

ICGI **Comparative Genomics&Bioinformatics** Workgroup Co-Chair Candidate

Dr. **Daojun Yuan**

Associate Professor

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I am profoundly honored to be nominated as a co-chair for the ICGI workgroup. If selected, I will commit my full dedication to serving this community by collaborating closely with the chair to organize activities for the Comparative Genomics and Bioinformatics Workshop. A central priority of our efforts will be advancing cotton genomics and leveraging bioinformatics tools to translate genomic insights into impactful research and genetic improvements for cotton. Below is a concise summary of my credentials and professional background:

Daojun Yuan earned his Ph.D. in Genetics and Crop Breeding from Huazhong Agricultural University in 2014 under the mentorship of Prof. Xianlong Zhang. From 2015 to 2019, he conducted postdoctoral research in the laboratories of Prof. Joshua A. Udall (Brigham Young University, Provo, USA) and Prof. Jonathan F. Wendel (Iowa State University, Ames, USA).

With nearly two decades of experience in cotton genomics, I have authored over 50 publications in leading journals such as *Nature Genetics*, *Advanced Science*, and *Journal of Advanced Research*, which have collectively garnered over 4,700 citations. Among my key contributions are the pioneering assembly of the *Gossypium barbadense* draft genome (*Scientific Reports*, 2015) and high-quality reference genomes for *G. hirsutum* and *G. barbadense* (*Nature Genetics*), alongside genomes of diploid species including *G. longicalyx*, *G. raimondii*, and *G. turneri*. Additionally, I conducted deep resequencing of 643 accessions spanning wild, domesticated, and allopolyploid cotton lineages, integrating these data with existing resources to resolve evolutionary relationships and unravel mechanisms of parallel domestication. These high-quality genomes and large-scale genomic datasets have been openly

shared with the global cotton research community, where they serve as foundational tools for genetic, genomic, and molecular breeding studies—advancing efforts to meet the rising demand for sustainable fiber production.

Selected publications:

1. Xinlin Yan, Shenglong Kan, Meixia Wang, Yongyao Li, Luke R Tembrock, Wenchuang He, Liyun Nie, Guanqing Hu, **Daojun Yuan***, Xiongfeng Ma*, Zhiqiang Wu*. Genetic diversity and evolution of the plastome in allotetraploid cotton (*Gossypium* spp.). *Journal of Systematics and Evolution* 2024, 62(6): 1118-1136.
2. Meng Qingying, Gu Jiaqi, Xu Zhongping, Zhang Jie, Tang Jiwei, Wang Anzhou, Wang Ping, Liu Zhaowei, Rong Yuxuan, Xie Peihao, Hui Liuyang, Udall Joshua A., Grover Corrinne E., Wendel Jonathan F., Jin Shuangxia, Zhang Xianlong, **Yuan Daojun***. Comparative analysis of genome sequences of the two cultivated tetraploid cottons, *Gossypium hirsutum* (L.) and *G. barbadense* (L.). *Industrial Crops and Products* 2023, 196: 116471.
3. Wang Nian, Li Yuanxue, Meng Qingying, Chen Meilin, Wu Mi, Zhang Ruiting, Xu Zhiyong, Sun Jie, Zhang Xianlong, Nie Xinhui*, **Yuan Daojun***, Lin Zhongxu*. Genome and haplotype provide insights into the population differentiation and breeding improvement of *Gossypium barbadense*. *Journal of Advanced Research* 2023, 54:15-27.
4. Jie Zhang, Jianying Li, Sumbul Saeed, William D Batchelor, Qingying Meng, Fuhui Zhu, Jiawei Zou, Zhongping Xu, Huan Si, Qiongqiong Wang, Xianlong Zhang, Huaguo Zhu, Shuangxia Jin*, **Daojun Yuan***. Identification and functional analysis of lncRNA by CRISPR/Cas9 during the cotton response to sap-sucking insect infestation. *Frontiers in Plant Science* 2022, 13: 784511.
5. **D. Yuan***, C.E. Grover, G. Hu, M. Pan, E. R. Miller, J.L. Conover, S.P. Hunt, J.A. Udall*, J. F. Wendel. Parallel and Intertwining Threads of Domestication in Allopolyploid Cotton. *Advanced Science* 2021, 2003634.
6. Jianying Li, **Daojun Yuan**, Pengcheng Wang, Qiongqiong Wang, Mengling Sun, Zhenping Liu, Huan Si, Zhongping Xu, Yizan Ma, Boyang Zhang, Liuling Pei, Lili Tu,

Longfu Zhu, Ling-Ling Chen, Keith Lindsey, Xianlong Zhang, Shuangxia Jin*, Maojun Wang*. Cotton pan-genome retrieves the lost sequences and genes during domestication and selection. Genome biology 2021, 22:1-26.

7. Maojun Wang#, Lili Tu#, **Daojun Yuan#**, De Zhu, Chao Shen, Jianying Li, Fuyan Liu, Liuling Pei, Pengcheng Wang, Guannan Zhao, Zhengxiu Ye, Hui Huang, Feilin Yan, Yizan Ma, Lin Zhang, Min Liu, Jiaqi You, Yicheng Yang, Zhenping Liu, Fan Huang, Baoqi Li, Ping Qiu, Qinghua Zhang, Longfu Zhu, Shuangxia Jin, Xiyan Yang, Ling Min, Guoliang Li, Ling-Ling Chen, Hongkun Zheng, Keith Lindsey, Zhongxu Lin*, Joshua A Udall*, Xianlong Zhang*. Reference genome sequences of two cultivated allotetraploid cottons, *Gossypium hirsutum* and *Gossypium barbadense*. Nature genetics 2019, 51(2).224–229.

8. **Yuan D#**, Tang Z#, Wang M#, Gao W, Tu L, Jin X, Chen L, He Y, Zhang L, Zhu L et al. The genome sequence of Sea-Island cotton (*Gossypium barbadense*) provides insights into the allopolyploidization and development of superior spinnable fibres. Scientific reports 2015, 5.17662.

9. Wang M, **Yuan D***, Gao W, Li Y, Tan J, Zhang X*. A comparative genome analysis of PME and PME1 families reveals the evolution of pectin metabolism in plant cell walls. PLoS One 2013, 8(8).e72082.

10. **Yuan D**, Tu L, Zhang X. Generation, annotation and analysis of first large-scale expressed sequence tags from developing fiber of *Gossypium barbadense* L. PLoS One 2011, 6(7).e22758.