**The genetic basis of adaptation in Arabidopsis lyrata**

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### Introduction

The genetic basis of adaptation is a central question in evolutionary genetics (Orr 1998). It is not known if adaptations are due to changes in regulatory or protein coding parts of the genes, if they occur though many small of few large mutations, or what is the role of interaction between genes and environment. An interesting question is whether similar adaptations occur using similar mutations and same genes in different populations and species (Hoekstra and Coyne 2007).

*Arabidopsis lyrata* is an outcrossing perennial relative of selfing *Arabidopsis thaliana*. It occurs in isolated populations scattered in Europe and North-America. Transplant studies have shown that populations are locally adapted (Leinonen et al. 2008).

We focus here on two populations, one from a northern, high altitude site (Spiterstulen, Norway) and the second originating from Central Europe (Plech, Germany) (Fig. 1). We study the response of the reproductive and morphological characters to environmental cues that are known to affect flowering, and the genetic basis for these differences.

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### Material and methods

We made an F2 cross between Plech and Spiterstulen *A. lyrata* populations using two independent grandparents from each population.

#### Growth conditions

We grew F2 plants together with parental populations and F1 plants in growth chambers with three different combinations of photoperiod, vernalization and nutrient treatments. When vernalized, 5 week old rosettes were exposed to 4°C at 8 h photoperiod, for 9 weeks time, and then returned to normal growth conditions.

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#### Traits scored

<table>
<thead>
<tr>
<th>Trait</th>
<th>GC01</th>
<th>GC05</th>
<th>GC05</th>
<th>GC05</th>
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</thead>
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<tr>
<td>Rosette area</td>
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<td>14hDV.rosheight1</td>
<td>14hDV.rosheight1</td>
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<tr>
<td>Leaf ratio</td>
<td>14hDV.leafratio3</td>
<td>14hDV.leafratio3</td>
<td>14hDV.leafratio3</td>
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</tr>
<tr>
<td>Total nb of shoots</td>
<td>14hDV.totnbflo3wa7</td>
<td>14hDV.totnbflo3wa7</td>
<td>14hDV.totnbflo3wa7</td>
<td>14hDV.totnbflo3wa7</td>
</tr>
<tr>
<td>Inflorescence height</td>
<td>14hDV.heightinflo5</td>
<td>14hDV.heightinflo5</td>
<td>14hDV.heightinflo5</td>
<td>14hDV.heightinflo5</td>
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<tr>
<td>Number of inflorescence flowers</td>
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<td>14hDV.nbinf1</td>
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<tr>
<td>Days to bolting</td>
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<td>14hDV.daystoflo7</td>
<td>14hDV.daystoflo7</td>
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</tr>
</tbody>
</table>

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### Results and discussion

Populations showed significant differences in most traits in the three growth conditions. Plech generally flowered more probably, earlier, and more vigorously than Spiterstulen; further, Plech rosettes were smaller and flatter.

Flowering probability and timing were plastic, responding positively to fertilization and vernalization in both parents, F1 and F2 (Fig. 2). Reproductive effort, on the other hand, was plastic only in Plech; inflorescence shoot number, flower number, and inflorescence height were strongly canalized in Spiterstulen. Respectively, only Spiterstulen showed plastic response of rosette height to vernalization, while the rosette was always very flat in Plech.

We detected a modest number of QTLs for flowering, reproductive investment and morphology (Fig. 3), each of the QTLs explaining 5 to 25% of the total variance in F2. Plech alleles generally promoted flowering and reproductive investment as expected. Some QTLs (e.g. bottom of chromosome 2 and beginning of chromosomes 4 and 7) were detected in many environments, and the same areas had QTLs for both flowering and morphological/reproductive traits, suggesting possible pleiotropic effects of genes in developmental pathways.

We present our experimental design as a demonstration of how QTL analysis can be used to test hypotheses about the genetic basis of adaptation.

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### Conclusions

The two populations showed contrasting responses to environmental cues, suggesting canalization of crucial traits due to adaption to local environments.

The genetic architectures of natural variation in flowering in *A. lyrata* and *A. thaliana* seem to be different. While the variation in *A. thaliana* is mainly governed by FRI and FLC, our results suggest that differences between *A. lyrata* populations in flowering time are due to more subtle mutations mainly at other loci.

We are currently studying additional crosses, and carrying out association studies and analyses of sequence variation at flowering time candidate genes.

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**References**


Stefanovic R, Badr H, Plech, Germany

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**Figure 1.** *A. lyrata* plants in Spiterstulen grow on an alpine river banks exposed to flood and hard winter conditions; in Plech they grow on rocky outcrops.

**Figure 2.** Timing of flowering in parental populations and F2 plants in GC05 experiment.

**Figure 3.** QTLs detected in three experiments.