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Development of genic SSR markers from transcriptome sequencing of pear buds

基于‘酥梨’芽转录组的SSR标记开发

Key words: Genic marker, Simple sequence repeat, Transcriptome, *Pyrus*, Genetic diversity

关键词：SSR标记， 转录组，梨属，遗传多样性

- Pears are considered to be typically self-incompatible and interspecies compatible, phylogenetic relationships within the genus *Pyrus* are complicated and difficult to be established.

- The transcriptome database offers an attractive alternative to complement existing SSR collections for assessing molecular phylogeny and genetic diversity in the *Pyrus* species.

- A total of 8375 genic SSR loci were discovered from transcriptomic unigenes, a set of 104 genic SSR markers were developed and twenty-eight polymorphic loci were further validated.

- These polymorphic SSR markers showed high polymorphism demonstrating their effectiveness in analyzing *Pyrus* genetic relationships and confirming the potential value of a pear transcriptome database for the development of new SSR markers.

Transcriptome Database of Pear Bud

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Identification of SSR Loci

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Primer Design and Polymorphism Testing

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Polymorphic Marker Validation

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Confirmed the potential value of a pear transcriptome database for the development of new SSR markers and their effectiveness in analyzing *Pyrus* genetic relationships