Gene-by-Environment Interactions in *Arabidopsis thaliana* in Response to Precipitation Extremes

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Introduction

Climate change is predicted to disrupt agriculture and increase food scarcity [1]. In the Midwestern United States, climate change will have an effect on global food supply: the region produces about 30% of the corn and soybeans grown worldwide [2].

In the last 30 years, rainfall in the Midwest has increased in the spring months, while drought and increased temperatures can lead to evaporation and drier soils in the summer [3]. These rapid changes to seasonal cycles of precipitation and temperature provide challenges to plant growth and reproduction [4]. Investigating the genetic architecture of plant response to these conditions is important to understanding how and which plants will survive in the changing environment.

This experiment models the natural environmental conditions by growing 100 recombinant inbred lines (RIL) of the plant *Arabidopsis thaliana* in soil that is saturated during the early growth period then allowed to dry out. Five phenotypes were measured to search for gene-by-environment interactions. A quantitative trait locus (QTL) analysis was performed in order to identify specific areas of the genome that affect these traits.

Methods

A set of seeds from 100 recombinant inbred lines of *Arabidopsis thaliana* were obtained from the *Arabidopsis* Biological Resource Center at the Ohio State University (stock number CS1899). After planting, plants were raised in growth chambers at constant 25°C and 24-hour light conditions. The control plants were watered regularly for optimal growth. The soil for the experimental plants was saturated for the first two weeks then watered optimally for 30 days, and finally allowed to dry out. Three plants from each line were phenotyped daily (figure 1).

Five phenotypes were collected: days to sprout, days to leaf, days to flower, days to bolt, and days to seed.

In order to detect gene-by-environment interactions, a two-way mixed model analysis of variance (ANOVA) was used. The fixed effect is the precipitation condition (control or experimental) and the random effect is the recombinant inbred line (RI line).

$$Y_{ijk} = \mu + Condition_i + Line_j + (Condition_i \times Line_j) + e_{ijk}$$

Figure 1: Experimental (left) and control (right) plant beds after 6 weeks of growth

Results

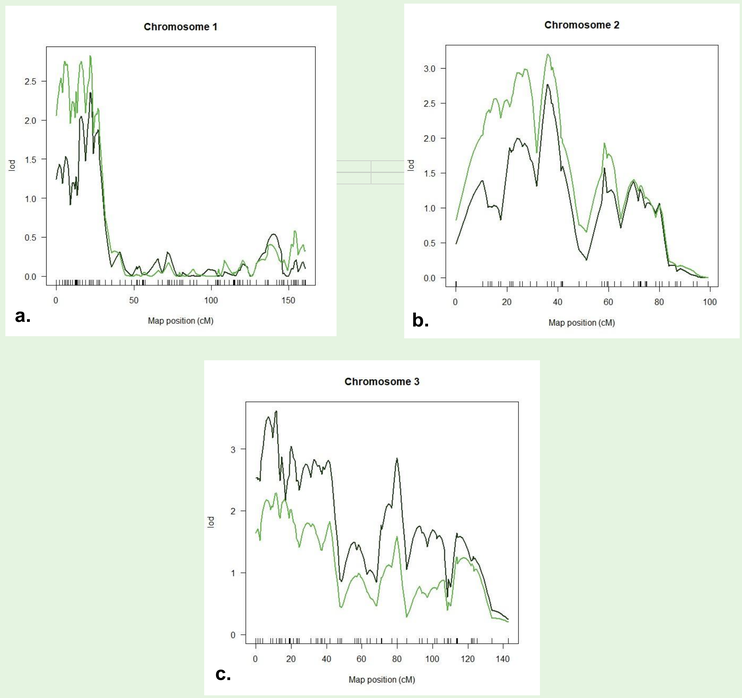

Figure 1: QTL analysis of days to bolt (dark green) and days to flower (light green) on a) chromosome 1, b) chromosome 2, and c) chromosome 3. The 5% significance threshold is 2.60.

Trait	Chr	LOD	Position (cM)
Flower	1	2.83	21.7
Flower	2	3.20	36.0
Bolt	2	2.77	36.0
Bolt	3	3.62	11.5

Table 1. Chromosome (chr), LOD scores, and positions in centimorgans (cM) of the four QTL.

Unsurprisingly, precipitation condition had a significant effect on all traits ($p \leq 0.04$). The effect of the recombinant inbred line is the genetic effect. Line had a significant effect ($p \leq 0.005$) on all traits except that of days to germinate. Of most interest to this study is the interaction of line and condition, the gene x environment interaction. This was significant for days to seed ($p = 0.03$), days to bolt ($p = 2.8 \times 10^{-11}$), days to flower ($p < 2.2 \times 10^{-16}$), and days to leaves ($p < 2.2 \times 10^{-16}$).

Through QTL analysis, we have identified two QTL for days to flower and two QTL for days to bolt. By performing the QTL analysis, we were able to identify regions of the genome that have effects on the timing of growth in plants of the control and experimental groups combined. The next phase of analysis will identify QTL for the areas of the genome with different effects in the two environmental conditions, the gene-by-environment effect.

Discussion

The results of the analysis suggest that there is genetic variation within this recombinant inbred line panel of *Arabidopsis thaliana* in responding to the environmental conditions. Some of the lines respond better to the environmental challenge than others. Furthermore, the QTL analysis shows that we can detect regions of the genome responsible for the developmental patterns seen in the experiment. While the days to growth for leaf, germ and seed did not have statistically significant QTL, we identified QTL for the days to bolt and flower.

Our next steps are to investigate the environmental impact on stomatal density. This will be determined by counting the stomata in sections of the plant leaves in both environmental conditions. QTL analysis of gene-by-environment effects will be completed shortly in order to determine which areas of the genome affect response to the environment. This spring we will also replicate the experiment to increase the number of individual phenotypes. The long-term goal of the project is to identify genes and alleles that allow plants to thrive in the changed climate.

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Citations

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4. Lippmann, R., et al. 2019. Development of wild and cultivated plants under global warming conditions. Current Biology 29: R1326-R1338