DECLARATION OF SARAH TISHKOFF

I, Sarah Tishkoff, declare under penalty of perjury, that the following statements in this declaration are true. The scientific descriptions and views set forth herein are each stated to a reasonable degree of scientific probability.

1. I am the David and Lyn Silfen University Professor of Genetics and Biology at the University of Pennsylvania. I obtained a dual B.S. degree from the University of California at Berkeley in Anthropology and Genetics in 1989, a master's degree from Yale in Human Genetics in 1992 and a PhD from Yale in Genetics in 1996.

2. The focus of my research is characterization of genomic variation across ethnically diverse human populations in order to make inferences about human evolutionary history and the genetic basis of variable traits including disease risk. Although we study variation on a global level, I have particular expertise studying African genetic variation.

3. As indicated in my CV (attached) I have participated in numerous workshops pertaining to genetics and race, and have been an advisor on projects sponsored by the National Institutes of Health to characterize genomic variation in globally diverse populations. I have published over 100 articles and book chapters, many of which focus on characterizing global patterns of genetic variation and impact on concepts such as human origins and race and my work has been cited over 22,800 times. My 2009 paper published in the high-profile journal *Science*, which characterized patterns of genetic variation on a global level in over 4,500 individuals including more than 2,000 from geographically diverse regions of Africa, has been cited over 1,200 times. I also have expertise studying the genetic basis of physiologic differences between individuals and populations. My 2007 paper published in Nature Genetics on the genetic basis of lactose tolerance in East Africans has been cited over 1,300 times.

4. I write to offer my opinion about whether or not there is a biological basis for racial classification as currently required for application for a marriage license in Virginia.

Genetic Differences in Humans

5. The human genome is composed of 23 pairs of chromosomes and the chromosomes are composed of DNA. DNA is composed of a "sequence" of letters: A, C, G, T (nucleotides), arranged in different orders. Some of these nucleotides code for proteins which are the building blocks of our cells and determine variable traits. Other parts of the genome do not code for any traits, but accumulate changes (mutations) over time which can be useful for tracking population histories.

6. Numerous recent advances in genomics technology allow us to characterize nucleotide variation in large numbers of individuals and relatively low cost and thereby to obtain unprecedented information about patterns of human genetic variation and how that variation impacts variable human traits, including, for example, height, skin color, and disease risk. The technologies include analyses of microsatellites (short tandem repeats of 1 – 5 nucleotides that are highly variable among individuals, such as "CACACACA"), Single Nucleotide Polymorphism (SNP) genotyping arrays that enable us to determine which nucleotide variants an individual has at millions of sites across the genome, and low cost sequencing technologies (referred to as "nextgen sequencing") that has enabled sequencing of nearly all 3 billion nucleotides in the human genome. These technologies can be used to characterize genetic variation at the level of individuals, populations, and geographic regions. These datasets have been generated in ethnically diverse populations from across the globe.

7. Having originated in Africa about 300,000 years ago, *homo sapiens* continued to diversify genetically within Africa for about 200,000 years, before human populations

encompassing a subset of African genetic diversity left that continent. Whereas all humans share more than 99% of the nucleotide sequences in their genomes, decades of genetic research have established that there is greater genetic diversity among different population groups *within Africa* than *among populations in the rest of the world*. Using some statistical approaches, greater genetic difference can be observed between African Maasai and African Khoisan individuals than between Chinese and Swedish individuals. This exemplifies the disutility of a genetic categorization that would put the former two into a single "black" race, while the latter two would be in two "white" and "Asian" races.

8. Using the genomic datasets referenced above, it is possible broadly to define genetically grouped ancestral populations, and also a contemporary individual's ancestry from those populations, associated with a given geographic area to which *homo sapiens* dispersed upon leaving Africa about 100,000 years ago. But there are no firm genetic boundaries between regions, and many individuals have mixed geographic, and thus genetic, ancestry. Individuals from Pakistan, for example, tend to show mixed European, Middle Eastern and Indian ancestry, and those from Central Asia tend to show mixed ancestry from East Asia, Europe and the Middle East. Such mixed genetic ancestry is more prevalent in proportion to historic migration events – voluntary or forced – followed by procreation between persons of different ancestry.

9. The above applies with full force to the population of the United States. Individuals who self-identify as African American, for example, routinely have European as well as African ancestry, as inferred by genetic data. Indeed, many have predominantly European ancestry as inferred from genetic data, regardless of how they may look or self-identify.

Earlier and Conventional Classifications of Humans

10. Prior to the flourishing of human genetic studies in recent decades, conventional racial categorization, dating back a few hundred years, was an effort to understand human differentiation as part of a broader attempt to classify plants and animals on earth. However, even at that time, social classifications were entwined with biological classifications. Further, these racial classifications were interpreted as being hierarchical, with those of European ancestry being at the top of the hierarchy. That hierarchical racial classification was used as a justification for colonialism, slavery, and genocide. Beginning in the mid-twentieth century, race has also featured in social scientific and political discourse addressing the consequences of racial discrimination. But for the past several decades, as human genetics has broadened and deepened our understanding of our own species, the concept of biologically defined discrete races has for the most part disappeared from mainstream scientific discourse. Apart from the fact that the "race" concept is fraught with historical and social difficulty, it does not serve any useful purpose in most human population genetics research, which is conducted without racializing its subjects.

11. In this country, since the demise of the Jim Crow laws there exists no standards even purporting to clarify racial identity. We are what we say we are. Thus, Tiger Woods is a self-described "Cablinasian" (combination of Caucasian, black, Native American and Asian ancestry). The federal racial guidelines provided by OMB Directive No.15 that frame most of our national and professional discourse on race expressly proclaim that they are not scientifically based, and indeed they are not. But none of this is science, and scientists cannot rely on such categorization – much the less on the "mixed" and "other" races that are acceptable categories for governmental purposes, including Virginia's marriage license application.

Race and Ancestry

12. It is important to differentiate between *ancestry* and *race,* as my colleagues and I point out in the attached article "Taking Race Out of Human Genetics," *Science* (Vol. 351, Feb. 5, 2016), at 565. From the standpoint of genetics, the study of ancestry is not the study of "race." From the standpoint of genetics, the study of ancestry is a serious scientific enterprise addressing a person's genomic heritage. Like all science, it is a mode of organizing verifiable knowledge – in this case about individual or population origins, similarities and dissimilarities. Studies of ancestry give rise to research data that is testable and replicable by other studies. The study of ancestry permits creation of a genetic record of our past demographic and evolutionary history, including migration and inter-marriage. This cannot be done using conventional racial categories.1

13. Human skin color varies due to adaptation to environments with differing amounts of ultra-violet (UV) exposure from the sun. Dark skin, which protects against UV degradation of folate, a significant inhibitor of birth defects, is common in many regions of the world with high levels of UV exposure, e.g. sub-Saharan Africa, southern India and Papua New Guinea. As modern humans migrated north out of Africa into regions of lower UV, problems associated with

---

1The same objections do not apply to the study of racism and the efforts to extirpate it and its consequences. If race is, in the words of anthropologist Ashley Montgague, *Man's Most Dangerous Myth* (1942), it is a myth with dramatic and malign consequences that continue to demand attention. Victims of racism demand assistance not because they are members of a race, but because they have been racialized and victimized as a result. One need not have subscribed to the Nazis' notion that Jews comprised a race to have worked to rescue them. I do not address such matters here, except to say that one need not trade in "race" in order to work to extirpate from our society the maleficent results of immature or specious race science, initially associated with the works of Gobineau and Blumenbach, ranking people according to their physiology. See also, Sussman, *The Myth of Race* (2014).

lack of folate faded and were replaced with problems associated with insufficient production of vitamin D, lack of which can cause development problems. Lighter skin was adaptive, as it was more receptive to vitamin D production, and no longer caused the UV exposure problems associated with equatorial regions. Differences in skin color reflect ancestral exposure to more or less severe sunlight, not "race."

14. Skin color does not divide humankind into difference races. A graphic example of the disutility and misleading nature of "racial" identification based on skin color are the Biggs twins, born July 3, 2006 in Birmingham, England to a mother of European ancestry and a father of African ancestry. The two girls, fraternal twins, have similar features except that one has fair skin, brown hair and blue eyes, and the other has dark skin, black hair and brown eyes. See, the photograph of the twins filed with the complaint beginning this lawsuit, and on-line documentation available by Googling <Biggs Twins>.

15. The United States Supreme Court's astute observation in *United States v. Thind* to the effect that "'the innumerable varieties of mankind run into one another by insensible degrees,' and to arrange them in sharply bounded divisions is an undertaking of such uncertainty that common agreement is practically impossible," is graphically demonstrated by the photographs of human beings throughout the world taken by the Brazilian photographer Angelica Dass, published under the name *Humanae*. See photographs depicting the hues of human beings filed with the complaint, and on-line photographs available by Googling <Humanae Project – Angelica Dass>.

Race, Genetics and Medicine

16. Genetic research in medicine focuses on identifying mutations that can cause health problems or offer health benefits – or both, as addressed in the following paragraph. The

identification of a group of persons likely to have that mutation, once identified, is made not with reference to "race," but with reference to genetic ancestry, regardless of conventional racial identification.

17. Historically, malaria has killed hundreds of thousands of persons each year. Populations surviving in areas where malaria is prevalent have evolved – been naturally selected for – a genetic defense to that disease, called sickle cell trait. Persons with sickle cell trait may be immune to malaria, or suffer from its effects far less than others. However, if a child inherits a sickle cell trait from both parents, the child is at risk of sickle cell anemia, a serious, debilitating illness. In this country, where malaria is not a serious health risk, the sickle cell trait serves no prophylactic function, and thus is a genetic and medical liability. Virtually all persons with sickle cell anemia trace their ancestry to malarial-infected locations, many in African and Mediterranean regions. It is this ancestry that determines their condition, not their "race." The reason that African-Americans in particular should be tested for sickle cell trait is not that they are part of a black race, but because their ancestry lies disproportionally in malarial areas, rendering them as a group disproportionally at risk for sickle cell anemia.

The Meaninglessness and Disutility of "Multiracial," "Mixed." and "Other" Races

18. The classification "multiracial" – whatever its utility, if any, for other purposes – is meaningless and useless for genetic, medical or other "hard" scientific purposes. Indeed, it is worse than worthless, in that it purports to impart meaning and significance to a catch-all category that has no integrity, substance or consequence. Someone whose parents are Chinese and Italian is conventionally "multiracial," as is someone whose parents are Yoruba (from Nigeria) and native Alaskan. Such a multifarious categorization may be mandated by political or social imperatives, but it is not science and cannot aid science.

19. The racial classifications "other" and "mixed" are equally meaningless and worse than useless for genetic, medical or other scientific purposes. Like "multi-racial," these terms purport to impart meaning and significance to catch-all categories that mix apples, oranges and baseballs. Such a scheme of categorization is not science and cannot aid science. Members of the "multiracial," "mixed" or "other" groups no more share genotypes or phenotypes than they share any other trait whatsoever, be it genetic, socioeconomic, educational, cultural or other.

Conclusion

20. In sum, there is no biological or genetic basis to conventional racial classification, and almost all human geneticists recognize this fact. The maintenance of conventional racial categories, whatever its consequences socially, psychologically and politically, is irrelevant to, not to say disruptive of, scientific study of the human species.

Sarah Tishkoff

Dated: August 22, 2019

Curriculum Vitae
Sarah A. Tishkoff, Ph.D.

Date: 06/04/2017

Address: 428 Clinical Research Building
415 Curie Boulevard
Philadelphia, PA 19104-6145 USA
tishkoff@mail.med.upenn.edu

Citizenship: U.S. citizen

Education:

1989	B.S.	University of California, Berkeley (Anthropology & Genetics)
1992	M.Phil.	Yale University (Human Genetics, Kenneth Kidd adviser)
1996	Ph.D.	Yale University (Genetics, Kenneth Kidd adviser)

Postgraduate Training and Fellowship Appointments:

1997-2000	Postdoctoral Fellow, Pennsylvania State University, Department of Biology (Andrew Clark adviser)
1997	Visiting Research Fellow, South African Institute of Medical Research, University of the Witwatersrand, Department of Human Genetics (Trefor Jenkins adviser)

Faculty Appointments:

2000-2005	Assistant Professor, University of Maryland, Department of Biology
2005-2007	Associate Professor, University of Maryland, Department of Biology
2008-2012	David and Lyn Silfen University Associate Professor, Department of Genetics, Perelman School of Medicine and Department of Biology, School of Arts and Sciences, University of Pennsylvania (Penn Integrates Knowledge Associate Professor)
2012-present	David and Lyn Silfen University Professor, Department of Genetics, Perelman School of Medicine and Department of Biology, School of Arts and Sciences, University of Pennsylvania (Penn Integrates Knowledge Professor)

Other Appointments:

2008-present	Member, Genomics and Computational Biology (GCB) Graduate Group, Biomedical Graduate Studies, Perelman School of Medicine, University of Pennsylvania
2008-present	Member, Penn Genome Frontiers Institute (PGFI), University of Pennsylvania
2008-present	Member, Genetics and Gene Regulation (GGR) Graduate Group, Biomedical Graduate Studies, Perelman School of Medicine, University of Pennsylvania
2008-present	Member, Center for Genes and Complex Traits (CGACT), University of Pennsylvania
2010-present	Member, Center of Excellence in Environmental Toxicology (CEET), University of Pennsylvania
2010-present	Member, Institute for Immunology (IFI), University of Pennsylvania

2011-present	Member, Diabetes and Endocrinology Research Center (DERC), University of Pennsylvania
2011-present	Member, Institute for Diabetes, Obesity, and Metabolism (IDOM), University of Pennsylvania
2012-present	Research Associate, Population Aging Research Center (PARC), University of Pennsylvania
2013-present	Member, Skin Disease Research Center (SDRC), University of Pennsylvania

Awards, Honors and Membership in Honorary Societies:

1987	U.C. Berkeley President's Undergraduate Fellowship
1989	U.C. Berkeley University High Honors
1989	U.C. Berkeley Anthropology Honors
1989-1994	National Institutes of Health Predoctoral traineeship
1991-1992	Fulbright/DAAD Predoctoral fellowship for research in Germany with Dr. Svante Pääbo
1996-1998	NSF Sloan Postdoctoral fellowship in molecular evolution
1998-2003	Burroughs/Wellcome Fund Career Award in the Biomedical Sciences
2001-2006	David and Lucile Packard Career Award in Science and Engineering
2003	Univ. of MD College of Life Sciences Faculty Excellence Award for Junior Faculty
2003	Featured as one of the "Ten Most Brilliant" young scientists in the U.S. by Popular Science Magazine, September, 2003
2008	Penn Integrates Knowledge (PIK) University Endowed Chair, University of Pennsylvania
2009	NIH Pioneer Award
2009-2011	Penn Fellow, University of Pennsylvania
2011	Invited Lecturer, Holiday Lectures on Science, HHMI
2012	Invited Lecturer, W. E. B. Du Bois Lectures, W.E.B. Du Bois Institute for African and African American Research, Harvard University
2012	Keynote Speaker, The Genomics of Common Disease, Potomac, Maryland
2013	Keynote Speaker, Symposium in honor of the 10th anniversary of the Human Genome Project, NHGRI, NIH
2013	Plenary Speaker, The Endocrinology Society Meeting
2013	Semi-Finalist for HHMI Investigator Competition
2013	Eugene Perrin Lecture on Health Sciences and Peace, Wayne State University
2014	Laureate Lecture, School of Medicine, University of Pittsburgh
2014	Plenary Speaker, Society of Molecular Biology and Evolution, San Juan
2014	Keynote Speaker, 11th International Conference on Zebrafish development and Genetics
2015	Wolk Lecture, Colgate University, Hamilton, NY
2017	14th Annual CC Li Lecture, University of Pittsburgh
2017	Evelyn Spritz Lecture in Human Genetics and Genomics, University of Colorodo School of Medicine, Boulder, CO
2017	Elected to the National Academy of Sciences

Memberships in Professional and Scientific Societies and Other Professional Activities:

International:

2000-present	Leakey Foundation (Grants Reviewer)
2005-present	African Society of Human Genetics (Member)
2005-2006	Wellcome Trust, UK, Fellowship Reviewer
2006-2009	Biotechnology and Biological Sciences Research Council (BBSRC), UK (Grant Reviewer)
2008-2010	FTC Portugal (national science council), Portugal (Grant Reviewer)
2008	Wellcome Trust, UK, Grant Reviewer
2010	Wellcome Trust, UK, Sanger Institute Programme Reviewer
2013-present	Faculty of 1000 (F1000) (Contributing Member)

National:

2000-present	American Association for Anthropological Genetics
2000-present	American Association for the Advancement of Science (Member)
2000-present	American Association of Physical Anthropologists (Member)
2000-present	American Society of Human Genetics (Member)
2000-present	National Science Foundation, Physical Anthropology (Grants Reviewer)
2000-present	Society for Molecular Biology and Evolution (Member)
2000-2007	Society for the Study of Evolution (Member)
2003-2005	National Human Genome Research Institute (NHGRI), National Institutes of Health (NIH) Advisory Panel Member, Research Planning and Evaluation Group, Ethical, Legal and Social Issues
2004	GRAD (Genetic Research of the African Diaspora) Project, Howard University Genome Sciences Center (Advisory Panel Member)
2004	National Human Genome Research Institute (NHGRI), National Institutes of Health (NIH) Advisory Panel Member "Race and Genetics"
2005	Genetics of Health and Disease Study Section, National Institute of General Medical Sciences, National Institutes of Health (Ad Hoc Member)
2005	"Race and Genetics," National Coalition for Health Professional Education in Genetics (Advisory Panel Member)
2006	Genes, Genomics, and Genetics Study Section, National Institutes of Health (Ad Hoc Member)
2006-present	Advisory Panel Member, "The New Genetics and the Trans-Atlantic Slave Database", Harvard University, Afro-American Studies Program, organized by Henry Louis Gates, Jr.
2007	National Science Foundation (CAREER Program Review Panel Member)
2007	Race and Ancestry in Clinical Genetics and Population Research Workshops, Broad Institute (Advisory Panel Member)
2007-present	National Human Genome Research Institute (NHGRI), National Institutes of Health (NIH) Member, Consultation and Oversight Group NHGRI Sample Repository
2008-present	Genetics Society of America (Member)
2008-2010	National Evolutionary Synthesis Center (NESCent) Scientific Advisory Board
2009	Keystone Symposia Genetics/Genomics Study Group (Scientific Advisory Panel)
2009	National Institutes of Health (Challenge Grants Reviewer)
2009-present	National Human Genome Research Institute (NHGRI), National Institutes of Health

	(NIH) 1000 Genomes Samples Advisory Committee
2010-present	Chair, Committee to Study African American ancestry using genomic studies as part of the working group "The New Genetics and the Trans-Atlantic Slave Database", Harvard University, Afro-American Studies Program, organized by Henry Louis Gates, Jr.
2010-present	Association for Women in Science (Member)
2010	International Centers of Excellence for Malaria Research (ICEMR), NIAID, NIH (Grant Review Panel)
2011-2013	Member, Genetics, Variation, and Evolution (GVE) Study Section, NIH
2011	National Institutes of Health (Workshop Participant - "Genomic Opportunities for Studying Sickle Cell Disease")
2012-2013	National Institutes of Health (H3Africa Common Fund Initiatives Review Panel)
2012-2013	Smithsonian National Museum of Natural History/NHGRI (Advisory Council)
2012-2013	Reviewer, Canada Research Chair applications, Canadian Institutes of Health Research
2012-2013	American Society of Human Genetics (Member, Nominating Committee)
2013-2014	American Society of Human Genetics (Chair, Nominating Committee)
2013-2015	Genetics, Variation, and Evolution (GVE) Study Section, NIH (Chair)
2013-2014	Selection Committee, Gilbert S. Omenn Prize at the Foundation for Evolution, Medicine and Public Health (Member)
2014-2015	Selection Committee, Gilbert S. Omenn Prize at the Foundation for Evolution, Medicine and Public Health (Chair)
2016-2019	Director, American Society of Human Genetics
2016	Co-Chair, Study Section to Review MIRA grants, NIGMS, NIH
2016-present	Advisory Board, International Society for Evolution, Medicine, and Public Health
2016 - present	Member, Executive Director of the American Society of Human Genetics Search Committee

Local:

2009-2010	Franklin Institute Scientific Advisory Panel

Editorial Positions:

1997-present	Reviewer: Nature; Human Molecular Genetics; Molecular Biology and Evolution; Human Genetics; European Journal of Human Genetics; Nature Reviews; PLOS Genetics; Annals of Human Genetics; Human Biology; The American Journal of Physical Anthropology; The American Journal of Human Genetics; Science; Nature Genetics; PLOS Biology; Genome Research; Trends in Genetics; Genetics, among others.
2005-2016	Associate Editor, Molecular Biology and Evolution Journal
2007-present	Editorial Board, Genome Research Journal
2010-2013	Associate Editor, The Quarterly Review of Biology
2011-present	Associate Editor, G3 (Genes, Genomes, Genetics)
2011-present	Member, Editorial Board, Evolution, Medicine, and Public Health
2016-present	Associate Editor PLOS Genetics

Academic and Institutional Committees:

2001-2002	UMD, Behavior, Ecology, Evolution, Systematics Graduate Admissions Committee
2001-2004	UMD, Biology Computational Biology Search Committee
2002-2003	UMD, Biology Faculty Advisory Committee
2002-2006	UMD, Howard Hughes Medical Institute Undergraduate Fellowship Advisory Board
2003-2004	UMD, Biology Chair Search Committee
2003-2006	UMD, Advisory Board for Bioinformatics Course Curriculum Development
2004-2005	UMD, Biology Department Comparative Genomics Faculty Search Committee
2004-2005	UMD, CBMG Department Functional Genomics Faculty Search Committee
2004-2006	UMD, Behavior, Ecology, Evolution, Systematics Graduate Steering Committee
2005-2006	UMD, Computational Biology Faculty Search Committee
2006-2007	UMD, College of Chemistry and Life Sciences Instrumentation and Core Facility Committee
2006-2007	UMD, Biology Graduate Admissions Committee
2008-2009	Member, Cell and Molecular Biology (CAMB), Genetics and Gene Regulation (GGR) Graduate Student Review Committee
2008-2009	Member, Genomics Faculty Search Committee, Penn Genome Frontiers Institute (PGFI)
2008-2010	Member, Faculty Advisory Panel on Global Health, School of Medicine (SOM)
2009-2011	Member, PGFI Scientific Advisory Committee
2009-2010	Member, Evolutionary Biology Faculty Search Committee, Department of Biology, School of Arts and Sciences (SAS)
2010-2011	Member, Penn Fellows Advisory Committee on topic of "Global Engagement at Penn"
2010-2011	Member, GCB Graduate Group Admissions Committee
2010	Chair, GCB Graduate Group Committee to develop and grade the genomics and genetics section prelim exam for second year students
2010	Panelist, Penn Preview
2010-2011	PCBI Faculty Search Committee
2011	Panelist, Penn Preview
2011-2012	Member, GCB Graduate Group Fellowship Committee
2011-2012	Evolutionary Medicine and Information Biology Faculty Search Committee, CHOP
2011-2014	Member, Advisory Committee for PA DOH Grant - Improving Vision & Preventing Visual Impairment in Urban African Americans & Rural Amish (PI: Dwight Stambolian)
2011-2012	Member, The Role of Penn Medicine in the World Working Group, SOM
2013	Member, PSOM Global Health Research Subcommittee
2013-present	Member, Department of Genetics Search Committee for IBI Assistant Professor
2013-2014	Member, SAS Planning Group on Diversity, Difference, and Community
2013-2014	Member, SAS Planning Committee for selection of Freshman reading material for the “Year of Health”
2013-2014	Member, SOM, Task Force to Assist with Planning Child Care Facility
2014-2017	Member, SOM, Committee on Academic Freedom and Responsibility
2014-2018	Member, SOM, Penn Medicine Awards of Excellence Selection Committee
2014 – present	Member, SAS, Department of Biology, Graduate Student Advising and Assessment Committee

2014 – 2015	Member, SAS Planning Group on Big Data
2014 – present	Member, Penn Program on Race, Science, and Society (PRSS) working group
2015 – 2016	Member, SOM, Search Committee for Chair of Cell and Developmental Biology
2015 - 2018	Member, University Disciplinary Hearing Panelist
2016-2017	Member, SOM, Faculty Search Committee, Department of Genetics
2017	Member, SAS, Awards Committee
2017	Member, SOM, Child Care Implementation Committee
2017	Member, SOM, review committee for the Department of Medical Ethics and Health Policy

Major Academic and Clinical Teaching Responsibilities:

Masters, PhD and Postdoctoral Mentorships:

2000-2008 M.A. Student Advisor:

- Hannah Hutton, (03/11-12/14)
- Kristin Kaercher (09/05-09/08)
- Bailey Levis (09/04-12/06)
- Kweli Powell (08/00-06/04)
- Lisa Pfeiffer (01/01-08/08)

2001-present Ph.D. Student Advisor:

- Derek Kelly, GCB program (06/15 – present)
- Meagan Rubel, Anthropology program (06/13 – present)
- Sameer Soi, GCB program (06/09-present)
- Felicia Gomez (09/06-05/13; postdoctoral fellow Washington State University St. Louis)
- Jibril Hirbo (08/03-12/10; postdoctoral fellow, Vanderbilt University)
- Alessia Ranciaro (06/04-06/08; research scientist, University of Pennsylvania)
- Holly Mortensen (06/01-06/08; bioinformatician, EPA)

2003-2008 Visiting Ph.D. Student Advisor:

- Gil Tomas (10/03-07/04)

2001-present Postdoctoral Advisor:

- Eric Mbunwe (10/16 – present)
- Shaohua Fan (03/15- present)
- Marcia Holsbach Beltrame (10/14 – present)
- Nicholas Crawford (03/14 – present)
- Matthew Hansen (09/13-present)
- Yancy Lo (11/15 – 12/16) (Research Scientist, Institute of Biological Informatics, University of Pennsylvania)
- Joseph Lachance (12/10-12/14) (Assistant Professor, Georgia Institute of Technology)
- Renata Afi Rawlings-Goss (10/11-08/14) (Co-Executive Director of the South Big Data Innovation Hub, Georgia Institute of Technology)

- Simon Thompson (09/09-04/14) (Research Coordinator at Global Alliance for Chronic Diseases, UK)
- Alessia Ranciaro (07/08-06/14) (Senior Research Scientist, University of Pennsylvania)
- Michael Campbell (09/07-06/14) (Assistant Professor, Howard University)
- Jibril Hirbo (12/10-12/13) (Research Scientist, Vanderbilt University)
- Laura Scheinfeldt (2009-2013) (Associate Professor, Temple University)
- Clara Elbers (07/10-02/13) (Research Scientist, Amsterdam Medical Center)
- Bart Ferwerda (07/10-6/12) (Research Scientist, Amsterdam Medical Center)
- Wen-Ya Ko (06/07-12/12) (Assistant Professor, Yang-Ming University, Taiwan)
- Joe Jarvis (08/08-10/11) (Senior Research Associate, Coriell Institute)
- Charla Lambert (11/08-01/10) (Cold Spring Harbor Laboratories)
- Floyd Reed (03/05-03/08; Assistant Professor, University of Hawaii)
- Katy Gonder (01/02-07/07; Associate Professor, Drexel University)
- Eduardo Tarazano-Santos (3/01-11/03; Associate Professor, Universidade Federal de Minas Gerais, Brazil)
- Brian Verrelli (02/01-11/03; Associate Professor, Virginia Commonwealth University)
- Agnes Awomoyi (03/01-01/03; Research Associate, Ohio State University)

PhD Committee Memberships:

2000-present Ph.D. Committee Member:

UMD: Eduardo Eizirik, Matthew Kostek, Colin Rose, Paul Zwiers, Jonathan Beadell, Peng Yue, Bailey Levis.

Penn: Natalie Miller, Yang Jiao, Sesh Sundararaman, Sameer Soi, Hannah Hutton, Meagan Rubel, Mitra Eghbal, Adam SanMiguel, Katie Siewert, Kelsey Johnson

2014 - 2015 Penn: Candidacy exam committee for Alexander Berry (Biology), and Kelsey Johnson (GGR)

Supervised Undergraduate Internships:

2001-2004 UMD: supervised 2 students/year in the honors internship program (BSCI 399H)

2001-2008 UMD: supervised between 2-3 students/year in undergraduate internships (BSCI 399 or 279)

2008-present Penn: supervised between 2-3 undergraduate students/year who did research in lab (BIOL 399 or 499)

2001-present Undergraduate Research Advisor:

Current: Elizabeth Eyermann,

Past: Daniel Wagner, Amy House, Emily Ashcraft, Chintan Patel, Jim Pineno, Prasad Acharya, Karena Sylvester, Radhika Akkapeddi, Hawa

Almansoori, Kathy Deljou, Sarah Hall, Sara Roschwalb, Aiman Saleh, Jonathan Hodax, Fizza Shaikh, Daniel Richard, Ning Lu, Ebuka Nwokoye, Jennifer Kessler, Nikhil Joshi, Sandra Winters, Esther Whitlock, Brittany Taylor, Sarah Akkoush, Isabel Fan, Dan Zinshteyn (graduate student, Cornell), Evan Daugharty (graduate student, Harvard), Robyn Jordan, Charles Washington (research fellow, University of Missouri); Avery Davis (graduate student, Harvard University), Robbie, Berg, John Russell, Kristin Mullen, Christopher Nagle, Tina Kartika, Stephanie Fagbemi, Arielle Fogel, Juliette Rando

2004-2009	High School Research Advisor: Aiman Saleh (2004-2005), Joseph Mustapha (2009)
2010 - present	BGS Summer Undergraduate Internship Program (SUIP), Michelle Haring (2010; graduate student Michigan State University), Guarav Luthria (2014; finishing undergraduate studies at UBMC), Alec Downie (2015; summer intern from Yale), Jake Haut (2015; summer intern from Rochester Institute of Technology)

Courses Taught:

2001-2006	UMD, BIOL 608 Topics in Human Evolutionary Genetics (graduate seminar) (6-14 students/semester, taught once/year)
2001-2007	Established and implemented a new interdisciplinary, inter-institutional graduate training program in Human Evolutionary Biology with GWU, Howard, and UMD; devised the program and curriculum and met bi-yearly on the PI and graduate admissions committees
2002	Developed a new course and curriculum for an advanced undergraduate course in Human Genetics (BSCI 416 The Biology of the Human Genome); also developed a Webpage for this course
2002-2007	UMD, BSCI 416 The Biology of the human genome (35-75 students/ class taught once/year)
2008-2011	Penn, Fall, Medical Genetics, first year medical school class (one lecture 2008, two lectures 2009, one lecture 2010, one lecture 2011)
2008-2009	Penn, Spring, Biol 121, Introductory Biology (one lecture/year in 2008 and 2009)
2008-2009	Penn, Fall, Biol 221, Molecular Biology and Genetics (one lecture/year in 2008 and 2009)
2009-present	Penn, Spring, Biol 422, Genomics of Human Disease and Evolution (formerly called "Human Genetics and Genomics"), 30 - 35 undergraduate and graduate students (3 hrs/week, total of 42 lecture hours in the semester in 2009, 2011, 2013, 2015)
2010-present	Penn, Spring, Biol 522, Human Evolutionary Genomics, Graduate/Advanced Undergraduate Seminar, 15 undergraduate students/1 graduate student (joint CAMB/Biology; 3 hrs/week in 2010, 2012, 2014, 2016)
2011	Lecturer, University of Pennsylvania Biology Department's Teacher Professional Development Series
2011-present	Penn, Spring, CAMB 550, Genetic Principles (one lecture, one discussion session in 2011, 2 lectures and one discussion session in 2012, 2 lectures and one discussion session in 2013 and 2014)
2004,	Lecturer, Jackson Labs Course in Mammalian Genetics, Bar Harbor, ME

2010-2014	
2011	Lecturer, Yale Undergraduate course in "Evolutionary Medicine" taught by Stephen Stearns
2011	Lecturer, Pinkham Course in the Basic Sciences, Swedish Hospital, Seattle Washington
2011	Lecturer, HHMI Holliday Series, live and videotaped broadcast to high school students
2012	Lecture at Bryn Mawr to students in Biol 327, "Evolutionary Genetics and Genomics"
2012	Lecture and discussions with M.D. and Ph.D. students in the Public Health
2012	Certificate Program (PHCP), School of Medicine, University of Pennsylvania "Dinner With Interesting People," Lecture and discussion with freshman students, McClelland Hall, University of Pennsylvania
2013	Penn, Spring, Biol 422, Genomics of Human Disease and Evolution, 39 students (3 hrs/week, total of 42 lecture hours)
2014	Taught Penn Preceptorial on African Genomics: Implications for human evolution and disease
2016	Responsible Conduct of Research lecture on ethics and genomics.
2017	Lecturer, Biol 221 Introduction to Genetics (3 lectures on population genetics)

Lectures by Invitation:

1995:	
Jan, 1995	Oxford University, Department of Genetics, John Radcliffe Hospital, UK
Jan, 1995	University of Munich, Department of Zoology, Germany
Feb, 1995	Sapienza University, Rome, Department of Biology, Italy
Apr, 1995	Northwestern University, Department of Anthropology
Sep, 1995	Penn State University, Department of Anthropology
1996:	
Feb, 1996	New York Consortium in Evolutionary Primatology
1997:	
Jan, 1997	University of Barcelona, Department of Biological Sciences, Spain
Feb, 1997	Stanford University, Department of Anthropology
Apr, 1997	Human Biology Association meeting, symposium on "Interpreting Patterns of Human Genetic Diversity", St. Louis
Jun, 1997	Trinational Workshop on Molecular Evolution, Munich, Germany
Aug, 1997	University of the Witwatersrand, Department of Human Genetics, South Africa
Aug, 1997	University of Pretoria, Department of Mammalian Genetics, South Africa
1998:	
Jan, 1998	Columbia University, Department of Anthropology
Feb, 1998	University of New Mexico, Department of Anthropology
Feb, 1998	Mt. Sinai Medical School, Department of Human Genetics
Apr, 1998	American Association of Anthropological Genetics/American Association of Physical Anthropology, Symposium on Genetics and Origins of Human Diversity
May, 1998	University of Connecticut at Storrs, Department of Anthropology
Jun, 1998	Trinational Workshop of Molecular Evolution, Vancouver, CA
1999:	
Jan, 1999	American Association for the Advancement of Science Meeting, Symposium on

	"The Emergence of modern Human Form" organized by Dr. Loring Brace
Feb, 1999	National Cancer Institute, Frederick, MD
Feb, 1999	Department of Biology, University of Maryland
May, 1999	Symposium on "Pattern and Implications of Human Genetic Variation" organized by Dr. Joanna Mountain, Stanford University, Dept. of Anthropological Sciences
Jun, 1999	Symposium on "Genome Diversity and Evolution" organized by Dr. Masatoshi Nei, in conjunction with the 1999 annual meeting of the American Genetic Association, Penn State University
Jun, 1999	Department of Biology, New York University
Jun, 1999	Department of Molecular Biology and Development, Cornell University
Nov, 1999	Symposium on "The Emergence of Modern Human Form", organized by Dr. C. Loring Brace, American Association of Anthropologists meeting, Chigaco, Ill.
2000:	
Apr, 2000	Symposium on "Modern Human Origins", organized by Dr. C. Loring Brace, American Association of Physical Anthropology meeting, San Antonio, TX.
Dec, 2000	Department of Anatomy, Howard University Medical School, Washington D.C.
2001:	
Feb, 2001	Symposium on "Know Thyself: The Human Genome Project", sponsored by the Wilson Center for Leadership in the Public Interest, Hampden Sydney College, Hampden-Sydney VA
Mar, 2001	Symposium on "Human Dimensions of Biodiversity", sponsored by the Human Biology Assoc. and the International Assoc. of Human Biology, Kansas City, MO
Oct, 2001	"Why is the study of African genetic diversity important for understanding modern human origins and the genetic basis of human disease?", Symposium on African Genetic Diversity, American Society of Human Genetics Meetings, San Diego, CA
Nov, 2001	Invited participant in panel discussion on "Where do people come from and how do we know? Reconciling Interdisciplinary approaches to questions of origins", American Association of Anthropology. Washington D.C.
2002:	
Feb, 2002	Dept. of Human Genetics, Univ. of Maryland, Baltimore, MD.
Apr, 2002	Symposium on "Northeast African Biocultural diversity," American Association of Physical Anthropology, Buffalo, NY
Apr, 2002	Dept of Epidemiology, School of Medicine, University of Pennsylvania, Philadelphia, PA
May, 2002	Symposium on Theoretical and Empirical Advances in the Study of Effective Population Size, Smithsonian Institute, Washington D.C.
Jun, 2002	National Institute on Deafness and Other Communication Disorders, NIH, Rockville, MD
Jun, 2002	Laboratory of Malaria and Vector Research," National Institute of Allergy and Infectious Diseases/NIH, Bethesda, MD
Sep, 2002	Keynote Speaker, 3rd MeHarry/Vanderbilt Alliance Genetics Symposium, Nashville, TN
Sep, 2002	Packard Foundation Career Awardee Meeting, Monterey, CA
Oct, 2002	5th International Meeting on Single Nucleotide Polymorphism and Complex Genome Analysis," Reykjavik, Iceland
Oct, 2002	Whitehead Press Seminar, MIT, Boston, MA
Nov, 2002	Biosciences Symposium, University of Maryland, College Park, MD

Nov, 2002 Meeting on East African Genetics, University of Khartoum, Khartoum, The Sudan

2003:

Feb, 2003 US/Egyptian Joint Workshop on Anthropology, Cairo, Egypt

Mar, 2003 Dept. of Epidemiology, Johns Hopkins University, Baltimore, MD

Mar, 2003 Distinguished speaker, Computational Molecular Biology Symposium, Carnegie Mellon University, Pittsburgh, PA

Mar, 2003 Distinguished Lecture Series, Laboratory of Genomic Diversity, National Cancer Institute, NIH, Frederick, MD

Apr, 2003 National Cancer Institute, NIH, Rockville, MD

May, 2003 Workshop on genetic and linguistic history of Bantu populations of Africa, University of Lyon, Lyon, France

Jun, 2003 National Institute of Mental Health, NIH, Baltimore, MD

Jun, 2003 "Journey of Man: A look at our amazing human history" (lecture/commentary on a newly released documentary on the evolutionary history of the Y chromosome in humans), National Institute of General Medical Sciences, NIH, Baltimore, MD

Oct, 2003 Symposium on host/pathogen coevolution sponsored by the Genetics and Genomics Training Grant, Harvard University, Cambridge, MA

Nov, 2003 Biosciences symposium, University of Maryland, College Park, MD

Nov, 2003 Dept. of Biology, University of Pennsylvania, Phila., PA

2004:

Feb, 2004 The Institute of Genome Research, Rockville, MD

Feb, 2004 Dept. of Biology, Georgetown University, Washington, D.C.

Feb, 2004 Gordon Conference on Molecular Evolution, Ventura, CA.

Mar, 2004 Symposium on Genomics and Society: Implications for the future health of Africa, Cairo, Egypt.

Mar, 2004 Workshop on Race and Genetics, NIGR, NIH, Bethesda, MD

Apr, 2004 Symposium on Human Ecological Immunity: Models and Methods for Future Research, AAPA/HBA meetings, Tampa, Florida

May, 2004 Symposium on The Future of Human and Medical Genetics Based on Contributions of Arno G. Motulsky, Genome Sciences, University of Washington School of Medicine (One of seven international scientists chosen by Dr. Motulsky to speak at a symposium in honor of the establishment of an endowed chair in his name)

Sep, 2004 American Association of Anthropology workshop on Race and Genetics, Washington D.C.

Nov, 2004 Invited by graduate students in the Biological Sciences Program as part of their Women in Science seminar series, Case-Western University, Cleveland, OH

2005:

Jan, 2005 Monell Chemical Senses Center, University of Pennsylvania, Philadelphia, PA

Apr, 2005 Marshfield Medical Research Institute, Marshfield, WI

Apr, 2005 Symposium on Bridging theory and data in the context of anthropological genetics, AAPA meeting, Milwaukee, WI

May, 2005 National Museum of Natural History, Smithsonian, Washington D.C.

Jul, 2005 Invited Lecturer, Mammalian Genetics Course, Jackson Labs, Bar Harbor, Maine

Dec, 2005 Dept. of Human Genetics, University of Chicago, Chicago, Illinois

Dec, 2005 Dept. of Biology, Duke University, Durham, NC

2006:

Jun, 2006 NHGRI, NIH, Bethesda, MD

Aug, 2006	Keynote Speaker for Workshop on The Genomic Revolution and the Origin of Humanity, McMaster University, Hamilton, Ontario
Oct, 2006	Symposium on natural selection and infectious disease, American Society of Human Genetics meeting, New Orleans, Louisiana
Nov, 2006	Frontiers in Biology Seminar Series, Department of Genetics, Stanford University, Stanford, CA

2007:

Feb, 2007	Dept of Genetics, Rutgers University, New Brunswick, NJ
Feb, 2007	Program in Human Genetics, University of Maryland, Baltimore, MD
Mar, 2007	Department of Genetics, University of Pennsylvania, Philadelphia, PA
Apr, 2007	High School Teachers Workshop, University of Maryland, Baltimore, MD
May, 2007	Biology of the Genome Meeting, Cold Spring Harbor, NY
May, 2007	Keynote speaker, American Institute of Biological Sciences Symposium, Washington D.C.
May, 2007	US Naval Observatory, Washington D.C.
May, 2007	Symposium on "Genetics of Infectious Disease", The Human Genome Organization meeting, Montreal, Canada
Jul, 2007	Human Genetics and Genomics Gordon Research Conference, Newport RI
Sep, 2007	Wellcome Trust Sanger Institute in Cambridge, UK
Oct, 2007	Banbury Conference on Human Variation, Cold Spring Harbor, NY
Oct, 2007	National Institute of Diabetes and Digestive and Kidney Diseases, NIH, Bethesda, MD
Nov, 2007	Keynote speaker, African Society of Human Genetics conference, Cairo, Egypt

2008:

Feb, 2008	Gordon Research Conference on Molecular Evolution, Ventura, CA
Feb, 2008	Keystone Symposium on Complex Traits: Biologic and Therapeutic Insights, Santa Fe, NM
Mar, 2008	Department of Molecular Microbiology and Immunology and the Division of Infectious Diseases, Johns Hopkins University, Baltimore, MD
Mar, 2008	Division of Medical Genetics, Children's Hospital of Philadelphia (CHOP), Philadelphia, PA
Apr, 2008	Burroughs Wellcome Foundation, Plasmodium Meeting, London, England
Apr, 2008	Division of Nutritional Sciences, Cornell University, Ithaca, NY
May, 2008	Keynote Speaker, Evolution and Medicine Lecture Series, NIGMS, NIH (filmed for video archive)
Jun, 2008	Invited speaker, Society for Molecular Biology and Evolution and European Society of Human Genetics Meeting, Barcelona, Spain.
Jun, 2008	Society for Molecular Biology and Evolution Meeting, section on infectious disease evolution
Sep, 2008	Symposium in honor of Charles Darwin, Smurfit Institute of Genetics, Dublin, Ireland
Oct, 2008	Banbury Meeting on Ancestry in Human Populations, Cold Spring Harbor, NY
Oct, 2008	Workshop on Natural Selection, Ethics, and Disease, NIH, Bethesda, MD
Oct, 2008	Human Genome Variation Meeting, Toronto, Canada
Nov, 2008	Genetics Colloquium in Honor of Charles Darwin, University of Wisconsin, Madison, WI

2009:

Jan, 2009	Genomics Colloquium in honor of Charles Darwin, University of Cincinnati, Cincinnati, OH
Feb, 2009	Symposium on Adaptation in honor of Charles Darwin, organized by Eric Green, AAAS Meeting, Chicago, IL.
Feb, 2009	University of Pennsylvania Museum of Archaeology and Anthropology, Darwin's Legacy in 21st Century Biology Symposium, Philadelphia, PA
Mar, 2009	African Society of Human Genetics Conference, Yaounde, Cameroon
Mar, 2009	Wellcome Trust Meeting, Yaounde, Cameroon
Apr, 2009	Keynote speaker at Case Western University as part of their celebration of he 150th anniversary in 2008-09 of the publication of the Darwin-Wallace paper, Cleveland, OH
Apr, 2009	Invited speaker, American Academy of Physical Anthropologists Meeting, Chicago, IL
Apr, 2009	Making History Campaign, University of Pennsylvania held in Washington, DC
May, 2009	Cold Spring Harbor Symposium in honor of Charles Darwin titled "Evolution - the Molecular Landscape"
May, 2009	Linguistics and Genetics Workshop, Center for Behavior, Evolution, and Culture, UCLA, Los Angeles, CA
May, 2009	Darwin Symposium Series, UCLA, Los Angeles, CA
Jul, 2009	Duke University, HOMINID Project group
Oct, 2009	Conference on Host Genetics Control of Infectious Diseases, Pasteur Institute, Paris, France
Oct, 2009	Keynote Speaker, Special Symposium on the 200th anniversary of the birth of Charles Darwin, American Society of Human Genetics Meeting, Honolulu, HI
Nov, 2009	North Carolina State, Genomics Program, Raleigh, NC
Dec, 2009	Sackler Colloquia "In the Light of Evolution IV: The Human Condition" National Academies of Sciences, Irvine, CA
Dec, 2009	Penn Alumni Event "Engaging Minds", NYC Times Center

2010:

Jan, 2010	Department of Biology, Addis Ababa University, Ethiopia
Jan, 2010	University of Botswana, Gaborone, Botswana
Jan, 2010	The Malaria Research and Training Unit, Bamako, Mali
Feb, 2010	African American Origins Workshop organized by Henry Louis Gates, Harvard University
Feb, 2010	NIH workshop on lactose intolerance, Washington, DC
Mar, 2010	UC San Diego, Genomics Seminar Series
Mar, 2010	Center for Academic Research and Training in Anthropology (CARTA), Human Origins Workshop, UCSD
Apr, 2010	Global Health Program of the Bill & Melinda Gates Foundation, Meeting focused on studies of vaccine efficiency in developing countries
Apr, 2010	SUNY Stony Brook, Department of Ecology and Evolutionary Biology
May, 2010	Keynote Speaker, Genomics Retreat, Univ of Utah
Jun, 2010	BioMAPS Institute for Quantitative Biology, summer school speaker, Rutgers University
Jul, 2010	Invited Lecturer, Jackson Labs, Annual Short Course on Experimental and Medical Mammalian Genetics, Bar Harbor, ME
Oct, 2010	Meeting on "Beyond the Genome: The true gene count, human evolution and disease

	genomics", Harvard University Medical School, Boston, MA
Oct, 2010	Keynote Speaker, Human Genetics Institute of New Jersey, Rutgers University
Nov, 2010	University of Washington, Genome Sciences, Invited by graduate students
Dec, 2010	Department of Biostatistics and Epidemiology, Johns Hopkins University
Dec, 2010	Arnold D. Kates Lecturer, Bowdoin College, ME

2011:

Jan, 2011	Department of Genetics, Mt Sinai University, New York
Feb, 2011	Session Titled "Humans Without Borders: Evolutionary Processes at Work in Humans and Their Relatives", AAAS Meeting
Mar, 2011	Keynote Speaker, African Society of Human Genetics Meeting, Cape Town, South Africa
Mar, 2011	Lecture at Centre for San Studies, University of Botswana, Gaborone, Botswana
Apr, 2011	Department of Ecology and Evolutionary Biology, Princeton University, Princeton, NJ
Jun, 2011	Department of Genetics, Harvard University (Graduate Student Invited Lecture)
Jun, 2011	The Sheba Legacy Meeting "The Genetics of migrant and isolated populations 1961-2011" Dan Accadia, Israel
Jun, 2011	CHOP/Penn Next Generation Sequencing Symposium
Jul, 2011	Invited Lecturer, Jackson Labs Annual Short Course on Mammalian Genetics, Bar Harbor, ME
Sep, 2011	Department Seminar, Panel Discussion on BBC Film, Advanced Seminar in undergraduate course "Evolutionary Medicine". Yale University, New Haven, CT.
Oct, 2011	Department of Anthropology, Washington University St. Louis, St. Louis, MO
Oct, 2011	HHMI Holiday Lectures, live and videotaped broadcast to high school students, Washington, DC
Nov, 2011	Roland Pinkham Basic Science Lecture, University of Washington, Seattle, WA.
Dec, 2011	NESCent Workshop on Language Evolution, Durham, NC

2012:

Jan, 2012	Department of Pathology and Medicine at the Philadelphia VA Medical Center (PVAMC)
Jan, 2012	Affymetrix, Santa Clara, CA
Jan, 2012	Symposium on Human Genomic Variation, UC Berkeley.
Feb, 2012	Armauer Hansen Research Institute, Addis Ababa, Ethiopia
Mar, 2012	Keynote Speaker, Genetics of the Peoples of Africa and the Transatlantic Diaspora, University of North Carolina, Chapel Hill, NC
Apr, 2012	W.E.B. Du Bois Lecture Series, W.E.B. Du Bois Institute for African and African American Studies, Harvard University
Apr, 2012	Center for Academic Research and Training in Anthropogeny, UCSD, San Diego.
Jul, 2012	Invited Lecturer, Jackson Labs Short Course in Mammalian Genetics, Bar Harbor, ME
Sep, 2012	Keynote Speaker, Genomics of Common Diseases 2012 organized by Nature Genetics and Wellcome Trust, Potomac, MD.
Sep, 2012	Keynote Speaker, Bioinformatics & Genomics (B & G) Retreat 2012 at Pennsylvania State University
Oct, 2012	13th Annual Genetics Symposium, Vanderbilt Center for Human Genetics Research, Nashville, TN

2013:

Jan, 2013	University of Pennsylvania Anthropology Colloquium
Feb, 2013	Eugene Perrin Lecture on Health Sciences and Peace, Wayne State University, Detroit, MI
Feb, 2013	University of Pennsylvania, FOCUS on Health & Leadership for Women
Mar, 2013	Williams College, Williamstown, MA
Mar, 2013	Four Field Colloquium series, Department of Anthropology, University of Michigan, Ann Arbor, MI
Apr, 2013	Keynote speaker, GET (Genomes, Environment, Traits) conference, Boston, MA
Apr, 2013	Keynote speaker, Symposium in honor of the 10th anniversary of the Human Genome Project, NHGRI, NIH
May, 2013	Plenary Speaker, Genetics and Genomics Section, American Thoracic Society International Conference in Philadelphia
Jun, 2013	Plenary Lecturer, Endocrine Society (ENDO) meeting 2013, San Francisco, CA
Jul, 2013	Invited Lecturer, Jackson Labs Short Course in Mammalian Genetics, Bar Harbor, ME
Sep, 2013	Plenary Speaker, Clarke Forum for Contemporary Issues, Dickinson College, Carlisle, Pennsylvania
Sep, 2013	Discussant, The African Diaspora: Integrating Culture Genomics and History Symposium, Smithsonian Museum/NHGRI
Oct, 2013	Invited Lecturer, Penn Institute for Computational Science (PICS) Kickoff Symposium
Oct, 2013	Symposium in honor of Kenneth Kidd, Massachusetts General Hospital, Harvard, Boston, MA
Oct, 2013	Plenary Speaker, Dean's Distinguished Lecture series, Rowan College, PA
Nov, 2013	Interdisciplinary Sciences Seminar Series, Gettysburg College, PA
Nov, 2013	Yale University, Department of Ecology and Evolutionary Biology

2014:

Jan, 2014	Lecture, Neonatology Research Seminar, University of Pennsylvania
Feb, 2014	Department of Ecology and Evolutionary Biology, Brown University
Feb, 2014	Invited Speaker, Alabama Lectures on Life's Evolution (ALLELE), University of Alabama, Huntsville
Mar, 2014	Invited Speaker, Cell Symposium: Evolution of Modern Humans - From Bones to Genomes, Meliá, Sitges, Spain
Apr, 2014	Invited Speaker, the 7th Annual Dartmouth Integrative Biology Symposium
Apr, 2014	Keynote Speaker, RECOMB 2014 (Research in Computational Molecular Biology) Pittsburgh, PA
Apr, 2014	Invited Lecturer, Department of Pathology Grand Rounds, University of Pennsylvania
May, 2014	Cornell Center for Comparative and Population Genomics
May, 2014	Laureate's Lecture, School of Medicine, University of Pittsburgh
Jun, 2014	Keynote Speaker, International Conference on Zebrafish Development and Genetics, Madison Wisconsin
Jun, 2014	Plenary Speaker, Society for Molecular Biology and Evolution, San Juan, Puerto Rico
Jul, 2014	Invited Speaker, Principals in Population Genetics: A coalescence of community to celebrate Andy Clark, Cornell

Jul, 2014	Invited lecturer, Jackson Labs Course in Mammalian Genetics, Bar Harbor, ME
Dec, 2014	High Risk/High Reward Symposium, NIH

2015:

Jan, 2015	University of Yaounde, Cameroon
Feb, 2015	Plenary Speaker, Advances in Genome Biology and Technology (AGBT) meeting, Marco Island, Florida
Apr, 2015	Wolk Lecture, Colgate University, Hamilton, NY
Apr, 2015	Invited Speaker, Genomics, Genetics, and Systems Biology (GGSB) symposium on Human Evolution, University of Chicago
Apr, 2015	Invited Speaker, PASEF, University of Pennsylvania
May, 2015	Department of Human Genetics, UCLA, Los Angeles, CA
May, 2015	Invited Speaker, Center for Excellence in Environmental Toxicology Annual symposium, University of Pennsylvania
May 2015	Invited Speaker, New York Genome Center Genentech, San Francisco, CA
June, 2015	Invited Lecturer, Jackson Labs, 56th Annual Short Course on Medical and Experimental Mammalian Genetics, Bar Harbor, ME
July, 2015	Department of Biology, McMaster University, Hamilton, Ontario, CA
Sept, 2015	Keynote Speaker, Biological Graduate Studies 30th anniversary Symposium, University of Pennsylvania
Oct, 2015	Harris Lewin Pioneer Lecture, University of Illinois, Urbana-Champaign
Oct, 2015	Invited Speaker, Bioinformatics and Systems Biology Symposium Series, UCSD, San Diego, California (rescheduled)
Nov, 2015	Invited Speaker, AAAS Meeting Symposium on "The Human Story in Africa", Washington DC

2016:

Feb, 2016	Darwin Lecture, Duquesne University, Pittsburgh, PA
Feb, 2016	Darwin Lecture, Center for Genomics and Systems Biology, NYU, New York, NY
March 2016	Department of Systems Biology, Columbia University, New York, NY
April 2016	Keynote Speaker, Genomics and Systems Biology Retreat, UCSD, CA
May 2016	U of Utah School of Medicine Benning Medical Society Lecture
May 2016	Invited Speaker, Keystone Symposia on "Understanding the Function of Human Genome Variation", Uppsala, Sweden.
July, 2016	Invited Lecturer, Jackson Labs 57th Human and Mammalian Genomics Course, Bar Harbor, ME
Sept, 2016	Colloquium on the Biology of Populations, Princeton University
Oct, 2016	Invited Speaker, Symposium on Pharmacogenetics, ASHG
Nov, 2016	Featured speaker at Genomics and Heath Disparities Lecture sponsored by NHGRI/NIH and FDA.
Dec, 2016	Invited Lecture, Duke University Program in Genetics and Genomics

2017:

March, 2017	Rutgers University, graduate student invited speaker
April 2017	14th Annual CC Li Lecture, University of Pittsburgh
May, 2017	Evelyn Spritz Lecture in Human Genetics and Genomics, University of Colorodo School of Medicine, Boulder, CO
June, 2017	World Science Festival, New York, NY

June, 2017	Marabou Symposium on "Nutrition and Human Evolution"
August, 2017	Department of Human Genetics, Vanderbilt University
Sept. 2017	Keynote Speaker, International Pigment Cell Conference, Denver, CO

Organizing Roles in Scientific Meetings:

Oct, 2000	Co-organized a workshop on "African Genetic Diversity" at the American Society of Human Genetics meeting Philadelphia, PA
Oct, 2001	Co-organized and moderated a symposium on "Genetics of African Populations: Implications for studies of human origins and human disease," American Society of Human Genetics Meeting San Diego, CA
Oct, 2001	Co-organized a workshop on "African Genetic Diversity" at the American Society of Human Genetics meeting San Diego, CA
Oct, 2002	Co-organized a workshop on "African Genetic Diversity" at the American Society of Human Genetics meeting Baltimore, MD
Oct, 2010	Co-organizer and Moderator, Session on next generation sequencing studies of human variation at "Beyond the Genome: The true gene count, human evolution and disease genomics" in celebration of the 10th anniversary of Genome Biology Journal, Harvard Medical School Boston, MA
Nov, 2010	Chair, Genomics Session, American Society of Human Genetics Annual Meeting Washington, DC
Apr, 2012	Co-organizer and moderator, Workshop on "Co-evolution of genes and culture", Center for Academic Research and Training in Anthropology (CARTA), UCSD San Diego, CA
March 2016	Co-Organizer of Working Group to study the Impact of Ecotourism on Indigenous Culture, University of Pennsylvania
June, 2016	Organizer of Symposium on Evolution and Disease in Africa, International Society for Evolution, Medicine, and Public Health
Oct, 2017	Co-Organizer of Working Group to study The Global Impacts of Race on Biomedicine

Grants:

Current:

Adaptation to diet and its impact on the gut microbiome and genomic variation in ethnically diverse Africans, National Science Foundation, BCS-1317217, 2013 – 2016 (Sarah Tishkoff, PI)

Integrative Nutrigenomic and Metabolomic Analyses of Africans with Variable Diets, National Institutes of Health, 1R01DK104339-01, 12/01/14 – 11/30/18 (Sarah Tishkoff, PI)

Integrative Genomic of Body Size and Metabolism in Ethnically Diverse Africans, National Institutes of Health, 1R01GM113657-01, 01/15/15 – 01/14/19 (Sarah Tishkoff, PI).

The Population Genetics of Divergence, National Institutes of Health, 2R01 GM078204-05, 01/01/15 – 12/31/16 (Jody Hey, PI)

Past:

Statistical Methods for Next-generation sequence data, National Institutes of Health, 5R01GM097505-02, 2013 – 2016 (Hongzhe Lee, PI). Goal: development of novel statistical methods and computational tools for statistical and probabilistic modeling of large-scale next-generation sequence (NGS) data motivated by important biological questions and experiments.

Population Genomics of Geographically and Ethnically Diverse Africans, National Human Genome Research Institute, F32HG006648, 2011-2014 (Joseph Lachance, PI), (Role in grant: Mentor for Joseph Lachance, Goal: Population genomics analysis of ethnically diversity Africans)

African Odyssey: An Integrative Genomics Analysis Of Complex Physiologic Traits, National Institutes Of Health, 5-DP1-OD-006445, 2009-2014 (Sarah Anne Tishkoff, PI), (Role in grant: PI, Goal: To use evolutionary biology, genomics, and systems biology approaches to dissect the genetic architecture of complex physiological traits across ethnically and geographically diverse Africans.)

African Integrative Genomics, PGFI Special Initiatives Funding, 1/2010-7/2013 (Tishkoff, PI), (Role in grant: PI, Goal: RNA Sequencing of RNA obtained from white cells from ethnically diverse Africans)

Collaborative Research: Genetic Bases For The Evolution Of Human Diet, National Science Foundation, BCS-0827436, 10/2008-9/2013 (Sarah Anne Tishkoff, PI) (Role in grant: PI, Goal: To study the evolution of diet during human origins.)

African Diversity and the Genetics of Human Health, National Human Genome Research Institute, 5-F32-HG005292-03, 9/2009-10/2011 (Joe Jarvis, PI), (Role in grant: Mentor for Joseph Jarvis, Goal: postdoctoral training to study association mapping in structured populations)

Doctoral Dissertation Improvement: Patterns Of Genetic Diversity And Signatures Of Natural Selection At The Intercellular Adhesion Molecule-1 (ICAM-1) And CD36 Loci, Directorate For Social, Behavioral And Economic Sciences/NSF, 0925802, 9/2009-8/2010 (Sarah Anne Tishkoff, PI), (Role in grant: PI, Goal: To fund graduate student research of Felicia Gomez to study nucleotide diversity at malaria susceptibility loci)

Association Mapping In Structured Populations, Stanford University, 26275940-49517-A, 8/2007-7/2011 (Carlos Bustamante, PI: Sarah Anne Tishkoff, Co-Principal Investigator), Goal: To develop novel statistical methods for association mapping in structured populations. Note: Originally applied for this joint NSF/NIH RFA as a full PI (multiple PIs). NIH awarded Bustamante as the sole PI and Tishkoff as a co-PI.)

Genetic History Of East Africa, National Science Foundation, BCS-0905858, 4/2007-3/2010 (Sarah Anne Tishkoff, PI), (Role in grant: PI, Goal: To reconstruct human evolutionary history of East African populations.)

Molecular, Statistical, And Bioinformatics Analysis Of Plasmodium And Human Genome Co-Evolution, Human Frontier Science Program Organization, GRP0054/2006-C, 12/2006-11/2010 (Sarah Anne Tishkoff, PI), (Role in grant: PI, Goal: To study co-evolution of human and Plasmodium falciparum genomes.)

Variation At Malaria Resistance Genes In Africans, National Institutes Of Health, 5-R01-GM-076637-05REVISED, 6/2006-12/2010 (Sarah Anne Tishkoff, PI), (Role in grant: PI, Goal: To characterize nucleotide diversity at loci involved in malarial resistance in African populations.)

Characterizing a Genetic History of African Populations, NRSA Postdoctoral Fellowship, 1/2006-1/2008 (Floyd Reed, PI), (Role in grant: Mentor for Floyd Reed, Goal: Postdoctoral Fellowship to characterize genetic substructure in Africans using a genome-wide panel of markers.)

Genetic History of East African Populations, Leakey Foundation, 1/2006-1/2007 (Sarah Anne Tishkoff, PI), (Role in grant: PI, Goal: To conduct fieldwork in Kenya and Ethiopia in order to collect DNA samples obtained from whole blood.)

The Co-Evolution of Human Plasmodium Genomic Interactions, Keck Foundation, 1/2006-1/2007 (Awadalla, PI: Sarah Anne Tishkoff, Co-Investigator), (Role in grant: Co-PI, Goal: to study variation at malaria susceptibility loci)

Genetic Structure of African and African American Populations, Center for Medical Genetics, Mammalian Genotyping Service, 1/2005-1/2006 (Sarah Anne Tishkoff, PI), (Role in grant: PI, Two competitive awards to have the Marshfield panel of 800 microsatellite and 400 in/del markers genotyped in ~3000 samples. Goal: to determine genetic structure of African and African American populations and identify markers and populations useful for gene mapping studies.)

Nucleotide Variability and Signatures of Natural Selection at the Human Vasopressin Type 2 (AVPRS) and Oxytocin Receptor (OTR) Loci, NSF Doctoral Dissertation Improvement Grant, 1/2005-1/2006 (Sarah Anne Tishkoff, PI), (Role in grant: PI, Goal: To fund PhD work of Lisa Pfeiffer to resequence the vasopressin type 2 and oxytocin receptor genes in geographically diverse populations in order to identify functionally significant mutations.)

Genetic Structure of African and African American Populations, Center for Medical Genetics, Mammalian Genotyping Service, 1/2004-1/2005 (Sarah Anne Tishkoff, PI), (Role in grant: PI, Two competitive awards to have the Marshfield panel of 800 microsatellite and 200 in/del markers genotyped in ~3200 samples. Goal: to determine genetic structure of African and African American populations and identify markers and populations useful for gene mapping studies.)

Genetic History of Kenyan Populations, Leakey Foundation, 1/2003-1/2006 (Sarah Anne Tishkoff, PI), (Role in grant: PI, Goal: To provide funding for a Kenyan PhD student studying genetic diversity of Kenyan populations.)

The Co-Evolution Of Human And Plasmodium Genomic Interactions, David And Lucile Packard Foundation, 2001-19049/2001-19049A, 11/2001-10/2006 (with extensions through 2009) (Sarah Anne Tishkoff, PI), (Role in grant: PI, Career Award)

Integrative Human Evolutionary Biology, NSF IGERT Training Grant, 1/2000-1/2007 (Sarah Tishkoff, PI: Greg Wray, Co-Investigator), (Role in grant: Co-PI, Goal: to provide interdisciplinary graduate training in human evolutionary biology.)

Genetic Variation Among Linguistically Diverse Tanzanian Populations: Implications for East African History and Modern Human Origins, NSF, BCS 9905396, 1/1999-1/2004 (Sarah Anne Tishkoff, PI), (Role in grant: PI, Goal: to obtain DNA samples and to characterize genetic diversity amongst linguistically diverse Tanzanian populations in order to reconstruct population histories and modern human origins.)

Genetic Diversity of Tanzanian Hunter-Gatherer Populations, Leakey Foundation, 1/1999-1/2001 (Sarah Anne Tishkoff, PI), (Role in grant: PI, Goal: to characterize genetic diversity and history of hunter-gatherer populations of Tanzania.)

Genetic History of Tanzanian Populations, Wenner Gren Foundation, 1/1999-1/2001 (Sarah Anne Tishkoff, PI), (Role in grant: PI, Goal: to characterize genetic diversity and evolutionary history of Tanzanian populations.)

Molecular Sequence Variation in G6PD and Its Role in Malarial Resistance, Burroughs/Wellcome Fund Career Award, 1/1998-1/2005 (Sarah Anne Tishkoff, PI), (Role in grant: PI, Goal: to characterize nucleotide diversity at the G6PD locus and determine the evolutionary forces resulting in high levels of G6PD deficiency mutations.)

Bibliography:

Research Publications, peer reviewed:

1. Ruano, G., Deinard, A. S., Tishkoff, S., Kidd, K. K.. Detection of DNA sequence variation via deliberate heteroduplex formation from genomic DNAs amplified en masse in "population tubes" PCR Methods and Applications 3(4): 225-31, 1994.

2. Risch, N., K.K. Kidd, and S.A. Tishkoff. Genetic data and the African origin of humans. Science 274: 1548-1549, Nov 1996.

3. Tishkoff, S.A., K.K. Kidd, and N. Risch. Interpretations of Multiregional Evolution. Science, letter to the editor 274, Nov 1996.

4. Michalatos-Beloin*, S., Tishkoff*, S. A., Bentley, K. L., Kidd, K. K., Ruano, G.. Molecular haplotyping of genetic markers 10 kb apart by allele-specific long-range PCR. Nucleic Acids Research 24(23): 4841-3, 1996 Notes: *These authors contributed equally.

5. Tishkoff, S. A., Ruano, G., Kidd, J. R., Kidd, K. K.. Distribution and frequency of a polymorphic Alu insertion at the plasminogen activator locus in humans. Human Genetics 97(6): 759-64, 1996.

6. Tishkoff, S.A., E. Dietzsch, W. Speed, A.J. Pakstis, K. Cheung, J.R. Kidd, B. Bonné-Tamir, A.S. Santachiara-Benerecetti, P. Moral, E. Watson, M. Krings, S. Pääbo, N. Risch, T. Jenkins, and K.K. Kidd. Global patterns of linkage disequilibrium at the CD4 locus and modern human origins. Science 271(5254): 1380-7, 1996.

7. Zietkiewicz, E., Yotova, V., Jarnik, M., Korab-Laskowska, M., Kidd, K. K., Modiano, D., Scozzari, R., Stoneking, M., Tishkoff, S., Batzer, M., Labuda, D.. Nuclear DNA diversity in worldwide distributed human populations. Gene 205(1-2): 161-71, 1997.

8. Tishkoff, S. A., Goldman, A., Calafell, F., Speed, W. C., Deinard, A. S., Bonne-Tamir, B., Kidd, J. R., Pakstis, A. J., Jenkins, T., Kidd, K. K.. A global haplotype analysis of the myotonic dystrophy locus: implications for the evolution of modern humans and for the origin of myotonic dystrophy mutations. American Journal of Human Genetics 62(6): 1389-402, 1998.

9. Zietkiweicz, E., V. Yotova, M. Jarnik, M. Korab-Laskowska, K.K. Kidd, D. Modiano, R. Scozzari, M. Stoneking, S. Tishkoff, M. Batzer, and D. Labuda. Genetic structure of the ancestral population of modern humans. Journal of Molecular Evolution 47: 146-155, 1998.

10. Destro-Bisol, G., Maviglia, R., Caglia, A., Boschi, I., Spedini, G., Pascali, V., Clark, A., Tishkoff, S.. Estimating European admixture in African Americans by using microsatellites and a microsatellite haplotype (CD4/Alu). Human Genetics 104(2): 149-57, 1999.

11. Tishkoff, S.A., A.J. Pakstis, S. Michalatos-Beloin, G. Ruano, and K.K. Kidd. A comparison of molecular and statistical methods for estimating haplotype frequencies as illustrated by highly polymorphic STRP data. American Journal of Human Genetics 67(2): 518-22, Aug 2000.

12. Tishkoff SA, Pakstis AJ, Stoneking M, Kidd JR, Destro-Bisol G, Sanjantila A, Lu R, Deinard AS, Sirugo G, Jenkins T, Kidd KK, and Clark AG. Short Tandem-Repeat Polymorphism/Alu Haplotype Variation at the PLAT Locus: Implications for Modern Human Origins. American Journal of Human Genetics 67(4): 901-925, Oct 2000.

13. Tishkoff, S. A., Pakstis, A. J., Ruano, G., Kidd, K. K.. The accuracy of statistical methods for estimation of haplotype frequencies: an example from the CD4 locus. American Journal of Human Genetics 67(2): 518-22, 2000.

14. Tishkoff, S. A., Varkonyi, R., Cahinhinan, N., Abbes, S., Argyropoulos, G., Destro-Bisol, G., Drousiotou, A., Dangerfield, B., Lefranc, G., Loiselet, J., Piro, A., Stoneking, M., Tagarelli, A., Tagarelli, G., Touma, E. H., Williams, S. M., Clark, A. G.. Haplotype diversity and linkage disequilibrium at human G6PD: recent origin of alleles that confer malarial resistance. Science 293(5529): 455-62, 2001.

15. Verrelli, B. C., McDonald, J. H., Argyropoulos, G., Destro-Bisol, G., Froment, A., Drousiotou, A., Lefranc, G., Helal, A. N., Loiselet, J., Tishkoff, S. A.. Evidence for balancing selection from nucleotide sequence analyses of human G6PD. American Journal of Human Genetics 71(5): 1112-28, 2002.

16. Drousiotou, Anthi, Elias Touma, Nicoletta Andreou, Jacques Loiselet, Michalis Angastiniotis, Brian Verrelli, Sarah Tishkoff. Molecular characterization of G6PD deficiency in Cyprus. Blood Cells Molecular Disease 33: 25-30, 2004.

17. Smith MW, NJ Patterson, JA Lautenberger, AL Truelove, GJ McDonald, BD Kessing, Z Yi, G deThe, M. Essex, P. J. Kanki, JP Phair, JJ Goedert, D Vlahov, RE Ferrell, SM Williams, SA Tishkoff, CA Winkler, FM DeLaVega, T Woodage, D Altshuler, JJ Sninsky, DA Gilbert, DA Hafler, SJ O'Brien, and DE Reich. A high density ancestry map for disease gene discovery in African Americans. American Journal of Human Genetics 74(5): 1001-13, 2004.

18. Tishkoff, S. A., Kidd, K. K.. Implications of biogeography of human populations for "race" and medicine. Nature Genetics 36(11 Suppl): S21-7, 2004.

19. Verrelli, B.J. and S.A. Tishkoff. Signatures of selection and gene conversion associated with human color vision variation. American Journal of Human Genetics 75(3): 363-75, 2004.

20. Evans PD, Gilbert SL, Mekel-Bobrov N, Vallender EJ, Anderson JR, Vaez-Azizi LM, Tishkoff SA, Hudson RR, Lahn BT.. Microcephalin, a gene regulating brain size, continues to evolve adaptively in humans. Science 309: 1717-20, 2005.

21. Mekel-Bobrov N, Gilbert SL, Evans PD, Vallender EJ, Anderson JR, Hudson RR, Tishkoff SA, and Lahn BT.. Ongoing adaptive evolution of ASPM, a brain size determinant in Homo sapiens. Science 309: 1720-2, 2005.

22. Shriver MD, Rui Mei, Esteban J. Parra, Vibhor Sonpar, Indrani Halder, Sarah A. Tishkoff, Theodore G. Schurr, Sergev I. Zhadanov, Ludmilla P. Osipova, Tom Brutsaert, Jonathan Friedlaender, Lynn B. Jorde, W. Scott Watkins, Michael J. Bamshad, Gerardo Gutierez, Halina Loi, Hajime Matsuzaki, George Argyropoulos, Jose Fernandez, Rick A. Kittles, Joshua M. Akey, and Keith Jones. Large-scale SNP analysis reveals clustered and continuous patterns of human genetic variation. Human Genomics 2(81): 81-89, 2005.

23. Tarazona-Santos, E., Tishkoff, S. A.. Divergent patterns of linkage disequilibrium and haplotype structure across global populations at the interleukin-13 (IL13) locus. Genes and Immunity 6(1): 53-65, 2005.

24. Awomoyi A, G. Sirugo, M.J. Newport, and S.A. Tishkoff . Global distribution of a novel trinucleotide microsatellite polymorphism (ATA)n in intron 8 of the SLC11A1 gene and susceptibility to pulmonary Tuberculosis. European Journal of Immunogenetics 33(1): 11-5, 2006.

25. Reed FA, Tishkoff SA.: Positive selection can create false hotspots of recombination. Genetics 172(3): 2011-4, 2006.

26. Verrelli, B. C., Tishkoff, S. A., Stone, A. C., Touchman, J. W.. Contrasting histories of G6PD molecular evolution and malarial resistance in humans and chimpanzees. Molecular Biology and Evolution 23(8): 1592-601, 2006.

27. Wang, J., Song, L., Gonder, M. K., Azrak, S., Ray, D. A., Batzer, M. A., Tishkoff, S. A., Liang, P.. Whole genome computational comparative genomics: A fruitful approach for

ascertaining Alu insertion polymorphisms. Gene 365: 11-20, 2006.

28. Tishkoff, S.A, Gonder, M.K, Henn, B.M., Mortensen H., Fernandopulle, N., Gignoux C., Knight, A, Underhill, P.A., Ramakrishnan, U, Reed, F.A., Mountain, J.L.. History of click-speaking populations of Africa inferred from mtDNA and Y chromosome genetic variation. Molecular Biology and Evolution 24(10): 2180-2195, July 2007.

29. Gonder, M. K., Mortensen, H. M., Reed, F. A., de Sousa, A., Tishkoff, S. A.. Whole-mtDNA genome sequence analysis of ancient African lineages. Molecular Biology and Evolution 24(3): 757-68, 2007.

30. Lind, J. M., Hutcheson-Dilks, H. B., Williams, S. M., Moore, J. H., Essex, M., Ruiz-Pesini, E., Wallace, D. C., Tishkoff, S. A., O'Brien, S. J., Smith, M. W.. Elevated male European and female African contributions to the genomes of African American individuals. Human Genetics 120(5): 713-22, 2007.

31. Shimada, Makoto K, Karuna Panchapakesan, Sarah Tishkoff , Alejandro Q. Nato, Jr., and Jody Hey. Divergent haplotypes and human history as revealed in a worldwide survey of X-linked DNA sequence variation. Molecular Biology and Evolution 24(3): 687-98, 2007.

32. Tishkoff, S. A., Reed, F. A., Ranciaro, A., Voight, B. F., Babbitt, C. C., Silverman, J. S., Powell, K., Mortensen, H. M., Hirbo, J. B., Osman, M., Ibrahim, M., Omar, S. A., Lema, G., Nyambo, T. B., Ghori, J., Bumpstead, S., Pritchard, J. K., Wray, G. A., Deloukas, P.. Convergent adaptation of human lactase persistence in Africa and Europe. Nature Genetics 39(1): 31-40, 2007.

33. Henn, B. M., Gignoux, C., Lin, A. A., Oefner, P. J., Shen, P., Scozzari, R., Cruciani, F., Tishkoff, S. A., Mountain, J. L., Underhill, P. A.. Y-chromosomal evidence of a pastoralist migration through Tanzania to southern Africa. Proceedings of the National Academy of Sciences 105(31): 10693-8, 2008.

34. Tishkoff, S. A., Reed, F. A., Friedlaender, F. R., Ehret, C., Ranciaro, A., Froment, A., Hirbo, J. B., Awomoyi, A. A., Bodo, J. M., Doumbo, O., Ibrahim, M., Juma, A. T., Kotze, M. J., Lema, G., Moore, J. H., Mortensen, H., Nyambo, T. B., Omar, S. A., Powell, K., Pretorius, G. S., Smith, M. W., Thera, M. A., Wambebe, C., Weber, J. L., Williams, S. M.. The genetic structure and history of Africans and African Americans. Science 324(5930): 1035-44, 2009.

35. Bryc, K., Auton, A., Nelson, M.R., Oksenberg, J.R., Hauser, S.L., Williams, S., Froment, A., Bodo, J.M, Wambebe, C., Tishkoff*, S.A., and Bustamante, C.D.*. Genome-wide patterns of population structure and admixture in West Africans and African Americans. Proceedings of the National Academy of Sciences 107(2): 786-91, Jan 12 2010 Notes: * Contributed equally as co-senior authors.

36. Scheinfeldt, L. B., Soi, S., Tishkoff, S. A.. Colloquium paper: working toward a synthesis of archaeological, linguistic, and genetic data for inferring African population history. Proceedings of the National Academy of Sciences 107 Suppl 2: 8931-8, 2010.

37. Gonder, Mary Katherine, Locatelli, Sabrina, Ghobrial, Lora, Mitchell, Matthew W., Kujawski, Joseph T., Lankester, Felix J., Stewart, Caro-Beth, Tishkoff, Sarah A.. Evidence from Cameroon reveals differences in the genetic structure and histories of chimpanzee populations. Proceedings of the National Academy of Sciences 108(12): 4766-71, March 22 2011.

38. Ko, W. Y., Kaercher, K. A., Giombini, E., Marcatili, P., Froment, A., Ibrahim, M., Lema, G., Nyambo, T. B., Omar, S. A., Wambebe, C., Ranciaro, A., Hirbo, J. B., Tishkoff, S. A.. Effects of Natural Selection and Gene Conversion on the Evolution of Human Glycophorins Coding for MNS Blood Polymorphisms in Malaria-Endemic African Populations. American Journal of Human Genetics 88(6): 741-54, June 2011.

39. Mortensen, H.;Froment, A.; Lema, G.; Bodo, J.M.; Ibrahim, M.; Nyambo, T.B.; Omar, S.A.; Tishkoff, S.A.. Characterization of Genetic Variation and Natural Selection at the Arylamine N-Acetyltransferase (NAT) Genes In global human populations. Pharmacogenomics 12(11): 1545-58, November 2011.

40. Huang, L., Jakobsson, M., Pemberton, T.J., Muntaser, I., Nyambo, T., Omar, S., Pritchard, J.K., Tishkoff, S.A., Rosenberg, N.A.. Haplotype variation and genotype imputation in African populations. Genetic Epidemiology 35(8): 766-80, Dec 2011.

41. Cabral, W. A., Barnes, A. M., Adeyemo, A., Cushing, K., Chitayat, D., Porter, F. D., Panny, S. R., Gulamali-Majid, F., Tishkoff, S. A., Rebbeck, T. R., Gueye, S. M., Bailey-Wilson, J. E., Brody, L. C., Rotimi, C. N., Marini, J. C.. A founder mutation in LEPRE1 carried by 1.5% of West Africans and 0.4% of African Americans causes lethal recessive osteogenesis imperfecta. Genetics in medicine : official journal of the American College of Medical Genetics 14(5): 543-51, 2012.

42. Campbell, M. C., Ranciaro, A., Froment, A., Hirbo, J., Omar, S., Bodo, J. M., Nyambo, T., Lema, G., Zinshteyn, D., Drayna, D., Breslin, P. A., Tishkoff, S. A.. Evolution of functionally diverse alleles associated with PTC bitter taste sensitivity in Africa. Molecular biology and evolution 29(4): 1141-53, 2012.

43. Jarvis, J. P., Scheinfeldt, L. B., Soi, S., Lambert, C., Omberg, L., Ferwerda, B., Froment, A., Bodo, J. M., Beggs, W., Hoffman, G., Mezey, J., Tishkoff, S. A.. Patterns of ancestry, signatures of natural selection, and genetic association with stature in Western African pygmies. PLoS genetics 8(4): e1002641, 2012.

44. Lachance, J., Vernot, B., Elbers, C. C., Ferwerda, B., Froment, A., Bodo, J. M., Lema, G., Fu, W., Nyambo, T. B., Rebbeck, T. R., Zhang, K., Akey, J. M., Tishkoff, S. A.. Evolutionary history and adaptation from high-coverage whole-genome sequences of diverse African hunter-gatherers. Cell 150(3): 457-69, 2012.

45. Mangino, M., Hwang, S. J., Spector, T. D., Hunt, S. C., Kimura, M., Fitzpatrick, A. L., Christiansen, L., Petersen, I., Elbers, C. C., Harris, T., Chen, W., Srinivasan, S. R., Kark, J. D., Benetos, A., El Shamieh, S., Visvikis-Siest, S., Christensen, K., Berenson, G. S.,

Valdes, A. M., Vinuela, A., Garcia, M., Arnett, D. K., Broeckel, U., Province, M. A., Pankow, J. S., Kammerer, C., Liu, Y., Nalls, M., Tishkoff, S., Thomas, F., Ziv, E., Psaty, B. M., Bis, J. C., Rotter, J. I., Taylor, K. D., Smith, E., Schork, N. J., Levy, D., Aviv, A.. Genome-wide meta-analysis points to CTC1 and ZNF676 as genes regulating telomere homeostasis in humans. Human Molecular Genetics, 15;21(24):5385-94. Dec. 2012.

46. Pickrell, J. K., Patterson, N., Barbieri, C., Berthold, F., Gerlach, L., Guldemann, T., Kure, B., Mpoloka, S. W., Nakagawa, H., Naumann, C., Lipson, M., Loh, P. R., Lachance, J., Mountain, J., Bustamante, C. D., Berger, B., Tishkoff, S. A., Henn, B. M., Stoneking, M., Reich, D., Pakendorf, B.. The genetic prehistory of southern Africa. Nature Communications 3: 1143, 2012.

47. Scheinfeldt, L. B., Soi, S., Thompson, S., Ranciaro, A., Woldemeskel, D., Beggs, W., Lambert, C., Jarvis, J. P., Abate, D., Belay, G., Tishkoff, S. A.. Genetic adaptation to high altitude in the Ethiopian highlands. Genome Biology 13(1): R1, 2012.

48. Steinberg, K. M., Antonacci, F., Sudmant, P. H., Kidd, J. M., Campbell, C. D., Vives, L., Malig, M., Scheinfeldt, L., Beggs, W., Ibrahim, M., Lema, G., Nyambo, T. B., Omar, S. A., Bodo, J. M., Froment, A., Donnelly, M. P., Kidd, K. K., Tishkoff, S. A., Eichler, E. E.. Structural diversity and African origin of the 17q21.31 inversion polymorphism. Nature Genetics 44(8): 872-80, 2012.

49. Wang, X., Mitra, N., Secundino, I., Banda, K., Cruz, P., Padler-Karavani, V., Verhagen, A., Reid, C., Lari, M., Rizzi, E., Balsamo, C., Corti, G., De Bellis, G., Longo, L., Beggs, W., Caramelli, D., Tishkoff, S. A., Hayakawa, T., Green, E. D., Mullikin, J. C., Nizet, V., Bui, J., Varki, A., Benjamin, B., Blakesley, R., Bouffard, G., Brooks, S., Chu, G., Coleman, H., Dekhtyar, M., Gregory, M., Guan, X., Gupta, J., Han, J., Hargrove, A., Ho, S. L., Johnson, T., Legaspi, R., Lovett, S., Maduro, Q., Masiello, C., Maskeri, B., McDowell, J., Montemayor, C., Novotny, B., Park, M., Riebow, N., Schandler, K., Schmidt, B., Sison, C., Stantripop, M., Thomas, J., Vemulapalli, M., Young, A.. Specific inactivation of two immunomodulatory SIGLEC genes during human evolution. Proceedings of the National Academy of Sciences of the United States of America 109(25): 9935-40, 2012.

50. Aminkeng, F., Ross, C. J., Rassekh, S. R., Brunham, L. R., Sistonen, J., Dube, M. P., Ibrahim, M., Nyambo, T. B., Omar, S. A., Froment, A., Bodo, J. M., Tishkoff, S., Carleton, B. C., Hayden, M. R.. Higher frequency of genetic variants conferring increased risk for ADRs for commonly used drugs treating cancer, AIDS and tuberculosis in persons of African descent. The Pharmacogenomics Journal Apr 16. doi: 10.1038/tpj. 2013.

51. Gomez, F., Tomas, G., Ko, W. Y., Ranciaro, A., Froment, A., Ibrahim, M., Lema, G., Nyambo, T. B., Omar, S. A., Wambebe, C., Hirbo, J. B., Rocha, J., Tishkoff, S. A.. Patterns of nucleotide and haplotype diversity at ICAM-1 across global human populations with varying levels of malaria exposure. Human Genetics 132(9): 987-99, 2013.

52. Ko, W.Y., Rajan, P., Gomez, F., Scheinfeldt, L., An, P., Winkler, C.A., Froment, A., Nyambo, T.B., Omar, S.A., Wambebe, C., Ranciaro, A., Hirbo, J.B., Tishkoff, S.A..

Identifying Darwinian selection acting on different human APOL1 variants among diverse African populations. American Journal of Human Genetics 93(1): 54-66, 2013.

53. Prado-Martinez, J., Sudmant, P.H., Kidd, J.M., Li, H., Kelley, J.L., Lorente-Galdos, B.,Veeramah, K.R., Woerner, A.E., O'Connor, T.D., Santpere, G., Cagan, A., Theunert, C., Casals, F., Laayouni, H., Munch, K., Hobolth, A., Halager, A.E., Malig, M., Hernandez-Rodriguez, J., Hernando-Herraez, I., Prüfer, K., Pybus, M., Johnstone, L., Lachmann, M., Alkan, C., Twigg, D., Petit, N., Baker, C., Hormozdiari, F., Fernandez-Callejo, M., Dabad, M., Wilson, M.L., Stevison, L., Camprubí, C., Carvalho, T., Ruiz-Herrera, A., Vives, L., Mele, M., Abello, T., Kondova, I., Bontrop, R.E., Pusey, A., Lankester, F., Kiyang, J.A., Bergl, R.A., Lonsdorf, E., Myers, S., Ventura, M., Gagneux, P., Comas, D., Siegismund, H., Blanc, J., Agueda-Calpena, L., Gut, M., Fulton, L., Tishkoff, S.A., Mullikin, J.C., Wilson, R.K., Gut, I.G., Gonder, M.K., Ryder, O.A., Hahn, B.H., Navarro, A., Akey, J.M., Bertranpetit, J., Reich, D., Mailund, T., Schierup, M.H., Hvilsom, C., Andrés, A.M., Wall, J.D., Bustamante, C.D., Hammer, M.F., Eichler, E.E., Marques-Bonet, T.. Great ape genetic diversity and population history. Nature. Jul 25;499(7459):471-5. 2013.

54. Wang S, Lachance J, Tishkoff SA, Hey J, Xing J. Apparent Variation in Neanderthal Admixture among African Populations is Consistent with Gene Flow from Non-African Populations. Genome Biol Evol. 5(11):2075-81. 2013.

55. Ferreira Z, Hurle B, Andrés AM, Kretzschmar W, Mullikin J, Cherukuri P, Cruz P, Gonder MK, Stone A, Tishkoff S, Swanson W; NISC Comparative Sequencing Program, Green E, Clark AG, Seixas S. Sequence diversity of Pan troglodytes subspecies and the impact of WFDC6 selective constraints in reproductive immunity. Genome Biol Evol. Jan;5(12):2512-23, 2013.

56. Elbers, C. C., Garcia, M. E., Kimura, M., Cummings, S. R., Nalls, M. A., Newman, A. B., Park, V., Sanders, J. L., Tranah, G. J., Tishkoff, S. A., Harris, T. B., Aviv, A.. Comparison Between Southern Blots and qPCR Analysis of Leukocyte Telomere Length in the Health ABC Study. The journals of gerontology. Series A, Biological sciences and medical sciences, May;69(5):527-31. 2014.

57. Campbell, M.C., Ranciaro, A., Zinshteyn, D., Rawlings-Goss, R., Hirbo, J.B., Thompson, S.I., Woldemeskel, D., Froment, A., Rucker, J.B., Omar, S.A., Bodo, J.-M., Nyambo, T., Belay, G., Drayna, D., Breslin, P.A.S., Tishkoff, S.A. Origin and differential selection of allelic variation at TAS2R16 associated with salicin bitter taste sensitivity in Africa. Molecular Biology and Evolution, 31(2):288-302, 2014.

58. Ranciaro, A., Campbell, M.C., Hirbo, J.B., Ko, W.-Y., Froment, A., Destro-Bisol, G., Kotze, M.J., Ibrahim, M., Nyambo, T., Omar, S.A., Tishkoff, S.A. Genetic origins of lactase persistence and the spread of pastoralism in Africa, American Journal of Human Genetics, 3;94(4):496-510, 2014.

59. Campbell MC, Ranciaro A, Zinshteyn D, Rawlings-Goss R, Hirbo J, Thompson S, Woldemeskel D, Froment A, Omar SA, Bodo JM, Nyambo T, Belay G, Drayna D, Breslin PA, Tishkoff SA. Limited evidence for adaptive evolution and functional effect of allelic variation at rs702424 in the promoter of the TAS2R16 bitter taste receptor gene in Africa. J Hum Genet.

Jun;59(6):349-52. 2014.

60. Elhassan N, Gebremeskel EI, Elnour MA, Isabirye D, Okello J, Hussien A, Kwiatksowski D, Hirbo J, Tishkoff S, Ibrahim ME. The Episode of Genetic Drift Defining the Migration of Humans out of Africa Is Derived from a Large East African Population Size. PLoS One. May 20;9(5):e97674. 2014.

61. Rawlings-Goss, Renata A., Michael C Campbell and Sarah A Tishkoff. Global Population-specific Variation in miRNA associated with Cancer Risk and Clinical Biomarkers. BMC Medical Genomics, Aug 28;7:53. doi: 10.1186/1755-8794-7-53. 2014

62. Lazaridis I, Patterson N, Mittnik A, Renaud G, Mallick S, …… Tishkoff SA, Singh L, Thangaraj K, Villems R, Comas D, Sukernik R, Metspalu M, Meyer M, Eichler EE, Burger J, Slatkin M, Pääbo S, Kelso J, Reich D, Krause J. Ancient human genomes suggest three ancestral populations for present-day Europeans. Nature. 18;513(7518):409-13. 2014

63. Lachance, J. Tishkoff S.A. Biased gene conversion skews allele frequencies in human populations, increasing the disease burden of recessive alleles. Am J Hum Genet. 2;95(4):408-20. 2014.

64. Mangino M, Christiansen L, Stone R, Hunt SC, Horvath K, Eisenberg DT, Kimura M, PetersenI, Kark JD, Herbig U, Reiner AP, Benetos A, Codd V, Nyholt DR, Sinnreich R, Christensen K, Nassar H, Hwang SJ, Levy D, Bataille V, Fitzpatrick AL, Chen W, Berenson GS, Samani NJ, Martin NG, Tishkoff S, Schork NJ, Kyvik KO, Dalgård C, Spector TD, Aviv A. "DCAF4, a novel gene associated with leucocyte telomere length." J Med Genet. Mar;52(3):157-62. 2015.

65. Karmin M, Saag L, Vicente M, Sayres MA, Järve M, ……. Lachance J, Tishkoff S, …..M, Thomas MG, Tyler-Smith C, Underhill PA, Willerslev E, Nielsen R, Metspalu M, Villems R, Kivisild T. A recent bottleneck of Y chromosome diversity coincides with a global change in culture. Genome Res. Apr;25(4):459-66. 2015

66. Nam K, Munch K, Hobolth A, Dutheil JY, Veeramah KR, Woerner AE, Hammer MF; Great Ape Genome Diversity Project, Mailund T, Schierup MH. Extreme selective sweeps independently targeted the X chromosomes of the great apes. Proc Natl Acad Sci U S A. May 19;112(20):6413-8. 2015

67. 1000 Genomes Project Consortium. A Global Reference for Human Genetic Variation. Nature. Oct 1; 526 (7571):68-74. 2015

69. Hsieh P, Veeramah KR, Lachance J, Tishkoff SA, Wall JD, Hammer MF, Gutenkunst RN. Whole-genome sequence analyses of Western Central African Pygmy hunter-gatherers reveal a complex demographic history and identify candidate genes under positive natural selection. Genome Res. Mar:26(3):279-90. 2016

70. Sobota RS, Stein CM, Kodaman N, Scheinfeldt LB, Maro I, Wieland-Alter W, Igo RP Jr, Magohe A, Malone LL, Chervenak K, Hall NB, Modongo C, Zetola N, Matee M, Joloba M,

Froment A, Nyambo TB, Moore JH, Scott WK, Lahey T, Boom WH, von Reyn CF, Tishkoff SA, Sirugo G, Williams SM. A Locus at 5q33.3 Confers Resistance to Tuberculosis in Highly Susceptible Individuals. Am J Hum Genet. Mar 3:98(3):514-24. 2016.

71. Jacobson DR, Alexander AA, Tagoe C, Garvey WT, Williams SM, Tishkoff S, Modiano D, Sirima SB, Kalidi I, Toure A, Buxbaum JN. The prevalence and distribution of the amyloidogenic transthyretin (TTR) V122I allele in Africa. Mol Genet Genomic Med. Jul 14;4(5):548-56. 2016

72. Mallick S, Li H, Lipson M, Mathieson I, Gymrek M, Racimo F, Zhao M, Chennagiri N, Nordenfelt S, Tandon A, Skoglund P, Lazaridis I, Sankararaman S, Fu Q, Rohland N, Renaud G, Erlich Y, Willems T, Gallo C, Spence JP, Song YS, Poletti G, Balloux F, van Driem G, de Knijff P, Romero IG, Jha AR, Behar DM, Bravi CM, Capelli C, Hervig T, Moreno-Estrada A, Posukh OL, Balanovska E, Balanovsky O, Karachanak-Yankova S, Sahakyan H, Toncheva D, Yepiskoposyan L, Tyler-Smith C, Xue Y, Abdullah MS, Ruiz-Linares A, Beall CM, Di Rienzo A, Jeong C, Starikovskaya EB, Metspalu E, Parik J, Villems R, Henn BM, Hodoglugil U, Mahley R, Sajantila A, Stamatoyannopoulos G, Wee JT, Khusainova R, Khusnutdinova E, Litvinov S, Ayodo G, Comas D, Hammer MF, Kivisild T, Klitz W, Winkler CA, Labuda D, Bamshad M, Jorde LB, Tishkoff SA, Watkins WS, Metspalu M, Dryomov S, Sukernik R, Singh L, Thangaraj K, Pääbo S, Kelso J, Patterson N, Reich D. The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. Nature. Oct 13;538(7624):201-206. 2016.

73. Pagani L, Lawson DJ, Jagoda E, Mörseburg A, Eriksson A, Mitt M, Clemente F, Hudjashov G, DeGiorgio M, Saag L, Wall JD, Cardona A, Mägi R, Sayres MA, Kaewert S, Inchley C, Scheib CL, Järve M, Karmin M, Jacobs GS, Antao T, Iliescu FM, Kushniarevich A, Ayub Q, Tyler-Smith C, Xue Y, Yunusbayev B, Tambets K, Mallick CB, Saag L, Pocheshkhova E, Andriadze G, Muller C, Westaway MC, Lambert DM, Zoraqi G, Turdikulova S, Dalimova D, Sabitov Z, Sultana GN, Lachance J, Tishkoff S, Momynaliev K, Isakova J, Damba LD, Gubina M, Nymadawa P, Evseeva I, Atramentova L, Utevska O, Ricaut FX, Brucato N, Sudoyo H, Letellier T, Cox MP, Barashkov NA, Škaro V, Mulahasanovic L, Primorac D, Sahakyan H, Mormina M, Eichstaedt CA, Lichman DV, Abdullah S, Chaubey G, Wee JT, Mihailov E, Karunas A, Litvinov S, Khusainova R, Ekomasova N, Akhmetova V, Khidiyatova I, Marjanović D, Yepiskoposyan L, Behar DM, Balanovska E, Metspalu A, Derenko M, Malyarchuk B, Voevoda M, Fedorova SA, Osipova LP, Lahr MM, Gerbault P, Leavesley M, Migliano AB, Petraglia M, Balanovsky O, Khusnutdinova EK, Metspalu E, Thomas MG, Manica A, Nielsen R, Villems R, Willerslev E, Kivisild T, Metspalu M. Genomic analyses inform on migration events during the peopling of Eurasia. Nature. Oct 13;538(7624):238-242. 2016

73. Hansen ME, Hunt SC, Stone RC, Horvath K, Herbig U, Ranciaro A, Hirbo J, Beggs W, Reiner AP, Wilson JG, Kimura M, De Vivo I, Chen MM, Kark JD, Levy D, Nyambo T, Tishkoff SA,* Aviv A.*. Shorter telomere length in Europeans than in Africans due to polygenetic adaptation. Hum Mol Genet. Jun 1;25(11):2324-2330. 2016. *Co-Senior Author

Research Publications, peer-reviewed reviews:

1. Tishkoff, S.A. and S.M. Williams. Genetic Analysis of African populations: Human evolution and complex disease. Nature Reviews Genetics 3(8): 611-21, 2002.

2. Tishkoff, S.A. and B.J. Verrelli. Patterns of human genetic diversity: Implications for human evolutionary history and human disease. Annual Review Genomics and Human Genetics 4: 293-340, 2003.

3. Tishkoff, SA and B.J. Verrrelli. Role of evolutionary history on haplotype block structure in the human genome: implications for disease mapping. Current Opinion in Genetics and Development 13(6): 569-75, 2003.

4. Reed, F.A. and S.A. Tishkoff. African human diversity, origins, and migrations. Current Opinion in Genetics and Development 16(6): 597-605, 2006.

5. Campbell, M. C., Tishkoff, S. A.. African genetic diversity: implications for human demographic history, modern human origins, and complex disease mapping. Annual Review Genomics and Human Genetics 9: 403-33, 2008.

6. Sirugo, G., Hennig, B. J., Adeyemo, A. A., Matimba, A., Newport, M. J., Ibrahim, M. E., Ryckman, K. K., Tacconelli, A., Mariani-Costantini, R., Novelli, G., Soodyall, H., Rotimi, C. N., Ramesar, R. S., Tishkoff, S. A., Williams, S. M.. Genetic studies of African populations: an overview on disease susceptibility and response to vaccines and therapeutics. Human Genetics 123(6): 557-98, 2008.

7. Lambert, C. A., Tishkoff, S. A.. Genetic structure in African populations: implications for human demographic history. Cold Spring Harbor symposia on quantitative biology 74: 395-402, 2009.

8. Campbell, M. C., Tishkoff, S. A. The evolution of human genetic and phenotypic variation in Africa. Current Biology 20(4): R166-73, 2010.

9. Vitti, J. J., Cho, M. K., Tishkoff, S. A., Sabeti, P. C. Human evolutionary genomics: ethical and interpretive issues. Trends in Genetics 28(3): 137-45, 2012.

10. Joseph Lachance and Sarah A. Tishkoff. Population Genomics of Human Adaptation. Annual Review of Ecology, Evolution, and Systematics, 44:123-143, 2013.

11. Lachance, J., Tishkoff, S. A. SNP ascertainment bias in population genetic analyses: why it is important, and how to correct it. BioEssays: news and reviews in molecular, cellular and developmental biology 35(9): 780-6, 2013.

12. Scheinfeldt, L. B., Tishkoff, S. A. Recent human adaptation: genomic approaches, interpretation and insights. Nature reviews. Genetics 14(10): 692-702, 2013.

13. Campbell, M., Hirbo J., J. Townsend, S.A. Tishkoff. The Peopling of the African Continent and the Diaspora into the New World, Current Opinion in Genetics & Development, 15;

29C:120-132. 2014.

14. Stone RC, Horvath K, Kark JD, Susser E, Tishkoff SA, Aviv A.. Telomere Length and the Cancer-Atherosclerosis Trade-Off. PLoS Genet. 2016 Jul 7;12(7):e1006144. 2016

15. Beltrame MH, Rubel MA, Tishkoff SA. Inferences of African evolutionary history from genomic data. Curr Opin Genet Dev. Dec;41:159-166. 2016.

16. Fan S, Hansen ME, Lo Y, Tishkoff SA. Going global by adapting local: A review of recent human adaptation. Science. Oct 7;354(6308):54-59. 2016.

15. Nielsen R, Akey JM, Jakobsson M, Pritchard JK, Tishkoff S, Willerslev E. Tracing the peopling of the world through genomics. Nature. Jan 18;541(7637):302-310. 2017

Editorials, Reviews, Chapters, including participation in committee reports (print or other media):

1. Heard, E., Tishkoff, S., Todd, J. A., Vidal, M., Wagner, G. P., Wang, J., Weigel, D., Young, R.. Ten years of genetics and genomics: what have we achieved and where are we heading? Nature Reviews Genetics 11(10): 723-33, 2010.

2. Scheinfeldt, L. B. and Tishkoff, S. A. Living the high life: high-altitude adaptation. Genome Biology 11(9): 133, 2010.

3. Tishkoff, S.. Interview with Sarah Tishkoff: perspectives for genetic research in African populations. Interview by Giovanni Destro-Bisol. Human biology 83(5): 637-44, 2011.

4. Williams, S.M and Tishkoff, S.A.. Exploring genomic studies in Africa. Genome Medicine 3(7):45. 2011.

5. Tishkoff, S.A. Strength in Small Numbers. Science, 349 (6254):1282-1283. 2015

6. Yudell M, Roberts D, DeSalle R, Tishkoff S. Science and Society: Taking race out of human genetics, Science, Feb 5:351(6273):564-5. 2016

Books:

1. Tishkoff, S.A., K.K. Kidd, and A.G. Clark. "Inferences of modern human origins from variation in CD4 haplotypes" Proceedings of the Trinational Workshop on Molecular Evolution. M.K. Uyenoyama and A. von Haeseler (eds.). Duke University Publications Group, Page: 181-198, 1998.

2. Tishkoff, S.A. and B.J. Verrelli. G6PD deficiency and malarial resistance in humans: insights from evolutionary genetic analyses Evolutionary Aspects of Infectious Disease. K. Dronamraju (eds.). Cambridge University Press, 2004.

3. Tishkoff, S.A. and M.K. Gonder. Human origins within and out of Africa. Anthropological Genetics. M. Crawford (eds.). Cambridge University Press, 2006.

4. Simpson, Kathleen, Tishkoff, Sarah. Genetics: from DNA to designer dogs. Textbook. National

Geographic, 2008.

5. J. B. Hirbo, A. Ranciaro, and S. A. Tishkoff. Population Structure and Migration in Africa: Correlations Between Archeological, Linguistic, and Genetic data. Causes and Consequences of Migration Benjamin Campbell and Michael H. Crawford (eds.). Cambridge University Press, 2012.

6. Wen-Ya Ko, Felicia Gomez, and Sarah A. Tishkoff. Rapid evolution of human erythrocyte-specific genes involved in malaria susceptibility. Evolution in the fast lane: Rapidly evolving genes and genetic systems. Rama S. Singh, Jianping Xu, and Rob J. Kulathinal (eds.). Oxford University Press, 2012.

7. Gomez, F., W.-Y. Ko, A. Davis, and S. A. Tishkoff.. Impact of Natural Selection due to Malarial Disease on Human Genetic Variation. "Primates, Pathogens and Evolution. Developments in Primatology: Progress and Prospects" J.F. Brinkworth and K. Pechenkina (eds.). Springer publishing, New York. 38: 117-160, 2013.

8. Gomez, F., J. Hirbo, and S.A. Tishkoff. African Population Genetic History and Evidence for Local Adaptation in African Populations. Who Are We? Human Diversity and Race from a Contemporary Genetics Perspective. Chakravarti, A. (eds.). Cold Spring Harbor Press, 2014.

Abstracts:

1. Mortensen, H.M, K. Gonder, J. Hirbo, S.A. Tishkoff. Genetic history of linguistically diverse Tanzanian populations inferred from mtDNA. Meeting on "Genomics and Society: Implications for the future health of Africa" sponsored by the African Genomics Initiative, Cairo, Egypt March 2004 Notes: Poster.

2. Gonder, M.K. and S.A. Tishkoff. Complete mitochondrial genome sequencing of Tanzanians implies an east African origin of modern humans. American Association of Physical Anthropology, Tampa, FL April 2004 Notes: Poster.

3. Hirbo, J. K. Gonder, J. Hodax, A. Knight , J. Mountain, and S. Tishkoff. Y chromosome genetic variation in Tanzanian populations: implications for modern human origins. American Association of Physical Anthropology, Tampa, FL April 2004 Notes: Poster.

4. Mortensen, H.M, K. Gonder, J. Hirbo, S.A. Tishkoff. Ancient Migrations and Population Expansions in East Africa: Genetic Evidence for Tanzanian Prehistory. American Association of Physical Anthropology, Tampa, FL April 2004 Notes: Oral presentation.

5. Pfeifer, L., B.C. Verrelli, S.A. Tishkoff. Nucleotide sequence variation of the Arginine Vasopressin Type II Receptor (AVPR2) gene in ethnically diverse human populations. American Association of Physical Anthropology, Tampa, FL April 2004 Notes: Poster.

6. Powell, K. and S.A. Tishkoff. Genotype/Phenotype Analysis of Lactase Persistence in Tanzanian Populations. American Association of Physical Anthropology, Tampa, FL April 2004 Notes: Poster.

7. Ranciaro, A., E. Tarazona-Santos, S.A. Tishkoff. Patterns of genetic diversity, haplotype structure, and linkage disequilibrium at interleukin-4 (IL-4) and interleukin-13 (IL-13) in human populations. American Association of Physical Anthropology, Tampa, FL April 2004 Notes: Poster.

8. Tishkoff, S.A., B.C. Verrelli, E. Tarazona-Santos, A. Ranciaro. Co-evolution of malaria infection and the human genome: implications for human evolutionary history. American Association of Physical Anthropology, Tampa, FL April 2004 Notes: Oral presentation.

9. Gonder, M.K., H.M. Mortensen, F. Reed, S.A. Tishkoff. Demographic History of Khoisan Speakers of Tanzania Inferred from mtDNA Control Region Sequences. Genomes and Evolution meeting (sponsored by SMBE and AGA), Pennsylvania State University June 2004 Notes: Poster.

10. Liang P, J. Wang, L. Song, M.K. Gonder, S.A. Tishkoff, S. Azrak. Intra-species genome comparison reveals 802 polymorphic Alus and dynamic Alu distributions in the human genome. American Society of Human Genetics meeting, Toronto, Canada October 2004 Notes: Poster.

11. Pfeifer, L.A. B.C. Verrelli, and S.A. Tishkoff. Patterns of nucleotide sequence diversity among humans and great apes at the Arginine Vasopressin Type II Receptor Gene (AVPR2). American Society of Human Genetics meeting, Toronto, Canada October 2004 Notes: Poster.

12. Ranciaro A., E. Tarazona-Santos, S.A. Tishkoff. Patterns of genetic diversity, haplotype structure, and linkage disequilibrium at interleukin-4 (IL-4) and interleukin-13 (IL-13) in human populations. American Society of Human Genetics meeting, Toronto, Canada October 2004 Notes: Poster.

13. Reed, F.A. and Tishkoff S.A.. Demographic and selective history of African populations inferred from genome-wide genetic markers" AAPA meeting, Milwaukee, WI April 2005 Notes: Oral presentation.

14. Tishkoff, S.A., Gonder M.K, Mortensen, H., Hirbo, J, de Sousa, A., Miguel T, and Reed, F.A.. Demographic history of African populations inferred from mtDNA analysis. AAPA meeting, Milwaukee, WI April 2005 Notes: Oral presentation.

15. Reed, FA, Weber, J, and Tishkoff, SA.. The demographic pattern of human populations in Africa inferred from genome-wide genetic markers. SMBE meeting, Aukland, New Zealand June 2005 Notes: Oral presentation.

16. Tishkoff, S.A, Gonder, M.K, Henn, B.M., Mortensen H., Fernandopulle, N., Gignoux C., Knight, A, Underhill, P.A., Ramakrishnan, U, Reed, F.A., Mountain, J.L.. Origins of click-speaking populations in Africa inferred from mtDNA and Y chromosome data. SMBE meeting, Aukland, New Zealand June 2005 Notes: Oral presentation.

17. Reed, F.A., J. Weber, and S.A. Tishkoff. Genetic Structure of African Populations. National

Academies Keck Futures Initiative The Genomic Revolution: Implications for Treatment and Control of Infectious Disease Conference in Irvine, California November 2005 Notes: Poster.

18. Pfeifer LA and Tishkoff SA. Genetic variability and signatures of natural selection at the human vasopressin type 2 (AVPR2) receptor locus. Gordon Research Conference on Genes and Behavior, Ventura, CA February 2006 Notes: Poster.

19. Gonder, M.K. H.M. Mortensen, F.A. Reed, A. de Sousa, and S.A. Tishkoff. Whole mtDNA genome sequence analysis of ancient African lineages. American Association of Physical Anthropology meeting, Anchorage, Alaska April 2006 Notes: Oral presentation.

20. Mountain, J.L., Gonder, M.K., B.M. Henn , H. Mortensen, C. Gignoux , P. A. Underhill, U. Ramakrishnan, F. A. Reed and S. A. Tishkoff. Languages, clicks, and genetic diversity. Language and Genes: An interdisciplinary conference. University of California, Santa Barbara September 2006 Notes: Poster.

21. Campbell ,M.C., S.A. Tishkoff, C. D. Bustamante, J.H. Lee, A. Carracedo, E.J. Parra, R. DeSalle, R.L. Holloway. Intracontinental Distribution of Haplotype Variation: Implications for Human Demographic History. American Society of Human Genetics meeting, New Orleans October 2006 Notes: Poster.

22. Hirbo, J., S. Omar, M. Ibrahim, S. Tishkoff. Paternal History of Linguistically diverse East African Populations. American Society of Human Genetics meeting, New Orleans October 2006 Notes: Poster.

23. Ranciaro, A. F.A. Reed, J. Hirbo, K. Powell, M. Osman, S. Omar, M. Ibrahim, S.A. Tishkoff. Molecular characterization of lactase gene regulation in African populations. American Society of Human Genetics meeting, New Orleans, October 2006 Notes: Poster.

24. Reed, F. A., A. Froment, M.W. Smith, S.M. Williams, S.A. Omar, M.J. Kotze, G.S. Pretorius, M. Ibrahim, O. Doumbo, M. Thera, C. Wambebe, S.E. Dobrin, J.L. Weber, S.A. Tishkoff. The Genetic Structure of Human Populations in Africa. American Society of Human Genetics meeting, New Orleans, October 2006 Notes: Oral presentation.

25. Tishkoff, S.A., F.A. Reed, A. Ranciaro, B.F. Voight, C.C. Babbitt, J.S. Silverman, K. Powell, J.B. Hirbo, H. Mortensen, M. Osman, M. Ibrahim, S.A. Omar, S. Bumpstead, J.K. Pritchard, G.A. Wray, P. Delouckas. The Genetic Basis of Lactase Persistence in Africa; Evidence for Convergent Adaptation Due to a Shared Cultural Trait in Europeans and Africans. American Society of Human Genetics meeting, New Orleans October 2006. Notes: Oral presentation.

26. Mountain, J.L., M.K. Gonder, B.M. Henn , H. Mortensen, C. Gignoux , P. A. Underhill, U. Ramakrishnan, F. A. Reed and S. A. Tishkoff. Languages, clicks, and genetic diversity Cradle of Language Conference, Stellenbosch, South Africa November 2006 Notes: Poster.

27. Pfeifer, L.A, and S.A. Tishkoff. Nucleotide sequence variation and balancing selection at the oxytocin receptor (OXTR) locus in ethnically diverse human populations. American Association of Physical Anthropologists meeting, Philadelphia, PA April 2007 Notes: Poster.

28. Tishkoff, S.A., F.A. Reed, A. Froment, M.W. Smith, S.M. Williams, S.A. Omar, M.J. Kotze, G.S. Pretorius, M. Ibrahim, O. Doumbo, M. Thera, C. Wambebe, S.E. Dobrin, J.L. Weber. Ancient Population Structure and Migration in Africa Inferred from Genome-wide Genetic Markers American Association of Physical Anthropologists, Philadelphia, PA April 2007 Notes: Oral presentation.

29. Gomez, F., G. Tomas, F. Reed, S. Tishkoff, and J. Rocha. Nucleotide Diversity and Signatures of Natural Selection in Intercellular Adhesion Molecule -1 (ICAM-1). American Institute of Biological Sciences meeting, Washington DC May 2007 Notes: Poster.

30. Pfeifer, L.A. and S.A. Tishkoff. Nucleotide sequence variation of the oxytocin receptor (OXTR) locus in ethnically diverse human populations. American Institute of Biological Sciences meeting, Washington DC May 2007 Notes: Poster.

31. Reed, F.A., A. Froment, M.W. Smith, S.M. Williams, S.A. Omar, M.J. Kotze, G.S. Pretorius, M. Ibrahim, O. Doumbo, M. Thera, C. Wambebe, S.E. Dobrin, J.L. Weber, S.A. Tishkoff. Genetic Structure of Human Populations in Africa Inferred from Genomewide Polymorphic Markers Cold Spring Harbor meeting on "The Biology of Genomes" May 2007 Notes: Poster.

32. Kaercher, K and S.A. Tishkoff. Nucleotide sequence variation in Glycophorin A, B, & E receptor genes in ethnically diverse West African populations. Society of Molecular Biology and Evolution meeting, Halifax, Nova Scotia June 2007 Notes: Poster.

33. Pfeifer, L.A. and S.A. Tishkoff. Nucleotide sequence variation and signatures of selection at neuropeptide receptor loci in ethnically diverse human populations. Society of Molecular Biology and Evolution meeting, Halifax, Nova Scotia June 2007 Notes: Poster.

34. Gomez, F., G. Tomas, F. Reed, S.A. Tishkoff, and J. Rocha. Patterns of Nucleotide Diversity and Potential Signatures of Natural Selection at ICAM-1. American Society of Human Genetics meeting, San Diego, CA October 2007 Notes: Poster.

35. Hirbo, J.B., F. Reed, S.A. Omar, M. Ibrahim, and S.A. Tishkoff. Gene-language correlations in the Luo population of Kenya. American Society of Human Genetics meeting, San Diego, CA October 2007 Notes: Poster.

36. Jakobsson, M, F.A. Reed, T.J. Pemberton, G. Coop, D.F. Conrad, J.D. Wall, J.K. Pritchard, S.A. Tishkoff, N.A. Rosenberg. Linkage disequilibrium and haplotype variation in Sub-Saharan Africa. American Society of Human Genetics meeting, San Diego, CA October 2007 Notes: Oral presentation.

37. Ranciaro, A., F. Reed, J. Hirbo, K. Powell, M. Osman, H. Muntaser, O. Sabah, and S.A. Tishkoff. Origins of regulatory mutations at the LCT locus in African populations. American Society of Human Genetics meeting, San Diego, CA October 2007 Notes: Poster.

38. Babbitt, C.C., Swearingen, A.S., Ranciaro, A., Tishkoff, S.A., Wray, G.A.. Functional

interactions between cis-regulatory SNPs involved in lactase persistence. American Society of Human Genetics Meeting, Philadelphia, PA 2008 Notes: Poster.

39. Bryc, K., Nelson, M., Oksenberg, J., Hauser, S., Bustamante, C., Tishkoff, S.. Genome-wide patterns of population structure and admixture in Africans and African Americans. American Society of Human Genetics Meeting, Philadelphia, PA 2008 Notes: Oral presentation.

40. Campbell, M., Ranciaro, A., Froment, A., Drayna, D., Breslin, P, Tishkoff, S.. Evolutionary history of TAS2R38, a bitter-taste receptor gene, in diverse African populations. American Association of Physical Anthropology Meeting, Columbus, OH 2008 Notes: Poster.

41. Campbell, M., Ranciaro, A., Froment, A., Drayna, D., Breslin, P., Tishkoff, S.. Patterns of genetic diversity at TAS2R38, a bitter-taste receptor gene, in diverse African populations from Cameroon and Kenya. Society for Molecular Biology and Evolution Meeting, Barcelona, Spain. 2008 Notes: Poster.

42. Campbell, M., Ranciaro, A., Froment, A., Drayna, D., Breslin, P., Tishkoff, S.. Patterns of genetic diversity at TAS2R38, a bitter-taste receptor gene, in diverse African populations from Cameroon and Kenya. American Society of Human Genetics Meeting, Philadelphia, PA 2008 Notes: Poster.

43. Gomez, F., Tomas, G., Rocha, J., Tishkoff, S.. Patterns of Nucleotide Variation at ICAM-1 in Diverse African Populations. American Society for Human Genetics Annual Meeting. Philadelphia, PA. 2008 Notes: Poster.

44. Gomez, F., Tomas, G., Rocha, J., Tishkoff, S.. Patterns of genetic variation and signatures of natural selection at ICAM-1 in diverse African populations. [poster presentation] Human Genome Variation Conference. Toronto, Canada. 2008 Notes: Poster.

45. Hirbo, J.B., Omar, S.A., Ibrahim, M. and Tishkoff, S.A.. Genetic History of Human Populations of East Africa. 58th Conference of the American Society of Human Genetics, Philadelphia, PA 2008 Notes: Poster.

46. Ko, W.-Y., Kaercher, K., Tishkoff, S.A.. Natural selection on the erthrocyte surface glycoproteins in malaria-endemic human populations of Africa. 58th Meeting of the American Society of Human Genetics, Philadelphia, PA 2008 Notes: Poster.

47. Ranciaro, A., Reed, F., Hirbo, J., Powell, K., Osman, M., Muntaser, H., Sabah, O., Fremont, A., Tishkoff, S.A.. The evolutionary history of lactase persistence in Africa. American Society of Human Genetics, Philadelphia, PA 2008 Notes: Poster.

48. Tishkoff, S.A., Ko, W.-Y., Gomez, F., Reed, F.A.. Genetic Variation in Africa: Implications for evolution of infectious disease resistance. Society of Molecular Biology Mtg, Barcelona, Spain. 2008 Notes: Oral presentation.

49. Gomez, F., Tomas, G., Rocha, J., Tishkoff, S.. An evolutionary and population genetic approach to malaria susceptibility in Africa. Invited talk given at Ford Foundation Conference of

Scholars 2009 Notes: Oral presentation.

50. Gomez, F., Tomas, G., Rocha, J., Tishkoff, S.. Genetic variation at ICAM-1 in diverse African populations. American Journal of Physical Anthropology Suppl. Chicago, IL. 138(35), 2009 Notes: Oral presentation.

51. Hirbo, J.B., Ranciaro, A., Omar, S.A., Ibrahim, M., Tishkoff, S.A.. Complex genetic history of human populations in East Africa. 59th Conference of the American Society of Human Genetics, Honolulu, Hawaii 2009 Notes: Oral presentation.

52. Ranciaro, A., Hirbo, J., Reed, F., Campbell, M., Mustaser, H., Sabah, O., Destro-Bisol, G., Froment, A., Kotze, M.J., Nyambo, T.B., Tishkoff, S.A.. The history of lactase persistence in African populations. Meeting on Molecular Anthropology in the Genomic era-DNA Polymorphisms in Human Populations, Rome. 2009 Notes: Oral presentation.

53. Tishkoff, S.A., Campbell, M., Fromen, A., Hirbo, J., Ibrahim, M., Omar, S., Ranciaro, A.. The genetic basis of phenotypic variation in Africa: Evidence for local adaptation. American Association of Physical Anthropology Meeting, Chicago, IL. 2009 Notes: Oral presentation.

54. Tishkoff, S.A., Gomez, F., Froment, A., Ibrahim, M., Nyambo, T., Omar, S., Wambebe, C., Ko, W.-Y.. An evolutionary and population genetics approach for identifying malaria susceptibility loci in Africa. Meeting on Host Genetics Control of Infectious Diseases, Pasteur Institute, Paris, France 2009 Notes: Oral presentation.

55. Ko, W.-Y., Kaercher, K., Tishkoff, S.A.. Balancing and positive selection on different parts of the extracellular domain of erythrocyte surface receptors. Ecology and Evolution of Infectious Disease Meeting, Atlantic City, NJ March 2010 Notes: Poster.

56. Ko, W.-Y., Gomez, F., Tishkoff, S.A.. An evolutionary and population genetic approach to malaria susceptibility in Africa. American Society of Physical Anthropology Meeting, Albuquerque, NM. 141(146), April 2010 Notes: Oral presentation.

57. Ko, W.-Y., Kaercher, K., Tishkoff, S.A.:.Adaptive evolution of human glycophorin loci in malaria endemic African populations. Society for Molecular Biology and Evolution (SMBE) Annual Meeting, Lyon, France July 2010 Notes: Oral presentation.

58. Joseph P. Jarvis, Jibril Hirbo, Charla Lambert, Alessia Ranciaro, Laura Scheinfeldt, Sameer Soi, Simon Thompson, Sarah A. Tishkoff. Integrative genomic and phenotypic studies of variation in Africa. NIH Director's Pioneer Award Meeting, Bethesda, MD, Sept, 2010. Notes: Poster.

59. Campbell, M.C., Ranciaro, A., Froment, A., Zinshteyn, D., Bodo, J.-M., Drayna, D., Breslin, P., Tishkoff, S.A.. The Genetic Basis and Evolutionary History of PTC Bitter Taste Perception in Africa. American Society of Human Genetics Meeting, Washington, D.C. November 2010 Notes: Poster.

60. Gomez, F., Tishkoff, S.A.. Patterns of Genetic Variation at CD-36, a malaria susceptibility

locus, in Diverse African Populations. American Society of Human Genetics Annual Meeting, Washington, D.C. November 2010 Notes: Poster.

61. Ko, W.-Y., Kaercher, K., Tishkoff, S.A.. Adaptive evolution of human glycophorin loci in malaria endemic African populations. 60th Annual American Society of Human Genetics (ASHG) Meeting, Washington, D.C. November 2010 Notes: Oral presentation.

62. Ko, W.-Y., Gomez, F., Tishkoff, S.A.. An evolutionary and population genetic approach to malaria susceptibility in Africa. Invited Symposium: Pathogens and Human and Non-human Primate Evolution, American Association of Physical Anthropology Meeting. Albuquerque, New Mexico. 2010 Notes: Oral presentation.

63. Ranciaro, A., Tishkoff, S.A.. Evolutionary history of lactose intolerance in Africa. NIH Workshop on Health Implications of Lactose Intolerance, Bethesda, M.D. 2010 Notes: Oral presentation.

64. Campbell, M.C., Ranciaro, A., Froment, A., Zinshteyn, D., Bodo, J.-M., Drayna, D., Breslin, P., Tishkoff, S.A.. Ongoing Evolution of Human Bitter Taste Perception Associated with the TAS2R38 Locus in Africa. African Society of Human Genetics, Young Researcher's Forum, Cape Town, South Africa March 2011 Notes: Oral presentation.

65. Hirbo, J.B., Ranciaro, A., Omar, S.A., Ibrahim, M., Godfrey, L., Nyambo, T.B., Tishkoff, S.A.. Genetic History of human populations of East Africa. African Society of Human Genetics, Cape Town, South Africa. March 2011 Notes: Poster.

66. Ranciaro, A., Campbell, M.C., Zinshteyn, D., Hirbo, J., Omar, S., Bodo, J.-M., Nyambo, T., Thompson, S.R., Issa, D.M., Belay, G., Drayna, D., Breslin, P., Tishkoff, S.A.. Genetic basis of the receptor of taste perception TAS2R16 in African populations. African Society of Human Genetics Meeting, Cape Town, South Africa March 2011 Notes: Poster.

67. Ko, W.-Y., Gomez, F., Tishkoff, S.A.. Spatially heterogeneous selection on human ApoL1 variants among diverse African populations in trypanosomiasis endemic areas. Society for Molecular Biology and Evolutions (SMBE) Annual Meeting, Kyoto, Japan. July 2011 Notes: Oral presentation.

68. Ko, W.-Y., Tishkoff, S.A.. Genome-wide detection of local adaptation in diverse African populations. Young Researchers Conference on Evolutionary Genomics, Tokyo, Japan August 2011 Notes: Oral presentation.

69. Jarvis, J. Lachance, J., Soi, S.' Scheinfeldt, L.' Lambert, C.' Omberg, L.' Ferwerda, B.' Ranciaro, A., Hirbo, J., Beggs, W.' Froment, A., Bodo, J., Ibrahim. M., Lema, G., Nyambo, T., Omar, S., Wambebe, C., Hoffman, G., Mezey, J., Tishkoff, S.. African Integrative Genomics: Implications for Human Evolution and Disease. NIH Director's Pioneer Awards Meeting, Bethesda, MD, Sept, 2011.Note: Poster.

70. Elbers, C.C., Thompson, S.R., Ranciaro, A., Meskel, D.W., Belay, G., Tishkoff, S.A.. Amylase gene copy numbers and salivary amylase activity in ethnically diverse populations from

Ethiopia. International Congress of Human Genetics/American Society of Human Genetics meeting. Montreal, Canada. October 2011 Notes: Poster.

71. Meltz, K., Steinberg, F. Antonacci, J. M. Kidd, C. D. Campbell, P. Sudmant, L. Vives, M. Malig, L. Scheinfeldt, W. Beggs, M. P. Donnelly, K. K. Kidd, S. A. Tishkoff, E. E. Eichler. African genome sequencing reveals diversity and origin of the "European" 17q21.31 inversion polymorphism. International Congress of Human Genetics/American Society of Human Genetics meeting. Montreal, Canada. October 2011 Notes: Poster.

72. Soi, S., L. Scheinfeldt, C. Lambert, J. Hirbo, A. Ranciaro, S. Thompson, J. M. Bodo, A. Froment, M. Ibrahim, A. Juma, T. Nyambo, S. Omar, C. Wambebe, D. Meskel, G. Belay, S. A. Tishkoff. Demographic histories of African hunting-gathering populations inferred from genome-wide SNP variation. International Congress of Human Genetics/American Society of Human Genetics meeting. Montreal, Canada. October 2011 Notes: Oral presentation.

73. Scheinfeldt L.B., Soi S., Froment A., Bodo J., Wambebe C., Tishkoff S.A.. An interdisciplinary genomic approach to the study of adaptation and population histories in Sub-Saharan Africa. American Association of Physical Anthropology. Portland, Oregon. April 2012. Notes: Oral presentation.

74. Lachance, J., B. Vernot, C. Elbers, B. Ferwerda, A. Froment, J-M. Bodo, G. Lema, T. Nyambo, T. Rebbeck, K. Zhang, J. Akey, S. Tishkoff.. High-coverage population genomics of diverse African hunter-gatherers. Society for Molecular Biology and Evolution, Dublin, Ireland. June 2012. Notes: Poster.

75. Lachance, J., B. Vernot, C. Elbers, B. Ferwerda, A. Froment, J. Bodo, G. Lema, W. Fu, T. Nyambo, T. Rebbeck, K. Zhang, J. Akey, S. Tishkoff. Evolutionary history and adaptation inferred from whole-genome sequences of diverse African hunter-gatherers. Joint Congress on Evolutionary Biology, Ottawa, Canada. July 2012. Notes: Oral presentation.

76. Lachance J, Jarvis J, Soi S, Scheinfeldt L, Vernot B, Ranciaro, A, Hirbo J, Rawlings A, Beggs W, Froment, A, Bodo, J, Ibrahim. M, Lema G, Nyambo T, Omar S, Wambebe C, Akey J, Tishkoff S.. Integrative Genomics Analyses of African Populations. NIH Director's Pioneer Award Meeting, Bethesda, MD, Sept 2012. Notes: poster.

77. Scheinfeldt L, S. Soi, C. Lambert, D. Hu, A. Coulibaly, H. Hutton, C. Elbers, W-Y. Ko, W. Beggs, A. Ranciaro, S. Thompson, J. Hirbo, J.M. Bodo, O. Doumbo, M. Ibrahim, A. Froment, G. Lema, T. Nyambo, S. Omar, C. Wambebe, D. Meskel, G. Belay, S. Tishkoff.. Genome-wide signatures of natural selection in diverse African populations. American Society of Human Genetics. San Francisco, CA. November 2012. Notes: Poster.

78. Soi, S. L. Scheinfeldt, C. Lambert, J. Hirbo, A. Ranciaro, S. Thompson, J. Marie Bodo, M. Ibrahim, G. Lema, T. Nyambo, S. Omar, C. Wambebe, D. Meskel, G. Belay, A. Froment, S. A. Tishkoff. Genome-wide SNP variation in sub-Saharan Africa is influenced by cultural and ethno-linguistic affiliation. American Society of Human Genetics, San Francisco, CA. November 2012. Notes: Poster.

79. Rawlings, R., S. Tishkoff. Novel human variation in miRNAs associated with disease, biomarkers and drug metabolism. The RNA Society Meeting, Ann Arbor, MI May-June 2012 Notes: Poster.

80. Ferreira, Z., S. Seixas, A. Andres, W. Kretzschmar, J. Mullikin, W. Swanson, M. K. Gonder, S. Tishkoff, A. Stone, A. G. Clark, E. Green, B. Hurle. Reproduction and immunity driven natural selection in the hominid WFDC locus. American Society of Human Genetics, San Francisco, CA. November 2012 Notes: Poster.

81. Lachance, J., B. Vernot, C. Elbers, B. Ferwerda, A. Froment, J. Bodo, G. Lema, W. Fu, T. Nyambo, T. Rebbeck, K. Zhang, J. Akey, S. Tishkoff. Evolutionary history and adaptation inferred from whole-genome sequences of diverse African hunter-gatherers. American Society of Human Genetics, San Francisco, CA. November 2012 Notes: Oral presentation.

82. Rawlings-Goss, R. Afi., S. Tishkoff. Novel Human Variation in MicroRNAs associated with Disease, Biomarkers, and Drug Metabolism. American Society of Human Genetics, San Francisco, CA. November 2012 Notes: Poster.

83. P. H. Hsieh, K. R. Veeramah, J. Lachance, S. A. Tishkoff, J. D. Wall, M. F. Hammer, R. N. Gutenkunst. Inference of Natural Selection and Demographic History for African Pygmy Hunter-Gatherers. Society for Molecular Biology and Evolution, Chicago July 2013 Notes: Poster.

84. J. Lachance, S. Tishkoff. The evolutionary impact of GC-biased gene conversion on human populations. American Society of Human Genetics, Boston October 2013 Notes: Poster.

85. P. H. Hsieh, K. R. Veeramah, J. Lachance, S. A. Tishkoff, J. D. Wall, M. F. Hammer, R. N. Gutenkunst. Inference of Natural Selection and Demographic History for African Pygmy Hunter-Gatherers. American Society of Human Genetics, Boston October 2013 Notes: Poster.

86. S. Soi, L. B. Scheinfeldt, D. Diep, W. Beggs, N. Plongthongkum, S. A. Tishkoff*, K. Zhang*. Genetic and environmental variables contribute to genome-wide methylation variation in geographically diverse Africans. American Society of Human Genetics, Boston October 2013 Notes: Poster.*These authors contributed equally

87. R. A. Rawlings-Goss, S. Tishkoff**.** Global Patterns of miRNA Variation and Population-specific Differentiation Based on Whole Genome Sequence Data. American Society of Human Genetics, Boston, October, 2013. Notes: Poster

88. Lachance J. and S. A. Tishkoff. Scans of selection using whole genome sequences of diverse African hunter-gatherers reveal associations between pituitary loci and Pygmy stature. Society for Molecular Biology and Evolution, Chicago 2013. Notes: Oral presentation.

89. Lachance J. and S. A. Tishkoff. Scans of selection using whole genome sequences of diverse African hunter-gatherers reveal associations between pituitary loci and Pygmy stature, Society for the Study of Evolution, Snowbird, Utah 2013 Notes: Oral presentation.

90. Soi S, Hutton, H. Lachance J, Jarvis J, Scheinfeldt L, Vernot B, Ranciaro, A, Hirbo J, Rawlings A, Beggs W, Froment A, Bodo J, Ibrahim M, Lema G, Nyambo T, Omar S, Wambebe C, Akey J, K. Zhang, Tishkoff S.. Integrative Genomics Analyses of African Populations. NIH Common Fund High-Risk High-Reward Research Symposium, Nov 18 – 20, 2013. Notes: Poster

91. Lachance, J and S. Tishkoff. Biased gene conversion skews allele frequencies in human populations, increasing the disease burden of recessive alleles, Society for Molecular Biology and Evolution, San Juan, Puerto Rico, June 2014. Notes: Poster

92. Lachance, J and S. Tishkoff. Biased gene conversion skews allele frequencies in human populations, increasing the disease burden of recessive alleles. Society for the Study of Evolution, Raleigh, NC, June 2014. Notes: Poster

93. Alessia Ranciaro, Michael C. Campbell, Jibril B. Hirbo, Wen-Ya Ko, Alain Froment, Paolo Anagnostou, Maritha J. Kotze, Muntaser Ibrahim, Thomas Nyambo, Sabah A. Omar, Sarah A. Tishkoff. Society for Molecular Biology and Evolution, San Juan, Puerto Rico, June 2014. Notes: Poster.

94. Matthew E.B. Hansen, J. Lachance, S.A. Tishkoff. Anthropometric trait variation among diverse African populations: deviations from drift. Society for Molecular Biology and Evolution, San Juan, Puerto Rico, June 2014. Notes: Poster.

95. Michael C. Campbell, Alessia Ranciaro, Daniel Zinshteyn, Renata Rawlings-Goss, Jibril Hirbo, Simon Thompson, Dawit Woldemeskel, Alain Froment, Joseph B. Rucker, Sabah Omar, Jean-Marie Bodo, Thomas Nyambo, G. Belay, Dennis Drayna, Paul A.S. Breslin, Sarah A. Tishkoff Origin and Adaptive Evolution of Allelic Variation at TAS2R16 Associated with Salicin Bitter Taste Sensitivity in Africa. Society for Molecular Biology and Evolution, San Juan, Puerto Rico, June 2014. Notes: Oral presentation.

96. P. Hsieh, J. D. Wall, J. Lachance, S. A. Tishkoff, R. N. Gutenkunst, M. F. Hammer. Statistical inference of archaic introgression and natural selection in Central African Pygmies. American Society of Human Genetics Meeting, San Diego, CA, October, 2014. Notes: Oral presentation.

97. M. E. B. Hansen, M. Rubel, A. Bailey, K. Bittinger, A. Laughlin, A. Ranciaro, W. Beggs, S. Thompson, F. D. Bushman, S. A. Tishkoff. Characterizing gut microbiota variation across diverse rural African populations. American Society of Human Genetics Meeting, San Diego, CA, October, 2014. Notes: Poster.

98. K. E. Johnson, C. C. Elbers, S. R. Thompson, A. Ranciaro, D. W. Meskel, A. L. Mandel, G. Belay, S. A. Tishkoff. Correlations between *AMY1* copy number, diet and BMI in ethnically diverse African populations. American Society of Human Genetics Meeting, San Diego, CA, October, 2014. Notes: Poster.

99. Rubel MA, Hansen MEB, Bailey A, Bittinger K, Laughlin A, Beggs W, Ranciaro A, Thompson SR, Bushman FD, Tishkoff SA. Role of Environment and Diet on Microbiome Composition

in Diverse Rural Africans. American Society for Human Genetics, Baltimore, MD. 2015. Notes: Poster

100. Rubel MA, Hansen MEB, Bailey A, Bittinger K, Laughlin A, Beggs W, Ranciaro A, Thompson SR, Bushman FD, Tishkoff SA. Dietary and Environmental Factors Shaping African Gut Microbiomes. Society for Molecular Biology and Evolution, Gold Coast, Australia, 2016. Notes: Oral Presentation

101. Rubel MA, Hansen MEB, Bailey A, Bittinger K, Laughlin A, Beggs W, Ranciaro A, Thompson SR, Bushman FD, Tishkoff SA. Diet, Environment, and Parasites: Factors Shaping Rural African Gut Microbiomes. International Society for Evolution, Medicine, and Public Health, Durham, NC. 2016. Notes: Oral presentation

102. Rubel MA, Hansen MEB, Bailey A, Bittinger K, Laughlin A, Beggs W, Ranciaro A, Thompson SR, Bushman FD, Tishkoff SA. Environmental and Dietary Factors Shaping African Gut Microbiomes. American Association of Physical Anthropologists, Atlanta, GA. 2016. Notes: Poster

103. DE. Kelly, SH. Fan, MH. Beltrame, MEB. Hansen, S. Mallick, Thomas Nyambo, Sabah Omar, Dawit Meskel, Gurja Belay, Alain Froment, N. Patterson, D. Reich, SA. Tishkoff Characterization of local adaptation in Africa from whole genome sequence data. American Society of Human Genetics Meeting, Vancouver, BC. 2016. Notes: Poster

104. SH. Fan, DE. Kelly, MH. Beltrame, MEB. Hansen, S. Mallick, Thomas Nyambo, Sabah Omar, Dawit Meskel, Gurja Belay, Alain Froment, N. Patterson, D. Reich, SA. Tishkoff. Whole-genome sequence analyses provide new insights into the demographic history and local adaptation of African populations. American Society of Human Genetics Meeting, Vancouver, BC. 2016. Notes: Poster

105. Matthew E.B. Hansen, Joseph Lachance, Sameer Soi, Laura Scheinfeldt, Alessia Ranciaro, Simon Thompson, Jibril Hirbo, and Sarah A. Tishkoff. Anthropometric and cardiovascular trait variation among sub-Saharan African populations: the impact of subsistence practice and genetic ancestry. American Society of Human Genetics, Baltimore, MD 2015. Notes: Poster

106. Matthew E.B. Hansen, Joseph Lachance, Sameer Soi, Laura Scheinfeldt, Alessia Ranciaro, Simon Thompson, Jibril Hirbo, and Sarah A. Tishkoff. Anthropometric and cardiovascular trait variation among sub-Saharan African populations: the role of gender, subsistence, and genetic ancestry. Society for Molecular Biology and Evolution, Vienna, Austria 2015. Notes: Poster, won best post-doc poster award.

107. Matthew E.B. Hansen, Alessia Ranciaro, Simon Thompson, William Begs, Jibril Hirbo, Stephan J. Chanock, Meredith Yeager, and Sarah A. Tishkoff. Physiological trait and biomarker variation among sub-Saharan African populations: the impact of gender, subsistence, and genetic ancestry. Center of Excellence in Environmental Toxicology Symposium, Philadelphia, PA, Notes: Poster

108. Matthew E.B. Hansen, Alessia Ranciaro, Simon Thompson, William Begs, Jibril Hirbo, Stephan J. Chanock, Meredith Yeager, and Sarah A. Tishkoff. The impact of ancestry and subsistence practice on cardiovascular and anthropometric traits in sub-Saharan Africans.

International Society for Evolution, Medicine, and Public Health, Durham, NC. 2016. Notes: Oral presentation

Alternative Media:

Media/Public Outreach and Education:

I have assisted with public outreach and education (particularly at the high school and undergraduate college level) by the development of several websites and videos describing my research including:

- University of Maryland (http://www.inform.umd.edu/CampusInfo/Departments/InstAdv/newsdesk/dna/project.html). This was advertised in the Chronicle of Higher Education and has been made available as a teaching tool for high school and undergraduate students.
- Developed a Slide show with Peter Nichols at the University of Pennsylvania http://www.sas.upenn.edu/home/SASFrontiers/tishkoff.html.
- Featured in NIGMS "computing Life" website in which students could ask me questions about my research via the web. http://publications.nigms.nih.gov/computinglife/answers.htm
- Videotaped by the University of Pennsylvania Museum of Anthropology and Archeology for the exhibit on Human Origins (2008-present)
- Videotaped by the American Museum of Natural History in New York for their exhibit on Human Origins (2008-present)
- Videotaped by Cold Spring Harbor for a video to be used for educational purposes. I also helped them to develop a high school laboratory project for genotyping genetic variants associated with lactose intolerance in Africans.
- Videotaped by National Institute of Medical Sciences as part of their public education effort (http://publications.nigms.nih.gov/multimedia/captions/tishkoff-captions.html) (May 2008)
- Consultant and featured scientist for Genetics textbook for children published by National Geographic (2008)
- Videotaped commentary about publication of Neanderthal Genome on *Science magazine* website (May 2010).
- Production of a live webcast and video for HHMI as part of the Holiday Lectures series entitled "Bones Stones and Genes: The Origin of Modern Humans". The video, which also features an interview and filming of lab work at Penn, will be distributed to >20,000 high schools nationally and internationally (October 2011)
- Advisor for development of NIH Curriculum Supplement on Evolution and Medicine (2011)
- Production of Documentary for the University of Munich LMU (2012) "Good milk / bad milk" (http://www.evolutionoflife.com/en/observe/video/fiche/good-milk-bad-milk.html)
- Advisor for the Smithsonian National Museum of Natural History and NHGRI for production of an exhibit on the Human Genome (2012-2013).
- American Society of Cell Biology (ASCB) iBioSeminar, a web-based seminar series (http://www.ascb.org/ibioseminars/) (2013)
- Discussant, videotaped public symposium, The African Diaspora: Integrating Culture Genomics and History Symposium, Smithsonian National Museum of Natural History (2013)

- Featured on Ask Me Anything (AMA) on Reddit, September 26, 2015 answering questions on human genetics and human evolution. https://www.reddit.com/r/science/comments/3mgh26/science_ama_series_i_study_the_population_history/
- Panel Participant at World Science Festival in New York discussing topics on human evolution for a general audience. http://www.worldsciencefestival.com/programs/future-evolution-humans-masters-fate/ (2017)

My research has been the focus of 23 news articles and/or Perspectives in *Science*, *Nature,* or *Nature Genetics*:

- *Science* 271:1341, March 8, 1996
- *Science* 292:627-629, April 27, 2001
- *Science* 293:442-443, July 20, 2001
- *Science* 293:389, July 20, 2001
- *Science* 314:1672, December 15, 2006
- *Nature* 444:994-996, December 2006
- *Nature Genetics* 39:7-8, January 2007
- *Nature News* December 10, 2007
- *Nature News* April 30, 2009
- Science 324:575, May 2009
- *Nature Genetics 41, 642-642, June 2009*
- *Nature News* 26 April 2012
- *ScienceNOW* 26 April 2012
- *Nature 486, S16-S17 20 June 2012*
- *Nature News 26 July 2012*
- *Science 27* July 2012*: 396.*
- Science 27 July 2012: 394-396.
- *ScienceNOW* 26 July 2012
- *Nature 488, 8-8, 1 August, 2012*
- *Nature Genetics 44, 967-967 29 August 2012*
- *Nature News 20 Sept 2012*

I have been quoted in 33 additional Science and *Nature* news articles:

- *Science* 276: 535-536, April 25, 1997
- *Science* 282:654-655, October 23, 1998
- *Science* 300:1641, June 13, 2003
- *Science* 303:1319-1320, February 27, 2004
- *Science* 309:234-7, July 8, 2005
- *Nature* 456:18-21, November 5, 2008
- *Science*NOW 5 February 2009
- *Science*NOW 24 March 2010
- *Science* 327: 1566-1567, 26 March 2010
- *Science* 7 328: 680-684, May 2010
- *Science*NOW 3 June 2010

- *Nature News 5 September 2011*
- *Nature News 7 March 2011*
- *Nature 468, S13-S15 22 December 2010*
- *Nature News 3 June 2010*
- *Nature* 463, 857-857 17 February 2010
- *Nature News 25 January 2010*
- *Nature News 23 September 2009*
- *Science* 11 June 2010: 1342.
- *Science 263,* 16 July 2010
- *Science 331:*23-23, 7 January 2011
- *Nature News 5 September 2011*
- *Science 167,* 14 October 2011
- *Nature* 486, 17-17. 6 June 2012
- *Science*NOW 6 August 2012
- *ScienceNOW* 30 August 2012
- *Nature News 28 November 2012*
- *Nature News 27 August 2013*
- *Nature News* 29 January 2014
- *Science Vol. 343, March 2014*
- *Science News 8 August 2014*
- *Nature News* 8 Aug 2014
- *Science News,* March 2015

My research was featured in NIGMS Findings magazine, February 2009.

I have done numerous interviews with the media including two documentaries featured on Discovery channel and PBS, four radio interviews on BBC, five radio interviews on NPR, two radio interviews with WTOP, two radio interviews with CBC radio in Canada, an interview on the Koji Nnamdi show on WAMU in Washington, DC, and two interviews on Radio Times with Marty Moss-Cohane on WHYY in Philadelphia.

My research has been featured in hundreds of media reports including the *New York Times* (seven times), *Washington Post* (five times), *Baltimore Sun* (three times), *LA Times* (three times), *Philadelphia Inquirer* (five times), *US News and World Report*, *The Economist*, *National Geographic*, *Popular Science*, *Science News*, *Discovery News*, *The Christian Science Monitor*, *American Scientist*, *Scientific American*, *Newsday*, *Genome Web* News, *Associated Press*, CNN, ABC News, *Men's Health Magazine*, *Sports Illustrated*, *Discover Magazine,* among others.

SCIENCE AND SOCIETY

Taking race out of human genetics

Engaging a century-long debate about the role of race in science

By **Michael Yudell,[1]* Dorothy Roberts,[2] Rob DeSalle,[3] Sarah Tishkoff[2]**

In the wake of the sequencing of the human genome in the early 2000s, genome pioneers and social scientists alike called for an end to the use of race as a variable in genetic research (*1*, *2*). Unfortunately, by some measures, the use of race as a biological category has increased in the postgenomic age (*3*). Although inconsistent definition and use has been a chief problem with the race concept, it has historically been used as a taxonomic categorization based on common hereditary traits (such as skin color) to elucidate the relationship between our ancestry and our genes. We believe the use of biological concepts of race in human genetic research—so disputed and so mired in confusion—is problematic at best and harmful at worst. It is time for biologists to find a better way.

POLICY

Racial research has a long and controversial history. At the turn of the 20th century, sociologist and civil rights leader W. E. B. Du Bois was the first to synthesize natural and social scientific research to conclude that the concept of race was not a scientific category. Contrary to the then-dominant view, Du Bois maintained that health disparities between blacks and whites stemmed from social, not biological, inequality (*4*). Evolutionary geneticist Theodosius Dobzhansky, whose work helped reimagine the race concept in the 1930s at the outset of the evolutionary synthesis, wrestled with many of the same problems modern biologists face when studying human populations—for example, how to define and sample populations and genes (*5*). For much of his career, Dobzhansky brushed aside criticism of the race concept, arguing that the problem with race was not its scientific use, but its nonscientific misuse. Over time, he grew disillusioned, concerned that scientific study of human diversity had "floundered in confusion and misunderstanding" (*6*). His transformation from defender to detractor of the race concept in biology still resonates.

Today, scientists continue to draw wildly different conclusions on the utility of the race concept in biological research. Some have argued that relevant genetic information can be seen at the racial level (*7*) and that race is the best proxy we have for examining human genetic diversity (*8*, *9*). Others have concluded that race is neither a relevant nor accurate way to understand or map human genetic diversity (*10*, *11*). Still others have argued that race-based predictions in clinical settings, because of the heterogeneous nature of racial groups, are of questionable use (*12*), particularly as the prevalence of admixture increases across populations.

Several meetings and journal articles have called attention to a host of issues, which include (i) a proposed shift to "focus on racism (i.e., social relations) rather than race (i.e., supposed innate biologic predisposition) in the interpretation of racial/ethnic 'effects'" (*13*); (ii) a failure of scientists to distinguish between self-identified racial categories and assigned or assumed racial categories (*14*); and (iii) concern over "the haphazard use and reporting of racial/ethnic variables in genetic research" (*15*) and a need to justify use of racial categories relative to the research questions asked and methods used (*6*). Several academic journals have taken up this last concern and, with mixed success, have issued guidelines for use of race in research they publish (*16*). Despite these concerns, there have been no

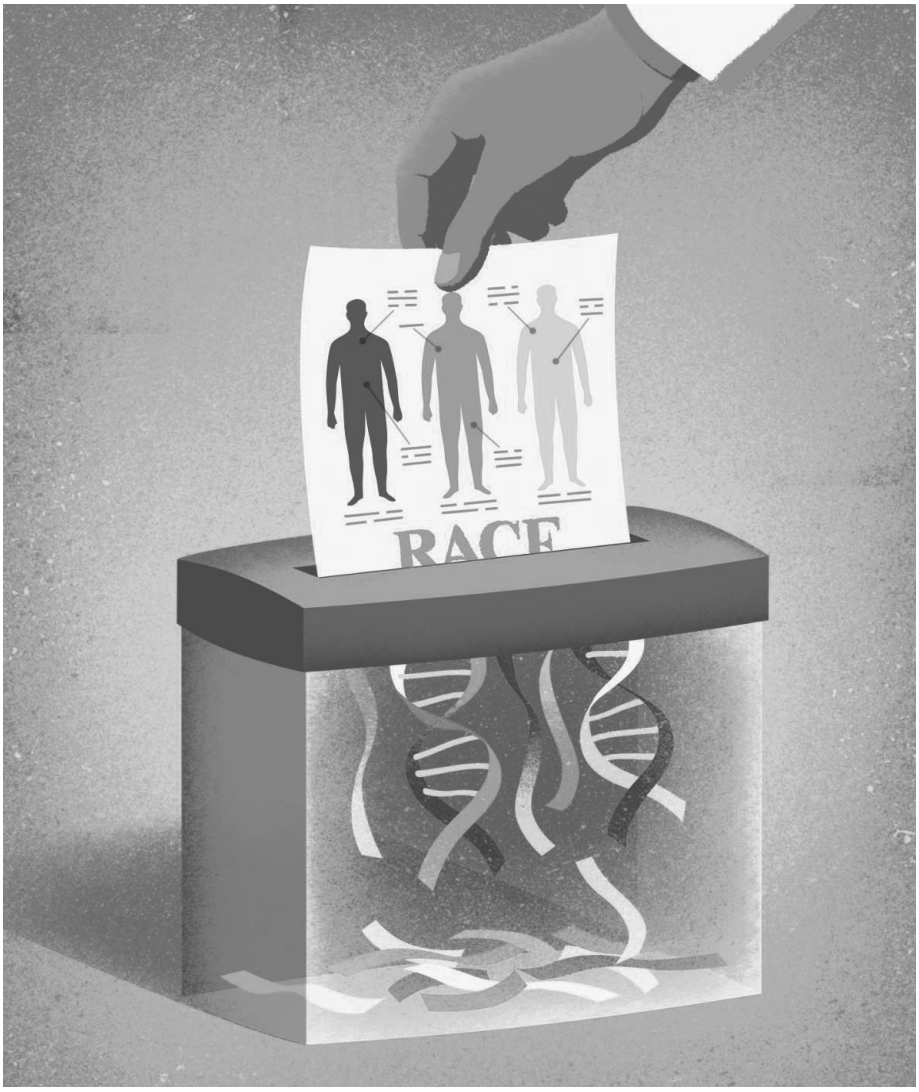

ILLUSTRATION: DAVIDE BONAZZI/@SALZMANART

[1]*Drexel University, Philadelphia, PA 19104, USA.* [2]*University of Pennsylvania, Philadelphia, PA 19104, USA.* [3]*American Museum of Natural History, New York, NY 10024, USA.*
**Corresponding author. E-mail: myudell@drexel.edu*

systematic attempts to address these issues and the situation has worsened with the rise of large-scale genetic surveys that use race as a tool to stratify these data (*17*).

It is important to distinguish ancestry from a taxonomic notion such as race. Ancestry is a process-based concept, a statement about an individual's relationship to other individuals in their genealogical history; thus, it is a very personal understanding of one's genomic heritage. Race, on the other hand, is a pattern-based concept that has led scientists and laypersons alike to draw conclusions about hierarchical organization of humans, which connect an individual to a larger preconceived geographically circumscribed or socially constructed group.

Unlike earlier disagreements concerning race and biology, today's discussions generally lack clear ideological and political antipodes of "racist" and "nonracist." Most contemporary discussions about race among scientists concern examination of population-level differences between groups, with

"...the use of biological concepts of race in human genetic research...is problematic at best and harmful at worst."

the goal of understanding human evolutionary history, characterizing the frequency of traits within and between populations, and using an individual's self-identified ancestry to identify genetic risk factors of disease and to help determine the best course of medical treatments (*6*).

If this is what race in contemporary scientific and medical practice is about, then why should we be concerned? One reason is that phylogenetic and population genetic methods do not support a priori classifications of race, as expected for an interbreeding species like *Homo sapiens* (*11*, *18*). As a result, racial assumptions are not the biological guideposts some believe them to be, as commonly defined racial groups are genetically heterogeneous and lack clear-cut genetic boundaries (*10*, *11*). For example, hemoglobinopathies can be misdiagnosed because of the identification of sickle-cell as a "Black" disease and thalassemia as a "Mediterranean" disease (*10*). Cystic fibrosis is underdiagnosed in populations of African ancestry, because it is thought of as a "White" disease (*19*). Popular misinterpretations of the use of race in genetics also continue to fuel racist beliefs, so much so that, in 2014, a group of leading human population geneticists publicly refuted claims about the genetic basis of social differences between races (*20*). Finally, the use of the race concept in genetics, an issue that has vexed natural and social scientists for more than a century, will not be obviated by new technologies. Although the low cost of next-generation sequencing has facilitated efforts to sequence hundreds of thousands of individuals, adding whole-genome sequences does not negate the fact that racial classifications do not make sense in terms of genetics.

More than five decades after Dobzhansky called on biologists to develop better methods for investigating human genetic diversity (*21*), biology remains stuck in a paradox that reflects Dobzhanky's own struggle with the race concept: both believing race to be a tool to elucidate human genetic diversity and believing that race is a poorly defined marker of that diversity and an imprecise proxy for the relation between ancestry and genetics. In an attempt to resolve this paradox and to improve study of human genetic diversity, we propose the following.

Scientific journals and professional societies should encourage use of terms like "ancestry" or "population" to describe human groupings in genetic studies and should require authors to clearly define how they are using such variables. It is preferable to refer to geographic ancestry, culture, socioeconomic status, and language, among other variables, depending on the questions being addressed, to untangle the complicated relationship between humans, their evolutionary history, and their health. Some have shown that substituting such terms for race changes nothing if the underlying racial thinking stays the same (*22*, *23*). But language matters, and the scientific language of race has a considerable influence on how the public (which includes scientists) understands human diversity (*24*). We are not the first to call for change on this subject. But, to date, calls to rationalize the use of concepts in the study of human genetic diversity, particularly race, have been implemented only in a piecemeal and inconsistent fashion, which perpetuates ambiguity of the concept and makes sustained change unfeasible (*16*). Having journals rationalize the use of classificatory terminology in studying human genetic diversity would force scientists to clarify their use and would allow researchers to understand and interpret data across studies. It would help avoid confusing, inconsistent, and contradictory usage of such terms.

Phasing out racial terminology in biological sciences would send an important message to scientists and the public alike: Historical racial categories that are treated as natural and infused with notions of superiority and inferiority have no place in biology. We acknowledge that using race as a political or social category to study racism and its biological effects, although fraught with challenges, remains necessary. Such research is important to understand how structural inequities and discrimination produce health disparities in socioculturally defined groups.

The U.S. National Academies of Sciences, Engineering, and Medicine should convene a panel of experts from biological sciences, social sciences, and humanities to recommend ways for research into human biological diversity to move past the use of race as a tool for classification in both laboratory and clinical research. Such an effort would bring stakeholders together for a simple goal: to improve the scientific study of human difference and commonality. The committee would be charged with examining current and historical usage of the race concept and ways current and future technology may improve the study of human genetic diversity; thus, they could take up Dobzhansky's challenge that "the problem that now faces the science of man [sic] is how to devise better methods for further observations that will give more meaningful results" (*21*). Regardless of where one stands on this issue, this is an opportunity to strengthen research by thinking more carefully about human genetic diversity. ■

REFERENCES AND NOTES

1. F. Collins, *Nat. Genet.* **36** (suppl.), S13 (2004).
2. M. W. Foster, R. R. Sharp, *Nat. Rev. Genet.* **5**, 790 (2004).
3. P. A. Chow-White, S. E. Green Jr., *Int. J. Commun.* **7**, 556 (2013).
4. W. E. B. Du Bois, *The Health and Physique of the Negro American* (Publ. no. 11, Atlanta Univ. Publications, Atlanta, GA, 1906).
5. T. Dobzhansky, *Genetics and the Origin of Species* (Columbia Univ. Press, New York, 1937).
6. M. Yudell, *Race Unmasked: Biology and Race in the 20th Century* (Columbia Univ. Press, New York, 2014).
7. E. G. Burchard *et al.*, *N. Engl. J. Med.* **348**, 1170 (2003).
8. Y. Banda *et al.*, *Genetics* **200**, 1285 (2015).
9. C. E. Powe *et al.*, *N. Engl. J. Med.* **369**, 1991 (2013).
10. D. Roberts, *Fatal Invention: How Science, Politics, and Big Business Re-Create Race in the Twenty-First Century* (The New Press, New York, 2012).
11. D. Serre, S. Pääbo, *Genome Res.* **14**, 1679 (2004).
12. P. C. Ng, Q. Zhao, S. Levy, R. L. Strausberg, J. C. Venter, *Clin. Pharmacol. Ther.* **84**, 306 (2008).
13. J. S. Kaufman, R. S. Cooper, *Am. J. Epidemiol.* **154**, 291 (2001).
14. T. R. Rebbeck, P. Sankar, *Cancer Epidemiol. Prev.* **14**, 2467 (2005).
15. L. M. Hunt, M. S. Megyesi, *J. Med. Ethics* **34**, 495 (2008).
16. A. Smart, R. Tutton, P. Martin, G. T. H. Ellison, R. Ashcroft, *Soc. Stud. Sci.* **38**, 407 (2008).
17. G. Lettre *et al.*, *PLOS Genet.* **7**, e1001300 (2011).
18. K. Bremer, H. E. Wanntorp, *Syst. Biol.* **28**, 624 (1979).
19. C. Stewart, M. S. Pepper, *Genet. Med.* (2015).
20. G. Coop *et al.*, *New York Times*, 8 August 2014, p. BR6.
21. T. Dobzhansky, *Mankind Evolving: The Evolution of the Human Species* (Yale Univ. Press, New Haven, CT, 1962).
22. S. M. Fullerton, J. H. Yu, J. Crouch, K. Fryer-Edwards, W. Burke, *Hum. Genet.* **127**, 563 (2010).
23. L. Braun, E. Hammonds, *Soc. Sci. Med.* **67**, 1580 (2008).
24. W. C. Byrd, M. W. Hughey, *Ann. Am. Acad. Pol. Soc. Sci.* **661**, 1 (2015).

ACKNOWLEDGMENTS

All authors contributed equally to the conceptualization of this paper. M.Y. wrote the first draft and revised it based on comments from coauthors. Special thanks to E. Arana for research assistance.

10.1126/science.aac4951