MiReN: An optimization tool for data-driven discovery of global regulatory phenomena during heat stress in rice seed

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In order to adapt to abiotic stress conditions, plants use a suite of strategies such as changing the levels of relative abundance of stress responsive genes and/or proteins that ultimately lead to the system-wide changes in the transcriptome, proteome, and metabolome. This project is aimed at understanding the heat stress response mechanisms in developing rice seed using optimization based data analyses from transcriptomics. In this work, a transcriptional analysis on developing rice seed under heat stress was performed to identify stress-responsive rice genes and transcription factors. MiReN, an MILP optimization-based tool was developed to decipher the minimal regulatory network using the time-series transcriptomic data. MiReN predicted important regulatory relationships for stress-responsive rice transcription factors and the minimal global regulatory network for rice seed in control and stress conditions. MiReN predictions were validated against published gene regulatory information for multiple global regulators in rice, including the stress-responsive gene Slender Rice 1 (*slr1*) and the disease resistance gene *Xa21*. A comparative analysis of the network topology revealed the shift in regulatory mechanisms in presence of stressors. With high-throughput multi-omics data being available, MiReN has the capability to efficiently identify stress biomarkers and opens up the potential to employ Artificial Intelligence for making decisions on robust engineering targets for crop stress-tolerance and yield. Informed from regulatory predictions and transcriptomic data, metabolic reconstructions of different rice tissues and modeling the interactions between them using multi-level and multi-objective modeling frameworks to develop a robust plant-scale rice model is underway. Our predictive mathematical model will identify biologically important and non-intuitive solutions to questions related to stress response mechanisms. This will impact the global food and agricultural industry by accelerating the development of tolerant plant varieties in an efficient and accurate fashion.