Dr Krishna R. Veeramah

Contact Information

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Research Interests

Human and non-human population genetics, paleogenomics, genomics methods development, approximate bayesian computation, three-spined stickleback evolutionary genomics, epigenetic ageing.

Education

University College London, London, UK

Ph.D. Human Genetics, Department of Genetics, Environment and Evolution, 2008

- Dissertation Topic: "An Investigation into the Distribution of Human Molecular Genetic Variation in sub-Saharan Africa"
- Advisor: Professor Mark G. Thomas

B.Sc. Human Genetics, 1st class, 2003

Academic Positions

Stony Brook University, Stony Brook, NY USA
Associate Professor **2020 - present**
Department of Ecology and Evolution

Assistant Professor **2014 - 2019**
Department of Ecology and Evolution

New York Genome Center, Stony Brook, NY USA
Affiliate faculty **2018 - present**

University of Arizona, Tucson, NY USA
Postdoctoral Research Assistant **2010 - 2013**
Michael Hammer Laboratory

University of California, Los Angeles, Los Angeles, CA USA
Postdoctoral Fellow **2008 - 2010**
John Novembre Laboratory, Department of History and Center for Society and Genetics

University College London, London, UK
Interim Lecturer **2007 - 2008**
Human Evolutionary Genetics, Department of Genetics, Environment and Evolution

Grants

HistoGenes: Integrating genetic, archaeological and historical perspectives on Eastern Central Europe, 400-900 CE. European Research Council Synergy Grant, value $1,251,928 awarded to SBU (co I. with P.I.s Professor Patrick Geary's, Walter Pohl, Tividar Vida & Johannes Krause, total grant $11,000,000) (2019)

Integrating Epigenomics with Life Stress Measurement to Predict Accelerated Aging. Stony Brook OVPR Seed Grant, value $65,000 (co I. with Dr Stacey Scott, PI, and Dr Kristin Bernard) (2019)

Postdoctoral Position In Ancient DNA. Institute for Advanced Study Research Grant, value $127,200 (2018)

Dynamics of Contemporary Genomic Evolution in Replicate Threespine Stickleback Populations. NIH R01, value $1,562,290 (2017)

Validating De Novo Mutations in a Whole Genome Sequenced Gibbon Quartet. Leakey Foundation, value $8,463 (2015)

Inferring Biological Relatedness And Genomic Ancestry Using 2nd Generation Sequencing. NSF Archaeology, value $100,646 (co P.I. with Professor Patrick Geary, Institute for Advanced Study, Princeton) (2015)

Identifying modifier genes in patients with SCN1A haploinsufficiency using whole exome sequencing. Dravet Syndrome Foundation grants, value $185,000 (co P.I. with Professor Michael Hammer, University of Arizona) (2013)

Tracing Longboard Migration through DNA Analysis. UCLA Transdisciplinary Seed Grant, value $24,100 (co P.I. with Professor Patrick Geary, Institute for Advanced Study, Princeton and Professor Robert Wayne, UCLA) (2011)

Wenner Gren Conference and Workshop Grants, value $10,000 (co P.I. with Dr Omer Gokcumen, Buffalo) (2009)

Other Honors and Awards

UCL Biology Postgraduate Symposium Poster Prize (2005)

BBSRC CASE PhD Studentship (2003)

University College London Biology Dean's list (2003)

Teaching Experience

Stony Brook University

Courses

EBH 380: Genomics (Fall 2015, 2016, 2017, 2018, 2019, 2020, 2021) - first six years co-taught with Jesse Hollister

EBH 381: Genomics Laboratory (Spring 2016, 2018, 2020, 2022, 2023) - first three years co-taught with Jesse Hollister

EBH 370: Advanced Human Genetics (Spring 2016, 2017, 2021) - first two years co-taught with Brenna Henn

BIO 367: Molecular Diversity Laboratory (Spring 2017, Spring 2019)

BEE 551: Principles of Evolution (Fall 2022, 2023) - co-taught with Tara Smiley

BEE 554: Population Genetics (Spring 2024)

BEE 690: Applications, Advances and Analysis in Ancient DNA - Graduate seminar (Spring 2015)

BEE 690: Current Trends and Practices in Speciation Genomics - Graduate seminar (Spring 2018)

BEE 690: Machine Learning Methods In Population Genomics - Graduate seminar (Spring 2021)

Guest lectures

BGE 510: Graduate Genetics - One guest lecture on Population Genetics (Spring 2018).

ANP 250: Forensic Anthropology - One guest lecture on DNA in Forensics (Fall 2018).

BEE 551: Principles of Evolution - Two guest lecture on next generation sequencing and Paleogenomics (Fall 2014, 2016).

BEE 569: Bayesian Data Analysis and Computation - One guest lecture on Approximate Bayesian Computation (Fall 2014).

Other Universities

Fundamentals of Molecular Biology (2nd Yr BSc Biology, UCL): Guest lectures (2007) Reproduction, Genetics and Development (2nd Yr Medicine, UCL): Guest lecture (2008)

Molecular Evolution (3rd Yr BSc Biology, UCL): Guest lecture (2008)

Languages, Genetics and Archaeology (MA/MSc Archaeology, UCL): Guest lecture (2008)

Using Genetics to Infer History (Upper Division Undergraduates, UCLA): Developed and taught course (2009-2010)

Cuisine, Nutrition and Genetics (Upper Division Undergraduates, UCLA): Guest lectures (2009)

Quantitative Biology Seminar, Next Generation Sequencing (Mathematics Graduate Students, UofA): Guest lecture (2012)

STUDENTS AND POSTDOCTORAL FELLOWS

Postdoctoral Advisor

Misha Lipatov (2015-2016)

Carlos Eduardo G. Amorim (2017-2018)

Deven Vyas (2018-present)

Kerry Reid (2019-2021)

Rachael Herman (2023-present)

PhD Advisor

Tian Yijie - E&E (2019-present)

Alexander Kwakye - Genetics (2021-present)

Sarah Vaccaro - E&E (2022-present)

Thomas Bertino - E&E (2023-present)

Taylor Medwig - Genetics rotations student (2016)

Shruti Iyer - Genetics rotations student (2017)

Samantha Henry - Genetics rotations student (2019)

Luiz Machado - Genetics rotations student (2021)

Masters Advisor

Jeffrey Gaillard (2020-present)

Matthew Dambrosio (2018-2019)

Matthew Marano (2018-2019)

Wei Jiang (2015-2016)

Giulia Bagarolo (visiting from University Ferrara) (2015)

PhD Student Committee Member:

Elise Lauterbur (E&E, Graduated)

Shyamalika Gopalan (E&E, Graduated)

Dave Carlson (E&E, Graduated)

Paul Donat (E&E)

Rachel Herman (E&E)
Anna McPherran (E&E, Graduated with MA)
Alejandro Gil Gomez (E&E)
William Thomas (E&E)
Alexandra Pamfilie (E&E)
Shruti Iyer (Genetics, Graduated)

Undergraduate Lab supervisor
Jonathon Gaige (Spring 2018, URECA award Summer 2018)
Mark Milhaven (Spring/Summer/Fall 2018)
Zain Khan (Spring 2018)
James Ancona (Spring 2018)
Priya Chohan (Fall 2018, Spring/Summer 2019)
Hillary Babalola (Fall 2018, Spring/Summer/Fall 2019)
Thomas Bertino (Fall 2018, Spring 2019, URECA award Summer 2019, now PhD Student)
Jared Mallozi (Summer/Fall 2019)
Guancheng Zeng (Fall 2019 - Spring 2021)
Abu Nafi (Fall 2019)
Jacqueline Ryan (Fall 2019)
Alexsandra Hernandez (Fall 2019)
Mariana Escobar Rodriguez (Fall 2020, Spring 2021)
Sarah Vaccaro (Fall 2020, Spring 2021, URECA award Summer 2021)
Hannah Oliver (Spring 2021)
Natalie Dzikowski (Spring 2021-Spring 2022, Lab Manager 2023)
Natalie Sokolow (Spring 2022-Summer 2023)
Arda Sinan Ates (Spring 2021-Fall 2023)
Julia Chivu (Spring 2022-Fall 2023
Vamsi Adabala (Spring 2022-Fall 2023)
Alina Feng (Spring 2022-Fall 2023)

PUBLICATIONS

Herman, R.W, Clucas, G, Younger, J, Bates J, Robinson B, Reddy S, Stepanuk, J, O'Brien, K, **Veeramah, K.R** & Lynch, H. Whole genome sequencing reveals stepping-stone dispersal buffered against founder effects in a range expanding seabird. (2024). Molecular Ecology.e17282

Escobar-Rodríguez, M. & **Veeramah, K.R**. Evaluation of ancient DNA imputation: a simulation study. (2024) Human Population Genetics and Genomics. 4(1):0002

Zavala, D.V, Dzikowski, N, Gopalan, S, Harrington, K, Pasquini, G, Mogle, J, Reid, K, Sliwinski, Graham-Engeland, J, Engelend, C.G, Bernard, K, **Veeramah, K.R** & Scott, S.B. *Epigenetic and chronological age: Associations with cognitive performance in daily life.* Journal of Gerontology: Biological Sciences (2023) The Journals of Gerontology, Series A: Biological Sciences and Medical Sciences. Online ahead of print.

Garcia-Olivares, V, Munoz-Barrera, Rubio-Roriguez, L.A, Jaspez, D, Diaz-de Usera, A, Inigo-Campos, A, **Veeramah, K.R** Alonso, S, Thomas, M.G, Lorenzo-Salazar, J.M, Gonzalez-Montelongo, R, & Flores, C. *Benchmarking of Human Y-chromosomal haplogroup classifiers with whole-genome* *and whole-exome sequence data.* (2023) Computational and Structural Biotechnology Journal. September 14

Vyas, DN, Koncz, I, Modi, A, Mende, BG, Tian, Y, Francalacci, P, Lari, M, Vai, S, Straub, P, Gallina, Z, Szeniczey, T, Hajdu, T, Pejrani Barrico, L, Giostra, C, Radzeviciute, R, Hofmanova, Z, Evinger, S, Bernert, Z, Pohl, W, Caramelli, D, Vida, T, Geary PJ, & **Veeramah, K.R**, Fine-scale sampling uncovers the complexity of migrations in 5th–6th century Pannonia. (2023) Current Biology (in press, available online)

Bird, N, Ormond, L, Awah, P, Caldwell, EF, Connell, B, Elamin, M, Fadlelmola, FM, Fomine, FLM, López, S, MacEachern, S, Moñino, Y, Morris, S, Näsänen-Gilmore, P, Nketsia, N, **Veeramah, K.R**, Weale, ME, Zeitlyn, D, Thomas, M.G. Bradman, N & Hellenthal G. *Dense sampling of ethnic groups within African countries reveals fine-scale genetic structure and extensive historical admixture.* (2023) Science Advances. 9(13)

Aguirre, WE, Reid, K, Rivera, J, Heins DC, **Veeramah, K.R** & Bell, MA.*Freshwater Colonization, Adaptation, and Genomic Divergence in Threespine Stickleback.* (2022) Integrative and Comparative Biology, 62:2:388-405

Olaechea-Lázaro, S, Garcia, O, González-Montelongo, R, Lorenzo-Salazar, J.M, Flores, C, Lopez, S, **Veeramah, K.R**, Hellenthal, G, Thomas, M.G & Alonso, S. *Complete mitogenome in a population sample from Cameroon.* (2021) Forensic Science International: Genetics. 55:102597

Min, K, Jannace, T.F, Si, H, **Veeramah, K.R**, Haley, J.D, & Konopka, J.B. *Integrative multi-omics profiling reveals cAMP-independent mechanisms regulating hyphal morphogenesis in Candida albicans.* (2021) Plos Pathogens. 17(8):e1009861.

Roberts Kingman, G.A, Vyas. D.N, Jones, F.C, Brady, S.D, Chen, H.I, Reid, K, Milhaven, M, Bertino, T.S, Aguirre, W.E, Heins, D.C, von Hippel, F.A, Park, P.J, Kirch, M. Absher, D.M Myers, R.M, Di Palma, F, Bell, M.A. Kingsley, D.M & **Veeramah, K.R**. *Predicting future from past: The genomic basis of recurrent and rapid stickleback evolution.* (2021) Science Advances. 7(25):eabg5285

Žegarac, A, Winkelbach, L, Blöcher, J, Diekmann, Y, Gavrilović, M.K, Porčić, M, Stojković, B, Milašinović, L, Schreiber, M, Wegmann, D, **Veeramah, K.R**, K.R, Stefanović, S & Burger, J. *Kinship, acquired and inherited status, and population structure at the Early Bronze Age Mokrin necropolis in northern Serbia.* (2021) Scientific Reports. 11(1):10072

Reid, K, Bell, M.A, & **Veeramah, K.R**. *Threespine Stickleback: A Model System For Evolutionary Genomics.*(2021) Annual Reviews of Genomics and Human Genetics. 22:357-383

Burger, J, Link, V, Blocher, J, Schulz, A, Sell, C, Pochon, Z, Diekmann, Y, Zegarac, A, Hofmanova, Z, Winkelback, L, Reyna-Blanco, C.S, Bieker, V, Orschiedt, J, Brinker, U, Scheu, A, Leuenberge, C, Bertino, T, Bollongino, R, Lidke, G, Stefanovic, S, Jantzen, D, Kaiser, E, Terberger, T, Thomas, M.G, **Veeramah, K.R** & Wegman, L. *Low Prevalence of Lactase Persistence in Bronze Age Europe Indicates Ongoing Strong Selection over the Last 3,000 Years.*(2020) Current Biology. 30 1-0

Okhovat, M, Nevonen, K.A, Davis, B.A, Michener, P, Ward, S, Milhaven, M, Harshman, L, Sohota, A, Fernandes, J.D, Salama, S.R, O'Neill. R.J, Ahituv, N, **Veeramah, K.R** & Carbone, L. *Co-option of the lineage-specific LAVA retrotransposon in the gibbon genome.*(2020) PNAS. 117 (32) 19328-19338

Lipson, M, Ribot, I, Mallick, S, Rohland, N, Olalde, I, Adamski, N, Broomandkhoshbacht, N, Lawson, A, López, S, Oppenheimer, J, Stewardson, K, Neba'ane Asombang, R, Bocherens, H, Bradman, N, Culleton, B.J, Cornelissen, E, Crevecoeur, I, de Maret, P, Fomine, F.L.M, Lavachery, P, Mbida Mindzie, C, Orban, R, Sawchuk, E, Semal, P, Thomas, M.G, Van Neer, W, **Veeramah, K.R**, Kennett, D.J, Patterson, N, Hellenthal, G, Lalueza-Fox, C, MacEachern, S, Prendergast, M.E & Reich, D. *Ancient West African foragers in the context of African population history.*(2020) Nature. 577(7792):665-670

Vai, S, Brunelli, A, Modi, Tassi, F, Vergata, C, Pilli, E, Lari, M, Susca, R.R, Giostra, C, Pejrani Baricco, L, Bedini, E, Koncz, I, Vidar, T, Mende, B.G, Winger, D, Loskotova, Z, **Veeramah, K.R**, Geary, P, Barbujani, G, Caramelli, D & Ghirotto, S. *A genetic perspective on Longobard-Era migrations.*(2019) Eur J Hum Genet. 27(4):647-656

Veeramah, K.R. *Primate Paleogenomics.* (2018) Paleogenomics. ed. Lindqvist, C. Population Genomics Series. Springer International Publishing

Veeramah, K.R. *The importance of fine-scale studies for integrating paleogenomics and archaeology.* (2018) Curr Opin Genetics Dev. 53:83-89

Amorim, C.E.G, Vai, S, Posth, C, Modi, A, Koncz, I, Hakenbeck, S, La Rocca, M.C, Mende, B, Bobo, D, Pohl, W, Pejrani Baricco, L, Bedini, E, Francalacci, P, Giostra, C, Vida, T, Winger, D, von Freeden, U, Ghirotto, S, Lari, M, Barbujani, G, Krause, J, Caramelli, D, Geary, P.J & **Veeramah, K.R**. *Understanding 6th-Century Barbarian Social Organization and Migration through Paleogenomics.* (2018) Nature Communications. 9:3547

Woerner, A.E, **Veeramah, K.R**, Watkins, J.C & Hammer, M.F. *The role of phylogenetically conserved elements in shaping patterns of human genomic diversity.* (2018) Mol Biol Evol. 35(9): 2284-2295

Pendleton, A.L, Shen, F, Taravella, A.M, Emery, S, **Veeramah, K.R**, Boyko, A.R & Kidd, J.M. *Comparison of village dog and wolf genomes highlights the role of the neural crest in dog domestication.* (2018) BMC Biology. 16:64

Oetjens, M.T, Martin, A, **Veeramah, K.R** & Kidd, J. *Analysis of the canid Y-chromosome phylogeny using short-read sequencing data reveals the presence of distinct haplogroups among Neolithic European dogs.* (2018) BMC Genomics. 19:350

Veeramah, K.R, Rott, A, Großc, M, van Dorp, L, López, S, Kirsanow, K, Sell, C, Blöcher, J, Wegmann, D, Link, V, Hofmanová, Z, Peters, J, Trautmann, B, Gairhosj, A, Haberstroh, J, Päffgen, B, Hellenthal, G, Haas-Gebhard, B, Harbeck M & Burger, J. *Population genomic analysis of elongated skulls reveals extensive female-biased immigration in Early Medieval Bavaria.* (2018) Proc Natl Acad Sci. 115(13):3494-3499

Botigue, L, Song, S, Scheu, A, Gopalan, S, Pendleton, A, Oetjens, M, Taravella, A, Seregély, T, Zeeb-Lanz, A, Arbogast, R.M, Bobo, D, Daly, K, Unterländer, M, Burger, J, Kidd, J & **Veeramah, K.R**. *Ancient European dog genomes reveal continuity since the early Neolithic.* (2017) Nature Communications. 8:16082

Geary, P, **Veeramah, K.R**. Mapping European population movement through genomic research. (2016) Medieval Worlds. 4:65-78

Broushaki, F, Thomas, M.G, Link, V, López S, van Dorp, L, Kirsanow, K, Hofmanová, Z, Diekmann, Y, Cassidy, L.M, Díez-Del-Molino, D, Kousathanas, A, Sell, C, Robson, H.K, Martiniano, R, Blöcher, J, Scheu, A, Kreutzer, S, Bollongino, R, Bobo, D, Davudi, H, Munoz, O, Currat, M, Abdi, K, Biglari, F, Craig, O.E, Bradley, D.G, Shennan S, **Veeramah, K.R**, Mashkour, M, Wegmann, D, Hellenthal, G, Burger, J. *Early Neolithic genomes from the eastern Fertile Crescent.* (2016) Science. 353(6298):499-503

Hofmanová, Z, Kreutzer S, Hellenthal, G, Sell, C, Diekmann, Y, Díez-Del-Molino, D, van Dorp, L, López S, Kousathanas, A, Link, V, Kirsanow, K, Cassidy, L.M, Martiniano, R, Strobel, M, Scheu, A, Kotsakis, K, Halstead, P, Triantaphyllou, S, Kyparissi-Apostolika, N, Urem-Kotsou, D, Ziota, C, Adaktylou, F, Gopalan, S, Bobo, D.M, Winkelbach, L, Blöcher, J, Unterländer, M, Leuenberger, C, Çilingirolu, Ç, Horejs, B, Gerritsen, F, Shennan, S.J, Bradley, D.G, Currat, M, **Veeramah, K.R**, Wegmann, D, Thomas, M.G, Papageorgopoulou, C, Burger, J. *Early farmers from across Europe directly descended from Neolithic Aegeans.* (2016) Proc Natl Acad Sci. 113(25):6886-6891

Hsieh, P, **Veeramah, K.R**, Lachance, J, Tishkoff, S.A, Wall, J.D, Hammer, M.F, Gutenkunst, R.N. *Whole genome sequence analyses of Western Central African Pygmy hunter-gatherers reveal a complex demographic history and identify candidate genes under positive natural selection.* (2016) Genome Res. 26(3):279-90

Stevison, L, Woerner, A, Kidd, J, Kelley J, **Veeramah, K.R**, McManus, K, Bustamante, C, Hammer, M.F, Wall, J. *The Time-Scale Of Recombination Rate Evolution In Great Apes.* (2016) Mol Biol Evol. 33(4):928-945

Nam, K, Munch, K, Holboth, A, Dutheil, J.Y, **Veeramah, K.R**, Woerner, A.E, Hammer, M.F, Great Ape Genome Diversity Project, Mailund, T & Schierup M.H. *Extreme selective sweeps independently targeted the X chromosomes of the great apes.* (2015) Proc Natl Acad Sci. 112(20):6413-6418

Veeramah, K.R, Woerner A.E, Johnstone, L, Gut, I, Gut, M, Marques-Bonet, T, Carbone, L, Wall, J.D & Hammer, M.F. *Examining Phylogenetic Relationships Among Gibbon Genera Using Whole Genome Sequence Data Using an Approximate Bayesian Computation Approach.* (2015) Genetics. 200(1):295-308

Karmin, M, ...83 other authors... **Veeramah, K.R**, Bradman, N, Hammer, M.H, Osipova, L.P, Balanovsky, O, Khusnutdinova, E,K, Johnsen, K, Remm, M, Thomas, M.G, Tyler-Smith, C, Underhill, P.A, Willerslev, E, Nielsen, R, Metspalu, M, Villems and, R & Kivisild, T. *A recent bottleneck of Y chromosome diversity coincides with a global change in culture.* (2015) Genome Res. 25(4):459-466

Vai, S, Ghirotto, S, Pilli, S, Tassi, F, Lari, M, Rizzi. E, Mata-Lalueza, L, Ramirez, O, Lalueza-Fox, C, Achilli, A, Olivieri, A, Torroni, A, Lanciono, H, Giostra, C, Bedini, E, Baricco, L.P, Matullo, G, Di Gaetano, C, Piazza, A, **Veeramah, K.R**, Geary, P, Caramelli & D, Barbujani, G. *Genealogical relationships between early medieval and modern inhabitants of Piedmont.* (2015) PLoS ONE. 10(1):e0116801

Karafet, T.M, Bulayeva, K.B, Bulayev, O.A, Gurgenova, F, Omarova, J, Yepiskoposyan, L, Savina, O.V, **Veeramah, K.R** & Hammer, M.F. *Extensive genome-wide autozygosity in the population isolates of Daghestan.* (2015) Eur J Hum Genet. 23(10):1405-1412.

McManus, K.F, Kelley, J.L, Song, S, **Veeramah, K.R**, Woerner, A.E, Stevison, L.S, Ryder, O.A, Kidd, J.M, Wall, J.D, Bustamante, C.D & Hammer, M.F. *Inference of Gorilla demographic and selective history from whole genome sequence data.* (2015) Mol Biol Evol. 32(3):600-12.

Mendez, F.L, **Veeramah, K.R**, Thomas, M.G, Karafet, T.M & Hammer, M.F. *Reply to "The 'extremely ancient' chromosome that isn't" by Elhaik et al.* (2015) Eur J Hum Genet. 23(5):567-568.

Carbone, L, Harris, R.A, Gnerre, S, **Veeramah, K.R**, ...78 other authors... Hammer, M.F, Marques-Bonet, T, Eichler, E.E, Fulton, L, Fronick, C, Muzny, D.M, Warren, W.C,Worley, K.C, Rogers, J, Wilson R.K & Gibbs, R.A. *Gibbon genome and the fast karyotype evolution of small apes.* (2014) Nature. 513 (7517):195-201.

Veeramah, K.R & Novembre J. *Demographic Events And Evolutionary Forces That Have Shaped European Genetic Diversity.* (2014) Cold Spring Harb Perspect Biol. 6(9):a008516.

Veeramah, K.R, Gutenkunst, N.R, Woerner, A.E, Watkins, J.C & Hammer, M.F. *Evidence for increased levels of positive and negative selection on the X chromosome versus autosomes in humans.* (2014) Mol Biol Evol. 31(9):2267-82.

Veeramah, K.R & Hammer, M.F. *The Impact of Whole Genome Sequencing on the Reconstruction of Human Population History.* (2014) Nat Rev Genet. 15(3):149-62

Yang, Y, Vasylyev D, Dib-hajj, F, **Veeramah, K.R**, Hammer, M.F, Dib-Hajj, S & Waxman, S. *Multi-state structural modeling and voltage-clamp analysis of epilepsy/autism mutation Kv10.2-R327H demonstrate the role of this residue in stabilizing the channel closed state.* (2013) J Neurosci. 33(42):16586-93.

Prado-Martinez, J, Sudmant, P.H, Kidd, J.M, Li, H, Kelley, J.L, Lorente-Galdos, B, **Veeramah, K.R**, ...64 other authors... Wall, J, Bustamante, C.D, Hammer, M.F, Eichler, E.E & Marques-Bonet, T. *Great ape genome diversity.* (2013) Nature 499(7459):471-5

Veeramah, K.R, Karafet, T.M, Wolf, D, Sampson, R & Hammer, M.F. *The KCNJ8-S422L variant previously associated with J-wave syndromes is found at an increased frequency in Ashkenazi Jews.* (2013) Eur J Hum Genet. 22(1):94-8

Veeramah, K.R, Johnstone, J, Karafet, T.M, Wolf, D, Sprissler, R, Salogiannis, J, Barth-Maron, A, Greenberg, M.E, Pazzi, M, Restifo, L.L, Talwar, D, Erickson, R.P & Hammer, M.F. *Exome sequencing reveals new causal mutations in children with severe epilepsies.* (2013) Epilepsia. 54(7):1270-81

Mendez, F.L, Krahn, T, Schrack, B, Krahn, A, **Veeramah, K.R**, Woerner, A.E, Fomine, F.L.M, Bradman, N, Thomas, M.G, Karafet, T.M & Hammer, M.F. *A divergent African American Y chromosome points to deep population structure in Central Africa.* (2013) Am J Hum Genet. 92(3):454-9.

Thompson, S.R, Humphries, S.E, Thomas M.G, Ekong, R, Tarekegn, A, Bekele, E, Creemer, O, Bradman, N & **Veeramah, K.R**. *The frequency of an IL-18-associated haplotype in Africans.* (2013) Eur J Hum Genet. 21(4):465-8

Veeramah, K.R, O'Brien, J.E, Meisler, M.H, Cheng, X, Dib-hajj, S.D, Waxman, S.G, Talwar, D, Girirajan, S, Eichler, E.E, Restifo, L.L, Erikson, R.P & Hammer, M.F. *De Novo Pathogenic SCN8A Mutation Identified by Whole-Genome Sequencing of a Family Quartet Affected by Infantile Epileptic Encephalopathy and SUDEP.* (2012) Am J Hum Genet. 90(3):502-510

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Wegmann, D, Kessner, D, **Veeramah, K.R**, Mathias, R.A, Nicolae, D.L, Yanel, LR,Sun, Y.V, Torgerson, D.G, Rafaels, N, Rucinski, I, Becker, L.C, Ruczinski, I, Beaty, T.H, Kardia, S.L.R, Meyers, D, Barnes, K.C, Becker, D.M, Freimer & N, Novembre, J. *Recombination rates in admixed* *individuals identified by ancestry-based inference.* (2011) Nat Genet. 43(9):847-53

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Beall, C.M, Cavalleri, G.L, Deng, L, Elston, R.C, Gao, Y, Knight, J, Li, C, Li, J.C, Liang, Y, McCormack, M, Montgomery, H.E, Pan, H, Robbins, P.A, Shianna, K.V, Tam, S.C, Tsering, N, **Veeramah, K.R**, Wang, W, Wangdui, P, Weale, M.E, Xu, Y, Xu, Z, Yang, L, Zaman, M.J, Zeng, C, Zhang, L, Zhang, X, Zhaxi, P & Zheng, Y.T. *Natural selection on EPAS1 (HIF2) associated with low hemoglobin concentration in Tibetan highlanders.* (2010) Proc Natl Acad Sci. 107(25):11459-64

Veeramah, K.R, Connell, B.A, Pour, N.A, Plaster, C, Powell, A, Zeitlyn, D, Mendell, N.R, Weale, M.E, Bradman, N & Thomas, M.G. *Little genetic differentiation as assessed by uniparental markers in the presence of substantial language variation in peoples of the Cross River region of Nigeria.* (2010) BMC Evol Biol. 10:92

Veeramah, K.R, Thomas, M.G, Weale, M.E, Mendell, N.R, Shephard, E.A, Bradman, N &Philips, I.R. *The potentially deleterious functional variant, FMO2*1, is at high frequency throughout sub-Saharan Africa.* (2008) Pharmacogenet Genomics. 18(10): 877-886

Veeramah, K.R, Zeitlyn, D, Fanso, V.G, Mendell, N.R, Connell, B.A, Weale, M.E, Bradman, N & Thomas, M.G. *Sex-Specific Genetic Data Supports One of Two Alternative Versions of the foundation of the ruling dynasty of the Nso' in Cameroon.* (2008) Curr Anthropol. 49:707-714

PREPRINTS

Veeramah, K.R, Brud, E & Eanes, W.F. *Florida Drosophila melanogaster genomes sampled 13 years apart show increases in warm-associated SNP alleles.* bioRxiv: https://doi.org/10.1101/2020.10.23.352732

Link, V, Kousathanas, A, **Veeramah, K.R**, Sell, C, Scheu, A & Wegmann, D *ATLAS: Analysis Tools for Low-depth and Ancient Samples.*bioRxiv: https://doi.org/10.1101/105346

Lipatov, M, Sanjeev, K, Patro & **Veeramah, K.R**. *Maximum Likelihood Estimation of Biological Relatedness from Low Coverage Sequencing Data.* bioRxiv: https://doi.org/10.1101/023374

INVITED PRESENTATIONS

Using hundreds of ancient genomes to understand the formation of Europe after the fall of the Roman Empire, Stony Brook Living World Lecture series, Stony Brook, NY (Nov 2022)

The Challenge of Generating and evaluating 4000 genomes from the Carpathian Basin, EHL Seminar, Princeton University, Princeton, NJ (Oct 2022)

Comparing and contrasting local genetic structure amongst densely sampled early medieval cemeteries,EMBO: EMBL Symposium Reconstructing the human past: using ancient and modern genomics, Heidelberg, Germany (Virtual due to illness) (Oct 2022)

A Fine-Scale Paleogenomic Analysis Of An Early Medieval Multigenerational Cemetery, UCONN SBU Archaeology Seminar Series, Zoom (Oct 2021)

Paleogenomics at Fine-Scales, Science in Archaeology Seminar Series, Mainz, Germany (Mar 2020)

Methods of Population Genetics, Presentation of ERC Synergy Grant, University of Vienna, Austria (Feb 2020)

The Rapid Genomic Evolution of Three-spined Stickleback, Program in Evolution, Ecology and

Conversation Biology seminar series, University of Illinois, Illinois (Oct 2019)

The Paleogenomics of Medieval Barbarians: Integrating ancient DNA with archaeology and history. The New York Regional Primatology Colloquium Series, New York, NY (Apr 2019)

The Paleogenomics of Medieval Barbarians: Integrating ancient DNA with archaeology and history. UC Davis Department of Anthropology Seminar, Davis CA (Apr 2019)

The Paleogenomics of Medieval Barbarians: Integrating ancient DNA with archaeology and history. Frontiers in Genomics 2018 series of seminars from the National University of México (UNAM), Campus Morelos (Oct 2018)

Using Paleogenomics To Illuminate The European Migration Period, IEMA Conference on Migration and Mobility, SUNY-Buffalo (Apr 2018)

Paleogenomics and the migration of Lombards. American Historical Association, Washington DC (Jan 2018)

Using ancient DNA to understand the wolf in your living room. Rhode Island University, RI (Nov 2017)

Ancient European Dog Genomes Reveal Continuity Since the Early Neolithic. Stony Brook University Paleobiology Seminar, NY (Oct 2017)

Ancient European Dog Genomes Reveal Continuity Since the Early Neolithic. Stony Brook University Libraries Presents: STEM Speakers Series, NY (Oct 2017)

Using ancient DNA to understand the wolf in your living room. Stony Brook Living Worlds, NY (Oct 2017)

Ancient European Dog Genomes Reveal Continuity Since the Early Neolithic. Bard College Biology Seminar, NY (Sept 2017)

The Lombards: A Framework for Integrating History, Archaeology, and Genomics. American Historical Association, Denver, USA (Jan 2017)

Ancient European dog genomes reveal continuity since the early Neolithic. CUNY Biology Department Seminar, NY (Dec 2016)

Understanding Medieval European Populations through Paleogenomics. EEB Seminar, University of Buffalo, NY (Dec 2015)

Using 2nd Generation Sequencing data to model the demographic history of European populations from the Migration Period. Genetic History: A Challenge to Historical and Archaeological Studies, Humboldt University, Berlin, Germany (Oct 2015)

Gibbon Origins and the Hominoid Slowdown. Biological Anthropology Seminar, Yale, (Jan 2015)

Contrasting the Impact of Natural Selection on the X chromosome and Autosomes amongst Apes. American Society of Human Genetics 2014, San Diego, USA (2014)

Genetics, migrations and ancestry in the 21st century. The bodies of our ancestors: ancient human remains and our past, Budapest, Hungary (2013)

Understanding Medieval Migration through Ancient DNA. Institute for Advanced Study seminar series, Princeton, New Jersey (2013)

Next Generation Sequencing in Children with Unclassified, Sporadic, Early-Onset Epileptic Encephalopathies—. UAGC & Illumina Next Generation Sequencing Seminar (2012), Phoenix Children's Hospital Neurology Grand Rounds (2012) and Genetics Grand Rounds, UMC (2012)

De novo pathogenic mutation of SCN8A identified by whole genome sequencing of a family quartet with infantile epileptic encephalopathy and SUDEP. Neurology Grand Rounds, UMC (2012)

Ancient DNA and its potential for genetic history. Genetic History & Medieval Studies International Workshop, Vienna (2012)

In depth analyses of population history. Application of Genomics to Anthropological Research Workshop, San Antonia, Texas (2012)

Genetic Diversity: An additional screwdriver in the historical scholar's toolbox. Thinking Across the African Past: Archaeological, Linguistic and Genetic Research on Precolonial African History Conference, Rice University (2011)

Sex-Specific Genetic Data Supports One of Two Alternative Versions of the foundation of the ruling dynasty of the Nso' in Cameroon. American Historical Association annual meeting, San Diego (2010)

Next Generation Sequencing Technologies. in Veeramah, K.R. (ed.) An Introduction to Human Genetics: The Biomedical & Life Sciences Collection, Henry Stewart Talks Ltd, London (online at http://hstalks.com/) (2009)

Stony Brook Service

University representative for Nassau Community College Biology Club (2016)

UG Bio Transfer Orientation Panel member (2015)

Admitted Student day representative for E&E (2014-2016)

College of Arts and Sciences Equal Employment Opportunity and Affirmative Action Committee (2015-2021)

College of Arts and Sciences admitted students Phon-a-Thon (2017)

Accepted high school student for Simon Summer Research Program (2015)

Genetics Graduate Admissions Committee (2018)

Genetics Graduate Admissions Interviewer (2018, 2024)

Center for Inclusive Education Faculty Career Month panel member - "preparing research and teaching statements for academic careers" (2018)

Institute For Advanced Computational Science Info session panelist (2018)

IDPAS program revision committee (2019-present)

College of Arts and Sciences Global Migration of People and Ideas working group (2019)

College of Arts and Sciences Promotion and Tenure Committee (PTC-J) (2021-2024)

Turner Fellowship Advisory Committee (2024-2026)

Other non-salaried Stony Brook appointments

Institute for Advanced Computational Science (IACS) affiliate faculty (2017-2020)

Genetics graduate program faculty (2016-present)

Interdepartmental Doctoral Program of Anthropological Sciences (IDPAS) faculty (2014-present)

Departmental Service

Graduate Admissions Committee (2015-2018)

Departmental Awards Committee (2016, 2017)

Proctor for E&E Graduate Prelims (2015, 2018)

E&E Retreat Organizer (2021, 2022)

Faculty mentor - Tara Smiley (2021-present)

E&E Masters Program director (2022-present)

E&E Masters Program Admissions Committee (2022-present)

E&E Graduate Prelim Committee - head (2024)

OTHER PROFESSIONAL SERVICE

Editor for the Human Population Genetics and Genomics (2020-present)

Senior Editor for the Annals of Human Genetics (2015-present)

Editorial board member for the American Journal of Biological Anthropology (2023-present)

Organizer of the DNA and History Faculty Seminar for UCLA Mellon Foundation Transforming the Humanities Initiative (2008-2010)

Co-Organizer of the workshop Genetic Anthropology at Fine Scales, Hilton Hawaiian Village, Honolulu, Hawaii Oct 25th-26th (2009)

Series Editor of An Introduction to Human Genetics: Fundamentals and Latest Advances, The Biomedical & Life Sciences Collection, Henry Stewart Talks Ltd, London (online at http://hstalks.com/) (2009)

Member of the Education Committee for the American Association of Anthropological Genetics (AAAG) (2011-present)

Long Island High School Science Fair judge (2015)

Long Island Biology Master Teachers lecture on CRISPR (2017)

Long Island Oceanside Library Science Café speaker (Oct 2017)

Society for Africanist Archaeologist 2018 Organizing Committee (2017)

Guest Editor for eLife (2018)

Instructor for AAAG Bioinformatics workshop (2018)

Member of Executive Committee for the NY Population and Medical Genomics (NY-PMG) working group (2020-present)

European Science Foundation Expert Reviewer (2020-present)

NSF panelist (2021-2022)

Organizer of the SBU-BARD Prison Initiative Biology Seminar Series at Eastern Correctional Facility (2022-present)

Manuscript reviewer for American Journal of Human Genetics, Bioinformatics, BMC Bioinformatics, BMC Biology, BMC Genomics, eLife, Current Biology, European Journal of Human Genetics, Evolution, Evolution: Education and Outreach, Environmental Biology of Fishes, Genetics, Genetics Selection Evolution, Genome Biology, Genome Biology and Evolution, Genome Research, Heredity, Human Biology, Human Heredity, Journal of Archaeological Science, Molecular Biology and Evolution, Molecular Ecology, Nature, Nature Communications, Nature Ecology and Evolution, Nature Reviews Genetics, PLOS Biology, PLOS Genetics, Proceedings of the National Academy of Sciences, Proceedings of the Royal Society B, SAGE Open, Science, Science Advances, Science and Education, Scientific Reports, The Quarterly Review of Biology

Grant reviewer for Austrian Science Fund, European Research Council, European Science Foundation, Hungarian Scientific Research Fund, Institute for Advanced Study Paris, Leakey Foundation, National Science Foundation Cultural Anthropology (Ad hoc), National Science Foundation Biological Anthropology (Ad hoc), National Science Foundation Biological Archaeology (Ad hoc), National Geographic Society, Natural Sciences and Engineering Research Council of Canada Discovery Grants program, Swedish Research Council