The first genome sequence of Chinese plum provides important resource for fruit improvement

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A Chinese research team, led by Beijing Forestry University, BGI, Beijing Lin Fu Ke Yuan Flowers Co., Ltd, and other institutes, has completed the first genomic sequence of *Prunus mume*, known as mei. This work is extremely important for the deeper understanding of Rosaceae evolution and provides an invaluable resource for the improvement of fruit trees. The latest study was published online today in *Nature Communications*.

As one of the longest-lived flowering fruit trees, the *P. mume* was domesticated in China more than 3,000 years ago. It belongs to Rosaceae, the third most economically important plant family in temperate regions, and is characterized by high nutrition, medical value, and tolerance to low temperature in winter. Writers and artists have extolled the beauty of its flowers, and the blossom is considered to be the symbol of Chinese national spirit. The availability of *P. mume* genome will open a new way for better decoding the mysteries of this fascinating tree.

The plantation technique that makes *P. mume* so diverse—the artificial grafting—also makes their genomes difficult to assemble. In this study, researchers sequenced the genome of *P. mume*, a wild species from Tibet in China, using a robust approach integrated with next-generation sequencing (NGS) and whole-genome mapping (WGM) technologies. Then they constructed a high-density genetic map by applying restriction-

site-associated DNA (RAD) marker strategy that further improves the quality of the genomic reference. Through all the efforts, researchers yielded the ~237Mb *P. mume* reference genome.

The poor phylogenetic resolution of the Rosaceae suggests rapid evolution within the family. In this study, the evolutionary analysis of *P. mume* genome demonstrated that there was no recent whole-genome duplication (WGD) event happened after the differentiation between *P. mume* and *Malus x domestica* (apple). However, the triplicated genomic arrangement was found in the *P. mume* genome by paleo-history analysis in *Prunus*.

Supported by the genomic data of apple and strawberry (*Fragaria vesca*), researchers successfully reconstructed nine ancestral chromosomes of Rosaceae family, and analyzed the chromosome fusion, fission and duplication history in three major subfamilies, including genera *Prunus*, *Malus* and *Fragaria*. Through analysis, they hypothesized that at least 11 fissions and 11 fusions occurred in *P. mume* from the nine common ancestral chromosomes. For apple, at least one WGD and five fusions took place to reach the 17-chromosome structure, compared with 15 fusions for strawberry to affect the 7-chromosome structure.

P. mume is one of the first trees that bloom in early spring, blooming even below 0°C. In this study, researchers investigated the genetic characteristics underlying the mechanisms related to acclimate to cold weather and release itself from dormancy. They found that dormancy-associated MADS-box transcription factors (DAM) family and C-repeat-binding transcription factors (CBF) were two important factors related with flowering dormancy.

As the saying goes, "Plum blossom incense from the cold weather", *P. mume* always has a special fragrance in winter. To understand its mechanism of floral scent, researchers identified a series genes related to

the biosynthesis of volatile compounds, such as benzyl alcohol acetyltransferase (BEAT) gene. They supposed the expansion of the BEAT gene family might increase the content of benzyl acetate and therefore induces the special fragrance of *P. mume*.

The disease resistance related-genes may benefit the future breeding improvement. In this study, researchers found many related genes expanded tremendously in the *P. mume* genome, such as leucine-rich repeat receptor-like kinase (LRR-RLK) genes, the nucleotide-binding site-coding resistant gene (NBS-coding R gene), and pathogenesis-related (PR) gene families. It was reported that PR proteins could mediate plant defence against pathogenic constraints and the general adaptation to stressful environments. Most PR gene families in *P. mume* were expanded notably especially PR10, suggesting their expansion might be related to the response of *P. mume* to salt, drought and fungal infection in roots and leaves.

Wenbin Chen, Project Manager of BGI, said, "The *P. mume* genome lays a solid foundation for identification of important economic traits, and provides a valuable resource for *P. mume* breeding and other Rosaceae species studies. The work here also brings a new approach for further exploring the biosynthesis of floral scent and regulation mechanism of early blooming in endodormancy, and other comparative genomics studies on Rosaceae species."

Provided by BGI Shenzhen

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