Publication

Lineage-specific adaptation to climate involves flowering time in North American Arabidopsis lyrata

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Adaptation to local climatic conditions is commonly found within species, but whether it involves the same intraspecific genomic variants is unknown. We studied this question in North American Arabidopsis lyrata, whose current distribution is shaped by postglacial range expansion from two refugia, resulting in two distinct genetic clusters covering comparable climatic gradients. Using pooled whole-genome sequence data of 41 outcrossing populations, we identified loci associated with three nichedetermining climatic variables in the two clusters and compared these outliers. Little evidence was found for parallelism in climate adaptation for single nucleotide polymorphisms (SNPs) and for genes with an accumulation of outlier SNPs. Significantly increased selection coefficients supported them as candidates of climate adaptation. However, the fraction of gene ontology (GO) terms shared between clusters was higher compared to outlier SNPs and outlier genes, suggesting that selection acts on similar pathways but not necessarily the same genes. Enriched GO terms involved responses to abiotic and biotic stress, circadian rhythm and development, with flower development and reproduction being among the most frequently detected. In line with GO enrichment, regulators of flowering time were detected as outlier genes. Our results suggest that while adaptation to environmental gradients on the genomic level are lineagespecific in A. lyrata, similar biological processes seem to be involved. Differential loss of standing genetic variation, probably driven by genetic drift, can in part account for the lack of parallel evolution on the genomic level.

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