

EMILIA HUERTA-SANCHEZ

ehuerta-sanchez@ucmerced.edu | 510-643-0060 | School of Natural Sciences, Merced, CA 95343

EDUCATION

PhD Applied Mathematics (08/2008)

Cornell University, Ithaca, NY

Advisors: Richard Durrett and Carlos Bustamante

M.S. Applied Mathematics (2005)

Cornell University, Ithaca, NY

B.A. Mathematics and B.A. French (2002)

Mills College, Oakland, CA

APPOINTMENTS

GeneTime Fellow, Trinity College Dublin, Ireland (Spring 2008)

Host: Prof. Dan Bradley

Visiting VIGRE Assistant Professor, University of California, Berkeley (2008-2009)

Department of Statistics

NSF Postdoctoral Research Fellow, University of California, Berkeley (2009-2012)

Departments of Statistics and Integrative Biology. Advisor: Rasmus Nielsen

Postdoctoral Research Fellow, University of California, Berkeley (2012-2014)

Center for Theoretical Evolutionary Genomics and Integrative Biology

Advisor: Rasmus Nielsen

Assistant Professor, University of California, Merced (July, 2014 - present)

School of Natural Sciences

TEACHING EXPERIENCE

Course Instructor

Fall 2010 Stat 98/198 (VIGRE seminar)

Fall 2009 Stat 98/198 (VIGRE seminar)

Spring 2009 Stat 134 (Introduction to Probability)

Fall 2008 Stat 20 (Introduction to Statistics)

Fall 2008 Stat 98/198 (VIGRE seminar)

Teaching assistant

Fall 2006 Single Variable Calculus (nominated for best TA)

Fall 2005 Multivariate Calculus

Guest Lecturer

Spring and Fall 2012 Workshops on next-generation sequence analysis. Taught a half-day course on methods to call SNPs and genotypes
Fall 2012 Genetics and Genomics. Taught one lecture on adaptation in humans
Fall 2013 Genetics and Genomics. Taught one lecture on Hardy-Weinberg equilibrium and on the fixation index, F_{ST}

MENTORING EXPERIENCE

Have mentored both undergraduate and masters students on population genetics projects: (1) understanding the relationship between gene-flow and positive selection and (2) assessing the power to detect selection when accounting for demographic history using 3-population summary statistics and (3) estimating demographic histories when samples sizes are large (> 1000 individuals).

Research interests

Population genetics, human genetics, demographic inference, natural selection, analyses of genetic variants from next-generation sequencing data, high altitude adaptation.

PUBLICATIONS

* Denotes joint first author

F. M. Key, B. Peter, M.Y. Dennis, **E. Huerta-Sánchez**, W. Tang, L. Prokunina-Olsson, R. Nielsen, A.M. Andrés. Selection on a variant associated with improved viral clearance drives local, adaptive pseudogenization of interferon lambda 4 (IFNL4). *PLoS Genet* 2014 DOI: 10.1371/journal.pgen.1004681.

E. Huerta-Sanchez*, X. Jin*, Asan*, Z. Bianba* et al. Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA. *Nature* doi:10.1038/nature13408, 2014. Received media coverage including on NPR, BBC, LA Times, San Francisco Chronicle, Slate.

L. Excoffier, I. Dupanloup, **E. Huerta-Sanchez**, V.C. Sousa, M. Foll. Robust demographic inference from genomic and SNP data. *PLoS Genet* 9(10): e1003905. Doi:10.1371/journal.pgen.1003905, 2013.

M. Fumagalli, F. Vieira, T. S. Korneliussen, T. Linderoth, **E. Huerta-Sanchez**, A. Albrechtsen, R. Nielsen. Quantifying population genetic differentiation from Next-Generation Sequencing data. *Genetics*, doi: 10.1534/genetics.113.154740. August 2013. (Chosen to be highlight for the *Genetics* November 2013 issue.)

M. Somel, M. Wilson Sayres, G. Jordan, **E. Huerta-Sanchez**, M. Fumagalli, A. Ferrer-Admetlla, R. Nielsen. A scan for human-specific relaxation of negative selection reveals unexpected polymorphism in the proteasome. *Mol Biol Evol.* 30(8): 1808–1815, 2013.

E. Huerta-Sanchez*, M. DeGiorgio*, L. Pagani*, A. Tarekegn, R. Ekong, T. Antao, A. Cardona, H. E. Montgomery, G. L. Cavalleri, P. A. Robbins, M. E. Weale, N. Bradman, E. Bekele, T. Kivisild, C. Tyler-Smith, R. Nielsen. Genetic signatures reveal high-altitude adaptation in a set of Ethiopian populations. *Mol Biol Evol.* 30(8): 1877–1888, 2013. Received media coverage including in NY Times and LA Times.

B. Peter, **E. Huerta-Sanchez** and R. Nielsen. Distinguishing between selective sweeps from standing variation and from a de novo mutation. *PLoS Genet.* 8(10) doi:10.1371/journal.pgen.1003011, 2012.

K. E. Lohmueller, A. Albrechtsen, Y. Li, S. Y. Kim, T. Korneliussen, N. Vinckenbosch, G. Tian, **E. Huerta-Sanchez** et al. Natural Selection Affects Multiple Aspects of Genetic Variation at Putatively Neutral Sites across the Human Genome. *PLoS Genet* 7(10): e1002326. doi:10.1371/journal.pgen.1002326, 2011.

X. Yi*, Y. Liang*, **E. Huerta-Sanchez***, X. Jin*, Z. X. P. Cuo*, J.E. Pool* et al. Archaeology Augments Tibet's Genetic History—Response. *Science* 329(5998):1467-1468, 2010.

X. Yi*, Y. Liang*, **E. Huerta-Sanchez***, X. Jin*, Z. X. P. Cuo*, J.E. Pool* et al. Sequencing of 50 human exomes reveals adaptation to high altitude. *Science* 329(5987):75-78, 2010. (Subject of a 'Perspectives' article in the same issue and media coverage)

Y. Li*, N. Vinckenbosch*, G. Tian*, **E. Huerta-Sanchez***, T. Jiang* et al. Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. *Nature Genetics* 42, 969-972, 2010.

C. Murray*, **E. Huerta-Sanchez***, F. Casey and D. Bradley. Cattle demographic history modelled from autosomal sequence variation. *Phil. Trans. R. Soc. B* 365:2531-2539, 2010.

E. Huerta-Sanchez, R. Durrett, and C. D. Bustamante. Population genetics of polymorphism and divergence under fluctuating selection. *Genetics* 178:325-337, 2008.

E. Huerta-Sanchez and R. Durrett. Wagner's canalization model. *Theoretical Population Biology* 71(2):121-130, 2007.

B. Gonzales, **E. Huerta-Sanchez**, C. Kribs, A. Ortiz-Nieves and T. Vazquez-Alvarez. Am I Too Fat? Bulimia as an Epidemic. *Journal of Mathematical Psychology* 47(5-6): 515-526, 2003.

E. Huerta-Sanchez, K. Rios-Soto, G. Jordan-Salivia. *The Effects of Mass Transportation During a Deliberate Release of Smallpox*. Technical report for the Mathematical and Theoretical Biology Institute (MTBI). Cornell University, Ithaca, NY Summer 2002.

E. Huerta-Sanchez, A. Lopez, D. Uminsky. Iterations of Even-Odd Splitting Map Can Make Integration Easier *The Pi Mu Epsilon Journal*. Vol. 11, No. 5, 241-250, 2001.

ORAL PRESENTATIONS

Adaptation to high altitude – an example of adaptive introgression in humans, MVZ, UC Berkeley, Berkeley, November 19 2014 (Invited Speaker)

Adaptation to high altitude – an example of adaptive introgression in humans, Biology Department,

San Francisco State University, October 2014 (*Invited Speaker*)

Adaptation to high altitude – an example of adaptive introgression in humans, Institute of Evolutionary Biology, University of Edinburgh, March 2014 (*Invited Speaker*)

Detecting and characterizing natural selection from next generation sequencing data, Trinity College Dublin, May 2013 (*Invited Speaker*)

Detecting and characterizing natural selection from next generation sequencing data, Pennsylvania State University, May 2013 (*Invited Speaker*)

Detecting and characterizing natural selection from next generation sequencing data, University of California Merced. March 2013 (*Invited Speaker*)

Detecting and characterizing natural selection from next generation sequencing data, University of Pennsylvania, January 2013 (*Invited Speaker*)

Is altitude adaptation in Tibet caused by selection on standing variation or from de novo mutations? High altitude and cold: adaptation to extremes, Cambridge UK. September 2012. (*Invited Speaker*)

Detecting selection to high altitude in Tibetans and Ethiopians. UC Berkeley Primate Biology group. May 2012.

Selection on standing variation is the more likely scenario responsible for the selective signature in the Tibetan population. Population Genomics Retreat, Churwalden/Lenzerheide, Switzerland. March 2012. (*Invited Speaker*)

Detecting and characterizing natural selection from next generation sequencing data, USC, December, 2011. (*Invited Speaker*)

Characterizing the genetic signature of high altitude adaptation in Tibetans. Society of Molecular Biology and Evolution (SMBE), Kyoto, Japan. 2011.

Sequencing of 50 human exomes reveals adaptation to high altitude. American Society of Human Genetics, Washington D.C., U.S.A. 2010

Sequencing of 50 human exomes reveals adaptation to high altitude. Society of Molecular Biology and Evolution (SMBE), Lyon, France. 2010.

Sequencing of 50 human exomes reveals adaptation to high altitude. Bay Area Population Genomics Conference, UC Berkeley, CA, USA. 2010. (*Invited Speaker*)

Modeling large family size: Lambda coalescent. Young investigators in Population Genetics Workshop, Tucson, Arizona, USA. 2008. (*Invited Speaker*)

Wagner's Canalization Model. Cornell Probability Summer School, Ithaca, NY. 2006. (*Invited Speaker*)

OUTREACH

Co-organized a professional session on Cracking the (bio)Code: How to Start a Research Career in Computational Biology at SACNAS, October 17, 2014.

Taught a lecture on human evolution and human adaptation to high school students in Spring 2013 and Spring 2014.

Participated in the 2013 University of California Museum Paleontology Short Course, a one-day conference highly attended by high school biology teachers.
(<http://www.ucmp.berkeley.edu/about/shortcourses/shortcourse13.php>)

Co-organized a series of lectures in evolutionary biology, forensics and medical genetics for freshman high school students in biology in Spring 2012, Spring 2013 and Spring 2014.

Participated in an outreach program highlighting my research for an educational website “Understanding Evolution” (http://evolution.berkeley.edu/evolibrary/article/0_0_0/huertasanchez_01) in 2012.

Undergraduate mentor for the Society for Molecular Biology and Evolution (SMBE) conference, 2010-2011. Guided undergraduates through their first academic conference experience.

Co-organized VIGRE seminar 2009, 2010, designed to introduce a diverse group of undergraduate students to statistics, content covered both practical applications in industry and academic research, and small research projects.

Co-organized Cal Day 2009, an annual university open house for prospective students and community members to visit the campus to meet the faculty and students to explore research and other activities.

Participated in the founding of the Summer Math Institute (SMI) in Cornell University, targeting underrepresented minorities and first generation college students for pre-PhD research training, and helped run the program in 2006.

Was on co-organizing committee for the Expanding Your Horizons (EYH) program, a one-day conference for middle school girls to experience the mathematical sciences in practical workshops, Cornell University, 2004-2007

OTHER EXPERIENCE

Member of the NSF Evolutionary Genetics grant review panel for the Evolutionary Processes Cluster of the Division of Environmental Biology, October 19-21, 2010, Arlington, VA.

Reviewer of numerous population genetic articles (in *Science*, *PLoS Genetics*, *Genetics*, *Genome Research*, *Molecular Biology and Evolution*, *The American Journal of Human Genetics*, *PLoS One*, *Annals of Applied Probability*, *BMC Evolutionary Biology*)

AWARDS AND HONORS

2012 National Institutes of Health (Diversity Supplement, 2 years)

2012 Selected as one of the 20 (out of more than 300 applicants) invited to interview for the Burroughs Wellcome Fund Career Awards at the Scientific Interface

2010 Society of Molecular Biology and Evolution Travel Grant

2009 NSF Postdoctoral Fellowship (3 years)

2008 Genetime Fellowship, EU Marie Curie Short-term Fellowship