Evolutionary and Comparative Genomics Workgroup Co-Chair Candidate

## Wangzhen Guo

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Upland cotton has the highest yield, and accounts for >95% of world cotton production. Decoding upland cotton genomes will undoubtedly provide the ultimate reference and resource for structural, functional, and evolutionary studies of the species. If elected, I will foster collaboration among all members to further develop this workgroup. I obtained my Ph.D. majored in crop genetics and breeding from Nanjing Agri. Univ. in 1997. My research interests have been on cotton genetic mapping construction and breeding utilization; genetic and epigenetic mechanisms of cotton fiber cell development; and polyploidy effects on genetic regulation. I and my team construct a functional markers-rich genetic map of allotetraploid cultivated cotton species, and further develop the structure, function, and evolution studies of tetraploid cotton species. I serve in several professional editorial boards of genomics-related journals. I organized the 3<sup>rd</sup> ICGI meetings held in Nanjing in 2002, and participated in several ICGI meetings. As an ICGI member, I will do my best to keep ICGI advantage in Evol/Comp Genomics using my knowledge and experiences.