GENETIC DIVERGENCE IN COMMON BEAN (PHASEOLUS VULGARIS L.)
LANDRACES FROM PARANÁ STATE

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Introduction

The common bean (Phaseolus vulgaris L.) is one of the most consumed crop in the world and its growth area is concentrated in Latin America, where is also registered the highest consumption. Brazil is the major producer and consumer of Phaseolus vulgaris L., and Paraná state is responsible for most of this production (25%). The landraces of common bean have been showing wide genetic variability for seed color, shape, brightness, size (in general large seeded cultivars are preferred), among other characteristics of cultivars used by farmers. These cultivars have demonstrated adaptability to several environmental conditions, which can be observed through the resistance to diseases and elevated yield potential (Rodíñio et al., 2003). Multivariate statistical methods have been used previously to analyze patterns of genetic diversity (Pereira et al., 1992). Due to its importance on Brazilian diet, the collection and evaluation of germplasm are very important to expand genetic basis of cultivars using genetic sources available. This work had the objective to quantify genetic variability in landraces cultivars collected in Paraná bean areas producer.

Material and Methods

The genetic divergence in 63 cultivars of common bean was evaluated using 11 morphoagronomic characters through multivariate statistics techniques. A randomized complete block design with four replications was used. The experimental unit was made up of four rows with 5 meters of length, spaced at 0.5 meters. The useful plot area consisted on two central rows, leaving a total of 5.0 m², with 48 plants. Genetic divergence was determined through multivariate techniques; the means were compared by the Scott-Knott’s test, at 5% probability. The grouping method used was the Mahalanobis’ generalized distance (D_m²), and for clustering the Tocher’s method and the Unweighted Pair Group Method with Arithmetic Mean (UPGMA). The relative contribution of each trait to diversity was determined by the Singh’s method (Singh, 1981). The analyses were carried out with the Genes Software (Cruz, 2001).

Results and Discussion

The results demonstrated that the first three canonic variables were the ones which contributed most for total variation of 82.88%, being them: plant height, number of days to flowering, and mean number of pod per plant. Using Tocher method, landraces and additional controls formed nine groups, being group I subdivided in seven subgroups (Figure 1). It was observed one subgroup composed mainly by cultivars of Carioca group. The UPMGA method clustered cultivars of different types, as Carioca and Jalo in distinguished groups. The most
divergent cultivars were Carioca Pitoco and Jalo vermelho, whereas the most similar were Carioca Pitoco and Carioca. In this study, the morphoagronomic characteristics proved to be efficient on discriminating landraces of common bean into Andean from Mesoamerican groups. These findings show the large genetic diversity of the Paraná landraces. Therefore, in the interpopulational selection is recommended to produce segregant populations from the crosses of Carioca and Jalo cultivars. These results evidenced the existence of genetic variability in bean cultivars used by farmers and multivariate analyses methods demonstrated efficiency to detect it separating in different groups the cultivars Carioca and Jalo. The cultivar Carnaval (33), Carioca Pitoco (16), Pérola (14) and Carnaval (27), due to the presence of highest productivity and being divergent, were indicated to generate populations in interpopulational selection programs.

Figure 1. Dendrogram of the 58 landraces and five cultivars (controls) of common bean, based on UPGMA method, using $D^2$ as a measure of dissimilarity.

References