

Hyperspectral GWAS Reveals Genetic Architecture of Photosynthetic Traits in *Populus trichocarpa*

Background/Objective

- Connecting poplar genotype to phenotype for feedstock improvement requires either increased labor or high-throughput phenotyping. Hyperspectral sensing offers a scalable alternative.

Approach

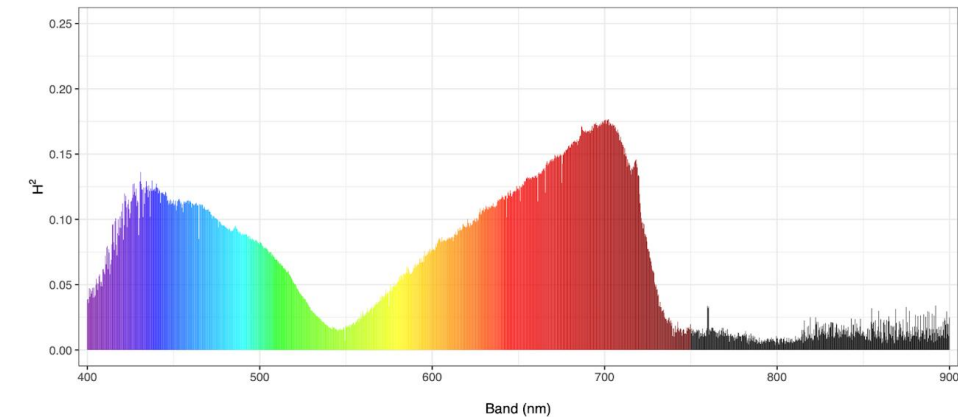
- A tower-based hyperspectral camera (400–900 nm) continuously monitored 595 trees (505 genotypes) of *Populus trichocarpa* under drought conditions in a common garden.
- Genome wide association studies (GWAS) were performed on 1423 wavebands and vegetation indices across three months of continuous measurements.

Results

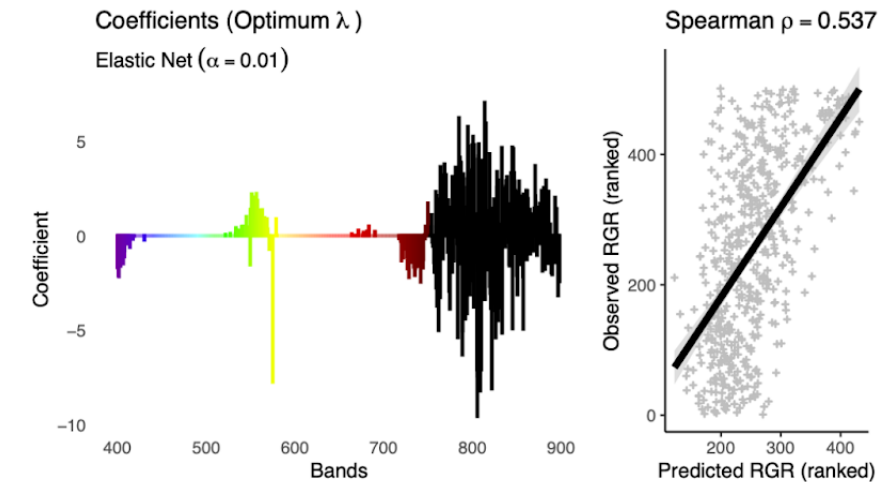
- Blue (450–500 nm) and red (650–700 nm) wavebands showed the highest heritability and most significant GWAS hits, yielding 98 significant SNP associations in the chlorophyll absorption spectra.
- Over 10 candidate genes involved in chloroplast function were identified, including plastid transcription regulators, pigment enzymes, and nitrogen assimilation genes.
- Temporal GWAS revealed dynamic genetic architecture shifting across the growing season, and an elastic net multivariate model predicted relative growth rate (RGR).

Significance/Impacts

- Hyperspectral GWAS is as a powerful approach for accelerating bioenergy crop breeding, revealing physiologically meaningful genetic variation that conventional methods miss.
- This approach enables more accurate, high-throughput selection strategies for poplar biomass improvement, as multivariate spectral models substantially outperform single indices for predicting tree growth.



Heritability (H^2) of hyperspectral bands



Spectral correlations with growth rate and elastic net predictions

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