

Chinese scientists reveal the genomic enigma of desert poplar

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In a collaborative study, researchers from Lanzhou University, BGI and other institutes have succeeded in unraveling the whole genome sequence of desert poplar, *Populus euphratica*, and the genetic bases underlying poplar to against salt stress. This work provides new insights for understanding the genetic basis of tree adaptation to salt stress and facilitating the genetic breeding of cultivated poplars for saline fields. The research results have been published online in [Nature Communications](#).

Trees are the lungs of the earth for that they can fix CO₂ - the major greenhouse gas - more efficiently. Forest trees rarely can grow in saline soils, but desert poplar is well-adapted to extreme desert environments and is an important species for studying the effects of salt stresses on trees. Notably, it maintains higher growth and photosynthetic rates than other poplar species at high salinity, and can survive concentrations of NaCl in nutrient solution up to 450mM. However, the knowledge of the genomic mechanisms of desert poplar under salt stress remains very limited.

Considering the limitation of next-generation sequencing for assembling complex genome and the high heterozygosity of desert poplar, researchers used a newly developed fosmid-pooling strategy to sequence and assemble the genome of this tree species. All the efforts yielded a high-quality [genome sequence](#) of desert poplar with high contiguity, coverage and accuracy, further demonstrating the feasibility of this fosmid-pooling approach for de novo sequencing and assembly of a

complex heterozygous genome.

The genome of desert poplar is very similar to that of the closely related mesophytic congener, *P. trichocarpa*. Researchers investigated the differences between the two genomes and suggested that *P. euphratica* diverged from *P. trichocarpa* within the last 8 to 14 million years. Although both species shared at least two whole-genome duplication (WGDs) and exhibited extensive collinearity across the gene space, species-specific genes involved in stress tolerance, such as "ion transport", "ATPase activity", "transcript factor activity" and "oxidoreductase activity", were selectively expanded and/or positively selected in the *P. euphratica* genome.

When studying the adaptation mechanisms to against salt stress, researchers found that several gene families likely to be involved in tolerance to salt stress contain significantly more gene copies in the *P. euphratica* lineage. They also compared the *P. euphratica* in response to salt stress with salt-sensitive poplar (*P. tomentosa*), and found some genes involved in ion transport and homeostasis, such as NhaD1, KUP3 and NCL, were distinctly upregulated under salt stress.

"The complete [genome](#) sequencing of desert poplar revealed the underlying genetic mechanisms of poplar to against salt stress, laying a solid foundation for accelerating the genetic breeding of cultivated poplars for saline and desert fields." said Junyi Wang, Project Manager at BGI, "Our work also demonstrate that trans-omic approach to study salt-tolerant plants is applicable on both herbaceous plant and woody plant, providing new insights into the comprehensive understanding of plants' salt tolerance and drought resistance."

Provided by BGI Shenzhen

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