

Scientists completed the first orchid whole genome sequencing

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As one of the most diverse plant family, orchid now has its first genome sequenced and the result is published at *Nature Genetics* as a cover article.

This study is an accomplishment of the Orchid Genome Project, an international collaboration led by Lai-Qiang Huang and Zhong-Jian Liu at Tsinghua University and National Orchid Conservation Center in Shenzhen China, with colleagues from different institutions, including Chengkong University in Taiwan, Ghent University in Belgium, and Institute of Botany of CAS in Beijing.

The team carried out whole [genome](#) sequencing on phalaenopsis equestris, which is an important parental species for breeding of commercial phalaenopsis strains. P. equestris is also the first plant with Crassulacean Acid Metabolism (CAM) for which the genome has been sequenced. The assembled genome contains 29,431 predicted protein-coding [genes](#). The average intron length is 2,922 base pairs, which is much longer than in any sequenced [plant genomes](#). Further analysis indicate that transposable elements in introns are the major reason why orchid genes have so big introns.

As heterozygosity post great challenge for whole [genome sequencing](#) and assembly, the orchid genome is by no means an exception. In the orchid genome, they found that contigs likely to be under-assembled owing to heterozygosity, are enriched for genes that might be involved in self-incompatibility pathways. Those genes could be candidates for further

research on the mechanism of self-incompatibility in orchid.

Like in many plant genomes, they also found evidence for an orchid-specific paleopolyploidy event that preceded the radiation of most orchid clades. This is possibly an important clue to why orchid developed into one of the largest plant families on earth.

By comparing with homolog genes in other plant genomes, they found gene duplication and loss in CAM genes along the lineage to orchid. This result suggests that gene duplication might have contributed to the evolution of CAM photosynthesis in *P. equestris*.

Finally, they found expanded and diversified families of MADS-box C/D-class, B-class AP3 and AGL6-class genes, which might contribute to the highly specialized morphology of orchid flowers.

All around the world, orchids are highly endangered species because of illegal collection and habitat loss. The [complete genome sequence](#) of *P. equestris* will provide an important resource to explore orchid diversity and evolution at the genome level. The [genome sequence](#) will also be a key resource for the development of new concepts and techniques in genetic engineering, such as molecular marker-assisted breeding and the production of transgenic plants, which are necessary to increase the efficiency of orchid breeding and aid [orchid](#) horticulture research.

Provided by Tsinghua University

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