## Dr. Amanda M Hulse-Kemp (Functional Genomics)

## USDA-ARS Bioinformatician / Adjunct Professor at North Carolina State University

I have been an active member of ICGI for nearly 15 years, with an eye towards utilizing bioinformatics to enhance cotton breeding programs. Our lab has been highly involved in development of the initial International Cotton SNP Consortium, developing the CottonSNP63K array. Recently we have also been leading the development of a replacement resource, the CottonSNP27K array. We strive to produce resources that can be used internationally for cotton improvement through the integration of marker assisted selection and genomic selection. Additionally, towards the Functional Genomics working group goals, we are working among many other projects aimed at deciphering gene function through trait mapping and biotechnology approaches. Leveraging bioinformatics to develop large datasets and implementation of advanced teaching methods through bioinformatics to enable user-friendly tools for deciphering gene function by cotton breeders and researchers. As in the past, we are still involved in producing many new high-quality reference genomes and resequencing various cotton materials.

I am a Bioinformatician with the USDA-ARS Genomics and Bioinformatics Research Unit located in Raleigh, NC at North Carolina State University. My research will continue to emphasize cotton bioinformatics, resource development and integration of genomics and bioinformatics tools for enhancing cotton breeding and utilization of currently available germplasm resources. I have strong collaborations with cotton researchers and breeders around the United States and Internationally. I've consistently participated in the International and Plant and Animal Genome Conference meetings and the ICGI group session since 2010. I envision strengthening the participation of students and the next generation in ICGI and have supported upcoming group member attendance.