

Dr. Joshua Udall completed a PhD at the University of Wisconsin-Madison. Dr. Udall first began working with cotton at Iowa State University with Dr. Jonathan Wendel. While at ISU, he created three different types of custom microarrays to investigate gene expression bias of tetraploid cotton. In 2006, Dr. Udall was hired at Brigham Young University (BYU, Provo, UT) in the Department of Plant and Wildlife Science. There his research continued in cotton as he created several large collections of ESTs and used the coding sequence alignment to identify useful SNPs in the cotton genome. A SNP-based map of the cotton genome was used to verify the *G. raimondii* genome sequence in Nature (Paterson et al. 2012). In addition to pursuing his research of polyploidy, his lab developed physical maps of cotton genomes using BioNano technology. Currently, he is working with large re-sequencing datasets of cotton to understand the domestication history of cotton and its untapped genetic diversity. Along with 6 Masters students, 1 Ph.D. student and postdocs, he has authored or co-authored 65 papers in peer reviewed journals. He was awarded Outstanding Research Scientist at BYU in 2014 and the Cotton Biotechnology Award in 2014. In 2019, Dr. Udall accepted a Plant Geneticist with the USDA-ARS, College Station, TX. At the same time, he served the Research Leader position for the Crop Germplasm Research Unit that has scientists working on cotton, pecan, sorghum, and warm-season grasses. Dr. Udall serves as an associate editor for G3 and Theoretical and Applied Genetics. He is also a member of the Genetics Society of America, the American Society of Plant Biologists, and the Crop Science Society of America.