

Constructing proteome and metabolome maps for genetic improvement of energy-related traits in soybean

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Although the genetic blueprint of soybean is represented by the genome, its phenotype is a product of that blueprint manifested as the production of proteins and metabolites influencing growth characteristics, stress responses, seed composition, and yield. We are using various tools of genomics and molecular breeding with an aim towards development of value-added soybeans that will help United States farmers to maintain their competitiveness and expand utilization of soybean crops (e.g. functional foods, industrial uses, biodiesel, etc). Profiling soybean gene products will lay the foundation for a systems biology approach to key processes such as seed development, which will lead to the genetic improvement of yield and seed composition. Being one of the major bio-energy crops, building a comprehensive map of proteins and metabolites for soybean will help make connections between regulatory or metabolic pathways not previously characterized. Another major benefit from these studies is the discovery of energy related traits including plant productivity and seed compositional traits for the genetic improvement of soybean. It is well known that environmental cues influence developmental phenotypes in plants. Different biotic stresses such as fungal diseases and abiotic stresses, such as drought and flooding, also elicit phenotypic responses from the genome. Thus, by studying the gene products, a direct correlation between response and specific peptides/metabolites can be made. This will lead to crop improvement either through breeding or transgenic efforts. Major objectives of this study are: a) to identify key soybean seed, leaf, and root proteins involved in development and biotic and abiotic stress responses; b) to establish a comprehensive set of chemical standards for soybean metabolites moving toward construction of a metabolome map with a focus on seed and drought effects on seed development and, c) to compile a database linking proteomic and metabolite information and associate this information to value-added soybean traits and markers for assisted breeding. We are utilizing GC/MS, LC/MS, and NMR approaches to identify key molecules for further characterization.