Relating Root Phenotype to Fitness and Flowering Time in Drought-stressed Arabidopsis thaliana Plants

The genetics of flowering time in the model annual plant species *Arabidopsis thaliana* has been studied intensively in the last 20 years and at least 54 genetic loci has been found to affect flowering time. At least three of them are polymorphic in nature: *FRI*GIDA (*FRI*), *FLOWERING LOCUS C* (*FLC*) AND *CRYPTOCHROME 2* (*CRY2*). Previous research found that allelic variation at the *FRI* and *FLC* loci can affect how efficiently plants use water. In Prof. Callahan’s lab I worked with two interesting natural populations of *Arabidopsis*: Shahdara that has a functional *FRI* allele and weak *FLC* allele and Bayreuth that has a non-functional *FRI* allele and strong *FLC* allele. By artificially crossing parents from these two populations, an experimental population of recombinant inbred (RI) lines was created. Recently, the French researchers who created this experimental population made it publicly available for researchers around the world. We used variation among these two parents and 18 RI lines to explore the effects of drought on fitness and root phenotypes. With Aqsa Shakoor, a Barnard Hughes intern, we planted 800 Arabidopsis plant representing the 20 genotypes. Forty replicates of each were planted and placed in five different treatments: mortality, control, rescue, root phenotype control and root phenotype rescue. In the mortality treatment, plants were deprived of water and we estimate the mean number of days each genotype could survive. We found no significant variation among them in survival time. Mean fruit number was estimated for each genotype in both the control and rescue treatments, allowing us to estimate reproductive fitness. We found that there was significantly higher fitness in the control treatment (18.8), where the number of fruits was double that in the rescue treatment (9.4). After a sublethal period of water deprivation, roots were harvested in root phenotype control and root phenotype rescue treatments. Length of roots did not differ significantly between treatments (control mean=9.18 and rescue mean=8.9) but differences in root length among genotypes were significant. Similarly, root dry weight did not differ between control and rescue treatments but varied among genotypes. A negative but non-significant correlation between mean fruit number and mean root length was found in both treatments. It is possible that plants are subject to a tradeoff, with bigger roots resulting in a smaller amount of fruits. These data are useful for planning future studies that will explore tradeoffs between survival and reproduction, and how both are related to the root phenotypes expressed under benign and stressful conditions.