

Researchers from China's Beijing Forestry University have unlocked a tool for fruit breeders and recorded the first genome sequence for *Prunus mume*, commonly known as the Chinese plum.



Unripe Chinese plums, Photo: SEKIUCHI

The study published online in *Nature Communications* explained *P. mume* is one of the first of its subfamily to have been sequenced. Understanding the fruit's make up can serve as a stepping stone to better evaluate the overall Rosaceae family, an umbrella for over 100 genera and 3,000 species.

Rosaceae, the rose family, is considered the third most economically important plant family in temperate regions, the report said. Fruits from the family contribute to an array of fresh, dried, juiced and processed products.

The family is characterized by rapid evolution and a recent divergence of genera. The phenotypic diversity has made it difficult to identify common morphological traits.

To break down the makeup of the plant, domesticated over 3,000 years ago in China, the research team followed the ancestral Rosaceae genome and evaluated three key genera: *Prunus*, *Malus* and *Fragaria*. Nine ancestral chromosomes of the Rosaceae family were reconstructed through the process.

They found 1,154 candidate genes for *P. mume* that define characteristics like flowering scent, flowering time and disease resistance.

The genome will help scientists and breeders better understand overall Rosaceae genomes, including their rapid evolution and genetic diversity.

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