

Genetic adaptation of Tibetan poplar (*Populus szechuanica* var. *tibetica*) to high altitudes on the Qinghai-Tibetan Plateau

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Abstract

Plant adaptation to high altitudes has long been a substantial focus of ecological and evolutionary research. However, the genetic mechanisms underlying such adaptation remain poorly understood. Here, we address this issue by sampling, genotyping, and comparing populations of Tibetan poplar, *Populus szechuanica* var. *tibetica*, distributed from low (~2000 m) to high altitudes (~3000 m) of Sejila Mountain on the Qinghai-Tibet Plateau. Population structure analyses allow clear classification of two groups according to their altitudinal distributions. However, in contrast to the genetic variation within each population, differences between the two populations only explain a small portion of the total genetic variation (3.64%). We identified asymmetrical gene flow from high- to low-altitude populations. Integrating with population genomic and landscape genomic manner, we detected a hot spot region containing ten genes under natural selection and associated with five environmental factors. These genes participate in abiotic stress resistance and regulating the reproductive process. Our results provide insight into the genetic mechanisms underlying high-altitude adaptation in Tibetan poplar.

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