Electronic Journal of Plant Breeding, 8(2): 626-628 (June 2017)
ISSN 0975-928X
DOI: 10.5958/0975-928X.2017.00095.3

Research Note

Selection indices in F_2 generation of mungbean (*Vigna radiata* (L.) Wilczek)

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(Received: 06 Dec 2016; Revised: 10 April 2017; Accepted: 30 April 2017)

Abstract
The discriminant function technique was used to construct selection indices in F_2 populations of mungbean (*Vigna radiata* (L.) Wilczek). Thirty one selection indices involving seed yield per plant and its four components were constructed using discriminant function technique. In general, the more the number of characters included in a selection index, the better was its performance. The index based on four characters *viz*., seed yield per plant, number of pods per plant, number of seeds per pod and plant height had highest genetic advance and relative efficiency 61.701g and 701.134 per cent, respectively followed by an index based on three characters *viz*., seed yield per plant, number of pods per plant and plant height which possessed genetic gain and relative efficiency of 16.59g and 696.474 per cent, respectively. The use of both these indices is advocated for selecting high yielding genotypes of mungbean.

Key words
Discriminant function, selection indices and relative efficiency

In India, mungbean is grown in an area of about 3.02 million hectare with total production of 1.50 million tonnes and productivity of 498 kg/ ha (Anonymous, 2016a). In Gujarat, mungbean is grown in an area of 0.117 million hectares with a total production of 0.073 million tonnes and a productivity of 625 kg/ha (Anonymous, 2016b). Thus, the productivity of mungbean is very low as in case of other pulse crop. Therefore, there is urgent need to improve the productivity of mungbean by proper breeding tools. Yield is governed by a polygenic system and is highly influenced by the fluctuation in the environment. Hence selection of superior genotypes based only on yield may not be much rewarding but the appropriate weightage should also be given to component traits. For that, an application of discriminant function developed by Smith (1936) helps to identify important combination of yield components useful for selection by formulating suitable selection indices. Most of the studies on this aspect are carried out using fix material. Many times, breeders use the information obtained from such material for the selection of desired genotypes in segregating material. In such a situation, it is of vital importance to obtain the information on selection indices from segregating material and also to compare it with fix material. Therefore keeping above said facts in mind, the present investigation was planned with 26 F_2 populations of mungbean to calculate discriminant functions for most efficient selection indices.

The present investigation was carried out at Pulses Research Station, Junagadh Agricultural University, Junagadh during *kharif* 2015-16 using F_2 progenies of 26 crosses. Above said 26 crosses were obtained by crossing 8 parents by all possible combinations. The selection material was grown in Randomized Block Design with three replications. Two rows of 4 m long spaced at 45 cm distance were allotted to each population. Immediately after germination, plants were thinned to maintain a distance of 10 cm between plants. Observations were recorded on 20 randomly selected plants in each cross combinations for characters *viz*., days to flowering, days to maturity, plant height, number of pods per plant, pod length, number of seeds per pod, number of leaves per plant, hundred seed weight and seed yield per plant. Selection indices were formulated by using four characters along with seed yield per plant for F_2 population. The respective genetic advance through selection was also calculated as per the formula suggested by Robinson *et al*. (1951). The relative efficiency of different discriminant functions in relation to straight selection for seed yield per plant were assessed and compared, assuming the efficiency of selection for seed yield per plant as 100 per cent. A part of analysis was done by Indostat software and remaining part was analysed in excel software prepared by faculties of Department of Genetics & Plant Breeding as per the book entitled "Biometrical methods in quantitative genetic analysis" by Singh, R.K. and Chaudhary, B.D. (1985), Kalyani Publishers, Ludhiana.

The plant breeder has certain desired plant characteristic in his mind while selecting for this he applies various weight to different traits for arriving on decisions. This suggests the use of selection index which gives proper weight to each of the two or more characters to be considered Hazel and Lush (1943) showed that the selection based on such an index is more efficient than selecting individually for the various characters and stated that the superiority of selection based on the index increases with an increase in the number of characters under selection. In the present study also the genetic advance and relative efficiency assessed for different indices increased considerably when selection was based on two or more characters.

For the construction of selection indices, the characters, which had high direct effect on seed yield, were considered. In this context, the seed yield per plant (X_1), along with its four components *viz*., number of pods per plant (X_2), number of seeds per pod (X_3), hundred seed weight (X_4) and plant height (X_5) were identified and considered for construction of selection indices. Thirty one selection indices were constructed in all the possible combinations of the four yield contributing and relative efficiency of different discriminant functions genetic gain and relative efficiency are given in Table 1, assuming the efficiency of straight selection for seed yield as 100 per cent.

The maximum genetic advance (GA) and relative efficiency (RI) in single character discriminant function was observed by number of pods per plant i.e. 8.944g and 375.483%, respectively. There was increase in genetic gain as well as relative efficiency with inclusion of an additional trait in the character combination. In the two character combinations (number of pods per plant and plant height) genetic gain 12.139g and relative efficiency was increased upto 509.194%. The best selection index was made by discriminant function with four character index (seed yield per plant, number of pods per plant, number of seeds per pod and plant height) with genetic gain (16.701 g) and RI (701.134 %) followed by an index of three characters (seed yield per plant, number of pods per plant and plant height) with genetic gain of 16.59g and R I of 696.474%.

The present study showed consistent increase in RI of succeeding index with simultaneous inclusion of each character. However, in practice the plant breeder might be interested in maximum gain with maximum number of characters with this view RI as per character was also worked out for each selection index. It was observed maximum RI per character was observed in selection index comprised of number of pods per plant and plant height (254.597%) followed by seed yield per plant, number of pods per plant and plant height (232.158%). It was interesting to note that number of pods per plant was combined with construction of selection index of two, three, four or five character systems where relative selection efficiency was increased. Therefore due weightage should be given to number of pods per plant. While formulating selection index of mungbean crop. The present study also revealed that the discriminant function method of making selections in plants appears to be the most useful than the straight selection for seed yield alone and hence, due weightage should be given to the important selection indices while making selection for seed yield advancement in mungbean.

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Table 1. Selection index, discriminant function, expected genetic advance in yield and relative efficiency from the use of different selection indices in 26 F_2 generations of Mungbean

Sr. No.	Selection index	Discriminant function	Expected genetic advance	Relative efficiency (%)	Relative coefficient per character (%)
(1)	(2)	(3)	(4)	(5)	(6)
1	X_1 seed yield per plant	0.737	2.382	100	100
2	X_2 Number of pods per plant	0.622	8.944	375.483	375.483
3	X_3 Number of seeds per pod	0.616	1.010	42.401	42.401
4	X_4 100-seed weight	0.450	0.338	14.190	14.190
5	X_5 Plant height	0.546	6.399	268.640	268.640
6	X_1 X_2	$1.199X_1+0.558\ X_2$	10.823	454.366	227.183
7	X_1 X_3	$0.744X_1+0.648\ X_3$	2.605	109.362	54.681
8	X_1 X_4	$0.751X_1\ +0.579X_4$	2.546	106.885	53.442
9	X_1 X_5	$0.935X_1\ +0.532X_5$	7.599	319.018	159.509
10	X_2 X_3	$0.618X_2\ +0.470X_3$	8.833	370.823	185.411
11	X_2 X_4	$0.606X_2\ +2.477X_4$	9.301	390.470	195.235
12	X_2 X_5	$0.637X_2\ +0.576X_5$	12.139	509.194	254.597
13	X_3 X_4	$0.107X_3\ -4.55X_4$	3.379	141.856	70.928
14	X_3 X_5	$0.724X_3\ +0.552X_5$	6.388	268.178	134.089
15	X_4 X_5	$-0.343X_4\ +0.531X_5$	6.285	263.584	131.792
16	X_1 X_2 X_3	$0.394X_1\ +0.723X_2\ +0.623X_3$	16.538	649.291	216.430
17	X_1 X_2 X_4	$0.387X_1\ +0.709X_2\ -0.032X_4$	16.121	676.784	225.594
18	X_1 X_2 X_5	$0.401X_1\ +0.719X_2\ +0.711X_5$	16.590	696.474	232.158
19	X_1 X_3 X_4	$0.502X_1\ +0.583X_3+0.447\ X_4$	6.896	289.504	96.501
20	X_1 X_3 X_5	$0.505X_1\ +0.540X_3\ +0.940X_5$	7.548	316.877	105.625
21	X_1 X_4 X_5	$0.500X_1\ +0.532X_4\ +0.986X_5$	7.279	305.584	101.861
22	X_2 X_3 X_4	$0.758X_2\ +0.611X_3\ +0.530X_4$	16.240	681.780	227.260
23	X_2 X_3 X_5	$0.762X_2\ +0.632X_3\ +0.200X_5$	16.479	691.814	230.604
24	X_2 X_4 X_5	$0.758X_2\ +0.632X_4\ +0.239X_5$	16.171	678.883	226.294
25	X_3 X_4X_5	$0.600X_3\ +0.904X_4\ +0.589X_5$	2.663	111.797	37.265
26	X_1 X_2 X_3 X_4	$0.380X_1\ +0.709X_2\ +0.703X_3\ -0.055X_4$	16.241	681.822	170.455
27	X_1 X_2 X_3 X_5	$0.396X_1\ +0.719X_2\ +0.613X_3\ +0.716X_5$	16.701	701.134	175.283
28	X_1 X_2 X_4 X_5	$0.385X_1\ +0.706X_2\ +-0.017X_4\ +0.831X_5$	16.301	684.341	171.085
29	X_1 X_3 X_4 X_5	$0.495X_1\ +0.558X_3\ +0.449X_4\ +1.004X_5$	7.535	316.331	79.082
30	X_2 X_3 X_4 X_5	$0.495X_2\ +0.627X_3\ +0.626X_4\ +0.238X_5$	16.255	681.150	170.287
31	X_1 X_2 X_3 X_4 X_5	$0.379X_1\ +0.705X_2\ +0.685X_3\ -0.037X_4\ +0.834X_5$	16.427	689.631	137.926

Correlation coefficient of number of pods per plant, number of seeds per pod, 100 seed weight and plant height with seed yield per plant was 0.607, -0.023, 0.188 and 0.254 at phenotypic level, respectively