

1. Highlights

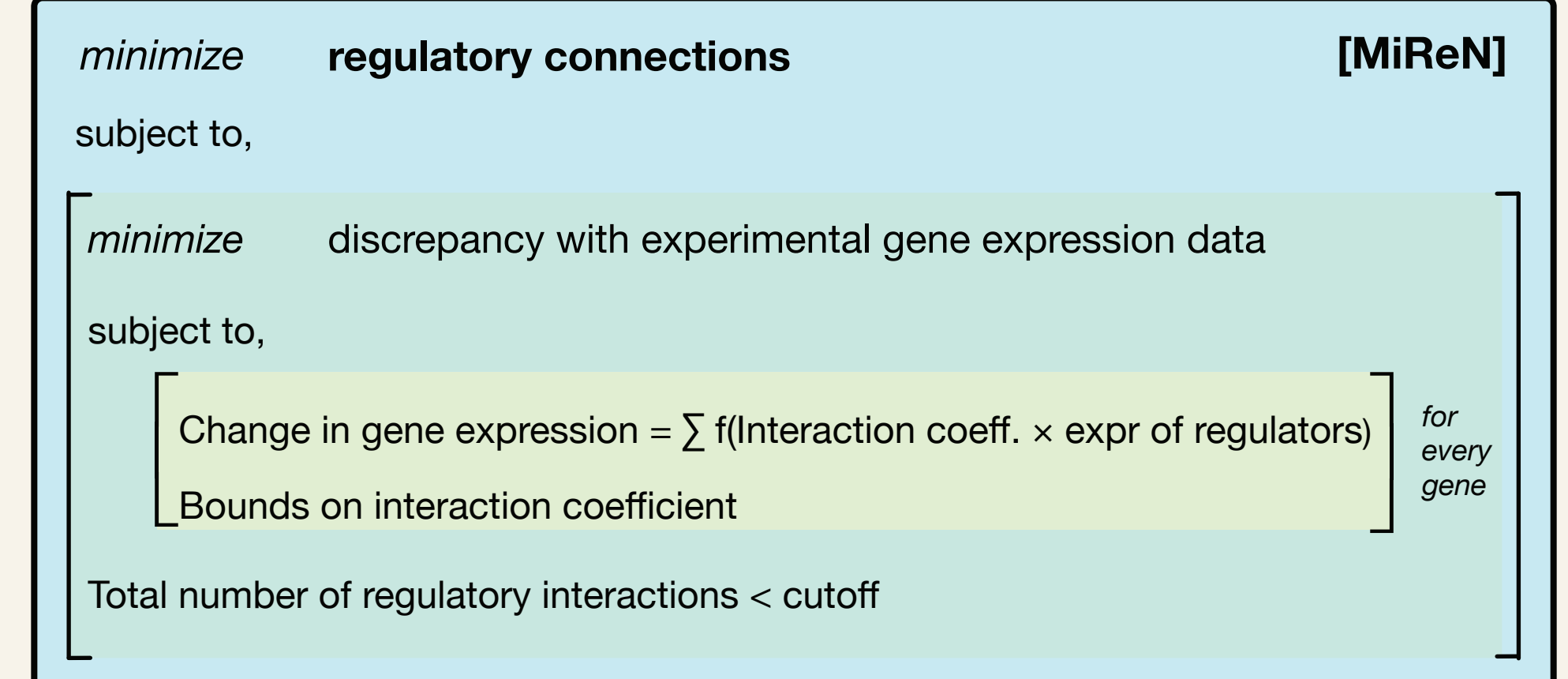
- Abiotic stresses during early seed development adversely affect the seed size and quality at maturity.
- To understand heat stress response in rice, a temporal transcriptomic analysis was performed.
- A mathematical optimization framework, **MiReN**, was developed to identify the minimal regulatory 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.

4. Minimal Regulatory Network (MiReN) Identifier

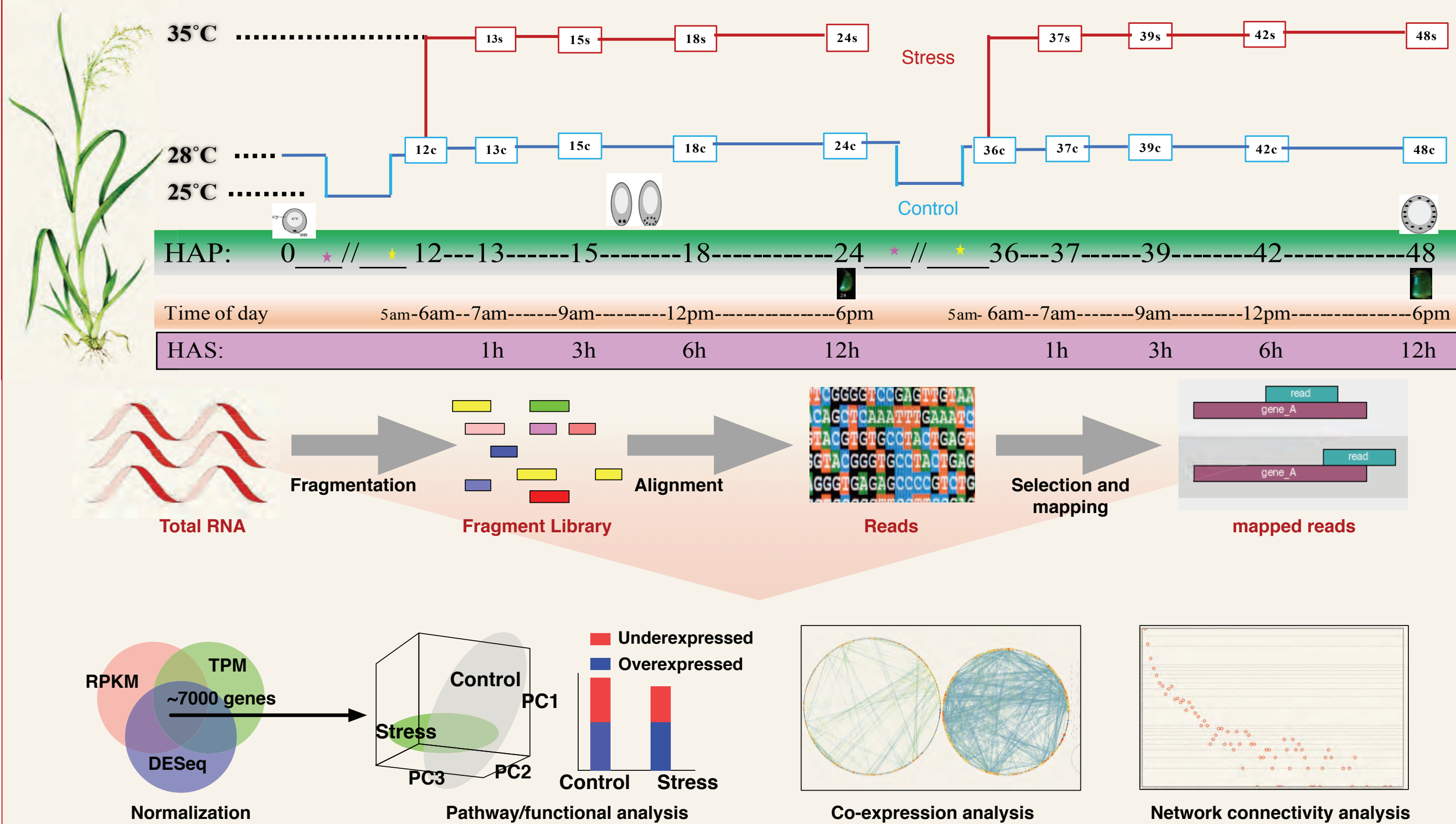
- Gene regulatory relationships are **hierarchical** and **not always linear**.
- MiReN finds the **minimal number of regulatory influence** on a gene that agrees with transcriptomic data.
- The **interaction coefficient** defines the extent of activation or inhibition of a gene by a regulator.

Challenges

$O(n^{n-1} + t)$
Smart cutoffs
Reduction
Variable Bounds



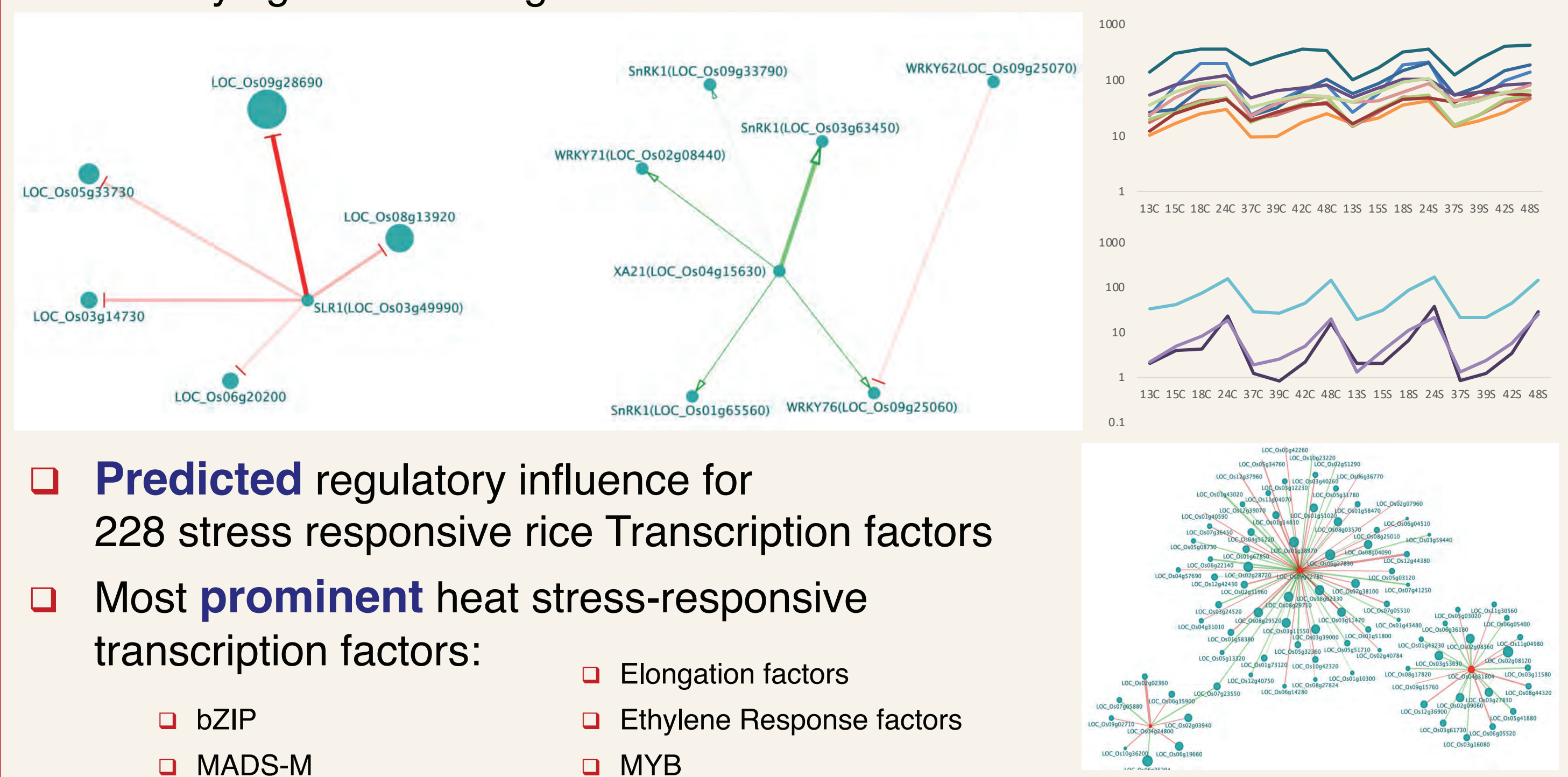
2. Transcriptomic Analysis of Rice Seed Under Heat Stress



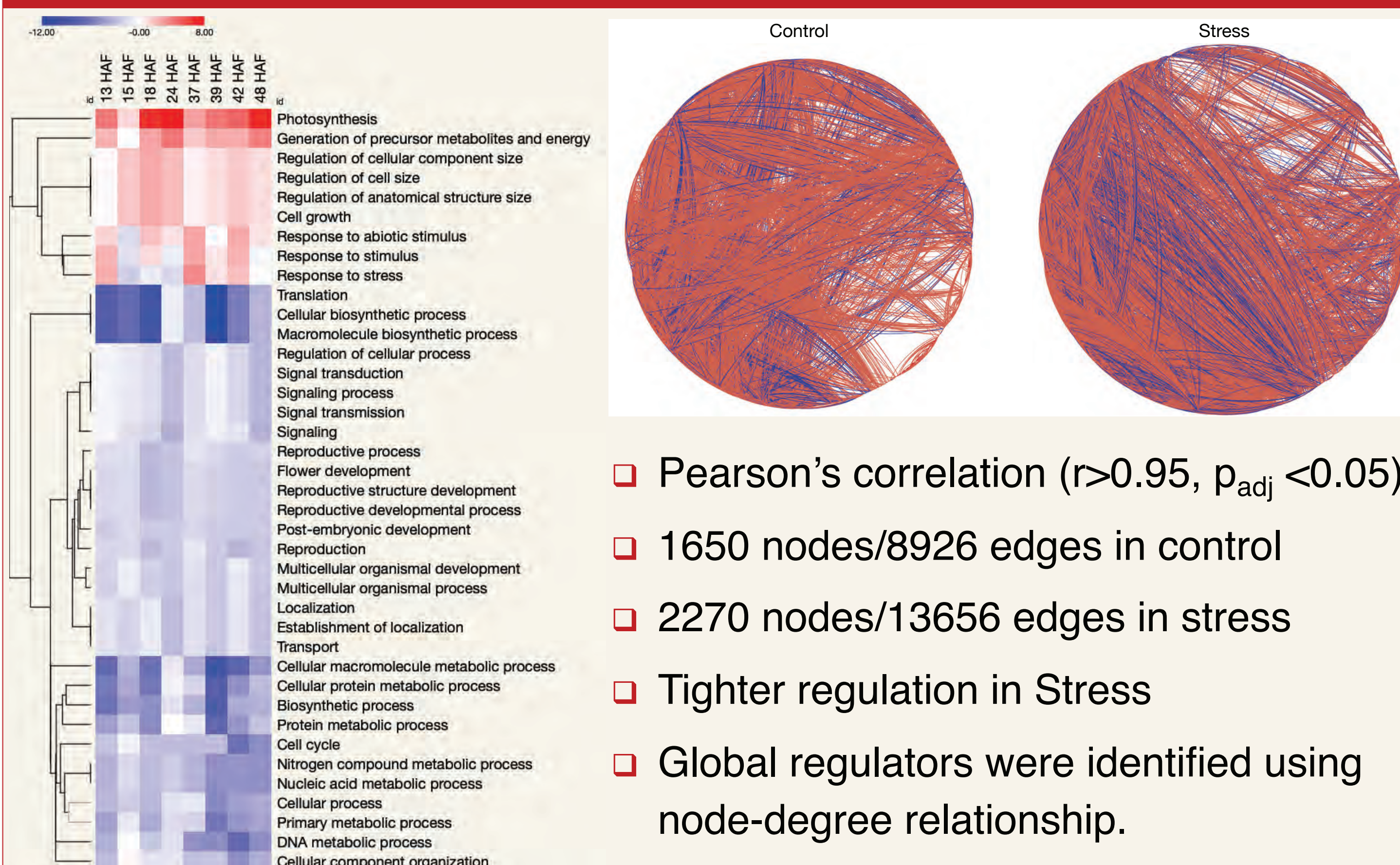
- 6755 stress-responsive genes
- 39 Cellular Processes GO terms identified

5. Identified Regulatory Relationships

- SLR1 represses** GA response pathway. (Jan and Komatsu 2006)
- Disease resistance gene **XA21 controls** several transcriptional repressors related to stress tolerance. (Seo et al 2011; Sharma et al 2013)
- Underlying circadian regulation?



3. Differential Gene Expression: Clustering



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.
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References

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