# COMPARISON OF BREEDING METHODS FOR FIBER CONTENT IN COMMON BEANS

**V.A. Pontes Júnior[1], P.G.S. Melo[1*], L.C. Melo[2], H.S. Pereira[2], J.L.C. Díaz[2], P.Z. Bassinello[2], A. Wendlend[2] and B.A.R. Paiva[1]**

[1]Universidade Federal de Goiás; and [2]Embrapa Arroz e Feijão, Brasil
[*]Corresponding author: pgsantos@gmail.com

The breeding program of common beans in Brazil is focused on the development of cultivars more adapted to weather variations, maintaining crop yield aggregated to other characteristics of interest such as fiber content, an important component in human diet, providing beneficial effects on health. Investigation of the available genetic variability as well as the quantification of fiber content in bean genotypes in Brazil are important and necessary, considering the low availability of information on this subject (Londero, 2008). The objective of this work was to compare raw fiber content of families obtained by different breeding methods.

Families were obtained from crosses between genitors CNFC 7812 and CNFC 7829, which are contrasting for fiber content, and conducted by three breeding methods: *bulk* ($F_{5:8}$), *bulk* within families $F_2$ ($F_{2:8}$) and Single Seed Descent - SSD ($F_{5:8}$) up to generation $F_8$. The experimental design was a completely randomized block with three replicates arranged in plots with four meter long rows spaced by 0.5 m and 15 seed/meter. The treatments were 45 families (F), 15 by method, 2 controls (C) and 2 genitors (G). Trials were conducted in four locations: Anapolis-GO (wet season 2009); Ponta Grossa-PR (wet season 2009 and dry season 2010); and Lavras-MG (dry season 2010). Methodology used to determine raw fiber content was the acid-base digestion, using the fiber determinator Tecnal® model TE-149. Individual and joint analyses of variance were performed using family mean values for raw fiber content through program Genes (Cruz 2006).

Family x Environment interaction (F x E) was observed in the joint analysis (Table 1), indicating different family behavior according to the four evaluated locations. Heritability ($h^2$) for this trait was 47. 61%, considered satisfactory to obtain selection gains. The largest $h^2$ estimate (64.47%) was obtained for the *bulk* method followed by *bulk* method within families (41.80%). In the SSD method, $h^2$ was equal to zero, indicating that this method presents difficulties in keeping genetic gain in time, as opposed by the bulk method the assures higher genetic gains over time. Families conducted by *bulk* ($P \leq 0.01$) and *bulk* within families ($P \leq 0.055$) showed significant differences for raw fiber content. SSD method did not show significant differences ($P \leq 0.05$). There were no significant differences between genitors, constrasting with values previously obtained, showing the contrast between them, this may indicate the existence of interaction Genitors x Environment. Also there were no significant differences between controls and methods, as well as controls *vs* families and genitors *vs* families. The SSD method provided the largest number of familes (eight) among the 20 best and the smaller number among the 20 worst families obtained. Looking at the general mean value obtained for raw fiber content among families (4.61%), the SSD method, undoubtedly, was the most efficient to generate superior families as well as the largest number of families surpassing the best genitor mean (4.46%) (Table 2). However, the low $h_2$ values obtained indicate its difficulty to maintain selection gains over time.

**Table 1.** Summary of the joint analysis of variance and analysis of variance of the three method evaluated for raw fiber content (%) of families $F_8$ evaluated in Anápolis/GO (wet season 2009), Ponta Grossa/PR (wet season 2009 and dry season 2010), and Lavras/MG (dry season 2010).

| Source of variation | Degree of freedom | Mean square | |
|---|---|---|---|
| | | Raw fiber content | P-value |
| Environment (E) | 3 | 0.674* | _ |
| Treatment (T) | 48 | 0.169* | _ |
| *Bulk d.*$F_2$ *Families* | 14 | 0.153 | 0.055 |
| *Bulk Families* ($F_{5:8}$) | 14 | 0.250 | 0.001 |
| SSD Families ($F_{5:8}$) | 14 | 0.084 | 0.509 |
| Controls (C) | 1 | 0.245 | 0.099 |
| Methods (M) | 2 | 0.007 | 0.923 |
| Genitors (G) | 1 | 0.020 | 0.639 |
| C *vs* F | 1 | 0.066 | 0.390 |
| G *vs* F | 1 | 0.150 | 0.196 |
| T x E | 144 | 0.178* | _ |
| Efetive error | 192 | 0.089 | _ |
| Mean | | 4.61 | |
| $h^2$ (%) | | 47.61(Bd.$F_2$: 41.80; *Bulk*: 64.47; SSD: 0) | |
| $CV_g$ (%) | | 2.17 | |
| $CV_g/CV_e$ | | 0.33 | |

Where: $h^2$: heritability; $CV_e$: weather coefficient of variation; $CV_g$: genetic coefficient of variation; *F test at 5% probability.

**Table 2.** Number of families in each method overcame the overall mean and the best genitor mean for raw fiber content.

| | Number of superior families | |
|---|---|---|
| Method | Overall mean | Best Genitor mean |
| *Bulk* $F_{2:8}$ | 8 | 12 |
| *Bulk* | 8 | 11 |
| SSD | 11 | 14 |

## REFERENCES

CRUZ, C. D. **Programa Genes**: versão Windows, aplicativo computacional em genética e melhoramento. Viçosa: Editora UFV, 2006. 175 p.

LONDERO, P. M. G., RIBEIRO, N. D., CARGNELUTTI FILHO, A. Teores de fibra e rendimento de grãos em populações de feijão. **Ciência e Agrotecnologia**, Lavras, v. 32, n. 1, p. 167-173, jan./fev., 2008.