

Reproducing early and often is the key to rapid evolution in plants

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Yale researchers have harnessed the power of 21st century computing to confirm an idea first proposed in 1916 — that plants with rapid reproductive cycles evolve faster. Their findings appear in the October 3rd edition of *Science*.

"Our study has profound consequence for the understanding of evolution made possible by the critical role of the computer in revealing major evolutionary patterns," said senior author Michael Donoghue, the G. Evelyn Hutchinson Professor of Ecology & Evolutionary Biology and Curator of Botany at Yale's Peabody Museum of Natural History.

Long involved with the Tree of Life Web Project, which is attempting to reconstruct the "tree" representing the genealogical relationships of all species on Earth, Donoghue has spearheaded the study of flowering plant evolution. In animals, the variation in rate of molecular evolution has been ascribed to differences in generation time, metabolic rate, DNA repair, and body size; in plants, the differences have been more difficult to determine.

The current analysis evaluated DNA sequence data for five major evolutionary lineages within the flowering plants, comparing genetic markers in their chloroplast, nuclear, and mitochondrial genomes. The authors also employed new methods for making some of the largest phylogenetic trees ever built.

A clear pattern emerged. Plants with a shorter generation time — from

the time they germinate to the time that a seed they produce germinates — generally show more rapid rates of molecular evolution. Longer-lived trees and shrubs, by contrast, evolve more slowly and show less variability in their rates of evolution. The study also showed that the difference in rate seen between herbs and woody plants has been maintained through evolutionary time.

"To give an idea of the scope of the data managed in this study, the largest data set contained over 4500 species, while typical tests of such hypotheses are based on less than 50 species in total," said Yale graduate student and lead author Stephen Smith.

For each branch on each limb of the "tree," the researchers calculated the rate of molecular evolution by determining the number of DNA nucleotide substitutions per site per million years.

Their analyses highlight the difficulty in using molecular data to infer the timing of evolutionary events, and suggest that new strategies may be necessary in using DNA sequence "barcodes" to identify plant species, and in setting conservation priorities.

"Our data indicate that some kinds of plants will be easy to ID and others will be much more difficult," said Smith. "The slower a plant species evolves, the harder it is to differentiate it from related plants. But our analyses point in a good new direction."

Source: Yale University

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