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Comparison of single seed descent, selective intermating and mass selection for seed size in greengram (*Vigna radiata* (L.) Wilczek)

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Summary. Three selection methods (single seed descent (SSD), mass selection and selective intermating) were applied simultaneously to a highly heterogeneous and broadly based population of greengram. Progeny developing after two cycles of selection were evaluated for yield and seven other economic characters. The relative efficacy of each selection method was judged on the basis of the number of high yielding progeny, mean yield of top 10% progeny, and mean of the highest yielding progeny. Selection after two cycles of selective intermating was found to be the best method for generating productive progeny although mass selection favouring smaller seeds was an equally efficient method. Both of these were found superior to SSD selection.

Key words: Greengram – *Vigna radiata* – SSD – Mass selection – Intermating

Introduction

Pedigree selection has commonly been used in breeding autogamous crops, including grain legumes. Although this method has been found quite useful for handling segregating materials, it has its drawbacks as have such methods as bulk selection, mass selection, early generation yield testing, etc. Alternative methods of selection, such as mass-pedigree, single seed descent (SSD), diallel selective mating and various forms of recurrent selection, have been proposed.

Many experiments have been conducted to compare the relative efficacy of these methods for developing productive genotypes of soybean (Voigt and Weber 1960; Empig and Fehr 1971; Leudders et al. 1973; Boerma and Cooper 1975), wheat (Knott and Kumar 1975; Tee and Qualset 1975), barley (Park et al. 1976), chickpea (Mishra et al. 1978; Dahiya et al. 1983; Bisen and Singh 1983; Bisen et al. 1985), pigeonpea (Green et al. 1980) and lentil (Haddad and Muehlbauer 1981). However, only limited information is available about the relative efficacy of these methods for developing high yielding genotypes of greengram, *Vigna radiata* L. Wilczek (Dahiya et al. 1983, 1984; Dahiya and Singh 1985).

In the present article we attempt to compare the relative efficacy of single seed descent (SSD), selective intermating (SI) and mass selection (MS) for seed size in greengram.

Materials and methods

A highly heterogeneous and heterozygous base population, developed from fifteen germplasm lines through multiple crossing, was advanced through SSD, SI and MS simultaneously. After two cycles of selection 68 progeny were developed through each method (Fig. 1 for detailed steps). These were evaluated for seed yield and its components during the rainy season, 1982 at Haryana Agricultural University, Hisar (29° 10′N and 75°46′E). For every entry, the mean of 5 plants was taken in each of the four replications for plant height, total pods per plant, clusters per plant, pods per cluster, and seed yield per plant. Pod length and seeds per pod were averaged over 20 pods in each replication. Days to flowering were recorded on a plot basis. Analysis of variance was done using the mean values suggested by Panse and Sukhatme (1978). The comparative efficacy of the selection methods was adjudged in terms of the number of productive lines evolved through each method as well as the productivity of these high yielding lines.

Results and discussion

A condensed form of analysis of variance for all eight characters are given in Table 1 for SSD, SI and MS. Highly significant differences among the 68 progeny developed through SSD were observed for all characters except seeds per pod. They also differed from the

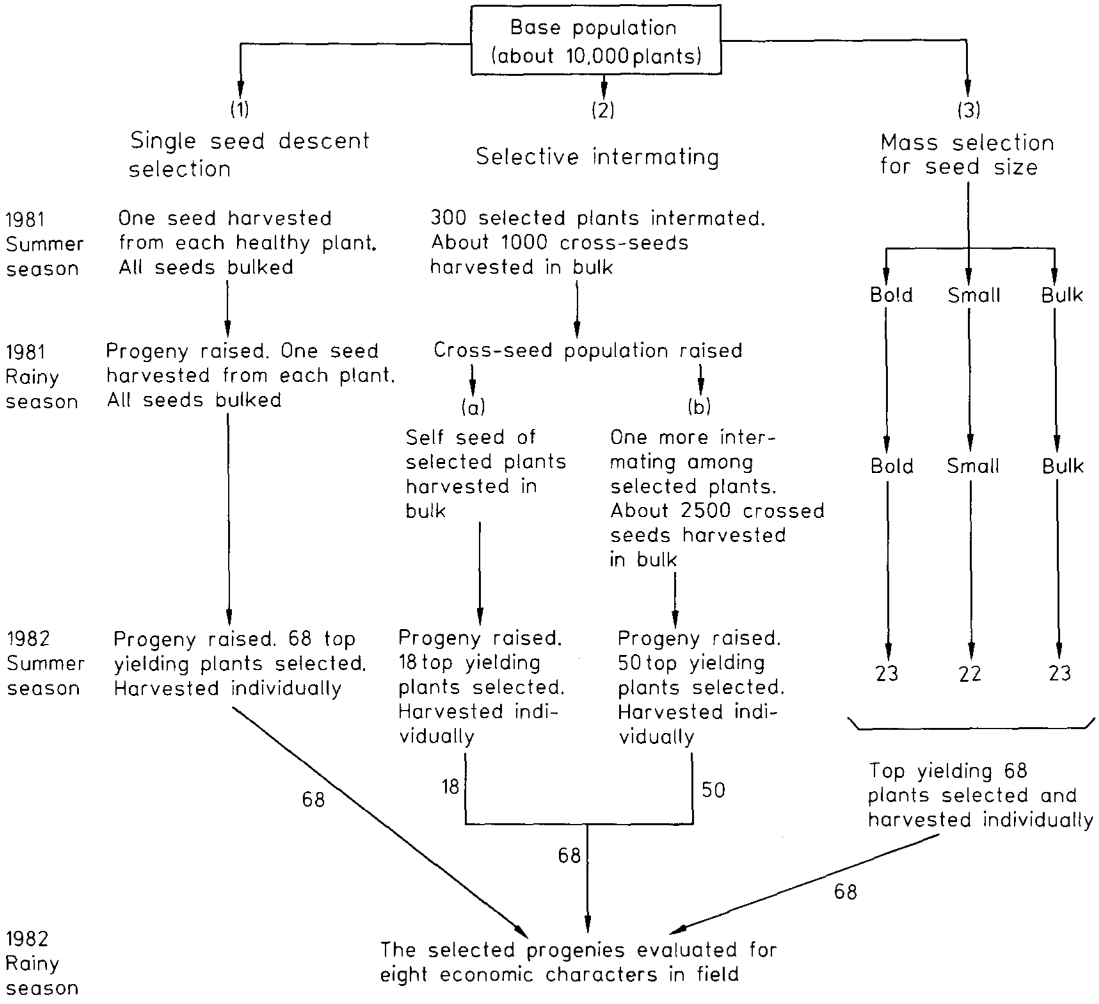

Fig. 1. Selection scheme

checks (K 851 and T 44) for days to 50% flowering, plant height, pods per plant and pods per cluster. The differences between the checks and progeny were fairly low for pod length and seeds per pod. Table 1 also shows significant values of mean squares for all eight characters among progeny developed through SI. Except for pods per cluster, pod length and seeds per pod, the progeny also differed from the check varieties. Progeny developed through selection after one cycle of selective intermating (one-cycle progeny) showed differences among themselves for all characters except seeds per pod and seed yield per plant. Progeny developed through selection after two cycles of SI (two-cycle progeny) were found to be significantly different from each other for all characters. These results indicate that two cycles of intermating are more effective than a single cycle in creating variability for characters like seeds per pod and seed yield per plant.

Progeny obtained after two cycles of MS had significant values of mean squares for only days to flowering, plant height, pods per plant and clusters per plant (Table 1). For the remaining characters there were no significant differences. They differed from the checks, however, for all characters except pod length. Porgeny developing from bold seeds differed among themselves for days to flowering and plant height only while progeny originating from smaller seeds had significant differences for days to flowering, pods per plant and clusters per plant. Similarly, progeny developing from bulk (unselected mass) seed were significantly different from each other for all characters except seeds per pod and seed yield per plant. Progenies of bold, small and bulk group differed from each other for days to flowering, pods per plant, clusters per plant and seed yield per plant.

The comparative efficacy of these three selection methods was judged on the basis of the number of productive progeny obtained through each method. Mean yield of the top 10% of the progeny and mean of the highest yielding progeny were two criteria used for

Table 1. Mean squares for eight characters in greengram progeny developed through SSD, selective intermating and mass selection for seed size (condensed form)

Selection method	Source of variation	d.f.	Mean squares 1	2	3	4	5	6	7	8
Single seed descent selection	Progeny	67	54.30**	358.18**	91.40**	6.99**	0.58**	0.23*	0.99	8.20**
	Checks vs progeny	1	142.80**	2,221.25**	449.13**	13.14	1.82*	0.02	0.51	8.49
	Error	207	4.20	68.35	46.34	4.08	0.37	0.15	0.80	4.07
Selective intermating	Progeny	67	36.15**	316.64**	102.91**	7.01*	0.66**	0.28**	1.17**	6.93**
	One-cycle progeny	17	34.97**	456.13**	109.32**	8.05*	1.06**	0.39**	0.30	4.18
	Two-cycle progeny	49	25.00**	201.63**	102.04**	5.64**	0.52**	0.25**	3.50**	7.92**
	One vs two progeny	1	602.39**	3,580.97**	36.45	0.03	0.77	0.02	4.57*	4.88
	Checks vs progeny	1	30.86*	449.88**	1,037.80**	71.74**	0.61	0.01	0.72	50.86**
	Error	207	5.28	75.68	50.02	4.90	0.41	0.16	0.70	3.51
Mass selection for seed size	Progeny	67	48.41**	237.49**	133.43**	7.29**	0.37	0.22	0.74	5.41
	Bold	22	47.08**	269.07**	59.37	4.84	0.34	0.21	1.02	3.74
	Small	21	24.41**	56.11	198.93**	7.15*	0.23	0.17	0.71	5.02
	Bulk	22	67.03**	380.49**	100.10**	9.01**	0.53*	0.27*	0.54	6.30
	Between groups	2	110.18**	221.75	626.87**	16.64*	0.28	0.22	0.04	18.23**
	Checks vs progeny	1	399.42**	3,219.02**	957.45**	53.07**	2.45**	0.01	6.42**	49.92**
	Error	207	8.06	76.27	48.33	4.40	0.31	0.17	0.67	4.23

*, ** Significant at $P = 0.05$ and 0.01, respectively

1: Days to 50% flowering; 2: Mature plant height (cm); 3: Pods per plant; 4: Clusters per plant; 5: Pods per cluster; 6: Pod length (cm); 7: Seeds per pod; 8: Seed yield per plant (g)

Table 2. Comparison of three selection methods for seed yield per plant in greengram progeny

Sr. no.	Selection method	Total no. progeny tested	% of progeny surpassing better check	Mean yield of top 10% progeny (g/plant)	Mean of the highest yielding progeny (g/plant)
1.	Single seed descent	68	10.29	8.81	9.57
2.	Selective intermating	68	30.88	8.84	9.90
	(a) One-cycle progeny	(18)	(22.22)	(7.83)	(8.25)
	(b) Two-cycle progeny	(50)	(34.00)	(9.10)	(9.90)
3.	Mass selection for seed size	68	30.88	7.96	8.57
	(a) Bold seeded	(23)	(21.74)	(7.49)	(7.97)
	(b) Small seeded	(22)	(45.45)	(8.30)	(8.57)
	(c) Bulk seeded	(23)	(26.09)	(7.42)	(7.58)

comparison. SI and MS were equally efficient selection methods in producing high yielding lines. Both of these methods produced equal numbers (30.8%) of such families (Table 2). SSD could generate only 10.29% highly productive families. Under MS, small seeded families produced the highest number (45.4%) of productive lines. Thirty-four per cent of the progeny developing after two cycles of intermating among selected plants were found to be productive. In this respect, therefore, MS favouring smaller seeds is a more effective method of selection. Two cycles of SI are better than one cycle for this purpose. The progeny developed through SI, particularly after two cycles of intermating, were more productive (mean 9.10 g/plant) than those produced through SSD (8.81 g/plant) and MS (7.96 g/plant). Even small seeded progeny (8.30 g/plant) could not compete with them in productivity. The highest yielding progeny (9.90 g/plant) of the experiment was developed through two cycles of SI.

These results indicate that two cycles of SI, and MS favouring smaller seeds are two very good selection methods for developing a higher number of productive families in greengram material. Although SI requires some emasculation and crossing work, it has a better chance of obtaining good segregants/recombinants as compared to the MS. Mass selection was found to be superior to pedigree selection and selection for yield per se (Dahiya et al. 1984) in greengram. Recurrent selection based on two cycles of intercrossing was also found to be better than the mass and pedigree selection methods in breaking undesirable linkages between yield and quality of cotton (Singh and Singh 1983). MS, on the other hand, is a comparatively easier and faster method for developing productive lines. Though some excellent progeny were selected through SSD, it is not as efficient as SI and MS, mainly because it yielded only a small number of productive families. However, SSD is economical and the most rapid method of generation advancement. In simulation studies, the SSD has been found quite effective at very low (10%) heritability (Casali and Tigchelaar 1975) and also retained more genetic variability (Haddad and Muehlbauer 1981). SSD selection has also been reported to be comparable to, or even better than, such traditional methods as pedigree, bulk, and/or early generation yield testing, for the development of superior pure lines of soybean, wheat, bengal gram, pigeonpea and lentil.

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