

# International consortium announce the first complete sequencing of pear genome

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An international pear genome consortium, comprised of seven universities and institutes, has completed the first pear genomic sequence in the world. The early access of pear genomic data is now available online (<http://peargenome.njau.edu.cn>). The international team includes researchers from Nanjing Agricultural University, BGI, Zhejiang Academy of Agricultural Sciences, University of Illinois at Urbana-Champaign, University of Georgia, University of Hawaii, and Tohoku University.

Pear (*Pyrus spp.*) is one of the major and oldest cultivated fruit trees in the temperate regions, which is likely to have originated during the Tertiary period (65 million years ago) in southwestern China. It 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.

Since pear [genome sequencing](#) project was initiated in April of 2010, the consortium has devoted great efforts on the de novo sequencing, assembly and annotation. The joint effort has yielded a high-quality diploid draft genome sequence for the commercially important Asiatic pear cultivar "Suli", *P. bretschneideri* Rehd. cv. Dangshansuli. A total of 97.1% of the estimated whole [genome size](#) has been assembled. These assembled scaffolds have been aligned and oriented to their corresponding 17 chromosomes using a high-density genetic map.

Professor Shaoling Zhang, the chief scientist and group leader of the

pear genome sequencing project at Nanjing Agricultural University, said, "The complete sequencing of the pear genome provides a solid scientific foundation for scientists to explore the complex [genetic characteristics](#) underlying the pear fruit tree, such as the key genes that related with the taste, color, storage, resistance for diseases and insects as well as yield improvement. Moreover, the genomic sequence provides an invaluable new resource for tracing pear's [evolutionary history](#)."

Professor Jun Wang, Executive Director of BGI, said, "The completion of the genome sequencing is a major step forward to understanding pear's important economic traits. We are making continuous efforts for decoding genomes of plants and animals that play a key economic role or are considered valuable food sources, as well as endangered species that have evolutionary or scientific importance. We would like to enhance the genomic research through collaborative projects with researchers worldwide for better understanding the genetics basis of plants and animals and boosting the further development of modern agriculture."

Provided by BGI Shenzhen

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