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COMPARISON OF THREE BREEDING METHODS FOR TRANSGRESSIVE SEGREGATION FOR YIELD AND ITS COMPONENTS IN GRASSPEA (*LATHYRUS SATIVUS* L.)

JIBAN MITRA* AND R. B. MEHRA

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

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ABSTRACT

The F_2 populations of 2 crosses of grasspea viz. 'RED' × 'P 28' and 'RED' × 'EC 242692' were advanced by following single seed descent, random bulk and pedigree methods up to F_5 generation during the period from 1992-93 to 1994-95 at Indian Agricultural Research Institute, New Delhi and IARI offseason nursery, Dharwad, Karnataka. The F_5 populations of these crosses were evaluated for comparing the relative efficiency of these 3 breeding methods in obtaining transgressiv segregants for yield and its components. The single seed descent method proved to be superior to random bulk and pedigree methods in producing greater frequency of transgressive segregants in F_5 generation for yield and its components, whereas the random bulk method showed a poor performance in this regard.

Key words: Grasspea, *Lathyrus sativus* L., transgressive segregation, yield components, single seed descent, random bulk, pedigree method

A breeder is more likely to be concerned with the production of transgressive segregants from a cross through a breeding method. Although transgressive segregants include lines which fall outside the range of performance of either parent, but only those being superior to better parent are of practical value. Single seed descent, random bulk and pedigree are the most commonly used conventional breeding methods for autogamous crops. The information on utility of different methods in obtaining transgressive segregants is scanty and particularly lacking in grasspea (*Lathyrus sativus* L.), where no report on generation advancement through any breeding method is available. The present investigation was carried out to compare 3 breeding method, viz. single seed descent, random bulk and pedigree in producing desirable transgressive segregants for yield and its components in grasspea.

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* Scientist, Western Regional Research Station (Indian Grassland and Fodder Research Institute), Avikanagar, 304 501, Rajasthan.

MATERIALS AND METHODS

The F_2 populations of 2 crosses of grasspea, 'RED' × 'P 28' and 'RED' × 'EC 242692' were advanced through single seed descent, random bulk and pedigree methods to F_5 generation during the period from 1992-93 to 1994-95 at Indian Agricultural Research Institute (IARI), New Delhi and IARI offseason nursery, Dharwad, Karnataka. However, F_2, F_3, F_4 and F_5 were grown in New Delhi during winter season of 1993-94 and Dharwad during rainy season of 1994-95, respectively. For single seed descent method, from a space-planted F_2 population of 500 genotypes in each cross, a single pod from each plant was collected and bulked seeds were sown to raise F_3 generation. The same procedure was followed to advance the 2 crosses up to F_5. In pedigree method, exerci [illegible]0% selection pressure on the same F_2 population, 50 phenotypically superior plants were selected to raise the individual plant progenies in F_3 generation. However, the family size was kept at 10 plants. In the F_3 generation, 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 2 superior-most plants from each superior family were chosen, thereby making a total of 50 plants. Population was advanced up to F_5 generation following the same procedure. The one-half of seeds harvested from all the F_2 individual plants was composited from which a random sample was taken to raise F_3 generation in random bulk method and this practice was repeated to advance the crosses up to F_5 generation. However, a population of 500 plants was maintained in each generation for each method. The frequency of transgressive segregants in positive direction for yield and its components in F_5 generation of 2 crosses was counted in each method.

RESULTS AND DISCUSSION

The single seed descent method resulted in the highest number of transgressive segregants for all the characters except seeds/pod in the cross 'RED' × 'P 28' and 100-seed weight in 'RED' × 'EC 242692' for which random bulk and pedigree methods, respectively showed the highest number of transgressive segregants (Table 1). The pedigree method, in general, ranked second in showing transgressive segregation for different characters, whereas the random bulk method performed the worst in this regard. The lines showing transgressive segregation for yield were critically examined whether these transgressants were showing transgressive segregation for other traits also (Table 2). Most of the transgressants for yield showed transgressive segregation

Table 1. Frequency of desirable transgressive segregants for yield and its components in two F_5 populations of two crosses of grasspea advanced by three breeding methods

Cross / Character	'RED' × 'P 28'			'RED' × 'EC 242692'		
	Breeding method					
	SSD	RB	PD	SSD	RB	PD
Pods/plant	114 (22.8)	39 (7.8)	56 (11.2)	141 (28.2)	55 (11.0)	84 (16.8)
Seeds/pod	16 (3.2)	36 (7.2)	12 (2.4)	19 (3.8)	17 (3.4)	10 (2.0)
100-seed weight	59 (11.8)	25 (5.0)	41 (8.2)	47 (9.4)	16 (3.2)	63 (12.6)
Yield/plant	91 (18.2)	21 (4.2)	43 (8.6)	69 (13.8)	19 (3.8)	56 (11.2)

SSD- Single seed descent, RB - Random bulk, PD-Pedigree., Figures in parentheses denote the percentage from a of total 500 plants in each method

for pods/plant indicating that pods/plant is a major yield contributing component. However, some such lines also showed transgressive segregation for seeds/pod and 100-seed weight, but in low frequency. No transgressant for yield was transgressant either for both seeds/pod and 100-seed weight or for all the three yield components, viz. pods/plant, seeds/pod and 100-seed weight simultaneously.

The ineffectiveness of pedigree method in producing transgressive segregation for yield and its components may be attributed to the genetic drift which is an important factor in determining probability of increase of desirable alleles within a single family. The separation of hybrid gene pool into a large number of families during generation advancement through pedigree method might have limited the opportunity of improvement within the family and reduced the chance of obtaining desirable gene combination because some potential lines may be lost owing to genetic drift in small families [2]. Furthermore, though selection in early generation for highly heritable character may be effective but there is doubt as to the effectiveness of selection for yield due to genotype × environment interaction [2, 3]. The random sample of seeds taken during generation advancement through random bulk method could not ensure the representation of previous generation and this procedure of sampling might have caused losses of some agronomically desirable individuals

Table 2. **Frequency of transgressive segregants for yield showing transgressive segregation for other traits in F_5 populations of two crosses of grasspea advanced by three breeding methods**

Cross	'RED' × 'P 28'			'RED × 'EC 242692'		
	Breeding method					
Character for which lines were transgressant	SSD	RB	PD	SSD	RB	PD
Only pods/plant	61	5	33	37	10	34
Only seeds/pod	6	11	3	3	6	5
Only 100-seed weight	17	5	5	14	2	12
Pods/plant & Seeds /pod	1	-	2	2	1	-
Pods/plant & seed weight	6	-	-	13	-	5
Total number of transgressive segregants for yield	91	21	43	69	19	56

SSD-Single seed descent, RB-Random bulk, PD-Pedigree

with favourable gene combination. However, seeds/pod was favourably affected by random bulk method concommitant with reduced seed size as small seeds might have a higher probability of being selected in random sample. Natural selection through intergenotypic competition and fecundity may also be a factor for reduced performance of random bulk [4]. The genetic drift and reduced variability in single seed descent method due to plant losses resulting from lack of germination of single seed, plant death or failure of some plants to produce at least one seed have also been reported [5-7]. But in this experiment, taking a single pod instead of single seed from each plant ensured the representation of previous generation and this might have reduced genetic drift and maintained a high variability resulting in higher number of transgressive segregants in single seed descen method. Thus, single seed descent method appears to be more attractive to plant breeder involved with grain legumes in general and grasspea in particular as compared to random bulk and pedigree methods.

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