

Title:

Connecting metabolism to development- The role of transcription factors and carbon partitioning

Abstract:

A fundamental question in cell biology is how central carbon metabolism is integrated with the development of multicellular organisms. Primary metabolites like lipids, carbohydrates, and amino acids play key roles from regulating gene expression to assimilation of storage reserves. The talk will highlight two such coordinated regulations. The first part will focus on the molecular characterization of the START (STeroidogenic Acute Regulatory (StAR)-related lipid Transfer) ligand-binding motif containing homeodomain leucine-zipper transcription factors (HD-Zip IV TFs). In plants, HD-Zip IV TFs are master regulators of gene expression during epidermal cell differentiation. START domain-containing proteins were first discovered in mammalian StAR cholesterol transporters. At least, fifteen human proteins contain START domains, about half of which bind specific sterols, phospholipids or sphingolipids. START proteins have been shown to be integral components of intracellular signaling pathways, and several are associated with human diseases, including cancer. The second part will examine lipids but in the context of carbon partitioning to improve soybean seed storage reserves. Soybeans produce 20% lipid and 40% protein that are important for food, feed and fuel. Previous research indicates a trade-off between lipid, protein, and carbohydrates including Raffinose Family Oligosaccharides (RFOs) and cell wall polysaccharides. In mature soybeans, a decline in lipid and protein level is accompanied with an increase in carbohydrates. This is economically unfavorable as it not only lowers the proportion of seed oil and protein, but carbohydrates have less value. The goal of this project is to gain a mechanistic understanding of whether altering carbon partitioning can overcome this trade-off to add value to the seed.