



ICAC's 82nd Plenary Meeting

International Hotel
Tashkent, Uzbekistan

29 Sept - 3 Oct 2024



Dr David Fang

Dr. David Fang is a Supervisory Research Geneticist and Research Leader of the Cotton Fiber Bioscience & Utilization Research Unit at USDA-ARS in New Orleans, Louisiana, USA. He leads a team studying cotton fiber biology using biochemical, genetic, molecular, and genomic methods and technologies. His personal research focuses on mapping important qualitative and quantitative traits of cotton using DNA markers and implementing them in breeding. Notably, he was the first cotton researcher to use a MAGIC population to identify genes and genetic loci that control fiber quality traits. Dr. Fang also uses various mutants to study fiber development, particularly fiber elongation and maturation. Since joining ARS, Dr. Fang has hosted and mentored eight post-docs in his laboratory.

Before joining USDA-ARS in 2008, Dr. Fang worked as the Molecular Cotton Breeder and Director of Molecular Breeding for Delta and Pine Land Company (D&PL) beginning in 1998. He founded the molecular cotton breeding program and transgenic testing laboratories for D&PL.

Dr. Fang has been active in the cotton research community, serving in various capacities, including as co-Chair and Chair of the International Cotton Genome Initiative (ICGI), co-Chair and Chair of ICGI's Structural Genomics Workgroup, and member of the Cotton Marker Database Advisory Committee. Outside the cotton community, he served as the Chair of the Membership Committee of the National Association of Plant Breeders. He actively serves the Tri-Societies and is the Chair or member of multiple committees. Currently, he is an editor of seven international journals, including the prestigious Theoretical and Applied Genetics and the CSSA's flagship journal Crop Science.

Dr. Fang has published 122 journal papers and edited two cotton books. His research work has been cited 7,720 times, and his h-index is 47 according to Google Scholar. Dr. Fang is a CSSA Fellow and the recipient of the Cotton Genetics Research Award in 2023.