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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

Identification of SSR Loci

Primer Design and Polymorphism Testing

Polymorphic Marker Validation

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