VARIABILITY STUDY OF 89 SNAP BEAN GENOTYPES USING THE AFLP MOLECULAR TECHNIQUE

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Introduction:
Snap bean is a vegetable cultivated by small farmers in some mountainous and hillside regions of Colombian. Since the research of snap bean has not had the same importance as common beans in Colombia, little competitive varieties, compared to the quality of the Blue Lake variety have been released, with a culti-variety with low tolerance to the biotic constraints of the tropic (Silbernagel et al., 1999). The lineages, coming from crossing this variety and other well adapted ones to the tropic genotypes of Phaseolus vulgaris, exhibit low commercial quality due to the rupture of the co-adapted genetic complex that determines the characteristics of the pod (Myers and Baggett, 1999). Using the AFLP technique, the genetic variability of 89 traditional varieties of snap bean (coming from primary and secondary domestication centers) was studied, to identify genotypes genetically closer to the Blue Lake type, combining desirable characteristics of the pod to be included in the set of basic materials associated to breed programs (Beattie et al., 2003). This way, the genetic base of the culture would be bigger, without breaking the link group regarding the pod quality.

Materials and methods:
Eighty-nine traditional varieties of snap bean were evaluated; two commercial related varieties of snap bean, presenting contrasting fibrousness (Blue Lake and Millenium); two commercial varieties of common bean (ICA-Pijao, Diacol-Calima) and two wild beans, these four with different genetic pool (G 23441, Guatemalan and G 21117 Colombian) were used as controls. From a binary matrix of 51 polymorphic bands, using the software Tree NTSYS and the DICE coefficient, the similarity analysis was obtained, which was compared with a previous group according to the phaseolin type (Andean and Mesoamerican) (Tofiño et al., 2004), with the purpose of knowing the process recombination between genetic pools and their relation with the increase of the desirable characteristics of the snap bean. The level of association and the degree of the variability between the analysis of molecular similarity and the morphologic grouping were also evaluated. Additionally, the total diversity, the population indexes, and the genetic flow using the software POPGENE, coming from the initial group of the genotypes by phaseolin type, were estimated.

Results and discussion:
The indexes of diversity and population structure, using the same technique, indicate a moderate genetic differentiation between genetic pools (Ht=0.225; Hs=0.2064; Gst=0.0827; Nm= 5.534; I= 0.3413), similar to the sample using iso-enzymes(Tofiño et al., 2004); also, a total diversity comparable to that found in studies in wild Mesoamerican beans (Ht = 0.22), and superior in reported common Mesoamerican beans (Ht= 0.12; Papa and Gepts, 2003). However, a general homogeneity within the sample was observed, because the similarity dendogram was split in two big groups at a level of 77% of similarity, different to other works made in common beans using the same technique, in which a minimum similarity of 24% was found (Nowosielski et al., 2002). Each group presents a genetic pool predominance of Mesoamerican or Andean genetic pool with intermediate genotypes, that is Andean individuals grouped with Mesoamerican
genotypes and vice versa, similar to the observed by Tofinó et al., 2004. In the same way, the genetic diversity was found bigger between individuals coming from Andean genetic pool (0.2225) than in individuals from Mesoamerican genetic pool (0.1902). This result suggests that the Andean genetic pool was enriched with the flow of genes coming from Mesoamerican genetic pool; since many individuals with Andean phaseolin are grouped with Mesoamerican individuals. The molecular analysis managed to discriminate the commercial controls appropriately because the dry Mesoamerican bean was grouped with genotypes of snap bean with Mesoamerican phaseolin, and the Andean control was grouped with genotypes of Andean-origin snap beans. On the other hand, the commercial controls of related snap bean were close grouped. These results strengthen the reach of the previously collected data, in spite of the low quantity of polymorphic bands. Additionally, the wild controls, although of Mesoamerican origin, were grouped together with genotypes of Andean-phaseolin snap bean. Also, the genotypes grouped according to their potential for the Latin American fresh market and their morphologic and fibrousness analysis, were close grouped under an index of similarity of 90%. Nevertheless, the genotypes G18722 and G10165, with contrasting fibrousness, were grouped together within the predominantly Andean group. Otherwise, the iso-enzymatic analysis allowed discrimination of genotypes with contrasting fibrousness in spite of the high morphologic similarity of the pod. According to the previous data (Tofinó et al., 2004), the iso-enzymatic analysis allows a fine discrimination of the pod quality characteristics regarding the other evaluated markers. Additionally, the diversity found in the germoplasm of snap beans using AFLP, the morphologic and biochemical description are similar to the recorded germoplasm of common beans and something inferior to the registered one previously in snap bean using other molecular markers (0.388) (Skroch and Nienhuis, 1995).

References:
SKROCH, P; NIENHUIS, J.1995. Qualitative and quantitative characterization of RAPD variation among snap bean (Phaseolus vulgaris) genotypes. TAG 91(6-7):1078-1085