Methylation-sensitive amplified polymorphism-based genome-wide analysis of cytosine methylation profiles in *Nicotiana tabacum* cultivars

J. Jiao[1,2]*, J. Wu[1]*, Z. Lv[3], C. Sun[2], L. Gao[1], X. Yan[1], L. Cui[1], Z. Tang[2], B. Yan[2] and Y. Jia[4]

[1]School of Basic Medicine, Xinxiang Medical University, Xinxiang, Henan, China
[2]Agronomic College, Sichuan Agriculture University, Ya'an, Sichuan, China
[3]The Third Affiliated Hospital of Xinxiang Medical University, Xinxiang, Henan, China
[4]Pharmacy College, Xinxiang Medical University, Xinxiang, Henan, China

*These authors contributed equally to this study.
Corresponding author: Y. Jia
E-mail: yljiacn@126.com

Genet. Mol. Res. 14 (4): 15177-15187 (2015)
Received April 7, 2015
Accepted July 31, 2015
Published November 25, 2015
DOI http://dx.doi.org/10.4238/2015.November.25.6

ABSTRACT. This study aimed to investigate cytosine methylation profiles in different tobacco (*Nicotiana tabacum*) cultivars grown in China. Methylation-sensitive amplified polymorphism was used to analyze genome-wide global methylation profiles in four tobacco cultivars (Yunyan 85, NC89, K326, and Yunyan 87). Amplicons with methylated C motifs were cloned by reamplified polymerase chain reaction, sequenced, and analyzed. The results show that geographical location had a greater effect on methylation patterns in the tobacco genome than did sampling time. Analysis of the CG dinucleotide distribution in methylation-sensitive polymorphic restriction fragments suggested that a CpG dinucleotide cluster-enriched area is a possible site of cytosine methylation in the tobacco genome. The sequence alignments of the *Nia1* gene (that encodes nitrate reductase) in Yunyan 87 in different regions indicate that a C-T transition might be responsible for the

tobacco phenotype. T-C nucleotide replacement might also be responsible for the tobacco phenotype and may be influenced by geographical location.

Key words: Methylation-sensitive amplified polymorphism; Nia1; Epigenetics; Methylation; Tobacco (*Nicotiana tabacum*); Phenotype

