

Curriculum Vitae



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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 species biodiversity, biosynthesis of important traits, and bioinformatics.

Professional Service

Journals: Nature, Cell, Nature Communications, Current Biology, BMC Evolutionary Biology, Bioinformatics, Molecular Ecology, Molecular Ecology Resources, Molecular Biology and Evolution, Systematic Biology, iSCIENCE

Grants: 英国UK Research & Innovation, 美国National Science Foundation, 波兰National Science Center

Funding

- National Natural Science Foundation of China, PI, 01/2021-12/2024, ¥520,000
- National Important Talents Program, PI, 01/2021-12/2023, ¥3,000,000
- Zhejiang 'Hundred Talents Program', PI, 12/2019-12/2025, ¥2,000,000

Recent Representative Publications

1. Yang L.#, Liu Z.#, Liu C.#, Shi Z., Pang L., Chen C., Chen Y., Pan R., Zhou W., Chen X.-X., Rokas A.*, Huang J.*, **Shen X.-X.*** 2022. HGT is widespread in insects and contributes to male courtship in lepidopterans. *Cell* in press (#co-first author, *corresponding author).
2. **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).
3. **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. 入选ESI高被引用论文, *Nature Ecol & Evol* 最具影响力论文之一.
 4. **Shen X.-X.***, Steenwyk J., LaBella A., Opulente D., Zhou X., Kominek J., Li Y., Groenewald M., Hittinger C., Rokas A.* 2020. Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota. *Science Advances* 6(45): eabd0079 (*corresponding author).
 5. **Shen X.-X.***, Li Y., Hittinger C., Chen X., Rokas A.* 2020. An investigation of irreproducibility in maximum likelihood phylogenetic inference. *Nature Communications* 11:6096 (*corresponding author).
 6. **Shen X.-X.***, Steenwyk J., Rokas A. 2021. Dissecting incongruence between concatenation- and quartet-based approaches in phylogenomic data. *Systematic Biology* 70(5):997-1014 (*corresponding author).
 7. Li Y., Steenwyk J., Chang Y., Wang Y., James T.Y., Stajich J.E., Spatafora J.W., Groenewald M., Dunn C., Hittinger C.T., **Shen X.-X.***, Rokas A.* 2021. A genome-scale phylogeny of the kingdom Fungi. *Current Biology* 31: 1653–1665 (*corresponding author, Cover story) 入选ESI高被引用论文.

Other Publications

8. **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.
9. **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.
10. **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.
11. 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)
12. **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.
13. **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.

14. **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.
15. 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* 29(15):2555–2562.
16. Li Y.#, Davod K.T.#, **Shen X.-X.**, Steenwyk J., Halanych K.M., Rokas A. 2020. Feature Frequency Profile-based phylogenies are inaccurate. *Proc. Natl. Acad. Sci. USA* 117: 31580-31581.
17. 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.
18. 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. Hulfachor, 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.
19. 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).
20. 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.
21. 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 communications*. 9: 1887. (*co-first authors).
22. 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.
23. Li Y., **Shen X.-X.**, Evans B., Dunn C.W.*, Rokas A.* 2021. Rooting the animal tree of life. *Molecular Biology and Evolution* 38(10):4322-4333 (*corresponding author).
24. Yang Y., Sun P., Lv L., Wang D., Ru D., Li Y., Ma T., Zhang L., **Shen X.-X.**, Meng F., Jiao B., Shan L., Liu M., Wang Q., Qin Z., Xi Z., Wang X., Davis C.C., Liu J. 2020. Prickly waterlily and rigid hornwort genomes shed light on early angiosperm evolution. *Nature Plants* 6(3):215–222.
25. Xu S.#, Liu Y.-X.#, Cernava T.#, Wang H., Zhou Y., Xia T., Cao S., Berg G., **Shen X.-X.**, Wen Z., Li C., Qu B., Ruan H., Chai Y., Zhou X., Ma Z., Shi Y., Yu Y.*, Bai Y.*, Chen Y.* 2022. *Fusarium* fruiting body microbiome member *Pantoea agglomerans* inhibits fungal pathogenesis by targeting lipid rafts. *Nature Microbiology* 7(6): 831-843 (#co-first author, *corresponding author).

26. Gonçalves C., Wisecaver J.H., Kominek J., Salema-Oom M., Leandro M.J., **Shen X.-X.**, Ofulente 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.
27. 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.
28. Steenwyk J., Buida III T.J., Li Y., **Shen X.-X.**, Rokas A. 2020. ClipKIT: a multiple sequence alignment-trimming algorithm for accurate phylogenomic inference. *PLoS Biology* 18: e3001007.
29. 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.
30. Steenwyk J., Buida III T.J., LaBella A.L., Li Y., **Shen X.-X.**, Rokas A. 2021. PhyKIT: a UNIX shell toolkit for processing and analyzing phylogenomic data. *Bioinformatics* 37(16):2325–2331.
31. Haase M.A.B.#, Kominek J.#, Ofulente D., **Shen X.-X.**, LaBella A., Zhou X., DeVirgilio J., Hulfachor A, Kurtzman C.P., Rokas A.*, Hittinger C.T.* 2020. Repeated horizontal gene transfer of GALactose metabolism genes violates Dollo’s law of irreversible loss. *Genetics* 217: iyaa012 (#co-first author; *corresponding author).
32. Mead M.#, Borowsky A.#, Joehnk B., Steenwyk J., **Shen X.-X.**, Sil A., Rokas A. 2020. Recurrent loss of abaA, a master regulator of asexual development in filamentous fungi, correlates with changes in genomic and morphological traits. *Genome Biology and Evolution* 12(7):1119–1130 (#co-first author).
33. Ely Z.A., Moon J.M., Sliwoski G.R., Sangha A.K., **Shen X.-X.**, LaBella A.L., Meiler J., Capra J.A., Rokas A. 2019. The impact of natural selection on the evolution and function of placentally expressed galectins. *Genome Biology and Evolution* 11(9):2574–2592.
34. Wang M., Fu H., **Shen X.-X.**, Ruan R., Rokas A., Li H. 2019. Genomic features and evolution of the conditionally dispensable chromosome in the tangerine pathotype of *Alternaria* and *alternata*. *Mol. Plant Pathol.* 20(10): 1425–1438.
35. Phillips, M. A., Steenwyk J.*, **Shen X.-X.**, Rokas A.* 2021. Examination of gene loss in the DNA mismatch repair pathway and its mutational consequences in a fungal phylum. *Genome Biology and Evolution* 13(10):1-12 (*corresponding author).
36. Tice, A. K.#, D. Žihala#, T. Pánek#, R. E. Jones, E. Salomaki, S. Nenarokov, F. Burki, M. Eliáš, L. Eme, A. J. Roger, A. Rokas, **Shen X.-X.**, J. F. H. Strasser, M. Kolíčko, M. W. Brown 2021. PhyloFisher: A phylogenomic package for resolving eukaryotic relationships. *PLoS Biology* 19: e3001365 (#co-first author).

Presentations

- **(Online talk) Shen X.-X.** “Opportunities and challenges in evolutionary genomics”. Invited by Institute of Microbiology, Chinese Academy of Sciences, May, 2022.
- **(Online talk) Shen X.-X.** “Opportunities and challenges in evolutionary genomics”. Invited by Agricultural University of Hebei, November, 2021.

- **(Talk) Shen X.-X.** “Challenges in phylogenomic inference”. Invited by Lanzhou University, June, 2021.
- **(Talk) Shen X.-X.** “Challenges in phylogenomic inference”. Invited by Kunming Institute of Botany, Chinese Academy of Sciences, May, 2021.
- **(Online talk) Shen X.-X.** “Challenges in phylogenomic inference”. Invited by the Banfield lab, University of California, Berkeley, April, 2021.
- **(Talk) Shen X.-X.** “Opportunities and challenges in genomics”. Invited by Institute of Zoology, Chinese Academy of Sciences, November, 2020.
- **(特邀大会报告) Shen X.-X.,** Hittinger C. T., Rokas A. “Can phylogenomics end incongruence”. Evolution 2019, Providence, Rhode Island, USA, June 21-25, 2019.
- **(特邀报告) Shen X.-X.** “Yeast evolution: loss is more”. Online talk invited by Chinese Genomics Online Meet-up (CGM). USA, May 2019
- **(大会报告) 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.
- **(大会报告) 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

- **The Thousand Youth Talents Program,** December 2020
- **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