1. Highlights
- Abiotic stresses during early seed development adversely affect the seed size and quality at maturity.
- To understand heat stress response in rice, a temporal transcriptomic analysis was performed.
- A mathematical optimization framework, MiReN, was developed to identify the minimal regulatory relationships in rice seed.
- A new, comprehensive, genome-scale metabolic model of rice seed is under development, enhanced by MiReN.
- A multi-tissue plant-scale model will allow us to answer important biological questions regarding stress response and will accelerate the development of stress-tolerant crop cultivars.

2. Transcriptomic Analysis of Rice Seed Under Heat Stress
- 6755 stress-responsive genes
- 39 Cellular Processes GO terms identified

3. Differential Gene Expression: Clustering
- Pearson's correlation (r>0.95, p_adj<0.05)
- 1650 nodes/8926 edges in control
- 2270 nodes/13656 edges in stress
- Tighter regulation in Stress
- Global regulators were identified using node-degree relationship.

4. Minimal Regulatory Network (MiReN) Identifier
- Gene regulatory relationships are hierarchical and not always linear.
- MiReN finds the minimal number of regulatory influence on a gene that agrees with transcriptomic data.
- The interaction coefficient defines the extent of activation or inhibition of a gene by a regulator.

Challenges
- \(O(n^{2-1} + l)\)
- Smart cutoffs
- Reduction Variable Bounds

5. Identified Regulatory Relationships
- SLR1 represses GA response pathway.
- Disease resistance gene XA21 controls several transcriptional repressors related to stress tolerance.
- Underlying circadian regulation?
- Predicted regulatory influence for 228 stress responsive rice Transcription factors
- Most prominent heat stress-responsive transcription factors:
  - BZIP
  - MADS-M
  - Ethylene Response factors

6. Future Directions
- Genome-scale metabolic model of rice seed is coming soon, integrated with regulatory information from MiReN.
- Tissue-specific models of plant root, seed, leaf, and stalk will be assembled into a plant-scale metabolic model.
- Knowledge gained from transcriptomic analyses and regulatory relationships will guide the development of stress-tolerant crop varieties.
- Artificial Intelligence for making decisions on robust engineering targets for crop stress-tolerance and yield from vast omics' databases is needed.

References