Xiaofan Zhou, Ph.D.

Integrative Microbiology Research Centre
South China Agricultural University
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CURRENT POSITION

2016-Present	Faculty, Integrative Microbiology Research Centre, South China Agricultural University

PAST POSITIONS

2011-2016	Postdoctoral Scholar, Vanderbilt University, USA Advisors: Antonis Rokas & Laurence J. Zwiebel
2006-2011	Ph.D. Student, The Pennsylvania State University, USA Advisor: Hong Ma
2005-2006	Research Assistant, Shanghai Jiao Tong University, P.R. China Advisor: Dabing Zhang
2004-2005	Undergraduate Thesis Student, Shanghai Jiao Tong University, P.R. China Advisor: Dabing Zhang

EDUCATION

2006-2011	Ph.D., Intercollege Graduate Program in Cell and Developmental Biology The Pennsylvania State University, USA
2001-2005	B.S., Biotechnology Shanghai Jiao Tong University, P.R. China

RESEARCH INTERESTS

- Functional and Comparative Genomics of Pathogenic Microorganisms
- High-throughput Sequencing Data Analysis
- Molecular Evolution, Phylogenetics, and Phylogenoimcs

SERVICE

Editorial roles:	Frontiers in Bioinformatics, Associate Editor Frontiers in Ecology and Evolution, Associate Editor Frontiers in Microbiology, Review Editor
Manuscript Reviewer:	Nature Communications, Current Biology, Nucleic Acids Research, Molecular Biology and Evolution, New Phytologist, Bioinformatics, Horticulture Research, BMC Evolutionary Biology, PLoS One, Insect Biochemistry and Molecular Biology, Annals of the Entomological Society of America, G3, Genes & Genomics, Molecular Genetics and Genomics.

<u>FIRST-AUTHOR PUBLICATIONS</u> (#: co-first author; *: co-corresponding author)

1. Chao Liu#, **Xiaofan Zhou**#, Yuanning Li, Chris Todd Hittinger, Ronghui Pan, Jinyan Huang, Xue-Xin Chen, Antonis Rokas, Yun Chen, Xing-Xing Shen, The Influence of the Number of Tree Searches on Maximum Likelihood Inference in Phylogenomics, *Systematic Biology*, 2024, 73(5):807-822.
2. Lin Chen#, Chengyu Li#, Bijun Li#, **Xiaofan Zhou**#, Yulin Bai, Xiaoqing Zou, Zhixiong Zhou, Qian He, Baohua Chen, Mei Wang, Yaguo Xue, Zhou Jiang, Jianxin Feng, Tao Zhou, Zhanjiang Liu*, Peng Xu*, Evolutionary divergence of subgenomes in common carp provides insights into speciation and allopolyploid success, *Fundamental Research*, 2024, 4(3):589-602.
3. Peng Yang#, Xuyi Ling#, **Xiaofan Zhou**#, Yuanxia Chen, Tiantian Wang, Xiaojing Lin, Yuanyuan Zhao, Yushi Ye, Linxuan Huang, Yewen Sun, Yuxin Qi, Dongming Ma, Ruoting Zhan*, Xueshuang Huang*, Jinfen Yang*, Comparing genomes of Fructus Amomi-producing species reveals genetic basis of volatile terpenoid divergence, *Plant Physiology*, 2023, 193(2):1244-1262.
4. Tiantian Yan#, **Xiaofan Zhou**#, Jieling Li#, Guanjun Li, Yali Zhao, Haojie Wang, Huaping Li*, Yanfang Nie*, Yunfeng Li*, FoCupin1, a Cupin_1 domain-containing protein, is necessary for the virulence of *Fusarium oxysporum* f. sp. *cubense* tropical race 4, *Frontiers in Microbiology*, 2022, 13:1001540.
5. Pankaj Bhatt#, **Xiaofan Zhou#**, Yaohua Huang, Wenping Zhang, Shaohua Chen, Characterization of the role of esterases in the biodegradation of organophosphate, carbamate, and pyrethroid pesticides, *Journal of Hazardous Materials*, 2021, 411:125026.
6. Yanqiu He#, **Xiaofan Zhou**#, Jieling Li, Huaping Li, Yunfeng Li*, Yanfang Nie*, In Vitro Secretome Analysis Suggests Differential Pathogenic Mechanisms between *Fusarium oxysporum* f. sp. *cubense* Race 1 and Race 4, *Biomolecules*, 2021, 11(9):1353.
7. Ming Hu#, Chuhao Li#, **Xiaofan Zhou**#, Yang Xue, Si Wang, Anqun Hu, Shanshan Chen, Xiuwen Mo, Jianuan Zhou, Microbial Diversity Analysis and Genome Sequencing Identify *Xanthomonas perforans* as the Pathogen of Bacterial Leaf Canker of Water Spinach (*Ipomoea aquatic*), *Frontiers in Microbiology*, 2021, 12:752760.
8. **Xiaofan Zhou**, Sarah Lutteropp, Lucas Czech, Alexandros Stamatakis, Moritz Von Looz, Antonis Rokas*, Quartet-based computations of internode certainty provide robust measures of phylogenetic incongruence, *Systematic Biology*, 2020, 69(2):308-324.
9. Yuyu Wang#, **Xiaofan Zhou#**, Liming Wang, Xingyue Liu*, Ding Yang* and Antonis Rokas*, Gene selection and evolutionary modeling affect phylogenomic inference of Neuropterida based on transcriptome data, *International Journal of Molecular Sciences*, 2019, 20(5):1072.
10. Xing-Xing Shen#, Dana A. Opulente#, Jacek Kominek#, **Xiaofan Zhou#**, Jacob L. Steenwyk, Kelly V. Buh, Max A.B. Haase, Jennifer H. Wisecaver, Mingshuang Wang, Drew T. Doering, James T. Boudouris, Rachel M. Schneider, Quinn K. Langdon, Moriya Ohkuma, Rikiya Endoh, Masako Takashima, Ri-ichiroh Manabe, Neza Cadez, Diego Libkind, Carlos A. Rosa, Jeremy DeVirgilio, Amanda Beth Hulfachor, Marizeth Groenewald, Cletus P. Kurtzman, Chris Todd Hittinger*, Antonis Rokas*, Tempo and mode of genome evolution in the budding yeast subphylum, *Cell*, 2018, 175(6):1533-1545.
11. **Xiaofan Zhou**, Xing-Xing Shen, Chris Todd Hittinger, Antonis Rokas*, Evaluating fast maximum likelihood-based phylogenetic programs using empirical phylogenomic data sets, *Molecular Biology and Evolution*, 2018, 35(2): 486-503.
12. Xin Yi#, Jiangwei Qi#, **Xiaofan Zhou#**, Mei Ying Hu, Guo Hua Zhong*, Differential expression of chemosensory-protein genes in midguts in response to diet of *Spodoptera litura*, *Scientific Reports*, 2017, 7(1): 296.
13. **Xiaofan Zhou**, David Peris, Jacek Kominek, Cletus P. Kurtzman, Chris Todd Hittinger, Antonis Rokas*, in silico Whole Genome Sequencer & Analyzer (iWGS): A computational pipeline to guide the design and analysis of *de novo* genome sequencing studies, *G3: Genes|Genomes|Genetics*, 2016, 6(11): 3655-3662.
14. **Xiaofan Zhou**, Antonis Rokas, Shelley L. Berger, Jürgen Liebig, Anandasankar Ray, Laurence J. Zwiebel*, Chemoreceptor evolution in Hymenoptera and its implications for the evolution of eusociality, *Genome Biology and Evolution*, 2015, 7(8): 2407-2416.
15. **Xiaofan Zhou**, Antonis Rokas*, Prevention, diagnosis, and treatment of high throughput sequencing data pathologies, *Molecular Ecology*, 2014, 23(7): 1679-1700.

16. **Xiaofan Zhou#**, David C. Rinker#, Ronald Jason Pitts, Antonis Rokas, Laurence J. Zwiebel*, Conserved and divergent elements comprise the chemoreceptive repertoire of the non-blood feeding mosquito *Toxorhynchites amboinensis*, *Genome Biology and Evolution*, 2014, 6(10): 2883-2896.
17. Ronald Jason Pitts#, Chao Liu#, **Xiaofan Zhou#**, Juan C. Malpartida, Laurence J. Zwiebel*, Odorant receptor-mediated sperm activation in disease vector mosquitoes, *Proceedings of the National Academy of Sciences, USA*, 2014, 111(7): 2566-2571.
18. David C Rinker#, **Xiaofan Zhou#**, Ronald Jason Pitts, The AGC Consortium, Antonis Rokas, Laurence J. Zwiebel*, Antennal transcriptome profiles of anopheline mosquitoes reveal human host olfactory specialization in *Anopheles gambiae*, *BMC Genomics*, 2013, 14(1): 749.
19. **Xiaofan Zhou#**, Jesse D. Slone#, Antonis Rokas, Shelley L. Berger, Jürgen Liebig, Anandasankar Ray, Danny Reinberg, Laurence J. Zwiebel*, Phylogenetic and transcriptomic analysis of chemosensory receptors in a pair of divergent ant species reveals caste-specific signatures of odor coding, *PLoS Genetics*, 2012, 8(8): e1002930.
20. **Xiaofan Zhou**, Zhenguo Lin, Hong Ma*, Phylogenetic detection of numerous gene duplications shared by animals, fungi and plants, *Genome Biology*, 2010, 11(4):R38.
21. **Xiaofan Zhou**, Hong Ma*, Evolutionary history of histone demethylase families: distinct evolutionary patterns suggest functional divergence, *BMC Evolutionary Biology*, 2008, 8:294.

CORRESPONDING-AUTHOR PUBLICATIONS (#: co-first author; *: co-corresponding author)

1. Yixiao Zhu, Yonglin Li, Chuhao Li, Xing-Xing Shen*, **Xiaofan Zhou***, A critical evaluation of deep-learning based phylogenetic inference programs using simulated data sets, *Journal of Genetics and Genomics*, 2025, 52(5):714-717.
2. Xiaoqing Wang#, Hongyu Shi#, Xiaoyan Wu, Xuemei Chen, Shaobo Liu, Qinglin Yu, Lian-Hui Zhang*, **Xiaofan Zhou***, Microbial diversity in coastal *Casuarina equisetifolia* forest and its potential in counteracting bacterial wilt infections, *Pest Management Science*, 2025, 81(8):4621-4634.
3. Bo Feng#, Yonglin Li#, Biyang Xu#, Hongyue Liu, Jacob L Steenwyk, Kyle T David, Xiaolin Tian, Carla Gonçalves, Dana A Opulente, Abigail L LaBella, Marie-Claire Harrison, John F Wolters, Shengyuan Shao, Zhaohao Chen, Kaitlin J Fisher, Marizeth Groenewald, Chris Todd Hittinger, Xing-Xing Shen, Shengying Li, Antonis Rokas*, **Xiaofan Zhou***, Yuanning Li*, Unique trajectory of gene family-evolution from genomic analysis of nearly all known species in an ancient yeast lineage, *Molecular Systems Biology*, 2025, 21(8):1066-1089.
4. Yuwei Liang#, Qiang Gao#, Fan Li#, Yunpeng Du#, Jian Wu#, Wenqiang Pan, Shaokun Wang, Xiuhai Zhang, Mingfang Zhang, Xiaoming Song, Linlin Zhong, Fan Zhang, Yan Li, Zhiwei Wang, Danqing Li, Qing Duan, Shenchong Li, Chunlian Jin, Peihua Zhang, Yang Gu, Zhong-Hua Chen, Klaus F X Mayer*, **Xiaofan Zhou***, Jihua Wang*, Liangsheng Zhang*, The giant genome of lily provides insights into the hybridization of cultivated lilies, *Nature Communications*, 2025, 16(1):45.
5. Xiaohui Wen#, Yuwei Liang#, Hongyan Shan#, Xiaojun Chang#, Xiaoming Song#, Shaoqin Shen, Yanhong Fu, Dan Chen, Fei Chen, Yueqing Li, Qian Guan, Qiang Gao, Qi Wang, Yonglin Li, Zhengjia Wang, Hongzhi Kong, Huan Liu*, Xiang Gao*, **Xiaofan Zhou***, Chris Thorogood*, Liangsheng Zhang*, The genome of giant waterlily provides insights into the origin of angiosperms, leaf gigantism, and stamen function innovation, *Plant Communications*, 2025, 6(6):101342.
6. Xiaoqing Wang, Chuhao Li, Shaohua Huang, Huagui Gao, Yonglin Li, Xuemei Chen, Liangzhou Huang, Jianhua Luo, Lian-Hui Zhang*, **Xiaofan Zhou***, Pathogenic and Comparative Genomic Analysis of *Ralstonia pseudosolanacearum* Isolated from Casuarina, *Plant Disease*, 2024, 108(9):2809-2819.
7. Xiuxiu Li#, Sheng Yu#, Zhihao Cheng#, Xiaojun Chang#, Yingzi Yun#, Mengwei Jiang#, Xuequn Chen, Xiaohui Wen, Hua Li, Wenjun Zhu, Shiyao Xu, Yanbing Xu, Xianjun Wang, Chen Zhang, Qiong Wu, Jin Hu, Zhenguo Lin, Jean-Marc Aury, Yves Van de Peer*, Zonghua Wang*, **Xiaofan Zhou***, Jihua Wang*, Peitao Lv*, Liangsheng Zhang*, Origin and evolution of the triploid cultivated banana genome, *Nature Genetics*, 2024, 56(1):136-142.

8. Siliang Zuo, Linghui Xu, Huiyan Zhang, Meiqian Jiang, Sifeng Wu, Lian-Hui Zhang, **Xiaofan Zhou***, Junxia Wang*, FlgI Is a Sec-Dependent Effector of *Candidatus* Liberibacter asiaticus That Can Be Blocked by Small Molecules Identified Using a Yeast Screen, Plants, 2024, 13(2):318.
9. Minghui Qiu#, Yonglin Li#, Qingmei Liu#, Xiaohan Zhang, Yulong Huang, Rui Guo, Ming Hu, Jianuan Zhou, **Xiaofan Zhou**, *Pseudomonas machongensis* sp. nov. and *Stenotrophomonas capsici* sp. nov., isolated from wilted pepper plants, *International Journal of Systematics and Evolutionary Microbiology*, 2024, 74(11):006550.
10. Wen-Juan Chen#, Shao-Fang Chen#, Haoran Song, Zeren Li, Xiaofang Luo, Xidong Zhang, **Xiaofan Zhou**, Current insights into environmental acetochlor toxicity and remediation strategies, *Environmental Geochemistry and Health*, 2024, 46(9):356.
11. Qingmei Liu, Chuhao Li, Xiaohan Zhang, Mengfan Ding, Xinyue Liao, Jinli Yan, Ming Hu, Leilei Yang, Xiaoqing Wang, Lisheng Liao, Peng Li*, **Xiaofan Zhou***, PhcX Is a LqsR-family response regulator that contributes to *Ralstonia solanacearum* virulence and regulates multiple virulence factors, *mBio*, 2023, 14(5):e0202823.
12. Qian He#, Juming Li#, Qingmei Liu#, Yonglin Li, Xinyue Liao, Jianuan Zhou, **Xiaofan Zhou**, Complete genome sequence resource of *Pantoea anthophila* CL1 causing soft rot disease in *Clausena lansium* (Wampee) in China, *Plant Disease*, 2023, 107(5):1613-1616.
13. Wen-Juan Chen#, Wenping Zhang#, Qiqi Lei#, Shao-Fang Chen, Yaohua Huang, Kalpana Bhatt, Lisheng Liao*, **Xiaofan Zhou***, *Pseudomonas aeruginosa* based concurrent degradation of beta-cypermethrin and metabolite 3-phenoxybenzaldehyde, and its bioremediation efficacy in contaminated soils, *Environmental Research*, 2023, 236:116619
14. Min Xu#, Qiang Gao#, Mengwei Jiang, Wenling Wang, Juan Hu, Xiaojun Chang, Dinggao Liu, Yuwei Liang, Yifan Jiang, Fei Chen, Chuhao Li, Haoran Huang, Feng Chen, Fan Li, Robert N Trigiano, Jihua Wang*, Chen Jiao*, **Xiaofan Zhou***, Liangsheng Zhang*, A novel genome sequence of *Jasminum sambac* helps uncover the molecular mechanism underlying the accumulation of jasmonates, *Journal of Experimental Botany*, 2023, 74(4):1275-1290.
15. Jianuan Zhou*, Steffen Kolb*, **Xiaofan Zhou***, Pathogen co-infections and plant diseases, *Frontiers in Plant Science*, 2023, 14:1189476.
16. Yuwei Liang#, Fan Li#, Qiang Gao#, Chunlian Jin, Liqing Dong, Qi Wang, Min Xu, Fuhui Sun, Bo Bi, Peng Zhao, Shenchong Li, Jiwei Ruan, **Xiaofan Zhou***, Liangsheng Zhang*, Jihua Wang*, The genome of *Eustoma grandiflorum* reveals the whole-genome triplication event, *Plant Biotechnology Journal*, 2022, 20(10):1856-1858.
17. Peng Yang, Haiying Zhao, Jieshu Wei, Yuanyuan Zhao, Xiaojing Lin, Jing Su, Fangping Li, Meng Li, Dongming Ma, Xukai Tan, Huilin Liang, Yewen Sun, Ruoting Zhan, Guozhen He*, **Xiaofan Zhou***, Jinfen Yang*, Chromosome-level genome assembly and functional characterization of terpene synthases provide new insights into the volatile terpenoid biosynthesis of *Wurfbainia villosa*, *Plant Journal*, 2022, 112(3):630-645.
18. Ming Hu, Yang Xue, Chuhao Li, Mingfa Lv, Lianhui Zhang, Matthew R Parsek, Guangtao Lu, **Xiaofan Zhou***, Jianuan Zhou*, Genomic and Functional Dissections of *Dickeya zeae* Shed Light on the Role of Type III Secretion System and Cell Wall-Degrading Enzymes to Host Range and Virulence, *Microbiology Spectrum*, 2022, 10(1):e0159021.
19. Mingfa Lv#, Yufan Chen#, Ming Hu, Qinglin Yu, Cheng Duan, Sixuan Ye, Jinfeng Ling, Jianuan Zhou, **Xiaofan Zhou***, Lianhui Zhang*, OhrR is a central transcriptional regulator of virulence in *Dickeya zeae*, *Molecular Plant Pathology*, 2022, 23(1):45-59.
20. Jianuan Zhou#, Ming Hu#, Anqun Hu#, Chuhao Li, Xinyue Ren, Min Tao, Yang Xue, Shanshan Chen, Chongzhi Tang, Yiwu Xu, Lianhui Zhang, **Xiaofan Zhou**, Isolation and Genome Analysis of Pectobacterium colocasium sp. nov. and Pectobacterium aroidearum, Two New Pathogens of Taro, *Frontiers in Plant Science*, 2022, 13:852750.
21. Yang Liu#, Stephen Dela Ahator#, Huishan Wang, Qishun Feng, Yinuo Xu, Chuhao Li, **Xiaofan Zhou***, Lian-Hui Zhang*, Microevolution of the mexT and lasR Reinforces the Bias of Quorum Sensing System in Laboratory Strains of Pseudomonas aeruginosa PAO1, *Frontiers in Microbiology*, 2022, 13:821895.

22. Chenxing Tan, Chuhao Li, Ming Hu, Anqun Hu, Yang Xue, **Xiaofan Zhou***, Jianuan Zhou*, Comparative Pathogenomic Analysis of Two Banana Pathogenic *Dickeya Strains* Isolated from China and the Philippines, *International Journal of Molecular Sciences*, 2022, 23(21):12758.
23. Yanfang Nie#, Guanjun Li#, Jieling Li, Xiaoshu Zhou, Yanzhi Zhang, Qingchuan Shi, **Xiaofan Zhou***, Huaping Li*, Xiao-Lin Chen*, Yunfeng Li*, A novel elicitor MoVcpo is necessary for the virulence of *Magnaporthe oryzae* and triggers rice defense responses, *Frontiers in Plant Science*, 2022, 13:1018616.
24. Ming Hu, Chuhao Li, Yang Xue, Anqun Hu, Shanshan Chen, Yufan Chen, Guangtao Lu, **Xiaofan Zhou***, Jianuan Zhou*, Isolation, characterization, and genomic investigation of a phytopathogenic strain of *Stenotrophomonas maltophilia*, *Phytopathology*, 2021, 111(11):2088-2099.
25. Xudan Xu#, Tian Ye#, Wenping Zhang, Tian Zhou, **Xiaofan Zhou***, Weijun Dai*, Shaohua Chen*, Identification of FadT as a Novel Quorum Quenching Enzyme for the Degradation of Diffusible Signal Factor in *Cupriavidus pinatubonensis* Strain HN-2, *International Journal of Molecular Sciences*, 2021, 22(18):9862
26. Tian Ye#, Tian Zhou#, Xudan Xu#, Wenping Zhang, Xinghui Fan, Sandhya Mishra, Lianhui Zhang, **Xiaofan Zhou***, Shaohua Chen*, Whole-genome sequencing analysis of quorum quenching bacterial strain *Acinetobacter lactucae* QL-1 identifies the FadY enzyme for degradation of the diffusible signal factor, *International Journal of Molecular Sciences*, 2020, 21(18):6729.
27. Li Zheng, Jun-jian Situ, Qing-feng Zhu, Ping-gen Xi, Yin Zheng, Hong-xia Liu, **Xiaofan Zhou***, Zi-de Jiang*, Identification of volatile organic compounds for the biocontrol of postharvest litchi fruit pathogen *Peronophythora litchii*, *Postharvest Biology and Technology*, 2019, 155:37-46.
28. Yue Zhong#, Meixin Yan#, Jinyan Jiang#, Zhihan Zhang, Junjun Huang, Lianhui Zhang, Yinyue Deng*, **Xiaofan Zhou***, Fei He*, Mycophenolic acid as a promising fungal dimorphism inhibitor to control sugar cane disease caused by *Sporisorium scitamineum*, *Journal of Agricultural and Food Chemistry*, 2019, 67(1):112–119.
29. Xin Yi, Song Shi, Peidan Wang, Yaoyao Chen, Qiqi Lu, Tianyi Wang, **Xiaofan Zhou***, Guohua Zhong*, Characterizing potential repelling volatiles for "push-pull" strategy against stem borer: a case study in *Chilo auricilius*, *BMC Genomics*, 2019, 20:751.
30. Peng Li*, Ying Zhang, Yuqingqing Sun, Xingxing Wu, Zhiyuan Wang, Jianuan Zhou, **Xiaofan Zhou***, Comparative genomic analysis of subspecies of *Pantoea stewartii* reveals distinct variations, *Journal of Plant Pathology*, 2019, 101(4):997–1004.
31. Ren Ren, Yazhou Sun, Yue Zhao, David Geiser, Hong Ma*, **Xiaofan Zhou***, Phylogenetic resolution of deep eukaryotic and fungal relationships using highly conserved low-copy nuclear genes, *Genome Biology and Evolution*, 2016, 8(9): 2683-2701.

INVITED TALKS

2025	Invited Speaker, 2025 Summer School on Bioinformatics, Zhongkai University of Agriculture and Engineering
2023	Invited Speaker, 2nd Haiqing Symposium, Shandong University
2020	Invited Speaker, Virtual Symposium on Phylogenomics, hosted by the Institute of Evolutionary Biology, Pompeu Fabra University
2019	Invited Speaker, The 4th Symposium on Systematic Biology, Beijing, P.R. China
2019	Invited Speaker, Functional Genomics Summit VI, Chengdu, P.R. China
2019	Faculty, 2019 Workshop on phylogenomics, Cesky Krumlov, Czech Republic
2018	Invited Speaker, 2018 Frontiers in Microbiology International Symposium, Guangzhou, P.R. China
2018	Invited Speaker, 1st Maritime Silk Road Life Sciences Forum for Young Scientists, Haikou, P.R. China
2018	Invited Speaker, Haixia Institute of Science and Technology, Fujian Agriculture and Forestry University, Fuzhou, P.R. China
2017	Faculty, 2017 Workshop on phylogenomics, Cesky Krumlov, Czech Republic