Homework #2 Zoe Portlas

Background

Red Spruce (*Picea rubens*) is a montane tree native to the Eastern United States and Canada. Its habitat is usually characterized as cool and moist (Blum, 1990), but it can also exist in warmer and drier sites. In this experiment, sites were separated by their climate of origin either being cool and wet or hot and dry based on the precipitation of the warmest quarter and the temperature of the warmest month. The expression of individuals from these habitats was assessed in response to a heat and a heat and drought treatment.

There were ten maternal families in the experiment, five families from each source climate, and there were three treatment groups in the experiment. The control group was watered every day and had a 16:8 L:D photoperiod, meaning a cycle of 16 hours of light at 23 °C followed by 8 hours of dark at 17 °C. The heat group experienced the same watering and photoperiod, but there was a 50% increase of temperature, so light/day was at 35 °C and dark/night was at 26 °C. Finally, the heat/drought group experienced the same photoperiod and temperatures as the heat group, but in addition, water was withheld.

Tissue was sampled on days 0, 5, and 10 for each of the groups. RNA was extracted from the whole seedlings, which includes root, stem, and needle tissue. This analysis focuses on the samples from day 10, which had 5 reps per source climate and treatment (total n = 30). Samples were quantified for RNA quantity and concentration on a Bioanalyzer, which is a chip based capillary electrophoresis machine. Samples with more than 1 ng/μL were sent to Cornell for 3’ tag sequencing. Library prep followed the LexoGen protocol for 3’ tag sequencing, which is useful for detecting short transcripts.

Bioinformatics

From QC assessments of raw reads to estimation of differential gene expression

Results

Conclusion

References

Blum, Barton M. "Picea rubens Sarg. Red Spruce." Silvics of North America 1 (1990): 250-259.