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IMPLEMENTATION OF SNP MARKERS TO IDENTIFY SOYBEAN VARIETIES COMMERCIALIZED IN URUGUAY

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Morphological, physiological and biochemical markers have been used to identify and differentiate varieties for years. The advance in genetic improvement has incorporated tools, such as the use of molecular markers to quickly and efficiently analyze germplasm under development. Molecular markers, especially SNP (Single Nucleotide Polymorphism) markers, have gained importance due to the advantage of being abundant in the genomes and polymorphic in populations. SNPs are routinely used in breeding programs, for phylogenetic and genetic diversity analysis and in association studies with agronomic traits, among others. This relevance is due to the ability to produce sequence information on an unprecedented scale that allows the detection of a large number of SNPs quickly and at low cost. Several sequencing methods have been developed to reduce the cost without compromising the quality of SNPs detected. Genotyping By Sequencing (GBS) is widely used and is based on the sequencing of a fraction of the entire genome, reducing complexity.

The purpose of this work is to determine a SNPs panel for identifying soybean varieties commercialized in Uruguay. Soybean varieties were genotyped by GBS to select a panel of SNPs markers. The varieties were genotyped by GBS and then bioinformatic tools were applied to obtain polymorphic SNPs in the population. After filtering SNPs by different quality parameters, a subset of 35 SNPs were selected. The 35 SNPs subset is at this moment under internal validation with different kind of samples. This 35 SNPs panel allow the identification of varieties under study and it will be helpful to control soybean seed trade.

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