

PingHsun (Benson) Hsieh

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[Google Scholar Profile](#)

Current Academic Appointment

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

Education

2016 Ph.D. Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ
2008 M.S. Computational Molecular Biology, University of Southern California, Los Angeles, 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

2010-2016 Graduate Research Associate, Department of Ecology and Evolutionary Biology, University of Arizona, AZ.
2008-2010 Statistical Genetic Programmer/Research Associate, 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 (K99HG011041). 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

Preprints & In Review

[1] **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. Opposing selective forces operating on human-specific duplicated *TCAF* genes in Neanderthals and humans. (In revision) [\[Link\]](#)

- [2] 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. A human-specific structural variation at the *ZNF558* locus controls a gene regulatory network during forebrain development. *bioRxiv* 2020.08.18.255562 (In revision) [\[Link\]](#)
- [3] 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, Zody MC, Eichler EE, SPARK Consortium. Recent ultra-rare inherited mutations identify novel autism candidate risk genes. *bioRxiv* 2020.02.10.932327 (In revision) [\[Link\]](#)

Peer-Reviewed Publications

- [15] 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, Kumar S, Lin J, Rausch T, Chen Y, Ren J, Santamarina M, Höps W, Ashraf H, Chuang NT, Yang X, Munson KM, Lewis AP, Fairley S, Tallon LJ, Clarke WE, Basile AO, Byrska-Bishop M, Corvelo A, Chaisson MJP, Chen J, Li C, Brand H, Wenger AM, Ghareghani M, Harvey WT, Raeder B, Hasenfeld P, Regier A, Abel H, Hall I, 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, Korbelt JO, Marschall T, Eichler EE. Haplotype-resolved diverse human genomes and integrated analysis of structural variation. *Science* 366, eabf7117 (2021). DOI: 10.1126/science.abf7117 [\[Link\]](#)
- [14] Logsdon GA, Vollger MR, **Hsieh PH**, Mao Y, Liskovych 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. The structure, function, and evolution of a complete human chromosome 8. *Nature* (Accepted) [\[Link\]](#)
- [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, Korbelt JO, Eichler EE. Recurrent inversion toggling and great ape genome evolution. *Nat Genet.* 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, Sorensen M, Munson K, Jiang W, Ventura M, Lamb BT, Conlon RA, Eichler EE. An evolutionary driver of interspersed segmental duplications in primates. *Genome Biol* **21**, 202 (2020). [\[Link\]](#)
- [11] **Hsieh PH**, Vollger MR, Dang V, Porubsky D, Baker C, Cantsilieris S, Hoekzema K, et al. Adaptive archaic introgression of copy number variants and the discovery of previously unknown human genes. *Science* 366, eaax2083 (2019). DOI: 10.1126/science.aax2083. [\[Link\]](#)

- [10] Hallmark B, Karafet TM, **Hsieh PH**, Osipova LP, Watkins JC, Hammer MF. 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. 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. 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. 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. Model-based analyses of whole-genome data reveal a complex evolutionary history involving archaic introgression in Central African Pygmies. *Genome Research* 26: 291 (2016) [\[Link\]](#)
- [4] **Hsieh PH**, Veeramah KR, Lachance J, Tishkoff S, Wall JD, Gutenkunst RN, Hammer MF. 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 (2016) [\[Link\]](#)
- [3] Coffman AJ, **Hsieh PH**, Gravel S, Gutenkunst RN. Computationally efficient composite likelihood statistics for population genetic inference. *Mol Bio Evol* 33:591 (2016) [\[Link\]](#)
- [2] Edwards T, Tollis M, **Hsieh PH**, Liu Z, Kusumi K, Culver M, Murphy RW. Assessing models of speciation under different biological scenarios; an empirical study using multi-locus and RNA-seq analyses. *Ecology and Evolution* 6:379 (2016) [\[Link\]](#)
- [1] **Hsieh PH**, Chen IY, Lin YT, Kuo SY. An XOR-based Reed-Solomon Algorithm for Advanced RAID Systems, *Proceedings of the 19th IEEE International Symposium on Defect and Fault Tolerance in VLSI Systems (DFT'04)*, Cannes, France. 2004. [\[Link\]](#)

Invited Talks

- 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, Dermeyer 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, 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

References

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