

# DNA sequencing unlocks relationships among flowering plants

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(PhysOrg.com) -- The origins of flowering plants from peas to oak trees are now in clearer focus thanks to the efforts of University of Florida researchers.

A study appearing online this week in the [Proceedings of the National Academy of Sciences](#) unravels 100 million years of evolution through an extensive analysis of plant genomes. It targets one of the major moments in plant evolution, when the ancestors of most of the world's flowering plants split into two major groups.

Together the two groups make up nearly 70 percent of all flowering plants and are part of a larger clade known as *Pentapetalae*, which means five petals. Understanding how these plants are related is a large undertaking that could help ecologists better understand which species are more vulnerable to [environmental factors](#) such as [climate change](#).

Shortly after the two groups split apart, they simultaneously embarked upon a rapid burst of new species that lasted 5 million years. This study shows how those species are related and sheds further light on the emergence of flowering plants, an evolutionary phenomenon described by [Charles Darwin](#) as an abominable mystery.

"This paper and others show flowering plants as layer after layer of bursts of evolution," said Doug Soltis, study co-author and UF distinguished professor of biology. "Now it's falling together into two big groups."

*Pentapetalae* has enormous diversity and contains nearly all flowering plants. Its two major groups, superrosids and superasterids, split apart between 111 million and 98 million years ago and now account for more than 200,000 species. The superrosids include such familiar plants as hibiscus, oaks, cotton and roses. The superasterids include mint, azaleas, dogwoods and sunflowers.

Earlier studies were limited by technology and involved only four or five genes. Those studies hinted at the results found in the new study but lacked statistical support, said study co-author Pam Soltis, distinguished professor and Florida Museum of Natural History curator of molecular systematics and evolutionary genetics.

The new study at UF's Florida Museum of Natural History analyzed 86 complete plastid genome sequences from a wide range of plant species. Plastids are the plant cell component responsible for photosynthesis.

Previous genetic analyses of *Pentapetalae* failed to untangle the relationships among living species, suggesting that the plants diverged rapidly over 5 million years. Researchers selected genomes to sequence based on their best guess of genetic relationships from the previous sequencing work.

Genome sequencing is more time-consuming for plants than animals because plastid DNA is about 10 times larger than the mitochondrial DNA used in studying animal genomes. But continual improvements in DNA sequencing technology are now allowing researchers to analyze those larger amounts of data more quickly.

The study provides an important framework for further investigating evolutionary relationships by providing a much clearer picture of the deep divergence that led to the split within [flowering plants](#), which then led to speciation in the two separate branches.

Eventually, researchers hope to match these evolutionary bursts with geological and climatic events in the earth's history. "I think we're starting to get to a point with a dated tree where we could start looking at what was happening at some of those time frames," Pam Soltis said.

Provided by University of Florida

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