

Charleston W.K. Chiang

charleston.chiang@med.usc.edu

Curriculum Vitae

Academic Appointment

- 2019-present Assistant Professor, University of Southern California
 Department of Quantitative and Computational Biology
 Dornsife College of Letters, Arts, and Sciences
- 2018-present Assistant Professor, University of Southern California
 Center for Genetic Epidemiology, Department of Preventive Medicine
 Keck School of Medicine

Education

parental leaves in 2013 and 2016.

- 2017# Postdoctoral Research Fellow, UCLA
 Center for Neurobehavioral Genetics, Semel Institute (Advisor: Nelson B. Freimer, M.D.)
- 2015# Ruth L. Kirschstein NRSA Postdoctoral Research Fellow, UCLA
 Department of Ecology and Evolutionary Biology (Advisor: John Novembre, Ph.D.)
- 2011 Ph.D., Genetics, Harvard University
 Division of Medical Sciences, Program in Biological and Biomedical Science
 Leder Human Biology and Translational Medicine Program Scholar
 Department of Genetics (Advisor: Joel N. Hirschhorn, M.D. Ph.D.)
- 2005 B.S., Microbiology, Immunology, and Molecular Genetics, UCLA
 Mathematics (minor), Statistics (minor)
 Summa Cum Laude, College Honors Program Scholar

Publications

12 (co-) first authorship (numerically bolded), **9** (co-) corresponding authorship (numerically bolded)

* equal contribution, † corresponding author, **bolded** name denotes group member

Through 2019, 16 out of 29 publications were in journals with impact factor (IF) > 8 at the year of publication.

46. Jeon S, de Smith AJ, Li S, **Chen M**, Muskens IS, Morimoto LM, Dewan AT, Mancuso N, Metayer C, Ma X, Wiemels JL[†], **Chiang CWK**[†]. "Genome-wide trans-ethnic meta-analysis identifies novel susceptibility loci for childhood acute lymphoblastic leukemia." *In preparation*
45. Kachuri L, **Jeon S**, DeWan AT, Metayer C, Ma X, Witte JS, **Chiang CWK**, Wiemels JL, de Smith AJ. "Genetic determinants of blood cell traits influence susceptibility to childhood acute lymphoblastic leukemia." *In preparation*
44. Qin X, **Chiang CWK**, Gaggiotti OE. "Deciphering signatures of natural selection via deep learning." *In preparation*
43. Qin X, **Chiang CWK**, Gaggiotti OE. "Kernel Local Fisher Discriminant Analysis of Principal Components (KLFDAPC) significantly improves the accuracy of predicting geographic origin of individuals." *In preparation*
42. Fernandez-Rhodes L, Graff M, et al. "Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traits – the Hispanic/Latino Anthropometry Consortium." *In preparation*

41. Ganel L, et al. "Mitochondrial genome copy number measured by DNA sequencing in human blood is strongly associated with metabolic traits via cell-type composition differences." *In review at Eur. J. Hum. Genet.* **medRxiv** (2021): <https://doi.org/10.1101/2020.10.23.20218586>
40. **Chiang CWK[†]**. "The opportunities and challenges of integrating population histories into genetic studies of diverse populations: a motivating example from Native Hawaiians." **arXiv** (2020): <https://arxiv.org/abs/2012.12532>
39. **Chen M[†], Chiang CWK[†]**. "Allele frequency differentiation at height-associated SNPs among continental human populations." *In review at Eur. J. Hum. Genet.* **bioRxiv** (2020): <https://www.biorxiv.org/content/10.1101/2020.09.28.317552v1>.
38. Chen L, Abel HJ, Das I, Larson DE, Ganel L, Kanchi KL, Regier AA, Young EP, Kang CJ, Scott AJ, Chiang C, Wang X, Lu S, Christ R, Service SK, **Chiang CWK**, Havulinna AS, Kuusisto J, Boehnke M, Laakso M, Palotie A, Ripatti S, Freimer NB, Locke AE, Stitzel NO, Hall IM. "Association of structural variation with cardiometabolic traits in Finns." **Am J Hum Genet** 2021 Apr 1;108(4):583-596. doi: 10.1016/j.ajhg.2021.03.008.
37. Graff M, et al. "Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry." **Am J Hum Genet** 2021 Apr 1;108(4):564-582. doi: 10.1016/j.ajhg.2021.02.011.
36. **Sun H*, Lin M***, Russell EM, Minster RL, **Chan TF, Dinh BL**, Naseri T, Reupena MS, Lum-Jones A, OLaGA Study Group, Cheng I, Wilkens LR, Le Marchand L, Haiman CA, **Chiang CWK[†]**. "The impact of global and local Polynesian genetic ancestry on complex traits in Native Hawaiians." **PLoS Genet.** 2021 Feb 11; doi: 10.1371/journal.pgen.1009273.
35. Iksan OA, Kisselev IA, Garshin AA, Skvortsova LA, Zhaniyazov ZA, Alpysbes MA, **Chiang CWK**, Musralina LZ, Zhunussova GS, Khussainova EM. "Analysis of the Kazakh tribe Baiuly based on the distribution of the Y-chromosome haplogroups." **Int J Biol Chem** 2021 Jan; 13(2):80-87. doi: 10.26577/ijbch.2020.v13.i2.10.
34. Pua CJ, et al. "Genetic Studies of Hypertrophic Cardiomyopathy in Singaporeans Identify Variants in TNNI3 and TNNT2 that Are Common in Chinese Patients." **Cir Genom Precis Med** 2020 Oct;13(5):424-434. doi: 10.1161/CIRCGEN.119.002823.
33. Chen MH, Raffield LM, Mousas A, et al. "Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 individuals from 5 Global Populations." **Cell** 2020 Sep 3;182(5):1198-1213.e14. doi:10.1016/j.cell.2020.06.045.
32. **Lin M**, Caberto C, Wan P, Li Y, Lum-Jones A, Tiirikainen M, Pooler L, Nakamura B, Sheng X, Porcel J, Lim U, Setiawan VW, Le Marchand L, Wilkens LR, Haiman CA, Cheng I, **Chiang CWK[†]**. "Population-specific reference panels are crucial for the genetic analyses: an example of the *CREBRF* locus in Native Hawaiians." **Hum Mol Genet** 2020 Aug 3;29(13):2275-2284. doi: 10.1093/hmg/ddaa083.
31. **Chen M[†]**, Sidore C, Akiyama M, Ishigaki K, Kamatani Y, Schlessinger D, Cucca F, Okada Y, **Chiang CWK[†]**. "Evidence of Polygenic Adaptation in Sardinia at Height-Associated Loci Ascertained from the Biobank Japan." **Am J Hum Genet** 2020 Jul 2;107(1):60-71. doi: 10.1016/j.ajhg.2020.05.014.
30. Marcus JH, Posth C, Ringbauer H, Lai L, Skeates R, Sidore C, Beckett J, Furtwangler A, Olivieri A, **Chiang CWK**, Al-asadi H, Dey K, Joseph TA, Liu CC, Der Sarkissian C, Radzeviciute R, Michel M, Gradoli MG, Marongiu P, Rubino S, Mazzarello V, Rovina D, La Fragola A, Serra RM, Bandiera P, Bianucci R, Pompianu E, Murgia C, Guirguis M, Orquin RP, Tuross N, van Dommelen P, Haak W,

Reich D, Schlessinger D, Cucca F, Krause J, Novembre J. “Genetic history from the Middle Neolithic to present on the Mediterranean island of Sardinia.” **Nat Comm** 2020 Feb 24;11(1):939. doi: 10.1038/s41467-020-14523-6.

29. de Smith AJ, Walsh KM, Morimoto LM, Francis SS, Hansen HM, **Jeon S**, Gonseth S, **Chen M**, **Sun H**, Luna-Fineman S, Antillón F, Girón V, Kang AY, Smirnov I, Shao X, Whitehead TP, Barcellos LF, Jolly KW, Healy J, Laverdière C, Sinnett D, Taub JW, Birch JM, Thompson PD, Pombo-de-Oliveira MS, Spector LG, DeWan AT, Mueller BA, **Chiang CWK**, Metayer C, Ma X, Wiemels JL. “Heritable variation at the chromosome 21 gene *ERG* is associated with acute lymphoblastic leukemia risk in children with and without Down syndrome.” **Leukemia** 2019 Nov;33(11):2746-2751. doi: 10.1038/s41375-019-0514-9.
28. Locke AE*, Steinberg KM*, **Chiang CWK***, Service S*, Havulinna A, Stell L, Pirinen M, Abel HJ, Chiang CC, Fulton RS, Jackson AU, Kang CJ, Kanchi KL, Koboldt DC, Larson DE, Nelson J, Nicholas TJ, Pietila A, Ramensky V, Ray D, Scott LJ, Stringham HM, Vangipurapu J, Welch R, Yajnik P, Yin X, Eriksson JG, Ala-Korpela M, Jarvelin MR, Manniko M, Laivouri H, FinnGen Project, Dutcher SK, Stitzel NO, Wilson RK, Hall IM, Sabatti C, Palotie A, Salomaa V, Laakso M, Ripatti S, Boehnke M, Freimer NB. “Exome sequencing of Finnish isolates enhances rare-variant association power.” **Nature** 2019 Aug;572(7769):323-328. doi: 10.1038/s41586-019-1457-z.
27. Sohail M, Maier RM, Ganna A, Bloemendal A, Martin AR, Turchin MC, **Chiang CWK**, Hirschhorn JN, Daly MJ, Patterson N, Neale B, Mathieson I, Reich D, Sunyaev SR. “Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies.” **eLife**. 2019 Mar 21;8. Pii: e39702. doi: 10.7554/eLife.39702.
26. **Chiang CWK**[†], Mangul S, Robles C, Sankararaman S. “A comprehensive map of genetic variation in the world’s largest ethnic group – Han Chinese.” **Mol Bio Evol** 2018 Nov 1;35(11):2736-2750. doi: 10.1093/molbev/msy170.
25. **Chiang CWK**[†], Marcus J, Sidore C, Biddanda A, Al-asadi H, Zoledziwska M, Pitzalis M, Busonero F, Maschio A, Pistis G, Steri M, Angius A, Lohmueller KE, Abecasis G, Schlessinger D, Cucca F, Novembre J[†]. “Genomic history of the Sardinian population.” **Nat Genet** 2018 Oct;50(10):1426-1434. doi: 10.1038/s41588-018-0215-8.
24. Ganna A, et al. “Quantifying the impact of rare and ultra-rare coding variation across the phenotypic spectrum.” **Am J Hum Genet**. 2018 Jun 7;102(6):1204-1211. doi: 10.1016/j.ajhg.2018.05.002.
23. Kim DS, et al. “Novel association of TM6SF2 rs58542926 genotype with increased serum tyrosine levels and decreased apoB-100 particles in Finns.” **J Lipid Res**. 2017 Jul;58(7):1471-1481. doi: 10.1194/jlr.P076034.
22. Ganel L, et al. “SVScore: an impact prediction tool for structural variation.” **Bioinformatics**. 2017 Apr 1;33(7):1083-1085. doi: 10.1093/bioinformatics/btw789.
21. Reid JS, Jeff J, et al. “A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape in >170,000 individuals of the GIANT Consortium.” **Nat Commun**. 2016 Nov 23;7:13357. doi: 10.1038/ncomms13357.
20. Chen CH, Yang JH, **Chiang CWK**, Hsiung CN, Wu PE, Chang LC, Chang J, Song IW, Yang SL, Chen YT, Liu FT, Shen CY. “Population structure of Han Chinese in the modern Taiwanese population based on 10,000 participants in the Taiwan Biobank project.” **Hum Mol Genet**. 2016 Dec 15;25(24):5321-5331. doi: 10.1093/hmg/ddw346.
19. **Chiang CWK**[†], Ralph P, Novembre J[†]. “Conflations of short identity-by-descent segments bias their

inferred length distribution.” **G3: Genes, Genomes, Genetics**. 2016 May 1; 6(5):1287-1296. doi: 10.1534/g3.116.027581.

18. Winkler TW, Justic AE, Graff M, Barata L, et al. “The influence of age and sex on genetic associations with body composition: a large-scale genome-wide interaction study.” **PLoS Genet**. 2015 Oct 1;11(10):e1005378. doi: 10.1371/journal.pgen.1005378. eCollection 2015 Oct.
17. Zoledziwska M*, Sidore C*, **Chiang CWK***, Sanna S*, Mulas A, Steri M, Busonero F, Marcus JH, Marongiu M, Maschio A, Del Vecchio DO, Floris M, Meloni A, Delitala A, Concas MP, Murgia F, Biino G, Vaccargiu S, Nagaraja R, Lohmueller KE; UK10K Consortium, Timpson NJ, Soranzo N, Tachmazidou I, Dedoussis G, Zeggini E; Understanding Society Scientific Group, Uzzau S, Jones C, Lyons R, Angius A, Abecasis GR, Novembre J, Schlessinger D, Cucca F. “Height-reducing variants and selection for short stature in Sardinia.” **Nat Genet**. 2015 Nov;47(11):1272-81. doi: 10.1038/ng.3368.
16. Sidore C, Busonero F, Maschio A, Porcu E, Naitza S, Zoledziwska M, Mulas A, Pistis G, Steri M, Danjou F, Kwong A, Ortega Del Vecchio VD, **Chiang CWK**, Bragg-Gresham J, Pitzalis M, Nagaraja R, Tarrier B, Brennan C, Uzzau S, Fuchsberger C, Atzeni R, Reinier F, Berutti R, Huang J, Timpson NJ, Toniolo D, Gasparini P, Malerba G, Dedoussis G, Zeggini E, Soranzo N, Jones C, Lyons R, Angius A, Kang HM, Novembre J, Sanna S, Schlessinger D, Cucca F, Abecasis GR. “Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers.” **Nat Genet**. 2015 Nov;47(11):1352-6. doi: 10.1038/ng.3403.
15. Yang WY, Platt A, **Chiang CWK**, Eskin E, Novembre J, Pasaniuc B. “Spatial localization of recent ancestors for admixed individuals.” **G3: Genes, Genomes, Genetics**. 2014 Nov 3; 4(12):2505-18. doi: 10.1534/g3.114.014274.
14. Wang SR, Agarwala V, Flannick J, **Chiang CWK**, Altshuler D, GoT2D Consortium, Hirschhorn JN. “Simulation of Finnish population history, guided by empirical genetic data, to assess power of rare variant tests in Finland.” **Am J Hum Genet**. 2014 May 1;94(5):710-20. doi: 10.1016/j.ajhg.2014.03.019.
13. Olalde I, Sanchez-Quinto F, Datta D, Marigorta UM, **Chiang CWK**, Rodriguez JA, Fernandez-Callejo M, Gonzalez I, Montfort M, Matas-Lalueza L, Civit S, Luiselli D, Charlier P, Pettener D, Ramirez O, Navarro A, Himmelbauer H, Marques-Bonet T, Lalueza-Fox C. “Genomic analysis of the blood attributed to Louis XVI (1754-1793), king of France.” **Sci Rep**. 2014 Apr 24;4:4666. doi: 10.1038/srep04666.
12. Olalde I, Allentoft ME, Sanchez-Quinto F, Santpere G, **Chiang CWK**, DeGiorgio M, Prado-Martinez J, Rodriguez JA, Quilez J, Rasmussen S, Ramirez O, Marigorta UM, Fernandez-Callejo M, Prada ME, Encinas JM, Nielsen R, Netea MG, Novembre J, Sturm RA, Sabeti P, Marques-Bonet T, Navarro A, Willerslev E, Lalueza-Fox C. “Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European.” **Nature**. 2014 Mar 13;507(7491):225-8. doi: 10.1038/nature12960.
11. Monda KL, Chen GK, Taylor KC, Palmer CD, et al. “A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry.” **Nat Genet**. 2013 Jun;45(6):690-6. doi: 10.1038/ng.2608.
10. Turchin MC*, **Chiang CWK***, Palmer CD, Sankararaman S, Reich D, Genetic Investigation of Anthropometric Traits (GIANT) Consortium, Hirschhorn JN. “Evidence of widespread selection on standing variation in Europe at height-associated SNPs.” **Nat Genet**. 2012 Sep;44(9):1015-9. doi: 10.1038/ng.2368.

9. **Chiang CWK**, Liu CT, Lettre G, Lange LA, Jorgensen NW, Keating BJ, Vedantam S, Nock NL, Franceschini N, Reiner AP, Demerath EW, Boerwinkle E, Rotter JI, Wilson JG, North KE, Papanicolaou GJ, Cupples LA, Genetic Investigation of Anthropometric Traits (GIANT) consortium, Murabito JM, Hirschhorn JN. "Ultraconserved elements in the human genome: association and transmission analyses of highly constrained single-nucleotide polymorphisms." **Genetics**. 2012 Sep;192(1):253-66.
8. Dauber A, Yu Y, Turchin MC, **Chiang CWK**, Meng Y, Demerath EW, Patel SR, Rich SS, Rotter JI, Schreiner PJ, Wilson JG, Shen Y, Wu BL, Hirschhorn JN. "Genome-wide association of copy number variation reveals an association between short stature and the presence of low frequency genomic deletions." **Am J Hum Genet**. 2011 Dec 9;89(6):751-9.
7. **Chiang CWK**, Gajdos ZKZ, Korn JM, Butler JL, Hackett R, Guiducci C, Nguyen T, Wilks R, Forrester T, Henderson KD, Le Marchand L, Henderson BE, Haiman CA, Cooper RS, Lyon HN, Zhu X, McKenzie CA, Palmert MR, Hirschhorn JN. "The efficacy of detecting variants with small effects on the Affymetrix 6.0 platform using pooled DNA." **Hum Genet**. 2011 Nov;130(5):607-21.
6. Zhu X, Young JH, Fox E, et al. "Combined admixture mapping and association analysis identifies a novel blood pressure genetic locus on 5p13: contributions from the CARE consortium." **Hum Mol Genet**. 2011 Jun 1;20(11):2285-95.
5. Kang SJ*, **Chiang CWK***, Palmer CD*, Tayo BO, Lettre G, Butler JL, Hackett R, Adeyemo AA, Guiducci C, Berzins I, Nguyen TT, Feng T, Luke A, Shriner D, Ardlie K, Rotimi C, Wilks R, Forrester T, McKenzie CA, Lyon HN, Cooper RS, Zhu X, Hirschhorn JN. "Genome wide association of anthropometric traits in African and African derived populations." **Hum Mol Genet**. 2010 Jul 1;19(13):2725-38.
4. **Chiang CWK**, Gajdos ZKZ, Korn JM, Kuruvilla FG, Butler JL, Hackett R, Guiducci C, Nguyen T, Wilks R, Forrester T, Haiman C, Henderson KD, Le Marchand L, Henderson BE, Palmert MR, McKenzie CA, Lyon HN, Cooper RS, Zhu X, Hirschhorn JN. "Rapid assessment of genetic ancestry in populations of unknown origin by genome-wide genotyping of pooled samples." **PLoS Genet**. 2010;6(3):e1000866.
3. **Chiang CWK***, Derti A*, Schwartz D, Chou MF, Hirschhorn JN, Wu C-t. "Ultraconserved elements: Analyses of dosage sensitivity, motifs, and boundaries." **Genetics**. 2008 Dec;180(4):2277-93.
2. Keating BJ, Tischfield S, Murray SS, *et al*. "Concept, Design and Implementation of a Cardiovascular Gene-centric 50K SNP Array for Large-scale Genomic Association Studies." **PLoS ONE**. 2008;3(10):e3583.
1. Dewing P, **Chiang CWK**, Sinchak K, Sim H, Fernagut P, Kelly S, Chesselet M, Micevych P, Albrecht KH, Harley VR, Vilain E. "Direct regulation of adult brain function by the male-specific factor SRY." **Curr Biol**. 2006, Feb 21;16(4): 415-420.

Contributed Abstracts: Talks

bolded name denotes group member

13. **Jeon S**, de Smith AJ, Musken IS, Metayer C, Ma X, Wiemels JL, **Chiang CWK**. "Multi-ethnic genome-wide association study of Acute Lymphoblastic Leukemia." International Genetic Epidemiology Society (IGES), Seoul, Korea, July 2020 (Online due to COVID-19). Best Poster/Lightning Talk Award.
12. **Chen M**, Sidore C, Akiyama M, Ishigaki K, Kamatani Y, Schlessinger D, Cucca F, Okada Y, **Chiang**

CWK. “Evidence of polygenic adaptation at height-associated loci in mainland Europeans and Sardinians.” Bay Area Population Genetics Meeting (BAPG), Berkeley, California, Nov 2019.

11. **Chen M**, Sidore C, Akiyama M, Ishigaki K, Kamatani Y, Schlessinger D, Cucca F, Okada Y, **Chiang CWK.** “Re-examining the evidence of polygenic adaptation at height loci in mainland European and Sardinia.” Southern California Evolution Meeting (Scale), Irvine, California, Oct 2019.
10. Lettre G, Chen MH, Raffield L, Mousas A, Jiang T, Akbari P, Sakaue S, Bao EL, Lareau CA, **Chen M, Chiang CWK**, Okada Y, Sankaran VG, Soranzo N, Reiner A, Johnson AD, Auer P, Blood-Cell Consortium. “The genetic architecture of hematological traits within and between populations.” American Society of Human Genetics (ASHG), Houston, TX, Oct 2019.
9. **Lin M**, Caberto C, Wan P, Lum-Jones A, Tiirikainen M, Le Marchand L, Wilkens L, Haiman C, Cheng I, **Chiang CWK.** “Oceanian reference panels are crucial for understanding the impact of a Polynesian-specific variant on adiposity in Native Hawaiians.” 23andMe Genome Research Day, Mountain View, California, Jun 2019.
8. **Chiang CWK**, Mangul S, Robles C, Kretzschmar WW, Cai N, Kendler KS, Sankararaman S, Flint J. “A comprehensive map of genetic variation in the world’s largest ethnic group – Han Chinese.” Society for Molecular Biology & Evolution (SMBE), Yokohama, Japan, Jul 2018.
7. **Chiang CWK**, Locke AE, Steinberg KM, Service S, Abel H, Havulinna AS, Chiang C, Stell L, Stringham HM, Jackson AU, Pirinen M, Ray D, Larson DE, Koboldt DC, Scott LJ, Fulton RS, Nelson J, Nicholas TJ, Yajnik P, Ramensky V, Stitzel NO, Wilson RK, Hall IM, Sabatti C, Ripatti S, Salomaa V, Palotie A, Laakso M, Boehnke M, Freimer NB. “Insights to the population structure and genetic architecture of cardiometabolic traits in 20,029 Finnish exomes.” American Society of Human Genetics (ASHG) Orlando, FL, Oct 2017.
6. **Chiang CWK**, Locke AE, Steinberg KM, Service S, Abel H, Havulinna AS, Chiang C, Stell L, Stringham HM, Jackson AU, Pirinen M, Ray D, Larson DE, Koboldt DC, Scott LJ, Fulton RS, Nelson J, Nicholas TJ, Yajnik P, Ramensky V, Stitzel NO, Wilson RK, Hall IM, Sabatti C, Ripatti S, Salomaa V, Palotie A, Laakso M, Boehnke M, Freimer NB. “Insights to the genetic architecture of cardiometabolic traits empowered by 20,000 exomes and the history of Finland.” Gordon Research Conference (GRC), Human Genetics & Genomics, Stowe, VT, Jul 2017.
5. **Chiang CWK**, Sidore C, Zoledziwska M, Marcus JH, Al-asadi H, Abecasis GR, Schlessinger D, Cucca F, Novembre J. “Population genetic insight to the study of human height.” International Society Evolution, Medicine & Public Health (ISEMPH), Durham, NC, Jun 2016.
4. Novembre J, **Chiang CWK**, Marcus J, Sidore C, Zoledziwska M, Steri M, Al-asadi H, Sanna S, Abecasis G, Schlessinger D, Cucca F. “The population structure and demographic history of Sardinia in relationship to neighboring populations.” American Society of Human Genetics (ASHG), San Diego, CA, Oct 2014.
3. **Chiang CWK**, Ralph P, Novembre J. “Conflations of short IBD blocks can bias inferred length of IBD blocks.” Society for Molecular Biology & Evolution (SMBE), San Juan, PR, Jun 2014.
2. Turchin MC, **Chiang CWK**, Palmer CD, Hirschhorn JN, GIANT consortium. “Intra-European allele frequency differences at height-associated SNPs suggest widespread selection on standing variation.” Cold Spring Harbor Laboratory (CSHL), The Biology of Genomes, Cold Spring Harbor, NY, May 2011.
1. **Chiang CWK**, Dewing P, Vilain E. “The genetic effect of the male-determining gene Sry on brain sexual dimorphism and function.” Southern California Conference of Undergraduate Research

(SCCUR), Whittier College, Whittier, CA, Nov. 2004.

Contributed Abstracts: Posters (Last 3 Years, out of 31 total)

bolded name denotes group member

15. **Chan TF, Chiang CWK**, Mancuso N. "Estimating heritability explained by local ancestry and evaluating confounding bias in admixture mapping from summary statistics." Biology of Genomes, CSHL, Cold Spring Harbor, NY, May 2021 (Online due to COVID-19).
14. **Fan C**, Mancuso N, **Chiang CWK**. "A genealogical estimate of genetic relationships." Probabilistic Modeling in Genomics, CSHL, Cold Spring Harbor, NY, Apr 2021 (Online due to COVID-19).
13. Kachuri L, **Jeon S**, Dewan AT, Metayer C, Ma X, **Chiang CWK**, Wiemels JL, de Smith AJ. "Genetic determinants of blood cell traits play a role in susceptibility to acute lymphoblastic leukemia." American Society of Hematology (ASH), San Diego, CA, Dec 2020.
12. **Fan C**, Mancuso N, **Chiang CWK**. "A genealogical estimate of genetic relationships." American Society of Human Genetics (ASHG), San Diego, CA, Oct 2020 (Online due to COVID-19). Reviewer's Choice Abstract
11. **Chiang CWK, Lin M, Sun H**, Russell EM, Minster RL, **Chan TF**, Naseri T, Reupena MS, Lum-Jones A, Cheng I, Wilkens LR, Le Marchand L, Haiman CA. "The challenges to study the impact of Polynesian genetic ancestry on the architecture of complex traits in Native Hawaiians." American Society of Human Genetics (ASHG), San Diego, CA, Oct 2020 (Online due to COVID-19).
10. **Chen M, Chiang CWK**. "Polygenic adaptation at height-associated loci among continental populations." American Society of Human Genetics (ASHG), San Diego, CA, Oct 2020 (Online due to COVID-19).
9. **Jeon S**, de Smith AJ, Muskens IS, Dewan AT, Metayer C, Ma X, Wiemels JL, **Chiang CWK**. "Multi-ethnic genome-wide association study identified novel loci associated with childhood acute lymphoblastic leukemia." American Society of Human Genetics (ASHG), San Diego, CA, Oct 2020 (Online due to COVID-19). Reviewer's Choice Abstract
8. **Chiang CWK**. "The impact of Polynesian genetic ancestry on the architecture of complex traits in Native Hawaiians, and the challenges to study them." Society for Molecular Biology & Evolution (SMBE), Quebec City, Canada, July 2020. (Conference canceled due to COVID-19)
7. **Fan C**, Mancuso N, **Chiang CWK**. "A genealogical estimate of genetic relationships." Biology of Genomes, CSHL, Cold Spring Harbor, NY, May 2020 (Online due to COVID-19).
6. **Lin M**, Caberto C, Wan P, Lum-Jones A, Tiirikainen M, Pooler L, Nakamura B, Sheng X, Le Marchand L, Wilkens L, Haiman C, Cheng I, **Chiang CWK**. "Oceanian reference panels are crucial for understanding the impact of a Polynesian-specific variant on adiposity in Native Hawaiians." American Society of Human Genetics (ASHG), Houston, TX, Oct 2019.
5. **Chen M**, Akiyama M, Sidore C, Ishigaki K, Okada Y, Kamatani Y, Schlessinger D, **Chiang CWK**. "Re-examining the evidence for polygenic adaptation at height-associated loci in mainland Europe and Sardinia." American Society of Human Genetics (ASHG), Houston, TX, Oct 2019. Reviewer's Choice Abstract
4. **Chen M**, Akiyama M, Sidore C, Ishigaki K, Okada Y, Kamatani Y, Schlessinger D, **Chiang CWK**. "Re-examining the evidence for polygenic adaptation at height-associated loci in mainland Europe and

Sardinia.” Gordon Research Conferenec (GRC), Human Genetics & Genomics, Waterville, NH, Jul 2019.

3. **Sun H, Lin M**, Wilkens L, Le Marchand L, Haiman CA, **Chiang CWK**. “The impact of global and local Polynesian genetic ancestry on complex traits in Native Hawaiians.” Biology of Genomes, CSHL, Cold Spring Harbor, NY, May 2019.
2. **Chen M**, Akiyama M, Sidore C, Ishigaki K, Okada Y, Kamatani Y, Schlessinger D, **Chiang CWK**. “Re-examining the evidence of polygenic adaptation at height-associated loci in mainland Europe and Sardinia.” Biology of Genomes, CSHL, Cold Spring Harbor, NY, May 2019.
1. **Chiang CWK**, Mangul S, Robles C, Sankararaman S. “A comprehensive map of genetic variation in the world’s largest ethnic group – Han Chinese.” American Society of Human Genetics (ASHG), San Diego, CA, Oct 2018.

Invited Talks and Colloquia

2020.01.22	Department Seminar, Department of Genetics University of Georgia, Athens, GA.
2019.09.09	Institute Seminar, International Laboratory of Human Genome Research (LIIGH) National University of Mexico (UNAM), Queretero, Mexico.
2019.08.29	Department Seminar, Quantitative Computational Biology Section Department of Biological Sciences, USC, Los Angeles, CA.
2018.06.08	Informatics Center for Neurogenetics and Neurogenomics (ICNN) Symposium University of California, Los Angeles (UCLA), Los Angeles, CA.
2018.04.18	Asian Evo Conference, Symposium on “Human Evolution and Adaptation” China National GeneBank, Shenzhen, China.
2018.04.13	Institute Seminar, Institute of Biomedical Sciences (IBMS) Academia Sinica, Taipei, Taiwan.
2017.04.13	Department Seminar, Center for Genetic Epidemiology University of Southern California, Los Angeles, CA.
2017.02.23	Department Seminar, Virginia Institute for Psychiatric and Behavioral Genetics (VIPBG) Virginia Commonwealth University, Richmond, VA.
2017.01.26	Department Seminar, Department of Anthropology University of Utah, Salt Lake City, UT.
2015.05.06	Institute Seminar, CAS-MPG Partnered Institute of Computational Biology Chinese Academy of Science, Shanghai, China.
2015.04.30	Department Seminar, Center for Genomic Sciences University of Hong Kong, Hong Kong, SAR, China.
2015.04.09	Institute Seminar, Institute of Biomedical Sciences (IBMS) Academia Sinica, Taipei, Taiwan.

Academic Awards and Recognitions

2020	Undergraduate Research Associate Program Award, USC (To support undergraduate researchers S. Rashid and S. Sommerer in AY 2020-21)
2017	ASHG Charles J. Epstein Trainee Award for Excellence in Human Genetics Research (Semifinalist)
2013-2015	National Institute of Health NRSA Postdoctoral Fellowship, F32
2010	Summer Institute in Statistical Genetics Travel Scholarship

2007-2010	National Science Foundation Graduate Fellowship
2005	Director's Fellowship, Yale University (declined)
2005	Phi Beta Kappa Society
2004	Ira J. and Shirley Spoon Honors Collegium Scholarship, UCLA
2003	Golden Key International Honour Society
2001	CRC Press Freshmen Chemistry Achievement Award
2001	The National Society of Collegiate Scholar
2001	Alpha Lambda Delta Honor Society
2001	Phi Eta Sigma Honor Society

Mentored Student and Postdocs

Abbreviations: **PIBBS**, Programs in Biomedical and Biological Sciences PhD program; **CBB**, Computational Biology and Bioinformatics PhD program; **MBBO**, Marine Biology and Biological Oceanography PhD program; **QB**, Quantitative Biology undergraduate program, USC.

Year	Name	Program	Role
<u><i>Current Trainee (at USC)</i></u>			
2021-current	Ying-Chu Lo, Ph.D.	USC-Taiwan Postdoctoral Fellow, USC	Postdoc advisor
2021-current	Xinghu Qin, Ph.D.	Postdoctoral Fellow, USC	Postdoc advisor
2018-current	Soyoung Jeon	Ph.D. student, PIBBS, USC	Co-PhD advisor
2019-current	Caoqi Fan	Ph.D. student, CBB, USC	PhD advisor
2019-current	Tsz Fung Chan	Ph.D. student, Epidemiology, USC	Co-PhD advisor
2020-current	Bryan Dinh	Ph.D. student, CBB, USC	PhD advisor
2020-current	Maria Ruggeri	Ph.D. student, MBBO, USC	External committee member
2021-current	Qianxi (Senkei) Feng	Ph.D. student, Epidemiology, USC	External committee member
2020-current	Xinyue (Camellia) Rui	B.S./M.S. student, Mathematics, USC Fall 2020 Provost Fellowship	MS advisor
2020-current	Sydney Rashid	B.S. student, QB, USC	--
2021-current	Echo Tang	B.S. student, QB, USC	--
2021-current	Jordan Cahoon	B.S. student, Comp Sci, USC	--
<u><i>Current Trainee (at other institutions)</i></u>			
2019-current	Olzhas Iksan	Ph.D. student, Genetics, Kazakh National Univ.	External committee member
<u><i>Former Trainee</i></u>			
2018-2019	Hanxiao Sun	M.S. student, Biostatistics, USC	MS advisor
2018-2020	Meng Lin, Ph.D.	Postdoctoral Fellow, USC	Postdoc advisor
2018-2021	Minhui Chen, Ph.D.	Postdoctoral Fellow, USC	Postdoc advisor
2019-2020	Samuel Sommerer	B.S. student, QB/Comp Sci, USC	--
<u><i>Rotation Students</i></u>			
2018 Spring	Kuochang Tseng	Rotation student, PIBBS, USC	--
2018 Spring	Charles Bramlett	Rotation student, PIBBS, USC	--
2018 Fall	Audrey Nickle	Rotation student, PIBBS, USC	--

Teaching

2020	Guest Lecturer, University of Southern California PM 533 (Genetic and Molecular Epidemiology), 1hr/term, Fall Term
2020	Guest Lecturer, University of Hawai'i Cancer Center Multiethnic Cohort T32 Postdoctoral Fellowship Seminar Series, 1hr, Spring Term
2019-2020	Guest Lecturer, University of Southern California BISC 577A (Computational Biology Laboratory), 2hrs/term, Fall Term
2009	Teaching Assistant, Harvard University. LS1B (Genetics, Genomics, and Evolution), Spring Term
2008	Guest Lecturer, Harvard Medical School. Genetics 228 (Genetics in Medicine; "Using Genetics Databases"), Fall Term
2007	Teaching Assistant, Harvard Medical School. Genetics 228 (Genetics in Medicine), Fall Term

Departmental and University Service

Abbreviations: **CGE**, Center for Genetic Epidemiology; **PIBBS**, Programs in Biomedical and Biological Sciences PhD program; **DPM**, Department of Preventive Medicine, USC; **QCB**, Department of Quantitative Computational Biology, USC.

Year	Role	Service
2021-	Member	DPM Junior Faculty Committee
2021	Member	DPM Statistical Genetics Curriculum Committee
2020-2021	Chair	CGE Seminar Series
2020	Webmaster	CGE webpage design and launch
2019-2021	Co-chair (2020-2021), Member (2019)	DPM Epidemiology Ph.D. Admission Committee
2019-2020	Member	PIBBS Ph.D. Admission Committee
2019	Member	QCB Faculty Search Committee
2018	Member	DPM Biostatistics Ph.D. Admission Committee

Professional Services and Scientific Communities

Editorship and Editorial Board:

Review Editor (Frontier in Genetics, 2018-2021)
Associate Editor (Frontier in Genetics, 2021-)

Invited Manuscript Reviewer:

Nature	Nature Genetics	Nature Communications
Am J of Hum Genet	Science	Science Advances
PNAS	Molecular Biology and Evolution	Human Molecular Genetics
Genetics	G3: Genes, Genomes, Genetics	Bioinformatics
PLoS Genetics	PLoS ONE	Eur J of Hum Genet
Human Genetics	Frontiers in Genetics	Nutrition and Diabetes
Scientific Reports		

American Society of Human Genetics (ASHG):

Member, 2007-present
Judge, DNA Day Essay Contest, 2014, 2015, 2017, 2021
Invited Abstract Reviewer, Evolutionary and Population Genetics, 2017
Mentor, Trainee-Mentor Luncheon, Evolution and Population Genetics, 2019
Member, Awards Committee, 2021-2023

Invited Grant Reviewer:

Human Frontier Science Program (Mail-in Reviewer, 2018)
Medical Research Council NIRG (Reviewer, 2019)

Symposia Organizer: 1st AsiaEvo Conference (2018)

Member: Society for Molecular Biology & Evolution (SMBE); American Society for Human Genetics (ASHG); American Association of Physical Anthropologists (AAPA)

Media Appearances, Engagement, and Coverage

“COVID-19 vaccine eligibility expands to anyone over the age of 16 in L.A. county”

USC Annenberg Media, Apr 13, 2021

<https://www.uscannenbergmedia.com/2021/04/13/covid-19-vaccine-eligibility-expands-to-anyone-over-the-age-of-16-in-la-county/>

“Polynesian ancestry linked to obesity in study of Native Hawaiians”

Genetic Obesity News, Feb 15, 2021

<https://geneticobesitynews.com/2021/02/15/polynesian-ancestry-linked-obesity-diabetes-heart-disease-risk-study/>

“Native Hawaiian genetic ancestry linked to metabolic diseases”

The Academic Times, Feb 11, 2021

<https://academictimes.com/native-hawaiian-genetic-ancestry-linked-to-metabolic-diseases/>

“Global, Local Polynesian Ancestry Influence Disease Risk Among Native Hawaiians”

Genomeweb, Feb 11, 2021

<https://www.genomeweb.com/genetic-research/global-local-polynesian-ancestry-influence-disease-risk-among-native-hawaiians#.YCWpKBNKjBI>

“Genetic ancestry linked to diabetes, heart failure and obesity among Native Hawaiians”

Keck School of Medicine News, Feb 11, 2021

<https://keck.usc.edu/genetic-ancestry-linked-to-diabetes-heart-failure-and-obesity-among-native-hawaiians/>

“Polynesian ancestry linked to obesity, diabetes in Native Hawaiians”

Honolulu Star Advertiser, Feb 11, 2021

<https://www.staradvertiser.com/2021/02/11/breaking-news/polynesian-ancestry-linked-to-obesity-diabetes-in-native-hawaiians/>

“Genetics contributes to diabetes, HF, obesity risk in Native Hawaiian individuals”

Healio, Feb 11, 2021

https://www.healio.com/news/cardiology/20210211/genetics-contributes-to-diabetes-hf-obesity-risk-in-native-hawaiian-individuals?utm_medium=social&utm_source=twitter&utm_campaign=scheduledpost

“Accuracy of Genotyping Chips Called into Question”

The Scientist, Jul 24, 2019

<https://www.the-scientist.com/news-opinion/accuracy-of-genotyping-chips-called-into-question--66198>

“Hidden Stories of Chinese Migration and Culture Found in Giant Genetic Study”
The New York Times, Oct 5, 2018
<https://www.nytimes.com/2018/10/05/science/china-genetics.html>

Outreach and Community Services

Hoyt Art Gallery, USC

Community outreach pairing local visual artist with biomedical researcher to collaborate for innovative artistic representation of ongoing research at Keck School of Medicine
2018 Partnered Biomedical Researcher

“How to get a postdoc” workshop, Department of Ecology and Evolutionary Biology, UCLA
2015 Panelist

Science in the News, Boston, MA.

Science in the News is a free evening seminar series for the public aimed at explaining and discussing today’s hottest scientific topics without the hype or exaggeration often introduced by media coverage.

2005-2006 Lecture Coordinator
“Stem Cells: Hope or Hype?” lecture series (2005)
“Obesity and Diabetes” lecture series (2006)

MATHCOUNTS, Suzanne Middle School, Walnut, CA

MATHCOUNTS is a nation-wide program for 6th to 8th grade students designed to elicit interest in mathematics through teamwork and competition.

2003-2005 Head Coach, Suzanne Middle School
1999-2003 Assistant Coach, Suzanne Middle School
2006, 2008, 2013 Volunteer, East San Gabriel Valley Chapter, CA