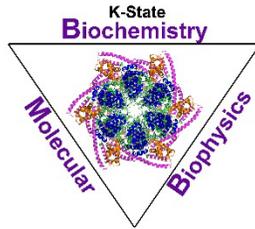


Ackert Hall, Room 120
Wednesday, April 3, 2024
4:00 P.M.



Coffee and Cookies
Chalmers Hall, Room 168
3:45 P.M.

Biochemistry
&
Molecular
Biophysics

Seminar

Understanding proteomic plasticity and the mechanisms behind amino acid rebalancing in seeds holds significant promise for biofortification efforts

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Seeds from various crops often lack several essential amino acids (EAAs), yet they remain valuable protein sources for both food and feed. Efforts to boost EAA levels by reducing or eliminating specific proteins have revealed complex regulation of seed amino acids, extending beyond the mere expression levels of seed storage proteins (SSPs) termed rebalancing. Surprisingly, despite significant knowledge of amino acid metabolic pathways, their regulation and genetic architecture underpinning their homeostasis, especially in seeds, remains elusive.

To address this, we've adopted integrative multi-omics approaches. Our studies involve comparing and contrasting candidate gene lists from diverse multi-omics strategies, including genome-wide association studies (GWAS), weighted gene correlation network analysis (WGCNA) of protein expression during kernel development, and transcriptome-wide association studies (TWAS) of proteins bound to amino acids of dry maize seeds. Functional analysis of the high-confidence candidate genes extracted from these multi-omic analyses has revealed multiple components of the translational machinery, particularly ribosomal proteins, suggesting a pivotal role of translation dynamics in shaping seed amino acid composition.

To further our understanding of the biological processes governing amino acid composition in seeds, we also conducted a proteomic developmental analysis of seed storage proteins mutant in maize, which exhibits proteomic reprogramming and rebalancing. This analysis has also provided strong support to the notion that targeting translation machinery for amino acid biofortification in seeds holds significant promise.