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# Comparison of mass, F<sub>2</sub>-derived family, and single-seed-descent selection methods in an interracial population of common bean

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Urrea, C. A. and Singh, S. P. 1994. Comparison of mass,  $F_2$ -derived-family, and single-seed-descent selection methods in an interracial population of common bean. Can. J. Plant Sci. 74: 461–464. Knowledge of comparative effectiveness of different selection methods is necessary for identification of superior genotypes, efficient management of populations, and use of available resources. Mass,  $F_2$ -derived-family, and single-seed-descent (SSD) selection methods were compared in an interracial population (ICA Pijao × Pinto UI 114) of common bean (*Phaseolus vulgaris* L.). The  $F_2$ -derived-family method involved elimination of low-yielding  $F_2$ -derived families in replicated yield trials in  $F_4$ ,  $F_5$  and  $F_6$ . Thirty-two random lines derived from each methods and the two parents were evaluated in a replicates-in-set design in two contrasting environments in Colombia in 1992. Mean seed yield of lines derived from the SSD method was significantly lower than yields obtained from the other two methods. Mean yield of lines derived from the pedigree method was the highest, indicating that even a low intensity of selection for yield among  $F_2$ -derived families was effective. The  $F_2$ -derived-family method also retained a comparatively higher proportion of lines with lighter-colored medium-sized seeds and indeterminate prostrate type III growth habit. Lines with darker and smaller seeds predominated in the mass and SSD methods. These two groups also had more erect type II lines than did the  $F_2$ -derived family method. On average, the SSD gave early maturing and the mass method late maturing lines. No line from any method outyielded ICA Pijao, the high-yielding parent. Two lines from the  $F_2$ -derived-family method, four lines from the mass method, and no lines from the SSD method significantly outyielded Pinto UI 114.

Key words: Common bean, Phaseolus vulgaris, selection methods, F2-derived family, seed yield

Urrea, C. A. et Singh, S. P. 1994. Comparaison des modes de sélection massale, généalogique modifiée et par descendance unipare dans une population interraciale de haricot. Can. J. Plant Sci. 74: 461-464. La connaissance de l'éfficacité comparative des différentes méthodes de sélection est nécessaire pour l'identification des génotypes de calibre supérieur, ainsi que pour la gestion des populations et l'utilisation des ressources disponibles. Nous avons comparé dans une population interraciale (ICA Pijao × Pinto UI 114) de haricot commun (Phaseolus vulgaris L.) trois méthodes de sélection: massale, généalogique modifiée et par descendance unipare (SDU). La sélection généalogique modifiée comporte l'élimination précoce des familles issues de la  $F_2$  au moyen d'essais de rendement avec répétitions en  $F_4$ ,  $F_5$  et  $F_6$ . Trente-deux lignées aléatoires issues de chaque méthode, ainsi que les deux géniteurs, ont été évaluées en 1992 dans un dispositif avec répétitions dans deux environnements différents en Colombie. Le rendement grainier moyen des lignées obtenu par SDU était significativement inférieur à ceux obtenus par les autres méthodes. C'est la méthode de sélection des familles issues de la F2 qui produisait le rendement le plus élevé, ce qui porte à penser que même une faible pression de sélection pour le rendement parmi les familles issues de F2 était efficace. Cette méthode conservait en outre une proportion relativement plus forte de lignées moins colorées, à graines de calibre moyen et à type de croissance prostré indéterminé, de type III, tandis que les lignées à graines foncées et plus petites dominaient dans les méthodes de sélection massale et SDU. Ces deux méthodes produisaient en outre relativement plus de lignées à port dressé de type II que la sélection familiale précoce. En moyenne, la SDU produisait des lignées précoces et la sélection massale des lignées tardives. Aucune lignée obtenue par l'une ou l'autre des trois méthodes de sélection ne dépassait le rendement de ICA Pijao, le géniteur à rendement élevé. Deux lignées issues de la sélection généalogique modifiée, quatre issues de la sélection massale et deux de la SDU surpassaient significativement le rendement de l'autre parent Pinto UI 114.

Mots clés: haricot, Phaseolus vulgaris, méthodes de sélection, sélection des familles issues de la F2, rendement grainier

Hybrid populations in self-pollinating crops, such as common bean (*Phaseolus vulgaris* L.), are usually managed by mass, pedigree, or single-seed-descent (SSD) selection methods or their modifications. In the mass and SSD methods, early generations are advanced without any selection and evaluation. Selection is often effected when considerable homozygosity has been reached. This allows handling a large number of hybrid populations and populations with a larger number of plants. The major drawback of these methods is the danger of losing desirable recombinants as a result of intergenotypic competition, natural selection, and random drift due to sampling errors. Also, these methods carry a large number of undesirable genotypes, which are eventually discarded in the advanced generations. In contrast, the pedigree method (especially combined with early-generation yield testing) permits identification of promising populations and families within populations. Undesirable populations and families are thus discarded sequentially as evaluation and selection progress. But extensive record-keeping is expensive and time-consuming. Thus, this method can usually be used only on comparatively few populations, provided selection

Abbreviations: SSD, single-seed descent.

gains are large enough to offset the increased costs and still offer advantages over other methods. A modification of the pedigree method, the  $F_2$ -derived-family method, involves early-generation selection for yield among  $F_2$ -derived families. Limited data are available on the effectiveness of this method. While in most crops information is available on the comparative effectiveness of various breeding methods, this information is currently lacking for the common bean, and providing this information is the objective of this study.

#### MATERIALS AND METHODS

An interracial cross was made between cultivars Pinto UI 114 and ICA Pijao. Pinto UI 114 is an indeterminate genotype with prostrate type III growth habit (Singh 1982) and medium-sized (25-40 g 100 seeds<sup>-1</sup>) seeds. Its characteristics conform to the race "Durango" (Singh et al. 1991). ICA Pijao possesses an indeterminate erect type II growth habit and small (<25 g 100 seeds<sup>-1</sup>) seeds. It belongs to the small-seeded lowland tropical race "Mesoamerica." Both are widely adapted and possess other contrasting characteristics, including days to maturity and resistance to bean common mosaic virus, bean golden mosaic virus, and rust caused by *Uromyces appendiculatus* (Pers.) Unger var. *appendiculatus*.

The  $F_2$  population of 648 plants was space-planted. At maturity, one pod from each plant was harvested and threshed in bulk for the mass method. All seeds were grown in  $F_3$ and, at harvest, the process was repeated as for  $F_2$ . This procedure was repeated until  $F_6$ . In the  $F_6$ , approximately 650 random plants were harvested individually. These were grown in plant-to-progeny rows in  $F_7$ , and seed was increased in  $F_8$ . Thirty-two random  $F_6$ -derived  $F_9$  lines were used for comparative trials.

For the SSD method, one pod from each of the 648  $F_2$  plants was harvested, threshed, kept in a separate envelope, and later planted in hill plots in  $F_3$ . A single pod was taken randomly from each hill plot to grow the next generation. This process was repeated until  $F_6$ . Only 228 of the original 648  $F_2$  plants were represented in  $F_6$ . These were then grown in plant-to-progeny rows in  $F_7$  and seed was increased in  $F_8$ . Thirty-two random  $F_2$ -derived  $F_9$  lines were used for comparative trials.

For the  $F_2$ -derived family method, the remaining seeds were harvested from each of the 648  $F_2$  plants that had provided one pod each for the mass and SSD methods. These were grown in plant-to-progeny rows in  $F_3$ . Plants within each  $F_3$  row were harvested in bulk. The  $F_2$ -derived families were tested in yield trials in  $F_4$ ,  $F_5$  and  $F_6$ . In each generation, only low-yielding families were eliminated. In  $F_7$ , 32 random families were selected, increased in  $F_8$ , and used for comparative trials in  $F_9$ . No selection was practised in any method for growth habit, maturity or seed characteristics.

The comparative trial was grown in a replicates-in-set design (Hallauer and Miranda 1988) in two contrasting environments (Quilichao and Popayán, Colombia) in 1992. Details such as soil types, temperatures, and agronomic management of nurseries were reported by Singh et al. (1992a). Each plot consisted of four rows, 3.4 m long.

Table 1. Mean and range for seed yield and maturity of 32 common bean lines from Pinto UI 114  $\times$  ICA Pijao selected by F<sub>2</sub>-derived-family, mass, or single-seed-descent methods and evaluated at Popayán and Quilichao, Colombia, in 1992

	Seed yi	eld (kg ha <sup>-1</sup> )	Maturity (d)		
Selection method	Mean	Range	Mean	Range	
F <sub>2</sub> -derived-family	2035	1606-2521	73.9	70.3-77.3	
Mass	1932	1255-2825	74.4	69.3-78.0	
Single-seed-descent	1628	877-2130	72.9	69.2-76.7	
Parents	2257	2012-2502	74.4	70.0-78.7	
LSD (0.05)	89		0.3		

The spacing between rows was 0.6 m at Quilichao and 0.5 m at Popayán. An average density of 200 000 plants ha<sup>-1</sup> was obtained at each location. Data were recorded for growth habit and days to maturity. At harvest, the two central rows, leaving head borders of 20 cm on either end, were taken for seed yield. Seed yield was adjusted to 14% moisture. Also, all entries were classified for seed color and 100-seed weight. Data for yield and days to maturity were tested for homogeneity of error variances (Bartlett 1947). These were then subjected to a combined analysis of variance, using a mixed model (McIntosh 1983), with selection methods fixed, and test environments considered as random effects. All data were analyzed, using the Proc Means Program of the Statistical Analysis System Institute, Inc. (SAS).

#### RESULTS

The mean squares due to selection methods were significant (P < 0.05) for seed yield and days to maturity (ANOVA not shown). The effects of location and location × selection method were not significant for either trait. Differences among lines within each selection method were highly significant (P < 0.01) for both traits.

Mean seed yield of lines derived from the SSD method was significantly (P < 0.05) lower than yields obtained from the mass and F<sub>2</sub>-derived-family methods (Table 1). The mean yield of lines developed from the mass method also was lower than that from the F<sub>2</sub>-derived-family method. Nonetheless, the differences between the highest yielding lines from the two methods were not significant. Two lines from the F<sub>2</sub>-derived-family method and four lines from the mass method significantly outyielded Pinto UI 114, but none outyielded ICA Pijao. No line from the SSD method yielded higher than either parent. The differences in mean values among the three methods for days to maturity were significant. On average, the SSD gave early maturing lines; the mass method, late maturing.

The frequency of lines for growth habit, seed size and seed color is shown in Table 2. Two lines out of 32 obtained from the  $F_2$ -derived-family method had erect type II growth habit, whereas both the SSD and mass method had 9 type II lines. The remaining 23 were prostrate type III. For seed size, a higher proportion of lines in the  $F_2$ -derived-family method had medium-sized seed than in the other two methods. The mass method had the fewest lines with medium-sized seeds. The  $F_2$ -derived-family method also

family, or single-seed-descent methods and evaluated at Popayan and Gunthav, Colombia, in 1992									
Selection method	Growt	Growth habit <sup>z</sup>		Seed size <sup>y</sup>		Seed color			
	II	III	Small	Medium	Pinto	Black	Others		
Mass	9	23	28	4	4	12	16		
F <sub>2</sub> -derived family	2	30	19	13	19	1	12		
Single-seed-descent	9	23	24	8	9	9	14		
Parental characteristics <sup>x</sup>	Р	U	Р	U	U	Р			

Table 2. Frequency for growth habit, seed size and seed color for 32 common bean lines from Pinto UI 114 × ICA Pijao selected by mass, F2-derived-Justed at Ponaván and Quilichao, Colombia, in 1992

<sup>z</sup>Growth habit: II, indeterminate erect; III, indeterminate prostrate, according to Singh (1982). <sup>y</sup>Seed size: small, <25 g 100 seeds<sup>-1</sup>; medium, 25-40 g 100 seeds<sup>-1</sup>.

\*P, ICA Pijao; U, Pinto UI 114.

retained the highest number of lines with pinto-type spotted seed coat color, whereas the black and nonparental off-type seed coat colors predominated in the SSD and mass selection methods.

#### DISCUSSION

Choice of selection method usually depends on the number of populations being managed, inheritance of traits under selection, and availability of resources and screening methods. But comparative yield and other agronomic qualities of lines developed from different methods must also be considered. That the mean yield of lines derived from the SSD method was significantly lower than yields of lines developed by the F2-derived-family and mass methods should be of concern. Although one random pod from each hill was taken to advance the generations (on average, a pod contains five seeds), a considerable loss in population occurred between the  $F_2$  and  $F_6$  generations of the SSD. This was not a random process: comparatively high-yielding genotypes and genotypes possessing larger and lighter colored seeds were apparently eliminated. Thus, under tropical environments and field conditions, use of the SSD method for common bean would not be recommended. This is in contrast to results reported in cowpea [Vigna unguiculata (L.) Walp.] by Ntare et al. (1984), greengram [Vigna radiata (L.) Wilczek] by Dahiya et al. (1986), and wheat (Triticum aestivum L.) by Knott and Kumar (1975) and Pawar et al. (1985). In these studies, the SSD was at least as good as or better than the bulk method or the pedigree method involving early-generation yield testing.

The F<sub>2</sub>-derived-family method produced lines with the highest mean yield, followed by those of the mass method. But the difference between the yields of the highest yielding lines obtained from the two methods was not significant (P > 0.05). Unlike the mass method, The F<sub>2</sub>-derivedfamily method contained genotypic mixtures rather than advanced generation pure lines. It is therefore not possible to know whether the extra cost and labor involved in recordkeeping and conducting yield trials for the F2-derivedfamily method would be worthwhile. The major reason for using this method would be to find promising populations and promising families within populations in  $F_3$ ,  $F_4$  and  $F_5$ . Singe-plant selections could then be made to identify and develop high-yielding cultivars.

The three groups of lines differed in relative frequencies for growth habit, seed size and seed color. As these traits are also important to common bean growers and consumers, they should be considered during selection. For example, with the F2-derived-family method, if genotypes with erect type II growth habit are desired, they should be grouped together and tested separately from other growth habit types. As it was, type II genotypes were probably differentially eliminated because of their low yields compared with type III. Similarly, in the mass selection method, separate bulks could be formed in F<sub>2</sub> or F<sub>3</sub>, based on seed size and color. Differences in growth habit and seed characteristics affect intergenotypic competition in common bean (Hamblin 1975; Lépiz 1982; Dessert 1987; Vieira 1988). In this case, genotypes with small dark seeds were favored over those with larger, lighter colored seeds.

No line from any selection method outyielded the highyielding parent ICA Pijao, and only two lines from the F2-derived-family method and four lines from the mass method significantly outyielded the low-yielding parent Pinto UI 114. No selection had been applied in the SSD or mass method at any stage; thus, a random sample of 32 lines was probably not large enough to contain high-yielding genotypes. But this could be less likely for the F2-derived-family method, where yield tests were applied on all  $F_2$ -derived families from F<sub>4</sub> onward. Thus, a high-yielding genotype was less likely to be lost. A more convincing case could have been made had advanced-generation pure lines instead of  $F_2$ -derived  $F_6$  families (probably genotypic mixtures) been tested in  $F_9$ . The  $F_2$ -derived-family method differed from the standard pedigree method in that single-plant selections were not made among or within  $F_2$ -derived  $F_3$ ,  $F_4$ ,  $F_5$  and  $F_6$  families. Nienhuis and Singh (1988) and Singh et al. (1992b) reported that both ICA Pijao and Pinto UI 114 possess negative general combining ability. Thus, an alternative explanation could be that although the parents belonged to two different races of common bean, genes determining yield differences between two parents were apparently not complementary, additive or multiplicative.

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