SEQUENCING OF THE GENUS *Arabidopsis* REVEALS A COMPLEX HISTORY OF NON-BIFURCATING SPECIATION AND ABUNDANT TRANS-SPECIFIC POLYMORPHISM

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The prevailing notion of species as reproductively isolated units related to each other through a bifurcating species tree has become increasingly challenged. Under this model, gene trees should generally agree with the species tree, sister taxa should be equally closely related to an outgroup, and they should not share genetic variation unless they diverged too recently for genetic drift to have eliminated shared ancestral polymorphism. Advances in sequencing technology are finally making it possible to evaluate this model systematically. We sequenced multiple individuals from 27 described taxa representing the entire genus *Arabidopsis*. Whole genome cluster analysis identified seven distinct groups, corresponding to four common species — the model species *A. thaliana*, plus *A. arenosa*, *A. halleri* and *A. lyrata* — and three other species with very limited geographical distributions. However, at the level of gene trees, only the separation of *A. thaliana* from the remaining taxa was universally supported, and for all species, including *A. thaliana*, the high amount of ancestral polymorphism shared with other species suggested that reproductive isolation was considerably more recent than the estimated divergence times. By considering the distribution of derived alleles, we uncovered multiple cases of past and ongoing gene flow that contradicts a bifurcating species tree. Finally, we show that the pattern of sharing and divergence between taxa differs between gene ontologies, suggesting a role for selection.

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