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Positions & Education

Year	Position / Degree
2022–present	Postdoc, Institute for Genomic Diversity, Cornell University <i>Advisor: Edward Buckler</i>
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-K.**, 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. Thorhølludottir, D.A.V., **Hsu, S-K.**, 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-K.**, 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-K.**, 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-C., Tsai, Y-C., **Hsu, S-K.**, Ou, J-H., Liao, C-T., & Tung, C-W. (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., Lepak, N., Fu, Q., Buckler, E., & Romy, C. (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., La, T., Marand, A.P., Seetharam, A.S., Scheben, A., Stitzer, M., Wrightsman, T., Romy, M.C., & Buckler, E.S. (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.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., Long, E., Miller, Z.R., Romy, C., Seetharam, A., Stitzer, M., Wrightsman, T., Buckler, E., Monier, B., & **Hsu, S-K.** (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