

# The origin of flowers: DNA of storied plant provides insight into the evolution of flowering plants

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The newly sequenced genome of the *Amborella* plant will be published in the journal *Science* on 20 December 2013. The genome sequence sheds new light on a major event in the history of life on Earth: the origin of flowering plants, including all major food crop species. Credit: Sangtae Kim

The newly sequenced genome of the *Amborella* plant addresses Darwin's "abominable mystery"—the question of why flowers suddenly proliferated on Earth millions of years ago. The genome sequence sheds new light on a major event in the history of life on Earth: the origin of flowering plants, including all major food crop species. On 20 December 2013, a paper by the *Amborella* Genome Sequencing Project that includes a full description of the analyses performed by the project, as well as implications for flowering plant research, will be published in the journal *Science*. The paper is among three on different research areas related to the *Amborella* genome that will be published in the same issue of the journal.

*Amborella* (*Amborella trichopoda*) is unique as the sole survivor of an ancient evolutionary lineage that traces back to the last common ancestor of all flowering plants. The plant is a small understory tree found only on the main island of New Caledonia in the South Pacific. An effort to decipher the *Amborella* [genome](#)—led by scientists at Penn State University, the University at Buffalo, the University of Florida, the University of Georgia, and the University of California-Riverside—is uncovering evidence for the evolutionary processes that paved the way for the amazing diversity of the more than 300,000 [flowering plant](#) species we enjoy today.

This unique heritage gives *Amborella* a special role in the study of flowering plants. "In the same way that the [genome sequence](#) of the platypus—a survivor of an ancient lineage—can help us study the evolution of all mammals, the genome sequence of *Amborella* can help us learn about the evolution of all flowers," said Victor Albert of the University at Buffalo.

Scientists who sequenced the *Amborella* genome say that it provides

conclusive evidence that the ancestor of all flowering plants, including *Amborella*, evolved following a "genome doubling event" that occurred about 200 million years ago. Some duplicated genes were lost over time but others took on new functions, including contributions to the development of floral organs.



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"Genome doubling may, therefore, offer an explanation to Darwin's "abominable mystery"—the apparently abrupt proliferation of new species of flowering plants in fossil records dating to the Cretaceous

period," said Claude dePamphilis of Penn State University. "Generations of scientists have worked to solve this puzzle," he added.

Comparative analyses of the *Amborella* genome are already providing scientists with a new perspective on the genetic origins of important traits in all flowering plants—including all major food crop species. "Because of *Amborella*'s pivotal phylogenetic position, it is an evolutionary reference genome that allows us to better understand genome changes in those flowering plants that evolved later, including genome evolution of our many crop plants—hence, it will be essential for crop improvement," stressed Doug Soltis of the University of Florida.

As another example of the value of the *Amborella* genome, Joshua Der at Penn State noted "We estimate that at least 14,000 protein-coding genes existed in the last common ancestor of all flowering plants. Many of these genes are unique to flowering plants, and many are known to be important for producing the flower as well as other structures and other processes specific to flowering plants."

"This work provides the first global insight as to how flowering plants are genetically different from all other plants on Earth," Brad Barbazuk of the University of Florida said, "and it provides new clues as to how seed plants are genetically different from non-seed plants."

Jim Leebens-Mack from UGA noted that "The *Amborella* genome sequence facilitated reconstruction of the ancestral gene order in the 'core eudicots,' a huge group that comprises about 75 percent of all angiosperms. This group includes tomato, apple and legumes, as well as timber trees such as oak and poplar." As an evolutionary outsider to this diverse group, the *Amborella* genome allowed the researchers to estimate the linear order of genes in an ancestral eudicot genome and to infer lineage-specific changes that occurred over 120 million years of

evolution in the core eudicot.



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At the same time, *Amborella* seems to have acquired some unusual genomic characteristics since it split from the rest of the flowering plant tree of life. For example, DNA sequences that can change locations or multiply within the genome (transposable elements) seem to have stabilized in the *Amborella* genome. Most plants show evidence of recent bursts of this mobile DNA activity, "But *Amborella* is unique in that it does not seem to have acquired many new mobile sequences in the past

several million years," stated Sue Wessler of the University of California-Riverside. "Insertion of some transposable elements can affect the expression and function of protein-coding genes, so the cessation of mobile DNA activity may have slowed the rate of evolution of both genome structure and gene function."

In addition to its utility in retrospective studies of the evolution of flowering plants, the *Amborella* genome sequence offers insights into the history and conservation of *Amborella* populations. There are only 18 known populations of this very special angiosperm in mountainous regions New Caledonia.

"Resequencing of individual *Amborella* plants across the species' range reveals geographic structure with conservation implications plus evidence of a recent, major genetic bottleneck," noted Pam Soltis of the University of Florida. A similar narrowing of genetic variation occurred when humans migrated from Africa to found modern-day Eurasian populations.

**More information:** The complete genome sequence of *Amborella* has been deposited in Genbank—the U.S. National Institutes of Health database of publicly available gene sequences—and also is available in the [Amborella Genome Database](#).

"The *Amborella* Genome and the Evolution of Flowering Plants," *Science*, 2013.

In addition to the paper about the nuclear genome sequence, two other papers appear in this same issue: one that reports the complete mitochondrial genome sequence of *Amborella*, which contains large amounts of foreign DNA resulting from horizontal transfer (Rice et al. 2013); and another that describes the novel assembly and validation of the nuclear genome using a combination of approaches that can be

applied to other complex genomes of non-model species (Chamala et al. 2013).

Provided by Pennsylvania State University

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