

Analysis Of Flower Genes Reveals The Fate Of An Ancient Gene Duplication

23 August 2005

In a step that advances our ability to discern the ancient evolutionary relationships between different genes and their biological functions, researchers have provided insight into the present-day outcome of a single gene duplication that occurred over a hundred million years ago in an ancestor of modern plants.

The work is reported in *Current Biology* by a team led by Brendan Davies of the University of Leeds, England.

Gene duplication - a relatively uncommon event in which a single copy of a gene is transformed into two separate copies - is thought to play a key role in the evolution of new gene functions.

Duplications are important because they effectively allow at least one of the gene copies to evolve while the (likely important) function of the original gene can remain intact.

In this way, the duplication of pre-existing genetic information provides the raw material from which new gene functions can evolve, thereby contributing to the evolution of genetic complexity and the evolution of sophisticated life forms.

Very many such gene-duplication events have shaped the evolution of today's living species, but tracing the evolution of a specific single gene over millions of years of evolution - and over potentially several gene-duplication events - can pose a significant challenge.

One way in which this can be overcome is for researchers studying a particular modern-day gene to look at neighboring genes in different related species.

Genes derived from a common ancestral gene region will still share similarities in neighboring gene sequences, both in terms of gene identity and the order such sequences appear within the

chromosome. This kind of preserved gene order is known as genome synteny.

In the new work, researchers have used synteny to clarify the evolution of genes essential for the development of floral reproductive organs, stamens and carpels.

The subjects of their work were two genes that appear to play identical functions in two different plant species: the AGAMOUS (AG) gene of the mustard plant *Arabidopsis thaliana* and the PLENA (PLE) gene of the snapdragon, *Antirrhinum majus*. Both genes are required for the development of flower reproductive structures, and when these genes are mutated, the plants form so-called double flowers, in which petals and sepals replace stamens and carpels.

AG and PLE are very closely related genes, and they clearly have nearly identical function, suggesting that they are derived from the same single gene inherited from a common ancestor.

However, analysis of synteny in the AG and PLE regions unambiguously showed that AG and PLE are not derived from the same ancestral gene, but that they instead represent two different products of a gene-duplication event that occurred around 125 million years ago in a common ancestor of *Arabidopsis* and *Antirrhinum*.

The other genes created in that ancient gene-duplication event became altered, in different ways, so that they now have new functions in *Arabidopsis* and *Antirrhinum*.

These findings provide one of the first demonstrations of how an essential developmental function can be randomly assigned to either product of a gene-duplication event. The work defines a new standard for the evidence required to establish the evolutionary relationships of genes from different species.

APA citation: Analysis Of Flower Genes Reveals The Fate Of An Ancient Gene Duplication (2005, August 23) retrieved 1 December 2022 from <https://phys.org/news/2005-08-analysis-genes-reveals-fate-ancient.html>

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