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Anatércia Ferreira Alves
Universidade Estadual da Região Tocantina do Maranhão, anaterciaa@yahoo.com.br

José Eustáquio de Souza Carneiro
Universidade Federal de Viçosa

Pedro Crescêncio Souza Carneiro
Universidade Federal de Viçosa

Deurimar Herênio Gonçalves Júnior
Universidade Estadual da Região Tocantina do Maranhão

Wallysson Nascimento Lima

See next page for additional authors

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Authors

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Anatércia Ferreira Alves [1*], José Eustáquio de Souza Carneiro[2], Pedro Crescêncio Souza Carneiro[2], Deurimar Herênio Gonçalves Júnior[1], Wallysson Nascimento Lima, Aurilene Barros da Silva[1].

[1]Universidade Estadual da Região Tocantina do Maranhão – UEMASUL. Rua Godofredo Viana, 1300 – Centro. Cep: 65900-100. Imperatriz, MA. Brasil. *e-mail: anaterciaa@yahoo.com.br
[2]Universidade Federal de Viçosa-UFV, Campus Universitário, S/N, Centro. Cep: 36571-000 - Viçosa, MG. Brasil

INTRODUCTION

In the a breeding program leading, various strategies can be used and they are capable to yield good results. However, hybridization is a routine in current breeding programs and it has been the main new bean lines source (Menezes Júnior et al. 2013). The big difficulty in the autogamous plants breeding is finding two parents who bring together all the interest phenotypes. In this case, the alternative would be to promote successive cycles of selection and interbreeding of the best individuals or the best families (Geraldi 1997). The genetic progress periodic estimation is fundamental to guide the plant breeders about the selective strategies used and the alternatives that could be adopted to increase their efficiency. Thus, the procedures commonly used to compare selective cycles are the different cycles families or lines evaluation, which can be done using common witnesses (Ramalho 1996). The work objective was to estimate the genetic progress of two recurrent selection cycles based on the evaluation of families with common controls.

MATERIAL AND METHODS

The experiments were carried out at the Experimental Station of Coimbra, belonging to the Department of Plant Sciences of the Federal University of Viçosa (UFV). The base population, zero cycle (C_0), it was obtained by the combination of 20 carioca type grains, with favorable phenotypes for several agronomic interest characters. The parents were recombined in a circulating diallel design, with each parent participating in two crosses, generating 20 populations. From these populations, the families were derived and evaluated for three generations, in the generations $F_{2:4}$ and $F_{2:5}$. The same recombination procedure and C_0 evaluation were performed in cycle one (C_I).

The genetic progress for productivity was estimated based on the $F_{2:3}$ generations families performance (2007 and 2010 winter crops, being 380 families), $F_{2:4}$ (2008 and 2011 drought crops, 160 families) And $F_{2:5}$ (2008 and 201 winter harvests, 40 families) of both C_0 and C_I cycles, respectively. Initially, a pooled variance analysis was performed and the family means adjusted by the control effect of the two experiments. Using the adjusted averages, the genetic progress was estimated. Statistical analyzes were performed with the help of the GENES program (Cruz, 2006).

RESULTS AND DISCUSSION

Table 1 shows the adjusted productivity averages for families $F_{2:3}$, $F_{2:4}$ and $F_{2:5}$ and controls evaluated in the C_0 and C_I cycles, and the respective genetic gains obtained. In all generations, the C_I families were higher than the C_0 families. This superiority was also verified in relation to controls. Estimates of genetic progress (GP) were obtained considering the families of each generation. Genetic gains for grain yield were 23.7%, 14.2% and 16.6% for the generations $F_{2:3}$, $F_{2:4}$ and $F_{2:5}$, respectively (Table 1). There was an overestimation of genetic progress when families were used in each cycle with the use of common controls when compared with other studies with simultaneous evaluation progress (Alves et al, 2015).

Table 1 - Average grain productivity (kg.ha^{-1}) and their respective genetic progress from the pooled analysis with common controls in the $F_{2:3}$, $F_{2:4}$ e $F_{2:5}$ generations.

Generation	Cycle	Grain Productivity Averages
$F_{2:3}$	C_0	3021
	C_I	3736
	Test	3044
	GP(%)	**23.7**
$F_{2:4}$	C_0	3295
	C_I	3762
	Test	3189
	GP(%)	**14.2**
$F_{2:5}$	C_0	3639
	C_I	4242
	Test	3491
	GP(%)	**16.6**

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