

# Single nucleotide polymorphism DNA marker development in common bean

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The common bean is an important source of protein, dietary fiber, iron and other minerals, complex carbohydrates, vitamins and calories for millions of people in developing and developed nations in South America and Eastern and Southern Africa. Because the common bean is closely related to soybean, many of the thousands of SNP-containing sequence tagged sites (STS) available in soybean might be of use in common bean without the need for *de novo* SNP marker development. In soybean, SNPs occur at a frequency of about one SNP per 1000 nucleotides in genomic DNA and they can be used to directly detect alleles responsible for a trait of interest. Every SNP in context with its surrounding genomic sequence is unique. SNPs can mark functionally important allelic differences, and SNPs that flag individual alleles of known genes have been used widely as molecular markers. Recent work at the USDA, Beltsville resulted in SNP discovery in *P. vulgaris* via the analysis of an 864 PCR primer sets designed to soybean ESTs. Annealing temperatures of 48 and 58 °C were used to amplify genomic DNA of bean genotypes BAT93, Jalo EEP558, DOR364 and G19833 (international population parental). The percentage of primer sets that amplified a single band in *P. vulgaris* was 46.3%. A total of 391 amplicons from each of the four genotypes were sequenced from both ends for SNP discovery. The forward and reverse sequence reads of the 4 genotypes were aligned and analyzed to discover SNPs using Phred, Phrap and PolyBayes software. From the 391 STS analyzed, 91 (23.3%) had at least one SNP, with 1 to 23 SNPs/STS, producing a total of 304 single base polymorphisms in the 4 bean genotypes. A second set of 960 primers derived from soybean Bacterial Artificial Chromosome-end sequences was tested at the same annealing temperatures. The percentage of amplification in *P. vulgaris* was 35.61% and 346 primer sets were used in the amplification and sequence analysis of the same 4 bean genotypes. The alignment of the 346 sets of 8 sequence traces resulted in the discovery of 529 SNPs in 89 of the 346 STS. In total, 833 common bean SNPs were discovered in 180 different STS, which represents a significant increase in the tools available for genetic mapping and diversity analysis.

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