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Evolutionary origin of Rosaceae-specific active non-autonomous *hAT* elements and their contribution to gene regulation and genomic structural variation

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Abstract Transposable elements account for approximately 30 % of the *Prunus* genome; however, their evolutionary origin and functionality remain largely unclear. In this study, we identified a *hAT* transposon family, termed *Moshan*, in *Prunus*. The *Moshan* elements consist of three types, *aMoshan, tMoshan*, and *mMoshan*. The *aMoshan* and *tMoshan* types contain intact or truncated transposase genes, respectively, while the *mMoshan* type is miniature inverted-repeat transposable element (MITE). The *Moshan* transposons are unique to Rosaceae, and the copy numbers of different *Moshan* types are significantly correlated. Sequence homology analysis reveals that the *mMoshan* MITEs are direct deletion derivatives of the *tMoshan* progenitors, and one kind of *mMoshan* containing a *MuDR*-derived fragment were amplified predominately in the peach genome. The *mMoshan* sequences contain *cis*-regulatory elements that can enhance gene expression up to 100-fold. The *mMoshan* MITEs can serve as potential sources of micro and long noncoding RNAs. Whole-genome re-sequencing analysis indicates that *mMoshan* elements are highly active, and an insertion into *S-haplotype-specific F-box* gene was reported to cause the breakdown of self-incompatibility in sour cherry. Taken together, all these results suggest that the *mMoshan* elements play important roles in regulating gene expression and driving genomic structural variation in *Prunus*.

Keywords *Prunus* · MITEs · Micro-RNAs · Peach · *hAT* transposon

Introduction

Transposable elements (TEs) are widely distributed in almost all organisms, and occupy a large fraction of many eukaryotic genomes (Kidwell 2002). TEs are grouped into two classes, retrotransposons (class I) and DNA transposons (class II) based on the mechanism of their transposition (Seberg and Petersen 2009). Retrotransposons move by a copy-and-paste mechanism *via* an RNA intermediate, whereas, DNA transposons move by a cut-and-paste process. TEs of both classes are further divided into autonomous and non-autonomous types. Autonomous transposons encode the proteins (also known as transposases) necessary for their own transposition, whereas, non-autonomous TEs do not encode transposases and their mobilization requires the supply of transposases produced by autonomous elements (Wicker et al. 2007). Most TEs in eukaryotic genomes are non-autonomous, and are presumed to be remnants of autonomous TEs that have

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