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DEVELOPMENT OF FUNCTIONAL MARKERS ASSOCIATED WITH PHENOTYPIC TRAITS FOR IDENTIFICATION IN SOYBEAN

Document prepared by experts from Uruguay

Summary

The organization of agricultural systems requires the verification of the genetic identity and purity of varieties. The increase in the number of varieties to be evaluated and the narrow genetic base of the soybean varieties make the identification of the varieties through the evaluation of phenotypic descriptors very difficult. The International Union for the Protection of New Varieties of Plants (UPOV) has recognized the utility of molecular markers associated with descriptive phenotypic characteristics. With the target of developing that type of marker for variety identification, six genic and genomic SSR were selected *in silico* through gene search, expressed sequences (ESTs) and sequences included in QTL intervals (*Sat286*, *Satt229*, *GmPrx1*, *GMES1173*, *Satt571 and GmHi*). These six markers with two previously reported markers (allele specific *GmF35H* and a genic SSR *SoyF3H*) were validated using a group of 35 soybean genotypes. The SSRs *GmPrx1* and *GmHi* selected for seed coat peroxidase and hilum color respectively were monomorphic. The mean Polymorphism Information Content (PIC) value within the selected group of markers was 0.48 with an average of 3.12 allele per locus. The *GmF35H* marker discriminated the 35 soybean varieties according to the flower color (white and purple). Discrimination tests showed a high percentage of accurate classification of growth habit (95.8%) and pubescence color (80.6%) traits with the *SSR Sat286* and *SoyF3H* respectively. Accurate classification values for pod color (74.2%) and leaflet size (73.5%) were intermediate using SSR *GMES1173* and *Satt571* (*GmPin1*) respectively. The marker *Satt229* was not effective at discriminating (low percentage of accurate classification) for flowering time (50%) and maturity (42.8%). These results indicate that molecular markers selected in, or close to, sequences of interest can be integrated into a genetic identification system as complementary markers to the classic phenotypic descriptors of soybean varieties.

Keywords: *Glycine max L.*, SSR mining, molecular characterization.

Mariela, Ibarra [1]; Ariel, Castro [2]; Fabián, Capdevielle [3].

[1] Instituto Nacional de Semillas (INASE). Cam. Bertolotti s/nºy R. 8, Km. 29. Barros Blancos. Canelones, Uruguay. Correo electrónico: mibarra@inase.org.uy.
[2] Universidad de la República, Facultad de Agronomía, EEMAC. Departamento de Producción Vegetal. Ruta 3 Gral. Artigas Km. 363. Paysandú, Uruguay.
[3] Instituto Nacional de Investigación Agropecuaria. Unidad de Biotecnología. Estación Experimental INIA Las Brujas. Ruta 48 km. 10. Rincón del Colorado. Canelones, Uruguay.

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