## RELATIONSHIPS AMONG OIL CONTENT, PROTEIN CONTENT AND SEED SIZE OF GOSSYPIUM ACCESSIONS IN THE U.S. NATIONAL COTTON GERMPLASM COLLECTION

Lori Hinze **USDA-ARS-SPARC College Station**. TX **Patrick Horn** University of North Texas **Denton**. TX Neha Kothari Texas A&M AgriLife Research **College Station, TX** Jane Dever Texas A&M AgriLife Research Lubbock, TX James Frelichowski **USDA-ARS-SPARC College Station, TX** Kent Chapman University of North Texas Denton, TX **Richard Percy** USDA-ARS-SPARC **College Station, TX** 

## <u>Abstract</u>

Low-field, time-domain <sup>1</sup>H nuclear magnetic resonance was used to quantify oil and protein content within 2,254 plant introductions of cotton (Gossypium spp.) including wild species, landraces, and adapted cultivars from around the world as represented in the US National Cotton Germplasm Collection. This specific group of plant introductions (accessions) is collectively known as the Gossypium Diversity Reference Set (GDRS). Within the GDRS, seed oil and protein averaged approximately the same (21.5%), with protein content encompassing a wider range of variability. Seed index ranged from 18 grams/100 seeds (wild G. barbadense accession GB-0096) down to less than 1 gram/100 seeds (several accessions from the C and G genomes). In addition, oil was positively correlated with seed index (r = 0.44) for the GDRS while oil and protein had a negative correlation (r = -0.31). Seed quality analyses were also conducted to explore relationships between oil and protein reserves and seed size in different cotton genomes (one tetraploid and eight diploid) and species (six tetraploid and 28 diploid). The tetraploid genome tended to have the highest oil content (21.7%) and largest seed sizes (9.6g) when compared with the diploid genomes. Of the diploid genomes, the K genome had the highest oil content (21.4%), and the A genome had the highest protein content (23.8%). For the cultivated tetraploid species, these seed quality components were evaluated relative to cultivated and wild types, as well as any known wild race classifications. Cultivated accessions of G. barbadense and G. hirsutum tended to have higher oil (22.7%) than the wild types (20.9%). Protein decreased in response to increasing oil content within G. hirsutum accessions but did not change within G. barbadense. The G. hirsutum Stoneville (SA) sub-collection had higher average oil content (22.7%) and slightly lower protein content (21.2%) than accessions in the G. hirsutum Texas (TX) sub-collection (21.0% and 22.0%, respectively). G. hirsutum wild type races richmondii and mocó had the highest oil content (23.6% and 23.4%, respectively) while race marie-galante had the highest protein (23.0%). These analyses provide a more comprehensive knowledge of cottonseed components to facilitate effective utilization of accessions in the US National Cotton Germplasm Collection by breeding programs interested in enhancing these seed traits.