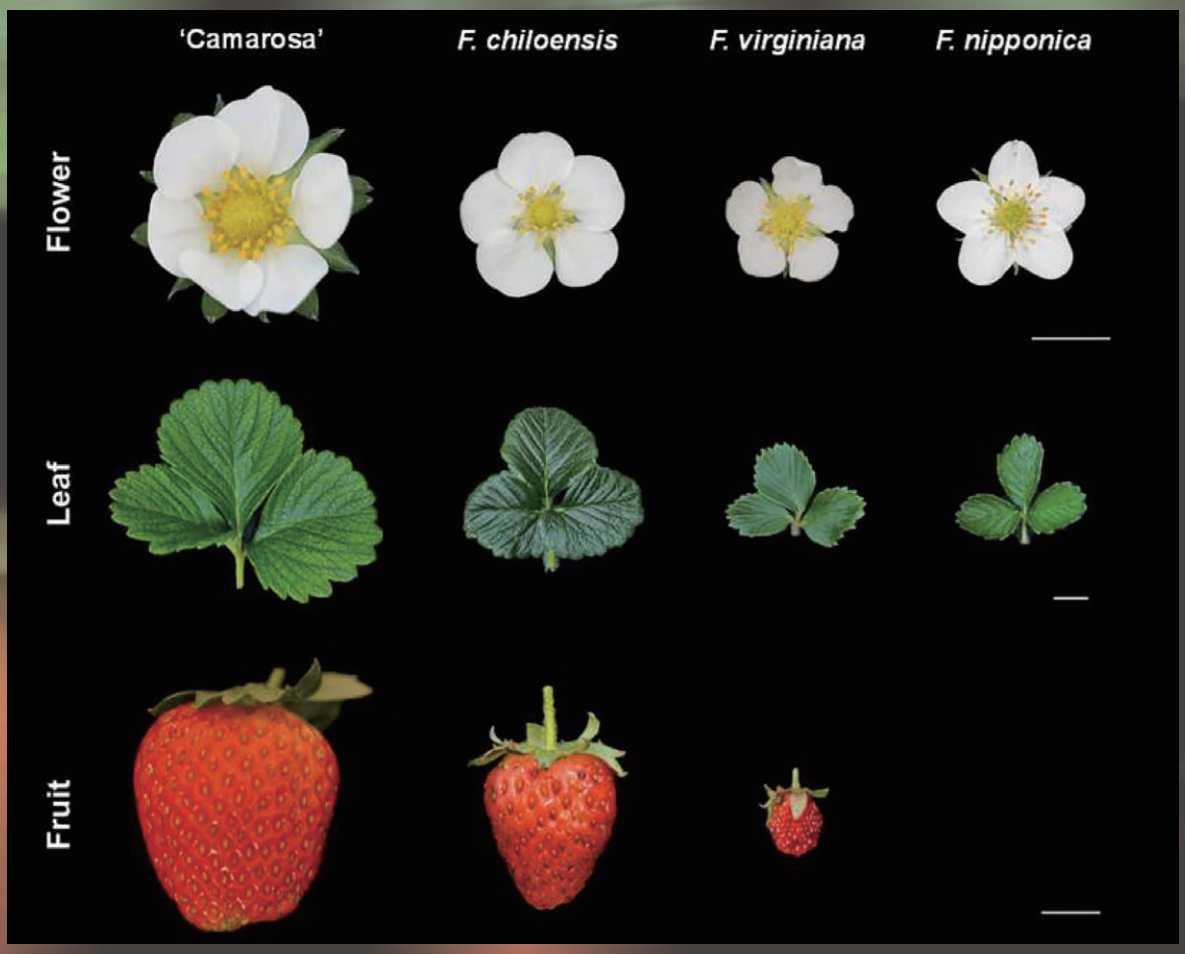
Wild Origins and Domestication Syndrome of the Garden Strawberry Revealed

By YAN Fusheng

Sweet, juicy strawberries are among the world's most beloved fruits. But how did the modest wild berries of past centuries transform into the plump, flavorful varieties we enjoy today? The tangled genomic history underlying cultivated strawberries' origin, as well as the associated molecular interactions during domestication, has long mystified scientists. Now, an international collaboration lifts the veil.



Morphological features of *F. chiloensis*, *F. virginiana*, *F. nipponica*, and the cultivar 'Camarosa'. Scale bar, 1 cm. (Credit: *Nature Plants*)

Reported in *Nature Plants* on August 3, 2023, a team of researchers, jointly led by Dr. ZHU Andan from the Kunming Institute of Botany (KIB) under the Chinese Academy of Sciences, Dr. Jeffrey P. Mower from the University of Nebraska-Lincoln in the US, and Dr. RUAN Jiwei from the Horticultural Research Institute under the Yunnan Academy of Agricultural Sciences revealed the wild origins of the modern strawberry.

The ancestry of the juicy, red strawberries we enjoy today can be traced back to two wild species, namely *Fragaria chiloensis* and *Fragaria virginiana*. They are octoploid species that have eight sets of chromosomes, which contributes to the genetic complexity of this fruit. These American natives journeyed across the Atlantic in the 18th century and hybridized to produce the large, sweet fruits that now grace our tables. But the convoluted origins of modern strawberries remained shrouded in mystery, until now.

Like playing genomic detective, an international team of scientists pieced together clues hidden in the DNA of wild and cultivated strawberries. They generated high-resolution genome sequences for *F. chiloensis* and *F. virginiana*. These genomic maps exposed the secrets of the two wild species' divergence and contributions to strawberry domestication over centuries of breeding programs.

Think of the strawberry genomes as books with relatively intact chapters but shuffled pages. The researchers had to reconstruct and separate the genetic texts of the two wild species, which had become interleaved through hybridization and duplication. Using cutting-edge DNA sequencing and computational approaches, they resolved the distinct "chapters" – the sets of chromosomes, and "paragraphs" – the genes, for each ancestral strain.

Scientists likened this process to "unzipping" the descendants to reveal their wild origins. The team also sequenced the genome of another diploid species, *Fragaria nipponica*, to help decipher the cryptic genetic codes. Together, the three high-quality genome assemblies unlocked a treasure trove of evolutionary insights.

Most notably, they enabled the accurate assignment of the intricate strawberry genomes into four subgenomes labeled A to D. The data reveal that subgenome A originates from *Fragaria vesca*, while the other three from *Fragaria iinumae*. This contradicts prior hypotheses suggesting different wild diploid ancestors. The new evidence reshapes our understanding of how wild *Fragaria* species hybridized and duplicated their genomes on the path to cultivated strawberry.

Aside from origins, the sequences uncover how gene expression patterns were coordinated and shifted among subgenomes during domestication. Stress responses visible in genes and some transcription factors display some of the most dynamic changes. The researchers propose that these expression adjustments may have enabled strawberries to survive new environments during breeding. Intriguingly, subgenome contributions are not equal – A dominates, while D shows extensive gene loss.

Such insights elucidate the consequences of the convoluted genomic history that complicates strawberry breeding today. In addition, they also reveal untapped potential for genetic improvements using wild germplasms.

So next time when you savor a sweet strawberry, do appreciate the fruit from centuries of natural evolution as well as human innovation. This international team's genomic decryption further unveils the convoluted code underlying the fruits' transformation from wild berries to modern delicacies.

Reference

Jin, X., Du, H., Zhu, C., Wan, H., Liu, F., Ruan, J., . . . Zhu, A. (2023). Haplotype-resolved genomes of wild octoploid progenitors illuminate genomic diversifications from wild relatives to cultivated strawberry. *Nature Plants*, 9(8), 1252-1266. doi:10.1038/s41477-023-01473-2