

Evolution can cause a rapid reduction in genome size

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Flowers of *Arabidopsis lyrata* (left) und *Arabidopsis thaliana* (right). Credit: Ya-Long Guo/MPI for Developmental Biology

(PhysOrg.com) -- It would appear reasonable to assume that two closely related plant species would have similar genetic blueprints. However, scientists from the Max Planck Institute for Developmental Biology in Tübingen, working in cooperation with an international research team have now decoded, for the first time, the entire genome of the lyre-leaved rock cress (*Arabidopsis lyrata*), a close relative of the thale cress (*Arabidopsis thaliana*), the model plant used by geneticists. They discovered that the genome of the lyre-leaved rock cress is fifty percent bigger than that of the thale cress. Moreover, these changes arose over a very short period in evolutionary terms. This new high-quality genome analysis will provide a basis for further detailed comparative studies on the function, ecology and evolution of the plant genus *Arabidopsis*.

Genome size among the different species of the plant kingdom varies significantly. At the upper end of the currently known spectrum, scientists have identified the herb Paris or true-lover's knot (*Paris quadrifolia*), whose [genome](#) is a good thousand times longer than that of the carnivorous plants from the genus *Genlisea*. However, these plants are so distantly related that it is almost impossible to identify the evolutionary forces at work in the individual species. Therefore, researchers from Detlef Weigel's Department of Molecular Biology at the Max Planck Institute for [Developmental Biology](#) in Tübingen working in cooperation with an international research team selected for their genome study a species closely related to the thale cress (*Arabidopsis thaliana*), probably the most widely studied flowering plant in genetics. The species in question was lyre-leaved rock cress (*Arabidopsis lyrata*) which, unlike thale cress, is unable to self-fertilise. "Thale cress and lyre-leaved rock cress shared an ancestor around ten million years ago, after which their evolutionary lineages diverged," explains Ya-Long Guo from the MPI for Developmental Biology.

The genome of the thale cress has been fully decoded for some time now: it has a sequence of 125 million base pairs, which are also referred to as the letters of the genetic alphabet, and includes 27,025 genes distributed on five chromosomes. The sequencing of the genome of a North American phylum of the lyre-leaved rock cress yielded a base sequence which, at 207 million base pairs or letters, is over 50 percent bigger than that of the thale cress. However, the scientists assume that these letter sequences do not form meaningful words and texts in all areas of the genome, and that the difference between the two species of the mustard family (*Brassicaceae*), in terms of their number of genes, is not quite so significant: the lyre-leaved rock cress has around 32,670 genes distributed on eight chromosomes.

The researchers also established that considerable elements have been lost from some parts of the thale cress genome. However, most of the

differences in the genome size of the two species are accounted for by hundreds of thousands of small deletions which mostly arose in regions located between the genes or in the transposons, sequences of DNA that can move. A smaller genome appears to offer advantages during the natural selection of individuals. This is backed up by the following detail from the new findings: transposons that have a negative effect on the surrounding genes appear to be particularly prone to deletion through selection. According to the scientists, elements are still being lost from the thale cress genome. “We assume that the genetic make-up of the plants’ shared ancestors is far more extensively preserved in the lyre-leaved rock cress – they also had eight chromosomes. We consider the thale cress with its more streamlined genome as the form derived through evolution,” says Ya-Long Guo.

What surprised the Tübingen-based researchers was how much bigger the lyre-leaved rock cress genome was than that of the thale cress. Through their analysis, the scientists have laid the foundations for further insights into how [evolution](#) in plants can take effect on the level of genes and molecules.

More information: Tina T. Hu et. al. The Arabidopsis lyrata genome sequence and the basis of rapid genome size change. *Nature Genetics* (10 April 2011), [doi: 10.1038/ng.807](https://doi.org/10.1038/ng.807)

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