# Delivering the goods: leveraging functional genomics to understand cofactor trafficking

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https://genomicscience.energy.gov/research/sfas/bnlqpsi.shtml

**Project Goals: The Quantitative Plant Science Initiative (QPSI) is a capability that aims to bridge the knowledge gap between genes and their functions. A central aspect of our strategy is combining genome-wide experimentation and comparative genomics with molecular-level experimentation. In this way, we leverage the scalability of 'omics data and bioinformatic approaches to capture system-level information, while generating sequence-specific understanding of gene and protein function. By incorporating molecular-level experimentation in our workflow, we are addressing the question of how a protein functions and establishing mechanistic insight into how sequence variation impacts phenotype. This knowledge serves as a touchstone for accurate genome-based computational propagation across sequenced genomes and forms the foundation for robust predictive modeling of plant productivity in diverse environments.**

Transition metals occupy numerous and often essential positions within the biochemical framework of the cell. As protein cofactors, these elements have expanded the breadth of protein-catalyzed reactions and enabled pivotal energy-intensive reactions. To use metal ions as catalysts, the cell must balance a fundamental dichotomy: nutrient and toxin. Metal homeostasis has evolved to tightly modulate the availability of metals within the cell, avoiding cytotoxic interactions due to excess and protein inactivity due to deficiency. Even in the presence of homeostasis processes, however, low bioavailability of these essential metal nutrients in soils can negatively impact crop health and yield. While research has largely focused on how plants assimilate metals, acclimation to metal-limited environments, such as marginal soils, requires a suite of strategies that are not necessarily involved in metal transport. The identification of these assimilation-independent mechanisms provides an opportunity to improve metal-use efficiency and optimize feedstock yield in low nutrient soils without supplementing with expensive and environmentally damaging fertilizers.

By leveraging phylogenomic and data-mining analyses combined with an inter-disciplinary experimental approach, we have discovered a novel transferase that delivers zinc to an essential zinc-dependent enzyme during zinc deficiency. We provide evidence that this function is universally conserved from fungi to plants, where duplication has resulted in analogous pathways in the cytosol and chloroplast. Based on biochemical and phenotype analysis, this ancient and conserved mechanism is required during Zn insufficiency to ensure protein translation fidelity.

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