



Richard Drury/The Image Bank/Getty

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Two new *Arabidopsis thaliana* resources from the 1001 Genomes Project promise to substantially facilitate research into how genetic and epigenetic variation can lead to phenotypic diversity on a species-wide level.

In the first of two publications in *Cell*, the 1001 Genomes Consortium report the re-sequenced genomes of 1,135 high-quality natural inbred strains (accessions) of *A. thaliana* from Europe, Central Asia, North Africa and North America. With 10,707,430 biallelic single-nucleotide polymorphisms (SNPs) and 1,424,879 small insertions and deletions (indels; up to 40 bp long) called within the nuclear genomes — as well as a further 2,842 and 824 biallelic SNPs in chloroplast and mitochondrial genomes, respectively — the resulting map of genetic variation represents the densest variant map for any organism, say the authors.

The detailed patterns of genetic variation reveal novel insights into the plant's global population structure, migration patterns and evolutionary history. Overall, the study suggests that modern *A. thaliana* strains represent a complex mixture of survivors from multiple glacial refugia, which are geographical locations that provided a habitat during the last ice age that enabled species survival. Descendants of a specific refugium have undergone population expansion, which may have been the result of human influence.

The second paper, by Kawakatsu *et al.*, reports the results from the 1001 Epigenomes Project, and includes 1,107 DNA methylomes from 1,028 accessions and 1,203 transcriptomes from 998 accessions. For a total of 866 accessions, SNP and small indel data from the 1001 Genomes Project are available in addition to methylomes and transcriptomes from rosette leaves, which will enable the correlation of genetic determinants with epigenetic and transcriptomic variation in future studies.

The strains exhibited high variability in average DNA methylation levels, and methylation correlated strongly with a strain's geographical origin and its climate. For example, methylation levels within transposable elements showed positive correlation with latitude and precipitation, and negative correlation with warmer temperatures, supporting the idea that methylation has a role in environmental adaptation. Additional analysis of physical genome maps (contigs) for nine accessions, representing the genomes with the greatest diversity, showed that epigenomic variation is shaped by structural variants, with the majority of loci (92%) containing transposable elements.

The detailed, curated and publicly available collection of natural *A. thaliana* accessions should greatly advance our knowledge of the evolution of genetic and epigenetic diversity, and should yield insights into fundamental molecular processes and environmental adaptations. Just like Scheherazade, the legendary storyteller in *One Thousand and One Nights*, these resources are a treasure trove of new t(h)ales.

Linda Koch

ORIGINAL ARTICLES 1001 Genomes Consortium. 1,135 genomes reveal the global pattern of polymorphism in *Arabidopsis thaliana*. *Cell* **166**, 481–491 (2016) | Kawakatsu, T. *et al.* Epigenomic diversity in a global collection of *Arabidopsis thaliana* accessions. *Cell* **166**, 492–505 (2016)

FURTHER READING Taudt, A. *et al.* Genetic sources of population epigenomic variation. *Nat. Rev. Genet.* **17**, 319–332 (2016)

WEB SITES

1001 Genomes Project: <http://1001genomes.org>

1001 Epigenomes Project: <http://1001epigenomes.org>