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Genome-wide profiling of genetic variation in *Agrobacterium*-□□ transformed rice plants

Key words: **Transformation, Genome-wide variation, Transfer DNA, Transposon, Rice**

Research Summary

1. Genomes of 5 independent transformed rice were sequenced at the depth of 24-fold coverage on average.

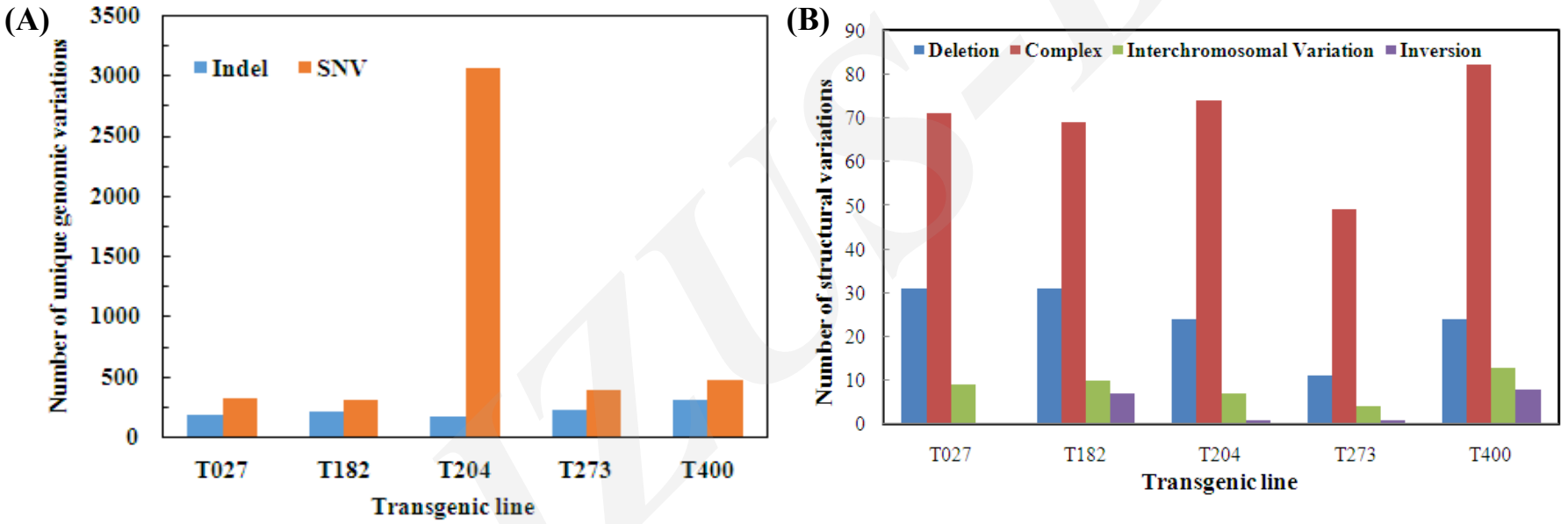
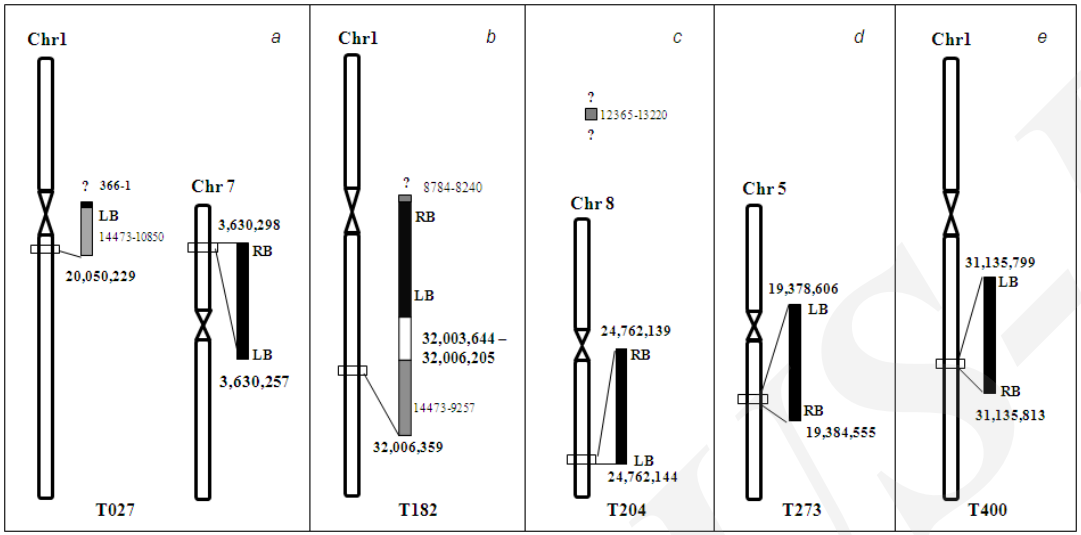


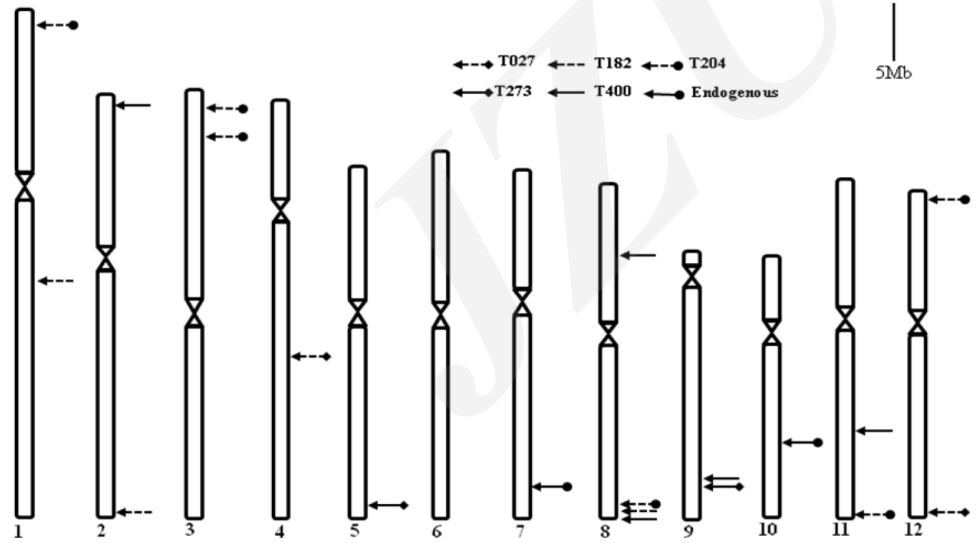
Fig1. SNV, Small InDel (A) and Structural variations(B) detected uniquely in transgenic lines.

2. The numbers of single nucleotide variation (SNV), insertion/deletion (Indel), and different types of structural variations were examined.

(A)



(B)



3. **The insertion of transfer DNA (T-DNA) and plasmid backbone sequences (A), as well as activation of other transposable elements (TEs) were examined (B, *Tos 17*) in the transformed plants.**

Innovation points

- **The spectra and frequency of different types of genetic variation in transformed rice plants generated *via Agrobacterium*-mediated transformation were disclosed at the genome-wide level and at single nucleotide resolution.**
- **T-DNA and plasmid backbone DNA sequences were identified in different configurations, highlighting the importance of genome-wide analysis for safety assessment.**
- **The results greatly enriched our knowledge of the genetics and genomics of *Agrobacterium*-transformed plants.**

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