Kirk E. Lohmueller, Ph.D.
Department of Integrative Biology
University of California
1005 Valley Life Sciences, Building No. 3140
Berkeley, CA 94720-3140
klohmueller@ucla.edu

CURRICULUM VITAE

EDUCATION:

2010 ***Ph.D. in Genetics***
Cornell University, Ithaca, NY
Focus on population genetics with a Biometry (Biostatistics) minor

2005 ***Bachelor of Science in Biology, (Magna Cum Laude)***
Georgetown University, Washington, DC

CONTINUING EDUCATION AND TRAINING:

2010 ***FOR283: Forensic Biology (Credited)***
University of California, Davis Extension, Davis, CA

2010 ***ETX280: Forensic DNA typing (Credited)***
University of California, Davis Extension, Davis, CA

EMPLOYMENT:

Starting March 2013 ***University of California, Los Angeles, CA***
Assistant Professor
Department of Ecology and Evolutionary Biology

2010-Present ***University of California, Berkeley, CA***
Miller Research (Postdoctoral) Fellow
Advisor: Dr. Rasmus Nielsen

RESEARCH INTERESTS:

Population and evolutionary genetics

-Using genetic variation data to learn about population history.

-Understanding how natural selection has shaped the human genome with a special emphasis on negative selection and on the interaction of selection with demography.

-Population genetic inferences from next-generation sequencing data.

Genetics of complex traits

-Developing and applying methods for association studies with rare variants

-Using population genetic information to inform studies of human disease.

Forensic genetics

-Population genetic and statistical issues in forensic DNA typing, particularly with low-level DNA profiles.

PREVIOUS RESEARCH:

2005-2009 ***Cornell University, Ithaca, NY***
Graduate Student Research Assistant
Advisors: Dr. Andy Clark & Dr. Carlos Bustamante

Research on human population genetics focusing on human demographic history and natural selection.

2004-2005 ***Georgetown University, Washington, DC***
Undergraduate Research Assistant—Biology Department
Advisor: Dr. John Braverman

Statistical analyses on large genetic variation datasets.

2002-2004 ***Georgetown University, Washington, DC***
Undergraduate Research Assistant—Institute for Molecular and Human Genetics
Advisor: Dr. Lee-Jun Wong

Single nucleotide polymorphism (SNP) genotyping on human DNA samples. Extensively used PCR and electrophoresis.

1998-2001 ***Whitehead/MIT Center for Genome Research, Cambridge MA***
High School Student Research Assistant
Advisor: Dr. Joel Hirschhorn

Review and meta-analysis of genetic association studies.

TEACHING:

2013 ***Population Genetics in Forensic DNA Analysis, Richmond, CA***
Designed and led a 3-day course on basic population genetics and statistics in forensic DNA analysis. Sponsored by the California Association of Criminalists

2012 ***University of California, Los Angeles, CA***
Gave two lectures on coalescent theory to the CS229: Current Topics in Bioinformatics course

2006 ***Cornell University, Ithaca, NY***
Teaching assistant for Population Genetics course

2004 ***Georgetown University, Washington, DC***
Teaching assistant for Biochemistry course

2003 & 2004 ***Georgetown University, Washington, DC***
Teaching assistant for Genetics course

2003 ***Georgetown University, Washington, DC***
Teaching assistant for Introductory Biology II course

AWARDS AND HONORS:

2011 ***Selected as a semifinalist for the Burroughs Wellcome Career Award at the Scientific Interface***
I was one of the top 79 (out of 445) applicants who were invited to submit the full application.

2010 ***Selected as a semifinalist for the Burroughs Wellcome Career Award at the Scientific Interface***
I was one of the top 79 (out of 445) applicants who were invited to submit the full application.

2010 ***Selected as a Platform Session moderator for the American Society of Human Genetics annual meeting***

2010 ***Trainee Research Semifinalist, American Society of Human Genetics***
Awarded to top abstracts submitted for presentations at the 2010 meeting.

2005 ***Chapman medal***
Awarded to the best senior thesis presentation in the Biology Department at Georgetown University.

FELLOWSHIPS AND FUNDING:

2010-2013 ***Miller Postdoctoral Research Fellowship, UC Berkeley***

2010 ***NIH Ruth Kirschstein National Research Service Award***
(I used 6 months before switching to the Miller)

2010 ***NSF Postdoctoral Research Fellowship in Biology***
(I declined this fellowship)

2005-06; 2007-09 ***NSF Graduate Research Fellowship***

2005 ***Cornell Presidential Genomics Fellowship***
(I declined this fellowship)

2004-2005 ***Barry Goldwater Scholarship***
Competitively awarded to students wishing to pursue careers in math and science.

2001-2005 ***Georgetown-Hughes Undergraduate Research Scholarship***
An award from the Howard Hughes Medical Institute (through Georgetown University) to sponsor students' research during the summer.

OTHER PROFESSIONAL ACTIVITIES:

Mentored undergraduate summer student Alison Feder (Summer 2010).

Co-editing (with Rasmus Nielsen) a textbook entitled *Human Population Genomics* to be published by Springer.

Invited reviewer for:
Science
Nature Genetics
Molecular Biology and Evolution

Proceedings of the Royal Society B
PLoS Biology
PLoS Computational Biology
PLoS Genetics
PLoS ONE
Genetica
Genetics
Proceedings of the National Academy of Sciences
Genome Research
American Journal of Human Genetics
Human Molecular Genetics
BMC Medical Genetics
European Journal of Human Genetics
Fronteirs in Evolutionary and Population Genetics.

PUBLICATIONS:

1. **Lohmueller KE*,** Sparsø T*, Li Q, Andersson E, Korneliussen T, Albrechtsen A, Banasik K, Grarup N, Hallgrimsdottir I, Kiil K, Kilpeläinen T, Krarup N, Pers T, Sanchez G, Jørgensen T, Sandbæk A, Lauritzen T, Kristiansen K, Brunak S, Li Y, Hansen T, Wang J, Nielsen R, Pedersen O. Exome sequencing of 2,000 Danish individuals and the role of rare coding variants in type 2 diabetes, Submitted. **(*Contributed equally).**

2. DeGiorgio M, **Lohmueller KE**, Nielsen R. A model-based approach for identifying signatures of balancing selection in genetic data, Submitted.

3. **Lohmueller KE,** Rudin N, Inman K. Analysis of allelic drop-out using the Identifiler® and PowerPlex® 16 forensic STR typing systems I. Estimation of drop-out probabilities, Submitted.

4. **Lohmueller KE,** Rudin N, Inman K. Analysis of allelic drop-out using the Identifiler® and PowerPlex® forensic STR typing systems II. Evaluation of estimated drop-out probabilities, Submitted.

5. **Lohmueller KE**, Rudin N. Calculating the weight of evidence in low-template forensic DNA casework. *Journal of Forensic Sciences*, 2013; 58 Suppl 1:S243-9.

6. Rasmussen M*, Guo X*, Wang Y*, **Lohmueller KE*,** and 54 additional co-authors. Aboriginal Australian genomic sequence obtained from hundred-year-old lock of hair reveals separate human dispersals into Asia. *Science*, 2011; 334:94-98 **(*Contributed equally).**

7. **Lohmueller KE**, Albrechtsen A, Li Y, Kim SY, Korneliussen T, Vinckenbosch N, Tian G, Huerta-Sanchez E, Feder A, Grarup N, Jørgensen T, Jiang T, Witte DR, Sandbæk A, Hellmann I, Lauritzen T, Hansen T, Pedersen O, Wang J, Nielsen R. Natural selection affects multiple aspects of genetic variation at putatively neutral sites across the human genome. *PLoS Genetics* 2011; 7:e1002326.

8. Kim SY, **Lohmueller KE**, Albrechtsen A, Li Y, Korneliussen T, Tian G, Grarup N, Jiang T, Andersen G, Witt D, Jorgensen T, Hansen T, Pedersen O, Wang J, Nielsen R. Estimation of allele frequency and association mapping using next-generation sequencing data. *BMC Bioinformatics*, 2011; 12:231.

9. **Lohmueller KE**, Bustamante CD, Clark AG. Detecting directional selection in the presence of recent admixture in African Americans. *Genetics*, 2011; 187:823-835.

10. Boyko A, Quignon P, Li L, Schoenebeck J, Degenhardt JD, **Lohmueller KE**, et al. A simple genetic architecture underlies quantitative traits in dogs, *PLoS Biology* 2010; 8:e1000451.

11. **Lohmueller KE**, Bustamante CD, Clark AG. The effect of recent admixture on inference of ancient population history. *Genetics* 2010; 185:611-622.

12. **Lohmueller KE,** Degenhardt JD, Keinan A. (Letter to the Editor) Sex-averaged recombination and mutation rates: A comment on Labuda et al., *Am J Hum Genet* 2010; 86:978-980.

13. **Lohmueller KE.** (Letter to the Editor) Graydon et al. provide no new evidence that forensic STR loci are functional. *Forensic Sci Int Genet* 2010; 4:273-274.

14. vonHoldt BM, Pollinger JP, **Lohmueller KE**, et al. Genome-wide SNP and haplotype analysis reveals a rich history underlying dog domestication. *Nature* 2010; 464:898-902.

15. Wall JD, **Lohmueller KE**, Plagnol V. Detecting ancient admixture and estimating demographic parameters in multiple human populations. *Mol Biol Evol* 2009; 26:1823-1827.

16. **Lohmueller KE**, Bustamante CD, Clark AG. Methods for human demographic inference using haplotype patterns from genome-wide SNP data. *Genetics* 2009; 182:217-231.

17. Auton A, Bryc K, Boyko AR, **Lohmueller** KE, Novembre J, Reynolds A, Indap A, Wright MH, Degenhardt J, Gutenkunst RN, King KS, Nelson MR, Bustamante CD. Global distribution of genomic diversity underscores rich complex history of continental human populations. *Genome Research* 2009; 19:795-803.

18. Boyko AR, Williamson SH, Indap AR, Degenhardt JD, Hernandez RD, **Lohmueller KE**, Adams MD, Schmidt A, Sninsky JJ, Sunyaev SR, White TJ, Nielsen R, Clark AG, Bustamante CD. Assessing the evolutionary impact of amino acid mutations in the human genome. *PLoS Genetics* 2008; 4: e1000083.

19. **Lohmueller KE,** Indap AR, Schmidt S, Boyko AR, Hernandez RD, Hubisz MJ, Sninsky JJ, White TJ, Sunyaev SR, Nielsen R, Clark AG, Bustamante CD. Proportionally more deleterious genetic variation in European than in African populations. *Nature* 2008; 451:994-997.

20. Olshen AB, Gold B, **Lohmueller KE**, Struewing JP, Satagopan J, Stefanov SA, Eskin E, Kirchhoff T, Lautenberger JA, Klein RJ, Friedman E, Norton L, Ellis NA, Viale A, Lee CS, Borgen PI, Clark AG, Offit K, Boyd J. Analysis of genetic variation in Ashkenazi Jews by high density SNP genotyping. *BMC Genetics* 2008; 9:14.

21. **Lohmueller KE**, Mauney MM, Reich DE, Braverman JM. Variants associated with common disease are not unusually differentiated in frequency across populations. *Am J Hum Genet* 2006; 78:130-136.

22. **Lohmueller KE**, Wong LJC, Mauney MM, Jiang L, Felder RA, Jose PA, Williams SM. Patterns of genetic variation in the hypertension candidate gene *GRK4*: ethnic variation and haplotype structure. *Ann Hum Genet* 2006; 70:27-41.

23. Patterson N, Hattangadi N, Lane B, **Lohmueller KE**, Hafler DA, Oksenberg JR, Hauser SL, Smith MW, O'Brien SJ, Altshuler D, Daly MJ, Reich D. Methods for high-density admixture mapping of disease genes. *Am J Hum Genet* 2004; 74:979-1000.

24. **Lohmueller KE**, Pierce CL, Pike M, Lander ES, Hirschhorn JN. Meta-analysis of genetic association studies supports a contribution of common variants to susceptibility to common disease. *Nat Genet* 2003; 33:177-182.

25. Hirschhorn JN, **Lohmueller K**, Byrne E, Hirschhorn K. A comprehensive review of genetic association studies. *Genet Med* 2002; 2:45-61.

INVITED SEMINARS:

1. Insights into human history and natural selection from genome sequencing data. Seminar for the Department of Molecular and Cellular Biology, University of California, Berkeley, CA, March 2012.

2. Insights into human history and natural selection from genome sequencing data. Seminar for the Bioinformatics Interdepartmental Ph.D. Program Seminar Series, University of California, Los Angeles, CA, February 2012.

3. Insights into human history and natural selection from genome sequencing data. Seminar for the Department of Biology, Dartmouth College, Hanover, NH, February 2012.

4. Insights into human history and natural selection from genome sequencing data. Seminar for the Department of Human Evolutionary Biology, Harvard University, February 2012.

5. Insights into human history and natural selection from genome sequencing data. Seminar for the Department of Biology, University of Maryland, February 2012.

6. Insights into human history and natural selection from genome sequencing data. Seminar for the Department of Biological Statistics and Computational Biology, Cornell University, Ithaca, NY, January 2012.

7. Insights into human history and natural selection from genome sequencing data. Seminar for the Center for Complex Biological Systems, University of California, Irvine, CA, January 2012.

8. Insights into human history and natural selection from genome sequencing data. Seminar for the Department of Genetics, Stanford University, Palo Alto, CA, January 2012.

9. Insights into human history and natural selection from genome sequencing data. Seminar for the Department of Medicine & Lung Biology Center, University of California, San Francisco, CA, November 2011.

10. Insights into human history and natural selection from genome sequencing data. Seminar for the Department of Biological Sciences, University of Southern California, Los Angeles, CA, November 2011.

11. Understanding the importance of natural selection across the human genome and in different human populations. Seminar for the Bioinformatics Interdepartmental Ph.D. Program Seminar Series, University of California, Los Angeles, CA, May 2011.

12. Negative natural selection affects multiple aspects of genetic variation across the human genome. Seminar for the Mathematical and Computational Biology Seminar Series, University of California, Berkeley, CA, April 2011.

13. Understanding patterns of negative selection throughout the human genome. Seminar for the Department of Genetics, Harvard Medical School, Boston, MA, January 2011.

14. Natural selection and patterns of genetic variation in the human genome. Seminar for the Ecology and Evolution Colloquium at San Francisco State University, San Francisco, CA, November 2010.

SELECT CONFERENCE PRESENTATIONS AND OTHER SEMINARS:

1. **Lohmueller KE.** Exome sequencing and the heterogeneity of complex traits. Platform presentation at the 7th Bay Area Population Genomics Conference, Palo Alto, CA, February 2013.

2. Inman K, Rudin N, **Lohmueller KE**. Calculating Likelihood Ratios Incorporating a Probability of Drop-out: A New Web-based Tool. Platform presentation at the California Association of Criminalists meeting, Hayward, CA, May 2012.

3. Inman K, Rudin N, **Lohmueller KE**. Calculating Likelihood Ratios Incorporating a Probability of Drop-out: A New Web-based Tool. Platform presentation at the California Association of Criminalists Northern Study Group meeting, Bakersfield, CA, May 2012.

4. **Lohmueller KE,** Rudin N, Inman K. Approaches to measure the strength of DNA evidence exhibiting possible stochastic effects. Platform presentation at the DNA workshop during the California Association of Criminalists meeting, Sacramento, CA, October 2011.

5. **Lohmueller KE**, Nielsen R. Signatures of negative natural selection on sites that are not evolutionarily conserved across species. Platform presentation, The 12th International Meeting on Human Genome Variation and Complex Genome Analysis (HGV2011), Berkeley, CA, September 2011.

6. **Lohmueller KE,** Rudin N, Inman K. Performance of statistical approaches to measure the strength of DNA evidence exhibiting possible stochastic effects. Poster presentation, 8th International Conference on Forensic Inference and Statistics, Seattle, WA, July 2011.

7. **Lohmueller KE**, Rudin N. The application of likelihood ratios using allelic drop-out probabilities to case samples, Poster presentation, 8th International Conference on Forensic Inference and Statistics, Seattle, WA, July 2011

8. **Lohmueller KE,** Rudin N, Inman K. Performance of statistical approaches to measure the strength of DNA evidence exhibiting possible stochastic effects. Platform presentation, Abstract A143, American Academy of Forensic Sciences, Chicago, February 2011.

9. **Lohmueller KE**, Albrechtsen A, Li Y, Kim SY, Corneliusen T, Vinckenbosch N, Tian G, Huerta-Sanchez E, Feder A, Jiang T, Hellmann I, Pedersen O, Wang J, Nielsen R, and the LuCamp Consortium. Genome-wide patterns of allele frequency variation estimated from low-coverage Illumina sequencing of 2,000 Danish individuals. Platform presentation, Abstract 21, American Society of Human Genetics, Washington, DC, November 2010.

10. **Lohmueller KE,** Rudin N, Inman K. Analysis of allelic drop-out using the IdentiFiler STR multiplex. Poster presentation at the 21st International Symposium on Human Identification, San Antonio, TX, October 2010.

11. **Lohmueller KE,** Rudin N, Inman K. Tools for estimating the weight of DNA evidence for difficult DNA profiles. Platform presentation at the DNA workshop during the California Association of Criminalists meeting, Oakland, CA, October 2010.

12. **Lohmueller KE.** Understanding the persistence of deleterious polymorphisms in natural populations. Seminar at Georgetown University, Washington, DC, October 2009.

13. **Lohmueller KE.** Understanding human demography and its implications for deleterious polymorphism. Seminar at Oxford University, Oxford, UK, February 2009.

14. **Lohmueller KE.** Understanding human demography and its implications for deleterious polymorphism. Seminar at Harvard University, Boston, MA, February 2009.

15. **Lohmueller KE.** Understanding human demography and its implications for deleterious polymorphism. Seminar at the University of California, San Francisco, CA, January 2009.

16. **Lohmueller KE.** Understanding human demography and its implications for deleterious polymorphism. Seminar at the University of California, Berkeley, CA, January 2009.

17. **Lohmueller KE**, Auton A, Bustamante CD, Clark AG. Inference of human demographic parameters using haplotype patterns from genome-wide SNP data. Platform presentation, Abstract 127, American Society of Human Genetics, Philadelphia, PA, 2008.

18. **Lohmueller KE,** Indap AR, Schmidt S, Boyko AR, Hernandez RD, Hubisz MJ, Sninsky JJ, White TJ, Sunyaev SR, Nielsen R, Clark AG, Bustamante CD. "Out-of-Africa" genetic load—Proportionally more deleterious variation in European than in African populations. Platform presentation. Abstract 270, The Biology of Genomes, Cold Spring Harbor, 2007.

19. **Lohmueller KE**, Mauney MM, Reich DE, Braverman JM. Population differentiation among SNPs associated with common disease. Platform presentation, Abstract 150, American Society of Human Genetics, Toronto, 2004.

20. Hirschhorn JN, **Lohmueller KE**, Pearce CL, Pike M, Lander ES. Meta-analysis of genetic association studies supports a role for common variants in common disease risk. Poster presentation, Abstract 1101, American Society of Human Genetics, Baltimore, 2002.