

## New Genetic Study Helps Solve Darwin's Mystery About Ancient Evolution of Flowering Plants

*ScienceDaily* (Apr. 11, 2011) — The evolution and diversification of the more than 300,000 living species of flowering plants may have been "jump started" much earlier than previously calculated, a new study indicates.

According to Claude dePamphilis, a professor of biology at Penn State University and the lead author of the study, which includes scientists at six universities, two major upheavals in the plant genome occurred hundreds of millions of years ago -- nearly 200 million years earlier than the events that other research groups had described. The research also indicates that these upheavals produced thousands of new genes that may have helped drive the evolutionary explosion that led to the rich diversity of present-day flowering plants. The study, which provides a wealth of new genetic data and a more precise evolutionary time scale, is expected to change the way biologists view the family trees of plants in general and flowering plants in particular.



*Amborella trichopoda*, a flowering plant. *Amborella trichopoda* is a basal angiosperm and the earliest surviving branch of the angiosperm tree of life. This plant was included in the Ancestral Angiosperm Genome Project. (Credit: Sangtae Kim)

The research findings are posted on the early online website of the journal *Nature* on 10 April 2011, and later will be published in the journal.

"We began with some intense genomic detective work -- combing through nine previously sequenced plant genomes, plus millions of new gene sequences that the Ancestral Angiosperm Genome Project (<http://ancangio.uga.edu/>) had gathered from the earliest surviving lineages of flowering plants," dePamphilis said. "We knew that, at some point in ancient history, one or more important genetic metamorphoses had occurred in the ancestor of flowering plants, and we also knew that these metamorphoses could explain the enormous success of so many species living on the Earth today. Most importantly, we suspected that these important changes had been driven by a common mechanism instead of by many independent events." DePamphilis explained that, after examining volumes of molecular evidence, his team discovered and calculated the dates for two instances of a special kind of DNA mutation -- called a polyploidy event -- that revolutionized the flowering-plant lineage.

"A polyploidy event is basically the acquisition, through mutation, of a 'double dose' of genetic material," explained Yuannian Jiao, a graduate student at Penn State and the first author of the study. "In vertebrates, although genome duplication is known to occur, it generally is lethal. Plants, on the other hand, often survive and can sometimes benefit from duplicated genomes." Jiao explained that, over the generations, most duplicated genes from polyploidy events simply are lost. However, other genes adopt new functions or, in some instances, subdivide the workload with the genetic segments that were duplicated, thereby cultivating more efficiency and better specialization of tasks for the genome as a whole.

Jiao also explained that, although ancient events of polyploidy have been well documented in plant-genome-sequencing projects, biologists had dated the earliest polyploidy event in flowering plants at around 125 to 150 million years ago. "There were hints that even earlier events had occurred, but no good evidence," Jiao said. "That's what makes our team's findings so exciting. We identified at least two major events -- one occurring in the ancestor of all seed plants about 320 million years ago, and another occurring in the flowering-plant lineage specifically, about 192 to 210 million years ago. That's up to 200 million years earlier than such events were assumed to have taken place."

DePamphilis added that such polyploidy events probably set in motion a kind of genomic renaissance, and that present-day varieties now are reaping the rewards. "Thanks to events such as these, where vast stretches of DNA have been duplicated and added to the genome, flowering plants have been able to evolve new and better functions. They have seized on the opportunity to become so diverse, so exquisite, and so prevalent," dePamphilis said. He explained that his team was able to trace the history of some of the major genes that define how flowering plants work. "Some of these new genes led to true innovations and have become vital parts of the genetic toolkit for the regulation of flower development," he said. "In other words, without the genes that these polyploidy events helped to create, flowering plants as we know them today probably would not exist."

DePamphilis also said that, thanks to the two polyploidy events that his research team identified, flowering plants may have enjoyed a distinct evolutionary advantage that allowed them to survive harsh climate changes and even mass extinctions. One such extinction that was accompanied by more-recent polyploidy events in several flowering-plant groups was the Cretaceous-Tertiary extinction event (the K-T event) -- a mass extinction of animals and plants that occurred approximately 65.5 million years ago that may have been triggered by a massive asteroid impact.

"Ever since Charles Darwin so famously called the rapid diversification of flowering plants in the fossil record an 'abominable mystery,' generations of scientists have worked to solve this puzzle," dePamphilis said. "We used to say that most of the hundreds of thousands of successful species of flowering plants show genetic traces of ancient polyploidy events. The further we push back the date of when these events happened, the more confidently we can claim that, not most, but all flowering plants are the result of large-scale duplications of the genome. It's possible that the important polyploidy events we've identified were the equivalent of two 'big bangs' for flowering plants."

In addition to dePamphilis and Jiao, other researchers who contributed to the study include Norman J. Wickett, Lena Landherr, Paula E. Ralph, Lynn P. Tomsho, Yi Hu, Stephan C. Schuster, and Hong Ma from Penn State; Saravanaraj Ayyampalayam and Jim Leebens-Mack from the University of Georgia; André S. Chanderbali, Pamela S. Soltis, and Douglas E. Soltis from the University of Florida; Haiying Liang from Clemson University; Sandra W. Clifton from Washington University; and Scott E. Schlarbaum from the University of Tennessee.

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