



## Transposable elements in *Phyllostachys pubescens* (Poaceae) genome survey sequences and the full-length cDNA sequences, and their association with simple-sequence repeats

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Genet. Mol. Res. 10 (4): 3026-3037 (2011)

Received January 5, 2011

Accepted March 31, 2011

Published December 6, 2011

DOI <http://dx.doi.org/10.4238/2011.December.6.3>

**ABSTRACT.** *Phyllostachys pubescens* is a woody bamboo with the highest ecological, economic, and cultural values of all bamboos in Asia. There is more genomic data available for *P. pubescens* than for any other bamboo species, including 2.12-Mb genome survey sequences (GSS) and 11.4-Mb full-length cDNA sequences (FL-cDNAs) currently deposited in GenBank. Analysis of these sequences revealed that transposable elements (TEs) are abundant, diverse and polyphyletic in the *P. pubescens* genome, of which Ty3-gypsy and Ty1-copia are the two most abundant families. Phylogenetic analysis showed that both elements probably arose before the Bambusoideae separated from the other Poaceae subfamilies. We found evidence that the distribution of some intragenic TEs correlated with transcript profiles, of which *Mutator* elements preferred to insert in the transcripts of transcription factors. Additionally, we found that the abundance of SSRs in TEs (4.56%) was significantly higher than in GSS (0.098%) and in FL-cDNAs (2.60%) in *P. pubescens* genome, and TA/AT and

CT/AG repeats were found to be intimately associated with *En/Spm* and *Mutator* elements, respectively. Our data provide a glimpse of the structure and evolution of *P. pubescens* genome, although large-scale sequencing of the genome would be required to fully understand the architecture of the *P. pubescens* genome.

**Key words:** *Phyllostachys pubescens*; Transposable elements; Genome survey sequences; Full-length cDNA sequences; Simple-sequence repeats