Breeding & Applied Genomics Workgroup Co-Chair Candidate

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Upland cotton has the highest yield, and accounts for >95% of world cotton production. The sequence information of four cotton species, *G. arboreum*, *G. raimondii*, *G. hirsutum*, and *G. barbadense*, has been released. These significant genomic progresses will greatly enhance the cotton breeding & applied genomics wider and deeper. I would like to serve the global cotton breeding & applied genomics research in ICGI community in next cycle. I obtained my Ph.D. majored in crop genetics and breeding from Nanjing Agri. Univ. in 1997. Now, I am a professor and the Chair of the Department of Plant Genetics and Breeding in College of Agriculture at Nanjing Agricultural University, and Deputy Director of State Key Laboratory of Crop Genetics and Germplasm Enhancement. I also serve as the Chair of Structural Genomics Workgroup of International Cotton Genome Initiative (ICGI). My research interest is in cotton genomics and molecular breeding. I and my colleagues have developed an integrated research program from elucidating molecular mechanisms to developing molecular breeding methodology, leading to the improvement of agronomic traits, including high quality, biotic and abiotic stress tolerance. As the first or corresponding author, I have published more than 50 research papers in high-impact journals, including Nature Biotechnology, Genome Biology, Plant Physiology and Journal of Experimental Botany et al. As principle participants, I have also published five textbooks and monographs, developed five new cotton varieties, and received 11 patents and seven national or provincial awards. As reviewer, I have good experiences to serve in several professional editorial boards of genomics-related journals. If elected, I will foster collaboration among all members to further develop this workgroup, and do my best to keep ICGI advantage in Breeding & Applied Genomics using my knowledge and experiences.