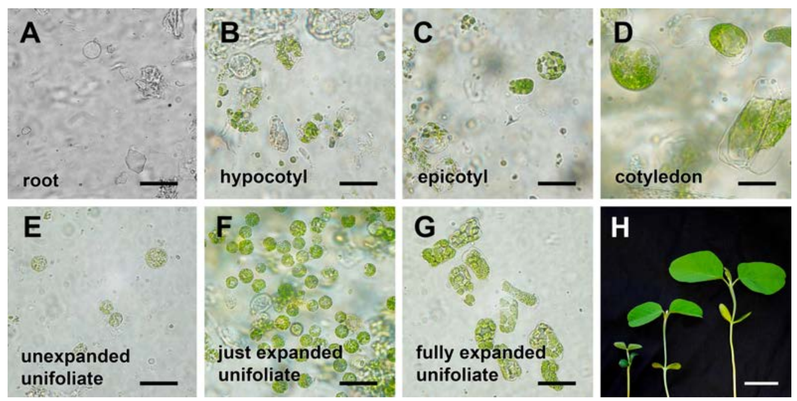
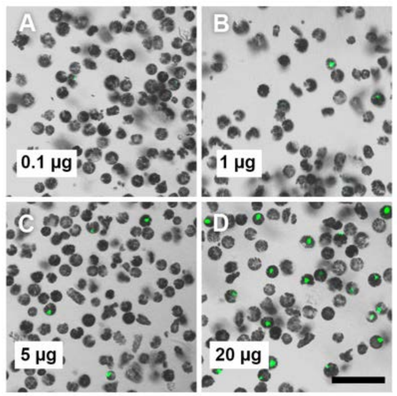
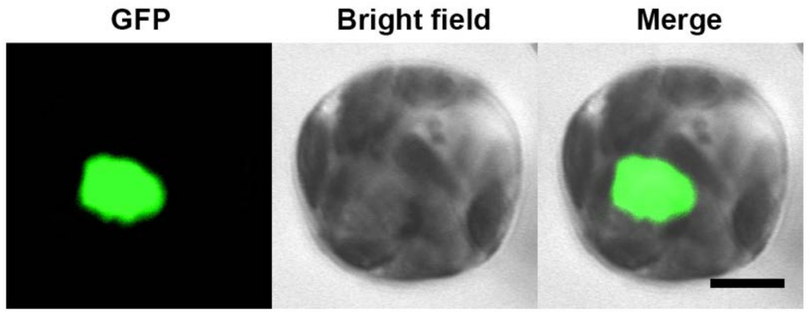
AUTONOMY RESEARCH CENTER FOR STEAHM

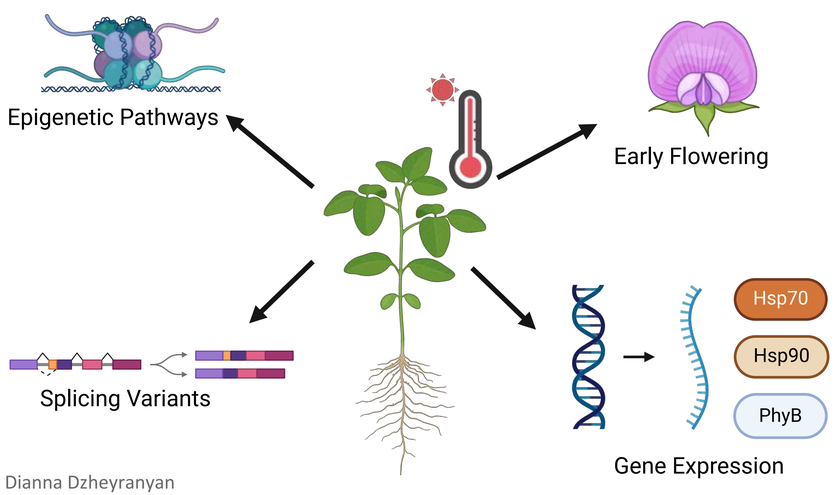
Autonomy for Sustainability

On the Challenge of Sustainable Agriculture and Ecosystem Under Diverse Environments

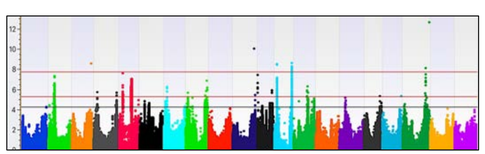


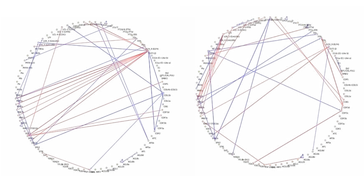






Dianna Dzheyranyan





Synopsis

- Sustainable crop production and natural ecosystems under changing environments remain a significant challenge.
- It is important to mitigate the impact of changing environments and to expand crop cultivation to novel environments.
- There is a significant knowledge gap:
  - How do specific environmental variables affect plant performance?
  - What genetic or epigenetic factors control plant responses to such environmental variables?

Research Objective

- Gain better understanding of how crop plants perceive and acclimate to environmental variables.
- Clarify the molecular mechanisms controlling plant's developmental transition in response to temperature fluctuations.
- Build mathematical models of the gene regulatory network to enable prediction of plant response to diverse environments.

Research Approach

- Characterizing temperature-specific expression of epigenetic factors and splicing isoforms using RNA-sequencing and quantitative reverse transcription polymerase chain reaction (qRT-PCR).
- Identifying downstream genes using network inference algorithms.
- Experimentally validating inferred regulatory networks using CRISPR genome editing and chromatin immunoprecipitation technologies.
- Develop differential equation models of the gene regulatory networks.

Research Results and Products

- Identified alternative splicing variants and epigenetic factors that plants may employ in order to respond to temperatures.
- Obtained inferred regulatory networks involving epigenetic mechanisms and circadian clock genes.
- Empirically verified several inferred regulatory interactions.

Commercialization and/or Societal Impact Opportunities

- **Application:** Prediction of crop performance and engineering climate resilient plants
- **Key Values:** Sustainable agriculture and ecosystem
- **Potential Customers:** Biotech industry, agriculture and seed company, breeders

Team Names & Collaborators

Fellow:
Dr. Upeksha Hemamali

Faculty:
Dr. Yoshie Hanzawa

Collaborator:
Dr. Eric Deeds (UCLA)

Citations

Alcantara, M; Iftikhar, H; Kagan, K; Dzheyranyan, D; Abbasi, P; Alamilla, A; et al.; Hanzawa, Y (2023). Clarifying the Temporal Dynamics of the Circadian Clock and Flowering Gene Network Using Overexpression and Targeted Mutagenesis of Soybean *EARLY FLOWERING 3-1* (*GmELF3-1*). microPublication Biology. 10.17912/micropub.biology.000935.

Alcantara, M; Iftikhar, H; Dzheyranyan, D; Kagan, K; Abbasi, P; Alamilla, A; et al.; Hanzawa, Y (2023). Elucidating the Temporal Patterns of Gene Expression in the Inferred Regulatory Interactions of *GmCOL1b* in *Glycine max*. microPublication Biology. 10.17912/micropub.biology.000924.

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