

Genome duplication drives evolution of species

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The plant species *Arabidopsis kamchatica*, which belongs to the rockcress genus, originated from the combination of two species. Credit: Lucas Mohn, UZH

Many wild and cultivated plants arise through the combination of two species. The genome of these so-called polyploid species often consists of a quadruple set of chromosomes—a double set for each parental species—and thus has about twice as many genes as the original species. About 50 years ago, evolutionary biologists postulated that this process

drives evolution, leading to new species. Due to the size and complexity of such genomes, however, proving this theory on a genetic level has been difficult.

An international team of researchers headed up by Timothy Paape and Kentaro Shimizu from the Department of Evolutionary Biology and Environmental Studies of the University of Zurich (UZH) has now provided the experimental confirmation of this theory. To do so, the scientists from Switzerland and Japan used plant [species](#) *Arabidopsis kamchatica*, which is part of the rockcress genus. They sequenced the genomes of 25 individuals of the polyploid species from around the world, as well as 18 individuals of its parental species in order to study its natural genetic diversity.

Arabidopsis kamchatica arose through the natural hybridization of the two parental species *A. halleri* and *A. lyrata* between 65,000 and 145,000 years ago. With 450 million base pairs, its [genome](#) is somewhat small for a polyploid plant, but still very complex. Using state-of-the-art sequencing methods and technology as well as bioinformatics tools, the researchers were able to determine the genetic sequence of the plant individuals.

Due to the large amount of genetic information, *A. kamchatica* is better equipped to adapt to new environmental conditions. "With these results, we have demonstrated on a molecular-genetic level that genome duplications can positively affect the adaptability of organisms," says plant scientist Timothy Paape. The multiple gene copies enable the plant to assume advantageous mutations while keeping an original copy of important genes.

The usefulness of the double genome for *A. kamchatica* can be seen in its wider distribution—at both low and high altitude—compared with its parental plants. Its habitat ranges from Taiwan, Japan and the Russian

Far East to Alaska and the Pacific Northwest region of the United States. "Knowing the genomic and evolutionary context also helps us understand how genetic diversity allows [plants](#) to adapt to changing environmental conditions," says Kentaro Shimizu. The recently published research was supported by the University Research Priority Program Evolution in Action: From Genomes to Ecosystems of the University of Zurich.

More information: Timothy Paape et al, Patterns of polymorphism and selection in the subgenomes of the allopolyploid *Arabidopsis kamchatica*, *Nature Communications* (2018). [DOI: 10.1038/s41467-018-06108-1](#)

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