

## **Statement by Xiyin Wang**

At present, I am leading the bioinformatics group in the Plant Genome Mapping Laboratory (headed by Prof. Paterson), and have led bioinformatics/comparative genomics groups in 8 international whole-genome sequencing projects of plant genomes, including cotton. Together with colleagues, I inferred a decaploid ancestor of cotton and characterized the complex cotton genome after rounds of polyploidizations. At present, I am working on cotton population genomics data, aiming at understanding its domestication and functional innovation.

As to publications, I have authored 55 high-impact papers, being the first author in 17 of them, and the corresponding author in 7 of them, contributing to the understanding of biology of multiple plants at divergent scales, from genome instability, genome repatterning, homoeologous chromosomal recombination, chromosome number reduction, and evolution of regulatory pathway and gene families.

As to database and software development, I conceived the idea and contributed to the construction of Plant Genome Duplication database (PGDD), which is being highly accessed (~8 million annual records) from more than 180 counties and regions. I developed the algorithms behind ColinearScan and partial of MCSCAN, and did the related programming.

As to grant application, I have rich grant application experiences in both USA and China, and as a PI achieved a NSF grant ~\$500,000 and quite several grants totaled ~\$1,000,000 in China. At present, I am developing a next-generation genome alignment tool supported by the NSF grant.

If elected as the chair of ICGI comparative genomics group, I would devote myself in understanding the functions of key gene families and evolutionary changes of cotton genomes, esp. constructing a cotton-genus comparative genomics database, exploiting gene colinearity and relating gene homology to specific polyploidization events, which will benefit innovational researches from the cotton community.