

# VARIABILITY AMONG AND WITHIN COMMON BEAN PROGENIES FROM SEGREGATING POPULATIONS

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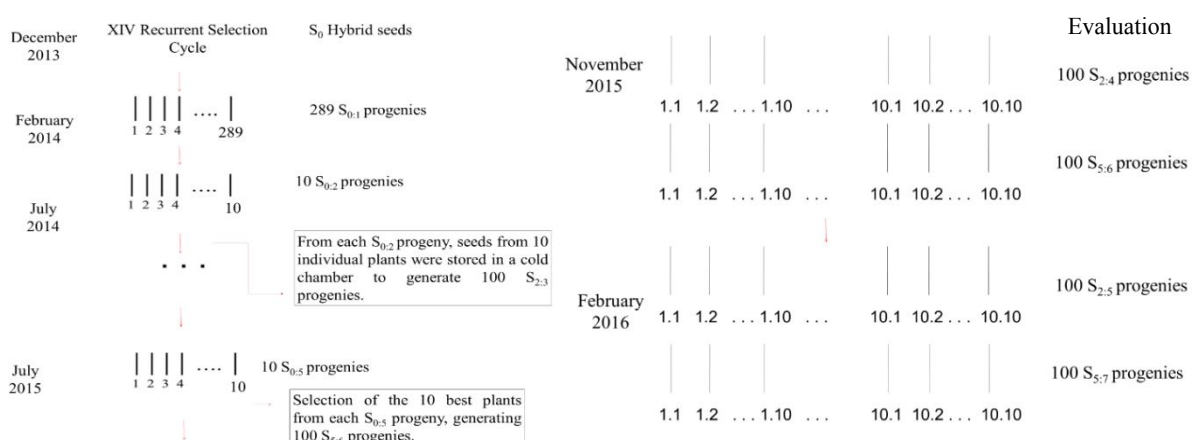
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## INTRODUCTION

Bulk within progenies derived from  $F_2$  plants (Frey 1954) is one of the most used breeding methods for common bean in Brazil. The original proposal was that from  $F_2$  generation, individual plants would be harvested and sowed by lines,  $F_{2:3}$  progenies. At harvesting time, these progenies would also be handled individually. A bulk from each progeny is used to generate the next generation. This means that each progeny is conducted by bulk method. This process is repeated until  $F_{2:6}$  or further generations, when the progenies are evaluated in experiments with replications. Many common bean breeding programs in Brazil use bulk within  $F_2$  progenies (Bulk/ $F_2$ ). However, the progenies are evaluated in experiments with replication from  $F_{2:3}$  generation. When applying this procedure, very often no selection is applied within the progenies, even at final stages, before releasing the new cultivars for farmers. Therefore, this new cultivar might be a multiline. In this way, this variability within progenies is not well explored. In our work the variation between and within progenies conducted by Bulk/ $F_2$  method was estimated aiming to guide future works that also uses this method.

## MATERIAL AND METHODS

The segregating population used came from the Universidade Federal de Lavras (UFLA) recurrent selection program for grain yield. Details about obtainment of original population and conduction of selection cycles are presented by Silva et al. (2010). Twenty progenies were recombined to generate the fourteenth cycle (CXIV). In July 2014, 100  $S_{0:2}$  progenies were evaluated using 10x10 lattice with tree replications. Plots consisted of two rows of two meter length. Seeds from ten progenies, taken at random, were divided into two sub-samples. The first sub-sample was stored in a cold chamber; however, the second sub-sample was proceeded further using the Bulk/ $F_2$ ( $S_0$  progenies) method. A scheme of how the process was conducted is shown in Figure 1: Inbreeding Generations Scheme.



In November, 2015 and February 2016 lattice 10x10 design was used, but in the first case with two replications and in the second case, with tree replications. All seasons were conducted at Lavras, Minas Gerais, Brazil. The trait under evaluation was grain yield. Genetic parameters were estimate according to Ramalho et al. (2012).

## RESULTS AND DISCUSSION

Considering the adopted method, each “S<sub>2:4</sub>” progeny represent the variation within S<sub>0</sub> progenies after four inbreeding generations. For the same reason, “S<sub>5:6</sub>” progenies represent the variation within S<sub>0</sub> after six inbreeding generations.

Heritability estimates among progenies were higher than the heritability estimates within progenies (Table 1). However, as expected, as inbreeding increased, the difference between the estimates decreased. It is also important to point that some within heritability estimates can be considered as null, since their lower limit estimates are negative.

When few plants were used to represent the variation within progenies, it is possible to infer that expressive variability was released. Not selecting within progenies derived from F<sub>2</sub> plants at final stages, as it has been done sometimes, leads to a new cultivar that is actually a multiline. If there are advantages or disadvantages when adopting this strategy for a trait such as grain yield, should still be more studied and explored.

**Table 1-** Heritability ( $h^2$ ) and grain yield (GY) mean estimates and its confidence intervals (lower limit - LL - and upper limit - UL).

|         | S <sub>2:4</sub> /S <sub>2:5</sub> |                           |        | S <sub>5:6</sub> /S <sub>5:7</sub> |                          |        |
|---------|------------------------------------|---------------------------|--------|------------------------------------|--------------------------|--------|
|         | LL                                 | $h^2$                     | UL     | LL                                 | $h^2$                    | UL     |
| Between | 0.115                              | 0.67                      | 0.885  | 0.56                               | 0.81                     | 0.945  |
| Within  | -0.93                              | 0.25                      | 0.74   | -0.185                             | 0.48                     | 0.845  |
|         | LL                                 | GY (Kg.ha <sup>-1</sup> ) | UL     | LL                                 | GY(Kg.ha <sup>-1</sup> ) | UL     |
|         | 2452.5                             | 2711.0                    | 3025.0 | 2479.5                             | 2881.5                   | 3325.5 |

\* The heritability estimate, grain yield and confidence intervals are based on November 2015 and February 2016 estimates means.

## ACKNOWLEDGEMENTS

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