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GENETIC DIVERGENCE IN COMMON BEAN GENOTYPES CULTIVATED IN NORTH OF MINAS GERAIS, BRAZIL

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INTRODUCTION: Common bean (*Phaseolus vulgaris* L.) presents a very great diversity of grains forms and color. It is a culture of great relevance for the Brazilian economic scenario, since its great importance and preference in the Brazilians food. The advance of genetic breeding has increased the number of cultivars with ideal characteristics of crop. However, the extensive use of one or more genetically similar cultivars provides narrowing of the genetic basis. Genetic diversity provides strategies that avoid the use of genetically similar cultivars and thereby avoid problems of origin mainly of biotic character. Thus, it is required that cultivars are not only adapted and productive, but also genetically divergent. Therefore, the objective of this work was to evaluate the genetic diversity of 25 common bean genotypes evaluated in the VCU tests in the north of Minas Gerais.

MATERIAL AND METHODS: The test carried out in Janauba were composed of 25 common bean genotypes of the carioca commercial group, selected among the breeding programs of UFV, UFLA, EPAMIG and EMBRAPA Rice and Bean. Soil preparation was conventional one, with a plowing and two harrowing. The area was then grooved and fertilized using a mechanized seeder adjusted for 0.5 m spacing between rows with a planting density of about 15 plants m^{-1}. The plots consisted of four rows of plants, 4 m in length, and additional irrigation was used. Grain yield, mean number of pods per plant (PPL), average number of grains per pod (GPP) and mass of 100 grains (M100) were evaluated. The data were submitted to analysis of variance for all the studied characteristics. The effect of the genotypes when significant were compared by the Scott-Knott test, at 5%. The generalized distance of Mahalanobis was used for the determinate genetic divergence among genotypes (SINGH, 1981). Tocher optimization method was used for the clustering. The analyzes were performed using the computational application in GENES genetic and statistical.

RESULTS AND DISCUSSION: Analysis of clustering using the Tocher method, based on the dissimilarity matrix, made it possible to distribute the genotypes in 11 different groups (Figure 1). Group I was composed of the genotypes CNFC 11965, RCII-2.19, BRSMG Majestoso, CVIII-2, MAIV-15.204 and MAIV-18.259. The genotypes P-18,163, Pérola, BRSMG Talismã, CVIII-5 and VC-17 represented respectively by groups 6, 7, 8, 9, 10 and 11 formed groups with only one genotype each one. These genotypes showed high diversity in relation to the others.

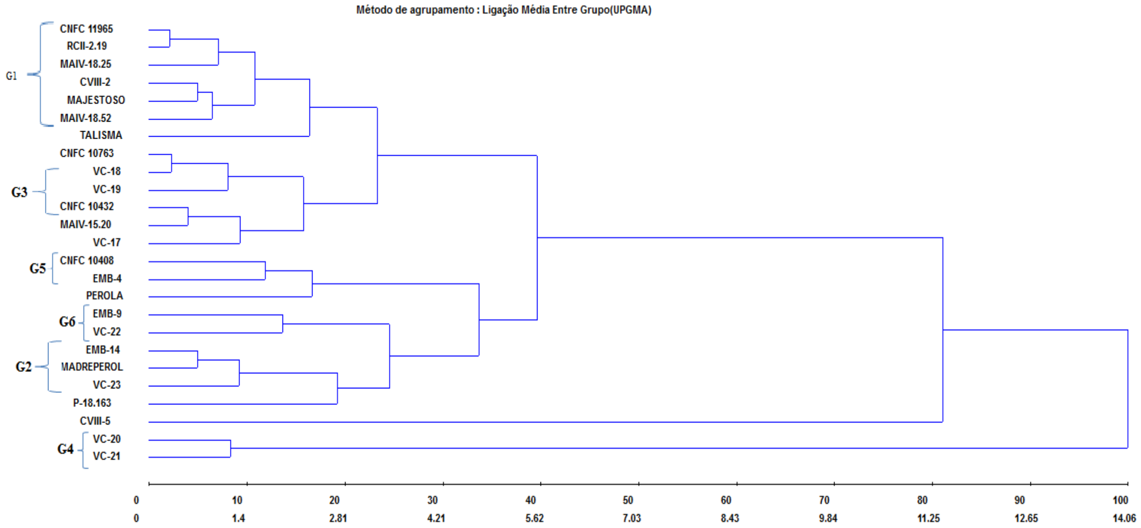

Figure 1. Representative dendrogram of the clustering of 25 common bean genotypes by the UPGMA method, based on the dissimilarity estimated from grain yield and yield components (Janaúba-MG, 2017).

The Table 1 shows the contribution of the characteristics to the divergence, it is observed that from the four evaluated characteristics, it was the number of pods per plant (35.85%) that more contributed to the divergence, while the mass of one hundred grains (12.77%) presented the smallest contribution.

Table 1. Relative contribution of the characters average number of pods per plant (PPL), average number of grains per pod (GPP) and mass of 100 grains (M100) and yield (PROD) for diversity by Singh method (1981) generalized distance of Mahalanobis.

Caracteres	S.j	Value in %
PPL	673.475392	35.8505
GPP	666.935651	35.5023
M100	239.928674	12.7719
PROD	298.228379	15.8753

CONCLUSION: There is genetic divergence among the genotypes studied in the VCU tests conducted in the north of Minas Gerais. The P-18.163, Pérola, BRSMG Talismã, CVIII-5 and VC-17 genotypes are the most divergent.

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