

Pear genome provides new insight into breeding improvement and evolutionary trace analysis

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An international research team led by Nanjing Agricultural University and BGI, has completed the first genomic sequence of pear by an approach using the combination of BAC-by-BAC strategy and next-gen sequencing. The pear genome not only provides an invaluable new resource for breeding improvement of this important crop, but also sheds new light on the genome evolution and other genome-wide comparative studies. The results were published online in *Genome Research*.

As one of the oldest [fruit crops](#), pear has more than 3,000 years of cultivation history and is likely to have originated during the Tertiary period ([65 million years](#) ago) in southwestern China. This important fruit crop is genetically diverse with more than 5,000 [cultivars](#) and accessions present all over the world that could be divided into two major groups, the European or "Occidental" pears and the Asiatic or "Oriental" pears.

Unlike many crops, pear is known to be highly heterozygous, which is a big challenge for de novo assembly based on current strategies. In this study, researchers sequenced and assembled the [pear genome](#), *P. bretschneideri* Rehd. cv. Dangshansuli using a combination of BAC-by-BAC and next generation sequencing technology. This approach is developed by BGI, which can be used to study the genomes with high level of heterozygosity and/or repetitive sequences. After data process, the assembled pear genome size is about 512.0 Mb, with a total of

42,812 protein-coding genes.

In this study, researchers identified repetitive sequences of 271.9 Mb, accounting for 53.1% of the pear genome. By comparison with the apple genome, they found the size differences between pear and apple genome were mostly contributed by content diversity in transposable elements (TEs), while genic regions are similar in both species.

Through [comparative genomics](#) and evolution analysis, researchers found pear, apple and strawberry shared an ancient whole-[genome duplication](#) (WGD) event that took place about 140 million years ago. About 30~45 million years ago, pear and apple shared a recent WGD event. After the two WGD events, pear and apple diverged from each other about 5.4~21.5 million years ago. Moreover, researchers inferred that the nine ancestral chromosomes formerly reported in apple, are not only the origin of the Pyreae tribe, but also serve as the ancestors of the whole Rosaceae family.

The availability of pear genome sequence provides an invaluable new resource for biological studies. In the study, researchers worked on the mechanisms underlying important biological processes of pear including stone cell formation, sugar accumulation, aroma formation. Six candidate SFB genes were predicted to be related with self incompatibility, and 66 lignin synthesis-related gene families were identified, including HCT genes associated with lignin synthesis, C3'H and CCOMT that related with the accumulation of both G-lignin and S-lignin, as well as three gene families of S6PDH, SDH, and SOT that involved in sorbitol metabolism. Furthermore, researchers also found that the metabolism of α -linolenic acid was likely to play an important role in aroma formation in pear fruit.

Zhiwen Wang, Project Manager of BGI, said, "BAC to BAC strategy is an excellent method to assemble the genomes with high heterozygosity.

The completed sequencing of pear genome offers invaluable data resource for better tracing the evolutionary history of Rosaceae crops. I expect that our efforts could promote the breeding improvement and yield more delicious pears."

Provided by BGI Shenzhen

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