

Upholding “good science” in human origins research: A response to Chan et al (2019)

Rebecca Rogers Ackermann^{1,2}, Sheela Athreya³, Wendy Black^{4,2}, Graciela S. Cabana⁵, Vincent Hare^{1,2}, Robyn Pickering^{6,2}, Lauren Schroeder^{7,2}

1 Department of Archaeology, University of Cape Town, Cape Town, South Africa

2 Human Evolution Research Institute, University of Cape Town, Cape Town, South Africa

3 Department of Anthropology, Texas A & M University, College Station, Texas, U.S.A.

4 Archaeology Unit, Department of Research and Exhibitions, Iziko Museums of South Africa

5 Department of Anthropology, University of Tennessee, Knoxville, Tennessee, U.S.A

6 Department of Geological Sciences, University of Cape Town, Cape Town, South Africa

7 Department of Anthropology, University of Toronto Mississauga, Mississauga, Canada

**** resubmitted 16 Nov 2019 as Matters Arising to *Nature***

In regards to: Chan, et al (2019) Human origins in a southern African palaeo-wetland and first migrations. *Nature*. <https://doi.org/10.1038/s41586-019-1714-1>

ABSTRACT: The recent publication by Chan et al (2019) entitled “Human origins in a southern African palaeo-wetland and first migrations” fails to meet scientific standards for publication in two ways. First, it neglects consideration of the entire body of scientific evidence around human origins, which leads to their unsupportable claim of a purported “homeland” for our species within southern Africa. Second, it reinforces ongoing dynamics of racialization within the science of human origins, including through the implicit treatment of current-day southern Africans as relics of times past. The publication of this study represents a failure of the research and editorial process to uphold thorough and ethically responsible science.

Increasingly, we as scientists recognize that “good science” entails both empirically *and* ethically sound research through community partnerships, inclusion of a diversity of research perspectives, and a thoughtful and thorough consideration of research implications. Simply put, “good science” can no longer be defined solely through strict adherence to empirically-driven, hypothetico-deductive methodologies; it must also be ethically responsible. In this context, the recent publication by Chan et al (2019) fails to meet these standards by neglecting a vast body of evidence from a broad range of

research on human evolution, ignoring concerns and findings emanating from the social sciences and humanities, and consequently inadvertently reinforcing racialized and “othering” narratives of human origins.

A glaring shortcoming of the study is that the empirical claims made in this paper are not supported by the preponderance of genomic and palaeoanthropological data. Chan et al (2019) examined a limited portion of African continental human genomic diversity, made sweeping claims about our species’ history based on living populations, and ultimately concluded that their results locate a southern African “homeland” for our species, *Homo sapiens*. This conclusion is fundamentally flawed. Extensive fossil and DNA evidence (e.g. ¹⁻⁴) from throughout Eurasia and Africa shows that the emergence of our species is complex and reticulate, and that even within Africa, our evolution is not reducible to a single locality or time period (e.g. ⁵). The last decade in particular has brought a landslide of autosomal studies of ancient genomes refuting simple replacement models of human origins.

Further, Chan et al.’s study uses uniparental mtDNA data as a proxy for populations, although it is well known that mtDNA data alone is not sufficient to represent “population” histories, much less reconstruct species-level trees ⁶. Moreover, current best practices for estimating past dispersal patterns dictate the use of extensive autosomal data from both living and ancient samples. The authors then rely on a loose correspondence between select maternal sublineage divergence dates from their total data set and inadequate paleoclimatic data (principally, two marine cores off the coast of Namibia – see below) to declare the time, place, and ecological setting of our species’ origin. However, neither their diagnosis of an origin point nor of dispersals can be based on their mitogenomic data alone; their inferences are something to be tested, not assumed. Drawing sweeping conclusions about places of origin from analyses of this tiny part of the extant human genome is deeply problematic and outdated, something that is well understood among anthropological geneticists whose work reconstructs population histories.

The paper's empirical claims are also unsupported by the existing body of archaeological and palaeoenvironmental work from Africa. Chan et al. omit several important palaeoclimatic data sets from their analysis, including from pollen, terrestrial stable isotopes, and a key marine core off the Limpopo catchment ⁷. The sole two Atlantic marine cores used by Chan *et al.* appear to include leaf wax isotope records that are uncorrected for important secular effects, including vegetation changes (for δD , e.g. ⁸) and shifts in atmospheric CO₂ across glacial-interglacial cycles (for $\delta^{13}C$, e.g. ⁹). Furthermore, changes in hydroclimate - if indeed present - do not necessarily imply simple changes in human populations. In fact, there is well-documented evidence showing that populations of *Homo* persisted throughout episodes of rapid climate change (e.g. ¹⁰), and dispersed widely over a range of environments during the Pleistocene. The African archaeological record also demonstrates that Pleistocene material culture originates and persists in multiple localities across a wide array of palaeoecological settings ⁵. These are all points for which Chan *et al.* provide no discussion. By all measures of good model building, archaeological and palaeoenvironmental data should have been foundational to this study, but instead were largely ignored or referenced *post hoc* rather than being used to test clear hypotheses.

Lastly and most importantly, in addition to their stated community engagement, the authors would have benefitted from a more diverse team that included social scientists and humanists, scholars who are knowledgeable about the range of human biological and behavioural diversity, both past and present, but are also mindful of how power structures and language impact how we narrate results about ourselves. Such a team could have provided important corrective perspectives on deeply offensive words and approaches in the study, such as the ubiquitous use of the word "homeland", a South African apartheid term for a territory set aside for "black" South Africans (a racial category of the apartheid regime). Similarly, explicit phrases used in Chan et al., such as "southern Africa is home to contemporary populations that represent the earliest branch of human genetic phylogeny" and "contemporary populations who represent the earliest human lineages", situate the study within colonial and racist scientific ideology, where living Africans such as the Khoesan peoples are continuously treated as primitive "missing links" ¹¹⁻¹³. The idea that hypothetical past hunter-gatherer groups were

isolated in a “homeland” for 70,000 years also reproduces colonial ideas of living populations as human fossils caught in the past ¹⁴, a notion that is inconsistent with ethnographic data demonstrating that hunter-gatherers engage in far flung (hundreds of kilometres) individual networks (e.g. ¹⁵), and as such, are dynamic groups that have been adapting and retooling their social systems for tens of thousands of years. Finally, the use of giraffes, lions, and zebras (i.e. undomesticated animals that do not cohabit with humans) to validate their hypotheses problematically implies that humans, in particular living Africans, can be understood by using wild animals as proxies. This set of unfortunate phrasing may have been unintentional on the part of the authors, but could have been caught via substantial engagement with anthropologists who work on these issues. Minimally, it should have been caught in the review process. Instead, these ideas were picked up by the popular press, magnified and widely disseminated throughout southern Africa and beyond, serving to reinforce outdated and irresponsible perspectives on race, human diversity and human origins.

In sum, Chan et al.'s study not only ignores important fossil, genomic, climatic, and archaeological evidence, but also serves to reproduce a form of scientific racism that is so deeply embedded in western science that it is often normalized by non-experts. Such egregious overstep on the part of Chan et al. may result from the fact that the team lacked anthropologists or similar specialists in human evolution. Lack of engagement with more broadly relevant literature and a more diverse group of scholars, even if unintentional, serves to marginalise previous work and existing bodies of knowledge. This behaviour in turn contributes to the hegemonic bias of western science in terms of whose data contributes to our output and whose does not. These problems stem from continued adherence to a narrow perspective on what constitutes “good science”, and demonstrate how urgently we need to broaden our awareness of power and privilege when any scientific work is conducted, particularly when it comes to how our species' story is written. We need to work harder at all levels – from research design through the editorial process to outreach – to uphold and disseminate thorough and ethically responsible science.

- 1 Ackermann, R. R., Mackay, A. & Arnold, M. L. The hybrid origin of “modern” humans. *Evolutionary Biology* **43**, 1-11 (2016).
- 2 Prufer, K. *et al.* A high-coverage Neandertal genome from Vindija Cave in Croatia. *Science (New York, N. Y.)* **358**, 655-658, doi:10.1126/science.aao1887 (2017).
- 3 Reich, D. *et al.* Genetic history of an archaic hominin group from Denisova Cave in Siberia. *Nature* **468**, 1053-1060, doi:10.1038/nature09710 (2010).
- 4 Trinkaus, E. Early Modern Humans. *Annual Review of Anthropology* **34**, 207-230, doi:10.1146/annurev.anthro.34.030905.154913 (2005).
- 5 Scerri, E. M. L. *et al.* Did Our Species Evolve in Subdivided Populations across Africa, and Why Does It Matter? *Trends in ecology & evolution* **33**, 582-594, doi:10.1016/j.tree.2018.05.005 (2018).
- 6 Rosenberg, N. A. & Nordborg, M. Genealogical trees, coalescent theory and the analysis of genetic polymorphisms. *Nature Reviews Genetics* **3**, 380-390, doi:10.1038/nrg795 (2002).
- 7 Smith, E. I. *et al.* Humans thrived in South Africa through the Toba eruption about 74,000 years ago. *Nature* **555**, 511, doi:10.1038/nature25967 (2018).
- 8 Sachse, D. *et al.* Molecular Paleohydrology: Interpreting the Hydrogen-Isotopic Composition of Lipid Biomarkers from Photosynthesizing Organisms. *Annual Review of Earth and Planetary Sciences* **40**, 221-249, doi:10.1146/annurev-earth-042711-105535 (2012).
- 9 Hare, V. J., Loftus, E., Jeffrey, A. & Ramsey, C. B. Atmospheric CO₂ effect on stable carbon isotope composition of terrestrial fossil archives. *Nature Communications* **9**, 252, doi:10.1038/s41467-017-02691-x (2018).
- 10 Potts, R. Variability selection in hominid evolution. *Evolutionary Anthropology: Issues, News, and Reviews* **7**, 81-96, doi:10.1002/(sici)1520-6505(1998)7:3<81::aid-evan3>3.0.co;2-a (1998).
- 11 Athreya, S. & Ackermann, R. R. in *Interrogating Human Origins: Decolonisation and the Deep Past* (eds M. Porr & J. Matthews) (Routledge, 2018).
- 12 Kuljian, C. *Darwin's Hunch: Science, Race and the Search for Human Origins*. 352 (Jacana Media (Pty) Ltd, 2016).
- 13 Schrire, C. An inquiry into the evolutionary status and apparent identity of San hunter-gatherers. *Human Ecology* **8**, 9-32, doi:10.1007/bf01531466 (1980).
- 14 Appadurai, A. Putting Hierarchy in Its Place. *Cultural Anthropology* **3**, 36-49, doi:10.1525/can.1988.3.1.02a00040 (1988).
- 15 Hitchcock, R. K. & Ebert, J. I. Modeling Kalahari Hunter-Gatherer Subsistence and Settlement Systems: Implications for Development Policy and Land Use Planning in Botswana. *Anthropos*, 47-62 (1989).