

DNA methylation changes facilitated evolution of genes derived from Mutator-like transposable elements

2016

Posted by : webmaster

Posted on : 2016/5/6 11:40:21

Jun Wang, Yeisoo Yu, Feng Tao, Jianwei Zhang, Dario Copetti, Dave Kudrna, Jayson Talag, Seunghee Lee, Rod A. Wing and Chuanzhu Fan

Genome Biology 2016 17:92

DOI: 10.1186/s13059-016-0954-8 © Wang et al. 2016

Received: 1 October 2015 Accepted: 14 April 2016 Published: 6 May 2016

<http://www.genomebiology.com/2016/17/1/92>

Abstract

Background

Mutator-like transposable elements, a class of DNA transposons, exist pervasively in both prokaryotic and eukaryotic genomes, with more than 10,000 copies identified in the rice genome. These elements can capture ectopic genomic sequences that lead to the formation of new gene structures. Here, based on whole-genome comparative analyses, we comprehensively investigated processes and mechanisms of the evolution of putative genes derived from Mutator-like transposable elements in ten *Oryza* species and the outgroup *Leersia perieri*, bridging ~20 million years of evolutionary history.

Results

Our analysis identified thousands of putative genes in each of the *Oryza* species, a large proportion of which have evidence of expression and contain chimeric structures. Consistent with previous reports, we observe that the putative Mutator-like transposable element-derived genes are generally GC-rich and mainly derive from GC-rich parental sequences. Furthermore, we determine that Mutator-like transposable elements capture parental sequences preferentially from genomic regions with low methylation levels and high recombination rates. We explicitly show that methylation levels in the internal and terminated inverted repeat regions of these elements, which might be directed by the 24-nucleotide small RNA-mediated pathway, are different and change dynamically over evolutionary time. Lastly, we demonstrate that putative genes derived from Mutator-like transposable elements tend to be expressed in mature pollen, which have undergone de-methylation programming, thereby providing a permissive expression environment for newly formed/transposable element-derived genes.

Conclusions

Our results suggest that DNA methylation may be a primary mechanism to facilitate the origination, survival, and regulation of genes derived from Mutator-like transposable elements, thus contributing to the evolution of gene innovation and novelty in plant genomes.

Keywords

Comparative genomics DNA methylation GC content Molecular evolution MULEs New genes
Oryza Recombination rate