Variation in plasticity within and between Populus tremuloides (Aspen), naturally occurring clones.

ERIN MULLINS, 2016

Mentor(s): Vladimir Douhovnikoff

One clone (genet) can be composed of many trees (ramets) and members of the same genet are identical in their genotype (Suvanto and Latva-Karjanmaa, 2005).

In order to study clones, proper identification is necessary. Microsatellites are considered a DNA fingerprinting technique that allows for individual clones to be identified and can allow for spatially distributed samples to be assigned to genets. Microsatellites repeat 1-4 base pairs of the sequences of DNA. Microsatellites are codominant and one of the most reliable techniques for mapping genetic populations and identifying clones (Suvanto and Latva-Karjanmaa, 2005).

I have been developing a line of research that uses Populus tremuloides (Aspen) as an in situ model species, which includes naturally occurring clones. This species is prevalent on the Bowdoin property situated on the former Brunswick Navy base and establishing permanent plots for current and future research are the core goal of this project. Using six different microsatellite primers I was able to identify and map multiple aspen stands. Since clonal species include genets with multiple ramets that are genetically identical, they are ideal species for the study of ecological plasticity, as we know that any variation in their phenotype is not a result of genetic variation (Douhovnikoff and Dodd, 2004). Having genotyped and assigned over 200 stems within four stands to specific genets we are now exploring variation in morphologically plastic traits such stomatal densities and gmax as well as epigenetic methylation at the DNA scale. This work allows us to identify and quantify plant responses to environmental variation within genotype, between genotype, between sites, and across spatial dimensions (de Witte and Stöcklin, 2010).

After collecting samples from the trees at each site, I extracted the DNA, amplified the samples using the thermo cycler and six different primers (WPMS14, WPMS17, WPMS18, WPMS 19, WMPS20, PTR2, and PTR14), and then sent a 2ul sample to a UPenn lab for them to perform an advanced sample analysis. With the data that they send back to us, I then do data analysis to determine which alleles are present in each sample to identify which clone they identify with.

Then, using this data and the mapping of the Aspen population, I have been able to track differences in the phenotypes, due to light, shading, or water, despite having the same genotypes. We have begun the process of comparing phenotypes within and between genets by looking at the number and sizes of the stomata on each of the leaf samples collected. We have predicted that there is more variation within a genet than between genets since these trees rarely reproduce sexually, so they must be very plastic to the different environmental conditions. As we continue to look at the data we have collected, we hope to be able to understand the plasticity of this clonal species.
References:

