangarai local	1192.90	7	Cumbu 1	271.67
8	Uthangarai local	4407.32	8	Cumbu 2	1125.05	8	PT 6067	269.48
9	PT 6675	3353.43	9	PT 6709	889.67	9	Pothu Cumbu	266.99
10	PT 6580	4595.75	10	PT 6580	1160.01	10	Dhanashakti	264.87
11	Cumbu 1	4202.18	11	Cumbu 1	1044.22	11	ICMB 06111	261.73
12	PT 6710	3504.43	12	Nattu Cumbu	917.32	12	Kuttu Cumbu 1	258.77
13	Cumbu 2	5014.71	13	PT 6675	1246.76	13	PT 6582	255.68
14	PT 6677	5347.53	14	PT 6710	1322.76	14	PT 6581	254.53
15	Nattu Cumbu	4956.63	15	Dhanashakti	1228.38	15	Uthangarai local	253.64
16	Shoolagiri local	4623.84	16	Shoolagiri local	1157.39	16	Shoolagiri local	249.49
17	PT 6708	3495.95	17	PT 6677	890.62	17	Kuttu Cumbu 2	248.22
18	Dhanashakti	4003.25	18	Kizikuppam local	1022.98	18	PT 6583	243.76
19	PT 6059	4693.84	19	PT 6708	1161.96	19	PT 6710	239.95
20	PT 6029	4627.32	20	PT 6067	1150.06	20	PT 6677	234.61
21	PT 6674	4604.56	21	PT 6705	1138.56	21	PT 6708	231.91
22	PT 6067	4851.61	22	PT 6029	1189.34	22	PT 6675	230.93
23	PT 6707	4364.27	23	PT 6707	1098.40	23	PT 6707	228.83
24	Kizikuppam local	4516.95	24	PT 6059	1109.43	24	PT 6029	223.97
25	PT 6705	4412.87	25	PT 6674	1090.38	25	PT 6674	218.04
26	ICMB 06111	4964.10	26	ICMB 06111	1209.88	26	PT 6709	215.73
27	PT 6583	5912.73	27	PT 6583	1398.39	27	ICMB 99222	193.74
28	Kuttu Cumbu 3	5524.03	28	Kuttu Cumbu 1	1319.02	28	PT 6676	191.94
29	Kuttu Cumbu 1	4560.45	29	Kuttu Cumbu 3	1095.49	29	PT 6059	184.16
30	Kuttu Cumbu 2	3718.94	30	Kuttu Cumbu 2	897.27	30	Kuttu Cumbu 3	176.00
31	Pothu Cumbu	5469.87	31	Pothu Cumbu	1282.47	31	ICMB 98222	174.39

Table 7. Estimates of genetic advance and relative efficiency of selection indices in different combination for yield and yield attributing traits

S. No.	Based on the equal weights	GA	RE
1	$X_3 X_{16}$	96.40	1890.93
2	$X_3 X_{13} X_{16}$	128.73	2525.05
3	$X_3 X_{11} X_{13} X_{16}$	151.96	2980.65
4	$X_3 X_{11} X_{12} X_{13} X_{16}$	168.61	3307.33
5	$X_3 X_4 X_{11} X_{12} X_{13} X_{16}$	178.95	3510.16
6	$X_1 X_3 X_4 X_{11} X_{12} X_{13} X_{16}$	183.28	3594.97
7	$X_1 X_3 X_4 X_9 X_{11} X_{12} X_{13} X_{16}$	197.62	3876.38
8	$X_1 X_3 X_4 X_6 X_9 X_{11} X_{12} X_{13} X_{16}$	197.62	3876.38
9	$X_1 X_3 X_4 X_6 X_7 X_9 X_{11} X_{12} X_{13} X_{16}$	197.44	3872.82
10	$X_1 X_3 X_4 X_6 X_7 X_9 X_{10} X_{11} X_{12} X_{13} X_{16}$	193.78	3800.92
11	$X_1 X_2 X_3 X_4 X_6 X_7 X_9 X_{10} X_{11} X_{12} X_{13} X_{16}$	189.75	3721.92
12	$X_1 X_2 X_3 X_4 X_6 X_7 X_8 X_9 X_{10} X_{11} X_{12} X_{13} X_{16}$	184.33	3615.54
13	$X_1 X_2 X_3 X_4 X_6 X_7 X_8 X_9 X_{10} X_{11} X_{12} X_{13} X_{15} X_{16}$	177.10	3473.73
14	$X_1 X_2 X_3 X_4 X_6 X_7 X_8 X_9 X_{10} X_{11} X_{12} X_{13} X_{14} X_{15} X_{16}$	163.88	3214.45
15	$X_1 X_2 X_3 X_4 X_5 X_6 X_7 X_8 X_9 X_{10} X_{11} X_{12} X_{13} X_{14} X_{15} X_{16}$	114.23	2240.53
Based on genotypic correlation coefficient with yield			
1	$X_{13} X_{16}$	45.16	540.99
2	$X_3 X_{13} X_{16}$	61.82	740.50
3	$X_3 X_{12} X_{13} X_{16}$	70.04	839.03
4	$X_3 X_{11} X_{12} X_{13} X_{16}$	76.94	921.60
5	$X_3 X_4 X_{11} X_{12} X_{13} X_{16}$	80.42	963.36
6	$X_1 X_3 X_4 X_{11} X_{12} X_{13} X_{16}$	82.23	985.02
7	$X_1 X_3 X_4 X_9 X_{11} X_{12} X_{13} X_{16}$	88.11	1055.47
8	$X_1 X_3 X_4 X_6 X_9 X_{11} X_{12} X_{13} X_{16}$	88.11	1055.47
9	$X_1 X_3 X_4 X_6 X_9 X_{10} X_{11} X_{12} X_{13} X_{16}$	89.64	1073.74
10	$X_1 X_3 X_4 X_6 X_7 X_9 X_{10} X_{11} X_{12} X_{13} X_{16}$	90.01	1078.23
11	$X_1 X_3 X_4 X_6 X_7 X_9 X_{10} X_{11} X_{12} X_{13} X_{15} X_{16}$	89.86	1076.40
12	$X_1 X_2 X_3 X_4 X_6 X_7 X_9 X_{10} X_{11} X_{12} X_{13} X_{15} X_{16}$	89.48	1071.86
13	$X_1 X_2 X_3 X_4 X_6 X_7 X_8 X_9 X_{10} X_{11} X_{12} X_{13} X_{15} X_{16}$	87.36	1046.44
14	$X_1 X_2 X_3 X_4 X_6 X_7 X_8 X_9 X_{10} X_{11} X_{12} X_{13} X_{14} X_{15} X_{16}$	83.39	998.92
15	$X_1 X_2 X_3 X_4 X_5 X_6 X_7 X_8 X_9 X_{10} X_{11} X_{12} X_{13} X_{14} X_{15} X_{16}$	68.29	818.04
Based on path direct effect			
1	$X_{13} X_{15} X_{16}$	20.89	143.03
2	$X_{10} X_{13} X_{15} X_{16}$	36.56	250.38
3	$X_{10} X_{13} X_{14} X_{15} X_{16}$	44.96	307.87
4	$X_3 X_{10} X_{13} X_{14} X_{15} X_{16}$	51.42	352.11
5	$X_2 X_3 X_{10} X_{13} X_{14} X_{15} X_{16}$	54.66	374.34
6	$X_1 X_2 X_3 X_{10} X_{13} X_{14} X_{15} X_{16}$	57.33	392.61
7	$X_1 X_2 X_3 X_5 X_{10} X_{13} X_{14} X_{15} X_{16}$	57.33	392.61
8	$X_1 X_2 X_3 X_5 X_7 X_{10} X_{13} X_{14} X_{15} X_{16}$	57.89	396.44
9	$X_2 X_3 X_5 X_6 X_7 X_{10} X_{13} X_{14} X_{15} X_{16}$	58.44	400.22
10	$X_1 X_2 X_3 X_5 X_6 X_7 X_8 X_{10} X_{13} X_{14} X_{15} X_{16}$	58.25	398.93
11	$X_1 X_2 X_3 X_5 X_6 X_7 X_8 X_{10} X_{12} X_{13} X_{14} X_{15} X_{16}$	56.88	389.55
12	$X_1 X_2 X_3 X_4 X_5 X_6 X_7 X_8 X_{10} X_{12} X_{13} X_{14} X_{15} X_{16}$	54.96	376.42
13	$X_1 X_2 X_3 X_4 X_5 X_6 X_7 X_8 X_9 X_{10} X_{12} X_{13} X_{14} X_{15} X_{16}$	52.49	359.47
14	$X_1 X_2 X_3 X_4 X_5 X_6 X_7 X_8 X_9 X_{10} X_{11} X_{12} X_{13} X_{14} X_{15} X_{16}$	47.30	323.91

Table 8. Estimates of genetic advance and relative efficiency for yield and yield attributing traits

S. No.	Variables	EW		GCC		PDE	
		GA	RE	GA	RE	GA	RE
1	Days to 50% spike emergence (X1)	2.61	51.13	2.58	30.91	-0.29	-2.00
2	Leaf sheath length (X2)	1.29	25.35	1.41	16.94	0.21	1.40
3	Leaf length (X3)	2.67	52.42	3.82	45.75	2.88	19.70
4	Leaf width (X4)	0.33	6.43	0.35	4.23	0.03	0.23
5	Flag leaf length (X5)	3.82	74.93	4.64	55.61	2.57	17.61
6	Flag leaf width (X6)	0.32	6.22	0.36	4.27	0.10	0.71
7	Number of nodes (X7)	0.24	4.77	0.30	3.60	0.15	1.02
8	Panicle length (X8)	1.20	23.52	1.50	17.95	0.73	5.00
9	Panicle diameter (X9)	0.42	8.20	0.42	5.08	-0.03	-0.19
10	Number of productive tillers (X10)	-0.36	-7.10	-0.29	-3.43	0.38	2.59
11	Plant height (X11)	-7.50	-147.20	-2.95	-35.28	17.40	119.16
12	Total grains per panicle (X12)	585.48	11484.29	555.85	6658.38	-197.29	-1351.09
13	Thousand grain weight (X13)	1.40	27.50	1.68	20.12	0.95	6.51
14	Biological yield (X14)	-0.32	-6.23	2.12	25.42	9.21	63.09
15	Harvest index (X15)	6.40	125.50	8.52	102.11	11.76	80.55
16	Single plant yield (X16)	5.10	100.00	8.35	100.00	14.60	100.00

EW: Based on the equal weights, GCC: Based on genotypic correlation coefficient with yield, PDE: Based on path direct effect, GA: Genetic Advance, RE: Relative efficiency

and relative efficiency, it helps to identify the genotypes and combination of traits towards the improvement of the dependent traits like grain yield. A similar type of results was reported by Kour *et al.* (2018) and Prasanna *et al.* (2013).

Relative efficiency of the selection index increases with an increase in the number of component characters up to some extent and then start to decline after reaching the optimum number of characters (Basavaraja and Sheriff, 1992; Shah *et al.*, 2016). The main reason for the above findings was the expected genetic gain and relative efficiency will be on higher side whenever correlated traits are present together (Kumar *et al.*, 2012; Pritchard *et al.*, 1972). In this investigation, negative expected genetic gain observed for days to 50 per cent flowering and total grains per panicle indicates that it is not a positive character for higher yield rather it depends on other components characters for higher yield (Sarker *et al.*, 2013).

The traits which are common under all these three methods of economic weights and had high genetic advance and relative efficiency for leaf length, flag leaf length, thousand grain weight and grain yield per plant. A plant breeder is always interested to have maximum genetic gain with the incorporation of minimum characters in the selection index (Singh *et al.*, 2013). The maximum genetic gain for grain yield per plant can be obtained by selecting the traits like leaf sheath length, leaf length, flag leaf length, flag leaf width, the number of nodes, panicle

length, the number of productive tillers, thousand grain weight, biological yield, harvest index and single plant yield in combination. These traits are recommended for selection which helps simultaneously to improve the yield.

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