

## MOLECULAR REGULATORY NETWORKS OF CLIMATE ADAPTATION



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As sessile organisms, plants are not able to escape unfavorable conditions. Therefore, natural plant populations are typically well adapted to their local abiotic and biotic environments. Timing of growth and development according to local seasonal cues is a prerequisite for their survival, but plants need to tolerate also extreme weather events as well as disease and pest outbreaks that are becoming more common because of the climate change. Genetic variation is crucial for adaptation. In wild populations, adaptation occurs through natural selection of advantageous genetic variation during a large number of generations. In plant breeding, however, useful variation is harnessed more efficiently through human selection that often uses genetic markers to predict the phenotype in advance. Epigenetic variation that regulates gene activities without changing the DNA sequence is an alternative and more flexible mechanism to adapt to new environments.

Wild plant populations provide natural repositories of genetic and epigenetic information about their adaptation to local environments. Woodland strawberry is a particularly useful model species for climate adaptation studies because of its wide geographical distribution in Europe, from Mediterranean to sub-Arctic zone. Local woodland strawberry populations are well adapted to their

environments, as exemplified by a clear cline in the emergence of flowers in plants that originate from natural populations across the latitudinal gradient. In the photo, the most southern plant is just starting to flower (left), while the northernmost plant (right) is already full of flowers.

To explore genetic variation contributing to climate adaptation in woodland strawberry, we have gathered a unique collection of 225 woodland strawberry accessions covering the geographical distribution of the species in Europe and sequenced their genomes. In this project, we will search for genetic and epigenetic variation in gene promoters between locally adapted populations and explore how these variations affect gene expression genome wide. These data will enable us to identify gene expression networks with potential roles in climate adaptation, and finally,

functional roles of selected networks will be tested using genome-edited plants. This new knowledge on the mechanisms of adaptation in natural populations will advise plant breeders how to develop crop cultivars that are better adapted to climate change.

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