

Brenna M. Henn

Curriculum Vitae

Associate Professor
Department of Anthropology
Genome Center
University of California, Davis

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Academic and Administrative Appointments

Current Position:

Associate Professor (1/2018 – present)
Dept. of Anthropology
Genome Center

UC Davis, Davis CA

Past Positions:

Assistant Professor (1/2013 – 12/2017)
Dept. of Ecology and Evolution
Graduate Program in Genetics
Interdepartmental Doctoral Program in Anthropological Sciences

Stony Brook University (SUNY), Stony Brook NY

EDUCATION AND PROFESSIONAL EXPERIENCE

Education

Postdoc (1/2010-12/2012)
Dept. of Genetics, School of Medicine
Advisor: Dr. Carlos Bustamante

Stanford University, Stanford CA

Ph.D. (9/2003-4/2009)
Dept. of Anthropological Sciences
Committee: Dr. Joanna Mountain, Dr. Richard Klein, Dr. Marcus Feldman
Thesis: Inferring Human Migration Patterns within Africa Using Calibrated Mitochondrial and Y-Chromosome Mutation Rates

Stanford University, Stanford CA

M.S. (9/2002-1/2005, coterminal with B.A.)
Dept. of Anthropological Sciences
Advisor: Dr. Joanna Mountain
Thesis: What Explains the Discrepancy Between Phylogenetic and Pedigree-Based Mitochondrial Mutation Rates?

Stanford University, Stanford CA

B.A. (9/1999-6/2003)
Dept. of Philosophy: *specialization* History and Philosophy of Science

Stanford University, Stanford CA

Other Professional Experience

Ancestry.com, San Francisco CA
Population Genetics Consultant (12/2011-2/2012)
23andMe Inc., Mountain View CA
Scientist, Population Genetics (4/2009-11/2009)
Population Genetics Consultant (4/2007-4/2009)

Research Topics:

Population Genetics, Genomics, Human Evolution, Africa, Genetic Architecture, Genetic Load, Mutation Rates

Personal Statement:

I began my PhD research by studying the deep population structure and complex migration patterns of African hunter-gatherer groups. I continue to be interested in diverse, indigenous populations from around the world who harbor genetic and phenotypic variation that is often overlooked in more commonly studied populations. Motivated by my prior PhD (2009) training in anthropology, I aim to approach questions of human genomic and phenotypic diversity from an interdisciplinary standpoint. My lab uses population genetic and quantitative genetic theory to model processes in human evolution, paired with extensive genomic and phenotypic data from Sub-Saharan African populations. The lab is committed to understanding genetic diversity in under-represented populations and testing the hypothesis that the determinants of phenotypic traits and disease in these populations may be influenced by alleles that are population-specific. We are broadly interested

in refining models of human migration and understanding the adaptive significance of healthy phenotypes such as life history traits, pigmentation, height, and infectious disease resistance. We continue to also focus on the complex demographic history of African populations. In collaboration with African geneticists, we currently work with populations at several field sites in South Africa, Namibia and Ethiopia to collect DNA samples, demographic data and biomedical phenotypes. In January 2018, I joined the Dept. of Anthropology and the Genome Center at UC Davis as an Associate Professor.

GRANTS, HONORS, PROFESSIONAL SERVICE

Honors

- NSF Graduate Research Fellowship Program (GRFP) – Honorable Mention 4/2003
- NSF Research Education for Undergraduates Grant 9905574 6/2002-9/2002

Consortia Membership

- African Genome Variation Project, Wellcome Trust / Sanger Centre
- Human Health and Heredity in Africa, H3Africa Network
- CAAPA

Ongoing External Research Support

Ref #: R35 GM133531-01 [\$1,908,719] **PI:** Brenna Henn **Date:** 09/2019 – 08/2024

Funding Agency: National Institutes of Health (NIH) / NIGMS

Title: MIRA: Improving Inference of Genetic Architecture and Selection with African Genomes

Goal: Generate genomes from Southern Africa to test portability of genetic architecture across populations, especially related to height, pigmentation and evolutionary traits. Characterize unique recombination and mutational patterns in Khoe-San and Himba populations. Advance bioinformatic tools for admixed African populations. Continue community engagement in African cohorts.

Role: PI

Ref #: NA [\$150,000] **PI:** Paul Norman **Date:** 09/2019 – 08/2020

Funding Agency: IHC Health Services / Intermountain Sequencing

Title: Integrating Complex Genomic Architecture with Resistance Phenotypes to Understand Tuberculosis Susceptibility

Goal: Sequence 100 South African genomes to provide a reference panel for GWAS imputation. Perform RNAseq on 25 individuals as part of a TB susceptibility cohort after isolating NK cells and stimulating with *Mycobacterium tuberculosis* (contrast host expression before and after stimulation)

Role: Co-I

Ref #: 2R01HL104608-06 [\$50,000] **PI:** Kathleen Barnes **Date:** 01/2018 – 12/2022

Funding Agency: National Institutes of Health (NIH) / NHLBI

Title: New approaches for empowering studies of asthma in populations of African descent

Goal: Our goal in this renewal is to apply an integrative, multi-omics approach to understand the molecular architecture underlying asthma, building upon the 5-year CAAPA program, where >16,000 asthmatics and non-asthmatics have already been GWAS-genotyped, and GWAS and/or whole genome sequencing (WGS) data are available on more than 100,000 non-CAAPA samples.

Role: Consultant to sequence and curate genomes from African countries for ancestry inference

Ref #: 1753951 [\$31,514] **PI:** Brenna Henn **Date:** 03/2018 – 02/2020

Funding Agency: National Science Foundation

Title: Doctoral Dissertation Research: Epigenetic age estimation in human bone

Goal: Developing forensic epigenomic age estimation tools for diverse populations utilizing bone samples from recently deceased individuals

Role: Advisor to Shyamalika Gopalan (PhD student)

Completed Research Support

Ref #: R01GM118652-01 [\$112,925] **PI:** Sohini Ramachandran **Date:** 06/2016 – 09/2019

Funding Agency: National Institutes of Health (NIH) / NIGMS

Title: Novel statistical methods to localize genomic elements underlying adaptive evolution

Goal: The major goal of this project is to develop a suite of statistical methods for localizing mutations genes, gene sets, and networks undergoing adaptive evolution from genomic data alone.

Role: Co-I to develop and apply new selection methods to human genomic datasets

Ref #: N/A [\$24,500] **PI:** Brenna Henn **Date:** 01/2017 – 09/2018

Funding Agency: Leakey Foundation

Title: Testing for Ancient Population Structure in Southern Africa via Extensive DNA Collection

Goal: Collect 500 DNA samples from the Cederberg Mountains, South Africa to identify cryptic KhoeSan population structure among 'Coloured' populations and model ancient divergence.

Role: PI, principal field researcher

Ref #: P30 AG017253-12 [\$30,000] **PI:** Alan Garber **Date:** 07/2011 -06/2012

Funding Agency: National Institutes of Health (NIH), NIA

Title: Combining Measures of Senescence with Genomic Data for Isolated African Populations

Goal: Assess measures of age using traditional ethnographic techniques for KhoeSan populations in the Kalahari. Use exome data to identify genetic variation in genes relevant to senescence among the eldest of the cohort (between 70-100 years old).

Role: Principal investigator for Seed Grant

Completed Trainee Support

Ref #: 2016-DN-BX-0011 [\$148,959] **PI:** Shyamalika Gopalan **Date:** 08/2016 – 07/2019

Funding Agency: National Institute of Justice (NIJ) / Dept. of Justice

Title: Graduate Research Fellowship in Science, Technology, Engineering and Mathematics

Goal: Developing forensic epigenomic age estimation tools for diverse populations

Role: Advisor to Shyamalika Gopalan (PhD student)

Ref #: 5K12GM102778-03 [\$116,375] **PI:** Jorge Benach **Date:** 08/2012 – 07/2017

Funding Agency: National Institute of Health (NIH)

Title: IRACDA - The New York Consortium for the Advancement of Postdoctoral Scholars

Goal: IRACDA NY-CAPS Program is designed to provide balanced training in research, teaching and professional development for postdoctoral fellows aimed at pursuing highly productive academic careers as scholar-teacher-researchers.

Role: Advisor to Dr. Elizabeth Atkinson (Postdoctoral fellow, awarded 3 years funding)

Ref #: N/A [approx. \$96,000]

PI: Laura R. Botigué

Date: 04/2014 – 08/2016

Funding Agency: Beatriu de Pinós Programme, Spain

Title: Postdoctoral Fellowship

Goal: Estimation of demographic parameters from human genomic data and quantifying purifying selection in African populations

Role: Advisor to Dr. Laura Botigué (Postdoctoral fellow, 2 years full postdoctoral stipend)

Editorial Boards and Peer Review Service

- *Journal Peer Review:* Nature, Science, Nature Genetics, Proceedings of the National Academy of Science, Proceedings of the Royal Society-B, PLoS Genetics, PLoS One, European Journal of Human Genetics, Molecular Biology and Evolution, American Journal of Physical Anthropology, Molecular Ecology, Genome Biology and Evolution, Journal of Human Evolution, International Journal of Epidemiology, Genetics, Current Biology, American Journal of Human Genetics
- *Grant Reviewer:* National Institutes for Health (Early Career Reviewer, GCAT), National Science Foundation, National Geographic Society, Leakey Foundation
- *Invited Guest Editor:* PNAS (2015, 2016)
- *Associate Editor:* Molecular Biology and Evolution (2016 – 2017)

Public Outreach

De Hoop Human Origins Museum (consulting scientist, South Africa), Faces of America (PBS), First Man (Documentary movie: Germany), Quarks & Co (WDR - Germany), By the Light of a Million Fires (Documentary movie: Firestick Productions), The Spittoon (guest blogger)

University Service, Advising, Classes

Courses Taught

UC Davis

- ANT 157L: Advanced Human Genetics Lab: upper division undergraduate computational lab course (in Spring 2020)
- ANT 153: Human Genetics: Mutation and Migration - upper division undergraduate lecture course
- ANT 253: Human Genetics Seminar - graduate student seminar

SUNY Stony Brook

- BEE 690: Seminar in Modern Human Origins and Migrations – graduate student seminar
- BIO 302/ EBH 302: Human Genetics - upper division undergraduate lecture course
- BIO 303/ EBH 370: Advanced Human Genetics Lab - upper division undergraduate / graduate computational lab course
- BGE 510: Graduate Genetics*, 1st year graduate student lecture course [*Partial teaching contribution]

Postdoctoral Fellows

- Austin Reynolds
- Elizabeth Atkinson **completed*
 - *Current position:* Broad Institute & Massachusetts General Hospital, Dr. Mark Daly's Lab, postdoctoral scholar
- Laura R. Botigué **completed*
 - *Current position:* tenure-track Junior Group Leader at the Center for Research in Agricultural Genomics, Barcelona, Spain

Graduate Students

- Natalie Swinford (PhD, Evolutionary Anthropology)
- Dana Al-Hindi (PhD, Evolutionary Anthropology)
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- Shyamalika Gopalan (PhD, Ecology and Evolution, SUNY Stony Brook) **graduated*
 - *Current position:* Postdoc at USC in Human Genetics
- Meng Lin (PhD, Genetics, SUNY Stony Brook) **graduated*
 - *Current position:* Postdoc at USC in Human Genetics
- Caitlin Uren (PhD, Molecular Genetics, *co-supervisor, Stellenbosch University, South Africa) **graduated*
- Rebecca Siford (MA, Ecology and Evolution) **graduated*
 - *Current position:* PhD in Anthropology, Arizona State University
- Evan Sticca (MA, Ecology and Evolution) **graduated*
 - *Current position:* PhD in Human Genetics, Colorado Center for Personalized Medicine, UC Anschutz

Undergraduate Honors

- Cole Williams (BS, Genetics, UC Davis) **graduated*
 - *Current position:* Staff bioinformatician, Colorado Center for Personalized Medicine, UC Anschutz
- Angela Taravella (BA, Anthropology, SUNY Stony Brook) **graduated*
 - *Current position:* PhD in Evolutionary Biology, Arizona State University

Publications and Submitted Manuscripts

* indicates equal authorship contribution

1. GL Wojcik, M Graff, KK Nishimura, R Tao, J Haessler, CR Gignoux, ..., **BM Henn**, ... KE North, U Peters, EE Kenny, CS Carlson. (2019) Genetic analyses of diverse populations improves discovery for complex traits. **Nature**. 570: 514-518.
2. Lin M, Siford RL, Martin AR, Nakagome S, Möller M, Hoal EG, Bustamante CD, Gignoux CR, **Henn BM**. Rapid evolution of a skin-lightening allele in southern African KhoeSan. **Proc Natl Acad Sci** (2018) 115(52):13324-9.
3. M Jobin, H Schurz, **BM Henn**. (2018) IMPUTOR: Phylogenetically Aware Software for Imputation of Errors in Next-Generation Sequencing. **Genome Biology and Evolution**, 10(5): 1248-1254.
4. N Nemat-Gorgani, HG Hilton, **BM Henn**, M Lin, CR Gignoux, JW Myrick, CJ Werely, JM Granka, M Möller, EG Hoal, M Yawata, N Yawata, L Boelen, B Asquith, P Parham, PJ Norman. Different Selected Mechanisms Attenuated the Inhibitory Interaction of KIR2DL1 with C2+ HLA- C in Two Indigenous Human Populations in Southern Africa. (2018) **J of Immun**, 200(8): 2640-2655.
5. **BM Henn**, T Steele, TD Weaver. (2018) Clarifying Distinct Models of Modern Human Origins. **Current Opinion in Genetics and Development**, 53: 146-153.
6. EG Atkinson, AJ Audesse, JA Palacios, DM Bobo, AE Webb, S Ramachandran, **BM Henn**. (2018) No Evidence for Recent Selection at FOXP2 among Diverse Human Populations. **Cell**. 174(6), 1424-1435.
7. LA Sugden, EA Atkinson, S Rong, **BM Henn**, S Ramachandran (2018) Localization of adaptive variants in human genomes using Bayesian one-dependence estimation. **Nature Comm**. 9 (1) 703.
8. AR Martin, M Lin, JM Granka, JW Myrick, X Liu, A Sockell, EG Atkinson, CJ Werely, M Möller, DM Kingsley, EG Hoal, X Liu, MW Feldman, CR Gignoux, CD Bustamante, **BM Henn** (2017) An Unexpectedly Complex Architecture for Skin Pigmentation in Africans. **Cell**. 171 (6), 1340-1353. e14
9. O Carja, JL Maclsaac, SM Mah, **BM Henn**, MS Kobor, MW Feldman, HB Fraser. (2017) Worldwide patterns of epigenetic variation. **Nature Ecol and Evol**. 1 (10) 1577.
10. S Gopalan, O Carja, M Fagny, E Patin, JW Myrick, L McEwen, SM Mah, MS Kobor, A Froment, MW Feldman, L Quintana-Murci, **BM Henn** (2017) Trends in DNA methylation with age replicate across diverse human populations. **Genetics**. 206, 1659-1674.
11. C Uren, M Möller, PVD Helden, **BM Henn**, EG Hoal (2017) Population Structure and Infectious Disease Risk in Southern Africa. **Mol Genet Genomics**: doi 10.1007/s00438-017-1296-2
12. KF McManus, A Taravella, **BM Henn**, CD Bustamante, M Sikora, OE Cornejo (2017) Population Genetic Analysis of the DARC Locus (Duffy) Reveals Adaptation from Standing Variation Associated with Malaria Resistance in Humans. **PLoS Genetics**. e1006560.
13. S Mallick, H Li, M Lipson, I Mathieson, ... **BM Henn**, ... , S Pääbo, J Kelso, N Patterson, D Reich. (2016) The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. **Nature** 538(7624): 201-206.
14. C Uren, M Kim, AR Martin, D Bobo, CR Gignoux, PDv Helden, M Möller, EG Hoal, **BM Henn** (2016) Fine-Scale Human Population Structure in Southern Africa Reflects Ecogeographic Boundaries. **Genetics** 204(1): 303-314.
15. JD Monzón, EG Atkinson, **BM Henn**, JL Benach (2016) Population and evolutionary genomics of *Amblyomma americanum*, an expanding arthropod disease vector. **Genome Biology and Evolution** 8(5): 1351-1360.
16. IJ Wallace, LR Botigué, M Lin, JB Smaers, **BM Henn**, FE Grine (2016) Worldwide variation in hip fracture incidence weakly aligns with genetic divergence between populations. **Osteoporosis International** 27:2867.
17. **BM Henn***, LR Botigué*, S Peishl*, I Dupanloup, M Lipatov, BK Maples, AR Martin, S Musharoff, H Cann, M Snyder, L Excoffier*, JM Kidd*, CD Bustamante* (2016) Feature Article: Distance from Sub-Saharan Africa Predicts Mutational Load in Diverse Human Genomes. **Proc Natl Acad Sci**. 113(4): E440-E449.

18. G Hilton, PJ Norman, N Nemat-Gorgani, A Goyos, JA Hollenbach, **BM Henn**, CR Gignoux, LA Guethlein, P Parham. (2015) Loss and Gain of Natural Killer Cell Receptor Function in an African Hunter-Gatherer Population. **PLoS Genetics** 11(8): e1005439
19. PH Sudmant, S Mallick, BJ Nelson, F Hormozdiari, N Krumm, J Huddleston, BP Coe, C Baker, S Nordenfelt, M Bamshad, LB Jorde, OL Posukh, H Sahakyan, WS Watkins, L Yepiskoposyan, MS Abdullah, CM Bravi, C Capelli, T Hervig, JTS Wee, C Tyler-Smith, GV Driem, IG Romero, A R Jha, S Karachanak-Yankova, D Toncheva, D Comas, **BM Henn**, T Kivisild, A Ruiz-Linares, A Sajantila, E Metspalu, J Parik, R Villems, EB Starikovskaya, G Ayodo, CM Beall, AD Rienzo, MF Hammer, R Khusainova, E Khusnutdinova, W Klitz, C Winkler, D Labuda, M Metspalu, SA Tishkoff, S Dryomov, R Sukernik, N Patterson, D Reich, EE Eichler. (2015) Global diversity, population stratification, and selection of human copy-number variation. **Science** 349(6253): aab3761.
20. **BM Henn**, LR Botigué, CD Bustamante, AG Clark, S Gravel. (2015) Estimating the Mutation Load from Human Genomes. **Nature Reviews Genetics** 16(6): 333-343.
21. I Lazaridis, N Patterson, A Mittnik, G Renaud, ..., **BM Henn**, ..., M Slatkin, S Pääbo, J Kelso, D Reich, J Krause. (2014) Ancient human genomes suggest three ancestral populations for present-day Europeans. **Nature** 503:409-413.
22. AR Martin*, HA Costa*, T Lappalainen, **BM Henn**, JM Kidd, MC Yee, F Grubert, HM Cann, M Snyder, SB Montgomery, CD Bustamante. (2014) Analysis of Diverse Human Transcriptomes Reveals Differentiated Regulatory Architecture. **PLoS Genetics** 10(8): e1004549.
23. JM Kidd*, TJ Sharpton*, D Bobo, PJ Norman, AR Martin, ML Carpenter, M Sikora, CR Gignoux, N Nemat-Gorgani, A Adams, M Guadalupe, X Guo, Q Feng, Y Li, X Liu, P Parham, EG Hoal, MW Feldman, KS Pollard, JD Wall, CD Bustamante, **BM Henn**. (2014) Exome capture from saliva produces high quality genomic and metagenomic data. **BMC Genomics** 15:262.
24. M Sikora, ML Carpenter, A Moreno-Estrada, **BM Henn**, PA Underhill, F Sánchez-Quinto, I Zarac, M Pitzalis, C Sidore, F Busonero, A Maschio, A Angius, C Jones, J Mendoza-Revilla, G Nekhrizovh, D Dimitrovah, N Theodossievi, TT Harkins, A Keller, F Maixner, A Zinkl, G Abecasis, S Sanna, F Cucca, CD Bustamante. (2014) Population genomic analysis of ancient and modern genomes yields new insights into the genetic ancestry of the Tyrolean Iceman and the genetic structure of Europe. **PLoS Genetics** 10(5): e1004353
25. M Daya, LVD Merwe, U Galal, M Moller, M Salie, E Chimusa, JM Galanter, PV Helden, **BM Henn**, CR Gignoux, E Hoal. (2013) A Panel of Ancestry Informative Markers for the Complex Five-Way Admixed South African Coloured Population. **PLoS One** 8(12): e82224
26. ER Chimusa, M Daya, M Möller, Raj Ramesar, **BM Henn**, PD van Helden, NJ Mulder, EG Hoal. (2013) Determining Ancestry Proportions in Complex Admixture Scenarios in South Africa Using a Novel Proxy Ancestry Selection Method. **PLoS One** 8(9): e73971
27. GD Poznik, **BM Henn**, MC Yee, E Sliwerska, GM Euskirchen, AA Lin, M Snyder, L Quintana-Murci, JM Kidd, PA Underhill, CD Bustamante. (2013) Sequencing Y Chromosomes Resolves Discrepancy in Time to Common Ancestor of Males versus Females. **Science** 341(6145): 562-565
28. LR Botigué*, **BM Henn***, S Gravel, BK Maples, CR Gignoux, E Corona, G Atzmon, E Burns, H Ostrer, C Flores, J Bertranpetit, D Comas, CD Bustamante. (2013) Gene flow from North Africa contributes to differential human genetic diversity in Southern Europe. **Proc Natl Acad Sci** 110(29): 11791-6
29. AM Casto, **BM Henn**, JM Kidd, CD Bustamante, MW Feldman. (2013) EDA2R/AR Intergenic Region is the Most Divergent Genomic Segment between Africans and Asians in the Human Genome. **Hum Biol.** 84(6) 641-694
30. **BM Henn**, MW Feldman, LL Cavalli-Sforza (2012) The Great Human Expansion. **Proc Natl Acad Sci.** 109(44): 17758-17764. [Faculty of 1000]
31. J Granka, **BM Henn**, CR Gignoux, JM Kidd, CD Bustamante, MW Feldman. (2012) Limited Evidence for Classic Selective Sweeps in African Populations. **Genetics** 192:1049-1064.
32. **BM Henn***, L Hon*, JM Macpherson, N Eriksson, S Saxonov, I Pe'er, JL Mountain (2012) Cryptic Distant Relatives are Common in both Isolated and Cosmopolitan Genetic Samples. **PLoS One** 7 (4): e34267
33. CL Campbell, PF Palamara, M Dubrovsky, LR Botigué, M Fellous, G Atzmon, C Oddoux, A Pearlman, L Hao, **BM Henn**, E Burns, CD Bustamante, D Comas, E Friedman, I Pe'er, H Ostrer (2012) North African

Jewish and non-Jewish populations form distinctive, orthogonal clusters. **Proc Natl Acad Sci.** 109(34):13865-13870

34. **BM Henn***, L Rodríguez-Botigué*, S Gravel, W Wang, A Brisbin, JK Byrnes, K Fadhlou-Zid, PA Zalloua, A Moreno, J Bertranpetit, CD Bustamante, D Comas (2012) Genomic Ancestry of North Africans Supports Back-to-Africa Migrations. **PLoS Genetics** 8(1): e1002397
35. A Keller, A Graefen, M Ball, M Matzas, V Boisguerin, F Maixner, P Leidinger, R Khairat, A Franke, J Mayer, J Spangler, S McLaughlin, M Shah, C Lee, TT Harkins, A Sartori, A Moreno-Estrada, **BM Henn**, PA Underhill, J Chiaroni, M Sikora, CD Bustamante, EE Vigl, M Samadelli, G Cipollini, J Haas, H Katus, B Meder, N Blin, E Meese, CM Pusch, A Zink. (2012) New Insights into the Tyrolean Iceman's Origin and Phenotype as Inferred by Whole-Genome Sequencing. **Nature Communications** 3:698
36. **BM Henn**, CD Bustamante, JL Mountain, MW Feldman (2011) Reply to Hublin and Klein: Locating a geographic point of dispersion in Africa for contemporary humans. **Proc Natl Acad Sci.** 108(28): E278
37. **BM Henn**, CR Gignoux, M Jobin, JM Granka, JM Macpherson, JM Kidd, L Rodríguez-Botigué, S Ramachandran, L Hon, A Brisbin, AA Lin, PA Underhill, D Comas, KK Kidd, P Parham, PJ Norman, CD Bustamante, JL Mountain, MW Feldman. (2011) *Feature Article*: Hunter-gatherer genomic diversity suggests a southern African origin for modern humans. **Proc Natl Acad Sci.** 108(13): 5154-5162. [Faculty of 1000]
38. S Gravel, **BM Henn**, R Gutenkunst, AR Indap, GT Marth, AG Clark, 1000 Genomes Consortium, CD Bustamante (2011) Demographic history and rare allele sharing among human populations. **Proc Natl Acad Sci.** 108(29): 11983-11988
39. CR Gignoux*, **BM Henn***, JL Mountain (2011) Rapid, global demographic expansions after the origins of agriculture. **Proc Natl Acad Sci.** 108(15): 6044-6049. PMID: 3076817
40. CD Bustamante and **BM Henn** (2010) Human Origins: Shadows of early migrations. **Nature** 468(7327): 1044-1045. PMID: 21179156
41. **BM Henn**, S Gravel, A Moreno-Estrada, S Acevedo, CD Bustamante. (2010) Fine-scale population structure and the era of next-generation sequencing. **Hum Mol Genet.** 19(2): R221-R226. PMID: 2953744
42. J Chiaroni, RJ King, NM Myres, **BM Henn**, A Ducourneau, MJ Mitchell, G Boetsch, I Sheikha, AA Lin, M Nik-Ahd, J Ahmad, F Lattanzi, RJ Herrera, ME Ibrahim, A Brody, O Semino, T Kivisild and PA Underhill. (2009) The emergence of Y-chromosome haplogroup J1e among Arabic-speaking populations. **Eur J Hum Genet.** 18(3): 348-53. PMID: 2987219
43. **BM Henn**, CR Gignoux, MW Feldman and JL Mountain. (2009) Characterizing the time-dependency of human mitochondrial DNA mutation rate estimates. **Mol Biol Evol.** 26(1): 217-230. PMID: 18984905
44. **BM Henn**, C Gignoux, AA Lin, PJ Oefner, P Shen, R Scozzari, F Cruciani, SA Tishkoff, JL Mountain and PA Underhill. (2008) Y-chromosomal evidence of a pastoralist migration through Tanzania to southern Africa. **Proc Natl Acad Sci.** 105(31): 10692-10297. PMID: 2504844
45. SA Tishkoff, MK Gonder, **BM Henn**, H Mortensen, A Knight, C Gignoux, N Fernandopulle, G Lema, TB Nyambo, U Ramakrishnan, FA Reed, and JL Mountain (2007) History of click-speaking populations of Africa inferred from mtDNA and Y chromosome genetic variation. **Mol Biol Evol.** 24(10): 2180-2192. PMID: 17656633
46. A Knight, PA Underhill, HM Mortensen, LA Zhivotovsky, AA Lin, **BM Henn**, D Louis, M Ruhlen, and JL Mountain (2003) African Y chromosome and mtDNA divergence provides insight into the history of click languages. **Current Biol.** 13(6): 464-473. PMID: 12646128