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## Genome-wide analysis and expression profile of the bZIP gene family in poplar

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**摘要**

**Background**

The bZIP gene family, which is widely present in plants, participates in varied biological processes including growth and development and stress responses. How do the genes regulate such biological processes? Systems biology is powerful for mechanistic understanding of gene functions. However, such studies have not yet been reported in poplar.

**Results**

In this study, we identified 86 poplar bZIP transcription factors and described their conserved domains. According to the results of phylogenetic tree, we divided these members into 12 groups with specific gene structures and motif compositions. The corresponding genes that harbor a large number of segmental duplication events are unevenly distributed on the 17 poplar chromosomes. In addition, we further examined collinearity between these genes and the related genes from six other species. Evidence from transcriptomic data indicated that the bZIP genes in poplar displayed different expression patterns in roots, stems, and leaves. Furthermore, we identified 45 bZIP genes that respond to salt stress in the three tissues. We performed co-expression analysis on the representative genes, followed by gene set enrichment analysis. The results demonstrated that tissue differentially expressed genes, especially the co-expressing genes, are mainly involved in secondary metabolic and secondary metabolite biosynthetic processes. However, salt stress responsive genes and their co-expressing genes mainly participate in the regulation of metal ion transport, and methionine biosynthetic.

### Conclusions

Using comparative genomics and systems biology approaches, we, for the first

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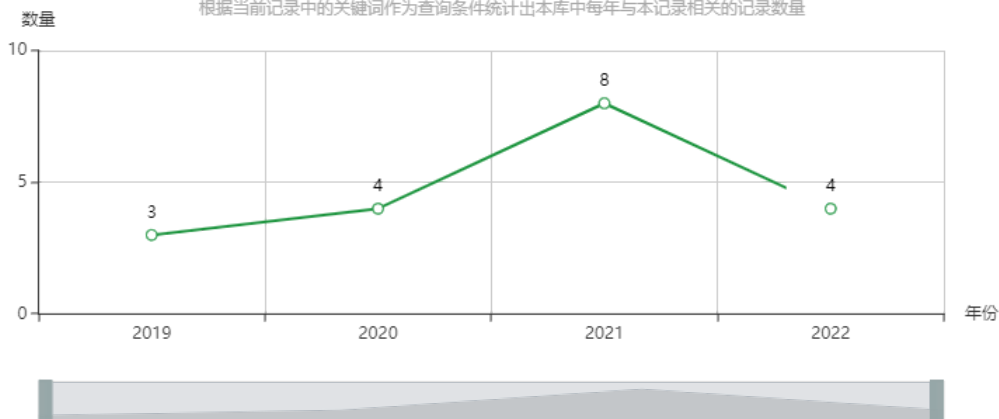
poplar. It appears that the bZIP gene family plays significant roles in regulation of poplar development and growth and salt stress responses through differential gene networks or biological processes. These findings provide the foundation for genetic breeding by engineering target regulators and corresponding gene networks into poplar lines.

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