

Biological Anthropology

One Year in Biological Anthropology: Species, Integration, and Boundaries in 2010

Libby Cowgill

ABSTRACT The year 2010 in biological anthropology has been marked by continuing questions regarding temporal and geographical species boundaries and by queries into what it means to be human. The lines of evidence we use to reconstruct our biosocial past often exist in a state of dynamic tension; however, opportunities for integration do occur, and these collaborative endeavors were notable in 2010. Here I focus on boundaries and integration in four separate areas. First, I discuss recent genetic advances in our understanding of human evolution. Second, I review a virtual issue of the *American Journal of Physical Anthropology* that emphasized bioarchaeology in Asia. Third, I highlight several articles in the *Proceedings of the National Academy of Sciences* that focus on speciation, human genetics, and the evolution of unique human characteristics. Last, I address the recent controversy over the language used in the American Anthropological Association's Long-Range Plan. [*biological anthropology, annual review 2010, Neandertal DNA, Asian bioarchaeology*]

The 2011 William S. Pollitzer Travel Award Essay Question for students seeking funding to attend the American Association of Physical Anthropology meetings is: "In the age of personalized genomics, genetic ancestry testing, and medical genetic testing, do disciplines such as osteology, paleontology, primatology, human adaptation, etc. have relevance anymore for understanding modern human evolution and biology?" It's a good question, one that will hopefully induce students to think about a variety of critical factors in our discipline. It is a question that begs students to consider the unique contributions of different subdisciplines within biological anthropology and how they add to our understanding of humans and their place in nature. I think it also implies a gentle tension between diverse lines of evidence and types of knowledge, an issue that frequently arises in the professional sphere and one of which students should be aware. The question also touches on the constant need for integration, reflection, and reevaluation, both within biological anthropology itself and within the wider field of anthropology as a whole. What are the unique contributions of different perspectives in anthropology? How should we define them? Can they be integrated into a cohesive whole that enhances understanding in a way that is more than simply a sum of its parts?

These are wonderful questions for 2010 in particular, as some of the most innovative research and frustrating challenges within biological anthropology touch on these issues. Although defining a theme for an entire year of research remains a daunting task, the unifying thread of these questions can be traced through much of the literature published in biological anthropology in 2010. Numerous studies, if viewed from a broader anthropological perspective, addressed the issue of boundaries, lines, and divisions that are expanding, contracting, and permeable, both for areas of study and for organisms themselves. A large variety of studies examined temporal and geographic boundaries of the human species, focused on areas of the globe previously overlooked, emphasized analyses of speciation and taxonomy, and explored the characteristics that make humans unique. Overlaying this, however, were issues of boundaries and integration of perspectives within our discipline. At times, these perspectives seemed to be in the constant dynamic tension implied by the AAPA travel-award question; at other times, they were integrated into such a seamless whole that one can't help but be enthusiastic about future collaborations and interdisciplinary pursuits that may yield further insights into what it means to be human, both biologically and culturally.

Although these issues and questions tie together much of the relevant literature in this review, it is still possible to view the year in discrete intellectual “chunks.” Therefore, this review is divided into four broad sections. The first section addresses some of the main issues in paleoanthropology this year, where genetic approaches to human evolutionary diversity, speciation, and our understanding of the human fossil record made several important contributions. The second section delves into recent bioarchaeological research in Asia, as skeletal biologists expand their research programs into a region that, although not precisely ignored, perhaps deserves more interest and attention within the discipline. The third section focuses on a recent issue of the *Proceedings of the National Academy of Sciences* in which scholars from a diverse array of fields brought their varying perspectives to issues of the human condition. Lastly, the fourth section touches briefly on the recent internal controversy over the changes made to the American Anthropological Association’s (AAA) Long-Range Plan.

SPECIES, PALEOANTHROPOLOGY, AND ANCIENT DNA

In introductory classes to biological anthropology, both instructors and the authors of numerous textbooks have been tempted to present the origin of modern humans as two equally plausible, mutually exclusive evolutionary scenarios: the Out of Africa hypothesis and the Multiregional Evolution hypothesis. These models can be expressed succinctly on a single PowerPoint slide, have historically been both suggested and supported by influential scholars in the field, and can be massively simplified for undergraduate consumption and, hopefully, comprehension. The good news is this: we can stop doing this now. The bad news is that a more current representation of the consensus that most researchers have reached is likely to be more complex and convoluted. In addition, it can likely only be represented by models of human evolution destined to befuddle introductory students everywhere, complete with multiple slides, wandering migration arrows, question marks, and unapologetic blank spaces.

In May of this year, Richard Green and colleagues (2010) published the first complete draft sequence of the Neandertal genome, and the unexpected results were greeted with surprise and enthusiasm from much of the anthropological community. Up until this point, only analyses of mitochondrial DNA from Neandertals had been undertaken, and all results had indicated that Neandertal mitochondrial DNA was outside of the range of recent modern human variation, providing no direct evidence for interbreeding between Neandertals and early modern humans (Briggs et al. 2009; Krings et al. 1997; Ovchinnikov et al. 2000). Information from the nuclear genome, however, appears to present a somewhat different picture. Green and colleagues (2010) compared the Neandertal genome to recent human genomes from a variety of locations around the globe, hypothesizing that if there was no interbreeding between Neandertals and early modern humans, Neandertal nuclear DNA should be equally

similar to all modern human DNA, regardless of geographic location. However, their results indicated that Neandertal nuclear DNA is more similar to that of non-African individuals than it is to DNA of those inside Africa. This pattern is best explained by interbreeding between early modern humans and local archaic populations in Europe and Asia. Green and colleagues also suggested that the proportion of Neandertal ancestry for non-African populations today is between one and four percent. As others have pointed out, however, this is perhaps best thought of as a minimum contribution of archaic DNA to the modern human genome, as it only considers the contribution of Neandertal DNA specifically (Hawks 2010). Given the potential for social and genetic contact between modern and archaic humans in Asia, the actual amount of admixture could be considerably higher than this research suggests.

The reaction of the paleoanthropological community to this research has been surprisingly mixed, which likely reflects, at least in part, the increased specialization of subfields within the larger discipline of biological anthropology as a whole. Although some scholars expressed overwhelming enthusiasm (Hawks 2010), others exhibit a restrained skepticism (see Klein’s comments in Wade 2010a). Some researchers seemed almost surprised that Green and colleagues hadn’t expected the results their study produced and noted that at least some archaeologists and skeletal morphologist have been proposing less strict Out of Africa models for some time. As one researcher commented, “After all these years the geneticists are coming to the same conclusions that some of us in the field of archaeology and human paleontology have had for a long time. What can I say? If the geneticists come to this same conclusion, that’s to be expected” (see Zilhão’s comments in Saey 2010). Despite differences in opinion on the meaning of the results, the convergence of different research approaches toward a similar conclusion is a welcome relief to the many scholars ready to at last move past discussions of “who was having sex with who in the Pleistocene” (see Trinkaus’s comments in Schmid 2010).

In addition to the Neandertal genome, Johannes Krause and colleagues (2010) continued to expand our current understanding of mitochondrial DNA diversity in the Late Pleistocene with their analysis of a distal phalanx from southern Siberia. Krause and colleagues presented a complete mitochondrial sequence from an unknown hominin little finger found in Denisova Cave in the Altai Mountains, a region known to be occupied by roughly contemporaneous Neandertals and early modern humans. Based on the genetic evidence, the authors argued that the Denisova Cave specimen represents a distinct mitochondrial DNA lineage that diverged from the lineage leading to living modern humans approximately one million years ago. Dubbed “X-Woman” by the media (and “The Yeti” and “Pinkyanthropus” by some of my more satirical colleagues), this analysis represents a significant contribution to the expanding sample of data on mitochondrial DNA from this time period and, in addition

to recent analyses of “hobbits” from the island of Flores, raises interesting questions about just how much morphological and genetic diversity was present during the Late Pleistocene.

Although Krause and colleagues carefully refrained from designating the Denisova Cave specimen a new species, others within the popular press were less hesitant (e.g., Brown 2010). Care must be taken, however, to avoid making such claims based on limited bodies of evidence. In a somewhat tongue-in-cheek analysis of the third molar from the Romanian early modern human Oase 2, Erik Trinkaus (2010) presented an interesting criticism of some of the claims made about the Denisova Cave “pinkie.” The third upper molars of the Oase 2 specimen present a unique morphology and are so large that they fall 3.65 standard deviations from the modern human mean. Had they been found in isolation and not in the securely situated context of a clearly modern human skull, some would have undoubtedly thought they represented yet another morph of Late Pleistocene hominin. Furthermore, following the logic and assumptions that Krause and colleagues (2010) used to reconstruct the divergence times of the Denisova Cave mtDNA lineage from that of modern humans, Trinkaus concluded that the Oase 2 specimen would have diverged from modern humans and Neandertals at a completely implausible date of 4.2 million years ago. Trinkaus readily admitted that these conclusions are “silly.” Although two separate mitochondrial lineages may conceivably have a divergence date, two third molars most certainly do not. However, his analysis of the Oase 2 third molar serves as a cautionary tale of how we analyze and interpret ranges of human variation in the past, particularly when evidence is limited.

Given the above contributions, discussions of species, phylogeny, and ranges of variation have been plentiful this year. Some scholars, because of their adherence to a very strict biological species concept, may prefer to banish the species name *Homo neanderthalensis* from the human family tree based on their clear interfertility with modern *Homo sapiens*. In general, however, the human family tree continued its trend toward increasing “bushiness” and taxonomic diversity. This trend includes the announcement of a new species of australopithecine this year: *Australopithecus sediba* (Berger et al. 2010). The two new partial skeletons, dating between 1.95 and 1.78 million years ago, were found in cave deposits at the Malapa site in South Africa and represent a new species that Lee Berger and colleagues believe was descended from *Australopithecus africanus*. The new specimens are a notable contribution to what many call the “muddle in the middle”: the confusing and contentious evolutionary time span proceeding and including the origin of our genus. If nothing else, the *Australopithecus sediba* specimens remind us of exactly how mysterious this time period can be. They exhibit a unique mosaic of both primitive and derived evolutionary characteristics, displaying long arms, a small body, and a small brain (~420 cc) combined with *Homo*-like features of the dentition, pelvis, teeth, and face.

The curious blend of ancestral and derived characteristics present in *Australopithecus sediba* inevitably raises questions about what morphological characteristics are important when considering whether or not to welcome a species into our genus. Although the authors emphasized the *Homo* affinities of the two specimens, they ultimately included the skeletons in the genus *Australopithecus*, likely primarily because of the very small brain size of the type specimen. Historically, brain size was the predominant criteria under which specimens were assigned to the genus *Homo*, and although rubicon for *Homo*-appropriate brain size has been relaxed significantly, the legacy of that mindset still remains. Other researchers, however, have argued that perhaps *Australopithecus sediba* would be a better fit within our genus based on dental characteristics and features of the mandible (see Anton’s and Johanson’s comments in Balter 2010). Still others are concerned that the diagnosis of a new species may be unwarranted, given that some of the shared features between *Australopithecus sediba* and *Homo* could be related to the juvenile status of the new species’ type specimen (see White’s comments in Balter 2010). The last 15 years have introduced a variety of new species, many of whom are potential candidates for the ancestor of our genus; although all have expanded our understanding of morphological variation during this evolutionary period, only time will tell whether they will continue to be recognized as unique variants.

EXPANDING BOUNDRIES: THE ASIAN FRONTIER

The above research on the finger bone from Denisova Cave is part of a broader body of literature this year that focused on biological anthropology in Asia. Although paleoanthropology in Asia has a rich history dating back to the discovery of *Homo erectus* by Dutch anatomist Eugene Dubois, the intensification of research on Asian bioarchaeology and population genetics is overdue. This February, the *American Journal of Physical Anthropology (AJPA)* published a virtual, online-only issue focused entirely on recent advances in Asian skeletal biology and genetics, including work on ancient DNA, genetics of living people, craniometrics, activity patterns, and body proportions. The virtual issue is a compellation of work published in *AJPA* over the last two years and contains notable articles from 2008 through 2010. The geographic range of articles spans the entire continent, with research emphases ranging from Japan to India to Siberia.

Several genetic analyses focused on reconstructing relationships among both extant and historical indigenous populations in Asia (Adachi et al. 2010; Fu et al. 2010; Jin et al. 2010; Kim et al. 2010; Krithika et al. 2010; Lertrit et al. 2010; Matsukusa et al. 2010; Wang et al. 2010; Zhang et al. 2010). Among these, Patcharee Lertrit and colleagues (2010) presented the first analysis of ancient DNA from Thailand, which explored the relationship between mtDNA sequences from two Bronze and Iron Age archaeological sites in Northeastern Thailand and those of modern samples from various ethnic populations of East and Southeast Asia. Yuquin Fu and colleagues (2010) investigated the patterns of

mitochondrial DNA variation in the inhabitants of a cemetery in Kublai Khan's Upper Capital in Inner Mongolia and found that the maternal lineages of these individuals are of Asian Han-Chinese origin, in spite of the presence of typical European morphological craniofacial features in several of the individuals. In an analysis of ancient mitochondrial DNA of 16 Jomon individuals who were the descendents of Japanese Pleistocene nomads, Noboru Adachi and colleagues (2010) showed evidence of a shared haplogroup between Jomon individuals and Native Americans, which supports previous hypotheses of genetic affinity between the two groups. S. Krithika and colleagues (2010) presented an analysis of extant South Asian tribal populations that incorporated both nuclear DNA microsatellites with linguistic data in populations from India. Hirotaka Matsukusa and colleagues (2010) found that genetic data from maternal, paternal, and autosomal sources contradicts archaeological data about the ancestry of individuals from the Sakishima islands, which are part of the Japanese archipelago. Lastly, both Fan Zhang and colleagues (2010) and Kijeong Kim and colleagues (2010) detected evidence of population admixture from populations in the west in different regions of Asia approximately 3,000 to 2,000 years ago.

Contributions to the special issue from skeletal morphologists also touched on population history as well as added additional information on activity patterns, health, growth, and body proportions in Asia populations (Choy et al. 2010; Hanihara and Ishida 2010; Hanihara et al. 2010; Hoover and Matsumura 2010; Lieverse et al. 2010; Temple 2010; Temple et al. 2010). Two studies in the virtual issue used craniometric data to explore population affinity among East Asian groups (Hanihara and Ishida 2010; Hanihara et al. 2010). Kyungcheol Choy and colleagues (2010) used correlations among stable isotope analyses, burial type, age, and sex to draw conclusions about variation in diet and status in a fourth- to seventh-century cemetery in South Korea. In a Neolithic–Bronze Age sample from Siberia, Angela Lieverse and colleagues (2010) detected a pattern of variation in musculoskeletal markers that was consistent with watercraft use. Daniel Temple and colleagues (2010) compared the limb proportions of Jomon individuals to Yayoi groups, who are more recent immigrants to Japan from mainland Asia, and found that Jomon limb proportions were similar to those of populations from temperate-tropical climates, reflecting morphological change among the Jomon since their migration to the Japanese Islands. In addition to differences in limb proportions, Jomon and Yayoi groups differed in the prevalence of enamel hypoplasias, with Yayoi displaying fewer enamel defects, likely because of their reliance on stable wet rice economies (Temple 2010).

A few additional articles and books focusing on Asian paleoanthropology are worth noting here. Two new books were published on the Asian fossil record. Hong Shang and Erik Trinkaus (2010) published a detailed description of a direct-dated early modern human from China. The volume on the individual from Tianyuan Cave presented an analysis

of the paleobiology and context of the most complete early modern human from this region. A recent volume, *Asian Paleoanthropology: From Africa to China and Beyond*, edited by Christopher Norton and David Braun (2010), added the first compellation of papers focusing specifically on the peopling of Asia two million years ago and covered both the archaeology and human paleontology of almost every major region of the Asian continent. In addition, a number of articles made important contributions. This year's *Yearbook of Physical Anthropology* contained a valuable synthesis of the Late Middle Pleistocene fossil record in Eastern Asia and presented a detailed evaluation of taxonomic issues unique to this time period and region (Bae 2010). In addition, fragmentary human remains dated to more than 100,000 years ago in South China may represent the earliest modern human from this region, based on the presence of a chin on the mandibular remains (Liu et al. 2010).

Lastly, one of the most heated debates to ever strike Asian paleoanthropology may finally be winding down, based on Leslie Aiello's thorough and measured review of our current understanding of the *Homo floresiensis* material (Aiello 2010). When the fossil material from Flores was published in 2004–05 (Morwood et al. 2004, 2005), the partial skeleton of LB 1 and other material assigned to *Homo floresiensis* sparked vitriolic controversy. Debates over whether the Flores hominins represent a new species or pathological individuals have been, to put it mildly, livening up the meetings of American Association of Physical Anthropology ever since. Aiello's (2010) recent review of the last five years of research on the "hobbits" from Liang Bua Cave is significant in that it represented a pleasant departure from the polarized discussions that have colored previous studies of this material. To the best of my knowledge, Aiello is not strongly associated with the previous research on the Flores specimens, and so her review of the evidence carries particular weight. Although many researchers will still hope for an additional Flores specimen that possesses both a small brain and body before completely closing the door on the pathology argument, Aiello concluded that, to date, none of the proposed pathologies fully account for all the morphological features seen in LB1. Furthermore, the pathologies proposed cannot explain this specimen's numerous features that strongly resemble earlier phases of human evolution. Although Aiello's opinion cannot be taken as the voice of all researchers in this ongoing discussion, her review of the evidence likely marks an important contribution on the road to consensus.

THE HUMAN CONDITION

A *Proceedings of the National Academy of Sciences* supplement was published this year that resulted from the Arthur M. Sackler Colloquium of the National Academy of Sciences and was the fourth in a series titled "In the Light of Evolution." This collection of articles, "In the Light of Evolution IV: The Human Condition," brings together a diverse compilation of work by anthropologists, evolutionary biologists, and philosophers of science to shed light on wide-ranging

issues in phylogeny, the human genome, and the evolution of several features unique to the human species (Awise and Ayala 2010). In their introductory article to the collection, John Awise and Francisco Ayala referred to the collection as part of an emerging field of “anthropogeny, [which] seeks to understand the evolutionary origins of humans and their biological and cultural traits” (2010:8897). In spite of this new designation, I would argue that the research presented in the colloquium falls under the sphere of biological anthropology and represents a truly innovative attempt at integrating a diverse body of perspectives and backgrounds, all dedicated to elucidating human biological and social history. The various contributions are best divided into three areas (Awise and Ayala 2010): (1) human phylogeny and taxonomy, (2) human genetics, and (3) the cultural evolution of the unique human cognitive and social system.

Although all 16 articles cannot be reviewed in detail here, some stand out as touching on areas of study that have been focused on in general in 2010, while others are particularly succinct synopses of ongoing, important research. Bernard Wood (2010) discussed the current state of affairs in the reconstruction of hominin family tree, addressing some of the major challenges facing scholars when attempting to establish relationships among a list of human ancestors that appears to grow by the year. Juan Luis Arsuaga (2010) emphasized similar issues with an interesting article on the ultimate form of the hominin family tree and thus the broader pattern of speciation within our lineage, using the fossil specimens from Sima de los Huesos as the focal point of discussion. Nina Jablonski and George Chaplin (2010) presented a brief summary of our current understanding of one of the best-documented examples of natural selection operating in human populations: skin color. John Awise (2010) evaluated the human genome for evidence of intelligent design and instead found numerous instances of imperfect systems that are overly complicated or that function suboptimally because of their evolutionary history. The contribution by Laura Scheinfeldt and colleagues (2010) was a particularly elegant example of the types of inferences that can be achieved by combining multiple lines of evidence. These authors used current evidence from linguistics and archaeology to contextualize what is known from genomewide studies of African populations, achieving a picture of African population history that has been enhanced through the use of information from studies of genetics, language, and material culture.

Debatably, some of the most exciting articles in the *PNAS* supplement included a variety of different perspectives converging on the common theme of human uniqueness—and, therefore, the combination of characteristics that define “humanity.” Kristen Hawkes (2010) shed light on the unique human life cycle with a discussion of the extension of the female lifespan past the cessation of fertility. In this elaboration of the “grandmother hypothesis,” Hawkes supplied an additional dimension, overall “frailty,” to clarify the relationship between reproductive success and extended

survival. Peter Richerson and colleagues (2010) discussed potential interactions between cultural and genetic evolution and the potential for cultural change to create novel environments where genes are exposed to new and different selective regimes. This perspective is particularly useful in examining genetic changes that occurred with the transition to sedentary agriculturalism, and the authors examined the associated genetic changes linked to dietary change and population expansion during the agricultural transition in some detail. Both Steven Pinker (2010) and Terrence Deacon (2010) focused on the evolution of human language. Pinker (2010) explored the history of theorization on the origin of language, dating back to contrasting viewpoints of Darwin and Alfred Russel Wallace on this issue. Combining two hypotheses about the evolution of human intelligence, Pinker argued that humans fill a “cognitive niche” and that the unique human cognitive faculties that evolved in the context of this niche can be co-opted for alternate purposes, including language. Deacon (2010) addressed the difficulty some researchers have had in generating plausible evolutionary hypotheses for the origin of language because of the problems associated with explaining the selective advantage of earlier, simplistic forms of language and argued that the evolutionary milieu in which modern language evolved was likely one of relaxed selective pressure at the organismal level. Lastly, Francisco Ayala (2010) presented an interesting discussion of the biological and cultural basis of morality, eventually concluding that while individual societal norms are a product of cultural evolution, the capacity for morality itself is an exaptation of the unique set of human intellectual abilities.

BOUNDARIES AND INTEGRATION IN THE AAA

Although it is entirely possible that the definition of *anthropology* has been discussed and debated more than sufficiently over the last month of 2010 for the satisfaction of most of our discipline, no treatment of boundaries, integration, and identity in 2010 would be complete without at least a mention of the recent internal and public controversy. As most of us are aware, during the 2010 AAA meetings, changes were made to the Long-Range Plan that included the removal of the word *science* and its replacement with the goal of advancing “public understanding of humankind” (AAA 2010a) and a list that “includes, but is not limited to” (AAA 2010b) various different approaches to anthropological research. The seemingly unanticipated firestorm that followed occurred primarily on the Internet and now totals commentary on this issue in over 100 articles, scientific blogs, and other academic news sources (see Lende 2010 for links to much of the commentary on this issue). In a recent response to the public controversy by the AAA, the association states that the controversy was exaggerated and partially inflamed by the explosion of media coverage (AAA 2010a). It is certainly true that some of the opinions expressed online and in other forms of popular media represent the most extreme standpoints on the issue (e.g., Carl 2010; Dreger

2010; Wade 2010b). However, while the revisions to the Long-Range Plan were likely intended to be more inclusive, the outcry, both publicly and internally, seems to indicate that some scholars felt marginalized by the recent changes and that the controversy itself is not an issue completely constructed by the popular media but, rather, one about which our discipline is very actively concerned.

The commentary on this issue has been fast and furious, with seemingly more reasoned voices chiming in toward the latter half of the discussion. Although most of the relevant points on both sides have been made, allow me to make just a few more. As a biological anthropologist whose research perspectives are strongly “scientific,” I feel compelled to note that the voices involved in this discussion represent only a small subset of the range of opinions on this issue as a whole. In general, among many of my colleagues in biological anthropology, the ongoing debate has been met with a collective yawn, as though the removal of the word *science* from the AAA Long-Range Plan is a mildly disappointing but not terribly surprising development. Because of this, the more extreme voices on the side of science may be less visible within the anthropological community (although not in the media) as many biological anthropologists have long since stopped paying their AAA membership dues.

Which is, of course, exactly why it is important for those of us within biological anthropology who still support a strongly integrated four-field approach to continue discussing this issue. In his recent piece in the *Yearbook of Physical Anthropology* this year, Agustín Fuentes (2010) called for increased communication between biological anthropologists of different emphases and the other subdisciplines within anthropology; recent controversies such as this present an opportunity to do so. Biological anthropologists who are still involved in this discussion are, by virtue of their involvement, individuals who are still profoundly interested in maintaining four-field ties within American anthropology and maintaining intellectual contact with other AAA members. The issue of whether or not the specific word *science* should be included in the Long-Range Plan is, in fact, a small one. However, the fervor surrounding this discussion is evidence in itself of larger issues of identity and integration that merit continued focus. In the rush to find some measured resolution to this issue and to provide intelligent counterpoints to opinions at the extreme edges of the debate, it is easy to lose sight of the fact that, even if only in the minds of some, these are real concerns within anthropology, and thus it is healthy for us as a discipline to continue our discussion. We should be interested from a practical standpoint in how such issues affect our working environments within departments, the public perception of our discipline, and whether we and our graduate students continue to be eligible for science-related funding opportunities. More importantly, we should be able to examine these issues through our unique scholarly perspectives as anthropologists, as researchers interested

in shifting boundaries, dynamic identities, and changing definitions.

Libby Cowgill *Department of Anthropology, University of Missouri, Columbia, Columbia, MO 65211-1440; cowgill@missouri.edu; <http://web.missouri.edu/~cowgill/>*

NOTE

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