Background & Rationale

Roots are the primary route for water and nutrient uptake in plants. Neighboring plants compete for these nutrients and adjust their root system architecture (RSA) and total body plan accordingly. The degree to which the RSA is modified depends on the identity of these competitors. Many plants are capable of ‘kin recognition’ (KR), i.e. the ability to distinguish genetic relatedness among conspecifics. These studies have established that KR induces obvious phenotypic changes to the RSA. Little is known about the molecular mechanisms associated with the KR response. Our lab is attempting to identify the metabolomic, proteomic, and genomic elements associated with KR in the model plant Arabidopsis thaliana.

Hypothesis: Competitive interactions between plants of the same ecotype (KIN) versus those between members of different ecotypes (STRANGER) results in differential protein expression.

Significance: Characterizing proteins which are differentially expressed during KR will help to identify the elements associated with detection of and response to competitors.


What is 2d-gel electrophoresis?

Proteins are separated by isoelectric point, then by molecular weight (size) on a gel. Individual proteins are resolved as unique ‘spots’ that can be analyzed for changes in intensity (protein expression) between samples. The location of a protein on a gel is unique, and can be used to identify it by database searches and excised for verification by mass spectrometry.

Experimental Design

1. Collect A. thaliana seedlings
2. Grow for 30 d
3. Protein extraction
4. 2-D gel

Progress

SDS-PAGE Preliminary Gel

2D Gels

Conclusion/Future Experiments

- Differential protein expression between STRANGER samples is observable.
- Future experiments: (i) Increasing the protein loading concentration to improve gel resolution
(ii) Running the 2D gels for Solo and Kin Samples 
(iii) Identifying protein bands.