COMPARISON OF BREEDING METHODS FOR IMPROVEMENT OF YIELD AND ITS COMPONENTS IN GRASSPEA

JIBAN MITRA* AND R. B. MEHRA

Division of Genetics,
Indian Agricultural Research Institute, New Delhi 110 012

ABSTRACT

Three breeding methods, viz., pedigree, single seed descent and random bulk were compared for their relative efficiency in terms of change in population mean in F_4 over F_3 and in F_5 over F_3 as well as F_4 generations for yield and its components in two crosses of grasspea, namely, RED × P 28 and RED × EC 242692. In general, single seed descent method proved to be superior to random bulk and pedigree methods in showing maximum changes in population mean for different characters, whereas random bulk method showed the worst performance in this regard.

Key Words : Grasspea; *Lathyrus sativus* L., breeding methods, pedigree, single seed descent, random bulk, population mean

Several breeding methods such as pedigree, mass-pedigree, bulk, single seed descent and diallel selective mating system have been proposed for handling segregating generation of self-pollinated crops and these methods have their merits and demerits [1, 2]. However, the information on valid comparison of these different alternative methods is scanty and particularly in grasspea, no report on generation advancement through any breeding method is available. Again, the change in population mean in advanced generations would be an important parameter for comparing the efficiency of different breeding methods. In view of these, the present experiment was conducted to compare the relative efficiency of three breeding methods, viz., pedigree, single seed descent and random bulk for change in population mean in F_4 over F_3 and F_5 over F_3 as well as F_4 generations in grasspea.

MATERIALS AND METHODS

Three breeding methods, viz., pedigree, single seed descent and random bulk were followed to advance two crosses of grasspea, namely, RED × P 28 and RED

*Present address: Western Regional Research Station, Indian Grassland and Fodder Research Institute, Avikanagar 304 501

× EC 242692 from F_2 to F_5 generations during the period from 1992-93 to 1994-95 at Indian Agricultural Research Institute (IARI), New Delhi and IARI offseason nursery, Dharwad, Karnataka. All the three methods were started from the same F_2 population of 500 genotypes in each cross. In pedigree method, exercising 10% selection pressure on F_2, 50 phenotypically superior plants were selected to raise individual plant progenies. In F_3, the family size was kept at 10 plants and between-family and within-family selection were exercised with selection intensity of 50% and 20%, respectively which amounted to a selection intensity of 10% on population basis. Thus, 25 superior families and two superior-most plants from each superior family were chosen, thereby making a total of 50 plants. The same procedure was repeated to advance the crosses up to F_5 generation. Single seed descent method was followed by collecting a single pod from each of 500 F_2 plants to raise F_3 generation and the population was advanced to F_5 generation following the same procedure. The one-half of seeds harvested from all the F_2 individual plants (including those selected for pedigree method) was composited and a random sample of seeds was taken to raise F_3 generation in random bulk method. The same procedure was followed up to F_5 generation. However, a population of 500 plants was maintained in each generation for each method. The data for yield and its components were recorded on all 500 single plants in F_3, F_4 and F_5 populations for each cross in each method. The change in population mean (%) of F_4 and F_5 over F_3 and F_5 over F_4 was estimated as difference between mean of succeeding generation and that of preceeding generation expressed in percentage of mean of preceeding generation.

RESULTS AND DISCUSSION

The change in population mean from F_3 to F_4 to F_5 and F_3 to F_5 in the two crosses under different breeding methods are depicted in Table 1. The change in mean of F_4 from F_3 population in both the crosses was higher in single seed descent method as compared to random bulk and pedigree methods for all the characters except seeds per pod in RED × P 28. The same trend was observed in the change in F_5 population mean over F_3 and F_4. Single seed descent was the best among the three methods. However, the magnitude in change in mean of F_5 over F_4 was less than that of F_5 over F_3. Among the traits studied, pods per plant showed, in general, the best performance in change in population mean. In contrast, very negligible change and sometimes, in negative direction was observed in seeds per pod. In general, pedigree method was intermediate between single seed descent and random bulk, whereas random bulk showed the worst performance in changing the population mean. Actually, random bulk method faces a major problem of sampling error during

Table 1. Changes in population mean for yield and its components under different breeding methods in F_4 and F_5 populations of two crosses of grasspea

Generations / Characters	Change in population mean (%)					
	F_4 over F_3 (%)		F_5 over F_4 (%)		F5 over F_3 (%)	
	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2
Single seed descent						
Pods/plant	32.16	26.79	17.23	9.87	54.94	39.30
Seeds/pod	6.01	8.13	−1.56	−0.94	4.30	7.19
100-seed wt. (g)	7.16	7.09	1.86	−0.27	10.81	1.44
Yield/plant (g)	25.87	19.03	14.74	8.79	44.44	29.45
Random bulk						
Pods/plant	9.20	6.19	−0.14	0.14	9.04	6.36
Seeds/pod	3.16	1.37	2.21	0.63	4.98	1.64
100-seed wt. (g)	1.23	0.91	0.59	2.61	1.56	3.51
Yield/plant (g)	4.02	2.41	−3.59	6.58	0.29	9.19
Pedigree						
Pods/plant	21.15	17.81	6.61	4.86	27.64	23.92
Seeds/pod	7.07	3.14	2.55	1.92	9.90	5.28
100-seed wt. (g)	5.92	4.03	2.45	2.10	8.56	6.20
Yield/plant (g)	17.61	13.42	9.01	8.94	28.19	23.59

Cross 1: RED × P 28., Cross 2: RED × EC 242692

generation advancement [3]. Instead of sowing all the material, a sample of seeds was taken to advance the generation which could not represent the previous generation. This problem of sampling might have caused genetic drift and losses of some superior genotypes resulting in poor performance of random bulk method in change in population mean, whereas the ineffectiveness of pedigree method may be attributed to the inefficiency of selection on a single F_2 plant basis due to genotype × environment interaction and non- additive gene action [4]. The selection in F_2 population might have excluded some lines which would have performed well in advanced generations if selected. However, the inadequacy of directional selection in pedigree method was also reported by Allard and Hansche [5]. The higher change in population mean in

desirable (positive) direction in single seed descent method may be due to change in gene and genotypic frequency as a result of natural selection aiding in desirable direction [6]. Again, the higher change in population mean indicates the higher probability of obtaining superior genotypes through selection in advanced generations. Thus, it may be inferred that single seed descent method is superior to pedigree and random bulk methods in evolving superior genotypes in advanced generations in self pollinated crops.

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