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A COMPARISON OF TWO BREEDING PROCEDURES IN TWO CROSSES OF MUNGBEAN (*VIGNA RADIATA* (L.) WILCZEK)

R. P. SINGH, B. D. SINGH AND R. N. SINGH

Department of Genetics and Plant Breeding
Institute of Agricultural Sciences, Banaras Hindu University, Varanasi 221005

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ABSTRACT

Two breeding methods, single-seed descent (SSD) and bulk (B) were compared in the segregating generations of two crosses (HG 19 x Black Neelalu (BN) and ML 5 x BN) of mungbean, *Vigna radiata* (L.) Wilczek. Yield trials were grown in F_3, F_4 and F_5 generations. There was no evidence for a directed shift in mean performance for days to maturity, No. of branches and seeds/pod. There were sporadic differences in variance and CV estimates of bulk and SSD populations most likely due to sampling error. The estimates of heritability and genetic advance were moderate to high, indicating that improvement through selection would be feasible. There was no consistent difference in the expected genetic advance from the three SSD and the bulk populations.

Key words: *Vigna radiata*, mungbean, single-seed descent, bulk method, genetic advance.

The bulk breeding method allows handling of a large number of crosses with relatively little effort. Studies have shown that natural selection exerts dynamic influence on the composition of bulk population in each generation, producing changes in gene frequencies [1, 2]. Often natural selection can be in direct conflict with the breeder's objectives to avoid which the single-seed descent (SSD) method has been proposed as a modification of the bulk scheme [3–5]. The SSD method, despite the small population size, is expected to maintain more genetic variability than the bulk method.

The present study aims to compare the effects of single-seed descent and bulk methods to analyse certain genetic parameters in the segregating generations of two crosses in mungbean.

MATERIALS AND METHODS

The material comprised F_2 seeds derived from two mungbean crosses, namely, HG 19 x Black Neelalu (BN) and ML 5 x BN. The F_2 seeds from each cross were divided into four groups of 500 seeds each and designated as bulk (B), SSD_1 (single-seed descent-1), SSD_2 and SSD_3; the three SSD schemes differed in terms of the spacings used for maintaining these populations, but in the yield trials uniform spacing was provided for all the populations.

The spacings used for maintaining the SSD_1, SSD_2 and SSD_3 and B populations were 15 x 5, 15 x 3, 10 x 3 and 30 x 5 cm, respectively, which were also maintained in the subsequent generations (F_3 and F_4). All plants in B population were harvested in bulk and a random sample of about 500 seeds was used to raise the next generation. The remaining seeds from the bulk population in each generation were used to conduct yield trial in the next cropping season. In view of heavy plant loss, each SSD population was reinitiated from 300 F_2 seeds, while in F_4 and F_5, 3–4 seeds from each plant of the previous generation were sown per hill and then thinned to one plant per hill just before flowering [6]. The yield trials were planted from the remaining seeds of each population with the uniform spacing of 30 x 10 cm for each population.

The yield trial in F_3 was planted according to a nested design with three replications using cv. K 851 as check. Each population had a plot of 3 m long 5 rows, and spacings 30 x 10 cm. Twenty five random plants from the central three rows were used to record observations on days to maturity, number of branches and seeds per pod. The yield trials were planted using F_4 (spring) and F_5 (kharif) seeds from these populations in the same manner. Plot means were used for analysis of variance according to a 2-factor nested design, while data on individual plants of each population from all the replications were taken for determining variances, standard deviations (SD) and coefficient of variation. Broad sense heritability (%) and genetic advance (GA), as per cent of mean, were estimated according to the formulae proposed by Burton and Devane [7] and Johnson et al. [8], respectively.

RESULTS AND DISCUSSION

MEAN PERFORMANCE

The mean performance of the four different populations (B, SSD_1, SSD_2 and SSD_3) did not differ significantly either from the check or among themselves for days to maturity in F_3 of both crosses. In F_4, three SSD populations matured significantly later than the check variety in cross HG 19 x BN, while SSD_2 and bulk were significantly later than the check in cross ML 5 x BN. In F_5, the four populations of both crosses were significantly later than the check. However, the different populations were comparable with each other in the three generations of both the crosses. The number of branches and seeds/pod did not differ significantly either from the check or among the populations in the three generations of the two crosses (Table 1). Clearly, the means of the four populations did not differ from each other for any of the traits, indicating that there was no directed shift in either bulk or SSD populations. This is surprising, since the SSD populations are expected to show a much larger sampling error than the bulk populations due to the drastic plant loss in the SSD populations. One reason for this expectation not being met may be the large environmental influence. These findings are comparable to earlier reports [9–14].

VARIABILITY

Estimates of variance and CV from the four populations were higher than those from the check for number of branches and seeds/pod in both the crosses over three generations, except for F_3 bulk and SSD_1 of cross HG 19 x BN. The estimates of variance and CV for the SSD populations were either equal to or higher than those from the bulk population, except in F_4 and F_5 of the cross HG 19 x BN (No. of branches) and F_3 of cross ML 5 x BN (No. of branches) (Table 2). Variances and CV declined in F_4, whereas the F_3 and F_5

Table 1. Mean performance for certain traits of different populations from two crosses in mungbean

Cross	Population	Days to maturity			No. of branches			Seeds per pod		
		F_3	F_4	F_5	F_3	F_4	F_5	F_3	F_4	F_5
HG 19 x BN	K 851 (check)	81.7	67.7	68.7	3.3	2.1	3.3	9.5	9.6	10.3
	Bulk	79.0	72.3	73.0	3.7	2.2	4.4	9.6	9.5	10.7
	SSD$_1$	80.3	78.0	72.7	3.7	2.3	3.6	9.5	9.5	10.1
	SSD$_2$	82.0	75.0	73.0	3.9	2.2	3.1	9.4	9.1	9.9
	SSD$_3$	80.7	77.0	73.0	3.6	2.3	3.8	9.5	9.5	10.0
ML BN	K 851 (check)	80.7	69.0	67.3	2.9	2.1	3.3	8.7	9.5	10.6
	Bulk	80.7	76.7	72.7	3.6	2.2	3.6	9.5	9.1	10.3
	SSD$_1$	81.7	71.3	72.7	3.2	1.9	3.3	9.6	9.1	10.6
	SSD$_2$	80.7	77.0	73.3	3.5	2.4	3.6	9.1	9.1	10.6
	SSD$_3$	82.0	70.0	73.0	3.5	2.4	3.9	9.3	9.3	10.6
C.D., 5%		NS	5.0	1.6	NS	NS	NS	NS	NS	NS

Table 2. Variance and CV (%) for certain traits estimated from different populations of two crosses in mungbean

Cross	Population	F_3		F_4		F_5	
		variance	CV	variance	CV	variance	CV
		Number of branches					
HG 19 x BN	K 851 (check)	1.1	31.9	0.10	14.3	1.09	31.6
	Bulk	1.3	30.8	1.50	54.2	3.48	42.3
	SSD$_1$	1.3	31.3	0.90	41.5	1.91	38.0
	SSD$_2$	2.1	37.0	1.00	44.4	1.43	38.3
	SSD$_3$	1.4	33.3	1.20	47.5	2.36	40.9
ML 5 x BN	K 851	1.1	35.9	0.17	19.6	1.02	30.6
	Bulk	2.3	41.5	1.37	54.2	1.86	37.8
	SSD$_1$	1.7	40.9	1.05	54.5	2.45	47.7
	SSD$_2$	1.8	38.2	1.69	53.7	2.08	40.1
	SSD$_3$	1.3	32.2	1.59	51.4	2.82	43.2
		Seeds per pod					
HG 19 x BN	K 851 (check)	1.40	12.5	0.78	9.2	1.03	9.9
	Bulk	2.83	17.6	1.63	13.5	1.76	12.4
	SSD$_1$	3.30	19.2	1.13	11.9	3.42	18.3
	SSD$_2$	2.49	16.8	1.72	14.4	2.49	15.9
	SSD$_3$	1.97	14.7	1.08	11.0	3.00	17.3
ML 5 x BN	K 851 (check)	2.09	16.6	0.91	10.0	0.24	4.6
	Bulk	2.62	17.0	1.75	14.6	1.76	12.9
	SSD$_1$	3.40	19.3	1.63	14.1	1.20	10.4
	SSD$_2$	3.90	21.7	1.83	14.9	2.38	14.5
	SSD$_3$	2.63	17.4	1.52	13.3	1.61	12.0

estimates were comparable to each other; this was, most probably, due to environmental effects and not due to a genetic change in the population. Further, the differences in the estimates of variance and CV in the bulk and SSD populations were sporadic and would be due to sampling error.

HERITABILITY AND GENETIC ADVANCE

The estimates of heritability for number of branches ranged from 15.4 to 93.3 in the bulk and the three SSD populations of both the crosses, whereas, those for genetic advance (GA) varied from 9.5 to 106.7 7% of mean. For seeds/pod, heritability, ranged from 20.2 to 89.9 and GA from 6.3 to 27.0% of mean (Table 3). There was considerable variation among the estimates of heritability and GA.. Very low heritability estimates were obtained only in a few cases and in only one generation for one or the other population. Obviously, such estimates were due to sampling error/environmental effects. The moderate to high estimates of heritability indicate that an improvement for number of branches and seeds/pod through selection in these populations would be feasible.

The estimates of CV were generally more or less comparable in the different populations of a cross, particularly when compared over generations. This also shows that there was no detectable loss in variability in the SSD populations in spite of drastic plant loss in them [6]. These findings are in agreement with those of the previous investigations. Empig and Fehr [9] reported that the differences in genetic variances among SSD_1, restricted-cross

Table 3. Estimates of broad sense heritability (H) and genetic advance (GA) as percentage of mean for certain traits in different populations derived from two crosses in mungbean

Cross	Population	F_3		F_4		F_5	
		H	GA	H	GA	H	GA
		Number of branches					
HG 19 x BN	Bulk	15.4	9.5	93.3	106.7	68.7	60.3
	SSD_1	15.4	9.5	88.9	75.6	42.9	34.0
	SSD_2	47.6	36.7	90.0	84.3	23.8	19.1
	SSD_3	21.4	14.2	91.7	90.3	53.8	45.0
ML 5 x BN	Bulk	52.2	45.1	87.6	96.4	45.2	35.1
	SSD_1	35.3	29.4	83.8	93.3	58.4	56.7
	SSD_2	38.9	30.8	89.9	100.4	51.0	42.1
	SSD_3	15.4	10.1	89.3	96.3	63.8	56.8
		Seeds per pod					
HG 19 x BN	Bulk	50.5	18.4	52.1	14.4	41.5	10.7
	SSD_1	57.6	22.8	31.0	7.1	69.9	26.4
	SSD_2	43.8	15.2	54.7	16.3	58.6	19.4
	SSD_3	28.9	8.8	27.8	6.3	65.7	23.5
ML 5 x BN	Bulk	20.2	7.0	48.0	14.4	86.4	22.8
	SSD_1	38.5	15.7	44.2	12.7	80.0	17.0
	SSD_2	46.4	20.6	50.3	15.3	89.9	27.0
	SSD_3	20.5	7.5	40.1	10.9	85.1	21.0

bulk and maturity-group bulk populations in three crosses of soybean were not consistent. But Tee and Qualset [15] reported that 5 out of 6 SSD populations of Hybrid I in wheat had larger components of genotypic variance for heading date than the bulk populations, and there was a tendency of increased variance with each advancing generation in both the procedures, and the two methods did not indicate a consistent difference in the expected GA. Knott and Kumar [16] observed that the heritability values (regression of F_5 means over F_3 means) were fairly similar in early generation yield trials and single seed descent.

REFERENCES

1. C. R. Adair and L. W. Jones. 1946. Effects of environment on the characteristics of plants surviving in bulk hybrid populations of rice. J. Amer. Soc. Agron., **38**: 708–716.
2. C. A. Suneson and H. Stevans. 1953. Studies with bulk hybrid populations of barley. U. S. Dept. Agric. Tech. Bull.: 1067.
3. C. H. Goulden. 1939. Problems in plant selection. *In*: Proc. 7th Intern. Genet. Congr. (ed. R. C. Burnett). Cambridge Univ. Press, Edinburgh: 132–133.
4. J. E. Grafius. 1965. Short cuts in plant breeding. Crop Sci., **5**: 377.
5. C. A. Brim. 1966. A modified pedigree method of selection in soybean. Crop Sci., **6**: 220.
6. R. P. Singh, B. D. Singh and I. S. Singh. 1990. Plant loss in SSD populations of mungbean (*Vigna radiata* (L.) Wilczek). Indian J. Genet., **50**(1): 12.
7. G. W. Burton and E. W. Devane. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*). Agron. J., **45**: 478–481.
8. H. W. Johnson, H. F. Robinson and R. E. Comstock. 1955. Estimates of genetic and environmental variability in soybeans. Agron. J., **42**: 314–318.
9. L. R. Empig and W. R. Fehr. 1971. Evaluation of methods for generation advance in bulk hybrid soybean populations. Crop Sci., **11**: 51–54.
10. H. R. Boerma and R. L. Cooper. 1975. Comparison of three selection procedures for yield in soybeans. Crop Sci., **15**: 225–229.
11. M. A. Rahman and P. N. Bahl. 1985. Comparison of single-seed descent, mass selection and random bulk method in chickpea. Indian J. Genet., **45**: 186–193.

12. S. J. Park, E. J. Walsh, E. Reinbergs, L. S. P. Song and K. J. Kasha. 1976. Field performance of doubled haploid barley lines in comparison with lines developed by the pedigree and single-seed descent. Can. J. Plant Sci., **56**: 467–474.

13. I. S. Pawar, R. S. Paroda, M. Yunus and S. Singh. 1985. A comparison of three selection methods in two wheat crosses. Indian J. Genet., **45**: 345–353.

14. N. I. Haddad and F. J. Muehlbauer. 1981. Comparison of random bulk population and single-seed methods for lentil breeding. Euphytica, **30**: 643–651.

15. T. S. Tee and C. O. Qualset. 1975. Bulk populations in wheat breeding: comparison of single-seed descent and random bulk methods. Euphytica, **24**: 393–405.

16. D. R. Knott and J. Kumar. 1975. Comparison of early generation yield testing and a single-seed descent procedure in wheat breeding. Crop Sci., **15**: 295–299.