

# Towards an interdisciplinary perspective for the study of human expansions and biocultural diversity in the Americas

## 1 | INTRODUCTION

The timing and mode(s) of the initial human occupation of the Americas are among the most discussed topics in archaeology and biological anthropology, with hundreds of articles published in the last decades dedicated to the topic (for some comprehensive reviews, see References 1–3). Researchers have contributed to the debates through a vast range of disciplines, methodological and theoretical approaches, ranging from traditional archeological and bio-archaeological methods, to climate simulations and ancient DNA analyses. And yet, despite recent advances in the study of the biological variation and prehistoric expansions of populations into and within the Americas, there is still little consensus about key questions including the time and modes of human dispersion across the continents. This brings up a crucial question: why are we unable to find a consensus about the processes behind the initial settlements of the Americas?

There are certainly multiple factors contributing to our inability to build reliable interpretations on this topic. Some of them are common to all endeavors to reconstruct and study past human societies across the planet, and some are unique to the history of research in the Americas. As a result, it is not uncommon to find significant reevaluations of current models and hypotheses, either through new findings and new methodological innovations (see, e.g., the most recent findings of early footprints in New Mexico<sup>4</sup>), by the reanalysis of radiocarbon data accumulated over decades of research,<sup>5</sup> or due to new theoretical framings of available data (see Reference 6 as a good example). While these constant reevaluations of the origins of early inhabitants of the Americas are related to all aspects of this process (e.g., chronology, cultural diversity, adaptation, and biological diversity), here we focus on recent discussions about the origins of Native American biological diversity, which by itself has been the focus of a vast and prolific literature.

The study of biological diversity among early Native Americans has progressed at a remarkably fast pace in recent decades, and researchers new to this topic will probably find the process of reviewing the body of specialized literature daunting. Recent studies have drawn upon a wealth of different modern sources of information, including molecular (Y-chromosome, mitochondrial-DNA, autosomal markers), morphological (cranial, dental, and postcranial), and cultural (linguistic, lithic technology, and physical activity) data. The rapid incorporation of cutting-edge methods in the last decades has brought to the research of the early peopling and diversity of the

Americas the sequencing of whole ancient genomes,<sup>7,8</sup> registering high-quality morphological data with 3D surface and CT-scanners,<sup>9</sup> performing digital reconstructions of fragmented anatomical structures,<sup>10</sup> as well as accessing and sharing a large amount of data thanks to Big Data and Open Science initiatives.<sup>11</sup>

However, while these methodologically advanced studies are bringing new sources of information to the discussion, they have also siloed most of the discussions within the confines of specialized sub-disciplines, limiting the dialog between researchers from different backgrounds. Indeed, there are only a handful of projects that have taken advantage of multidisciplinary perspectives.<sup>12–17</sup> Consequently, recent discussions about the biological variation and migratory patterns of early Americans are mostly restricted to (re)interpretations of a few former models and rarely integrate discussions derived from analyzing different kinds of evidence. Evidently, this limitation can be largely explained as the result of the progressive degree of academic specialization required to handle each data type, as well as the substantial expertise and financial support needed to carry them out. Because of this natural tendency of specialization, we have reached a moment in which it is crucial to promote more dialog among research groups and stakeholders and integrate frameworks combining cultural, genetic, and morphological data to study migratory patterns and biological diversity among Native Americans.

With this shared goal in mind, the authors participated in an interdisciplinary symposium in the context of the 90th Annual meeting of the American Association of Physical (now Biological) Anthropologists (Figure 1). The symposium focused on debating how different kinds of evidence contribute to discuss various aspects of the origin and expansions of human populations across the Americas and included experts representing diverse career stages, gender, ethnicity, as well as different countries of origin. The diverse panel of specialists enriched the discussions by contributing their own perspectives from both South, Central, and North American backgrounds. The lessons learned from discussions held at the symposium, and the fact that all participants share the feeling that more interdisciplinary dialog is needed, prompted us to write this overview article. We had the opportunity to share ideas with specialists working with cranial morphology, dental metrics and non-metrics, linguistics, and DNA from prehistoric and/or extant populations, as they discussed their current work on ancient expansions and biocultural diversity in the Americas. While these disciplines cover only a fraction of research topics and disciplines focused on the human occupation of the Americas, the work presented highlights a series



FIGURE 1 Participant's online discussion at the 90th Annual meeting of the American Association of Physical Anthropologists

of common themes and emergent questions that are directly relevant to others as we collectively focus on the next stages of our research. We present here the main outcomes from our interdisciplinary debate in the hope that they will help to engage with a broader community of researchers and stakeholders and continue to promote space for interdisciplinary dialog within a naturally specializing academic environment.

## 2 | THE INTERDISCIPLINARY DEBATE

Any interdisciplinary debate starts with the recognition of the need to connect with other disciplines and to establish bridges that facilitate fruitful exchanges of knowledge and perspectives. As part of the discussion that motivated this article, we challenged ourselves to identify three main aspects of our research programs: their unique strengths, their limitations in reconstructing the past, and the challenges they face in connecting with discussions from other disciplines. These critical self-evaluations of our own work allowed us to establish the shared points of interest, potential venues for collaboration, and directions for future interdisciplinary engagement. Interestingly, the discussion of these three aspects of our research highlighted areas that go beyond the immediate recovery and analysis of data (e.g., practical, theoretical, and methodological difficulties), and also considered challenges related to management, political, and ethical aspects of research.

### 2.1 | Unique strengths of specific disciplines

The promising outcomes of exploring the origins of Native American biological diversity from multiple disciplinary lenses rests on the notion that each approach can contribute partially unique sources of information, while still overlapping explanations with other disciplines. There is, therefore, an expectation that each disciplinary contribution can balance its ability to highlight new information about early America's past, while still remaining connected to other discussions to promote cross-disciplinary dialogs. The strengths identified by our own self-analysis highlight this implicit balance in our research.

As a commonality, researchers working with genetics (both modern and ancient DNA), linguistics, cranial and dental morphology, recognize their contributions to reconstruct the history of biological diversity, modes of dispersal, and relationships of Native American populations. However, each discipline highlights the unique strength of its own methodological and theoretical approaches.

The most conspicuous advantage of genetic studies is the fine-scale level of information and detail that can be achieved from the ancient past, not only for identifying biological information at the individual level (e.g., sex and pathologies), but also for reconstructing population histories. The emerging and powerful approach of genetic analysis facilitates the reconstruction of major demographic and dispersion events associated with the peopling of the American continents<sup>18–21</sup> and can also contribute to the understanding of some smaller-scale mobility events.<sup>22–25</sup> With recent methodological

advances, genetic data shows the highest level of resolution when working with the human past.<sup>8,26,27</sup>

Linguistic data has the advantages of ready access and recoverability, often with very good coverage and consistency, from most languages still spoken or documented; and it can yield accurate diachronic descriptions of descent and interaction among languages. The thorough coverage and detailed maps now available of language and language family ranges<sup>28,29</sup> make it possible to estimate, with good accuracy, large-scale structural patterns, and times of first settlement such as the age of the Indigenous American linguistic population (linguistically based dates of at least ~24,000 years BP have recently been confirmed archeologically<sup>4,30,31</sup>).

Additionally, it is also relevant to recognize strengths related to the preservation of collections and dissemination of data. Researchers working with either cranial or dental variation focus almost exclusively on nondestructive approaches, which often translates into larger sample sizes of individuals from the early and middle Holocene.<sup>32–34</sup> Complementarily, the use of highly standardized data collection protocols, as well as the increasing generation of 3D models of skeletal remains, facilitates data sharing and the establishment of long-distance collaborations. Linguistic and genetic studies focused on recent populations also benefit from large comparative and accessible datasets.<sup>29,35</sup>

Morphological data, both cranial and dental (but also postcranial, although not included here), have the unique advantage of allowing non-destructive access for studying the individual's lifestyle and history.<sup>36</sup> In this way, it is possible to combine osteobiographic approaches aiming at describing the particularities of individuals during their lifetime (from the basic parameters of sex and age; habitual activities, diet, pathology, and health; to mortuary behavior associated with the individual), with an evolutionary one focused on mechanisms that acted on the population's biological diversity.<sup>37</sup> Researchers can go beyond the data fragmentation for publishing purposes and instead reach a more comprehensive understanding of the differential impact of multiple evolutionary mechanisms acting simultaneously on populations' biosocial history as well as lifestyle.

## 2.2 | Limitations in reconstructing the past

Similar to the strengths of each discipline, there are limitations in reconstructing the past that are shared by all. The main limitation relates to the gap for some regions and/or chronologies for which biological data is not available, a product of both differential sample preservation and the fact that there is scant archeological evidence of the oldest human presence in the continents.<sup>38</sup> In some countries, this is the result of lack of research funding for establishing systematic research projects, difficulties in getting access to collections, as well as the impossibility of accessing some areas due to political conflicts or missing data due to language extinction.

Besides the limitation in access to data, we want to emphasize the lack of a theoretical framework that allows combining different kinds of data. This is especially true when considering that each sort of data has different assumptions and estimates biological

relationships based on different rates of change, heritability, and time-scales.<sup>39</sup> Some types of data are more appropriate to describe wide population changes at larger scales (e.g., genomics and population history inferences), while others provide more fine-grained detailed information (e.g., bioarchaeology and life-history interpretations).<sup>40</sup>

There are methodological limitations shared by at least two disciplines: linguists and geneticists share limitations in the ability to quantify rates of evolutionary change, admixture/interaction, and reliable estimates of microevolutionary dynamics. Studies working with contemporary genetic and linguistic variation have limited accuracy in reconstructing early population events in the Americas, especially considering the impact of the European invasion on the biological and cultural diversity of Indigenous groups across the Americas, including a reduction in population sizes/diversity, forced relocations, and genetic and cultural admixture.<sup>41,42</sup>

There are also specific limitations for each discipline. A disadvantage of linguistic data is that it is not always possible to distinguish descent-based, contact-based, and random resemblances among languages and language families. Moreover, descent lines can rarely be traced back earlier than approximately 6000 years BP. Even with ancient genomes it can be difficult to pinpoint the tempo and mode of different microevolutionary mechanisms.<sup>43</sup> Additionally, particular genetic variation (mtDNA and Y-chromosome) only allows us to partially reconstruct the history of the populations under study due to the characteristics of their inheritance (uniparental) and responses to evolutionary forces.<sup>44–46</sup> Additional limitations are associated with the destructive and costly nature of ancient DNA analysis, which limits access to a large sample coverage.<sup>47,48</sup> Morphological studies also show a plethora of limitations, especially in disentangling the different evolutionary processes that shaped and structured Native American diversity.<sup>49</sup>

Finally, there are considerable challenges in studies trying to merge different kinds of data, as there are only a few cases where it is possible to study the same individuals, or even the same populations, using multiple methods. Additionally, the existing data gaps do not necessarily match across disciplines and often the categories used to describe periods, regions, and groups differ among data types, which has become a critical factor hindering interdisciplinary collaborations (see, References 50,51 for attempts to advance on the matter). Ultimately, the simplification of categories used in each discipline reduce the ability of anthropological studies to infer the complexity of the evolutionary processes in the American continents and the full range of biocultural diversity therein.

## 2.3 | Challenges for connecting with other disciplines

One of the main challenges that arose from our interdisciplinary debate is the lack of hypotheses and models that can be tested from multiple disciplinary perspectives. On one hand, many studies about the origin of Native American biological diversity are overly focused on describing patterns of variation,<sup>52</sup> rather than testing specific

hypotheses.<sup>53</sup> On the other hand, as pointed out by Dillehay,<sup>54</sup> most recent studies are not discussing new evidence in relation to previous models but rather dismissing them and proposing new ones (e.g., References 19,55 in Reference 54). As such, it becomes crucial that researchers state clear and testable models and/or hypotheses that integrate the biological, cultural, and linguistic domains. A theoretical framework in which different kinds of evidence can be evaluated is currently missing or not widely used.

Beyond the theoretical conceptualization of research programs, there is also a challenge in the combination of data derived from different sources and disciplines. To effectively combine data from different sources it will be necessary to also consider differences in the timing, rate of change, and geographic coverage of the datasets. For instance, the rate of change between morphologic, genetic, and linguistic data differs in such a way that their direct comparison requires consideration of evolutionary, ecological, and life-history processes at differing intensities and over different timescales.<sup>39,40,56</sup> Even though multidisciplinary analyses have been attempted in the past,<sup>57,58</sup> these studies have been unable to effectively consider the nuances associated with different sources of data, resulting in broad scoped models for the origins of Native American biological diversity. All disciplines carry with them limitations in chronological and geographic coverage, and frequently regions and periods covered by one type of data are unavailable for other types of data (e.g., there is a gap of morphological and aDNA data in the Amazon, which is a region well represented by recent DNA and linguistic data).

It is also important to make the limitations of each discipline and data type more explicit in the specialized studies, as a significant barrier in cross-disciplinary integration is the limited ability of researchers to critically assess the results from other disciplines. This is especially relevant in the context of the biological diversity of early Americans, as all the disciplines that contribute frequently to this discussion (biological anthropology, molecular anthropology, and linguistics) rely on highly specialized data types and analytical approaches, with assumptions that can be opaque to other researchers when not made explicit.

Last but not least, there is an urgent need to incorporate the perspectives from Indigenous communities into research projects about the origins and nature of the biological diversity of Native Americans. The authors collectively acknowledge that, despite the steps taken in this direction, we still need to be more proactive in this regard and collaborate with Indigenous scholars and representatives from the planning stages of projects. Collaboration with Indigenous communities must include care in promoting the use of traditional or preferred community names (see for a full critique<sup>59,60</sup>), informed consent, and continuous dialog on the status of the research (for a more comprehensive view on this subject, we recommend<sup>61–63</sup>).

### 3 | RECOMMENDATIONS AND FUTURE STEPS

The discussions held in the symposium that inspired this article highlighted the importance and need to more actively promote the

collaboration between scholars studying the settlement of the Americas from different perspectives. We share the belief that interdisciplinarity is the key to make progress on previous sub-method limitations or difficulties, and anthropological practice must be based on conducting real and balanced collaborations from the moment in which the research design is defined. To return to our introductory discussion, we argue that the path toward achieving a consensus on the time and mode of the settlement of the Americas runs through the active promotion of interdisciplinary debate. This emphasis must be made explicit, as the natural tendency of the disciplines working on this topic is to continue their specialization and isolation from other theoretical and methodological perspectives.

With this in mind, we conclude with a series of recommendations to promote more interdisciplinary discussion about the processes behind the origins and diversification of Native Americans. Evidently, this is far from being an exhaustive list, and we extend the invitation to colleagues to engage with us in other ways through which we can promote and benefit from the integration of multiple theoretical and methodological perspectives.

*Recommendation 1:* Research projects on Native Americans should be designed to include and balance multiple perspectives from their onset, especially those of Indigenous communities.

*Recommendation 2:* Studies should be explicit in how they interact with and test previous models and hypotheses, especially those promoted by other disciplines, to facilitate cross-disciplinary impacts.

*Recommendation 3:* Studies should make the assumptions and limitations of their data and methods explicit, allowing researchers from other disciplines to critically assess the reliability and limitations of studies.

*Recommendation 4:* Researchers should publish more articles that include data from several disciplines' methods (>3) that facilitate comprehensive explanations of the past and avoid data fragmentation. Discussions should not be limited to biological data but incorporate archaeology, ethnography, and oral histories.

*Recommendation 5:* Discussions about the migratory processes of early Native American populations should avoid broad generalizations, and must take into account regional realities, to avoid over-simplistic models about the human processes in the continents. At the very least, it is important to separate the settlement of South America from the settlement of North America, to recognize the very different histories of human presence in these continents.

### ACKNOWLEDGMENTS

We would like to thank the Executive Committee and the Program Committee from the AABA for providing an exciting space for the organization of our symposium. Special thanks to Leslea Hlusko for supporting us on the difficult road toward the organization of a virtual Symposium during a pandemic.

### CONFLICT OF INTEREST

The authors declare no potential conflict of interest.

## DATA AVAILABILITY STATEMENT

Data sharing is not applicable to this article as no new data were created or analyzed for this study.

Lumila P. Menéndez<sup>1,2</sup> , Kathleen S. Paul<sup>3</sup>  
 Constanza de la Fuente<sup>4</sup> , Tatiana Almeida<sup>5,6</sup>, Miguel Delgado<sup>7,8</sup>  


Gonzalo Figueiro<sup>9</sup> , Kelsey Jorgensen<sup>10</sup> , Susan Kuzminsky<sup>11,12</sup>,  
 María Clara Lopez-Sosa<sup>1</sup>, Johanna Nichols<sup>13</sup>, Mirjana Roksandic<sup>14</sup> ,  
 George Richard Scott<sup>15</sup> , Dennis O'Rourke<sup>16</sup> ,  
 Mark Hubbe<sup>17,18</sup> 

<sup>1</sup>Department of Anthropology of the Americas, University of Bonn,  
 Bonn, Germany

<sup>2</sup>Theoretical Biology Unit, Department of Evolutionary Biology, University  
 of Vienna, Vienna, Austria

<sup>3</sup>Department of Anthropology, University of Arkansas, Fayetteville,  
 Arkansas, USA

<sup>4</sup>Department of Human Genetics, University of Chicago, Chicago,  
 Illinois, USA

<sup>5</sup>Clinical Laboratory & BigData and Analytics, Hospital Israelita Albert  
 Einstein, São Paulo, Brazil

<sup>6</sup>Laboratorio de Estudios em Antropologia Biológica, Bioarqueología  
 e Evolución Humana, Universidad Federal do Rio Grande,  
 Rio Grande, Brazil

<sup>7</sup>Consejo Nacional de Investigaciones Científicas y Técnicas  
 (CONICET), República Argentina (CONICET), División Antropología,  
 Facultad de Ciencias Naturales y Museo, Universidad Nacional de La  
 Plata, La Plata, República Argentina

<sup>8</sup>Ministry of Education Key Laboratory of Contemporary Anthropology  
 Collaborative Innovation Center of Genetics and Development, School  
 of Life Sciences and Human Phenome Institute Fudan University,  
 Shanghai, China

<sup>9</sup>Departamento de Antropología Biológica, Universidad de la República,  
 Montevideo, Uruguay

<sup>10</sup>Department of Anthropology, Wayne State University, Detroit,  
 Michigan, USA

<sup>11</sup>Department of Anthropology and Applied Archaeology, Eastern New  
 Mexico University, Portales, New Mexico, USA

<sup>12</sup>Anthropology Department, University of California, Santa Cruz,  
 California, USA

<sup>13</sup>Department of Slavic Languages and Literatures, University of  
 California, Berkeley, California, USA

<sup>14</sup>Department of Anthropology, University of Winnipeg, Winnipeg,  
 Manitoba, Canada

<sup>15</sup>Department of Anthropology, University of Nevada-Reno, Reno,  
 Nevada, USA

<sup>16</sup>Department of Anthropology, University of Kansas, Lawrence,  
 Kansas, USA

<sup>17</sup>Department of Anthropology, Ohio State University, Columbus,  
 Ohio, USA

<sup>18</sup>Instituto de Arqueología y Antropología, Universidad Católica del  
 Norte, Antofagasta, Chile

## Correspondence

Lumila P. Menéndez, Department of Anthropology of the Americas,  
 University of Bonn, Bonn, Germany.  
 Email: menendez@uni-bonn.de

## ORCID

Lumila P. Menéndez  <https://orcid.org/0000-0002-7867-2910>  
 Kathleen S. Paul  <https://orcid.org/0000-0001-9744-4203>  
 Constanza de la Fuente  <https://orcid.org/0000-0002-2857-3615>  
 Miguel Delgado  <https://orcid.org/0000-0001-6221-1186>  
 Gonzalo Figueiro  <https://orcid.org/0000-0003-0433-932X>  
 Kelsey Jorgensen  <https://orcid.org/0000-0002-8681-5248>  
 Mirjana Roksandic  <https://orcid.org/0000-0003-0291-6357>  
 George Richard Scott  <https://orcid.org/0000-0003-2328-8003>  
 Dennis O'Rourke  <https://orcid.org/0000-0001-5196-3577>  
 Mark Hubbe  <https://orcid.org/0000-0003-4433-3942>

## REFERENCES

- Potter BA, Baichtal JF, Beaudoin AB, et al. 2018. Current evidence allows multiple models for the peopling of the Americas. *Sci Adv* 4(8): eaat5473.
- Smith HL, Kuzminsky SC, Linderholm A. 2020. Discerning dispersals along the Pacific and interior corridors: contributions of geometric morphometrics to the peopling of the Americas. *PaleoAmerica* 6(1): 109–130.
- Sutter RC. 2021. The pre-Columbian peopling and population dispersals of South America. *J Archaeol Res* 29:93–151.
- Bennett MR, Bustos D, Pigati JS, et al. 2021. Evidence of humans in North America during the last glacial maximum. *Science* 373(6562): 1528–1531.
- Prates L, Politis GG, Perez SI. 2020. Rapid radiation of humans in South America after the last glacial maximum: a radiocarbon-based study. *PLoS One* 15(7):e0236023.
- Pitblado BL. 2011. A tale of two migrations: reconciling recent biological and archaeological evidence for the Pleistocene peopling of the Americas. *J Archaeol Res* 19:327–375.
- De la Fuente C, Moreno-Mayar JV, Raghavan M. 2021. Early peopling of the Americas. A palaeogenetics perspective. In: Muñoz-Moreno ML, Crawford MH, editors. *Human migration: biocultural perspectives*. Oxford: Oxford University Press.
- Willerslev E, Meltzer DJ. 2021. Peopling of the Americas as inferred from ancient genomics. *Nature* 594(7863):356–364.
- Kuzminsky SC, Reyes Báez O, Arriaza B, et al. 2018. Investigating cranial morphological variation of early human skeletal remains from Chile: a 3D geometric morphometric approach. *Am J Phys Anthropol* 165(2):223–237.
- Menéndez LP, Rademaker K, Harvati K. 2019. Revisiting east–west skull patterns and the role of random factors in South America: cranial reconstruction and morphometric analysis of the facial skeleton from Cuncaicha Rockshelter (southern Peru). *PaleoAmerica* 5(4):315–334.
- Paschetta C, Gonzalez-José R, Lanata JL. 2017. De Como Cruzar Fronteras en la Ciencia. Homenaje a Héctor M. Pucciarelli. Puerto Madryn y San Carlos de Bariloche: Instituto Patagonico de Ciencias Sociales y Humanas e Instituto de Investigaciones en Diversidad Cultural y Procesos de Cambio.
- Barberena R, Menéndez L, le Roux PJ, et al. 2020. Multi-isotopic and morphometric evidence for the migration of farmers leading up to the Inka conquest of the southern Andes. *Sci Rep* 10(1):1–12.
- Delgado M, Rodríguez F, Kassadjikova K, et al. 2021. A paleogenetic perspective of the Sabana de Bogotá (northern South America)

population history over the Holocene (9000–550 cal BP). *Quat Int* 578:73–86.

[14] Fehren-Schmitz L, Llamas B, Lindauer S, et al. 2015. A re-appraisal of the early Andean human remains from Lauricocha in Peru. *PLoS One* 10(6):e0127141.

[15] Hoffecker JF, Elias SA, O'Rourke DH, et al. 2016. Beringia and the global dispersal of modern humans. *Evol Anthropol* 25(2):64–78.

[16] Scott GR, O'Rourke DH, Raff JA, et al. 2021. Peopling the Americas: not “out of Japan”. *PaleoAmerica* 7(4):309–332.

[17] Urban M, Barbieri C. 2020. North and south in the ancient Central Andes: contextualizing the archaeological record with evidence from linguistics and molecular anthropology. *J Anthropol Archaeol* 60: 101233.

[18] Ioannidis AG, Blanco-Portillo J, Sandoval K, et al. 2020. Native American gene flow into Polynesia predating Easter Island settlement. *Nature* 583(7817):572–577.

[19] Moreno-Mayar JV, Vinner L, de Barros Damgaard P, et al. 2018. Early human dispersals within the Americas. *Science* 362(6419):eaav2621.

[20] Posth C, Nakatsuka N, Lazaridis I, et al. 2018. Reconstructing the deep population history of central and South America. *Cell* 175: 1185–1197.

[21] Raghavan M, Steinfücken M, Harris K, et al. 2015. Genomic evidence for the Pleistocene and recent population history of Native Americans. *Science* 349:aab3884.

[22] Castro e Silva MA, Nunes K, Lemes RB, et al. 2020. Genomic insight into the origins and dispersal of the Brazilian coastal natives. *Proc Natl Acad Sci* 117(5):2372–2377.

[23] Flegontov P, Altiniski P, Changmai N, et al. 2019. Palaeo-Eskimo genetic ancestry and the peopling of Chukotka and North America. *Nature* 570:236–240.

[24] Nägele K, Posth C, Orbegozo MI, et al. 2020. Genomic insights into the early peopling of the Caribbean. *Science* 369(6502): 456–460.

[25] Ramallo V, Bisso-Machado R, Bravi C, et al. 2013. Demographic expansions in South America: enlightening a complex scenario with genetic and linguistic data. *Am J Phys Anthropol* 150(3):453–463.

[26] Liu Y, Mao X, Krause J, et al. 2021. Insights into human history from the first decade of ancient human genomics. *Science* 373(6562): 1479–1484.

[27] Orlando L, Allaby R, Skoglund P, et al. 2021. Ancient DNA analysis. *Nat Rev Methods Primers* 1(1):1–26.

[28] Dryer MS, Haspelmath M. 2013. The world atlas of language structures online, Leipzig: Max Planck Institute for Evolutionary Anthropology. <http://wals.info>

[29] Hammarström H, Forkel R, Haspelmath M, et al. 2021. Glottolog 4.4, Leipzig: Max Planck Institute for Evolutionary Anthropology. <http://glottolog.org>

[30] Nichols J. 2008. Language spread rates as indicators of glacial-age peopling of the Americas. *Curr Anthropol* 49(6):1109–1117.

[31] Nichols J. 2015. How America was colonized: linguistic evidence. In: Frachetti MD, Spengler RN III, editors. *Mobility and ancient society in Asia and the Americas*, New York: Springer. p 117–126.

[32] Delgado ME. 2017. Holocene population history of the Sabana de Bogotá region, northern South America: an assessment of the cranio-facial shape variation. *Am J Phys Anthropol* 162:350–369.

[33] Neves WA, Hubbe M, Correal G. 2007. Human skeletal remains from Sabana de Bogotá, Colombia: a case of Paleoamerican morphology late survival in South America? *Am J Phys Anthropol* 130:1080–1098.

[34] Pucciarelli HM, Perez SI, Politis GG. 2010. Early Holocene human remains from the Argentinean Pampas: additional evidence for distinctive cranial morphology of early South Americans. *Am J Phys Anthropol* 143(2):298–305.

[35] Reich D, Patterson N, Campbell D, et al. 2012. Reconstructing native American population history. *Nature* 488(7411):370–374.

[36] Hosek L, Robb J. 2019. Osteobiography: a platform for bioarchaeological research. *Bioarchaeol Int* 3(1):1–15.

[37] Hubbe M, Neves WA, do Amaral HL, et al. 2007. Brief communication: “Zuzu” strikes again—morphological affinities of the early holocene human skeleton from Toca dos Coqueiros, Piauí, Brazil. *Am J Phys Anthropol* 134(2):285–291.

[38] Dillehay TD. 1997. ¿Dónde están los restos óseos humanos del período pleistoceno tardío? Problemas y perspectivas en la búsqueda de los primeros americanos. *Bolet Arqueol PUCP* 1:55–63.

[39] Simpson GG. 1944. *Tempo and mode in evolution*, New York, NY: Columbia University Press.

[40] Pelletier F, Garant D, Hendry AP. 2009. Eco-evolutionary dynamics. *Philos Trans R Soc B* 364(1523):1483–1489.

[41] Llamas B, Fehren-Schmitz L, Valverde G, et al. 2016. Ancient mitochondrial DNA provides high-resolution time scale of the peopling of the Americas. *Sci Adv* 2(4):e1501385.

[42] Yaremko JM. 2016. *Indigenous passages to Cuba, 1515–1900*, Florida: University Press of Florida.

[43] Booth TJ. 2019. A stranger in a strange land: a perspective on archaeological responses to the palaeogenetic revolution from an archaeologist working amongst palaeogeneticists. *World Archaeol* 51(4):586–601.

[44] Fehren-Schmitz L, Harkins KM, Llamas B. 2017. A paleogenetic perspective on the early population history of the high-altitude Andes. *Quat Int* 461:25–33.

[45] O'Rourke DH. 2012. Why do we migrate? A retrospective. In: Crawford MH, Campbell MC, editors. *The causes and consequences of migration: an evolutionary perspective*, Cambridge: Cambridge University Press. p 527–536.

[46] Stoneking M. 2016. An introduction to molecular anthropology, New Jersey: John Wiley & Sons.

[47] Bardill J, Bader AC, Garrison NA, et al. 2018. Advancing the ethics of Paleogenomics. *Science* 360(6387):384–385.

[48] Prendergast ME, Sawchuk E. 2018. Boots on the ground in Africa's ancient DNA 'revolution': archaeological perspectives on ethics and best practices. *Antiquity* 92(363):803–815.

[49] Menéndez LP, Bernal V, Novellino P, et al. 2014. Effect of bite force and diet composition on craniofacial diversification of southern South American human populations. *Am J Phys Anthropol* 155(1):114–127.

[50] Eisenmann S, Bánffy E, van Dommelen P, et al. 2018. Reconciling material cultures in archaeology with genetic data: the nomenclature of clusters emerging from archaeogenomic analysis. *Sci Rep* 8:13003.

[51] Riede F, Hoggard C, Shennan S. 2019. Reconciling material cultures in archaeology with genetic data requires robust cultural evolutionary taxonomies. *Palgrave Commun* 5(1):1–9.

[52] Hubbe M, Terrazas Mata A, Herrera B, et al. 2020. Morphological variation of the early human remains from Quintana Roo, Yucatán peninsula, Mexico: contributions to the discussions about the settlement of the Americas. *PLoS One* 15(1):e0227444.

[53] Kuzminsky SC. 2013. Human craniofacial variation among Pacific Rim Populations through the Holocene: A test of the coastal migration hypothesis using 3D morphometric methods, Unpublished Ph.D. Thesis, University of California, Santa Barbara.

[54] Dillehay TD. 2019. Un ensayo sobre genética, arqueología y movilidad humana temprana: Comentado por Francisco Rothhammer y Luis Alberto Borrero, traducido por Matías Lépore. *Mundo De Antes* 13(2):11–65.

[55] Llamas B, Harkins KM, Fehren-Schmitz L. 2017. Genetic studies of the peopling of the Americas: what insights do diachronic mitochondrial genome datasets provide? *Quat Int* 444:26–35.

[56] Bromham L, Woolfit M, Lee MSY, et al. 2002. Testing the relationship between morphological and molecular rates of change along phylogenies. *Evolution* 56(10):1921–1930.

[57] González-José R, Bortolini MC, Santos FR, et al. 2008. The peopling of America: craniofacial shape variation on a continental scale and its interpretation from an interdisciplinary view. *Am J Phys Anthropol* 137(2):175–187.

ISSUES, NEWS, AND REVIEWS

- [58] Greenberg JH, Turner CG, Zegura SL, et al. 1986. The settlement of the Americas: a comparison of the linguistic, dental, and genetic evidence. *Curr Anthropol* 27(5):477–497.
- [59] Garrison NA, Hudson M, Ballantyne LL, et al. 2019. Genomic research through an indigenous lens: understanding the expectations. *Annu Rev Genomics Hum Genet* 20:495–517.
- [60] Hudson M, Nanibaa'A G, Sterling R, et al. 2020. Rights, interests and expectations: indigenous perspectives on unrestricted access to genomic data. *Nat Rev Genet* 21(6):377–384.
- [61] Claw KG, Anderson MZ, Begay RL, et al. 2018. A framework for enhancing ethical genomic research with indigenous communities. *Nat Commun* 9(1):1–7.
- [62] Garrison NA, Carroll SR, Hudson M. 2020. Entwined processes: rescripting consent and strengthening governance in genomics research with indigenous communities. *J Law Med Ethics* 48(1): 218–220.
- [63] Wagner JK, Colwell C, Claw KG, et al. 2020. Fostering responsible research on ancient DNA. *Am J Hum Genet* 107(2):183–195.