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Research Note

Selection Indices in Indian Mustard [*Brassica juncea* (L.) Czern & Coss]

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Abstract
The discriminant-function technique was used to construct selection indices in 50 genotypes of Indian mustard (*Brassica juncea*). Sixty-three selection indices involving seed yield per plant and its five 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 six characters *viz.,* seed yield per plant, biological yield per plant, harvest index, number of primary branches per plant, number of secondary branches per plant and number of siliquae per plant which had a genetic advance and relative efficiency of 122.10g and 1847.80% followed by and index based on five characters seed yield per plant, biological yield per plant, number of primary branches per plant, number of secondary branches per plant and number of siliquae per plant which possessed genetic gain and relative efficiency of 121.94g and 1845.33%, respectively. The use of both these indices is advocated for selecting high yielding genotypes of mustard.

Keyword: Mustard, selection indices, discriminant function,

In spite of great importance of rapeseed and mustard as oilseed crops, very limited research work has been done on the genetics of economic characters. As a result breeding work has been confined mainly to pureline selection or pedigree method of breeding. It is now well recognized that yield is a complex character and depends upon the action and interaction of a number of factors. It is felt that progress can be accelerated if simultaneous selection for most of the economic characters contributing to yield is considered. For this purpose, the utilization of an appropriate multiple selection criteria based on the selection indices would be more desirable. No wok on this problem has been undertaken on Indian mustard so far. An application of discriminat function developed by Fisher (1936) and first applied by Smith (1936) helps to identify important combination of yield components useful for selection by formulating suitable selection indices. Therefore, the object of the present study was to constuct and assesses the efficiency of selection indices in mustard.

A field trial was conducted using 50 diverse genotypes of mustard during *Rabi* 2011-12 in a randomized block design with three replications at Instructional Farm, College of Agriculture, Junagadh Agricultural University, Junagadh. Each entry was sown in a single row of 3.0 m length with a spacing of 60 x 10 cm. Observations were recorded on five plants selected at random for the seed yield per plant (X_1), biological yield per plant (X_2), harvest index (X_3), number of primary branches per plant (X_4), number of secondary branches per plant (X_5) and number of siliquae per plant (X_6). For constructing the selection indices, the characters with high and significant genetic correlation coefficients and sizable direct effects on seed yield were considered. The model suggested by Robinson *et al.* (1951) was used for the construction of selection indices and the development of required discriminant function. A total of 63 selection indices were constructed using six traits. 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 were assessed and compared, assuming the efficiency of selection for seed yield per plant as 100%.

Selection indices for seed yield per plant and other characters were constructed and examined to identify their relative efficiency in the selection of superior genotypes. The results on selection indices, discriminant functions, expected genetic gain and relative efficiency are presented in Table 1. The results showed that the genetic advance and relative efficiency assessed for different indices were higher than straight selection when the selection was based on component characters which further increased considerably with the inclusion of two or more characters. The highest efficiency was noted when five characters (X_1+X_2+X_3+X_4+X_5) or all the six characters were considered. Thus, selection indices are more reliable and realistic for selecting desirable genotypes since they are constructed by giving proper weightage on the characters associated with the seed yield per plant.

The maximum genetic advance (GA) and relative efficiency (RI) in single character discriminant function was 104.910 g and 1587.621 %, respectively for number of siliquae per plant which, however, genetic advance (GA), relative efficiency (RI) and relative efficiency per character increased up to 112.17 g, 1697.54 % and 848.77 %, respectively in two character combinations (X_2+X_6) and 117.76 g, 1782.13 % and 594.043 %, respectively in three characters combinations (X_2+X_5+X_6). Thus, there was an increase in the genetic gain as well as on relative efficiency with an increase in the character combinations. In four character combinations (X_1+X_2+X_5+X_6), the highest genetic advance, relative efficiency and relative efficiency per character were 120.98 g, 1830.84 % and 457.711 %, respectively. Whereas the maximum genetic advance, relative efficiency and relative efficiency per character in five characters combinations (X_1+X_2+X_4+X_5+X_6) were 121.94 g, 1845.33 % and 369.07% respectively. Robinson *et al.* (1951) in corn recorded a progressive increase in efficiency of selection indices with inclusion of every additional character in the index formula. Hazel and Lush (1943) also stated that the superiority of selection based on index increased with an increase in the number of characters under selection. In mustard, Singh and Singh (1974), Yadav and Singh (1988), Kakroo *et al*. (1994), Khulbe and Pant (1999) and Hussain *et al.* (2003) were also reported that an increase in characters resulted in an increase in genetic gain and that the selection indices improved the efficiency than the straight selection for seed yield alone.

Further, it was observed that the straight selection for seed yield was not that much rewarding (GA=6.61 g, RI=100 %) as it was through its components like biological yield per plant (GA=7.50 g, RI=113.45 %), harvest index (GA=4.16 g, RI=62.95 %), number of primary branches per plant (GA=1.03 g, RI=15.56 %), number of secondary branches per plant (GA=5.44 g, RI=82.26 %), number of siliquae per plant (GA=104.91 g, RI=1587.62 %) and/or in their combinations. The maximum efficiency in selection for seed yield was exhibited by a discriminant function involving seed yield per plant, biological yield per plant, harvest index, number of primary branches per plant, number of secondary branches per plant and number of siliquae per plant (X_1+X_2+X_3+X_4+X_5+X_6) which had a genetic advance, relative efficiency and relative efficiency per character of 122.10g, 1847.80 % and 307.97 %, respectively followed by an index of five characters (X_1+X_2+X_4+X_5+X_6) with 121.94 g genetic advance, 1845.33 % relative efficiency and 369.07 % relative efficiency per character. High efficiency in selection based on seed yield per plant, number of siliquae per plant, number of primary branches and number of secondary branches or in combination of all these four characters has been reported by Singh and Singh (1974), Chatterjee and Bhattacharyya (1986) and Karkoo *et al*. (1994).

The present study showed consistent increase in the relative efficiency of the succeeding index with simultaneous inclusion of each character. However, in practice, the plant breeder might be interested in maximum gain with minimum number of characters. In such a case, selection index consisting of four traits *viz*., seed yield per plant, biological yield per plant, number of secondary branches per plant and number of siliquae per plant could be advantageously exploited in the mustard breeding programmes. 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 yield advancement in mustard.

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Table 1.Selection index, discriminant function, expected genetic advance in seed yield and relative efficiency from the use of different selection indices of mustard

Sr. No.	Selection index	Discriminant function	Expected genetic advance	Relative efficiency (%)	Relative efficiency per character (%)
1	$X_{1:}$ Seed yield per plant	$0.621X_1$	6.608	100.000	100.000
2	$X_{2:}$ Biological yield per plant	$0.274\ X_2$	7.497	113.453	113.453
3	$X_{3:}$ Harvest index	$0.383\ X_3$	4.160	62.954	62.954
4	$X_{4:}$ No. of primary branches per plant	$0.613\ X_4$	1.028	15.557	15.557
5	$X_{5:}$ No. of secondary branches per plant	$0.687\ X_5$	5.436	82.264	82.264
6	$X_{6:}$ No. of siliquae per plant	$0.697\ X_6$	104.910	1587.621	1587.620
7	X_1+X_2	$1.623X_1$ - $0.021X_2$	16.873	255.344	127.672
8	X_1+X_3	$0.903X_1 + 0.269X_3$	11.654	176.366	88.183
9	X_1+X_4	$0.621X_1 + 0.720X_4$	6.921	104.736	52.368
10	X_1+X_5	$0.609X_1 + 0.695X_5$	9.497	143.714	71.857
11	X_1+X_6	$0.522X_1 + 0.700X_6$	107.168	1621.787	810.894
12	X_2+X_3	$0.402X_2 + 1.026X_3$	14.773	223.558	111.779
13	X_2+X_4	$0.216X_2 + 3.365X_4$	9.512	143.944	71.972
14	X_2+X_5	$0.196X_2 +1.438X_5$	14.364	217.378	108.689
15	X_2+X_6	$0.002X_2 + 0.745X_6$	112.174	1697.544	848.772
16	X_3+X_4	$0.371X_3 + 0.235X_4$	3.987	60.340	30.17
17	X_3+X_5	$0.348X_3 + 0.589X_5$	5.718	86.536	43.268
18	X_3+X_6	$0.724X_3 + 0.699X_6$	105.098	1590.465	795.233
19	X_4+X	$0.926X_4 + 0.689X_5$	6.005	90.879	45.440
20	X_4+X	$3.401X_4 + 0.699X_6$	105.440	1595.643	797.822
21	X_5+X	$2.667X_5 + 0.672X_6$	109.168	1652.055	826.028
22	$X_1+X_2+X_3$	$3.056X_1 – 0.354X_2 – 0.607X_3$	21.811	330.063	110.021
23	$X_1+X_2+X_4$	$1.703X_1 – 0.119X_2 + 4.213X_4$	18.300	276.936	92.312
24	$X_1+X_2+X_5$	$1.607X_1 – 0.104X_2 + 1.518X_5$	21.285	322.111	107.370
25	$X_1+X_2+X_6$	$2.019X_1 – 0.409X_2 + 0.748X_6$	115.381	1746.077	582.026
26	$X_1+X_3+X_4$	$0.967X_1 + 0.208X_3 – 0.197X_4$	11.791	178.440	59.480
27	$X_1+X_3+X_5$	$0.993X_1 + 0.172X_3 + 0.479X_5$	13.148	198.976	66.325
28	$X_1+X_3+X_6$	$0.344X_1 + 0.955X_3 + 0.706X_6$	107.712	1630.018	543.339
29	$X_1+X_4+X_5$	$0.594X_1 + 1.017X_4 + 0.732X_5$	10.155	153.671	51.224
30	$X_1+X_4+X_6$	$0.478X_1 + 3.572X_4 + 0.692X_6$	107.712	1630.023	543.341
31	$X_1+X_5+X_6$	$0.209X_1 + 2.764X_5 + 0.680X_6$	111.485	1687.128	562.376
32	$X_2+X_3+X_4$	$0.357X_2 + 1.062X_3 + 2.847X_4$	15.586	235.860	78.620
33	$X_2+X_3+X_5$	$0.348X_2 + 1.020X_3 + 1.223X_5$	18.329	277.380	92.460
34	$X_2+X_3+X_6$	$0.163X_2 + 1.326X_3 + 0.736X_6$	113.008	1710.168	570.056
35	$X_2+X_4+X_5$	$0.139X_2 + 3.318X_4 + 1.436X_5$	15.897	240.565	80.188
36	$X_2+X_4+X_6$	$-0.105X_2 + 6.822X_4 + 0.733X_6$	113.057	1710.908	570.303
37	$X_2+X_5+X_6$	$-0.299X_2 + 3.791X_5 + 0.726X_6$	117.763	1782.129	594.043
38	$X_3+X_4+X_5$	$0.348X_3 + 0.576X_4 + 0.643X_5$	6.209	93.968	31.323

Contd..

Table 1. contd..

Sr. No.	Selection index	Discriminant function	Expected genetic advance	Relative efficiency (%)	Relative efficiency per character (%)
39	$X_3+X_4+X_6$	$0.779X_3 + 3.364X_4 + 0.690X_6$	105.608	1598.181	532.727
40	$X_3+X_5+X_6$	$0.815X_3 + 2.615X_5 + 0.675X_6$	109.212	1652.718	550.906
41	$X_4+X_5+X_6$	$2.159X_4 + 2.632X_5 + 0.668X_4$	109.654	1659.408	553.136
42	$X_1+X_2+X_3+X_4$	$3.042X_1 – 0.399X_2 – 0.557X_3 + 3.070X_4$	22.516	340.740	85.185
43	$X_1+X_2+X_3+X_5$	$2.569X_1 – 0.265X_2 – 0.273X_3 + 1.268X_5$	24.759	374.681	93.670
44	$X_1+X_2+X_3+X_6$	$2.519X_1 – 0.438X_2 + 0.066X_3 + 0.740X_6$	116.067	1756.463	439.116
45	$X_1+X_2+X_4+X_5$	$1.685X_1 – 0.198X_2 + 4.125X_4 + 1.500X_5$	22.690	343.371	85.843
46	$X_1+X_2+X_4+X_6$	$2.182X_1 – 0.578X_2 + 7.902X_4 + 0.735X_6$	116.396	1761.444	440.361
47	$X_1+X_2+X_5+X_6$	$2.085X_1 – 0.736X_2 + 3.880X_5 + 0.728X_6$	120.982	1830.844	457.711
48	$X_1+X_3+X_4+X_5$	$1.021X_1 + 0.144X_3 + 0.193X_4 + 0.504X_5$	13.408	202.912	50.728
49	$X_1+X_3+X_4+X_6$	$0.162X_1 + 1.139X_3 + 4.074X_4 +0.700X_6$	108.265	1638.393	409.598
50	$X_1+X_3+X_5+X_6$	$-0.415X_1 + 1.542X_3 + 2.988X_5 + 0.694X_6$	112.088	1696.250	424.063
51	$X_1+X_4+X_5+X_6$	$0.182X_1 + 2.412X_4 + 2.764X_5 +0.675X_6$	112.038	1695.496	423.874
52	$X_2+X_3+X_4+X_5$	$0.301X_2 + 1.057X_3 + 2.894X_4 + 1.233X_5$	19.304	292.129	73.0323
53	$X_2+X_3+X_4+X_6$	$0.062X_2 + 1.429X_3 + 6.725X_4 + 0.725X_6$	113.851	1722.928	430.730
54	$X_2+X_3+X_5+X_6$	$-0.119X_2 + 1.414X_3 + 3.629X_5 + 0.719X_6$	118.247	1789.457	447.364
55	$X_2+X_4+X_5+X_6$	$-0.386X_2 + 5.904X_4 + 3.757X_5 + 0.716X_6$	118.610	1794.949	448.737
56	$X_3+X_4+X_5+X_6$	$0.845X_3 + 2.195X_4 + 2.619X_5 +0.670X_6$	109.735	1660.633	415.158
57	$X_1+X_2+X_3+X_4+X_5$	$2.568X_1 – 0.313X_2 – 0.233X_3 + 3.136X_4 + 1.233X_5$	25.516	386.140	77.228
58	$X_1+X_2+X_3+X_4+X_6$	$2.355X_1 – 0.493X_2 + 0.286X_3 + 6.933X_4 +0.728X_6$	116.931	1769.531	353.906
59	$X_1+X_2+X_3+X_5+X_6$	$13.037X_1 – 1.531X_2 – 8.100X_3 – 21.683X_5 + 0.922X_6$	99.559	1506.641	301.328
60	$X_1+X_2+X_4+X_5+X_6$	$2.226X_1 – 0.879X_2 + 6.980X_4 + 3.833X_5 + 0.717X_6$	121.940	1845.333	369.067
61	$X_1+X_3+X_4+X_5+X_6$	$-0.560X_1 + 1.690X_3 + 3.558X_4 + 2.960X_5 + 0.689X_6$	112.625	1704.377	340.875
62	$X_2+X_3+X_4+X_5+X_6$	$-0.203X_2 + 1.502X_3 + 5.927X_4 + 3.602X_5 +0.709X_6$	119.071	1801.919	360.384
63	$X_1+X_2+X_3+X_4+X_5+X_6$	$0.761X_1 – 0.282X_2 + 1.463X_3 + 6.187X_4 + 3.632X_5 + 0.712X_6$	122.102	1847.797	307.966