

## **Construction of Genetic Diversity Panel of USDA Peanut Germplasm Collection for Omics Research**

**C. CHEN\***, A. SANZ-SAEZ, Auburn University, Auburn, AL 36849; M.L. WANG, S. TALLURY, B. TONNIS USDA-ARS Plant Genetic Resources Conservation Unit, Griffin, GA 30223; J. YU, T. GUO, Iowa State University, Ames, IA 50011, P. DANG, USDA-ARS National Peanut Research Lab, Dawson, GA 39842.

Recent advances in sequencing technology and analysis tools have made omics research feasible for many species, including soybean, rice, maize, wheat, *Brachypodium distachyon*, *Brassica rapa*, *Brassicaoleracea*, and *Brassica napus* et al., which offers a much broader understanding of crop gene functions thus can be extremely useful in crop improvement. A well represented genetic diversity panel is critical for the success of omics research. Based on the current available data for the USDA peanut germplasm collection such as morphological traits, origins, chemical traits, and Arachis\_Axiom2 SNP array genotyping data, and pedigree information, we constructed a genetic diversity panel of 350 accessions to present an entire USDA peanut germplasm diversity, which included six botanical types, geographical distribution, unique genetic resource, significant donor parents of modern developed peanut cultivars. This panel will be used for genome wide association study (GWAS), development of high-throughput phenotyping system, and some other genomic research.