

Dr Qian-Hao Zhu is a principle research scientist at Agriculture and Food, CSIRO, Australia. He has been working on plant functional genomics and pre-breeding related works since moving to Australia in 2000. Taking the advantage of rapid progress in cotton genomics and releasing of cotton reference genome sequences, he has made significant contribution to cotton functional genomics by identification of several genes underlying the traits of classic mutants, such as the okra-leaf and fuzzless (both recessive and dominant) traits. He is on track to identify more genes related to fiber initiation and pest resistance. He has rich experience on non-coding RNAs and recently found that the cotton miR482 family has experienced significant expansion mediated by transposon capture and amplification. He is also involved in the CSIRO's genomic selection project with the aim to improve breeding efficiency. If elected, he'll be more closely working with world-wide colleagues not only in the space of functional genomics but also in all other areas to promote cotton genomics and pre-breeding works. Particularly, he'll advocate to set up a task force to create a unified cotton genome annotation system. Current, several cotton reference genomes with different gene ID for the same gene are used by the cotton community. It's not an easy task for people who uses one of the genomes to find the equivalent gene in another genome. Creating a set of unified annotated genes would make it easy for everyone to track cotton genes, some of them annotated differently, and facilitate cotton genomics studies.