STRATEGIES FOR SELECTING INDIVIDUALS IN COMMON BEAN BREEDING PROGRAMS

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INTRODUCTION:

In conducing of segregating populations using Bulk or Bulk within F_2 progenies methods, at the time of obtaining the progeny, the choice of individuals is usually performed visually. To improve efficient, the character data could be obtained, and the selection would be made using this information. For this, there are some alternatives, as mass selection, between and within selection, and also the use of mixed models, especially BLUP (Bernardo, 2002; Resende, 2007; Nunes et al., 2008). The aim of this study was to compare selection strategies in identifying the individuals who will lead to the best progenies in order to continue the selection process.

MATERIALS AND METHODS:

The experiment was conducted at experimental area of Universidade Federal de Lavras, Minas Gerais, Brazil. It was used the data of 51 $F_{2:4}$ progenies derived from the cross between CVIII8511 x RP-26 common bean lines. The experimental design was a random complete block with 20 replications and plots of one plant. The plant architecture and grain yield data were obtained per plant, and, furthermore, the sum of the standardized of those two variables ($\sum Z$) was estimated for simultaneous selection of both characteristics. The analysis of variance was performed by the mixed models method (BLUP) and by the least squares method (LS), and the results were used for comparing different selection strategies.

The phenotypic value per plant data were submitted to different selection strategies for later comparison with the data supplied by BLUP. In the mass selection, the 100 best and 100 worse individuals were selected in the $F_{2:4}$ generation in function of the $\sum Z$ regardless of the progeny or replication to which they belonged. In the stratified mass selection, the plants were divided in strata and each stratum was a replication. Thus, each stratum contained one plant from each progeny and there were a total of 51 plants per stratum. The five best and five worst individuals were selected from each stratum considering the $\sum Z$. As there were 20 replications, there were a total of 100 progenies in each group. To perform the between and within progeny selection, analysis of variance was carried out first using the least squares method to obtain the $\sum Z$ means of the 51 progenies. The six best progenies were selected from these means (11.7% between progenies selection intensity) and within these, the 16 best of the 20 existing plants. The same was done with the group of worst progenies, totaling 96 plants in each group. The selection strategies were compared with BLUP procedure by observing the coincidence of the selected individuals, and also through the selection differential in each strategy.

RESULTS AND DISCUSSION:

The coincidence of individuals selected by BLUP procedure and LS method was 100%. Bernardo (2002) commented that when the design is completely balanced, BLUP and LS supply the same information. Because each plot consisted of one plant, and 8.6% of the total were lost, it was inferred that with this loss level there was no advantage in BLUP compared to LS.

It was also estimated the coincidence of individuals selected by the different alternatives of selections with BLUP. Because individual BLUP provides an estimate that involves all the model variables, for example, the merit of the progeny, the individual in the progeny and even the replication where it is located (Resende, 2007), should present great coincidence in the individuals selected by between and within selection. Taking as reference the $\sum Z$, the coincidence was over 80%. Mass selection and stratified mass selection had lower concordance compared to BLUP (Table 1).

Table 1 - Coincidence (in %) of the best and worst plants selected by different selection strategies compared to BLUP, considering the $\sum Z$

Strategies	100 Best	100 Worst
Mass selection	44	36
Stratified mass selection	42	39
Between and within selection	83	84

The results obtained, in the first moment, allowed inference that mass selection was not efficient compared to BLUP. However, the selection by different strategies does not necessarily identify the same progeny/individual, but rather individuals similar in terms of performance. In this condition, the efficiency of the mass selection strategy would be underestimated. To demonstrate this fact, the selection differential of the different strategies was estimated. It was observed that the selection differential was greatest in the mass selection strategy, of 3.63, while for BLUP and between and within selection the selection differential was of 2.6 and 3.14, respectively. It should be emphasized, however, that in the selection gain expression (SG), the selection differential should be multiplied by the heritability (h^2). In the case of BLUP, $h^2 = 1.0$. In the between and within progeny selection, the h^2 between and h^2 within progeny selection should be used as weights. In the case of mass selection, it would be SG = selection differential $_x$ h_I^2, where h_I^2 is the heritability for selection at individual level, a value that is not normally high (Moreto et al, 2007). It can be inferred that the expected gain from mass selection and BLUP would be similar if h_I^2 was 74.3%, that is, $2.6/3.5 = 0.7428$. Although this h_I^2 estimate was not obtained, it would be difficult to be of this magnitude. However, the efficiency of mass selection compared to BLUP should not be considered of only 40%.

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