



# Molecular identification and genetic variation of varieties of *Styphnolobium japonicum* (Fabaceae) using SRAP markers

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Genet. Mol. Res. 15 (2): gmr.15027837

Received October 15, 2015

Accepted January 18, 2016

Published May 6, 2016

DOI <http://dx.doi.org/10.4238/gmr.15027837>

**ABSTRACT.** Thirty-four *Styphnolobium japonicum* varieties were analyzed using sequence-related amplified polymorphism (SRAP) markers, to investigate genetic variation and test the effectiveness of SRAP markers in DNA fingerprint establishment. Twelve primer pairs were selected from 120 primer combinations for their reproducibility and high polymorphism. We found a total of 430 amplified fragments, of which 415 fragments were considered polymorphic with an average of 34.58 polymorphic fragments for each primer combination. The percentage of polymorphic fragments was 96.60%, and four primer pairs showed 100% polymorphism. Moreover, simple matched coefficients ranged between 0.68 and 0.89, with an average of 0.785, indicating that the genetic variation among varieties was relatively low. This could be because of the narrow genetic basis of the selected breeding material. Based on the similarity coefficient value of 0.76, the varieties were divided into four major groups. In addition, abundant and clear SRAP fingerprints were obtained and could be used to

establish DNA fingerprints. In the DNA fingerprints, each variety had its unique pattern that could be easily distinguished from others. The results demonstrated that 34 varieties of *S. japonicum* had a relatively narrow genetic variation. Hence, a broadening of the genetic basis of breeding material is necessary. We conclude that establishment of DNA fingerprint is feasible by means of SRAP markers.

**Key words:** *Styphnolobium japonicum*; SRAP; Molecular identification; Genetic variation; DNA fingerprints