
BIOGRAPHICAL SKETCH

NAME: Deborah Ann Bolnick

eRA COMMONS USER NAME: dabolnick1

POSITION TITLE: Associate Professor, Department of Anthropology

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	Completion Date MM/YYYY	FIELD OF STUDY
Yale University, New Haven, CT	BA	05/1999	Anthropology
University of California, Davis, Davis, CA	MA	06/2001	Anthropology
University of California, Davis, Davis, CA	PhD	05/2005	Anthropology

A. Personal Statement

I have a broad background in anthropology, population genetics, ancient DNA studies, human biological variation, and the ethical, legal, and social implications of genetic research, especially for indigenous communities. My primary area of research investigates the patterns of genetic variation in Native American populations and how they have been shaped by culture, language, history, and geography. My laboratory analyzes both ancient and modern DNA samples to track changes in genetic diversity over time and to reconstruct the demographic and evolutionary history of Native American populations. In particular, we are interested in how early events in human prehistory (such as the initial peopling of the Americas) as well as more recent historical events (such as European contact/colonialism) shaped the patterns of genetic diversity that exist today in Native American communities. As part of this research, I work closely with indigenous individuals and communities in the southern United States. A second project in my laboratory is focused on developing methods for assessing DNA methylation patterns in ancient DNA extracted from human remains. These techniques will allow us to reconstruct epigenetic variation in ancient populations, which may help elucidate experiences of violence, stress, and malnutrition in ancient times. These research projects are conducted in collaboration with graduate students and postdoctoral researchers working in my lab, as well with members of the Native American communities participating in these studies.

My second area of research examines the ethical, legal, social, and political implications of genetic research, including the ways that genetic and biomedical studies intersect with Euro-American and Native American understandings of race, ethnicity, and identity. I work with an interdisciplinary group of scholars from around the country (including geneticists, physicians, social scientists, legal scholars, and bioethicists) to (a) investigate how genetic ancestry research influences and is influenced by understandings of race and ethnicity, (b) examine the scientific limitations and medical, ethical, legal, and social implications of commercial genetic ancestry tests, and (c) develop alternative approaches for scientific research on human biodiversity and racial/ethnic health disparities. I have also played a role in efforts to incorporate innovative training on race, genomics, health disparities, and the social determinants of health into the medical curriculum for the University of Texas Dell Medical School. My research therefore fits within the PRC's primary research areas of (1) Family Demography and Intergenerational Relationships and (2) Population Health. PRC administrative and development work has been, and continues to be, critical to supporting my research.

B. Positions and Honors

Positions and Employment

2005-2007 Lecturer/Research Fellow, Dept. of Anthropology, University of Texas at Austin
2007-2014 Assistant Professor, Dept. of Anthropology, University of Texas at Austin
2007- Faculty, Ecology, Evolution, and Behavior Graduate Program, University of Texas at Austin
2012- Faculty Research Associate, Population Research Center, University of Texas at Austin
2014- Associate Professor, Dept. of Anthropology, University of Texas at Austin

Other Experience and Professional Memberships

1999- Member, American Association of Physical Anthropology
1999- Member, American Anthropological Association (Biological Anthropology Section)

2003-2005	Executive Board, Biological Anthropology Section of the American Anthropological Association
2006-	Member, Society for American Archaeology
2007-2010	Genetics and Evolution Workshop Instructor, Texas Memorial Museum professional development series for Texas high school biology teachers
2010-	Member, American Association of Anthropological Genetics
2011-2014	Vice President, President, & Past President, American Association of Anthropological Genetics
2011-2014	Executive Committee, American Association of Anthropological Genetics
2012-2013	Editorial Board, <i>Human Biology</i>
2012-2013	<i>Human Biology</i> Editorial Search Committee
2013-2016	Ethics Committee, American Association of Physical Anthropologists
2015-2016	Annual Meeting Program Committee, American Association of Physical Anthropologists
2013-	Instructor and Steering Committee, Summer Internship for Indigenous Peoples in Genomics
2014	Co-organizer, Summer Internship for Native Americans in Genomics (SING) workshop
2014-	Member, Texas Archaeological Society
2015-	Chair, Ethics Committee, American Association of Anthropological Genetics
2016-	Annual Meeting Executive Program Committee, American Anthropological Association

Honors

1999	Phi Beta Kappa
1999	Edward Sapir Prize, Yale University
1999	<i>Summa cum laude</i> , Yale University
2011	University of Texas Society for Teaching Excellence

C. Contributions to Science

- Many of my early publications focused on using genetic data from extant populations to improve our understanding of Native American genetic diversity and population history. With my collaborators, I conducted the most extensive studies to date of genetic variation in eastern North America, analyzing mtDNA and Y chromosome variation in 605 individuals from 16 contemporary eastern North American populations. These studies showed that sociocultural and historical factors have played an important role in shaping the genetic structure of this region. In particular, post-marital residence practices strongly influenced population genetic structure, and European contact (in AD 1492) had significant but sex-specific genetic effects. Male-mediated European gene flow introduced non-native Y chromosome lineages into the indigenous gene pool, and the demographic collapse following European contact reduced mtDNA diversity in southeastern North America. The latter discovery was important because several earlier studies had suggested that this collapse had no discernible effect on Native American genetic variation. This research also showed that male and female demographic histories can differ substantially.
 - Malhi RS, Eshleman JA, Greenberg JA, **Weiss DA**, Schultz BA, Kemp BM, Kaestle FA, Lorenz JG, Johnson JR, Smith DG. 2002. The structure of diversity within New World mitochondrial DNA haplogroups: implications for the prehistory of North America. *American Journal of Human Genetics* 70:905-919.
 - Bolnick DA**, Smith DG. 2003. Unexpected patterns of mitochondrial DNA variation among Native Americans from the southeastern United States. *American Journal of Physical Anthropology* 122:336-354.
 - Bolnick DA**, Bolnick DI, Smith DG. 2006. Asymmetric male and female genetic histories among Native Americans from eastern North America. *Molecular Biology and Evolution* 23:2161-2174.
- In addition to studying contemporary diversity patterns, I analyze ancient DNA (aDNA) extracted from Native American skeletal remains. My work has helped advance this field methodologically and by pioneering new anthropological applications of aDNA data. First, my laboratory has developed a non-destructive method for extracting DNA from ancient human remains. Unlike most extraction protocols, our method isolates DNA from ancient teeth without breaking or powdering them and without exposing them to hazardous chemicals. This method keeps the sampled material intact and allows it to be safely returned to a museum curator or custodian. Because curators and Native American communities often will not approve destructive analyses of Native American remains, this method has made it possible to conduct genetic research using skeletal collections that could not otherwise be studied. Second, we are applying new

methods for detecting cytosine methylation to aDNA, allowing us to analyze epigenetic data from ancient human populations for the first time. These approaches may make it possible to reconstruct gene expression patterns in ancient populations and investigate the epigenetic effects of social and ecological stress in ancient times.

- a. **Bolnick DA**, Bonine HM, Mata-Miguez J, Kemp BM, Snow MH, LeBlanc SA. 2012. Non-destructive sampling of human skeletal remains yields ancient nuclear and mitochondrial DNA. *American Journal of Physical Anthropology* 147:293-300.
 - b. Smith RWA, Monroe C, **Bolnick DA**. 2015. Detection of cytosine methylation in ancient DNA from five Native American populations using bisulfite sequencing. *PLoS ONE* 10(5): e0125344.
3. My other main contribution to the field of aDNA research has been to show how aDNA data can be combined with archaeological, osteological, and ethnohistorical evidence to address important questions about Native American population history, the initial peopling of the Americas, and subsequent migrations within the Americas. I have contributed to collaborative studies of some of the earliest human remains found in North America, and these studies have improved our understanding of the first migrations into the Americas and the relationships between ancient and contemporary Native Americans. I have also studied aDNA from ~1800 year old remains from the Midwestern United States to show that migration and gene flow accompanied the trade and cultural exchange that occurred among many ancient communities in this region. This study also demonstrated that skeletal morphology can sometimes be a poor proxy for genes.
- a. **Bolnick DA**, Smith DG. 2007. Migration and social structure among the Hopewell: evidence from ancient DNA. *American Antiquity* 72:627-644.
 - b. Chatters JC, Kennett DJ, Stafford TW, Asmerom Y, Kemp BM, Polyak V, Blank AN, Beddows P, Reinhart E, Arroyo-Cabrales J, **Bolnick DA**, Malhi RS, Erreguerena PL, Morell-Hart S, Rissollo D. 2014. Late Pleistocene human skeleton and mtDNA links Paleoamericans and modern Native Americans. *Science* 344:750-754.
 - c. Raff JA, **Bolnick DA**. 2015. Does mitochondrial haplogroup X indicate ancient trans-Atlantic migration to the Americas? A critical re-evaluation. *Paleoamerica* 1:297-304.
 - d. **Bolnick DA**, Raff JA, Springs LC, Reynolds AW, Miró-Herrans AT. 2016. Native American genomics and population histories. *Annual Review of Anthropology*.
4. Working with collaborators and members of my lab group, I have also used both ancient and modern DNA datasets to evaluate changes in the Native American gene pool over time. In one analysis of 63 ancient and 98 modern populations from the Americas, we showed that continent-wide patterns have not changed substantially over the last several thousand years, and regional differences were established fairly early in prehistory. However, we also found that many regions exhibit some changes over time due to population movements, gene flow, and genetic drift. In other studies, we have tracked genetic changes over time at a single location to investigate whether the site experienced a population replacement at a time when the archaeological record indicates major shifts in cultural practices. In one case (at the town of Xaltocan in central Mexico), the genetic evidence suggests that a population replacement did occur, while in the other case (at a site in western Illinois), it appears that cultural changes occurred despite population continuity over time. Together, these studies demonstrate that genetic patterns have changed over time in some places but not others, and temporal sampling is necessary to reconstruct the processes that have shaped contemporary genetic diversity. Our work investigating changes in ABO blood group diversity over time provides an example of how such temporal sampling can help us understand the patterns of the genetic diversity that exist today.
- a. Halverson MS, **Bolnick DA**. 2008. An ancient DNA test of a founder effect in Native American ABO blood group frequencies. *American Journal of Physical Anthropology* 137:342-347.
 - b. Raff JA[†], **Bolnick DA**[†], Tackney J, O'Rourke DH. 2011. Ancient DNA perspectives on American colonization and population history. *American Journal of Physical Anthropology* 146:503-514.
[†] *equal contribution; one of five most accessed articles in AJPA in 2011*
 - c. Mata-Míguez J, Overholtzer L, Rodríguez-Alegría ER, Kemp BM, and **Bolnick DA**. 2012. The genetic impact of Aztec imperialism: ancient mitochondrial DNA evidence from Xaltocan, Mexico. *American Journal of Physical Anthropology* 149:504-516.

- d. Reynolds AW, Raff JA, **Bolnick DA**, Cook DC, Kaestle FA. 2015. Ancient DNA from the Schild site in Illinois: implications for the Mississippian transition in the Lower Illinois river valley. American Journal of Physical Anthropology 156:434-448.
5. As part of my research, I have also discussed the ethical, legal, social, and political implications of genetic research, including the ways that genetic studies and commercially-available genetic ancestry tests intersect with Euro-American and Native American understandings of race, ethnicity, and identity. My research has examined what companies claim about these tests, what the tests actually show, and how the tests shape American perspectives on race, ethnicity, kinship, group membership, and individual identity. I was one of the first scholars to publicly raise concerns (in 2003) about the scientific limitations and ethical issues associated with these tests. My co-authors and I subsequently called on professional genetic associations to develop recommendations on ancestry testing, and we encouraged federal agencies to help set industry standards for appropriate direct-to-consumer (DTC) genetic testing practices. The American Society of Human Genetics (ASHG) subsequently released a set of recommendations on ancestry testing and convened two roundtables of stakeholders to develop guidelines on genetic ancestry inference. The US Government Accountability Office and the Food & Drug Administration have also begun to engage the DTC genetic testing industry in recent years. I have also called for better training of scientists and medical practitioners about race, ethnicity, genetics, and health disparities.
- a. **Bolnick DA**, Fullwiley D, Duster T, Cooper RS, Fujimura JH, Kahn J, Kaufman JS, Marks J, Morning A, Nelson A, Ossorio P, Reardon J, Reverby SM, TallBear K. 2007. The science and business of genetic ancestry testing. Science 318:399-400.
- b. Lee SS, **Bolnick DA**, Duster T, Ossorio P, TallBear K. 2009. The illusive gold standard in genetic ancestry testing. Science 325:38-39.
- c. Fujimura JH, **Bolnick DA**, Rajagopalan R, Kaufman J, Lewontin RC, Duster T, Ossorio P, Marks J. 2014. Clines without classes: how to make sense of human variation. Sociological Theory 32:208-227.
- d. **Bolnick DA**. In press. Combating racial health disparities through medical education: the need for anthropological and genetic perspectives in medical training. Human Biology 87:349-359.

D. Research Support

Ongoing Research Support

BCS-1518079 (D. Bolnick, PI)

06/15/15-05/31/17

National Science Foundation

Identifying Genomic Signatures of Evolutionary and Cultural Change in Native Americans

This project investigates how Native American genetic diversity changed over time and across space in the Midwestern United States in response to sociocultural and demographic shifts over the last 1000 years.

Role: Principal Investigator

Responsibilities: For this project, I oversee the selection and collection of samples for genetic analysis, data collection and analysis, and the interpretation of the genetic data being collected. I also supervise and mentor the graduate students involved in the project.

BCS-1535841 (R. Hard, PI)

09/01/15-08/31/17

National Science Foundation

Understanding Long Term Relationships Between Environmental Change, Human Resilience, and Territoriality

This project is analyzing ancient DNA, stable isotopes, radiocarbon dates, and archaeological data from a site in the Texas Coastal Plain that was occupied over a 6000 year period, in order to address questions about the emergence and evolution of territorial systems in the Americas.

Role: Co-Principal Investigator

Responsibilities: For this project, I oversee the collection and analysis of ancient DNA data from the Morhiss site in Texas. I also work with the PI and other co-PIs to integrate genetic, isotopic, chronological, and bioarchaeological analyses.

SMA-1520308 (R. Hard, PI)

08/15/15-01/31/19

National Science Foundation

IBSS: The Evolution of Social Networks and the Robustness of Human Societies to Population Growth and Climate Change: A Deep Time Perspective

This interdisciplinary project combines bioeconomic modeling, social network analysis, ancient DNA analyses, and archaeological investigations to identify reasons why human societies in the Texas Coastal Plain often persisted but sometimes collapsed under conditions of population growth and environmental change.

Role: Co-Principal Investigator

Responsibilities: For this project, I oversee the collection and analysis of ancient DNA data, bioinformatic and biostatistical analyses of the genetic data, and the genetic demographic modeling. I also work with the PI and other co-PIs to integrate genetic, isotopic, chronological, and bioarchaeological analyses.

Completed Research Support

SMA-1408876 (D. Bolnick, PI)

08/01/14-10/31/16

National Science Foundation

The Impact of European Contact on Native American Evolutionary History

This project is investigating the impact of European contact on Native American genomic diversity by analyzing genome-wide diversity patterns in contemporary and ancient Native Americans from the southern US.

Role: Principal Investigator

Responsibilities: I supervised the data collection and analysis of genetic data, and mentored the postdoctoral fellow on research, teaching, and professional development skills over the course of the project.

003658-0029-2011 (D. Bolnick, PI)

07/01/12-08/31/15

Norman Hackerman Advanced Research Program

Assessing the Impact of European Contact on Native American Genomic Diversity and Disease Prevalence

This project collected and analyzed genetic data from contemporary and ancient Native Americans in order to investigate the impact of European contact on Native American genomic diversity and the prevalence of genetic diseases in Native Americans.

Role: Principal Investigator

Responsibilities: In this project, I supervised the collection of genetic data, mentored the undergraduates, graduate students, and postdoctoral researchers involved in the project, and took a leading role in analyzing the data and preparing results for publication.

BCS-1412501 (D. Bolnick, PI)

08/01/14-07/31/16

National Science Foundation

Doctoral Dissertation Improvement: Assessing the Demographic and Genetic Impact of Major Social Transitions in Historical Perspective

This project is analyzing genomic data from both ancient and contemporary residents of Xaltocan, Mexico in order to investigate how Aztec imperialism and the Spanish conquest affected the genetic composition of a rural Mexican community.

Role: Principal Investigator

Responsibilities: For this project, I supervised the data collection and analysis performed by graduate student who was undertaking this work as part of his dissertation research.

UTA12-000694 (D. Bolnick, PI)

06/15/12-08/31/16

Rock Art Foundation

Ancient DNA Analysis of the Prehistoric Inhabitants of the Lower Pecos Region of Texas

This project is analyzing ancient DNA from prehistoric skeletal remains in order to infer the biological ancestry of the sampled individuals and their genetic relatedness to other Native American populations.

Role: Principal Investigator

Responsibilities: For this project, I oversaw the collection and analysis of genetic data, prepared regular progress reports for the foundation, presented the results at academic conferences, and am contributing to the publications being prepared on this research.