

# Katherine Graham, Biochemistry

---

University: University of Missouri-Columbia  
Year in School: Senior  
Hometown: Hamilton, Illinois  
Faculty Mentor: Dr. Jay J. Thelen, Biochemistry  
Funding Source: MU Monsanto Undergraduate Research Fellowship

## **Revisiting the soybean seed filling proteome**

Katherine Graham, Ganesh Kumar Agrawal, Martin Hajduch, and Jay J. Thelen

Soybean seeds are an important source of proteins and fatty acids for human and animal nutrition as well as for non-edible uses, including industrial feed-stocks and combustible fuel. These components are mainly synthesized during the seed filling phase of seed development. A systematic and large-scale investigation of the protein components expressed during the seed filling phase and their quantification might uncover molecular mechanisms potentially involved in fine-tuned regulation of proteins and oils in seed. Towards this goal, we recently studied five sequential stages (2, 3, 4, 5, and 6 weeks after flowering) of seed development in soybean (cv Maverick) using two-dimensional gel electrophoresis (2-DGE) and matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF-MS), and reported 422 proteins representing 216 non-redundant proteins [Hajduch et al. (2005) *Plant Physiology* 137: 1397]. In this study, we have extended our investigation on soybean seed filling first by analyzing 960 trypsin-digested 2-D spots on liquid chromatography tandem MS and second by employing a complementary multi-dimensional protein identification technology (MudPIT). Of 960 spots analyzed, the identity of 531 spots was determined, representing 239 non-redundant proteins. These proteins were functionally classified into 13 major categories, where metabolism (26.4%), protein destination and storage (25.1%), and energy (10.9%) related proteins were highly represented. This data was used to provide a proteomic view on the pathways of carbon assimilation leading to oil synthesis in soybean seed and was compared with the previous report on the pathways in *Brassica napus* (cv Reston), which revealed differences in abundance and number of isoelectric species of the protein components between soybean and *Brassica*. This research was supported by NSF grants DBI-03324418 and DBI-0445287.

