# 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. crossref: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. crossref: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. crossref: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. crossref:**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. crossref: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. crossref: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. crossref: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. crossref:**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. crossref:**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. crossref: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. crossref:**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. crossref:**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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