Special Issue: What's in a Name?
Late Middle and Early Late Pleistocene Hominin Systematics

Middle Pleistocene Hominin Systematics: The "Chibanian Puzzle"

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ABSTRACT

The primary goal of the workshop "Meet the Chibanians" held at Novi Sad in 2023—and of the resulting papers—is to establish a broad consensus among the researchers on exactly how to describe the place of hominin fossils that cannot be easily assigned to *Homo erectus*, *H. neanderthalensis*, or *H. sapiens* from the late Middle and early Late Pleistocene across the Old World. A great deal of this discussion revolves around exactly how many hominin taxa were present during this period (Middle-Late Pleistocene) and how they were related to each other. We introduce the papers in this Special Issue of *PaleoAnthropology* and how they relate to the current state of research.

Understanding hominin evolution during the Chibanian age (i.e., Middle Pleistocene sub-epoch) continues to draw a great amount of attention from both the paleoanthropological and broader public communities (Athreya and Hopkins 2021; Bae 2010, 2024; Bae et al. 2024; Harvati and Reyes-Centeno 2022; Hawks 2025; Reed 2025; Rightmire 1996, 2004, 2008; Roksandic et al. 2018; 2022a; Stringer 1983, 2012; Tattersall 1986; Tattersall and Schwartz 2008). This is at least in part because it is usually considered that within the Chibanian, we might be able to find the last known ancestor of *Homo sapiens*. The Chibanian is a particularly important period given that the earliest modern humans now appear to date to ~315 ka in Northwest Africa (Hublin et al. 2017). The reason why the Chibanian continues to be referred to as the "Muddle in the Middle" is because several different hominin taxa that cannot be easily assigned to *Homo erectus*, *H. neanderthalensis*, or *H. sapiens* have been proposed to be penecontemporaneous. Traditionally, these fossils have been assigned to *H. heidelbergensis* and/or *H. rhodesiensis* or simply referred to as archaic *H. sapiens* or mid-Pleistocene *Homo*. In realizing how complex the Chibanian hominin fossil record is, however, over the past several decades a number of new hominin taxa (e.g., *H. floresiensis*, *H. naledi*, *H. luzonensis*, *H. longi*, *H. bodoensis*, *H. juluensis*) have been added to the taxonomic list; this updated list is serving to clarify (or further complicate) the human evolutionary picture (Bae 2024; Bae et al. 2024; Berger et al. 2015; Brown et al. 2004; Détroit et al. 2019; Ni et al. 2021; Reed 2025; Roksandic et al. 2022a, b). Of course, the Denisovans, who have recently been linked to *H. juluensis* (Bae 2024; Bae and Wu 2024; Wu and Bae 2025) or *H. longi* (Fu et al. 2025), and potential "ghost lineage(s)" (Prüfer et al. 2014), lead much of these recent discussions.

A great many of these discussions revolve around exactly how many hominin taxa were present during the Chibanian and how they were related to each other. For instance, we (Roksandic et al. 2022a, b) recently proposed to help clarify the situation by introducing a new species, *H. bodoensis*, while at the same time arguing to discontinue the use of *H. heidelbergensis* and *H. rhodesiensis* on the

Figure 1. NS'23 workshop participants (bolded) and guests in front of the "Meet the Chibanians" poster. Back row, left to right: ***Denne Reed, Lauren Schroeder,*** *Slobodan Marković, Dušan Mihailović,* ***Cosimo Posth****, Ivan Roksandic,* ***John Hawks, Frido Welker, Predrag Radović, Mary Silcox, Yosuke Kaifu, Jeff Schwartz, Xijun Ni****. Front row standing left to right: Jean Ives and Ana Majkić, Bojana Mihailović,* ***Mirjana Roksandic, María Martinón-Torres, Leslie C. Aiello, Christopher Bae****, Crouching:* ***Clement Zanolli and Xiujie Wu****.*

grounds that they have been poorly defined and/or are problematic based on ethical grounds. Advocates of these latter two taxa still abound (e.g., Delson and Stringer 2022; Sarmiento and Pickford 2022), and their camps have posed some relevant questions that cut to the core of the practice of paleontological taxonomy more generally. In turn, these discussions have brought to the forefront the meaning and appropriateness of the International Code of Zoological Nomenclature (ICZN) rules (hereafter, simply "the Code"), particularly as they are applied to the ancestors of us, modern humans, and the practice of anthropology and broader biological sciences more generally (Bae et al. 2023a; Figueiredo et al. 2023; Roksandic et al. 2023).

The purpose of taxonomy is to classify living organisms in a way that allows further communication about them. As such, taxonomic names enable the most direct communication about a group of objects/phenomena/organisms, and accordingly, they play an important role in scientific communication. Hominin systematics follow the same rules as other taxonomies; however, naming hominin species is a layered and complex task that needs to answer to a multitude of often conflicting demands. Although it may sound like an ephemeral and academic question, how we perceive and name species—in particular, in the context of human evolution—has strong implications on how we as researchers communicate our research findings to each other, and to the general public that has shown persistent interest in understanding our deep past. This is an important topic in the field of anthropology today, which is pushing towards diversifying researchers, opinions, and knowledge traditions. In the face of anthropology's 30 odd years of self-reflection and often self-congratulatory statements on decolonization of the field, we cannot allow the discipline to be the last one to recognize growing neo-colonialism, fascism, and racism in the West, but yet staunchly defend offensive names in the name of stability (Bae et al. 2023b; 2024; Roksandic et al. 2022b; 2023).

We initiated these important discussions at the 2019 Association for American Biological (then "Physical") Anthropologists conference that was held in Cleveland, Ohio. In an invited poster symposium, the session focused on the question of *H. heidelbergensis* and what, if anything, should be done with the taxon. In addition to the 15 presentations, more than 100 attendees participated, leading to a lively discussion. Although not everyone agreed, there seemed to be a great deal of support for the idea that *H. heidelbergensis* was nothing more than a wastebasket taxon and that it was probably time to remove the name from circulation. This led us to the realization that further discussion would be important to really understand the nature of Chibanian hominin systematics. As a result, we received funding from the Wenner-Gren Foundation and the Social Science and Humanities Research Council of Canada to organize a workshop that was held in Novi Sad, Serbia, in 2023 (Figure 1; Figure 2 below). At the Novi Sad meeting (hereafter, NS'23), we felt it would be a good opportunity to re-evaluate hominin taxonomy, the rules that govern it (especially Article 23 that covers the Code's Principle of Priority), and how these rules promote or impede proper communication in the biological sciences. After all, names are a means of communication and have to allow rather than impede proper understanding. Discussing these issues in a constructive environment provided by a workshop/symposium format resulted in a better understanding of the role of taxonomy in defining, describing, and understanding human evolutionary history, but also in leading toward the changes that are increasingly necessary in order to communicate our findings in a coherent way that—in simplifying the conclusions to make them easily understood by non-specialists and the general public—does not do so by

sacrificing clarity and accuracy. Although a shorter piece from the NS'23 workshop was published earlier and co-authored by all of the participants (Bae et al. 2024), this special issue of *PaleoAnthropology* further builds upon these discussions and provides an opportunity for some of the participants to present their own research ideas on the topic of Chibanian hominin systematics.

To briefly summarize the major conclusions drawn from the NS'23 meeting, where there was consensus or at least near consensus (see also Bae et al. 2024):

1. Much of the debate and misinterpretation in paleoanthropology, especially in how it is presented in the ever-interested media, arises from assuming that hominin species are understood through the **Biological Species Concept** (BSC). We called for the paleoanthropological community to explicitly say that the species concept used in their research is NOT, and cannot be, the BSC. Furthermore, rather than settling on one species concept that can be utilized across the board, we recognize that different types of analysis or methodological approaches would require different species concepts to be employed. Researchers studying species or phylogeny-related questions need to specify which species concept is used in their specific study and how it relates to their particular approach. Communication aimed at the general public should also follow these same principles to facilitate a more proper understanding of the evolutionary question(s) on hand.
2. The group decided that *H. heidelbergensis* should not be entirely discarded as a taxonomic unit. However, until demonstrable morphological connections between the Mauer mandible and any other fossil remains are identified, this should be a taxon restricted to only the Mauer mandible.
3. Changes need to be made to ICZN rules to allow for suppressing names linked to genocidal and colonial historical figures. The taxon that was discussed at great length in this context during the NS'23 meeting was *H. rhodesiensis*, named after the toponym Northern Rhodesia (a former British protectorate, now Zambia), which was named after Cecil Rhodes.

In addition to the earlier synthesis of the NS'23 meeting (Bae et al. 2024), here, we bring together eight papers from participants from said NS'23 meeting that discuss the issues surrounding the Chibanian hominin record from very different perspectives. As with the NS'23 participants more generally, the contributors to this *PaleoAnthropology* special issue (SI) are from different regions and academic traditions, stages in their careers, and demographics. We felt strongly about having as diverse a group of participants as we could bring together for the NS'23 meeting, and we are quite pleased that this diversity extended to this SI. The contributions range from more historical/methodological/conceptual (Hawks 2025; Reed 2025; Silcox 2025; Welker et al. 2025) to more analytical papers that focus on questions or fossils from specific regions, including one that focuses on the African record (Schroeder and Komza 2025) and three that focus on the Asian record (Kaifu and Athreya 2025; Ni et al. 2025; Wu and Bae 2025).

In the first paper in this SI, Reed (2025) reviews the nomenclature and taxonomy of Chibanian hominins and provides us with the list of currently **available** names. Reed (2025) also reviews some much-neglected information about the Code, the formatting of scientific names, their proper citation protocols, and many other relevant points that are useful to paleoanthropologists, as they often come from disparate disciplines within the field. The availability vs. **validity** of names is also brought forward as an important consideration in the context of hominin evolution. This paper is of utmost interest to anyone considering naming new species or redefining the hypodigm of known species and provides important clarifications for any further attempt to address the mechanism available in the Code to change, suppress, and remove problematic names. African nomenclature is quite complex, since almost every Chibanian fossil in Africa has received a taxonomic name at some point in the past. In addition to this problem, because hypodigms change as our knowledge progresses, the so often touted principle of priority as a cornerstone of taxonomic stability ultimately serves to create instability. The author discusses ethical concerns as worthy of exploration and offers mechanisms to deal with this issue in paleoanthropology.

Paralleling the concerns of formal nomenclature, Hawks (2025) presents the non-Linnean nomenclature and hominin classifications that are often used to avoid issues associated with the complexities of applying formal Latin names to what appears to be an ever-changing landscape of our own, very polymorphic species. The advantage that this "informal" taxonomy has over the binomial Linnean system is that it does not assume or discuss the status of a group as a species. Hawks discusses the origin and development of this informal taxonomy as it reflected and continues to reflect the changing paradigms in the field, from the classification of human races in the 18th and 19th centuries, to understanding regional and global patterns of fossil hominin variation. Another important aspect of the nomenclature issues Hawks (2025) addresses is the impact of molecular anthropology and ancient DNA on naming conventions. If the purpose of nomenclature is to enable accurate communication within the discipline, among related disciplines, and to the general public, using non-Linnean names allows for flexibility, but comes with the potential risk of losing clarity. It certainly does not help to reduce the proliferation of synonyms so prevalent in formal taxonomy to have a parallel system, but as long as formal Linnean taxonomy of the hominin fossil record is not overhauled, particularly when there is a clear need, this informal system will remain in place, for better or for worse.

The Silcox (2025) paper could be read as a cautionary tale coming from abundant Early Neogene primate fossil deposits in Wyoming. An early primate perspective draws the study of human evolution back into paleontology. Since they study our own species' evolution, paleoanthropologists are influenced and often constrained by concerns

that have little to do with science and all to do with the history of the field and the politics of the individual academics, academia in general, and the funders. Discussing the *Tetonius matthewi-Pseudotetonius ambiguus* lineage of omomyoids, the *Phenacolemur praecox-Phenacolemur fortior* lineage of paromomyids, and the *Arctodontomys nuptus-Microsyops angustidens* lineage of microsyopids provides us with a model in non-human primate evolution that can potentially elucidate the issues we are facing in hominin taxonomy. In all three cases, specimens that were intermediate both temporally and in terms of morphology were identified in the context of large alpha taxonomic revisions of the Southern Bighorn Basin collections for each group. A striking revelation that Silcox (2025) guides us through is that more fossils do not result in a simpler picture; quite the contrary, more fossils often mean a more complex picture where the taxonomy of specimens intermediate, both morphologically and temporally, needs to follow either of the two paths—lumping the whole lineage into one species or separating them into different species based on combined morphology and age. Silcox argues for retaining the end members of these lineages as distinct taxa and distinguishing intermediates from the other members of the lineages. This paleoprimatology discussion relates to the question of *Homo heidelbergensis* as follows: retaining a single name for the African, Asian, and European Chibanian hominins obscures diverse lineages that develop independently across three continents. It also does not allow for discussion of the movement and process of human evolution more generally. However, 23 (and growing) potentially valid taxa reported by Bae et al. (2024) and discussed in Reed (2025) are unlikely to all be useful going forward, and an attempt should be made to reach a consensus in hominin taxonomy in a larger working group.

Welker et al. (2025) review recent advances in molecular paleoanthropology, contributions of ancient DNA, and, increasingly, proteomics brought to the study of human evolution, and the issues the field is facing. While ancient DNA is rarely preserved from periods that predate the Late Pleistocene, it has contributed the key evidence that Neanderthals, Denisovans, modern humans, and an as-yet-unidentified "super-archaic" hominin group mated and interbred. Regular introgression effectively removed the species barrier, as defined by the BSC, between the different groups (as reflected in Silcox's [2025] use of *Homo sapiens neanderthalensis*). Alternatively, it makes the BSC obsolete or impractical in paleoanthropology. Further, most paleogeneticists talk about lineages rather than species. With rare exceptions such as Sima de los Huesos (Meyer et al. 2014) and the Holstein Stadel (Posth et al. 2017), ancient DNA can only provide indirect evidence for the Middle Pleistocene. Preservation of proteins is much better and can even reach back at least into the Early Pleistocene, if not earlier. Welker et al. (2025) review the potential contributions to phylogeny and taxonomy of the field with its increased time depth, and development of ever more sophisticated extraction methods that aim to minimize the impact of sampling on the precious fossil material.

The remaining papers focus on more specific issues related to a particular region and/or specific hominin fossils. Three papers in this SI are dedicated to the Asian hominin fossil record, and one is focused on Africa. The lack of papers on European Chibanians stands in contrast to the historical importance this geographic area played in paleoanthropological research and the development of explanatory models of human evolution. The long-held view that Neanderthals were the only occupants of Middle and early Late Pleistocene Europe, until the arrival of modern humans around 45–50 ka (Smith et al. 2024), is challenged with more recent finds (e.g., Ceprano, Mala Balanica; Manzi 2001; Manzi et al. 2010; Roksandic et al. 2011; 2018; 2023) and the reanalysis of sites with new analytical methods (e.g., Di Vincenzo et al. 2017; Harvati et al. 2019; Skinner et al. 2016). As such, the evolutionary position of *H. antecessor* (Bermúdez de Castro et al. 1997) in relation to European and other Chibanians remains unresolved (Bermúdez de Castro et al. 2017; Welker et al. 2020). Further, many interesting questions posed by the European record indicate that we might have reached the saturation point, and if so, then until more evidence becomes available, especially from Southeast and Eastern Europe, no new models can be proposed. Africa has been the focus of much recent research with re-dating and re-evaluation of the hominin material (Richter et al. 2017). However, it is the Asian record that is currently the focus of much productive research, and this is amply illustrated in this SI.

Schroeder and Komza (2025) examine eight African large-brained Chibanians using the approach derived from evolutionary quantitative genetics. Testing the null hypothesis of drift, they examine the evolutionary forces behind hominin variability reflected in both the rejection of the null hypothesis (more or less variation than expected under the null hypothesis of neutral selection) and the slope values indicating the direction. They conclude that the pattern of less between-group variation than expected may reflect stabilizing selection. Therefore, most of the variation is consistent with a single species under the **Ecological Species Concept** (ESC) of Van Valen (1976). Only four comparisons involving the Bodo 1 cranium show possible diversifying selection that could initiate some taxic diversity in Africa, although the hypothesis of neutral selection is not rejected in these cases. Lack of diversifying selection in hominin lineages could also be connected to the hominin "adaptive zone" itself, which is highly influenced by obligatory tool use. Either way, their Table 4 provides much food for thought on how morphological differences can be used in a novel way to examine taxonomy through the application of methods of quantitative genetics.

Three papers (Kaifu and Athreya 2025; Ni et al. 2025; Wu and Bae 2025) are focused on making sense of the Asian Chibanian record. Two of the papers (Kaifu and Athreya 2025; Wu and Bae 2025) utilize more traditional comparative morphological approaches, while the third paper (Ni et al. 2025) uses a phylogenetic approach. Interestingly, the three papers draw quite different conclusions from, more or less, the same set of hominin fossils. This example high-

lights methodological and theoretical differences in the field that are reflected in the interpretations of the same set of hominin fossils.

Wu and Bae (2025) provide a detailed fossil-by-fossil description of the Xujiayao materials. The Xujiayao site, located in the western part of the Nihewan Basin in northern China, was discovered and excavated in the 1970s (Norton and Gao 2008). The excavations yielded thousands of stone artifacts and paleontological remains, including a plethora of hominin fossils representing the remains of at least ten individuals. However, since their discovery, the Xujiayao fossils were simply assigned to the generic "archaic *H. sapiens*" category, a category that most scientists now consider to be obsolete. Interestingly, an earlier study of the Xujiayao fossil teeth suggested that they may represent a previously unknown hominin group (Xing et al. 2015). To date, a detailed description of the Xujiayao fossils has yet to be published outside of the Wu and Poirier (1995) synthesis. Here, Wu and Bae (2025) build on and contribute to a growing body of recent literature (Bae 2024; Bae and Wu 2024; Wu et al. 2022) that argues that the Xujiayao fossils, in addition to the Xuchang fossils, represent at least a new population (Julurens) or, more likely, a new species (*Homo juluensis*). The species assignment (*H. juluensis*) is based on the Xujiayao (holotype) and Xuchang (paratype) fossils.

It is always interesting to see how species names originate. For instance, when naming a species after a place, it is generally considered standard to add "ensis" after the place name. *Homo floresiensis* and *H. luzonensis* are good examples of this. When naming a species after an object, it is standard to add "i" after the object. A good example of this is *H. longi*. This raises the question, then, about how *H. juluensis* came about. The type specimen is from the Xujiayao site and, therefore, if we wanted to name it after the site, the accepted name should be "xujiayaoensis." The only problem with this, in our opinion, is that most non-Chinese researchers, including the public, would have trouble pronouncing the name, let alone remembering how to spell it. That is why Wu and Bae (Bae 2024; Bae and Wu 2024; Wu and Bae 2025; Wu et al. 2022;) decided to use the word "julu", which literally means "big head" and is easy to remember. The next step in the process would be to then assign "i" to "julu", but "jului" would be difficult for non-Chinese to remember and pronounce as well. For instance, some people would pronounce it "juluway", while others would pronounce it "juluwee". As such, Wu and Bae decided to buck the trend, so to speak, and came up with "juluensis", which is easy to remember and easy to pronounce. This may not follow the exact rules of The Code, but as emphasized here and elsewhere (e.g., Bae et al. 2024), science communication is an important aspect of what we, as scientists, are responsible for. If we come up with names that are difficult to remember or pronounce, it will be difficult to impossible for people, both academics and the public, to remember and use.

The primary question that has been raised about *H. juluensis* is the other fossils that Wu and Bae (2025) include in the hypodigm, namely the fossils from Penghu, Xiahe, Tam Ngu Hao 2, and, importantly, Denisova (here, and see Bae 2024; Bae and Wu 2024; Wu et al. 2022). Wu and Bae make the case to include the Denisovan fossils in *H. juluensis* based on morphological comparisons, particularly with the M2 and mandible. However, a recent paleoproteomics study published by Fu et al. (2025) argues that the Denisovan fossils should be assigned to *H. longi* instead. Nevertheless, given the current absence of comparable paleoprotein data from Xujiayao and/or Xuchang, it is difficult to simply discount the morphological similarities between the fossils. The next step in this debate seems to be to attempt to analyze samples from Xujiayao and Xuchang for aDNA and paleoproteomics to see how they fit in this picture (should Denisova be assigned to *H. juluensis*, *H. longi*, or something else altogether). Regardless, the Wu and Bae (2025) piece is a nice synopsis of the current state of Chibanian hominin paleontology in Asia and continues to build on such earlier syntheses they have contributed to (Bae 2024; Bae and Wu 2024; Bae et al. 2023; Wu et al. 2022).

Kaifu and Athreya (2025) present a fairly comprehensive synthesis of all of the major hominin fossils from eastern Asia from the Early to the early Late Pleistocene. Rather than assign species names to the different populations, they choose to assign them to paleodemes (which, in this context, may be considered synonymous with "populations"), largely divided by time units (early Calabrian, late Calabrian, early Chibanian, late Chibanian). As with earlier studies (e.g., Antón 2002; Baab 2010; Kaifu et al. 2010), Kaifu and Athreya (2025) found that *H. erectus* can be easily separated into regional variants (Zhoukoudian in the north and Indonesia in the south), though they find that the Hexian fossil somewhat toggles between the Zhoukoudian and Indonesian *H. erectus*. In Kaifu and Athreya's view, a case could be made for possible regional continuity between Zhoukoudian and the late Chibanian hominins like Jinniushan, Dali, and Harbin. They do note, however, that the hypothesis is only "weakly supported at present because there is no overlap in the range of variation exhibited by these two groups" (Kaifu and Athreya 2025: 386). They do propose a Hexian/Penghu/Xiahe p-deme that could represent one of possibly several Denisovan lineages. Interestingly, in the Kaifu and Athreya (2025) analysis, they find that Xuchang is more closely related to their Hexian p-deme, suggesting a possible close ancestor-descendant relationship. This does not agree with the Wu and Bae (2025) analysis that consistently found a close relationship between Xuchang and Xujiayao, the paratype and holotype of *H. juluensis*, respectively. However, this may be because the Xujiayao fossils were not included in the Kaifu and Athreya (2025) analysis. Regardless, these studies are just beginning to determine the degree of morphological variation present in the region, a record that is only beginning to be understood (Bae 2024; Bae and Wu 2024; Bae et al. 2023).

Ni et al. (2025) take a different approach to understanding Calabrian and Chibanian hominin variation. They use a phylogenetic method that has its roots in paleontology, where they assign 95 fossils to 55 operational taxonomic units and then run a cladistic analysis. The general con-

Figure 2. Participants in the NS'23 workshop in front of the Balanica cave complex overlooking the Sićevo Gorge near Niš, Serbia.

clusion they draw is that several broad groups can be created (*H. erectus/ergaster*, *H. neanderthalensis*, *H. sapiens*, and *H. longi*). Ni et al. (2025) do try to include the Denisovan fossils in the *H. longi* hypodigm, and the recent paleoproteomics study by Fu et al. (2025) lends further support for this relationship. However, Ni et al. (2025) did not include *H. juluensis* in their analysis because this new species was published after the core analysis for their study was done. Further, as mentioned above, we still do not know how the protein and/or aDNA from the Xujiayao and Xuchang fossils fit in all of this. It is important to keep in mind that while phylogenetic approaches are used in paleoanthropology (e.g., Collard and Wood 2000), in general, it is considered to be just one alternative method to the more traditional methods utilized in the Wu and Bae (2025) and Kaifu and Athreya (2025) studies—no better, no worse, just a different approach. In fact, see Kaifu and Athreya (2025) for a discussion of some of the problems with applying phylogenetic approaches to the hominin fossil record (also see Harrison 1993).

CONCLUSION

This SI of *PaleoAnthropology*, as well as the Wenner-Gren/SSHRC workshop in Novi Sad, did not provide the answers as to the number of species or the phylogeny of the hominin lineage(s). Rather, both questions demonstrate the need for the paleoanthropology community to reexamine the prevalent paradigms, assess the taxonomic units it uses, and engage in free and unfettered discussion of this relevant period in human evolution that eventually saw the emergence of our own species. Although we, as scientists and biologists, like to consider humans as part of the animal world, our evolution has a very different significance for both the scientific and public communities. How we communicate about our science matters, and how we name and categorize human ancestors is relevant to the ease with which we break down complex and multifaceted scientific advances into understandable information. Humans are excellent at building categories, and our language is based on this ability. However, as we are learning, biology does not operate in neatly delineated categories. Life is complex and messy, and while these categories are meaningful and useful, multiple phenomena happen in the fuzzy gray areas at their boundaries. Open-minded and vigorous discussions are needed to move the field forward and make sense of the growing and increasingly complex fossil record in order to answer questions like "the Chibanian Puzzle." Meetings like the 2019 AABA symposium and the NS'23 workshop, and these *PaleoAnthropology* proceedings, are important steps in the right direction.

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DATA AVAILABILITY STATEMENT

All relevant data are included in the text.

AUTHOR CONTRIBUTION

MR and CB conceptualized, wrote, and edited the paper.

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