**Project Idea: Survey of –pHB content**

**Feb 4, 2016**

We have some unique sample and data sets in the Mansfield Lab. For example, as part of the AGIP and POPCAN projects, hundreds of poplar genotypes were grown in common garden plots and harvested for extensive analysis. A full wood chem analysis was conducted along with various phenology and physiology traits as well as gene expression analysis. Included in this data is lignin content and composition (S:G ratio). But unfortunately the content of –pHB pendant groups in lignin was not determined. Many of the original processed wood samples remain in the lab and are available for further analysis. By measuring the –pHB content in these samples, it may be possible to gain a unique insight into the role of such pendant groups in lignin. In other words, does the –pHB content correlate to any other measured traits for these wood samples? I have already done a small survey of some of the samples and found considerable diversity in the –pHB content. What remains now is to systematically analyses many more samples. In addition to learning more about the role of –pHB pendant groups, if we can make use of the gene expression data it may be possible to identify which putative BAHD acyltransferase enzymes are differentially expressed in high and low –pHB genotypes.

Several sample sets exist in the lab – some of these details still need to be double-checked:

AGIP (Applied Genomics Innovation Program):

· Approximately 380 genotypes of *P. trichocarpa*

· Extractive-free ground wood available

· Lignin measured by Klason method

· SNP array data available

POPCAN – *P. trichocarpa*:

· Approximately 450 genotypes of *P. trichocarpa*

· Extractive-free ground wood available

· Lignin measured by unreliable “micro method”

· RNAseq data available

POPCAN – P. balsamifera:

• Approximately 50 genotypes of P. balsamifera

• Extractive-free ground wood available

• Lignin measured by unreliable “micro method”

• No sequencing data available

Emily’s AgCanSalix samples – *Salix eriocephala*:

• Approximately 300 genotypes of *S. eriocephala*

• Extractive-free ground wood available

• Lignin measured by Klason method

• No sequencing data available

We should most likely avoid the data sets where lignin content was measured using the unreliable “micro method” since the lignin values will be very important in our analysis (we will likely normalise the –pHB value by lignin content). Accordingly, it would probably be best to start with the AGIP samples. If we find some interesting results then we should consider adding other species. Since willows also have –pHB pendant groups in lignin, we could see if Emily would be keen to collaborate.

A brief overview of the project work flow:

Step 1 – Choose samples for analyses

Step 2 – Weight 30 mg of each sample, in duplicate

Step 3 – Conduct saponification reactions in batches and quantify –pHB by HPLC

Step 4 – Process data and look for trends and correlations

Step 5 – Discuss next steps, if any, to move forward