

# COMPARISON OF METHODS FOR CONDUCTING SEGREGANT POPULATIONS FOR FIBER CONTENT

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## INTRODUCTION

Among the autogamous plants, the common beans (*Phaseolus vulgaris* L.) is an outstanding crop in the Brazilian economy especially for its social role (RAMALHO et al., 1993). The nutritional quality of its grains makes it a crop of great importance for the country. The presence of fiber in the food is an important trait due to its direct benefits in human health. Comparisons among the methods of conducting segregant populations of common beans are still scarce and generally their objectives are related to grain yield (RAPOSO, 1999). So, it becomes relevant to quantify fiber content as well as to study the genetic variability of the trait in Brazilian genotypes. (LONDERO, 2005). This research had the following objectives: to quantify the content of crude fiber in populations conducted by three breeding methods, to verify if there is genetic variability among genotypes and to compare the methods utilized.

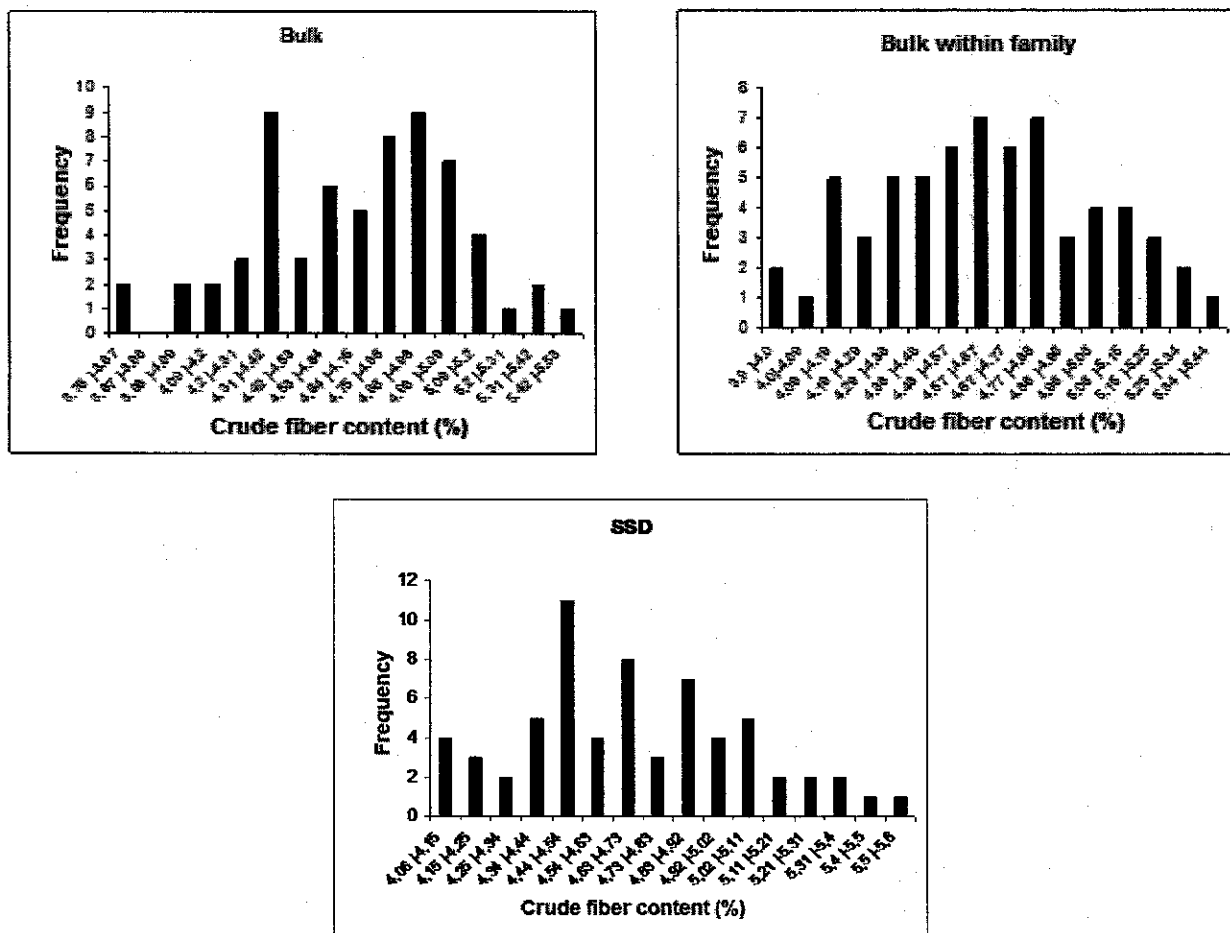
## MATERIALS AND METHODS

192 families of carioca common beans obtained by hybridization between the strains CNFC 7812 and CNFC 7829 were analyzed. These families were conducted by three breeding methods (SSD, Bulk and Bulk within family) up to the F<sub>7</sub> generation. For each method, 64 families were evaluated. The field trial was conducted at the location of Santo Antonio de Goiás, Goiás State, Brazil. The experimental design used was a lattice 14x14, with two replicates and plots were comprised of two rows four meters long spaced apart 0.5 m and seeded with 15 seeds per meter. The harvested grains were utilized for the quantification of crude fiber content by the AOAC (1997) modified method.

## RESULTS AND DISCUSSION

The lattice design was of little efficiency (98%), so the experiment was analyzed as a complete randomized block design. A significant difference among families was detected by the F test at the 10% probability level, in the analysis of variance. The coefficient of variation was 10.32%, which indicated a good experimental precision. The heritability estimate was low (16.7%), which lead to the conclusion that the trait is greatly influenced by the environment. There were no differences among family means for each method and so it was possible to compare methods utilizing the mean distribution within each method. It was observed, for the three methods, that genetic variability was present, an indication that it is possible to select superior families (Figure 1). The bulk method was the one that presented the greatest variation in crude fiber content amongst families and that can be observed by the amplitude of the variation of means. It was observed that the number of families obtained with mean crude fiber content greater than 5% (14 families) was similar for the three methods. When the twenty best families were selected across methods, it was realized that five families were obtained through the Bulk method within family, six through the Bulk method and eight through the SSD. The cultivar BRS Cometa was also present within the twenty best populations, showing the

highest value for fiber content (6.02 %). Among the twenty worst families, eight of them originated through the Bulk within family method and six through the other methods. The differences among fiber content and number of superior families among methods were negligible, so it is not possible to identify which method was more efficient for the development of superior families for the fiber content trait. Due to the high environmental influence on this trait, it would be highly advisable to evaluate families over a great range of environments.



**Figure 1.** Frequency distribution of crude fiber content obtained in analyses in 2008/2009 by the methods SSD; Bulk and Bulk within family.

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