

Curriculum Vitae



Xing-Xing Shen
Institute of Insect Sciences
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Education and Experience

- **Zhejiang University**, November 2019-Present
'Hundred Talents Program' Young Professor
- **Vanderbilt University**, December 2014-December 2019
Postdoctoral Fellow, Advised by Dr. Antonis Rokas
- **Sun Yat-sen University**, September 2009 – July 2014
Ph.D. in Biochemistry and Molecular Biology, Advised by Dr. Peng Zhang
- **Hainan University**, September 2005–July 2009
B.S. in Biotechnology

Research

My current research mainly focuses on utilizing computational approaches and genomic data in animal and fungi to shed light on questions in molecular phylogenetics, evolutionary biology, genomics, comparative genomics, and bioinformatics such as:

- a) Examining phylogenetic incongruence
- b) Reconstructing phylogenetic relationships
- c) Developing bioinformatics tool
- d) Exploring fungal pathogenicity (HGT, Convergence)

Professional Service

Reviewer: BMC Evolutionary Biology, Bioinformatics, Current Biology, Molecular Ecology, Molecular Ecology Resources, Molecular Biology and Evolution, Systematic Biology

Publications

1. Krassowski, T., J. Kominek, **Shen X.-X.**, D. A. Opulente, X. Zhou, A. Rokas, C. T. Hittinger, Wolfe K.H. 2019. Multiple Reinventions of Mating-type Switching during Budding Yeast Evolution. *Current Biology* in press.
2. Steenwyk, J. L., **Shen X.-X.**, A. L. Lind, G. G. Goldman, Rokas A. 2019. A robust phylogenomic timetree for biotechnologically and medically important fungi in the genera *Aspergillus* and *Penicillium*. *mBio* 10: e00925-19.
3. Steenwyk, J. L., D. A. Opulente, J. Kominek, **Shen X.-X.**, X. Zhou, A. L. Labella, N. P. Bradley, B. F. Eichman, N. Čadež, D. Libkind, J. DeVirgilio, A. B. Hulfactor, Kurtzman C.P., Hittinger C.T., Rokas A. 2019. Extensive loss of cell cycle and DNA repair genes in an

- ancient lineage of bipolar budding yeasts. *PLoS Biology* 17: e3000255.
4. Kominek J.*, Doering D.T.*, Opulente D., **Shen X.-X.**, Zhou X., Jeremy D., Hulfachor A.B., Groenewald M., Mcgee M., Karlen S., Kurtzman C.P., Rokas A., Hittinger C.T. 2019. Eukaryotic acquisition of a bacterial operon. *Cell* 176: 1356-1366. (*co-first authors).
 5. **Shen X.-X.***, Opulente D.A.*, Kominek J.*, Zhou X.*, Steenwyk J., Buh K.V., Haase M., Wisecaver J.H., Wang M., Doering D.T., Boudouris J., Schneider R., Langdon Q.K., Ohkuma M., Endoh R., Takashima M., Manabe R., Čadež N., Libkind D., Rosa C., DeVirgilio J., Hulfachor A., Groenewald M., Kurtzman C.P., Hittinger C.T., Rokas A. 2018. The tempo and mode of genome evolution in the budding yeast subphylum. *Cell* 175: 1533-1545. (*co-first authors).
 6. Krause D.J., Kominek J., Opulente D.A., **Shen X.-X.**, Zhou X., Langdon Q.K., DeVirgilio J., Hulfachor A., Kurtzman C.P., Rokas A., Hittinger C.T. 2018. Functional and evolutionary characterization of a secondary metabolite gene cluster in budding yeasts. *Proc. Natl. Acad. Sci. USA* 115: 11030-11035.
 7. Shi R., **Shen X.-X.**, Rokas A., Eichman B.F. 2018. Structural biology of the HEAT-like repeat family of DNA glycosylases. *BioEssays* 40: 1800133.
 8. Krassowski T.*, Coughlan A.Y.*, **Shen X.-X.**, Zhou X., Kominek J., Opulente D., Riley R., Grigoriev I. V., Maheshwari N., Shields D.C., Kurtzman C.P., Hittinger C.T., Rokas A., Wolfe K.H. 2018. Evolutionary Instability of CUG-Leu in the Genetic Code of Budding Yeasts. *Nature communication*s. 9: 1887. (*co-first authors)
 9. Gonçalves C., Wisecaver J.H., Kominek J., Salema-Oom M., Leandro M.J., **Shen X.-X.**, Opulente D., Zhou X., Peris D., Kurtzman C.P., Hittinger C.T., Rokas A., Gonçalves P. 2018. Evidence for loss and adaptive reacquisition of alcoholic fermentation in an early-derived fructophilic yeast lineage. *Elife*. 7:e33034.
 10. Zhou X., **Shen X.-X.**, Hittinger C.T., Rokas A. 2018. Evaluating Fast Maximum Likelihood-Based Phylogenetic Programs Using Empirical Phylogenomic Data Sets. *Molecular Biology and Evolution*. 35(2): 486-503.
 11. Shi R., Mullins E.A., **Shen X.-X.**, Lay K.T., Yuen P.K., David S.S., Rokas A., Eichman B.F. 2018. Selective base excision repair of DNA damage by the non-base-flipping DNA glycosylase AlkC. *EMBO Journal* 37: 63-74.
 12. **Shen X.-X.**, Hittinger C. T., Rokas A. 2017. Contentious relationships in phylogenomic studies can be driven by a handful of genes. *Nature Ecology & Evolution* 1: 0126.
 13. **Shen X.-X.**, Zhou X., Kominek J., Kurtzman C. P., Hittinger C. T., Rokas A. 2016. Reconstructing the backbone of the Saccharomycotina yeast phylogeny using genome-scale data. *G3: Genes / Genomes / Genetics*: 6: 3927-3939.
 14. **Shen X.-X.**, Salichos L., Rokas A. 2016. A genome-scale investigation of how sequence-, function-, and tree-based gene properties influence phylogenetic inference. *Genome Biology and Evolution* 8(8): 2565–2580.
 15. **Shen X.-X.**, Liang D., Chen M.Y., Mao R.L., Wake D.B., Zhang P. 2016. Enlarged Multilocus Dataset Provides Surprisingly Younger Time of Origin for the Plethodontidae, the Largest Family of Salamanders. *Systematic Biology* 65(1): 66-81.

16. **Shen X.-X.**, Liang D., Feng Y.J., Chen M.Y., Zhang P. 2013. A Versatile and Highly Efficient Toolkit Including 102 Nuclear Markers for Vertebrate Phylogenomics, Tested by Resolving the Higher-level Relationships of the Caudata. *Molecular Biology and Evolution* 30(10): 2235-2248.
17. Liang D.*, **Shen X.-X.***, Zhang P. 2013. One Thousand Two Hundred Ninety Nuclear Genes from a Genome-Wide Survey Support Lungfishes as the Sister Group of Tetrapods. *Molecular Biology and Evolution* 30(8): 1803-1807. (* first co-authors)
18. **Shen X.-X.**, Liang D., Zhang P. 2012. The Development of Three Long Universal Nuclear Protein-Coding Locus Markers and Their Application to Osteichthyan Phylogenetics with Nested PCR. *PLoS ONE* 7(6): e39256.62.
19. **Shen X.-X.**, Liang D, Wen J.Z., Zhang P. 2011. Multiple Genome Alignments Facilitate Development of NPCL Markers: A Case Study of Tetrapod Phylogeny Focusing on the Position of Turtles. *Molecular Biology and Evolution* 28(12): 3237-3252.

Presentations

- **Shen X.-X.**, Liang D., Zhao Z.L., Zhang P. 2012. On the root of the salamander tree: evidence from 15 nuclear protein-coding locus markers. 5th Asian Herpetological Conference Proceedings, Chengdu. P48.
- **Shen X.-X.**, Zhang P. 2010. The Development of New Nuclear Markers and Their Application to the Phylogenetic Position of Turtles. Chinese Herpetological Conference Proceedings, Guilin. P36

Awards and Honors

- **Vanderbilt Postdoc of the Year Award, Honorable Mention**, April 2019
- **The Second Prize for Excellent Graduate Students**, State Key Laboratory of Biocontrol, June 2014
- **National Scholarship for Doctoral Graduate Students**, Ministry of Education of the People's Republic of China, November 2013
- **Innovative Talents Foundation**, Sun Yat-sen University, August 2013– June 2014, 20,000 RMB
- **The Second Prize for Academic Excellence**, State Key Laboratory of Biocontrol, June 2013
- **National Scholarship for Doctoral Graduate Students**, Ministry of Education of the People's Republic of China, November 2012
- **The Second Prize for Excellent Graduate Students**, State Key Laboratory of Biocontrol, June 2012
- **Most Meritorious Oral Presentation**, Scientific Organizing Committee of the 5th Asian Herpetological Conference, June 2012
- **Excellent Graduate Students**, Sun Yat-sen University, November 2011
- **The First Prize for Academic Excellence**, State Key Laboratory of Biocontrol, June 2011
- **Collaboration Award**, State Key Laboratory of Biocontrol, June 2010

- **Merit Student**, Hainan University, September 2008
- **Outstanding Basketball Referees**, College of Agriculture, Hainan University, April 2008