

CHE-WEI HSU

Resnick Sustainability Institute Pioneer Postdoctoral Fellow ◇ *California Institute of Technology*

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PROFILE

Developmental biologist and single-cell data scientist studying how individual cells coordinate their developmental programs to build a resilient organism, and how that coordination adjusts when the environment changes. I combine single-cell and spatial genomics, 3D imaging, and genetic perturbation with biology-motivated modeling to follow regulation from the nucleus and cell to the form of the whole organ, from the first comprehensively annotated single-cell atlas of a plant organ to GeneSys, a generative model of developmental systems. Twelve peer-reviewed publications with more than 900 citations, six as first or co-first author, including *Science*, *Cell*, *Nature*, and a *Developmental Cell* cover article; openly released tools (GeneSys, COPILOT, scKB, ARVEX, ORVEX) that are taught in community workshops.

RESEARCH EXPERIENCE

2025 – present **Resnick Sustainability Institute Pioneer Postdoctoral Fellow**

Laboratory of Trevor Nolan, California Institute of Technology

- Lead 3D cellular morphogenesis profiling and spatial transcriptomic analysis of Arabidopsis root development.
- Develop the computational pipeline for PHYTOmap 3D single-cell spatial transcriptomics in intact roots (multi-round registration, 3D spot detection, cell-wall-based segmentation, anatomical annotation) and use it to link cellular morphology to gene expression in mutants.
- Contribute single-cell and gene-regulatory-network analyses to osmotic-stress and salinity time courses and to the lab's in vivo plant Perturb-seq and Virtual Root initiatives.

2024 – 2025 **Postdoctoral Researcher**

Laboratory of Sheng-Yang He, Duke University

- Applied AI-driven single-cell and structural modeling to uncover stress-responsive regulators and engineer heat-resilient plant immune receptors; single-cell profiling of immunity-challenged leaves under elevated humidity.

2023 – 2024 **Postdoctoral Researcher**

Laboratory of Philip Benfey (deceased 2023), Duke University

- Time-series single-cell analysis of brassinosteroid gene regulatory networks and of hormone-cell cycle interactions in the Arabidopsis root (*Science* 2023; *Cell* 2025).
- Built and annotated a single-cell atlas of the rice root and used it to reveal how root tissues adapt to soil compaction (*Nature* 2025); released the ORVEX browser.

2019 – 2022 **Graduate Research Associate**

Laboratory of Uwe Ohler, Berlin Institute for Medical Systems Biology (MDC-BIMSB), with the laboratory of Philip Benfey, Duke University

- Led construction of a comprehensively annotated single-cell atlas of the Arabidopsis root (*Developmental Cell* 2022, cover) and released the ARVEX browser.

- Developed COPILOT (non-arbitrary single-cell quality control) and scKB (fast raw-data processing); single-cell analysis of CRISPR-activation perturbations in human neuroblastoma cells (Cell Genomics 2025).

2018 – 2019 Graduate Research Assistant

Laboratory of Cheng-Ruei Lee, National Taiwan University

- Traced the geo-evolutionary history of *Arabidopsis thaliana* from large-scale ecotype genomic data (New Phytologist 2019, first author).

2016 – 2018 Graduate Research Assistant

Laboratory of Chih-Wei Tung, National Taiwan University

- Population genetics of rice: organelle genomics to guide conservation of the rice gene pool.

2014 – 2016 Undergraduate Research Assistant

Laboratory of Chii-Shen Yang, National Taiwan University

- Archaea-derived rhodopsin engineering for the design of bio-solar cells.

EDUCATION

2019 – 2022 Ph.D., Developmental Biology and Bioinformatics

Humboldt-Universität zu Berlin (research at MDC-BIMSB)

2016 – 2018 M.S., Agronomy (Crop Science Division)

National Taiwan University

2012 – 2016 B.S., Biochemistry

National Taiwan University

FELLOWSHIPS, AWARDS, AND HONORS

2026 – present Resnick Sustainability Institute Pioneer Postdoctoral Fellowship, Caltech

2022 Cover article, Developmental Cell (cover art contributed by C.-W. Hsu)

2025 Sigma Xi, The Scientific Research Honor Society

2024 Travel Award, International Conference on Arabidopsis Research, San Diego, CA

PUBLICATIONS

** co-first author. Twelve peer-reviewed articles and one preprint; more than 900 citations (Google Scholar).*

- 13** Jhu M.-Y., M. Minne, Z. Luo, H. Dörpholz, J. Yao, S. Mukhtar, F. Mathieu, M. Peirats-Llobet, T. Lee, P. Formosa-Jordan, S. Song, M. Libault, **C.-W. Hsu**, T.M. Nolan, T. Nobori, C.R. Anderton, R.J. Schmitz, D. Jackson, M. Moreno-Risueno, H. Nelissen, R. Simon, R. Sozzani, K. Sugimoto (2026). Unlocking the full potential of spatial omics in plants: practical challenges, solutions, and a path forward. *The Plant Cell*, koag282. doi:10.1093/plcell/koag282.
- 12** Haghani M., T.N. Chau, R. Alajoleen, C.-Y. Chen, S.A. Dip, V. Gurung, **C.-W. Hsu**, C. Kittivorawong, S. Kundu, X. Li, J. Luo, M. Salehin, M. Simenc, J. Yun, B.O.R. Bargmann, S. Li (2026). Cross-species plant single-cell analysis: community challenges and shared solutions. *Journal of Experimental Botany*. doi:10.1093/jxb/erag218.
- 11** **Hsu C.-W.**, C.-Y. Chen, T.M. Nolan, P.N. Benfey, U. Ohler (2025). GeneSys: generative modeling of developmental systems. *bioRxiv*. doi:10.1101/2025.08.20.671385. [first author; preprint]

- 10 Vučićević D., C.-W. Hsu, L.S.L. Zepeda, M. Burkert, A. Hirsekorn, I. Bilić, N. Kastelić, M. Landthaler, S.A. Lacadie, U. Ohler (2025). Sensitive dissection of a genomic regulatory landscape using bulk and targeted single-cell activation. *Cell Genomics*. doi:10.1016/j.xgen.2025.100984.
- 9 Zhu M.*, C.-W. Hsu*, L.L. Peralta Ogorek, I.W. Taylor, S. La Cavera, D.M. Oliveira, L. Verma, P. Mehra, M. Mijar, A. Sadanandom, F. Perez-Cota, W. Boerjan, T.M. Nolan, M.J. Bennett, P.N. Benfey, B.K. Pandey (2025). Single-cell transcriptomics reveal how root tissues adapt to soil stress. *Nature* 642, 721–729. doi:10.1038/s41586-025-08941-z. [co-first author]
- 8 Vukašinović N.*, C.-W. Hsu*, M. Marconi, S. Li, C. Zachary, R. Shahan, P. Szekley, Z. Aardening, I. Vanhoutte, Q. Ma, L. Pinto, P. Krupař, N. German, J. Zhang, C. Simon, J. Perez-Sancho, P.C. Quijada, Q. Zhou, L.R. Lee, J. Cai, E.M. Bayer, M. Fendrych, E. Truernit, Y. Zhou, S. Savaldi-Goldstein, K. Wabnik, T.M. Nolan, E. Russinova (2025). Polarity-guided uneven mitotic divisions control brassinosteroid activity in proliferating plant root cells. *Cell* 188, 2063–2080.e24. doi:10.1016/j.cell.2025.02.011. [co-first author]
- 7 Taylor I.W., O.R. Patharkar, M. Mijar, C.-W. Hsu, J. Baer, C.E. Niederhuth, U. Ohler, P.N. Benfey, J.C. Walker (2024). Arabidopsis uses a molecular grounding mechanism and a biophysical circuit breaker to limit floral abscission signaling. *Proceedings of the National Academy of Sciences* 121, e2405806121. doi:10.1073/pnas.2405806121.
- 6 Blanco-Touriñán N., S. Rana, T.M. Nolan, K. Li, N. Vukašinović, C.-W. Hsu, E. Russinova, C.S. Hardtke (2024). The brassinosteroid receptor gene BRI1 safeguards cell-autonomous brassinosteroid signaling across tissues. *Science Advances*. doi:10.1126/sciadv.adq3352.
- 5 Nolan T.M.*, N. Vukašinović*, C.-W. Hsu*, J. Zhang, I. Vanhoutte, R. Shahan, I. Taylor, L. Greenstreet, M. Heitz, A. Afanassiev, P. Wang, P. Szekely, A. Brosnan, Y. Yin, G. Schiebinger, U. Ohler, E. Russinova, P.N. Benfey (2023). Brassinosteroid gene regulatory networks at cellular resolution in the Arabidopsis root. *Science* 379, eadf4721. doi:10.1126/science.adf4721. [co-first author]
- 4 Hsu C.-W., R. Shahan, T.M. Nolan, P.N. Benfey, U. Ohler (2022). Protocol for fast scRNA-seq raw data processing using scKB and non-arbitrary quality control with COPILOT. *STAR Protocols* 3, 101729. doi:10.1016/j.xpro.2022.101729. [first author]
- 3 Shahan R.*, C.-W. Hsu*, T.M. Nolan, B. Cole, I. Taylor, L. Greenstreet, S. Zhang, A. Afanassiev, A.H.C. Vlot, G. Schiebinger, P.N. Benfey, U. Ohler (2022). A single-cell Arabidopsis root atlas reveals developmental trajectories in wild-type and cell identity mutants. *Developmental Cell* 57, 543–560.e9. doi:10.1016/j.devcel.2022.01.008. [co-first author; cover article, over 400 citations]
- 2 Carley L.N., J.P. Mojica, B. Wang, C.-Y. Chen, Y.-P. Lin, K. Prasad, E. Chan, C.-W. Hsu, R. Keith, C.L. Nuñez, C.F. Olson-Manning, C.A. Rushworth, M.R. Wagner, J. Wang, P.-M. Yeh, M. Reichelt, K. Ghattas, J. Gershenzon, C.-R. Lee, T. Mitchell-Olds (2021). Ecological factors influence balancing selection on leaf chemical profiles of a wildflower. *Nature Ecology & Evolution* 5, 1135–1144. doi:10.1038/s41559-021-01486-0.
- 1 Hsu C.-W., C. Lo, C.-R. Lee (2019). On the post-glacial spread of human commensal Arabidopsis thaliana: journey to the east. *New Phytologist* 222, 1447–1457. doi:10.1111/nph.15682. [first author]

SOFTWARE AND DATA RESOURCES

- **GeneSys**: deep generative model that simulates single-cell developmental and stress dynamics with encoded biological knowledge and prioritizes regulators (Hsu et al., 2025).
- **COPILOT**: biology-informed, non-arbitrary quality control for single-cell RNA-seq; taught annually at the Virginia Tech plant single-cell workshop (Hsu et al., 2022).
- **scKB**: fast scRNA-seq raw-data processing workflow (Hsu et al., 2022).

- **ARVEX**: Arabidopsis Root Virtual Expression eXplorer, interactive browser for the root atlas (2022).
- **ORVEX**: Oryza Root Virtual Expression eXplorer, interactive browser for the rice root atlas (2024).
- **PHYTOMap 3D pipeline**: registration, spot detection, 3D segmentation, and annotation for whole-mount spatial transcriptomics of intact roots (in preparation).

INVITED TALKS

- 5** SoCal Single-Cell Retreat, UC Riverside, CA. *Mapping single-cell transcriptomic and morphological dynamics in root development: towards 3D spatial transcriptomics.*
Apr 2026
- 4** Plant Spatial Omics Workshop, Kanagawa, Japan. *How brassinosteroids shape root development: towards single-cell spatial insights in 3D.*
Jan 2026
- 3** Masterclass 9, Applying Spatial Transcriptomics in Plants, Cambridge, UK. *Reconstructing Arabidopsis root spatial expression patterns with novoSpaRc.*
Feb 2024
- 2** Plant Cell Atlas workshop (online). *Non-arbitrary alternatives of basic quality control scheme for sc/snRNA-seq analysis: COPILOT.*
Nov 2023
- 1** Seminar, National Taiwan University, Taipei. *When root development meets single-cell RNA-seq.*
Apr 2023

CONTRIBUTED TALKS AND SEMINARS

- 9** International Conference on Arabidopsis Research, Singapore. *Mapping single-cell transcriptomic and 3D morphogenesis in Arabidopsis root.*
Jun 2026
- 8** OMG plant single-cell data analysis workshop, Virginia Tech, VA (invited). *Fast scRNA-seq raw data processing with scKB and non-arbitrary quality control with COPILOT.*
Jun 2026
- 7** Seminar, Michigan State University, MI. *Cellular-resolution root development under hormonal perturbations and environmental stress.*
Feb 2026
- 6** Plant and Animal Genome 33, San Diego, CA. *How hormone shapes root development: a single-cell view of brassinosteroids.*
Jan 2026
- 5** Plant Genomes, Systems Biology, and Engineering Symposium, Cold Spring Harbor Laboratory, NY. *GeneSys: a generative single-cell gene expression model reveals regulators and transitions in developmental systems.*
Dec 2025
- 4** Plant single-cell data analysis workshop, Virginia Tech, VA. *Non-arbitrary quality control for sc/snRNA-seq: COPILOT.*
Jun 2025
- 3** International Conference on Arabidopsis Research, San Diego, CA. *GeneSys: generative modeling for developmental systems.*
Jul 2024
- 2** Seminar, Duke University, NC. *Tributes to Philip Benfey.*
Oct 2023
- 1** IRTG seminar, Berlin, Germany. *Integrating single-cell data to construct and apply a whole-organ gene expression atlas.*
Feb 2023

POSTER PRESENTATIONS

- 4** Gordon Research Conference: Plant Cell Atlas, Portland, ME.
Aug 2025

- 3 International Conference on Arabidopsis Research, San Diego, CA.
Jul 2024
- 2 American Society of Plant Biologists annual meeting, Honolulu, HI.
Jun 2024
- 1 IRTG seminar, Berlin, Germany.
Feb 2023

TEACHING

- 2025, 2026 **Guest Lecturer**, Plant Single-Cell Data Analysis Workshop, Virginia Tech
- Designed and taught a hands-on module on scRNA-seq raw-data processing and non-arbitrary quality control, guiding trainees through the logic of each algorithmic step rather than pipeline execution alone.

MENTORING

Postdoctoral scholar: Chia-Yu Chen (2025 – present)

Graduate students: Rogelio Avila Silva (2025 – present), Chi Kuan (2024 – 2025), Stephanie Peak (2023 – 2025), Victoriia Huryn (2023 – 2024)

Undergraduate students: Michael Battiest (2026), Yunus-Emre Kurnaz (2021)

PROFESSIONAL SERVICE

- 2025 – present Plant Cell Atlas, Computation, Modeling, and AI Committee (member)
- 2024 – 2025 Topic Editor, Frontiers in Plant Physiology
- Aug 2026 Participant, International Spatial Omics Pre-Hackathon Workshop, Versailles, France (organizers R. Sozzani, B. Guillotin, M. Minne)
- 2021 – present Manuscript reviewer (more than 10 manuscripts): Nature, Nature Communications, Bioinformatics, The Plant Journal, Communications Biology, Physiologia Plantarum, Plant Methods, Genome Biology

TECHNICAL SKILLS

- **Computation:** Python, R, Bash; deep learning and generative modeling (variational autoencoder-based frameworks); high-performance and cloud computing; R Shiny application development; Git/GitHub.
- **Single-cell and spatial genomics:** scRNA-seq and snRNA-seq processing, quality control, integration, annotation, trajectory and gene-regulatory-network inference; time-series and perturbation (Perturb-seq) analysis; image-based spatial transcriptomics (PHYTOmap) and 3D image registration and U-Net-based cell segmentation.
- **Biology:** Arabidopsis and rice root development, hormone signaling, abiotic stress, and plant immunity; population and organelle genomics.

REFERENCES

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