Identification of the Icelandic accession of Arabidopsis thaliana

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The first Icelandic accession of *Arabidopsis thaliana* has been confirmed with cytogenetic markers and its origin inferred from whole-genome sequencing. The plants were found for the first time in May 2015, growing on warm geothermal soil around the hot spring Deildartunguhver in Reykholt, West Iceland (Fig. 1).

Figure 1. One of *Arabidopsis thaliana* plants growing on geothermal soil at Deildartunguhver (June 2017).

Flower buds and leaves were collected and used for cytogenetic analyses and DNA sequencing. Whole plant specimens were deposited at the Icelandic AMNH herbarium and were assigned accession number VA21379. The accession was identified as diploid with 2n=2x=10, as expected for this species. At meiosis I it formed five normal bivalents. Ribosomal FISH mapping revealed two pairs of 5S rDNA loci and two pairs of NORs (Fig. 2). Fine-scale chromosome painting using BAC clones specific for chromosomes At1 and At4 confirmed the standard structure of these chromosomes (Fig. 2).

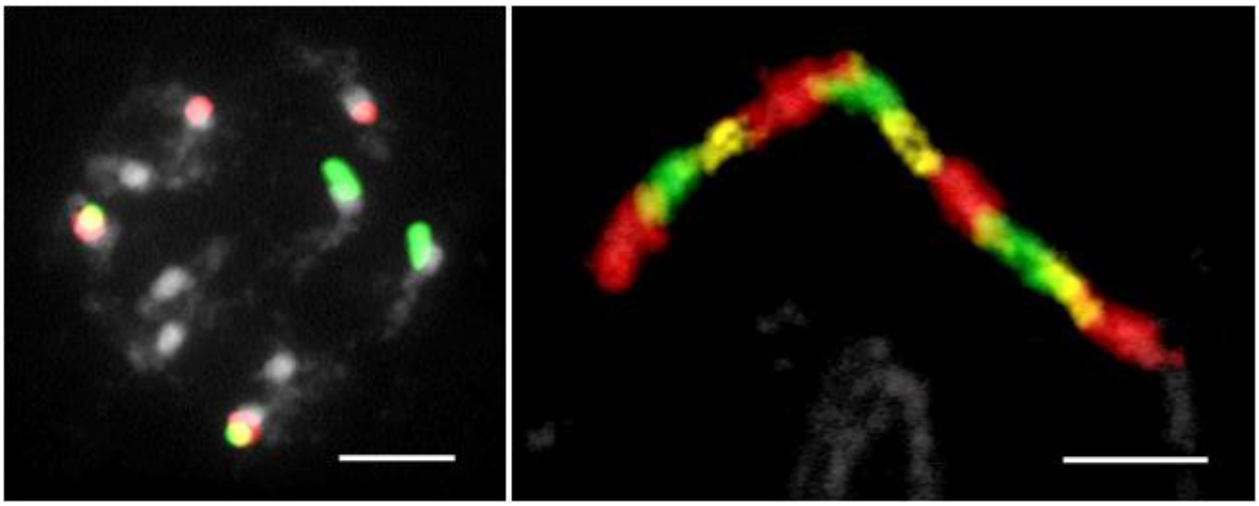

Figure 2. Cytogenetic study of the Icelandic accession of *Arabidopsis thaliana*. Left: Fluorescence *in situ* localization of 5S (red) and 45S (green) rDNA on ten mitotic chromosomes. Right: Fluorescent painting on pachytene chromosomes in meiosis, specifically showing painting of block A (~6.7Mb) on the upper arm of chromosome At1 using ten differently labelled BAC contigs (total 66 BAC clones). Chromosomes were counterstained with DAPI. Scale bars = 5 μm.

Furthermore, the painting revealed an absence of the 1.17-Mb paracentric inversion on the At4 short arm in the Icelandic accession, in contrast to the inversion-bearing *A. thaliana* accessions more prevalent in North America. The sequencing of multiplexed whole-genome libraries identified the Swedish accession Hamm-1 (CS76910 from Skåne) as the closest relative of the Icelandic accession, with, however, a markedly low SNPmatch score. We conclude that although the Icelandic accession appears to be more genetically related to populations from Scandinavia than to other European accessions, it did not originate from any of the populations represented in the global collection of the 1001 Genomes accessions of *A. thaliana*. Further evidence from an SEM investigation (unpublished) supports close relationship with Eurasian populations.

Reference: Mandáková T, Thorbjörnsson H, Pisupati R, Reichardt I, Lysak MA, Anamthawat-Jònsson K (2017) Icelandic Agricultural Sciences 30: 29-38

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