**Presentation Title:** A web-based platform for RNA-Seq data analysis and storage: a case study on soybean gene expression experiments
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**Abstract**

The availability of the soybean genome sequence and the rapid evolution of DNA sequencing technologies in recent years bring us exciting new promises for scientific discovery and its conversion into required technological breakthroughs in the production and use of soybean. In addition to be a major protein source in animal feeds, soybean is ranked number one among the chief oil crops in the world and is becoming a major crop for biodiesel production. As a leguminous crop, soybean fixes nitrogen in association with *Bradyrhizobium*, which significantly reduces the needs for ammonium-based fertilizer even in other crops.

In this presentation, it will be described using a web-based platform, Soybean Gene Express, for analyzing and storing RNA-Seq data from whole-genome transcription profiling experiments. It will be presented firsthand how Soybean Gene Express supports researchers going from raw data to visual reports comparing the different genes within same sample or comparing gene expression across different biological samples/conditions. Also, it will be explored the power of link-based integration with other sources of biological information and databases such as ontologies, KEGG pathways, Pfam, and others, to uncover the biological meaning of these data. The ultimate goal is to facilitate the discovery of new biological insights into fundamental molecular processes as responses to biotic and abiotic stresses in soybean.