GMR Genetics and Molecular Research
Online Journal
ISSN:1676-5680

Esterase polymorphisms for analysis of genetic diversity and structure of soybean (*Glycine max*) cultivars

L.C. Valentini, C.A. Mangolin, S.A.O. Collet and M.F.P.S. Machado

Departamento de Biologia Celular e Genética da Universidade Estadual de Maringá, Maringá, PR, Brasil

Corresponding author: M.F.P.S. Machado
E-mail: mfpsmachado@uem.br

Genet. Mol. Res. 10 (4): 2472-2481 (2011)
Received September 8, 2010
Accepted April 20, 2011
Published October 13, 2011
DOI http://dx.doi.org/10.4238/2011.October.13.4

ABSTRACT. We used native polyacrylamide gel electrophoresis to identify polymorphism levels in α- and β-esterase loci from leaf tissues of Brazilian soybean cultivars for the analysis of population genetic diversity and structure, and to investigate relationships between conventional and genetically modified cultivars. The cultivars included lines developed by a soybean-grower cooperative (CD), by EMBRAPA (BR), and "Roundup Ready" (RR) cultivars. Esterase isozymes recorded with α-naphthyl acetate and β-naphthyl acetate were produced from 14 loci. Two to three allelic variants were detected in leaves from 420 plants of 21 CD, BR, and RR cultivars at *Est-1*, *Est-2*, *Est-3*, *Est-5*, and *Est-14* loci. The estimated proportion of polymorphic loci in CD cultivars was 21.4%, and in BR and RR cultivars it was 28.6%. High and low H_O and H_E values were observed within CD and BR cultivars and a very high cultivar differentiation level was evident in the plants of the 21 CD, BR, and RR cultivars (F_{ST} = 0.3865). A low level of differentiation (F_{ST} = 0.0289) was detected between conventional and RR cultivars. Plants from cultivar BR37 had the highest level of genetic differentiation compared to the other cultivars. The genetic basis of BR cultivars (0.5538-0.9748) was found to be broader than the genetic

basis of CD cultivars (0.7058 for CD205 and CD209 and 0.9995 for CD205 and CD208). Higher genetic identity was detected between plants of CD and CDRR cultivars (I = 0.9816). Understanding the genetic structure of these populations can help provide specific culture strategies for each cultivar, depending on its level of heterozygosity.

Key words: Soybean; Esterase polymorphism; Genetic diversity

