Holstonia Bigfoot Investigations
Genesis Series No. 9

The Relict Hominin Hypothesis: State of the Scientific Field

Daniel H. Kegley
holstonia-investigations.org
Version of Record: This document constitutes the authoritative version of this work. Please cite the version available at holstonia-investigations.org. Revised editions, if issued, will be explicitly identified.

Dedicated to the memory of Dr. Jeff Meldrum and Dr. Jane Goodall

Introduction

Scientific discussion of alleged “relict hominins” (e.g., Bigfoot/Sasquatch) remains fringe relative to mainstream anthropology and zoology, largely because no *type specimen* or broadly accepted diagnostic biological material has been produced. Even so, a small body of academically affiliated writing has treated the question as (at minimum) an evidentiary and methodological problem—evaluating footprints, ecological plausibility, and the recurring failure of purported biological samples to survive rigorous scrutiny (Napier, 1973; Krantz, 1992; Meldrum, 2006; Daegling, 2004). The most defensible scientific posture is therefore conditional: the hypothesis is testable in principle, but currently underdetermined by admissible physical evidence.

Current research landscape

The modern “state of the field” is best described as a set of partial, disciplinary lenses applied to an unresolved claim.

Ichnology and biomechanics (footprint-centered arguments).
Work by Jeffrey Meldrum is frequently cited for arguing that *some* footprint casts and trackways exhibit internal consistency and biomechanical features (e.g., midfoot deformation, pressure ridges, stride variables) that merit analysis as potential biological traces rather than being dismissed *a priori* (Meldrum, 2004; Meldrum, 2006). Importantly, this line of work does not constitute species confirmation; it is best framed as a claim about *patterned morphology* that—if genuine—would imply an unknown track-maker and justify higher-quality documentation and independent replication.

Anthropological precedent and framing.
Earlier academic treatments (notably Napier and Krantz) approached Sasquatch as a problem spanning folklore, misidentification, hoaxing, and the occasional possibility of an unrecognized primate/hominin—again, without crossing the evidentiary threshold needed for taxonomic acceptance (Napier, 1973; Krantz, 1992). These contributions are most useful today as methodological baselines: what counts as evidence, what confounds recur, and what kinds of claims remain non-falsifiable without better materials.

Wildlife biology and ecological plausibility.
Bindernagel advanced an explicitly biological framing—treating Sasquatch as a hypothetical large omnivore/primate-like mammal occupying a low-density niche in forested landscapes (Bindernagel, 1998, 2010). This is best read as an argument about *ecological feasibility* rather than existence: large mammals can persist at low densities and still be hard to document, especially where detectability is poor and observations are irregular.

Formal niche modeling (a cautionary contribution).
A peer-reviewed ecological niche modeling exercise has been used to illustrate both the allure and the pitfalls of modeling with low-quality occurrence data: models can be generated, but outputs largely mirror input biases and assumptions (Lozier et al., 2009). In a monograph grounded in inference, this is useful as a methodological warning: ecological modeling is only as strong as sampling design, ground-truthing, and error structure.

Genetic investigations (and why standards matter).
The strongest *general* lesson from genetics is procedural: when the target is hominin-adjacent, contamination control, chain-of-custody, transparent methods, and independent replication are non-negotiable. In practice, widely publicized “Bigfoot DNA” claims have not produced a stable, broadly accepted molecular result; published analyses of submitted “anomalous primate” hair samples have instead tended to resolve to known animals (or otherwise fail to support an unknown primate) (Sykes et al., 2014). The field implication is straightforward: absent rigorous protocols and replicable results, genetics cannot function as confirmatory evidence here—it becomes another pathway for ambiguous or contaminated signals.

Consensus and skepticism

The prevailing scientific consensus remains that the claim is unproven because the evidentiary package is incomplete: no type specimen, no validated tissue series, no replicable genomic dataset, and no chain-of-custody materials that survive adversarial review (Loxton & Prothero, 2013; Daegling, 2004). Skeptical literature typically emphasizes (1) the high base rate of misidentification in eyewitness reports, (2) the strong incentive structure for hoaxing and legend-making, and (3) the absence of decisive physical evidence despite decades of public interest (Loxton & Prothero, 2013; Daegling, 2004; Schmitt & Daegling, 1999).

At the same time, some skeptical and pro-hypothesis authors converge on a limited point: footprint claims are the most *structurable* category of evidence—meaning they can be documented, measured, replicated, and compared—though interpretation remains contested (Napier, 1973; Meldrum, 2004; Daegling, 2004).

Emerging trends that change the background assumptions (not the conclusion)

Several developments in adjacent sciences don't "support Bigfoot," but they do weaken overly simple intuitions about what *should* exist in the record.

Late and geographically broad hominin diversity.
Discoveries of late-surviving and regionally distinct hominins demonstrate that hominin diversity persisted later and in more places than older, linear models suggested (Brown et al., 2004; Détroit et al., 2019). Genomic work likewise shows that substantial archaic diversity can be inferred from limited remains once DNA is recovered (Meyer et al., 2012; Reich et al., 2010). This supports a *background plausibility* claim about diversity—not a specific claim about North America.

Sedimentary DNA and presence without bones.
The recovery of hominin DNA directly from sediments shows that organisms can be detected genetically even where skeletal material is absent (Slon et al., 2017). For this monograph's logic, the relevance is methodological: it strengthens the case for non-invasive molecular strategies as a decisive future pathway—if implemented with stringent controls.

Overall assessment (framed as inference)

As of the current literature, the relict hominin hypothesis remains biologically *conceivable* but evidentially *unconfirmed*. The most credible contributions—whether sympathetic or skeptical—tend to share three commitments: (1) treat claims as testable hypotheses rather than settled facts, (2) prioritize evidence types that can be standardized (casts/trackways, chain-of-custody samples, replicable sequences), and (3) avoid cognition/evolutionary narratives that outrun the data. In short, scientific standards still

demand extraordinary evidence; meanwhile, developments in paleoanthropology and genetics remind us that absence of evidence can be ambiguous—but not exculpatory—when detectability is low and sampling is weak (Dennell & Roebroeks, 2005; Slon et al., 2017; Loxton & Prothero, 2013).

This state-of-the-field framing functions as context for the monograph's central stance: proceed by inference, modeling, and falsifiable protocols—while explicitly separating plausibility arguments from confirmation claims.

References

Bindernagel, J. A. (1998). *North America's great ape: The Sasquatch—A wildlife biologist looks at the continent's most misunderstood large mammal*. Beachcomber Books.

Bindernagel, J. A. (2010). *The discovery of the Sasquatch*. Hancock House.

Brown, P., Sutikna, T., Morwood, M. J., Soejono, R. P., Jatmiko, Saptomo, E. W., & Due, R. A. (2004). A new small-bodied hominin from the Late Pleistocene of Flores, Indonesia. *Nature, 431*(7012), 1055–1061.

Daegling, D. J. (2004). *Bigfoot exposed: An anthropologist examines America's enduring legend*. AltaMira Press.

Dennell, R., & Roebroeks, W. (2005). An Asian perspective on early human dispersal from Africa. *Nature, 438*(7071), 1099–1104.

Détroit, F., Mijares, A. S., Corny, J., Daver, G., Zanolli, C., Dizon, E., Robles, E., Grün, R., & Piper, P. J. (2019). A new species of *Homo* from the Late Pleistocene of the Philippines. *Nature, 568*(7751), 181–186.

Krantz, G. S. (1992). *Big foot-prints: A scientific inquiry into the reality of Sasquatch*. Johnson Books.

Lozier, J. D., Aniello, P., & Hickerson, M. J. (2009). Predicting the distribution of Sasquatch in western North America: Anything goes with ecological niche modelling. *Journal of Biogeography, 36*(9), 1623–1628.

Loxton, D., & Prothero, D. R. (2013). *Abominable science!: Origins of the yeti, Nessie, and other famous cryptids*. Columbia University Press.

Meldrum, D. J. (2004). Midfoot flexibility, fossil footprints, and Sasquatch steps: New perspectives on the evolution of bipedalism. *Journal of Scientific Exploration, 18*(1), 65–79.

Meldrum, D. J. (2006). *Sasquatch: Legend meets science*. Tom Doherty Associates.

Meyer, M., Kircher, M., Gansauge, M.-T., Li, H., Racimo, F., Mallick, S., Schraiber, J. G., Jay, F., Prüfer, K., de Filippo, C., Sudmant, P. H., Alkan, C., Fu, Q., Do, R., Rohland, N., Tandon, A., Siebauer, M., Green, R. E., Bryc, K., … Pääbo, S. (2012). A high-coverage genome sequence from an archaic Denisovan individual. *Science, 338*(6104), 222–226.

Napier, J. R. (1973). *Bigfoot: The yeti and Sasquatch in myth and reality*. E. P. Dutton.

Reich, D., Green, R. E., Kircher, M., Krause, J., Patterson, N., Durand, E. Y., Viola, B., Briggs, A. W., Stenzel, U., Johnson, P. L. F., Maricic, T., Good, J. M., Marques-Bonet, T., Alkan, C., Fu, Q., Mallick, S., Li, H., Meyer, M., Eichler, E. E., … Pääbo, S. (2010). Genetic history of an archaic hominin group from Denisova Cave in Siberia. *Nature, 468*(7327), 1053–1060.

Schmitt, D. O., & Daegling, D. J. (1999). Bigfoot's screen test. *Skeptical Inquirer, 23*(3), 20–25.

Slon, V., Hopfe, C., Weiß, C. L., Mafessoni, F., de la Rasilla, M., Lalueza-Fox, C., Rosas, A., Soressi, M., Knul, M. V., Miller, R., Stewart, J. R., Derevianko, A. P., Jacobs, Z., Li, B., Roberts, R. G., Shunkov, M. V., de Lumley, H., Perrenoud, C., Gušić, I., … Meyer, M. (2017). Neandertal and Denisovan DNA from Pleistocene sediments. *Science, 356*(6338), 605–608.

Sykes, B. C., Mullis, R. A., Hagenmuller, C., Melton, T. W., & Sartori, M. (2014). Genetic analysis of hair samples attributed to yeti, bigfoot and other anomalous primates. *Proceedings of the Royal Society B: Biological Sciences, 281*(1789), 20140161.