

Transcriptomics From Space: Linking Remote Sensing to Tree Gene Expression in a Diverse Set of Species Through the Growing Season and in Response to Water Deficit



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Background & Rationale

- The distribution and performance of individuals and species on the landscape is determined by the degree to which their traits fit the abiotic and biotic environment.
- Despite the key advances that have been made in trait-based plant ecology, major challenges remain.
- First, trait-based plant ecology tends to have narrow and shallow assays of plant function - a few easily-measured and static functional traits.
- Second, we are typically restricted to studying the distribution of plant function on the scale of 10's to 100's of meters.
- So, the grand challenge is to develop a feasible way to generate deep and broad assays of plant function in landscapes at or near the scale of individual plants.
- We propose that an integration of transcriptomics and remote sensing data can be accomplished to meet this grand challenge.**

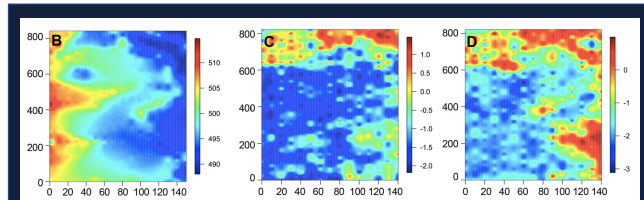


Figure 1: Community Transcriptomics in the Wabikon Lake Forest Dynamics Plot – Left) Topographic map of the forest plot. Center) Standardized effect size of the similarity in gene expression across all genes annotated as biological process as they respond to drought where red indicates dissimilar responses and blue indicates similar responses. Right) Standardized effect size of the similarity in gene expression across all genes annotated as molecular functions as they respond to drought where red indicates dissimilar responses and blue indicates similar responses. Note that species with similar gene expression responses to drought cluster at high elevation (i.e. drier) areas in the forest and species with dissimilar gene expression responses occur in lower elevation (i.e. wetter) areas of the forest (Swenson et al. 2017 Nat. Comm.).

Community Transcriptomics

- Nearly a decade ago we began the only community-wide studies of gene expression and remain the only studies of gene expression in tree communities.
- Key advances and results are:
 - Development of computational and statistical methods for comparative transcriptomics for communities of species including pairs of species that diverged >150 million years ago.
 - Gene expression responses to drought predicted species distributions along topographic and soil moisture gradients in the field (Figures 1 and 2).
 - Gene expression responses were superior predictors of tree distributions compared to phylogenetic or functional trait data.
 - Changes in gene expression throughout growing seasons are repeatable across sites and years.



Figure 3: Study Sites – Left) The location of the Wabikon Lake (Yellow Dot) and UNDERC (Blue Dot) Forest Dynamics Plots. Right) A diagram of the data layers collected in a typical forest dynamics plot – topography and the distribution and diameter of every individual tree with a diameter 1cm or greater. Plots are re-censused every year in order to track changes in species distributions and diversity and individual growth and mortality.

Study Sites & Resources

- This study will focus on two large forest dynamics plots (Figure 3) that are a part of the Smithsonian's ForestGeo network (forestgeo.si.edu)
 - Wabikon Lake Forest Dynamics Plot – Chequamegon Nicolet National Forest in Wisconsin
 - UNDERC Forest Dynamics Plot – University of Notre Dame Environmental Research Center on the Wisconsin – Michigan Border
- These sites are chosen because
 - We have a large transcriptomic and genomic data infrastructure for the species at these sites
 - The contain large forest plots with mapped and tagged trees
 - The UNDERC site is the core terrestrial NEON site for the Great Lakes Region

Objectives

- Establish the relationships between drought, spectral signatures and gene expression in the greenhouse (Figure 4).
- Prediction of species composition and gene expression for sub-plots in the two forest dynamics plots throughout the growing season (i.e. as water stress increases from spring to late summer) using DESIS, GEDI and ECOSTRESS data products.
- Field validation of predictions by collecting spectral and gene expression data from individuals in the sub-plots throughout the growing season during two years.
- Build predictions of gene expression on the regional scale to serve as a system for identifying forested regions experiencing severe drought.



Figure 4: Original Greenhouse Study of Gene Expression – The original greenhouse study investigated the gene expression of control and droughted individuals of over 20 Angiosperm and Gymnosperm species that dominate northern Wisconsin forests. The present study will conduct a similar greenhouse study to build a spectral library for these species while simultaneously quantifying their gene expression.

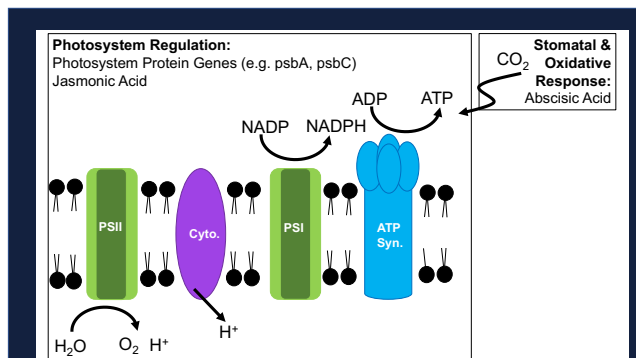


Figure 2: Identification of Genes and Functions Underlying Species Distributions Along Soil Moisture Gradients – Our previous work on the gene expression responses of Wisconsin trees to experimental drought identified individual gene ontologies and genes linked to the natural distribution of species along a soil moisture gradient (Swenson et al. 2017 Nat. Comm.). Specifically, genes related to the regulation of Jasmonic and abscisic acid, oxidative stress response and photosystem II were among those that were the best predictor of species distributions in the forest. Commonly-measured plant functional traits (e.g. SLA, %N, %P, wood density) and phylogenetic relatedness were weakly related to species distributions. In other words, our detailed transcriptomic assays uncovered the mechanisms underlying species distributions that functional traits could not.

Timing & Will This Work?

- Funding for the study began in September 2022
- The Swenson Lab and Illumina have begun a small study evaluating RNA quality and quantity from highly stressed seedling and adult samples using mRNA and totalRNA libraries.
 - Development of customized Illumina kits designed to knockdown ribosomal RNAs common in the study species.
- The greenhouse study will be conducted spring 2023
- Field campaigns will sample plots in the spring and late summer of 2023 and 2024.
- Prior to 2022 there were no studies clearly linking gene expression to spectral signatures. A recent study on rice has demonstrated a link between a gene related to phosphorus uptake and spectra that was used to successfully predict gene expression in experimental plots where phosphorus was manipulated (Takehisa et al. 2022 Plant, Cell, & Env.).

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