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

Analysis of DNA methylation patterns and levels in maize hybrids and their parents

T.J. Liu[1]*, L.F. Sun[1,2]*, X.H. Shan[1], Y. Wu[1], S.Z. Su[1], S.P. Li[1], H.K. Liu[1], J.Y. Han[1] and Y.P. Yuan[1]

[1]College of Plant Science, Jilin University, Changchun, China
[2]College of Agronomy, Heilongjiang Bayi Agricultural University, Development Zone, Daqing, China

*These authors contributed equally to this study.
Corresponding authors: J.Y. Han / Y.P. Yuan
E-mail: han_junyou@126.com / yuanyp@jlu.edu.cn

Genet. Mol. Res. 13 (4): 8458-8468 (2014)
Received September 24, 2013
Accepted March 20, 2014
Published October 20, 2014
DOI http://dx.doi.org/10.4238/2014.October.20.22

ABSTRACT. Heterosis is the superior performance of heterozygous individuals and has been widely exploited in plant breeding, although the underlying regulatory mechanisms still remain largely elusive. To understand the molecular basis of heterosis in maize, in this study, roots and leaves at the seedling stage and embryos and endosperm tissues 15 days after fertilization of 2 elite hybrids and their parental lines were used to estimate the levels and patterns of cytosine methylation by the methylation-sensitive amplification polymorphism method. The relative total methylation levels were lower in all the tissues of all hybrids than their corresponding mid-parent values, and the number of demethylation events was higher in the hybrids. These results implied that the decreasing trend and demethylation in hybrids relative to their parents may enable the derepression and possibly expression of many genes that were associated with the phenotypic variation in hybrids. To further analyze the observed methylation pattern changes, a total of 63 differentially displayed DNA fragments were successfully sequenced. Basic Local Alignment Search Tool analysis showed that 11

fragments shared similarity with known functional proteins in maize or other plant species, including metabolism, transposon/retrotransposon, development, stress response, and signal transduction, which indicated that these genes might play a significant role in maize hybrid vigor.

Key words: Heterosis; DNA methylation; Hybrid; Maize; Methylation-sensitive amplification polymorphism

