

SYSTEMS BIOLOGY AND FUNCTIONAL GENOMICS TO UNDERSTAND THE MOLECULAR MECHANISMS OF THE NITROGEN RESPONSE IN *ARABIDOPSIS THALIANA*

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Our long term goal is to understand how nitrogen (N) signaling intersects with other signaling networks to control plant growth and development. N availability is the most limiting factor for plant growth and agricultural productivity. Understanding the mechanisms involved in N sensing and response offers opportunities for improving N-use efficiency in plants or modifying the amino acid content of seeds, which are important issues for health, agriculture, and human nutrition. Recently we developed the first network models of the plant cell and identified gene network modules that are controlled by N and/or carbon metabolites. To build this model, we integrated known relationships among genes, proteins and molecules (extracted from public databases and/or generated with predictive algorithms) as well as experimental measurements obtained with microarray technology under different N treatments. We use novel visualization techniques to render the multivariate information in visual formats that facilitate extraction of biological concepts. Our systems approach provided specific hypotheses for transcriptional and post-transcriptional regulatory mechanisms of the plant response to changes in nitrogen availability. Recent works that address these hypotheses will be discussed. Although our main interest is in plants and using Arabidopsis as a model system, the tools we develop are generic and applicable to any organism whose genome is sequenced.

Selected references:

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