

ORCHID FEATURES, EVOLUTIONARY HISTORY INFORMED BY NEW GENOME

With the help of a new orchid genome sequence, an international team led by investigators in China, Belgium, Taiwan, and Japan has gained new insights into orchid evolution and adaptations.

Using a combination of short- and long-read sequencing, 10x Genomics scaffolding, and other approaches, the researchers came up with a draft genome sequence for *Apostasia shenzhenica*. Along with an annotation of the genome, helped along by new transcriptome sequences, they performed comparative genomics and phylogenetics analyses to look at orchid relationships and ancestral orchid features.

"The genome sequence of *A. shenzhenica*, an orchid belonging to a small clade that is sister to the rest of Orchidaceae, provides a reference for studying orchid evolution, revealing clear evidence of an ancient [whole genome duplication] shared by all orchids, facilitating reconstruction of the ancestral orchid gene toolkit, and providing insights into many orchid-specific features," the authors of the new study, published in *Nature* today, wrote. The study was led by investigators at the Shenzhen Key Laboratory for Orchid Conservation and Utilization and other centers in China, Belgium, Taiwan, and Japan.

After isolating genomic DNA from leaf, stem, and flower samples collected from *A. shenzhenica* plants in southeastern China, the researchers used Illumina HiSeq 2000 and PacBio RS sequencers to generate short and long reads to put together a draft genome for the plant and fill gaps.

The team estimated that the resulting genome — which also included sequences and scaffolds produced with 10x Genomics technology and spanned some 349 million bases — is nearly 94 percent complete.

With the new genome and RNA sequences generated for the same orchid tissues using Illumina HiSeq 2000 reads, the researchers identified 21,841 predicted protein-coding genes. More than 92 percent of those genes were represented in the transcriptome sequences.

From there, they analyzed *A. shenzhenica* sequences in conjunction with sequences from more than a dozen other plant species for a phylogenetic analysis based on a few hundred single-copy gene families. The investigators also searched for gene families that appeared to have ballooned or dwindled over the course of orchid evolution, along with other clues to past genome duplications or alterations.

For example, the team's analyses suggest that the *A. shenzhenica* lineage has undergone at least two whole-genome duplications: one event that occurred in the ancestors of orchids and lineages leading to pineapple, asparagus, and other monocot plants, and a more recent, orchid-specific whole-genome duplication that took place not long after Orchidaceae plants started diversifying.

And because the *A. shenzhenica* plant has some physical features that differ from those found in other orchids — including relatively rudimentary reproductive structures and an undifferentiated version of the labellum or lip that most orchids use to lure in pollinators — the investigators were able to begin teasing apart the genetic contributors to some specialized orchid traits.

"We identify new gene families, gene family expansions and contractions, and changes within MADS-box gene classes, which control a diverse suite of developmental processes during orchid evolution," the authors wrote, noting that their work "sheds new light on the genetic mechanisms underpinning key orchid innovations."

GENOMEWEB

