COMPARISON OF BREEDING METHODS FOR YIELD SELECTION IN COMMON BEAN SEGREGANT POPULATIONS

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INTRODUCTION

The genetic improvement of plants is among the major contributions of science to the welfare of society. It is estimated that about 50% of the increase in yield of major crops is attributed to the breeding (Raposo et al., 2000). The comparisons among the methods of conducting autogamic plants in segregant populations are very restricted, especially in Brazil. For common beans, the information about it was obtained in other countries (Urrea & Singh, 1994; Ranalli et al., 1996). Thus, it is important to evaluate the relative efficiency of the methods available under the conditions prevailing in the country. The objective of this study was to evaluate and to compare yield in segregating populations of common beans conducted by three breeding methods in order to improve efficiency.

MATERIALS AND METHODS

192 families of common beans with carioca grain type were obtained by hybridization between the lines CNFC 7812 and CNFC 7829. These families were conducted by three breeding methods (SSD, Bulk and Bulk within Family) up to the F_7 generation. For each method, 64 families were evaluated with a common control group of four cultivars. The field trial was conducted at Santo Antônio de Goiás, GO, Brazil. The experimental design used was lattice 14x14, with two replicates and plots were comprised of two rows four meters long spaced apart 0.5 m with 15 seeds per meter. The yield was obtained after harvest and weight of the grains converted to kg.ha[1].

RESULTS AND DISCUSSION

The analysis of variance showed that there were significant differences among treatments (Table 1). The bulk and SSD methods showed highly significant differences. There was no significant difference among the controls and controls x methods interaction. The yield had average heritability of 57% that indicates the possibility of success with the selection. The coefficient of variation (22%) indicated a normal experimental precision for beans. It was possible to select twenty best families among the three methods: ten families came from the bulk within the family method, six from the bulk method and four from SSD method and no control was selected. Among the twenty worst families, nine of them originated from the SSD method, six from the bulk method, three from bulk within the family method and two controls. The SSD method was the least efficient method to develop superior families for

yield, since the bulk within families method was the most efficient to develop superior families for this trait. Evaluating families with yield up 2,000 kg.ha^{-1}, it was observed that eleven families came from the bulk within family method, nine from bulk method and eight from SSD method. Considering these results, seems that the bulk within families method is superior when compared to the others, but it is necessary to evaluate these families in a larger number of environments to identify the effect of genotype x environment interaction on the efficiency of breeding methods.

Table 1. Analysis of variance for yield of families evaluated in Santo Antônio de Goiás, GO, Brazil in 2008/2009.

V.S.	D.F.	M.S.
Treatments	**195**	**280403.88****
Bulk within family	63	243582.513*
Bulk	63	320330.9108**
SSD	63	290899.6534**
Controls	3	168391.5676^{ns}
Controls x methods	1	275244.1463^{ns}
Between methods	2	22551.449^{ns}
Error effective	351	131847.8
Efficiency of the lattice (%)		107
CV (%)		22
Mean (kg.ha^{-1})		1647
h^2 (%)		57

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