

ICGI Comparative Genomics & Bioinformatics Workgroup Co-Chair Candidate

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At present, I am a professor and the dean of the School of Life Science at the North China University of Science and Technology. For years, I was leading the bioinformatics group in the Plant Genome Mapping Laboratory at the University of Georgia. So far, I have ever led bioinformatics/comparative genomics groups in ~20 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, and was working on cotton population genomics data, aiming at understanding its domestication and functional innovation.

As to publications, I have authored ~70 high-impact papers, being the first author in 17 of them, and the corresponding author in 20 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. Papers were cited 12300 times as to Google Scholar. A new publication of my group found that cotton diverged with cacao and durian much more recent than previous expected.

As to database and software development, I conceived the idea and contributed to the construction of Plant Genome Duplication database (PGDD), which has ~8 million annual records from >180 counties and regions. Together with colleagues, I developed the algorithms and statistics behind ColinearScan and MCSCAN.

If elected as the chair of ICGI comparative genomics group, I would be committed to push forward collaboration between cotton researches, especially those in comparative genomics and bioinformatics. By constructing a cotton-genus comparative genomics database, I will establish a collaborative platform to benefit innovational researches from the cotton community.