

Rose family study leads to new understanding of fruit diversity across geological time

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Among flowering plants, the rose family (called Rosaceae) displays an incredible diversity, including classic reds like the American beauty. But in addition to ornamentals making the perfect romantic gift, the Rosaceae family also includes vital staples of worldwide diets and cash crop economies. They exhibit an extraordinary range of variation in the size and shapes of trees, bushes and succulent fruits, from strawberries and raspberries, to Jonathan apples, plums, cherries, and almonds, to mouth-watering Georgia peaches.

For evolutionary biologists, Rosaceae provides an excellent opportunity to understand how fruit evolved from ancestral types to the present day dry or fleshy varieties that, with the help of animals, have spread to a worldwide distribution of about 3,000 known species.

In a new international collaboration between Chinese and U.S. institutions including Fudan University, Huanggang Normal College, the Pennsylvania State University and the Smithsonian Institution, led by Professors Hong Ma and Jun Xiang, the authors performed a tour de force evolutionary study of Rosaceae fruits from the analyses of 125 flowering plants with large gene sequence datasets, including those of 117 Rosaceae species.

Their results, published in the early online edition of the journal *Molecular Biology and Evolution*, have shown a new evolutionary picture

of Rosaceae plant size and shape, flowers and, importantly, fruits.

First, a new tree of life for Rosaceae was reconstructed using newly obtained nuclear gene sequences to investigate the evolution of fruit types and other characters in the context of geological times. They also found strong evidence of whole genome duplication that likely generated new genes contributing to Rosaceae diversity.

The new evolutionary tree traces the beginnings of the Rosaceae family as far back as about 120 million years ago (Mya), when the ancestor of Rosaceae separated from other families. Almost 20 million years later, the shrub subfamily Dryadoideae split from the other two subfamilies, immediately followed by a divergence of the two largest subfamilies at about 100 Mya around the boundary between the Early and Late Cretaceous. From there, further expansions over eons have culminated in the 3,000 species seen today.

In addition, their analysis of the many thousands of gene sequences yielded strong evidence for several whole [genome duplications](#) that probably facilitated specialization of tree size and fruits, not only supporting the hypothesis that the apple tribe (a large group with many genera) had two closely spaced whole genome duplications, but also revealing another one in the Amygdaleae tribe of the pitted fruits including plums, cherries, almonds, apricots and peaches.

"It is likely that the whole genome duplications detected here and environmental factors, such as animal feeding, have contributed to the evolution of the many fruit types in Rosaceae. The results in the paper provide a foundation for understanding fruit evolution in flowering plants," said Hong Ma, one of the supervisors of the study.

Next, from their newly developed evolutionary tree, they traced the evolutionary history of fruit shapes. The authors suggest that the

ancestral fruits of the subfamily with apples and peaches were likely a set of five aggregated follicles.

"Enlarged and fleshy fruits likely evolved via two distinct ways. In one, the inner fruit wall (or endocarp) became hard, forming nuculanium; in addition, the previously dry middle fruit wall (or pericarp) became fleshy and the number of carpels decreased to one or two, finally resulting in the drupe (pitted fruits, such as peach, plum, cherry, and apricot)," said Jun Xiang, who co-directed the project. "Alternatively, after five carpels became connate, the receptacle becomes urn-like and further enveloping the pistils, resulting in semi-inferior (such as hawthorn) and fully inferior (such as apple) ovaries."

But a rose family —by any other name— also means focusing on flowers. As for flowers, most Rosaceae species share some common ancestral characters, such as bearing a hypanthium, which is a connation of the receptacle and the basal part of perianth (sepals and petals) and stamens, and having pentamerous sepals and petals (wind-spread species tend to have no petals). However, pistil number and shape vary among different groups of the family. "An apocarpous pistil with superior ovary and numerous carpels is supported as the ancestral character of Rosaceae," said Ma.

The authors also conclude that the plants of Rosaceae species most probably evolved from shrubs. "Most species of the Rosoideae subfamily (including strawberry and raspberry) tend to diminish their sizes to perennial or annual herbs with small compound leaves and a mass of small dry seeds," said Hong Ma. "On the contrary, trees originated independently in the tribe with apple and pear and the tribe with pitted fruits in the peach subfamily (Amygdaloideae), with more light exposure and more leaves for harvesting light energy." "These advantages could have allow members of these tribes to produce more fruits per plant, and more fleshy and nutritious fruits to attract animals,"

said Jun Xiang.

The study has contributed to making Rosaceae an excellent system for studying fruit evolution using molecular biology, providing an important resource for understanding flowering plant evolution and improving fruit crops to the delight of consumer palettes.

Provided by Oxford University Press

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