

Surprises discovered in decoded kiwifruit genome

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The recent decoding of the kiwifruit genome has discovered that the fruit has many genetic similarities to other plant species, including potatoes and tomatoes, among other surprises.

(Phys.org) —A new study that decoded the DNA sequence of the kiwifruit has concluded that the fruit has many genetic similarities between its 39,040 genes and other plant species, including potatoes and tomatoes. The study also has unveiled two major evolutionary events that occurred millions of years ago in the kiwifruit genome.

"The kiwifruit is an economically and nutritionally important fruit crop. It has long been called 'the king of fruits' because of its remarkably high vitamin C content and balanced nutritional composition of minerals, dietary fiber and other health-benefits," says Zhangjun Fei, a scientist from the Boyce Thompson Institute at Cornell who contributed heavily

to study, which was conducted by a team of plant scientists from the United States and China and published Oct. 18 in *Nature Communications*.

"The genome sequence will serve as a valuable resource for kiwifruit research and may facilitate the breeding program for improved fruit quality and disease resistance," Fei says.

Kiwifruit originated from the mountains and ranges of southwestern China and was not really known to the world until the early 20th century, when farmers in New Zealand discovered the fruit and began breeding it as a commercial crop. It is a form of berry that grows on woody vines, much like grapes, and belongs to the order of Ericales, where blueberries, tea bushes and Brazil nuts are also classified.

One of the most remarkable findings of the study was uncovered when scientists observed a high percentage of similarities within the kiwifruit DNA. The data revealed two unusual mishaps that occurred in the process of cell division about 27 and 80 million years ago, when an extensive expansion of [genes](#) arose from an entire extra copy of the genome, followed by extensive gene loss.

Fei explains, "The kiwifruit genome has undergone two recent whole-genome duplication events."

When genes are duplicated, the extra genes can mutate to perform entirely new functions that were not previously present in the organism. This process, called neofunctionalization, can occur with no adverse effects in plants and, in the case of kiwifruit, was quite beneficial.

"The duplication contributed to adding additional members of gene families that are involved in regulating important kiwifruit characteristics, such as fruit vitamin C, flavonoid and carotenoid

metabolism," says Fei.

For the sequencing, the scientists used a Chinese variety called "Hongyang," which is widely grown in China, to produce the draft sequence. They then compared kiwifruit to the genomes of other representative [plant species](#) including tomato, rice, grape and the mustard weed Arabidopsis. They uncovered about 8,000 genes that were common among all five species. The comparison revealed important evolutionary relationships, including the development genes related to fruit growth, ripening, nutrient metabolism, and disease resistance.

Prior to the study, extensive research on the metabolic accumulation of vitamin C, carotenoids and flavonoids had been reported in kiwifruits, but genome sequence data, critical for its breeding and improvement, had never been available.

"The kiwifruit [genome sequence](#) represents the first of a member in the order Ericales, thus providing a valuable resource for comparative genomics and evolutionary studies," Fei says. "We expect to continue generating genome sequences from other kiwifruit varieties to investigate the genetic diversity of [kiwifruit](#) and elucidate regulatory networks of important biological processes."

The sequence is accessible online at the Kiwifruit Genome Database.

More information: bioinfo.bti.cornell.edu/kiwi

Provided by Cornell University

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