

research highlights

ARABIDOPSIS EVOLUTION

Roots in Africa

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The model species *Arabidopsis thaliana* has been particularly helpful in facilitating our understanding of fundamental biological mechanisms and evolutionary processes. The recent publication of 1,135 *A. thaliana* genomes from worldwide samples suggested that the vast majority of the accessions derived from a single recent population expansion, whereas a few Eurasian samples were relict lineages. To provide a more complete picture of the evolution of *A. thaliana*, Angela M. Hancock's group from the Max Planck Institute for Plant Breeding Research now sequence 78 African samples, providing new insights into the early evolution of *A. thaliana*.

Using phylogenomic and population genomic analyses, the researchers show that African samples harbour the highest diversity compared to other geographic populations, and represent the deepest history in the *A. thaliana* lineage. All African samples are as divergent as the relicts without close relatedness to the Eurasia cluster, suggesting that African accessions are native to this continent rather than being introduced from other regions. Analysis of S-locus variation reveals the coexistence of three loss-of-function S-haplogroups known to control selfing in a single African region, suggesting that the transition to selfing in *A. thaliana* evolved in one geographic area rather than separate regions, as predicted by previous studies.

Based on demographic inferences, the researchers propose a population dynamic model in which the ancient and recent splitting times of *A. thaliana* populations coincide with major climate transitions, such as the last interglacial and Abbassia pluvial, again demonstrating a key role of climate events in shaping species evolution.

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