

research highlights

FRUIT GENOMICS

New apple genome

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High-quality reference genomes not only facilitate our biological understanding of a species, but also pave the way for breeding. While many plant species have been sequenced using second-generation shotgun sequencing, the assemblies are often incomplete or inaccurate due to a high level of repeat content or heterozygosity. Now, using new sequencing and assembly technologies, Nicolas Daccord and Jean-Marc Celton from the Université d'Angers and colleagues report a high-quality reference genome for apple.

To overcome the issue associated with high heterozygosity rate, the researchers chose a doubled-haploid Golden Delicious line (GDDH13) for sequencing. By combining shotgun sequencing, single-molecule sequencing and optical mapping, a high-quality assembly of 649.7 Mb and consisting of 17 pseudochromosomes was

generated, with dramatically increased scaffold and contig sizes over the old apple genome.

The new assembly shows that transposable elements (TEs) represent over half of the apple genome. Estimation of the TE insertion age revealed that a major burst of TEs occurred around 21 million years ago. The burst coincided with the divergence between pear and apple, and also the uplift of the Tian Shan mountains

where apple originated, suggesting that the TE burst and related events may have promoted the species diversification and adaptive evolution.

The high-quality genome also provides a chance to examine genome-wide methylation patterns and epigenetically controlled processes in apple. Comparing the leaf and fruit methylomes, the researchers observed that most methylation differences occur at CHH sites, and some occur in genes that are probably involved in flower and fruit development. Comparing the methylomes between GDDH13 and an isogenic line of smaller fruit size, the researchers found candidate genes with different methylation levels that potentially contribute to the fruit size difference. Taken together, these data show that apple fruit development and fruit size are subjected to epigenetic regulation, and that methylation dynamics are important for apple fruit development.

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