

Abstract

Natural variation plays a central role in the evolution of species diversity. Variation within species is the substrate for natural selection and allows for evolutionary response towards changing environmental conditions. The process mediating this response that changes populations towards a better fit to the environment is termed adaptation. Adapted phenotypes are characterized by higher reproductive fitness which is conferred by a particular shape of expressed life history traits in a given environment. One of the most crucial life history traits for plants is the transition to flowering, which marks the onset of the reproductive phase. This process needs to be precisely aligned with the environment in order to ensure reproductive success, which is a hallmark of fitness. Variation in flowering time between and within species is hence thought to indicate adaptation to local conditions.

Arabis alpina, a perennial Brassicaceae, has a broad arctic-alpine distribution with major populations in the European Alps and Scandinavia. In this framework, adaptation can be studied on different spatial scales, allowing to address the role of continuous variation of environmental parameters and to test for parallel evolution of phenotypic and genotypic solutions to similar selection pressures.

In this study, variation in flowering time was characterized on a local scale, addressing the magnitude and distribution of flowering time variation as well as the underlying genetic basis. Flowering time was shown to be variable between and within populations of *A. alpina* within a region of the French Alps. Each population was characterized by a typical spectrum of flowering time and degree of flowering time variation. One population at Col du Galibier contained plants that flowered particularly early and flowering time variation was spatially structured with early and late flowering plants growing at opposite ends of a mountain range. Both sites differed in growing season length and monthly minimum temperatures, suggesting a role of environmental heterogeneity in flowering time differentiation. Neutral population genetic structure paralleled the distribution of flowering time phenotypes, which potentially resulted from a combination of limited gene flow and high inbreeding with strong local selection for traits related to flowering time. A major QTL for flowering time was identified on the upper arm of chromosome 8 that included the *PERPETUAL FLOWERING 1* (*PEP1*) locus, which encodes a potent repressor of flowering in the vernalisation pathway. While genetic analyses supported *PEP1* as a candidate gene underlying early flowering of plants from Galibier, no causal polymorphism could be detected at the *PEP1* locus.

The presented results indicate that considerable variation for flowering time occurs even within single populations of *A. alpina* and that this may be shaped by the interaction of environmental heterogeneity with genetic variation. The study system presented here may contribute to understanding the mechanisms that underlie local adaptation on small spatial scales and how these mechanisms shape life history evolution on a larger scale.