

# SELECTION OF BLACK BEAN GENOTYPES VIA MIXED MODELS FOR THE STATE OF PERNAMBUCO

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## RESUMO

The interaction of genotypes with the environment (G x E) is one of the great challenges of plant breeding programs. The evaluation of the genotypes must be carried out in different places and times of cultivation, thus allowing the recommendation of new cultivars for specific and / or general environments. The objective of this work was to select the best black bean genotypes based, simultaneously, on productivity, adaptability and stability. The experiments were conducted in the 2012 agricultural year in three municipalities in the state: Belém de São Francisco, Ibimirim and Petrolina. Fifteen black bean genotypes were evaluated, being 12 strains and three cultivars. A randomized block design with three replications was used. Each experimental unit consisted of 4 lines of 4 m spaced at 0.50 m. Based on the productivity data it was possible to estimate the genetic parameters through the procedure REML / BLUP (Restricted Maximum Likelihood) / BLUP (Best Linear Unbiased Prediction). Model 54 of the SELEGEN-REML / BLUP software was used to evaluate the genotypes. The selection of the best genotypes was made using the harmonic mean method of the relative performance of the predicted genetic values (MHPRVG). The average heritability was low (0.2398), while the accuracy was moderate (0.4889). When considering the selection of bean genotypes in all environments, 40% of these materials had averages higher than the general average (1,370.55 kg / ha). Selection based on each environment, two of the six best genotypes were also selected based on the genotypes with the best agronomic response, using the MHPRVG method, with the following lineages being selected: CNFP 10104 and CNFP 15171, surpassing the controls BRS Campeiro and IPR Uirapuru. It is concluded that the MHPRVG method provides optimized selection of genotypes in terms of productivity, adaptability and stability.

**PALAVRAS-CHAVE:** Genotype x environment interaction, Lineages, REML / BLUP

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