



Development of novel SCAR markers for genetic characterization of *Lonicera japonica* from high GC-RAMP-PCR and DNA cloning

J.L. Cheng^{1*}, J. Li^{1*}, Y.M. Qiu^{1,2*}, C.L. Wei^{1,3}, L.Q. Yang¹ and J.J. Fu^{1,3,4}

¹Key Laboratory of Epigenetics and Oncology,
The Research Center for Preclinical Medicine,
Sichuan Medical University, Luzhou, Sichuan, China

²Maternal and Child Health Care Hospital of Zigong, Zigong, Sichuan, China

³State Key Laboratory of Quality Research in Chinese Medicine,
Macau University of Science and Technology, Macau, China

⁴Judicial Authentication Center, Sichuan Medical University, Luzhou City,
Sichuan, China

*These authors contributed equally to this study.

Corresponding author: J.J. Fu

E-mail: fujunjiang@hotmail.com / fujunjiang@lzm.edu.cn

Genet. Mol. Res. 15 (2): gmr.15027737

Received December 16, 2015

Accepted January 15, 2016

Published April 27, 2016

DOI <http://dx.doi.org/10.4238/gmr.15027737>

ABSTRACT. Sequence-characterized amplified region (SCAR) markers were further developed from high-GC primer RAMP-PCR-amplified fragments from *Lonicera japonica* DNA by molecular cloning. The four DNA fragments from three high-GC primers (FY-27, FY-28, and FY-29) were successfully cloned into a pGM-T vector. The positive clones were sequenced; their names, sizes, and GenBank numbers were JYHGC1-1, 345 bp, KJ620024; YJHGC2-1, 388 bp, KJ620025; JYHGC7-2, 1036 bp, KJ620026; and JYHGC6-2, 715 bp, KJ620027, respectively. Four novel SCAR markers were developed by designing specific primers, optimizing conditions, and PCR validation. The developed SCAR markers were used for the genetic authentication

of *L. japonica* from its substitutes. This technique provides another means of developing DNA markers for the characterization and authentication of various organisms including medicinal plants and their substitutes.

Key words: High GC-content primers; RAMP-PCR; Sequence-characterized amplified region (SCAR); Genetic authentication; *Lonicera japonica*; Substitutes