SIMULTANEOUS SELECTION MODEL FOR PLANT SELECTION IN GREENGRAM

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Simultaneous seletion model based on Discriminant Function was applied to select the ____ genotype out of 63 greengram genotypes. 16 different sets of assigned weights were tried in the model to select the best genotype. The genotype LM 222 was selected as the best genotype by the model in 13 sets of weights out of 16 sets of weights.

Selection of promising genotypes for further breeding programme in a given set of genotypes is an important aspect in plant breeding. The selection of genotypes based on the phenotypic values of plant characters is seldom successful. Smith (1936) has suggested a model based on discriminant function to select genotypes considering (i) phenotypic values ; (ii) genotypic values of the different characters responsible for yield simultaneously. Goulden (1962) has given a worked out example with two sets of assigned weights for selecting genotypes without attributing any reason for assigning such weights. There is little work regarding the methods of assigning other weights. Therefore, different methods of assigning weights in Smith's model has been attempted in the present study in greengram (*Vigna radiata* L) with the following objectives :

1. To select the best greengram genotype from the given set ;

2. To verify whether the same genotype is being selected as the best in different methods of assigning weights to the plant characters.

MATERIALS AND METHODS

The data on 63 greengram genotypes obtained from field experiments conducted at Tamil Nadu Agricultural University during monsoon '82 have been used in the present study. Randomised block design was adopted in the experiment with two replications. Five plants of each genotype were selected at random in each replication and observations were made on the following eleven characters :

1) Seed yield (x_1)
2) Leaf weight (x_2)
3) Stem weight (x_3)
4) Root weight (x_4)
5) Leaf area (x_5)
6) Total dry matter production (x_6)
7) Number of pods (x_7)
8) 100 seed weight (x_8)
9) Number of clusters (x_9)
10) Number of branches (x_{10})
11) Plant height (x_{11})

The means of five plants values in each replication were used for further statistical analysis. The 63 genotypes were :

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1) PLS 269	32) PLS 304
2) PLS 327	33) PLS 322
3) AC 176	34) PS 414/1
4) AC 300	35) ML 26
5) MDU 2984	36) LM 35
6) LM 7	37) LM 254
7) LM 21	38) LM 263
8) LM 23	39) LM 279
9) LM 72	40) LM 361
10) LM 87	41) LM 366
11) PLS 266	42) CO 3
12) PLS 300	43) PLS 41
13) PLS 311	44) M 1
14) PLS 328	45) M 3
15) PLS 337	46) M 9
16) PLS 343	47) MS 8909
17) AC 205	48) LM 167
18) ML 26/10/3	49) LM 218
19) LM 89	50) LM 222
20) LM 85	51) LM 370
21) KM 1	52) LM 449
	53) NA 5
22) PLS 298	54) ML 1
23) MDU 1945	55) LM 150
24) MDU 2106	56) LM 152
25) LM 14	57) LM 220
26) LM 15	58) LM 228
27) LM 24	59) LM 275
28) LM 170	60) LM 360
29) LM 244	61) LM 419
30) LM 253	62) LM 469
31) LM 459	63) CO 4

The Smith's model involves finding the coefficients b_1, b_2.... b_p in the Discriminant Function,

$$I = b_1 x_1 + b_2 x_2 + \ldots + b_p x_p \quad (1)$$

where x_1 x_2 .... x_p are the characters

taken for study. The values of b_1 b_2.......b_p are obtained from the following equation

$$\underline{b} = P^{-1} G \underline{a} \quad (2)$$

where $\underline{b}$ is the vector of Co-efficients b_1 b_2 b_p to be estimated

P^{-1} is the inverse of phenotypic variance-covariance matrix. G is the genotypic variance-Covariance matrix $\underline{a}$ is the vector of coefficients assigned to each character.

The equation (2) is obtained such that the correlation between genotypic worth and phenotypic worth is maximum. (Singh and Choudhary, 1979).

After finding b_1...b_p from equation (2) they are substituted in the Discriminant Function (1)

The mean values of x_1 x_2...x_p for each genotype are substituted in equation (1) and the resulting value is called selection criteria for the corresponding genotypes. The selection criteria values are ranked and the genotype taking the first rank will be adjudged the best genotype. The expected genetic advance in selection through Discrimination Function is estimated by the formula,

$$X = K \times \frac{b^I G a}{V \overline{b^I P b}}$$

(Singh and Choudhary, 1979). where, k is the standard normal value for the percentage of genotypes selected.

If the genotypes were selected through direct selection based on their importance (i.e weights) then the expected genetic gain is estima-

Table 1 : The description and values of different assigned weights

Set No.	Description of the set	Assigned weights										
		a_1	a_2	a_3	a_4	a_5	a_6	a_7	a_8	a_9	a_{10}	a_{11}
1.	Equal weights	1	1	1	1	1	1	1	1	1	1	1
2.	Reciprocal of grand means	0.0856	0.2837	0.2592	1.2488	0.0021	0.0399	0.0283	0.2569	0.0972	0.5990	0.0265
3.	Reciprocal of SDs	0.1475	0.4058	0.3179	2.5691	0.0027	0.0671	0.0507	1.2826	0.1745	1.0014	0.0974
4.	Error variance	15.0209	1.8890	2.8666	0.0382	3.4656	66.128	115.83	0.0789	8.2037	0.2928	23.0496
5.	Co-efficient of variation	33.1500	38.987	43.885	24.805	39.836	32.470	30.411	7.2167	27.632	30.249	12.7208
6.	Unity to a_1 & zeroes to others	1	0	0	0	0	0	0	0	0	0	0
7.	Unity to a_2 & zeroes to others	0	1	0	0	0	0	0	0	0	0	0
8.	Unity to a_3 & zeroes to others	0	0	1	0	0	0	0	0	0	0	0
9.	Unity to a_4 & zeroes to others	0	0	0	1	0	0	0	0	0	0	0
10.	Unity to a_5 & zeroes to others	0	0	0	0	1	0	0	0	0	0	0
11.	Unity to a_6 & zeroes to others	0	0	0	0	0	1	0	0	0	0	0
12.	Unity to a_7 & zeroes to others	0	0	0	0	0	0	1	0	0	0	0
13.	Unity to a_8 & zeroes to others	0	0	0	0	0	0	0	1	0	0	0
14.	Unity to a_9 & zeroes to others	0	0	0	0	0	0	0	0	1	0	0
15.	Unity to a_{10} & zeroes to others	0	0	0	0	0	0	0	0	0	1	0
16.	Unity to a_{11} & zeroes to others	0	0	0	0	0	0	0	0	0	0	1

Table 2 : The set number of weights and the values of b's in each set

Set No.	Description of each set	Coefficient of discriminant function										
		b_1	b_2	b_3	b_4	b_5	b_6	b_7	b_8	b_9	b_{10}	b_{11}
1.	Equal weights	−22.5555	0.4124	21.5288	288.557	0.4723	−6.8120	7.0131	33.8355	5.2521	−9.3590	12.0172
2.	Reciprocal of grand means	−0.1248	−0.4402	0.4189	2.9717	0.0065	−0.1144	0.0744	0.4073	0.1418	0.2305	0.1276
3.	Reciprocal of SDs	−0.2066	−0.7662	0.7034	4.8823	0.0108	−0.1890	0.1216	1.3260	0.2416	0.4331	0.2290
4.	Error variance	−757338	274826	598731	8949390	13710.1	−194808	208933	1154680	113600	−293357	371031
5.	Coefficients of variation	−894.137	80.5678	815.731	11184.3	18.0918	−258.53	271.86	1343.72	188.34	−259.83	458.91
6.	Unity to a_1 and zeroes to others	0.1256	−0.8038	0.4953	−3.4694	0.0071	−0.1653	0.0950	0.3838	0.1466	−0.0453	0.1185
7.	Unity to a_2 and zeroes to others	−0.0207	0.1191	0.1199	1.4780	0.0029	−0.0841	0.0152	0.0542	0.0350	−0.0349	0.0725
8.	Unity to a_3 and zeroes to others	−0.0113	−0.3917	0.5334	2.1182	0.0040	−0.1221	0.0257	0.3103	0.0859	−0.1021	0.0668
9.	Unity to a_4 and zeroes to others	−0.0147	−0.0349	0.0356	0.3143	0.0005	−0.0066	0.0051	0.0035	−0.0034	−0.0151	0.0117
10.	Unity to a_5 and zeroes to others	−21.851	7.9470	17.2702	258.181	0.3955	−5.6195	6.0263	33.3209	3.2750	−8.4624	10.7325
11.	Unity to a_6 and zeroes to others	−0.1889	−2.0126	1.0605	9.6951	0.0197	−0.2464	0.2046	0.9416	0.3121	0.1160	0.2991
12.	Unity to a_7 and zeroes to others	−0.4850	−3.7457	8.9879	0.0497	0.0304	−0.2837	0.6021	−1.2115	0.5916	−0.5917	0.0822
13.	Unity to a_8 and zeroes to others	−0.0145	−0.0122	−0.0315	−0.0137	0.0004	−0.0038	0.0033	0.8846	0.0020	0.0150	−0.0005
14.	Unity to a_9 and zeroes to others	−0.2587	−0.4715	0.3413	−1.5120	0.0050	−0.1160	0.0825	−0.1272	−0.6359	−0.5220	−0.0502
15.	Unity to a_{10} and zeroes to others	−0.0395	−0.0698	0.0112	0.2184	0.0004	0.0054	0.0062	0.0026	−0.0033	0.6747	0.0127
16.	Unity to a_{11} and zeroes to others	0.1807	−0.1118	0.6646	5.5591	0.0069	−0.2699	−0.0527	0.7373	0.1746	−0.2913	0.5615

ted by the formula (Prem Narain *et. al.,* 1979)

$$Y = k \times \frac{a' \, G \, a}{V \overline{a' \, P \, a}} \quad \dots \quad \dots \quad (4)$$

The expected genetic gain in selecting genotypes through discriminant function than through direct selection is given by the formula (Prem Narain *et al.,* 1979).

$$(X/Y-1) \times 100 \quad\quad\quad (5)$$

The values of p^{-1} and G in equation (2) are unique for a given set of data. But the values of a_1, a_2,.. a_i...a_p *viz.,* the weights to the characters X_1, X_2... X_i...X_p respec·ively are not uniquely defined. It is to be assigned outside the given data. For example, if all the characters X_1, X_2, X_1...X_i..X_p are to be assigned equal weights, then $a_1=1$, $a_2=1$, ...$a_i=1$... $a_p=1$ should be assigned. Suppose the weightage is to be given only for x_1 and not for x_2,x_3 ..x_i...x_p then $a_1=1$, $a_2=0$, ...$a_i=0$ ...$a_p=0$ should be assigned. In general, if weightage is to be given only for x_i and not for other characters then a_i should be taken as 1 and other a's should be taken as zeroes. The different weights assigned to each character in the present study are furnished in Table 1.

RESULTS AND DISCUSSION :

The values of b_1, b_2 ...b_{11} estimated from each set of assigned weights are furnished in Table 2. The ranks of the selection criteria values of the genotypes and the expected genetic gain due to selection through Discriminant Function than through straight selection are furnished in Table 3.

The results in Table 3 revealed that the Genotype LM 222 ranked first almost in all sets of assigned weights except in set-12, set-13, and set-15. In set-12, the assigned weights were, 0,0,0,0,0,0,1,0,0,0,0, for x_1, x_2, x_3, x_4, x_5, x_6, x_7, x_8, x_9, x_{10} and x_{11} respectively. This set of assigned weights implies that importance was given only to the character x_7, *viz.,* "Number of Pods per plant". The failure of LM 222 to take first rank in set-12, might be that with respect to the character "Number of pods per plant" the genotype might not be the best among the 63 genotypes. The expected genetic gain in selecting genotypes through Discriminant Function than through straight selection was 8.13 per cent by assigning the weights to the plant characters in greengram as in set-12. The genotype M3 took the first rank in assigning the weights as in set-12. There was evidence from the data that the genotype M3 might be the best genotype if plants were selected through Smith's model of Discriminant Function by assigning importance only to the character ''Number of Pods per plant'' among the eleven characters in greengram. There is little information in Discriminant Function whether the same genotype would be the best genotype at all locations and seasons. The genotype LM 222 took the second rank when the assigned weights were as in set-12, which indicated that LM 222 is a better genotype if not the best.

LM 222 failed to take first rank in set-13 and this indicated that there was evidence in the data that it might not be the best genotype if plants were

Table 3 :   Ranks of selection criteria values and genetic gain

	Genotypes	Set 1	Set 2	Set 3	Set 4	Set 5	Set 6	Set 7	Set 8	Set 9	Set 10	Set 11	Set 12	Set 13	Set 14	Set 15	Set 16
1.	PLS 269	17	23	25	17	17	25	21	31	22	17	23	22	62	20	31	23
2.	PLS 327	42	43	41	40	41	37	43	1	39	40	39	43	7	45	42	43
3.	AC 176	35	34	31	33	35	40	31	38	36	33	38	54	10	53	4	31
4.	AC 300	37	38	43	38	37	30	42	42	33	35	37	18	63	17	44	50
5.	MDU 2984	22	27	22	21	22	39	20	23	28	21	32	57	2	62	17	42
6.	LM 7	20	12	23	20	20	26	16	25	20	20	24	30	57	30	12	13
7.	LM 21	47	52	51	47	47	53	50	57	53	47	54	52	16	31	36	54
8.	LM 23	9	16	16	8	9	19	10	16	10	8	14	14	34	21	50	18
9.	LM 72	38	40	40	37	38	45	36	45	40	37	42	47	47	56	6	38
10.	LM 87	19	25	28	18	19	27	17	24	19	18	27	29	60	22	53	12
11.	PLS 266	60	59	50	60	60	60	60	61	61	60	61	61	9	61	57	59
12.	PLS 300	58	62	63	58	58	63	57	63	62	38	63	62	39	57	61	58
13.	PLS 311	34	41	38	32	33	42	34	35	31	32	41	53	5	54	49	30
14.	PLS 328	59	58	58	59	59	58	59	58	58	59	58	56	8	58	58	56
15.	PLS 337	30	29	27	28	30	31	27	28	32	28	31	38	6	32	18	34
16.	PLS 343	28	32	34	25	26	35	26	33	25	25	33	34	29	39	37	33
17.	AC 205	62	61	60	62	62	59	62	60	60	62	60	59	19	60	59	60
18.	ML 26/10/3	63	63	62	63	63	62	63	62	63	63	62	60	20	59	62	63
19.	LM 84	43	44	45	43	43	44	37	41	41	43	44	41	61	37	33	37
20.	LM 85	61	60	61	61	61	61	61	59	59	61	59	58	28	55	50	62
21.	KM 1	44	47	48	42	44	51	40	49	46	42	50	46	27	44	46	47
22.	PLS 298	31	35	35	31	31	34	29	29	29	31	34	36	50	35	34	22
23.	MDU 1946	55	56	47	52	55	57	56	47	56	52	56	63	1	63	53	61

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
24.	MDU 2106	51	51	50	50	51	48	51	50	48	50	49	45	30	47	43	46
25.	LM 14	10	15	13	9	10	20	9	13	8	9	15	25	22	27	23	7
26.	LM 15	21	24	24	22	21	24	23	22	18	22	22	24	58	29	21	24
27.	LM 24	18	26	26	16	18	32	15	26	10	16	28	40	24	41	40	15
28.	LM 170	56	55	57	56	56	52	55	53	52	56	55	48	32	43	55	33
29.	LM 244	54	48	53	55	54	50	54	54	54	55	51	32	54	25	26	55
30.	LM 252	23	28	29	23	23	29	24	32	37	23	30	28	44	33	22	32
31.	LM 459	57	57	56	57	57	55	58	56	57	57	57	55	3	51	52	57
32.	PLS 304	45	42	42	45	45	38	41	40	45	45	43	33	35	24	33	40
33.	PLS 322	36	36	36	35	36	36	33	43	37	35	36	37	52	46	7	35
34.	PS 414/1	46	49	49	46	46	47	47	46	42	46	47	44	36	48	56	39
35.	ML 26	48	53	54	48	48	54	46	55	50	48	53	50	25	38	45	51
36.	LM 35	13	13	15	13	13	13	13	17	12	13	13	10	55	18	25	19
37.	LM 254	53	50	52	54	53	46	53	51	49	54	48	35	51	36	39	52
38.	LM 263	40	45	44	39	39	49	38	44	44	39	46	51	12	40	47	45
39.	LM 279	50	54	55	49	49	56	45	52	47	49	52	49	56	49	54	49
40.	LM 361	25	37	37	24	25	41	22	37	24	24	35	39	46	50	48	26
41.	LM 366	52	46	46	53	52	43	52	48	51	53	45	42	33	42	24	48
42.	CO 2	29	30	30	27	29	28	28	34	26	27	29	31	26	34	30	25
43.	PLS 41	6	6	6	6	6	6	6	6	6	6	6	4	41	2	2	14
44.	M 1	11	9	9	11	11	7	7	8	13	11	9	12	21	10	28	8
45.	M 3	2	3	3	2	2	3	3	3	2	2	3	1	48	3	27	3
46.	M 9	5	5	5	5	5	5	5	5	5	5	5	5	17	4	8	5
47.	MS 8909	16	14	14	13	16	15	19	12	17	19	16	15	43	11	13	17
48.	LM 167	7	8	8	7	7	9	8	9	7	7	7	8	37	12	11	9
49.	LM 218	15	11	11	15	15	10	14	11	14	15	12	13	18	9	9	10

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
50. LM 2 22	1	1	1	1	1	1	1	1	1	1	1	2	13	1	3	1
51. LM 370	8	7	7	10	8	12	11	7	11	10	10	11	53	5	5	11
52. LM 449	33	20	18	36	34	16	39	19	33	36	19	20	11	16	20	29
53. NA 5	14	12	12	14	14	11	18	14	15	14	11	6	31	13	10	28
54. ML 1	32	19	20	34	32	18	35	21	34	34	20	17	38	14	15	27
55. LM 159	39	31	33	41	40	22	47	36	35	41	25	23	40	28	16	41
56. LM 152	49	39	39	51	50	33	49	30	55	51	40	27	45	6	51	44
57. LM 220	3	2	2	3	3	2	2	2	2	3	2	3	14	7	1	2
58. LM 228	12	10	10	12	12	8	12	10	9	12	8	9	39	15	10	6
59. LM 275	24	17	17	26	24	17	25	15	21	26	17	16	42	19	32	20
60. LM 360	26	21	21	29	27	15	32	20	23	29	18	19	15	23	41	21
61. LM 419	41	33	32	44	42	23	44	27	38	44	26	26	23	26	29	36
62. LM 469	27	18	19	30	28	21	30	18	30	30	21	21	49	8	38	16
63. CO 4	4	4	4	4	4	4	4	4	4	4	4	7	4	52	14	4
Genetic gain (in per cent)	6.07	4.35	6.28	7.53	6.48	9.17	10.62	9.89	7.89	7.53	10.2	8.23	0.23	3.03	1.75	4.23

selected through Smith's model of Discriminant Function by assigning importance only to the character "100 seed weight" among the eleven characters in greengram.

The expected genetic gain in selecting genotypes through Discriminant Function than through straight selection was only 0.23 per cent. Hence the set of assigned weights was not useful in Discriminating the best genotype.

The genotype LM 222 failed to take the first rank, when the weights were assigned as in set-15. This indicated that there was evidence in the data that LM 222 might not be the best genotype when importance was given only to the character "Number of branches" among the characters under study in greengram if selection of genotypes was to be done through Discriminant Function. The expected genetic gain in selecting genotypes through Discriminant Function than through straight selection was 1.75 per cent by assigning weights to plant characters in greengram as in set-15. The genotype LM220 took the first rank and the genotype LM 222 took the third rank when the assigned weights were as in set-15. This indicated that LM 220 was the best genotype and LM 222 was a better genotype.

Equal importance to all the characters was assigned in set-1. The weights in set-2, set-3, set-4 and set-5 were the values estimated from the data. The weights in set-6, set-7, set 8, set-9, set-10, set-11, set-12, set-13, set-14 set-15 and set-16 were the values assigned outside the data. In cases of equal weights (set-1) and the values assigned from the data (set-2 to set-5)

the genotype LM 222 was selected as the best genotype by Smith's model of Discriminant Function. The expected genetic gains in the above six sets of assigned weights ranged from 4.35 per cent to 7.53 per cent. This indicated that assigning equal weights and unequal weights from the data to select genotypes through Discriminant Function has given more or less the same expected genetic gain. In assigning 16 sets of different weights to the eleven characters in greengram the genotype LM 222 has been selected as the best genotype out of 63 genotypes through Discriminant Function in the following 13 sets viz. set-1, set-2, set-3, set-4, set-5, set 6, set-7, set-8 set-9, set 10, set-11, set-14 and set-16. Therefore in 81 per cent of the cases LM 222 has been selected as the best genotype through Discriminant Function. Even in the sets where LM 222 did not happen to be the best genotype, it was ranked closer to the first rank (second rank in set-12 and third rank in set-15). Therefore, LM 222 may be considered as the best genotype except when importance is given to the characters "Pods per plant" and "Number of branches" if Smith's model of Discriminant Function is used in selecting genotypes.

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