

# Sheng-Kai Hsu

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## Positions & Education

Year	Position / Degree
2022–present	Postdoc, Institute for Genomic Diversity, Cornell University
2017–2021	Ph.D., Vienna Graduate School of Population Genetics, Univ. of Veterinary Medicine Vienna <i>Advisor: Christian Schlötterer</i>
2014–2015	M.Sc., Department of Agronomy, National Taiwan University <i>Advisor: Chih-Wei Tung</i>
2010–2014	B.Sc., Department of Agronomy, National Taiwan University

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## Publications

### Peer-reviewed Publications

1. **Hsu, S.**, Emmett, B.D., Haafke, A., Costa-Neto, G., Schulz, A.J., Lepak, N., La, T., AuBuchon-Elder, T.M., Hale, C.O., Raglin, S.S., Ojeda-Rivera, J.O., Kent, A.D., Kellogg, E.A., Roday, M.C., & Buckler, E.S. (2025). *Contrasting rhizosphere nitrogen dynamics in Andropogoneae grasses*. *The Plant Journal*, 123(1). <https://doi.org/10.1111/tpj.70319>
2. Thorhølludottir, D.A.V., **Hsu, S.**, Barghi, N., Mallard, F., Nolte, V., & Schlötterer, C. (2025). *Reduced Parallel Gene Expression Evolution With Increasing Genetic Divergence—A Hallmark of Polygenic Adaptation*. *Molecular Ecology*, 34(12). <https://doi.org/10.1111/mec.17803>
3. Lai, W., **Hsu, S.**, Futschik, A., & Schlötterer, C. (2025). *Pleiotropy increases parallel selection signatures during adaptation from standing genetic variation*. *eLife*, 13. <https://doi.org/10.7554/eLife.102321.3>
4. **Hsu, S.**, Lai, W., Novak, J., Lehner, F., Jakšić, A.M., Versace, E., & Schlötterer, C. (2024). *Reproductive isolation arises during laboratory adaptation to a novel hot environment*. *Genome Biology*, 25(1). <https://doi.org/10.1186/s13059-024-03285-9>
5. Buchner, S., **Hsu, S.**, Nolte, V., Otte, K.A., & Schlötterer, C. (2023). *Effects of larval crowding on the transcriptome of Drosophila simulans*. *Evolutionary Applications*, 16(10), 1671-1679. <https://doi.org/10.1111/eva.13592>

6. **Hsu, S.**, Belmouaden, C., Nolte, V., & Schlötterer, C. (2020). *Parallel gene expression evolution in natural and laboratory evolved populations*. *Molecular Ecology*, 30(4), 884-894. <https://doi.org/10.1111/mec.15649>
7. Jakšić, A.M., Karner, J., Nolte, V., **Hsu, S.**, Barghi, N., Mallard, F., Otte, K.A., Svečnjak, L., Senti, K., & Schlötterer, C. (2020). *Neuronal Function and Dopamine Signaling Evolve at High Temperature in Drosophila*. *Molecular Biology and Evolution*, 37(9), 2630-2640. <https://doi.org/10.1093/molbev/msaa116>
8. **Hsu, S.**, Jakšić, A.M., Nolte, V., Lirakis, M., Kofler, R., Barghi, N., Versace, E., & Schlötterer, C. (2020). *Rapid sex-specific adaptation to high temperature in Drosophila*. *eLife*, 9. <https://doi.org/10.7554/eLife.53237>
9. **Hsu, S.**, Jakšić, A.M., Nolte, V., Barghi, N., Mallard, F., Otte, K.A., & Schlötterer, C. (2019). *A 24 h Age Difference Causes Twice as Much Gene Expression Divergence as 100 Generations of Adaptation to a Novel Environment*. *Genes*, 10(2), 89. <https://doi.org/10.3390/genes10020089>
10. Lin, P., Tsai, Y., **Hsu, S.**, Ou, J., Liao, C., & Tung, C. (2018). *Identification of natural variants affecting chlorophyll content dynamics during rice seedling development*. *Plant Breeding*, 137(3), 355-363. <https://doi.org/10.1111/pbr.12584>
11. **Hsu, S.**, & Tung, C. (2017). *RNA-Seq Analysis of Diverse Rice Genotypes to Identify the Genes Controlling Coleoptile Growth during Submerged Germination*. *Frontiers in Plant Science*, 8. <https://doi.org/10.3389/fpls.2017.00762>
12. **Hsu, S.**, & Tung, C. (2015). *Genetic Mapping of Anaerobic Germination-Associated QTLs Controlling Coleoptile Elongation in Rice*. *Rice*, 8(1). <https://doi.org/10.1186/s12284-015-0072-3>

## Preprints

1. Elad Oren, Jingjing Zhai, Travis Rooney, Ruthie Angelovici, Charles Hale, Lara J. Brindisi, **Sheng-Kai Hsu**, Christine Gault, Jian Hua, Thuy La, Nicholas Lepak, Qin Fu, Edward Buckler, & Cinta Romay (2025). *Grass Rhizome Proteomics Reveals Convergent Freezing-Tolerance Strategies*. bioRxiv. <https://doi.org/10.1101/2025.05.15.654294>
2. Charles O. Hale, **Sheng-Kai Hsu**, Jingjing Zhai, Aimee J. Schulz, Taylor Aubuchon-Elder, Germano Costa-Neto, Allen Gelfond, Mohamed El-Walid, Matthew Hufford, Elizabeth A. Kellogg, Thuy La, Alexandre P. Marand, Arun S. Seetharam, Armin Scheben, Michelle Stitzer, Travis Wrightsman, M. Cinta Romay, & Edward S. Buckler (2025). *Extensive modulation of a conserved cis-regulatory code across 589 grass species*. bioRxiv. <https://doi.org/10.1101/2025.04.23.650228>

3. Michelle C. Stitzer, Arun S. Seetharam, Armin Scheben, **Sheng-Kai Hsu**, Aimee J. Schulz, Taylor M. AuBuchon-Elder, Mohamed El-Walid, Taylor H. Ferebee, Charles O. Hale, Thuy La, Zong-Yan Liu, Sarah J. McMorrow, Patrick Minx, Alyssa R. Phillips, Michael L. Syring, Travis Wrightsman, Jingjing Zhai, Rémy Pasquet, Christine A. McAllister, Simon T. Malcomber, Paweena Traiperm, Daniel J. Layton, Jinshun Zhong, Denise E. Costich, R. Kelly Dawe, Kevin Fengler, Charlotte Harris, Zach Irelan, Victor Llaca, Praveena Parakkal, Gina Zastrow-Hayes, Margaret R. Woodhouse, Ethalinda K. Cannon, John L. Portwood, II, Carson M. Andorf, Patrice S. Albert, James A. Birchler, Adam Siepel, Jeffrey Ross-Ibarra, M. Cinta Romy, Elizabeth A. Kellogg, Edward S. Buckler, & Matthew B. Hufford (2025). *Extensive genome evolution distinguishes maize within a stable tribe of grasses*. bioRxiv. <https://doi.org/10.1101/2025.01.22.633974>
4. Aimee J Schulz, Jingjing Zhai, Taylor AuBuchon-Elder, Mohamed El-Walid, Taylor Ferebee, Elizabeth Gilmore, Matthew Hufford, Lynn C Johnson, Elizabeth Kellogg, Thuy La, Evan Long, Zachary R Miller, Cinta Romy, Arun Seetharam, Michelle Stitzer, Travis Wrightsman, Edward Buckler, Brandon Monier, & **Sheng-Kai Hsu** (2023). *Fishing for a reelGene: evaluating gene models with evolution and machine learning*. bioRxiv. <https://doi.org/10.1101/2023.09.19.558246>

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