Genome and evolution of the shade?requiring medicinal herb Panax ginseng
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Summary
Panax ginseng C. A. Meyer, reputed as the king of medicinal herbs, has slow growth, long generation time, low seed production and complicated genome structure that hamper its study. Here, we unveil the genomic architecture of tetraploid P. ginseng by de novo genome assembly, representing 2.98 Gbp with 59 352 annotated genes. Resequencing data indicated that diploid Panax species diverged in association with global warming in Southern Asia, and two North American species evolved via two intercontinental migrations. Two whole genome duplications (WGD) occurred in the family Araliaceae (including Panax) after divergence with the Apiaceae, the more recent one contributing to the ability of P. ginseng to overwinter, enabling it to spread broadly through the Northern Hemisphere. Functional and evolutionary analyses suggest that production of pharmacologically important dammarane?type ginsenosides originated in Panax and are produced largely in shoot tissues and transported to roots; that newly evolved P. ginseng fatty acid desaturases increase freezing tolerance; and that unprecedented retention of chlorophyll a/b binding protein genes enables efficient photosynthesis under low light. A genome?scale metabolic network provides a holistic view of Panax ginsenoside biosynthesis. This study provides valuable resources for improving medicinal values of ginseng either through genomics?assisted breeding or metabolic engineering.

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