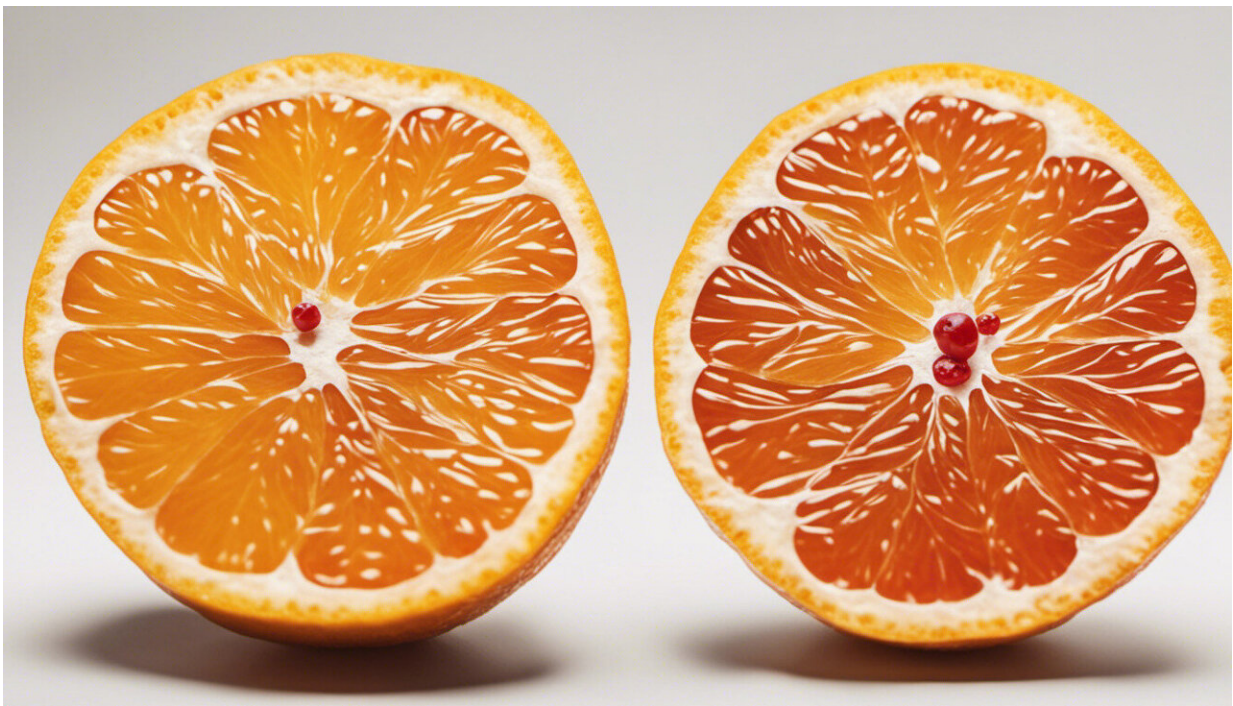


Sweet orange's parents and mechanism for producing vitamin C revealed in its draft genome sequence

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Credit: AI-generated image ([disclaimer](#))

The sweet orange, *Citrus sinensis*, has long dominated fruit production worldwide. Yet attempts to study this fruit's genetics and improve its desirable traits have proved difficult because it reproduces asexually and seedlings are nearly identical to the mother plant. Plant biologists had

even failed to determine with certainty which fruits had been crossed to produce the sweet orange, over 2,000 years ago in China. An international research team, including members from the A*STAR Genome Institute Singapore (GIS), has now broken the deadlock by sequencing the genome of the sweet orange. The team has also revealed the fruit's parentage: pummelo, which is similar to grapefruit, and mandarin, a small and easy-peeling orange.

Xiaoan Ruan of GIS along with Qiang Xu and Ling-Ling Chen of Huazhong Agricultural University, China, and their co-workers compared the orange's genome with those of pummelo, *C. grandis*, and mandarin, *C. reticulata*, using simple sequence repeat and single-nucleotide polymorphism markers—two types of short and highly variable [DNA sequence data](#).

One-quarter of the sweet orange's markers matched pummelo, and three-quarters matched mandarin. The researchers also knew that the sweet orange's chloroplast—the organelle that performs photosynthesis—originated in pummelo, indicating that this fruit was the maternal parent. Plants inherit DNA only from their 'fathers', whereas they inherit DNA, chloroplasts and mitochondria from their 'mothers'. Ruan and his co-workers therefore inferred that the original breeders first crossed a female pummelo with a male mandarin, and then crossed the resulting hybrid with a male mandarin, resulting in the asexual sweet orange.

The research team also mined the sequence data to uncover the [genetic underpinnings](#) of one of orange's most important traits: production of vitamin C, a powerful antioxidant essential for connective tissue building and wound-healing. They searched for genes similar to GalUR, which produces a key enzyme in the vitamin C production pathway and found 18 copies. Other vitamin-C-rich crops, such as papaya and apple, contain between 13 and 17 copies only. From studies of when and where genes

are expressed during development, the team observed that the GalUR genes are highly expressed in orange fruits. "GalUR may be the most important contributor to vitamin C accumulation in orange fruit," says Ruan.

Availability of the sweet orange genome will facilitate the study of many other important traits, including disease resistance, flavor, sugar content and fruit color, the team notes. "The findings provide new tools and approaches for future plant breeding using genetic modification or engineering for high-yield vitamin C production," says Ruan.

More information: Xu, Q. et al. The draft genome of sweet orange (*Citrus sinensis*). *Nature Genetics* 45, 59–66 (2013).

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