



## Research Note

### Discriminant function method of selection in groundnut (*Arachis hypogaea* L.)

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#### Abstract

One hundred diverse genotypes of groundnut were evaluated for 15 characters in order to construct selection indices. The characters, which had desirable correlation as well as moderate to high direct effect on pod yield per plant were considered as selection index criterion. The pod yield per plant ( $X_1$ ) along with its five components viz., days to maturity ( $X_2$ ), number of pods per plant ( $X_3$ ), kernel yield per plant ( $X_4$ ), biological yield per plant ( $X_5$ ) and harvest index ( $X_6$ ) were utilized for the construction of selection indices. The discriminant function had higher genetic gain and relative efficiency over straight selection for pod yield alone. The relative efficiencies of selection indices constructed in combinations of two or more characters were ranged from 105.90 to 536.06%, while genetic advance ranged from 12.75 to 64.58g. There was an increase in genetic gain and relative efficiency with inclusion of an additional trait in the character combination. A selection index consisting of pod yield per plant, days to maturity, number of pods per plant, kernel yield per plant and biological yield per plant and an index involving pod yield per plant, number of pods per plant, kernel yield per plant and biological yield per plant registered higher genetic gain and relative efficiency. These indices could be advantageously exploited in the groundnut breeding programmes for isolating high yielding genotypes.

**Keywords:** Groundnut, yield, discriminant function

Groundnut (*Arachis hypogaea* L.) is one of the most economic oilseed crops of the world. It is considered as the world's fourth largest source of edible oil and third most important source of vegetable protein (Desai *et al.*, 1999). Yield in crops is a quantitative trait and has a complex genetic control mechanism and hence, direct selection is not much effective on it. Since the economic part of groundnut known as pod is developed under the soil, the prediction of its performance based on aerial morphological characters is almost difficult (Weiss, 2000). The most desirable approach to improve characteristics such as pod yield is simultaneous selection based on related traits (Bos and Caligri, 2007). This can be done using selection index, which is multiple regressions of genotypic values on phenotypic values of several traits (Falconer, 1989). The use of selection index is superior in improving complex traits (Hasel and Lush, 1942). Furthermore, the selection indices approach aimed at determining the most suitable combination of traits with the intention of indirectly improving the pod yield in groundnut was well documented (Shettar, 1974; Bandyopadhyay *et al.* 1985 and Dobariya *et al.*, 2008).

The plant breeder has certain desired plant characteristics in his mind while selecting for particular genotype and for this he applies various weights to different traits for arriving on decisions. The better way of exploiting genetic correlations with several traits having high heritability is to construct an index which combines information on all the characters associated with yield. This suggests the use of selection index, which gives

proper weight to each of the two or more characters to be considered. Selection index was proposed for the first time by Smith (1936) on the basis discriminant function of Fisher (1936). Hazel and Lush (1943) and Robinson *et al.* (1951) showed that the selection based on such an index is more efficient than selecting individually for the various characters. Keeping these facts in view the present study was undertaken in order to construct selection indices for efficient selection in groundnut breeding programme.

The experimental material comprised of 100 genotypes of Spanish bunch groundnut. The list of genotypes along with their origin is given in Table 1. The genotypes were evaluated in a Randomized Block Design with three replications at the Main Oilseeds Research Station, J.A.U., Junagadh During *kharif* 2011. Each entry was sown in a single row of 2.0 m length with a spacing of 45 x 10 cm. The observations were recorded on five randomly selected plants from each entry and replication and their mean values were used. The observations were recorded on five randomly selected competitive plants from each genotype and replication for 15 characters viz., days to 50% flowering, days to maturity, plant height (cm), number of secondary branches per plant, number of pegs per plant, number of pods per plant, number of mature pods per plant, sound mature kernels (%), 100- kernel weight (g), kernel yield per plant (g), shelling out-turn (%), biological yield per plant (g), harvest index (%), oil content (%) and pod yield per plant (g).

Application of discriminant function as a basis for making selection on several characters simultaneously is aimed at discriminating the desirable genotypes from undesirable ones on the basis of their phenotypic performance. A model suggested by Robinson *et al.* (1951) was used for the construction of selection indices and the development of a required discriminant function. For the construction of selection indices, the characters, which had desirable correlation as well as moderate to high direct effect on pod yield per plant, were considered. In this context, the pod yield per plant ( $X_1$ ) along with its five components *viz.*, days to maturity ( $X_2$ ), number of pods per plant ( $X_3$ ), kernel yield per plant ( $X_4$ ), biological yield per plant ( $X_5$ ) and harvest index ( $X_6$ ) were identified and considered for the construction of selection indices.

Sixty three selection indices were constructed in all possible combinations of five yield contributing characters and pod yield per plant. Their respective genetic advances were calculated and relative efficiency of different discriminant functions in relation to the straight selection for pod yield was compared.

A total of 63 selection indices (Table 2) based on six characters constructed in all possible combinations revealed that the selection efficiency was not higher over straight selection for pod yield per plant when selection was based on individual components except selection index made-up of biological yield per plant. The results suggested that the selection indices containing single trait were not efficient to bring genetic improvement in groundnut for pod yield. This is due to the fact that yield is a cumulative effect of several traits and hence, selection for single trait is not expected to explain fully the genotypic variation for pod yield. However, it was believed that when two or more single-trait based indices were merged, the relative efficiency of the resulted index was better than using each of the single traits independently. 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 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. The relative efficiencies of selection indices constructed in combinations of two or more characters were ranged from 105.90 to 536.06%, while genetic advance ranged from 12.75 to 64.58g. The maximum genetic advance (GA) and relative efficiency (RI) in single character discriminant function were 45.59g and 378.43%, respectively which however, increased to 54.96g and 456.24%, respectively in two character combinations and 59.78g and 496.25%, respectively in three character combinations. Thus, there was an increase in the genetic gain as well as

relative efficiency with inclusion of an additional trait in the character combinations. In four character combinations, the highest genetic advance and relative efficiency were 62.06g and 515.10%, respectively. In five character combinations, the highest genetic advance and relative efficiency were 64.24g and 533.27%, respectively whereas, the maximum genetic advance and relative efficiency in case of six character combinations were 64.58g and 536.06%, respectively. Abraham (1990), Dobariya *et al.* (2008) and Bhosale (2011) were also with the same opinion that an increase in characters results in an increase in genetic gain and that the selection indices improve the efficiency of selection than the straight selection for yield alone.

In the present study, it was also observed that the straight selection for yield was not that much rewarding (GA=12.04g, RI=100.00%) as it was through its components like biological yield per plant (GA=45.59g, RI=378.43%) and harvest index (GA=12.71g, RI=105.50%) or in their combinations. The maximum efficiency in selection for pod yield was exhibited by a discriminant function involving pod yield per plant, days to maturity, number of pods per plant, kernel yield per plant, biological yield per plant and harvest index, which had a genetic advance and relative efficiency of 64.58g and 536.06%, respectively followed by an index of five characters *viz.*, pod yield per plant, days to maturity, number of pods per plant, kernel yield per plant and biological yield per plant, which had a genetic advance and relative efficiency of 64.24g and 533.27%. The best selection index identified for four character combinations involved pod yield per plant, number of pods per plant, kernel yield per plant and harvest index ( $X_1.X_3.X_4.X_5$ ) with 62.06g genetic advance and 515.17% relative efficiency. The best selection index identified for three character combinations included pod yield per plant, kernel yield per plant and biological yield per plant ( $X_1.X_4.X_5$ ) having expected genetic gain of 59.78g and a relative efficiency of 496.25% as compared to the straight selection for pod yield per plant. The underlying reason for usefulness of selection index is that yield is a cumulative effect of two or more correlated and co-heritable yield components such as number of pods per plant, kernel yield per plant, biological yield per plant and harvest index. Thus, the progress to be attained from indirect selection using one or more yield components is depended upon the direction and magnitude of genotypic correlation between the traits in selection index and yield. Lack of efficiency for selection based on a single trait therefore, may also be attributed to either low genotypic correlation and heritability or both of each trait with pod yield. It is interesting to note that the relative efficiency of two or more character combination indices increased

considerably when biological yield per plant was involved in an index, which suggested that the improvement in pod yield may be possible through improvement in biological yield per plant in groundnut.

Further, there was a consistent increase in the relative efficiency of the succeeding index with simultaneous inclusion of each character. Ideally all possible combinations of traits have to be examined so as to identify the combinations that contribute the most to the selection index. However, in practice, the plant breeder might be interested in maximum possible gain and relative efficiency with minimum number of characters in a selection index. From practical plant breeding point of view, however, the easiest and a relatively efficient index is the one which contains traits that are relatively easier to record in a better precision in the field and these records are collected in routine activity of research (Bos and Caligri, 2007). In such a case, selection index consisting of pod yield per plant, days to maturity, number of pods per plant, kernel yield per plant and biological yield per plant (X1.X2.X3.X4.X5) followed by a selection index involving pod yield per plant, number of pods per plant, kernel yield per plant and biological yield per plant (X1.X3.X4.X5) or pod yield per plant, days to maturity, kernel yield per plant and biological yield per plant (X1.X2.X3.X5) could be advantageously exploited in the groundnut breeding programmes. The results of the present study also revealed that the discriminant function method of making selection in plants appeared to be the most useful than the straight selection for pod yield alone and hence, due weightage should be given to the important selection indices while making selection for yield advancement in groundnut.

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**Table 1. List of Spanish bunch groundnut genotypes with their origin**

Sr. No.	Name of genotype	Origin	Sr. No.	Name of genotype	Origin
1	JB-FSD-383	Junagadh (Gujarat)	51	JB-468	Junagadh (Gujarat)
2	JB-765	Junagadh (Gujarat)	52	TG-3	Trombay (Maharashtra)
3	Dh-202	Dharwad (Karnataka)	53	J-22	Junagadh (Gujarat)
4	J-54	Junagadh (Gujarat)	54	JB-909	Junagadh (Gujarat)
5	502-1-P	United States of America	55	JB-452	Junagadh (Gujarat)
6	JB-714	Junagadh (Gujarat)	56	AH-7217	Nigeria
7	SHANFUNG	China	57	J-60	Junagadh (Gujarat)
8	GG-5	Junagadh (Gujarat)	58	JB-500	Junagadh (Gujarat)
9	GCP-513	DGR, Junagadh (Gujarat)	59	JB-FDR-17	Junagadh (Gujarat)
10	JB-655	Junagadh (Gujarat)	60	GJG-31	Junagadh (Gujarat)
11	J-27	Junagadh (Gujarat)	61	R-2001-3	Raichur (Karnataka)
12	JBE-346	Junagadh (Gujarat)	62	ICGV-91114	Hyderabad (Andhra Pradesh)
13	TG-36-B	Trombay (Maharashtra)	63	JL-24	Jalgaon (Maharashtra)
14	AK-159	Akola (Maharashtra)	64	GG-7	Junagadh (Gujarat)
15	JB-839	Junagadh (Gujarat)	65	GPBD-4	Dharwad (Karnataka)
16	J-33	Junagadh (Gujarat)	66	Dh-101	Dharwad (Karnataka)
17	ICG-7886	Hyderabad (Andhra Pradesh)	67	GPBD-5	Dharwad (Karnataka)
18	JB-680	Junagadh (Gujarat)	68	TMV(GN)-13	Vridhachalam (Tamil Nadu)
19	JB-60	Junagadh (Gujarat)	69	R-2001-2	Raichur (Karnataka)
20	GJG-9	Junagadh (Gujarat)	70	JL-501	Jalgaon (Maharashtra)
21	Dh -201	Dharwad (Karnataka)	71	TPG-41	Trombay (Maharashtra)
22	RPM-190	Udaipur (Rajasthan)	72	SG-99	Ludhiana (Punjab)
23	JB-302	Junagadh (Gujarat)	73	TAG-24	Trombay (Maharashtra)
24	JB-T5-455	Junagadh (Gujarat)	74	Girnar-3	Junagadh (Gujarat)
25	JB-T5-456	Junagadh (Gujarat)	75	TG-37-A	Trombay (Maharashtra)
26	ICGS-156	Hyderabad (Andhra Pradesh)	76	VG-9816	Vridhachalam (Tamil Nadu)
27	JB-443	Junagadh (Gujarat)	77	ICGV-00350	Hyderabad (Andhra Pradesh)
28	JB-564	Junagadh (Gujarat)	78	RG-425	Durgapura (Rajasthan)
29	JB-618	Junagadh (Gujarat)	79	PM-1	Udaipur (Rajasthan)
30	J-62	Junagadh (Gujarat)	80	PM-2	Udaipur (Rajasthan)
31	J-28	Junagadh (Gujarat)	81	VG-5	Vridhachalam (Tamil Nadu)
32	ICGV-92116	Hyderabad (Andhra Pradesh)	82	K-1333	Kadiri (Andhra Pradesh)
33	Girnar-1	DGR, Junagadh (Gujarat)	83	TG-68	Trombay (Maharashtra)
34	JB-667	Junagadh (Gujarat)	84	P-135-30086	Udaipur (Rajasthan)
35	JB-637	Junagadh (Gujarat)	85	ICGV-00351	Hyderabad (Andhra Pradesh)
36	JB-803	Junagadh (Gujarat)	86	Dh-218	Dharwad (Karnataka)
37	ICG-FDRS-10	Hyderabad (Andhra Pradesh)	87	ICGS- 901-A	Hyderabad ( Andhra Pradesh )
38	JB-747	Junagadh (Gujarat)	88	CTMG-7	Chintamani (Karnataka)
39	JL-272	Jalgaon (Maharashtra)	89	K-1392	Kadiri (Andhra Pradesh)
40	JDR-66	Junagadh (Gujarat)	90	K-1463	Kadiri (Andhra Pradesh)
41	JB-588	Junagadh (Gujarat)	91	K-1470	Kadiri (Andhra Pradesh)
42	J-63	Junagadh (Gujarat)	92	GAUG-1	Junagadh (Gujarat)
43	EC-21051	Argentina	93	ICR-3	Hyderabad (Andhra Pradesh)
44	JB-677	Junagadh (Gujarat)	94	ICR-48	Hyderabad (Andhra Pradesh)
45	JB-574	Junagadh (Gujarat)	95	Jun-27	DGR, Junagadh (Gujarat)
46	JB-FDR-59	Junagadh (Gujarat)	96	CSMG-2006-6	Mainpuri (Uttar Pradesh)
47	Khandesh	Maharashtra	97	RTNG-2	Shirgaon (Maharashtra)
48	J-32	Junagadh (Gujarat)	98	JB-757	Junagadh (Gujarat)
49	JB-612	Junagadh (Gujarat)	99	JL-286	Jalgaon (Maharashtra)
50	JB-510	Junagadh (Gujarat)	100	JL-220	Jalgaon (Maharashtra)



**Table 2. Selection index, discriminant function, expected genetic advance in yield and relative efficiency from the use of different selection indices in groundnut**

S.No.	Selection index	Discriminant function	GA	RE (%)
1	X1 (Pod yield/ plant)	0.925X1	12.04	100.00
2	X2 (Days to maturity)	0.999X2	9.79	81.33
3	X3 (Number of pods/plant)	0.972X3	7.61	63.18
4	X4 (Kernel yield/ plant)	0.942X4	7.91	65.66
5	X5 (Biological yield/plant)	0.990X5	45.59	378.43
6	X6 (Harvest index)	0.876X6	12.71	105.50
7	X1.X2	0.922X1 + 1.015X2	16.83	139.75
8	X1.X3	0.923X1 + 0.992X3	15.66	129.99
9	X1.X4	0.896X1 + 1.058X4	18.86	156.56
10	X1.X5	0.890X1 + 1.010X5	54.96	456.24
11	X1.X6	0.944X1 + 0.854X6	21.09	175.08
12	X2.X3	1.007X2 + 0.972X3	12.75	105.90
13	X2.X4	1.005X2 + 0.951X4	13.55	112.52
14	X2.X5	1.004 X2 +0.990X5	47.72	396.13
15	X2.X6	1.005X2 + 0.575X6	16.39	136.10
16	X3.X4	1.906 X3 +1.759X4	22.65	188.06
17	X3.X5	2.516X3 + 0.979X5	52.91	439.21
18	X3.X6	0.915X3 + 0.931X6	14.95	124.12
19	X4.X5	0.971X4 + 0.874X5	49.82	413.59
20	X4.X6	1.019X4 + 0.868X6	17.42	144.59
21	X5.X6	0.982X5 + 0.883X6	43.45	360.71
22	X1.X2.X3	0.920X1 + 1.016X2 + 0.992X3	19.81	164.43
23	X1.X2.X4	0.893X1 + 1.014X2 + 1.059X4	22.78	189.15
24	X1.X2.X5	0.886X1 + 1.016X2 + 1.010X5	57.11	474.12
25	X1.X2.X6	0.941X1 + 1.018X2 + 0.854X6	24.38	202.40
26	X1.X3.X4	0.895X1 + 0.989X3 + 1.059X4	21.86	181.51
27	X1.X3.X5	0.885X1 + 0.996X3 + 1.011X5	57.24	475.16
28	X1.X3.X6	0.944X1 + 0.985X3 + 0.852X6	23.43	194.52
29	X1.X4.X5	0.834X1 + 1.109X4 + 1.012X5	59.78	496.25
30	X1.X4.X6	0.458X1 + 1.071X4 + 0.930X6	27.12	225.16
31	X1.X5.X6	0.873X1 + 1.162X5 + 0.848X6	54.48	452.27
32	X2.X3.X4	1.006X2 + 0.977X3 + 0.952X4	16.51	137.11
33	X2.X3.X5	1.004X2 + 0.987X3 + 0.991X5	49.99	415.02
34	X2.X3.X6	1.007X2 + 0.970X3 + 0.873X6	18.43	153.00
35	X2.X4.X5	1.005X2 + 0.979X4 + 0.992X5	52.02	431.86
36	X2.X4.X6	1.003X2 + 1.019X4 + 0.867X6	20.88	173.32
37	X2.X5.X6	0.369X2 + 0.722X5 + 0.742X6	44.37	368.30
38	X3.X4.X5	1.075X3 + 0.932X4 + 0.327X5	52.13	432.78
39	X3.X4.X6	0.964X3 + 1.024X4 + 0.865X6	19.69	163.44
40	X3.X5.X6	0.392X3 + 1.007X5 + 0.911X6	45.50	377.75
41	X4.X5.X6	1.113X4 + 0.970X5 + 0.846X6	48.70	404.32
42	X1.X2.X3.X4	0.892X1 + 1.014X2 + 0.988X3 + 1.06X4	25.50	211.71
43	X1.X2.X3.X5	0.882X1 +1.017X2 + 0.995X3 + 1.012X5	59.38	492.97
44	X1.X2.X3.X6	1.0585X1 + 0.171X2 + 1.006X3 + 0.828X6	25.04	207.86
45	X1.X2.X4.X5	0.799X1 +0. 488X2 + 0.772X4 +0.832X5	61.90	514.39
46	X1.X2.X4.X6	0.835X1 + 1.014X2 + 1.099X4 + 1.013X6	30.17	250.50
47	X1.X2.X5.X6	0.969X1 + 1.020X2 + 0.984X5 + 0.852X6	56.75	471.12
48	X1.X3.X4.X5	0.874X1 + 0.977X3 + 1.164X4 + 0.845X5	62.06	515.17
49	X1.X3.X4.X6	0.874X1 + 0.977X3 + 1.164X4 + 0.845X6	29.36	243.76
50	X1.X3.X5.X6	0.700X1 + 1.044X3 + 0.723X5 + 0.743X6	56.81	471.64
51	X1.X4.X5.X6	0.965X1 + 1.002X4 + 0.986X5 + 0.743X6	60.01	498.17
52	X2.X3.X4.X5	0.463X2 + 0.963X3 + 0.836X4 + 0.854X5	32.32	268.33
53	X2.X3.X4.X6	1.005X2 + 0.964X3 + 1.024X4 + 0.865X6	23.00	190.95
54	X2.X3.X5.X6	1.014X2 + 0.996X3 + 0.982X5 + 0.880X6	48.22	400.26
55	X2.X4.X5.X6	1.008X2 + 1.113X4 + 0.970X5 + 0.845X6	51.07	423.91
56	X3.X4.X5.X6	0.989X3 + 1.112X4 + 0.971X5 + 0.845X6	51.11	424.26
57	X1.X2.X3.X4.X5	0.830X1 + 1.014X2 + 0.989X3 + 0.987X4 + 0.858X6	64.24	533.27
58	X1.X2.X3.X4.X6	0.870X1 + 1.014X2 + 0.977X3 + 1.100X4+1.014X6	32.34	268.49
59	X1.X2.X3.X5.X6	0.956X1 + 1.021X2 + 0.999X3 + 0.987X5 + 0.858X6	59.07	490.37
60	X1.X2.X4.X5.X6	4.894X1 + 0.882X2 + 1.185X4 + -0.133X5 + -1.778X6	60.03	498.36
61	X1.X3.X4.X5.X6	0.873X1 + 0.990X3 + 1.197X4 + 0.987X5 + 0.851X6	62.32	517.31
62	X2.X3.X4.X5.X6	1.008X2 + 0.989X3 + 1.112X4 + 0.970X5 + 0.844X6	53.44	443.66
63	X1.X2.X3.X4.X5.X6	0.866X1 + 1.015X2 + 0.990X3 + 1.198X4 + 0.989X5 + 0.854X6	64.58	536.06

GA= Expected genetic advance RE- Relative efficiency (%)