

# Transcriptional networks in the nitrate response of *Arabidopsis thaliana*

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## Abstract

Nitrogen is an essential macronutrient for plants and its availability is a key determinant of plant growth and development and crop yield. Besides their nutritional role, N nutrients and metabolites are signals that activate signaling pathways that modulate many plant processes. Because the most abundant inorganic N source for plants in agronomic soils is nitrate, much of the work to understand plant N-signaling has focused on this nutrient. Over the last years, several studies defined a comprehensive catalog of nitrate-responsive genes, involved in nitrate transport, metabolism and a variety of other processes. Despite significant progress in recent years, primarily using *Arabidopsis thaliana* as a model system, the molecular mechanisms by which nitrate elicits changes in transcript abundance are still not fully understood. Here we highlight recent advancements in identifying key transcription factors and transcriptional mechanisms that orchestrate the gene expression response to changes in nitrate availability in *A. thaliana*.