PingHsun Hsieh

Department of Genetics, Cell Biology, and Development

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Current Academic Appointment

2023-present   Assistant Professor
                 Department of Genetics, Cell Biology, and Development
                 University of Minnesota, Twin Cities, MN

Education

2016   Ph.D.   Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ

2008   M.S.   Computational Molecular Biology, University of Southern California, CA

2005   M.S.   Electrical Engineering, National Taiwan University, Taiwan

2002   B.S.   Computer Science and Information Engineering, National Central University, Taiwan

Previous Academic Appointments

2016-2022   Senior Fellow, Department of Genome Sciences, University of Washington, WA.

2010-2016   Research Associate, Department of Ecology and Evolutionary Biology, University of Arizona, AZ.

2008-2010   Statistical Genetic Programmer, Oregon Clinical and Translational Research Institute, OHSU, OR.

2007-2008   Research Assistant, Center of Excellence in Genomic Science, University of Southern California, CA.

2003-2005   Research Assistant, Department of Electrical Engineering, National Taiwan University, Taiwan.

Grants, Awards, and Scholarships

2020-2025   NIH Pathway to Independence Award (K99/R00). Role: PI.

2013   Charles J. Epstein Trainee Awards for Excellence in Human Genetics Research, semifinalist, American Society of Human Genetics

2013   Government Study Abroad Scholarship, Ministry of Education, Taiwan

2013   Galileo Circle Fellowship, University of Arizona, U.S.A.

2006-2008   Joint Initiative Graduate Merit Award, University of Southern California, U.S.A.

2001   National Science Council Research Creativity Award, Taiwan

Peer-Reviewed Publications

[21] Vollger MR, Dishuck PC, Harvey WT, DeWitt WS, Guitart X, Goldberg ME, Rozanski AN, Lucas J, Asri M, The Human Pangenome Reference Consortium, Munson KM, Lewis AP, Hoekzema K, Logsdon GA, Porubsky D, Paten B, Harris K, **Hsieh P**, Eichler EE. (2023).

Increased mutation rate and interlocus gene conversion within human segmental duplications. *Nature* (In revision).

[20] Porubsky D, Höps W, Ashraf H, **Hsieh PH**, Rodriguez-Martin B, Yilmaz F, Ebler J, Hallast P, Maggiolini FA, Harvey WT and Henning B, Audano PA, Gordon DS, Ebert P, Hasenfeld P, Benito E, Zhu Q, Human Genome Structural Variant Consortium (HGSVC), Lee C, Antonacci F, Steinrucken M, Beck CR, Sanders AD, Marschall T, Eichler EE, Korbel JO. (2022) Haplotype-resolved inversion landscape reveals hotspots of mutational recurrence associated with genomic disorders. *Cell* DOI: 10.1016/j.cell.2022.04.017 [Link]

[19] Johansson PA, Brattås PL, Douse CH, **Hsieh PH**, Pontis J, Grassi D, Garza R, Jönsson ME, Atacho DAM, Pircs K, Eren F, Sharma Y, Johansson J, Trono D, Eichler EE, Jakobsson J. (2021) A cis-acting structural variation at the ZNF558 locus controls a gene regulatory network in human brain development. *Cell Stem Cell* DOI: 10.1016/j.stem.2021.09.008 [Link]

[18] **Hsieh PH**, Dang V, Vollger MR, Mao Y, Huang T, Dishuck PC, Baker C, Cantsilieris S, Lewis AP, Munson KM, Sorensen M, Welch AE, Underwood JG, Eichler EE. (2021) Evidence for opposing selective forces operating on human-specific duplicated *TCAF* genes in Neanderthals and humans. *Nature Communications* DOI: 10.1038/s41467-021-25435-4 [Link]

[17] Wilfert AB, Turner TN, Murali SC, **Hsieh PH**, Sulovari A, Wang T, Coe BP, Guo H, Hoekzema K, Bakken TE, Winterkorn LH, Evani US, Byrska-Bishop M, Earl RK, Bernier RA, The SPARK Consortium, Zody MC, Eichler EE. (2021) Recent ultra-rare inherited mutations identify novel autism candidate risk genes. *Nature Genetics* DOI: 10.1038/s41588-021-00899-8 [Link]

[16] Mao Y, Catacchio CR, Hillier LW, Porubsky D, Li R, Sulovari A, Fernandes JD, Montinaro F, Gordon DS, Storer JM, Haukness M, Fiddes IT, Murali SC, Dishuck PC, **Hsieh PH**, Harvey WT, Audano PA, Mercuri L, Piccolo I, Antonacci F, Munson KM, Lewis AP, Baker C, Underwood JG, Hoekzema K, Huang T, Sorensen M, Walker JA, Hoffman J, Thibaud-Nissen F, Salama SR, Pang AWC, Lee J, Hastie AR, Paten B, Batzer MA, Diekhans M, Ventura M, Eichler EE. (2021) A high-quality bonobo genome refines the analysis of hominid evolution. *Nature* DOI: 10.1038/s41586-021-03519-x [Link]

[15] Logsdon GA, Vollger MR, **Hsieh PH**, Mao Y, Liskovykh MA, Koren S, Nurk S, Mercuri L, Dishuck PC, Rhie A, de Lima LG, Dvorkina T, Porubsky D, Mikheenko A, Bzikadze AV, Kremitzki M, Graves-Lindsay TA, Jain C, Hoekzema K, Murali SC, Munson KM, Baker C, Sorensen M, Lewis AM, Surti U, Gerton JL, Larionov V, Ventura M, Miga KH, Phillippy AM, Eichler EE. (2021) The structure, function, and evolution of a complete human chromosome 8. *Nature* DOI: 10.1038/s41586-021-03420-7 [Link]

[14] Ebert P, Audano PA, Zhu Q, Rodriguez-Martin B, Porubsky D, Bonder MJ, Sulovari A, Ebler J, Zhou W, Mari RS, Yilmaz F, Zhao X, **Hsieh PH**, Lee J, … , Flicek P, Stegle O, Gerstein MB, Tubio JMC, Mu Z, Li YI, Shi X, Hastie AR, Ye K, Chong Z, Sanders AD, Zody MC, Talkowski ME, Mills

RE, Devine SE, Lee C, Korbel JO, Marschall T, Eichler EE. (2021) Haplotype-resolved diverse human genomes and integrated analysis of structural variation. *Science* 366, eabf7117. DOI: 10.1126/science.abf7117 [Link]

[13] Porubsky D, Sanders AD, Höps W, **Hsieh PH**, Sulovari A, Sorensen M, Murali SC, Gordon D, Cantsilieris S, Pollen AA, Antonacci F, Marschall T, Korbel JO, Eichler EE. (2020) Recurrent inversion toggling and great ape genome evolution. *Nature Genetics* 2020;52(8):849-858. [Link]

[12] Cantsilieris S, Sunkin SM, Johnson ME, Anaclerio F, Huddleston J, Baker C, Dougherty ML, Underwood J, Sulovari A, **Hsieh PH**, Yafei M, Catacchio CR, Malig M, Welch A, … , Eichler EE. (2020) An evolutionary driver of interspersed segmental duplications in primates. *Genome Biology* **21,** 202. [Link]

[11] **Hsieh PH**, Vollger MR, Dang V, Porubsky D, Baker C, Cantsilieris S, Hoekzema K, Lewis AP, Munson KM, Sorensen M, Kronenberg ZN, Murali S, Nelson BJ, Chiatante G, Maggiolini FAM, Blanche H, Underwood JG, Antonacci F, Deleuze JF, Eichler EE. (2019) Adaptive archaic introgression of copy number variants and the discovery of previously unknown human genes. *Science* DOI: 10.1126/science.aax2083. [Link]

[10] Hallmark B, Karafet TM, **Hsieh PH**, Osipova LP, Watkins JC, Hammer MF. (2019) Genomic Evidence of Local Adaptation to Climate and Diet in Indigenous Siberians. *Molecular Biology and Evolution* 36 (2), 315-327 [Link]

[9] Kronenberg ZN, Fiddes IT, Gordon D, Murali S, Cantsilieris S, Meyerson OS, Underwood JG, Nelson BJ, Chaisson MJP, Dougherty ML, Munson KM, Hastie AR, Diekhans M, Hormozdiari F, Lorusso N, Hoekzema K, Qiu R, Clark K, Raja A, Welch AE, Sorensen M, Baker C, Fulton RS, Armstrong J, Graves-Lindsay TA, Denli AM, Hoppe ER, **Hsieh PH**, Hill CM, Pang AWC, Lee J, Lam ET, Dutcher SK, Gage FH, Warren WC, Shendure J, Haussler D, Schneider VA, Cao H, Ventura M, Wilson RK, Paten B, Pollen A, and Eichler EE. (2018) High-resolution comparative analysis of great ape genomes. *Science* 360, (6393), eaar6343 [Link]

[8] Prufer K., de Filippo C, Grote S., Mafessoni F, Korlevic P, Hajdinjak M, Vernot B, Skov L, **Hsieh PH**, Peyregne S, et al. (2017) A high-coverage Neandertal genome from Vindija Cave in Croatia. *Science* 358, 655-658. [Link]

[7] **Hsieh PH**, Hallmark B, Watkins J, Karafet TM, Osipova LP, Gutenkunst RN, Hammer MF. (2017) Exome sequencing provides evidence of polygenic adaptation to a fat-rich animal diet in indigenous Siberian populations. *Molecular Biology and Evolution* 34 (11), 2913-2926. [Link]

[6] Ragsdale AP, Coffman AJ, **Hsieh PH**, Struck TJ, Gutenkunst RN. (2016) Triallelic population genomics for inferring correlated fitness effects of same site nonsynonymous

mutations. *Genetics* 203 (1), 513-523. [Link]

[5] **Hsieh PH**, Woerner AE, Lachance J, Tishkoff S, Wall JD, Gutenkunst RN, Hammer MF. (2016) Model-based analyses of whole-genome data reveal a complex evolutionary history involving archaic introgression in Central African Pygmies. *Genome Research* 26: 291 [Link]

[4] **Hsieh PH**, Veeramah KR, Lachance J, Tishkoff S, Wall JD, Gutenkunst RN, Hammer MF. (2016) Whole genome sequence analyses of Western Central African Pygmy hunter-gatherers reveal a complex demographic history and identify candidate genes under positive natural selection. *Genome Research* 26: 279 [Link]

[3] Coffman AJ, **Hsieh PH**, Gravel S, Gutenkunst RN. (2016) Computationally efficient composite likelihood statistics for population genetic inference. *Molecular Biology and Evolution* 33:591 [Link]

[2] Edwards T, Tollis M, **Hsieh PH**, Liu Z, Kusumi K, Culver M, Murphy RW. (2016) Assessing models of speciation under different biological scenarios; an empirical study using multi-locus and RNA-seq analyses. *Ecology and Evolution* 6:379 [Link]

[1] **Hsieh PH**, Chen IY, Lin YT, Kuo SY. (2004) An XOR-based Reed-Solemon Algorithm for Advanced RAID Systems, *Proceedings of the 19th IEEE International Symposium on Defect and Fault Tolerance in VLSI Systems (DFT'04)*, Cannes, France. [Link]

Invited Talks

2022	Department of Genetics, Cell Biology, and Development, University of Minnesota, Twin Cities, MN
2022	Department of Medical Genetics, University of Wisconsin, Madison, WI
2022	Department of Biological Chemistry, University of California, Irvine School of Medicine, CA
2022	Department of Biochemistry & Molecular Biology, Penn State University College of Medicine, PA
2022	Institute of Genomic Medicine, Columbia University, NY
2022	Division of Genetics, Oregon National Primate Research Center, OR
2022	School of Biological Sciences, Georgia Institute of Technology, GA
2021	Pacific Northwest Research Institute, WA
2021	Canada Excellence Research Chair, McGill University, Quebec, Canada
2021	New York Genome Center, NY
2021	Children's Hospital of Philadelphia, University of Pennsylvania, PA
2021	Department of Biology, Syracuse University, NY
2021	Department of Biology, University of Texas, Arlington, TX
2020	PopGen Lunch series, Department of Genome Sciences, University of Washington, WA
2019	ComBi seminar, Department of Genome Sciences, University of Washington, WA
2016	Department of Applied Mathematics, University of Arizona, AZ

2015   Simons Center for Quantitative Biology, Cold Spring Harbor Laboratory, NY

2015   Department of Human Genetics, University of Chicago, IL

2015   Department of Genetics, University of Pennsylvania, PA

2015   Department of Genome Sciences, University of Washington, WA

Conference Presentations

[9] **Hsieh PH**, Vollger MR, Dang V, Porubsky D, Baker C, Cantsilieris S, Hoekzema K, et al. Adaptive archaic introgression of copy number variants introduces novel genes in humans. *American Society of Human Genetics*, Huston, U.S.A. 2019. (Poster)

[8] **Hsieh PH**, Kronenberg ZN, Cantsilieris S, Hoekzema K, Munson KM, Antonacci F, Ventura M, Eichler EE. Adaptive Evolution and Archaic Introgression of Copy Number Variants in Melanesians. *Society of Molecular Biology and Evolution*, Yokohama, Japan. 2018. (Poster)

[7] **Hsieh PH**, Hallmark B, Karafet TM, Hammer MF, Gutenkunst RN. Genetic Basis of Polygenic Adaptation in Indigenous Siberian Population Inferred using Exome Sequencing Data. *American Society of Human Genetics*, Baltimore, U.S.A. 2015. (Poster)

[6] **Hsieh PH**, Woerner AE, Wall JD, Lachance J, Tishkoff S, Gutenkunst RN, Hammer MF. Whole genome evidence of recurring archaic introgression in Western African Pygmies. *American Society of Human Genetics*, San Diego, U.S.A. 2014. (Oral)

[5] **Hsieh PH**, Wall JD, Lachance J, Tishkoff S, Gutenkunst RN, Hammer MF. Inference of Archaic Introgression in Central African Pygmies. *Society of Molecular Biology and Evolution*, Puerto Rico, U.S.A. 2014. (Oral)

[4] **Hsieh PH**, Veeramah KR, Lachance J, Tishkoff S, Wall JD, Gutenkunst RN, Hammer MF. Inference of Natural Selection and Demographic History for African Pygmy Hunter-Gatherers. *American Society of Human Genetics*, Boston, U.S.A. 2013. **Semifinalist for the Charles J. Epstein Trainee Award**. (Poster)

[3] **Hsieh PH**, Veeramah KR, Lachance J, Tishkoff S, Wall JD, Gutenkunst RN, Hammer MF. Demographic inference and whole genome scan for natural selection in pygmies from Central Africa. *American Society of Human Genetics*, San Francisco, U.S.A. 2012. (Poster)

[2] Bittner N, Dermyer L, **Hsieh PH**, Campbell P, Nachman MW. Molecular population genetics of Brca1 and Brca2, candidate genes for reproductive isolation in house mice. *Evolution*, Oklahoma, U.S.A. 2011. (Poster)

[1] Wilmot B, **Hsieh PH**, McWeeney SK. Considerations for algorithm selection and experimental design in detection of copy number variations in cancer. *ISMB/ECCB*, Sweden. 2009. (Poster)

Ad-hoc Journal Reviewer

Genome Research, *Bioinformatics*, *BMC Evolutionary Biology*, *Ecology and Evolution*, *Human Genetics*, *Frontier Ecology and Evolution*.

Teaching Experience

Fall, 2014	Graduate Teaching Associate, University of Arizona, Tucson AZ, USA Course: Key Concepts in Quantitative Biology.
Spring, 2011	Graduate Teaching Associate, University of Arizona, Tucson AZ, USA Course: Evolutionary Biology.
Fall, 2004	Graduate Teaching Associate, National Taiwan University, Taiwan. Introduction of Computer Programming

Professional Affiliations

Member, American Society of Human Genetics

Member, Society of Molecular Biology and Evolution