

Genetic analysis in *Phaseolus vulgaris* by molecular markers related to yield traits under drought tolerance.

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World agriculture has major challenges towards to overcoming barriers of future projections of climate changes such as global warming and the gradual reduction in water availability. As a consequence, increasing emphasis has been given to integration of genomic technologies to the programs of genetic breeding aiming the development of common bean varieties with higher yield potential and stability under adverse environmental conditions. The present study aimed to create a database of expressed gene sequences (EST) followed by the identification of candidate genes involved in response to water deficit and the development of segregating populations for drought tolerance in order to identify QTLs related to yield components in common bean under conditions of water deficit. From a large set of ESTs derived from genotypes BAT477 (tolerant) and Pérola (susceptible) genotypes subjected to a drought stress experiment, differentially expressed sequences were identified in which the automatic annotation by BLASTnr allowed the identification of drought-induced genes. From these sequences were developed markers to search for SNPs on candidate genes using genotypes for drought tolerance. Linkage analysis was performed on a segregating population of 140 families (F₂) and, so far, a total of 100 microsatellites were grouped on multiplex systems, and used to genotype the population. A preliminary linkage analysis revealed markers distributed across the *Phaseolus* genome, and the marker order generally agreed with those obtained on previous genetic maps. The phenotypic data of yield-related traits obtained on F_{2,4} - F_{2,5} generations under drought stress experiments in Porangatu – GO showed a normal distribution. In addition to the genomic resources generated, as well as the advance of knowledge in QTLs analysis, it were identified drought- tolerant lines that can, in a near future, to be used as genitors to the development of more drought tolerant common beans cultivars.

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