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Using high-throughput profiling to understand the genetic basis of soybean elemental composition

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The vast majority of the elements that make up a seed, with the exception of carbon and oxygen, are obtained from soil via the roots. These soil-derived elements are required for plant structure, metabolism, protein function, signaling, and proper osmotic and electrostatic potential. Elemental accumulation requires the integration of processes across biological scales, including interactions with the soil matrix and biota, subcellular localization, metabolism, and gas exchange. Thus, the elemental composition of seeds (the “ionome”), including both beneficial and toxic elements, is a consequence of complex plant-environment interactions with serious nutritional implications. High-throughput ionomics workflows allow a single inductively coupled plasma mass spectrometer (ICP-MS) to precisely analyze hundreds of samples for more than 20 elements per day. We have used ionomic profiling of ~100,000 soybean seeds to detect the genetic and environmental determinants of the ionome, observing variation across scales from within the canopy, across fields and between environments. Using modern genetic approaches such as QTL, GWAS and NAM GWAS, we can easily identify loci that control the ionome in a given environment, but there are large gene by environment interactions, so few loci are conserved across all environments. We are using several different approaches to integrate ionomic and other systems biology datasets to identify the causal genes underlying these phenotypes.