# 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 *Advisor: Christian Schlötterer* |
| 2014–2015 | M.Sc., Department of Agronomy, National Taiwan University *Advisor: Chih-Wei Tung* |
| 2010–2014 | B.Sc., Department of Agronomy, National Taiwan University |

## 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., Romay, 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. Thorhölludottir, 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-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.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-K.**, Barghi, N., Mallard, F., Otte, K.A., 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.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-K.**, 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-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.J., **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.O., **Hsu, S-K.**, Zhai, J., Schulz, A.J., Aubuchon-Elder, T., Costa-Neto, G., Gelfond, A., El-Walid, M., Hufford, M., Kellogg, E.A., & *et al.* (2025). *Extensive modulation of a conservedcis-regulatory code across 589 grass species*. bioRxiv. https://doi.org/10.1101/2025.04.23.650228
3. Stitzer, M.C., Seetharam, A.S., Scheben, A., **Hsu, S-K.**, Schulz, A.J., AuBuchon-Elder, T.M., El-Walid, M., Ferebee, T.H., Hale, C.O., 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.J., Zhai, J., AuBuchon-Elder, T., El-Walid, M., Ferebee, T., Gilmore, E., Hufford, M., Johnson, L.C., 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

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