Dynamic Changes in the *Populus* Leaf Proteome Revealed Across a Diurnal Period

Background

- Rhythmic biological processes synchronize plant behavior across cellular and molecular levels and play a major role in a plant's phenotypic plasticity.
- The characterization of this phenomenon at the proteome level under natural conditions is currently lacking for a model woody plant species

Approach

- High resolution mass spectrometry characterized the temporal dynamics of proteins expressed in *P. deltoides* leaves harvested every 2 h for 24 h in a growth chamber with a 12h/12h light/dark cycle.
- Advanced *de novo*-assisted data processing was employed to broadly characterize post-translational modifications (PTMs).

Outcome

- ~12% of the identified proteome showed significant rhythmic trends in abundance.
- 144 different PTM modifications were identified, and many PTMs exhibited rhythmic diurnal patterns of abundance.

Significance

- Understanding the temporal regulation in *Populus* provides a more complete understanding of how plants respond to environmental cues.
- Rhythmic patterns and oscillators play an important role in regulating numerous biological processes of agricultural and ecological importance (e.g., photosynthesis, plant development, and tolerance to various abiotic and biotic stresses); this work informs efforts to maximize feedstock traits in specific environments.

Shrestha, Him K., et al. "Temporal dynamics of protein and post-translational modification abundances in Populus leaf across a diurnal period." *Proteomics* (2021): 2100127. <u>https://doi.org/10.1002/pmic.202100127</u>



0 2 4 6 8 10 12 14 16 18 20 22 Time (hr)

Poplar leaf proteome showed five major trends among the diurnally regulated proteins with unique biological process enriched across the major trend. Gray indicates the dark cycle.



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Cluster 1 (319 proteins