

Sequencing of the genus *Arabidopsis* identifies a complex history of non-bifurcating speciation and abundant trans-specific polymorphism. DOI: 10.1038/ng.3617

(Vienna 18 July 2016) For the first time, researchers have sequenced the genomes of all of the species within an entire genus, revealing that the process of speciation is not as simple as previously thought. Species are the basic building blocks of biological classification and a species is generally defined as the largest group of organisms that can produce fertile offspring. The next layer of classification is the genus, which is a group of closely related species. The genus *Canis* for example includes wolves and dogs, *Canis lupus* where *lupus* is the species name, and *Canis aureus*, the European golden jackal. One of the major questions in evolutionary biology is how the process of speciation takes place – how does evolution drive one population to become different from another. Classic views of evolution describe this process as a split, where two groups separate and then evolve independently. In new work published today in *Nature Genetics* from an international consortium spearheaded by the lab of Magnus Nordborg from the Gregor Mendel Institute of Plant Molecular Biology (GMI) of the Austrian Academy of Sciences (OeAW), this model was tested by sequencing the genomes of 94 individuals corresponding to all 27 species of the genus *Arabidopsis*, a group of small weeds native to Europe which includes the model plant *Arabidopsis thaliana*. The work provides the details for how speciation, which is estimated to have begun around 6 million years ago, formed genetic variation across this genus.

Most interestingly, this work reveals that the process of speciation does not occur as a simple split. Although *A. thaliana* is believed to have separated from the other species 6 million years ago, they found that it shares more genetic variation in common with *A. lyrata* than any of the other species, demonstrating that *A. thaliana* and *A. lyrata* became reproductively isolated, and hence separate species, much later than previously thought. The researchers were also able to identify genes which had evolved very little over this time, identifying four genes involved in viral defense that share common variation across the genus, suggesting that evolution maintained this genetic variation. They went on to identify genetic variations which are unique to the different species, suggesting that these variants may have been important for speciation. For example, in a species which is known to grow in the presence of high levels of heavy metals, *A. halleri*, they identified variation in genes encoding metal-binding proteins that show evidence of selection. These will be useful targets for studying heavy metal accumulation in this species. In *A. lyrata*, the species with the northern-most range, they identified novel variants in genes involved in regulating circadian rhythms, likely in response to the dramatic changes in day-length in the far-north.

According to the lead author, Polina Novikova, „This work dramatically advances the use of *Arabidopsis* as a model for the study of speciation and evolution. Future plans include studying how genes have been shared across these species; whether these events were just random chance, or whether they made important contributions to the ability of these plants to adapt to their specific environments.“

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