

9-1-2015

Case Study on Ancestry Estimation in an Alaskan Native Family: Identity and Safeguards against Reductionism

Alyssa C. Bader

Department of Anthropology, University of Illinois at Urbana-Champaign, Urbana, IL, acbader2@illinois.edu

Ripan S. Malhi

School of Integrative Biology, University of Illinois at Urbana-Champaign, Urbana, IL

Recommended Citation

Bader, Alyssa C. and Malhi, Ripan S., "Case Study on Ancestry Estimation in an Alaskan Native Family: Identity and Safeguards against Reductionism" (2015). *Human Biology Open Access Pre-Prints*. 106.
http://digitalcommons.wayne.edu/humbiol_preprints/106

This Open Access Preprint is brought to you for free and open access by the WSU Press at DigitalCommons@WayneState. It has been accepted for inclusion in Human Biology Open Access Pre-Prints by an authorized administrator of DigitalCommons@WayneState.

Case study on ancestry estimation in an Alaskan Native family: Identity and safeguards against reductionism

Alyssa C. Bader¹, Ripan S. Malhi^{1,2,3}

¹Department of Anthropology, University of Illinois at Urbana-Champaign, Urbana, IL 61801

²School of Integrative Biology, University of Illinois at Urbana-Champaign, Urbana, IL 61801

³Carl R. Woese Institute for Genomic Biology, University of Illinois at Urbana-Champaign, Urbana, IL 61801

ABBREVIATED TITLE Genetic ancestry estimation and identity

KEY WORDS Ancestry, Identity, Genetic testing, Native American

CONTACT Alyssa Bader

607 S. Matthews Ave

109 Davenport Hall, M/C 148

Urbana, IL 61801

acbader2@illinois.edu

Issue: 87.4, Health disparities special issue

With advances in DNA genotyping and sequencing technology, in combination with computational developments, genetic ancestry estimation now provides the ability to identify the ancestral genetic composition of an individual or population or to learn about descendants of people or groups who “mixed” in the recent past (Royal et al. 2010). The ability to estimate ancestry or learn about admixture opens pathways to identify loci associated with disease through admixture mapping (Winkler et al. 2010), learn of genomic regions subject to natural selection through admixture driven selection (Tang et al. 2007), or learn about admixture history associated with European colonization (Verdu et al. 2014). At the individual level, genetic ancestry estimation is being used to verify family or national narratives (Cabana et al. 2006; Gibbon et al. 2011) or in law enforcement and forensic science (Shriver et al. 1997; Budowle et al. 2003).

Ancestry-based identity

Personal identity is multidimensional, complex, and intersectional (Medina 2004). Many different forms of individual identity – political, ethnic, religious, family – are related in part to notions of ancestry (Brodwin 2002). In the past, ancestry was often conceptualized as ‘blood,’ a metaphor representing “nation, nativity, heritage, class, family, kinship, and ancestry” (Bardill 2011). This metaphorical, symbolic blood did not necessarily require biological relatedness, but rather a deep sense of shared identity. However, the advent of genetic ancestry estimation has redefined symbolic ‘blood’ into the literal substance, where ancestry is empirically discoverable and measurable through the analysis of DNA markers (Bardill 2011). Thus, some individuals have utilized genetic ancestry estimation as evidence to authenticate membership in an ancestral community, such as African American individuals whose ancestors were forcefully dislocated from Africa and brought to the Americas as slaves (Nelson 2008). Genetic testing has also been

used as a resource for validating enrollment claims in several Native American tribes (TallBear 2013b). As most tribes require enrollees to prove biological descent from a tribe member listed on original roll documents, genetic parentage analysis has been widely used to verify parentage and support claims of descent (Bardill *in* NCAI Genetics Resource Center). Communities such as the Western Mohegan have attempted to use genetic ancestry estimation, rather than parental analysis, to gain federal recognition (see TallBear 2003 for more discussion).

The ability to demonstrate Native American ancestry and legally claim “Nativity” has profound social and economic implications in the United States, given the sociopolitical history between indigenous nations and the United States government, as well as the current status of federally recognized tribes as “nations within the nation” (Bardill 2011). Legal recognition provides access to benefits established through Native land claim settlements and federal treaties (TallBear 2003, TallBear 2013b). An individual can be legally recognized as Native through tribal enrollment and/or federal recognition via a Certificate of Indian Blood (more recently Certified Degree of Indian Blood). This status often depends on an individual’s ‘blood quantum’, a method employed by the United States government to measure and record Native ancestry since the early 1800s (TallBear 2003). An individual’s blood quantum is calculated by their hereditary relationship to tribal members recorded on original tribal rolls and treaty claims (Bardill *in* NCAI Genetics Resource Center). For example, an individual with three grandparents who were listed as ‘full-blooded’ on the tribal roll would have a blood quantum of 3/4, while an individual with only one Native grandparent who was recorded on the original roll with a blood quantum of 1/2 would themselves have a blood quantum of 1/8. This blood is symbolic (Bardill 2011), as it is based off of genealogical records. However, the capabilities of genetic ancestry testing mean that literal blood could potentially be used as a new measure of Native ancestry.

Though there are widely recognized problems with the blood quantum system (see TallBear 2003 for discussion), many indigenous scholars see genetic ancestry testing as potentially more problematic in terms of measuring “Nativity” (Bardill 2011; TallBear 2013b). While symbolic blood is somewhat negotiable, genetic analyses simplify an individual’s identity down to pure biology, excluding cultural and linguistic aspects of Native heritage (Bardill 2011). TallBear (2003) argues “tribal ideas of kinship and community belonging are not synonymous with biology”, suggesting the use of genetics to confer group membership could disenfranchise historical members of the tribal community. Other scholars agree, noting that interpreting the results of genetic ancestry estimation involves judging “genetic knowledge against other kinds of claims to authentic identity,” putting at stake “personal esteem and self-worth, group cohesion, access to resources, and the redressing of historical injustice” (Brodwin 2002). Clearly, the methods used to define and measure Nativeness have very real consequences for living individuals and communities; given these concerns, the debate of either employing blood quantum *or* genetic ancestry estimation is oversimplified and inadequate. A critical examination of genetic ancestry estimation alongside other forms of identity knowledge is needed to assess the ways molecular genetic information may interact with, rather than replace, other forms of knowledge.

Purpose of study and goals

This study engages members of one extended family with Alaskan Native ancestry in examining personal identity and ancestry. Three different forms of ancestry information – oral family history, genetic ancestry estimation, and document-based genealogy – are assessed to examine the ways in which these lines of evidence may complement and/or contradict each other. Interest in genetic ancestry estimation and its potential uses within the Native community

is quickly growing, but its relationship to other methods of measuring and/or describing other ancestry-related identity is woefully understudied. Given the unique sociopolitical and economic stakes related to indigenous ancestry, it is imperative that researchers critically examine how genetic ancestry estimation contributes to or impacts individual, family, and community narratives of indigenous ancestry. As widespread European colonization and subsequent treaty agreements occurred relatively late in the region now known as southeast Alaska and British Columbia, a family with Alaskan Native ancestry provides an interesting case study to explore these relationships. The Alaska Native Claims Settlement Act was not signed into law until 1971, an event during which several of the study participants were alive. Working with this family, the researchers had the opportunity to examine family oral history and historical and legal documents over several generations, both before and after the ANCSA was formally enacted.

MATERIALS AND METHODS

Data were collected from a single extended family (n=7) with members who are Alaskan Native. As the goal was to assess the relationship between multiple components of identity, the study examined both qualitative and quantitative data on individual identity. The data for this study was comprised of: oral family history (qualitative), historical and legal documentation (qualitative and quantitative), and genetic ancestry estimation (quantitative) (Table 1). This study was approved by the University of Illinois Institutional Review Board with protocol #13013.

Oral family history

In-person oral interviews were conducted by ACB with six living members of the extended family. The study participants comprised three generations of Alaskan Natives, as well as those who had married in to the family. Each interview was recorded via a digital voice

recorder, with the participants' consent. The questions asked discussed the individuals' self-identification, knowledge of their family history and ancestry, cultural affinities, and perspectives on genetic ancestry testing. Additionally, researchers were provided with access to oral history interviews of a family elder previously recorded by a family member.

Historical and legal documentation

Both publically accessible and family historical and legal documents were consulted to reconstruct a genealogy tracing the Alaskan Native ancestry within the family. The documents accessed dated back to 1900. These documents included census records, birth certificates, death certificates, baptismal and mission records, and Certificates of Indian Blood issued by the federal Bureau of Indian Affairs. Several family members had previously documented genealogical research, which was shared with the researchers by the participants and the sources verified. In addition to reconstructing a family tree, the historical and legal documents were used as ethnographic texts to collect data on the language used to identify and record individuals, especially non-White individuals (such as "color or race" and "tribe and clan"), in legal and historical documents throughout this period of history.

Genetic ancestry estimation

Each participant (n=7) was provided with a commercially available saliva collection kit from the genetic testing company 23andMe. The company employs a custom Illumina HumanOmniExpress-24 format chip which genotypes over 600,000 SNPs from across the genome, including the autosomal, mitochondrial, and Y chromosomes (23andMe Genotyping Technology). The 23andMe ancestry composition analysis program "FINCH" uses the same algorithm as a genetic analysis program commonly used by anthropological geneticists

(“BEAGLE,” Browning and Browning 2007). The participants registered their own 23andMe.com accounts (some with the help of ACB) to receive and manage their results. The participants then shared access to the ancestry portion of their test results with ACB (the health results remained private). When assessing the ancestry composition results provide by 23andMe, the authors compiled the conservative, standard, and speculative estimates of percent ancestry at the regional resolution level into a range of percent ancestry (reported in Figure 1). To assess the percent Native American, the 23andMe estimates for percent “Native American” and “Broadly East Asian and Native American” were combined.

RESULTS

Information from historical documents, individual interviews, and genetic ancestry estimation was compiled into an annotated genealogical tree (Figure 1). To focus the study, the family tree has been simplified by removing siblings so only one branch of descendants is shown.

Family oral history interview

When interviewed, each participant in this study identified himself or herself, at least in part, using race or ancestry. Five family members identified themselves as having Alaskan Native ancestry. Individuals articulated their Native ancestry in varying ways (see Figure 1), but each of the family members who identified as Native discussed their identity as stemming from family relationships and heritage, rather than an overall sense of cultural community.

For me it's kind of a sense of pride, that I'm from Alaska and I'm part Native I think of as a positive term and that my father's half Native... I use it with a sense of pride that that's where my heritage is from, although I don't do the things that probably reflect that heritage... I think as I grew older and became closer to my father I think I began to connect more with who I was, my heritage. (Individual 3)

I learned a lot from my Native uncles because the Native way of raising a kid back then... was to send the kid off with their uncles ...I was sent off every summer to fish with my uncles. I learned how to fish. I learned how to hunt; I learned how to clean animals; I learned how to fix things from my uncles. (Individual 5)

Individual interviews, in combination with previously recorded interviews provided by some participants, provide an oral narrative of family history going back to the early 1900's. The family identifies as having Native ancestry in the Tsimshian, Haida, and Tlingit communities of the area now known as southeast Alaska and British Columbia (Figure 2).

Historical and legal documentation

Textual analysis of historical documents such as census records, birth certificates, and death certificates show the terms used to describe non-White individuals as far back as the 1900 census. Censuses were collected once every ten years in the Alaska Territory from 1900-1940. Indigenous individuals were described by linguistic group or tribe, as well as simply identifying them as "Indian", "Mixed", or "Brown". Clans within tribes were not recorded, but specific tribal communities were sometimes recorded, such as "Hydah Klawock" or "Tsimpsean Metlakatlan". Documents in the mid to late 1900's transitioned away from tribal designations to modern race-based classifications: "Indian", "White", or "White/Indian". Race or ancestry information for the same individual was often inconsistent across documents (for example see Individuals 9 and 16, Figure 1).

More recent Certificates of Indian Blood indicate the blood quantum value assigned for each participant who claims Native ancestry. The CIBs recognize the family members as varying fractions of "IND" with no description of tribe or clan (Figure 3).

Genetic ancestry estimation

The genetic ancestry results broadly reflected each individual's self-reported ancestry, in terms of biogeographic ancestral groups, and supported all described and historically reported biological relationships. However, the proportion of Native ancestry estimated through the genetic ancestry test did not match the federally reported blood quantum of two of the four individuals with CIBs. The percent Native American was estimated to be lower than the recorded blood quantum of Individuals 1 and 2. Additionally, the genetic ancestry estimate did not have a level of resolution that could estimate regional, tribal, or clan-specific Native American ancestry.

DISCUSSION

Each study participant used race or ancestry as one component of self-described personal identity. Thus, ancestry-related identity is a key element of each individual's overall sense of self. The results of the document analysis and genetic ancestry estimation for this family reflected family oral history regarding ancestry, as well as individual ancestry-related identity. However, the case studies demonstrate several differences in the way ancestry-related identity is quantified between the three different forms of data.

Quantifying ancestry-related identity

Both historically and presently, the indigenous ancestry of individuals claiming to be Native has been measured according to symbolic blood quantum, a proportion estimation method. Individual identity is impacted by these legal definitions of 'how Native' an individual is. Genetic ancestry estimation has presented itself as a new method for quantitative ancestry measurement. Genetic ancestry testing companies are even marketing themselves to tribes

(TallBear 2013b), but genetic ancestry estimates are not necessarily compatible with blood quantum estimates, as demonstrated by this case study.

There are clear discrepancies in the relationship between blood quantum values and estimated genetic ancestry when the data for Individuals 1, 2, 3, and 5 are compared (Figure 1). Whereas blood quantum calculations rely on the assumption that ‘Nativity’ can be inherited in equal proportions from the mother and father, genetic ancestry estimation calculations are more variable. Individual 5 has a genetic ancestry estimate of 18.8-39.5% Native American. His defined blood quantum is much higher than the mean of this range (29.15%), at $\frac{3}{8}$ (37.5%). His biological son, Individual 3, inherited half that blood quantum for a value of $\frac{3}{16}$ (18.75%). Individual 3’s genetic ancestry estimate ranges from 13.1-25.2% Native American. Thus his defined blood quantum lies much closer to the average of his genetic ancestry composition estimate (19.15%). His children, Individual 1 (daughter) and Individual 2 (son) again inherited half of their father’s blood quantum, and are each documented as having a blood quantum of $\frac{3}{32}$ (9.38%). However, their genetic ancestry estimates vary. Individual 1 has a genetic ancestry estimate of 3.5-7.1% Native American, while her brother is estimated at a lower range of only 2.4-4.1% Native American. Importantly, in both siblings the range of estimated Native American genetic ancestry is less than their documented blood quantum. While the range of estimated Native American genetic ancestry for both their father and grandfather encompassed the defined blood quantum values, the estimated range of Native American genetic ancestry excludes the blood quantum values of the two siblings. Thus the genome-wide genetic ancestry estimation does not always concur with the symbolic quantification of Native ancestry measured through blood quantum. There are both biological and socio-political/historical reasons for these discrepancies.

Some of the factors influencing genetic ancestry estimates are well known, such as the importance of informative reference populations when estimating admixture (Royal et al. 2010; Weiss and Long 2009). The individuals in this family who were estimated to have Native American genetic ancestry had an average range of 13.6 percentage points when their Native American genetic ancestry estimates were compiled across confidence levels (conservative, standard, and speculative). In comparison, European genetic ancestry estimates ranged an average of only 5.0 percentage points across all study participants. Additionally, each individual with estimated Native American genetic ancestry had a much higher proportion of “unassigned” genetic ancestry (between 6.8-43.8% of the genome at the conservative confidence level) than individuals with only European genetic ancestry (less than 0.1-2% of the genome at the conservative confidence level). This suggests that at the computational stage, there is a much greater difficulty in confidently identifying Native American genetic ancestry than European genetic ancestry, which likely stems from the reference population. The reference population used by 23andMe to estimate genetic ancestry composition includes their customer databank as well as public reference datasets from research projects such as the 1000 Genomes Project, HapMap, and the Human Genome Diversity Project (23andMe Ancestry Composition Guide). Previous research has demonstrated that the clientele of direct-to-consumer genetic testing companies are predominantly white, middle-class individuals (Malhi 2009), suggesting that there is a dearth of comparative indigenous genetic information in the customer database of 23andMe. Public reference datasets also lack comprehensive representations of Native American genetic diversity (Malhi and Bader 2015). The only samples from the Americas collected by the 1000 Genomes Project are so-called “Ad Mixed American” from Los Angeles, Puerto Rico, Medellin, and Lima (1000 Genomes Project Consortium 2012). HapMap has no samples from the

Americas (International HapMap Consortium 2007). The Human Genome Diversity Project contains samples from only a few populations from southern North America (Pima and Maya) and South America (Karitiana, Surui, and Colombian; Cavalli-Sforza 2005). There is a clear lack of comparative reference samples for estimating genetic ancestry indigenous to northern North America.

An additional biological factor illuminated by this study is the unequal contribution of genetic material from paternal grandparents. Genome-wide comparisons of autosomal SNP contribution between the paternal grandmother and grandfather of Individuals 1 and 2 (sibling pair) demonstrate for both individuals the grandmother contributed a significantly higher proportion of the paternal genome compared to the grandfather (Figure 4). Given the perceived value of proving high proportions of Native ancestry, and the potential for genetic ancestry estimation to factor more prominently in tribal enrollment decisions, this variation of inheritance from grandparents is an important factor to consider. In this case study, each grandchild had a lower likelihood of inheriting genomic regions with indigenous ancestry because the paternal grandfather is the relative with indigenous ancestry. This resulted in each grandchild having a Native American genetic ancestry estimate which was lower than their documented blood quantum, even though their grandfather's recorded blood quantum fell within his estimated range of Native American genetic ancestry. This discrepancy may be a result of estimation error and/or variation in the meiotic process. Hypothetically, if the siblings in this case needed a 5% Native American genetic ancestry estimation to be legally recognized as part of the tribe, one sibling would be recognized while the other would not, solely as a result of processes of transmission genetics. If genetic ancestry estimation were used exclusive to other ancestry information, such

reductionism would tie a person's identity to natural variation of a cellular process that has little to no bearing on ancestry identity.

Whereas genetic ancestry estimates are a function of both genetic information and sociopolitical definitions, blood quantum values represent the interplay between sociopolitical and historical factors. Documented blood quantum is based on the estimated ratio of Native ancestry an individual was recorded as having on a tribal roll or claims settlement. Based on the discrepancies between documents examined pertaining to this family, it is clear that descriptions of the race, origins, or ancestry of indigenous individuals was highly variable in government records (Figure 1). As an example, Individual 9 was categorized as either "Indian" or "Hydah/Haida" on all documents examined except her son's birth certificate, when she was described as "White-Indian". It is unclear why this discrepancy occurred, or whether the description was contributed by her or the observation of a hospital staff person. According to family oral history, older generations of the family lived in an environment when Nativeness was discouraged and discriminated against.

My mom didn't talk about it much, but I started talking to Gramma (Individual 13) and that's when I discovered there was a period of time in her growing up where they were urged not to be Native. They were told you wanted to drop your Native ways and learn the Caucasian ways and that happened both in school and in church... (Individual 5)

Individual 16 also provides an example of variation in race and ancestry records over time. This individual was alternately described as having been born in Spain or Chile, and being "Brown Chilean", "White", "Mixed", and "Metlakatlan". Given the racial perceptions at that time, it is possible Individual 16 chose to identify as being born in Spain, and be perceived as European, rather than be Chilean born and thus regarded as non-White. Both these individuals demonstrate how variable government records are regarding ancestry, and thus how an

individual's blood quantum, based on reporting methods much like these, might vary from quantification of their estimated genetic ancestry. These examples also illustrate the ways in which individuals may have negotiated their own identities in response to their sociopolitical environment.

Acknowledging different perspectives and avoiding genetic essentialism

It is important to consider, when examining the differences between self-reported ancestry, legally documented ancestry, and genetic estimates of ancestry, that these different methods have different perspectives of ancestral 'time'. Molecular anthropologists and population geneticists are interested in human population history along an evolutionary time scale, a much deeper time scale than government initiated ancestry documentation. While indigenous origin stories are often juxtaposed to the narrative produced through population history analysis, it is possible to reconcile these two narratives as different perspectives on population history. As TallBear (2013a) describes, in genetic narratives of history "Landscapes are places *through* which humans and their molecules move and *settle*... Indigenous notion of *peoplehood* as emerging *in relation with* particular lands and waters and their nonhuman actors differ from the concept of a genetic population, defined as moving upon or through landscapes". Thus, while molecular narratives of genetic ancestry address the deep time history of the evolution and movements of people, indigenous origin narratives address the history of their people emerging within a homeland. Both narratives can be respected for their contributions to human history, and both have been demonstrated to complement each other.

A recent example of complementary narratives can be seen in Raghavan et al.'s (2014) analysis of ancient and present-day DNA from the North American arctic. Their analysis provided molecular evidence of a Paleo-Eskimo metapopulation that was genetically distinct

from modern Inuit peoples, which complemented long-held Inuit oral history narratives of encounters with the ancient Tuniit people (Raghavan et al. 2014). Inuit oral history has recorded encounters with a large, strong, and shy people called the Tuniit who lived and hunted in the Inuit region of Nunavut before the Inuit arrived (Bennett and Rowley 2004). According to their oral history, these people were eventually driven off the land by the ancestors of the Inuit (Bennett and Rowley 2004). Raghavan et al.'s (2014) analysis of ancient human DNA from the North American arctic suggests there were multiple waves of population movement into this region. An early migration of people entered the region approximately 6,000 years ago while a later population, the ancestors of the Inuit, moved into the North American arctic approximately 700 years ago (Raghavan et al. 2014). The ancestors of the Inuit completely replaced the previous inhabitants, who remained genetically distinct and were not assimilated (Raghavan et al. 2014). This genetic narrative parallels Inuit oral knowledge regarding their Tuniit predecessors in the North American arctic, demonstrating how indigenous and Western scientific ways of knowing can be used as complements to expand our understanding of human history.

In light of the aforementioned explanations, it is imperative that this disagreement between blood quantum and genetic estimates of Native ancestry is acknowledged. Academic research can impact federal policy, and thus the lives of individuals. President Obama recently issued an executive order that insight from behavioral science research be used specifically to improve the design of government policy (Office of the Press Secretary 2015). As interest in genetic ancestry estimation continues to grow, it may eventually be utilized in policy decisions such as federal recognition with the Bureau of Indian Affairs. This suggests researchers should work to better engage policy makers by ensuring their writing is accessible to non-scientists. Given that the quantification of Native ancestry has a very real impact on the lives and legal

rights of Native individuals, both scholars and community members must understand and be able to communicate the differences in what each of these methods of ancestry quantification actually represent, and how each form of knowledge intersects, contradicts, and complements the others. In the case of this family, utilizing family oral history and historical records helps provide some explanation for the discord between blood quantum and genetic ancestry estimation, providing a more holistic understanding of Native ancestry in this family. While much of this discussion deals with biological ancestry, whether symbolic or literal, it is important to remember that being Native American is not simply biological.

CONCLUSION

When compared, the results of all three forms of data – historical and legal documents, genetic ancestry estimation, and oral family history – concur at the broadest level with regards to the family's Alaskan Native ancestry. However, the quantification of ancestry-related identity is problematic when all three lines of evidence are compared at a finer scale. This study illustrates the benefits of a multi-component analysis when examining genetic ancestry and ancestry-related identity. Biological ancestry was one facet of personal identity for each individual in this study, though the importance of this aspect varied by individual. Clearly biogenetic ancestry should not be discounted when considering ancestry-related identity, but the problems with genetic ancestry estimation illustrated through this study demonstrate that relying solely on genetic ancestry estimation when investigating ancestry-related identity risks becoming overly reductionist. Using complementary sources of information on ancestry-related identity, such as historical and legal documents and family oral history, provides a more nuanced view to supplement biogenetic data, resulting in more informed interpretations of the data and its potential shortcomings. Using this

multi-component approach may help to safeguard against genetic essentialism when addressing ancestry-related identity.

Embracing indigenous collaboration

The conclusions of this study demonstrate the importance of comprehensive study design when conducting genetic research with indigenous communities, in order to consider the unique sociopolitical and biological history of these populations. Partnering with indigenous communities and providing training opportunities for Natives in genomics are two ways anthropological geneticists can improve their study design and interpretation of results (see Malhi and Bader 2015 for discussion).

In the past, genetic studies conducted with poor ethics and communication resulted in moratoriums on genetic research and a climate of distrust (see Schroeder et al. 2006 for discussion). However, advances in genetic technologies have the potential to benefit Native communities, when employed ethically. For example, First Nations in British Columbia who partner with RSM see a benefit of using data obtained through paleogenomic analysis (along with other lines of information) within the settler colonial legal system to provide evidence of consistent occupation of their territory over thousands of years (Cui et al. 2013). More research is needed to critically assess the ways in which emerging technologies and new sources of data intersect with existing Native knowledge. Indigenous (and indigenous studies) scholar Jessica Bardill stated “If Native peoples and nations replace traditional knowledge and understanding with scientific knowledge, traditional knowledge is risked and can be lost, but if it is used as one of many tools, traditional knowledge can possibly be enhanced” (Bardill 2011). The scientific community, too, will benefit from uniting traditional and emerging knowledge.

Acknowledgements The authors thank the organizers of the “Thinking Anthropologically About Genetics” session during the 2015 American Association of Physical Anthropologists annual meeting, for which this project was originally conceived. The funding for this project was provided by the Office of the Vice Chancellor of Research at the University of Illinois at Urbana-Champaign. Additionally, we would like to acknowledge the organizers and participants of the 2013 SING workshop as invaluable to this work. The exposure to indigenous scholars and students, and their perspectives and discussions on the ethics of genetic research in Indian Country provided an essential backdrop for this project.

Received 22 December 2015; revision received 9 April 2016.

LITERATURE CITED

1000 Genomes Project Consortium. 2012. An integrated map of genetic variation from 1,092 human genomes. *Nature*. 491(7422).

Ancestry composition guide. 23andMe.com:
<https://www.23andme.com/ancestry_composition_guide/>.

Bardill, J. D. 2011. *Beyond Blood and Belonging: Alternarratives for a Global Citizenry*. Doctoral dissertation. Department of English. Duke University: Durham, NC.

Bardill, J. Tribal enrollment and genetic testing. American Indian and Alaska Native Genetics Resource Center. National Congress of American Indians: <<http://genetics.ncai.org/tribal-enrollment-and-genetic-testing.cfm>>.

Bennet, J., S. Rowley, eds. 2004. *Uqalurait: An Oral History of Nunavut*. Montreal: McGill-Queen’s University Press.

Brodwin, P. 2002. Genetics, identity, and the anthropology of essentialism. *Anthropol. Quart.* 75(2):323-330.

Browning, S. R., B. L. Browning. 2007. Rapid and accurate haplotype phasing and missing data inference for whole genome association studies by use of localized haplotype clustering. *Am. J. Hum. Genet.* 81:1084-97.

Budowle, B., M. W. Allard, M. R. Wilson, et al. 2003. Forensics and mitochondrial DNA: Applications, debates, and foundations. *Annu. Rev. Genomics Hum. Genet.* 4:119-141.

Cabana, G. S., A. Merriwether, K. Hunley, et al. 2006. Is the genetic structure of Gran Chaco populations unique? Interregional perspectives on Native South American mitochondrial DNA variation. *Am. J. Phys. Anthropol.* 131:108-119.

Cavalli-Sforza, L. L. 2005. The Human Genome Diversity Project: Past, present and future. *Nat. Rev. Genetics.* 6:333-340.

Cui Y., J. Lindo, C. E. Hughes, et al. 2013. Ancient DNA analysis of mid-Holocene individuals from the Northwest Coast of North America reveals different evolutionary paths for mitogenomes. *PloS One.* 8(7).

Genotyping technology. 23andMe.com: < <https://www.23andme.com/more/genotyping/>>.

Gibbon S., R. V. Santos, M. Sans, eds. 2011. *Racial Identities, Genetic Ancestry and Health in South America: Argentina, Brazil, Columbia and Uruguay.* New York: Palgrave Macmillan.

International HapMap Consortium. 2007. A second generation human haplotype map of over 3.1 million SNPs. *Nature.* 449(18).

Malhi, R. S. 2009. Viewpoint on DNA tests for Native American ancestry from private business and academia. American Anthropological Association. Philadelphia, PA.

Malhi, R. S., A. C. Bader. 2015. Vital topics forum: Engaging Native Americans in genomic research. *Am. Anthropol.* 117(4).

Medina, J. 2004. Introduction: Identity and ethnicity. *J. Speculative Philos.* 18(2):93-98.

Nelson, A. 2008 The factness of diaspora: The social sources of genetic genealogy. In *Revisiting Race in a Genomic Age.* Koenig B.A., Lee S.S., Richardson S.S., eds. New Jersey: Rutgers University Press.

Obama, B. Sept. 15, 2015. Executive order: Using behavioral science insights to better serve the American people. The White House: Office of the Press Secretary.

Raghavan, M., M. DeGiorgio, A. Albrechtsen, et al. 2014. The genetic prehistory of the New World Arctic. *Science.* 345.

Royal, C. D., J. Novembre, S. M. Fullerton, et al. 2010. Inferring genetic ancestry: Opportunities, challenges, and implications. *Am. J. Hum. Gen.* 86:661-673.

Schroeder, K. B., R. S. Malhi, D. G. Smith. 2006. Opinion: Demystifying Native American genetic opposition to research. *Evo. Anthropol.* 15:88-92.

- Shriver, M. D., M. W. Smith, L. Jin, et al. 1997. Ethnic-affiliation estimation by use of population-specific DNA markers. *Am. J. Hum. Genet.* 60(4):957-964.
- Tang, K., K. R. Thornton, and M. Stoneking. 2007. A new approach for using genome scans to detect recent positive selection in the human genome. *Plos Biol.* 5(7):e171.
- TallBear, K. 2003. DNA, blood, and racializing the tribe. *Wicazo Sa. Review.* 18(1):81-107.
- TallBear, K. 2013a. Genomic articulations of indigeneity. *Soc. Stud. Sci.* 43(4):509-533.
- TallBear, K. 2013b. *Native American DNA: Trial Belonging and the False Promise of Genetic Science.* Minneapolis, MN: University of Minnesota Press.
- Verdu, P., T. J. Pemberton, B. M. Kemp, et al. 2014. Patterns of admixture and population structure in native populations of northwest North America. *Plos Genet.* 10(8):e1004530.
- Weiss, K. M., J. C. Long. 2009. Non-Darwinian estimation: My ancestors, my genes' ancestors. *Genome Res.* 19:703-710.
- Winkler, C. A., G. W. Nelson, and M. W. Smith. 2010. Admixture mapping comes of age. *Ann. Rev. Genom. Hum. Gen.* 11:65-89.

TABLE AND FIGURE CAPTIONS

Table 1. Table documenting the number of individuals who participated in each phase of the study.

Figure 1. Simplified family tree annotated with data compiled from historical documents, oral family history, and genetic ancestry profiles. Marriage between individuals is denoted by “+” symbol, “CB” refers to certificate of birth, “CD” is certificate of death, “CIB” represents Certificate of Indian Blood. Ancestry composition image adapted from 23andMe.com.

Figure 2. Map of what is now southeast Alaska and British Columbia, showing sites where various family members were reportedly born. The subset area is a portion of the traditional homeland of the Tlingit, Haida, and Tsimshian peoples.

Figure 3. Example of the Certificate of Indian Blood issued by the Bureau of Indian Affairs.

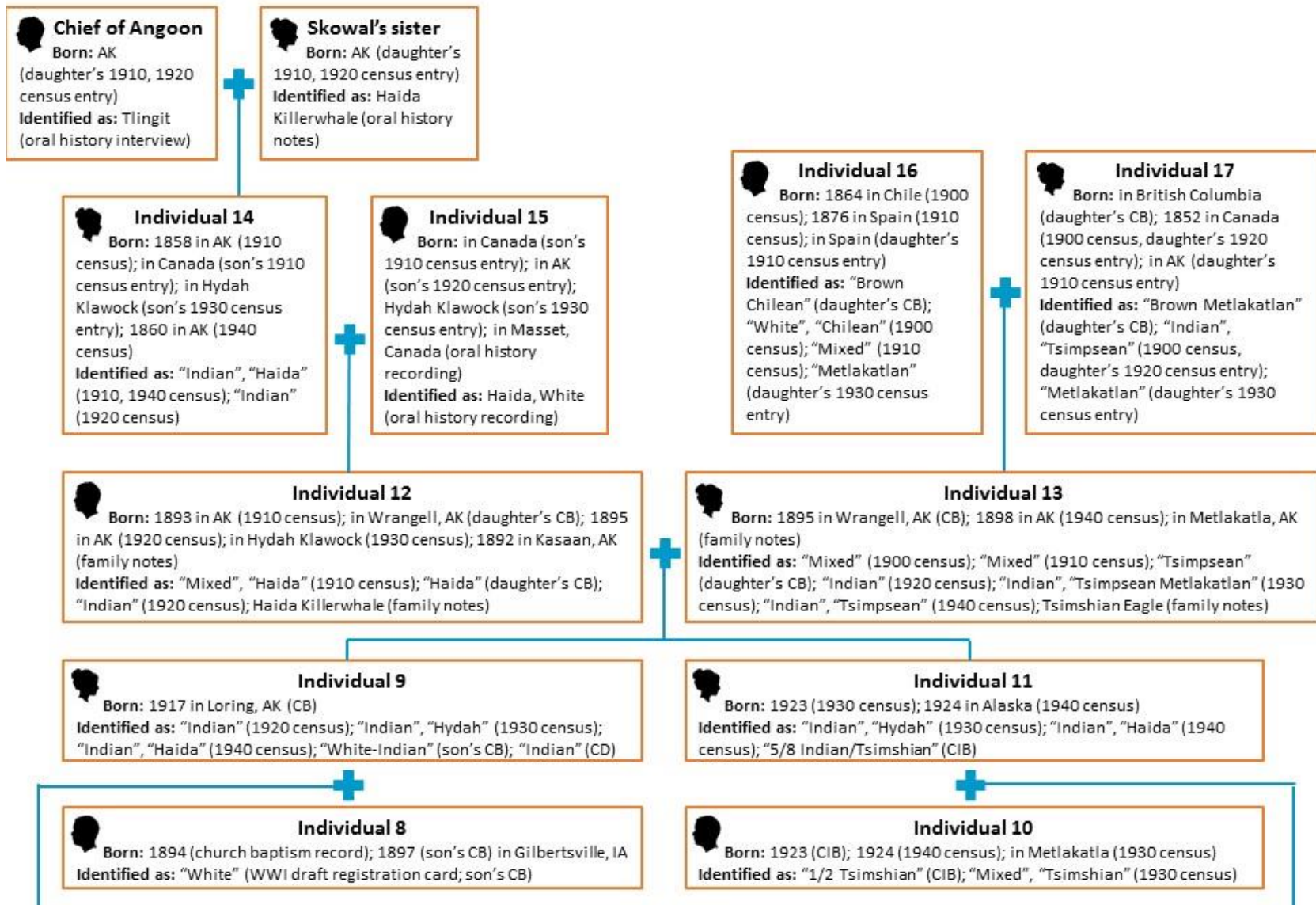
Figure 4. Side-by-side sibling analysis of genome-wide inheritance contributed by each paternal grandparent. Image adapted from 23andMe.com.

Table 1.

Study participants (n=7)	Submitted sample for genetic ancestry estimation (n=7)	Participated in oral interview (n=6)	Genealogical information shared (n=7)
Individual 1	X	No	X
Individual 2	X	X	X
Individual 3	X	X	X
Individual 4	X	X	X
Individual 5	X	X	X
Individual 6	X	X	X
Individual 7	X	X	X
Additional individuals represented in Figure 2 are ancestors identified through family oral history interviews and genealogical records.			

Figure 1. (next page, two facing pages)

Simplified and annotated genealogical tree for a family with Alaskan Native ancestry



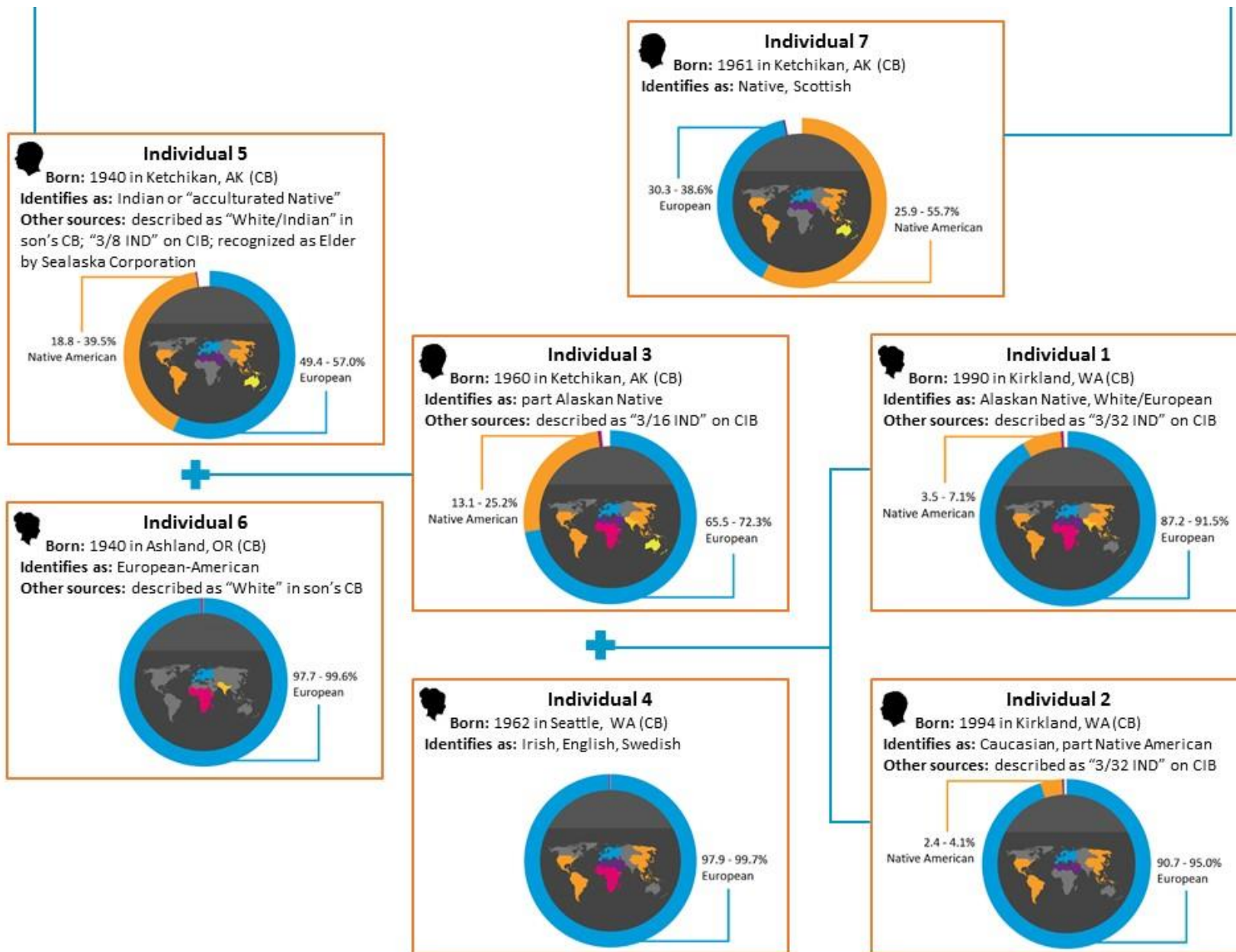


Figure 2.

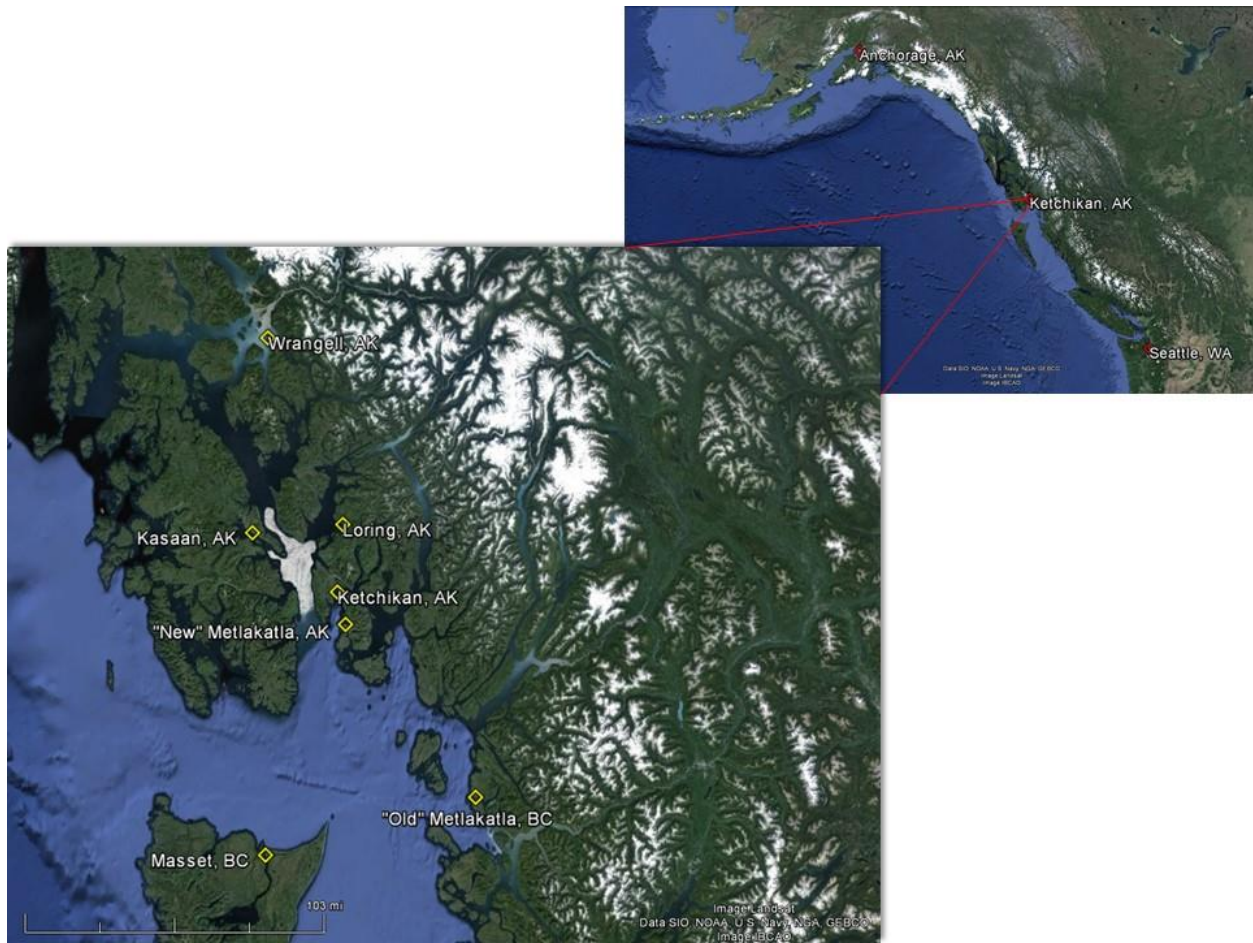


Figure 3.



UNITED STATES
DEPARTMENT OF THE INTERIOR
BUREAU OF INDIAN AFFAIRS
ALASKA REGION

CERTIFICATE OF INDIAN BLOOD (DESCENDANT)

This is to Certify that according to the records on file in this office,

████████████████████

is the direct descendant of an Alaska Native Enrollee who is listed on the Alaska Native Claims Settlement Act (ANCSA) Roll dated December 31, 1981, an official record of the Bureau of Indian Affairs.

Date of Birth: ██████████

Degree of Blood: ██████ IND

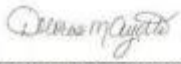
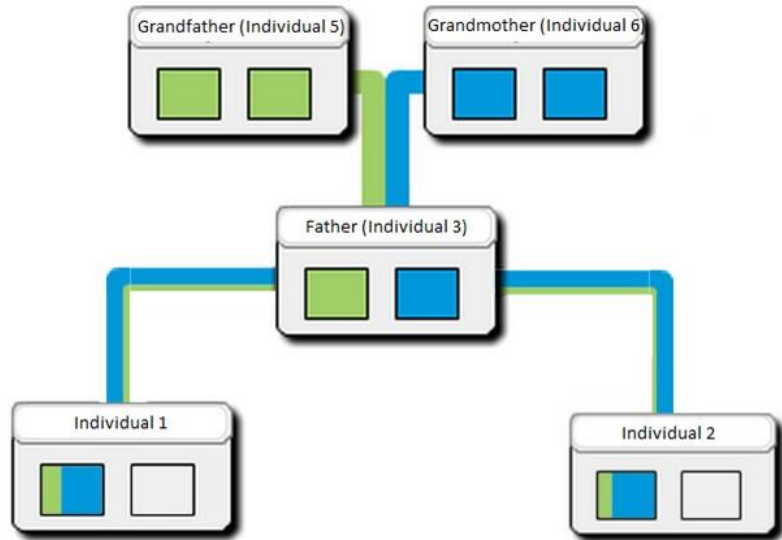
By: 
Dolores Ayotte, Acting Superintendent

Figure 4.

Sibling pair comparison of genome-wide inheritance from paternal grandparents



In a genome-wide comparison, Individual 1 inherited 34% of her paternal DNA from her paternal grandfather (Individual 5) and 66% from her paternal grandmother (Individual 6).

In a genome-wide comparison, Individual 2 inherited 24% of his paternal DNA from his paternal grandfather (Individual 5) and 76% from his paternal grandmother (Individual 6).