

Sheng-Kai Hsu

Email: sh2246@cornell.edu

Affiliation: Postdoc, Institute for Genomic Diversity, Cornell University

ORCID: 0000-0002-6942-7163

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

Publications

Peer-reviewed Publications

1. **Hsu, S.**, Emmett, B., Haafke, A., Costa-Neto, G., Schulz, A., Lepak, N., La, T., AuBuchon-Elder, T., Hale, C., Raglin, S., & *et al.* (2025). *Contrasting rhizosphere nitrogen dynamics in Andropogoneae grasses. The Plant Journal*, 123(1). <https://doi.org/10.1111/tpj.70319>
2. Thorhólludottir, D., **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-Y., Hsu, S-K., 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-K., Lai, W-Y., Novak, J., Lehner, F., Jakšić, A., 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., & 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., Karner, J., Nolte, V., Hsu, S-K., Barghi, N., Mallard, F., Otte, K., Svečnjak, L., Senti, K-A., & 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-K., Jakšić, A., 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-K., Jakšić, A., Nolte, V., Barghi, N., Mallard, F., Otte, K., & 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-K., & Tung, C-W. (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-K., & Tung, C-W. (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. Oren, E., Zhai, J., Rooney, T., Angelovici, R., Hale, C., Brindisi, L., Hsu, S-K., Gault, C., Hua, J., La, T., & *et al.* (2025). *Grass Rhizome Proteomics Reveals Convergent Freezing-Tolerance Strategies*. *bioRxiv*. <https://doi.org/10.1101/2025.05.15.654294>
2. Hale, C., Hsu, S-K., Zhai, J., Schulz, A., Aubuchon-Elder, T., Costa-Neto, G., Gelfond, A., El-Walid, M., Hufford, M., Kellogg, E., & *et al.* (2025). *Extensive modulation of a conserved cis-regulatory code across 589 grass species*. *bioRxiv*. <https://doi.org/10.1101/2025.04.23.650228>
3. Stitzer, M., Seetharam, A., Scheben, A., Hsu, S-K., Schulz, A., AuBuchon-Elder, T., El-Walid, M., Ferebee, T., Hale, C., La, T., & *et al.* (2025). *Extensive genome evolution distinguishes maize within a stable tribe of grasses*. *bioRxiv*. <https://doi.org/10.1101/2025.01.22.633974>

4. Schulz, A., Zhai, J., AuBuchon-Elder, T., El-Walid, M., Ferebee, T., Gilmore, E., Hufford, M., Johnson, L., Kellogg, E., La, T., & *et al.* (2023). *Fishing for a reelGene: evaluating gene models with evolution and machine learning*. bioRxiv. <https://doi.org/10.1101/2023.09.19.558246>

Last updated: 2025-07-08