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## GENETIC DISSIMILARITY AMONG GENOTYPES OF SNAP BEANS BASED ON YIELD AND PRODUCTION COMPONENTS

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**INTRODUCTION:** The snap bean belong to the same botanical Family and species of common bean (*Phaseolus vulgaris* L.), however is classified as a vegetable because its immature pods with tenuous grains are the consumed part, thus is essential the obtaining of genotypes that ally high yields and great pod quality. An alternative, which has been used to direct new improvement programs, is the study of genetic dissimilarity (Freiria et al., 2016).

The aim of this study is to evaluate the genetic dissimilarity of tem snap beans genotypes based on yield and production components, with the intent to identify the most promising crosses.

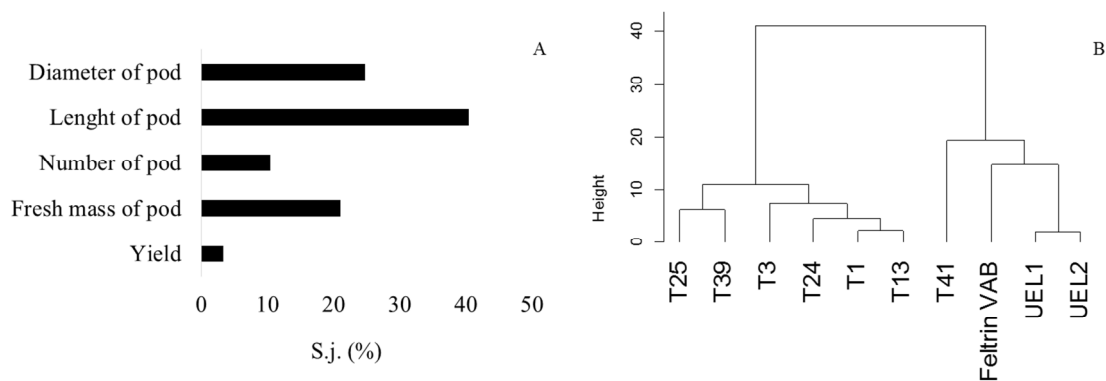
**MATERIAL & METHODS:** The rehearsal was conducted at Universidade Estadual de Londrina (UEL), located in latitude of 23°19'41.00” S, longitude of 51°12'18.19” W and altitude of 590 meters (Londrina, Parana state, Brazil). The design was completely randomized blocks with three repetitions, being each treatment composed by the tem genotypes of snap beans: Feltrin Vicenza Amarelo Baixo, UEL 1, UEL 2, T1, T3, T13, T24, T25, T39 and T41. Each parcel was composed by four lines (4m length) with a spacing of 0.50m between lines and were considered as borders the two external and 0.50m from the extremities of the central lines.

The seedling was in March 18<sup>th</sup> 2016 and the harvest realized in June 10<sup>th</sup> of the same year (fall/winter cultivation). Were measured the characteristics: Yield of pods (kg ha<sup>-1</sup>), unitary pod's fresh mass (g), number of pods per plant, pods diameter (mm) and length of pods (cm). For the dissimilarity analysis, the Mahalanobis generalized distance was estimated and was proceeded the cluster of UPGMA. The relative contribution of the characters was estimated based on Singh (1981). Also was made the main compounds analysis.

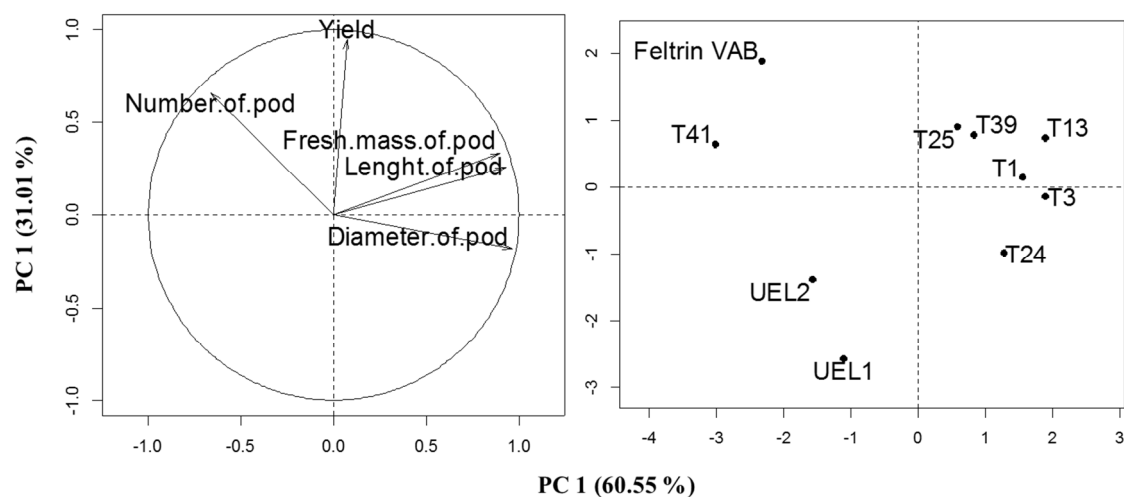
**RESULTS:** Based on Figure 1A it can be noted that the pods yield was the least contributor to dissimilarity (3.30%) and the pods length was the characteristic that presented the highest contribution, followed by pods diameter (40.49% e 24.73%, respectively). Based on UPGMA cluster (Figure 2B) is possible to make the separation of the genotypes into two groups, in 30% of genetic divergence: Group I – T25, T39, T3, T24, T1 and T13; and Group II – T41, Feltrin Vicenza Amarelo Baixo, UEL 1 and UEL 2. Results proximal to the ones obtained with the main compounds analysis (MCA) (Figure 2).

The Group I presented higher relation with the quality of pods, producing bigger pods in length and diameter, and with a higher unitary weight, consequently, pods with higher commercial appeal. Group II by the MCA was broken down into two new groups (Group IIa – T41 and Feltrin Vicenza Amarelo Baixo; and Group IIb – UEL 1 and UEL 2). The Group IIa presented higher association with the production vectors and number of pods per plant, which is, was constituted by more outputs genotypes. There was not observed any negative correlation among the vectors of the variables permitting to obtain productive genotypes and with a higher

Pods quality (Figure 2). Thus, the cross between the individuals of Group I with the ones from Group IIa showed promising to the obtainment of new materials.



**Figure 1.** Relative contribution of the characters to the genetic dissimilarity according to the method proposed (A) and representative UPGMA dendrogram of the genetic divergence of the ten snap beans genotypes, obtained based on the Mahalanobis dissimilarity matrix (B).



**Figure 2.** Main Components Analysis (MCA) of ten genotypes of snap beans to yield and pods production compounds.

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