Emergent Homin Theory

DNA Origins of the Worlds Homins

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Abstract

Three independent DNA studies have corroborated evidence that an archaic Homin has interbreed with Sub Saharan Africans. The Sykes DNA study of Kwhit and Zana's descendants 2012, The MUC 7E Oxford study of Homin introgression, 2017 and the Pan African study, 2019 that concluded not only was there a introgression with an archaic Homin but this Homin interbreed with Neanderthal also. This genetic evidence validates Emergent Homin Theory (EHT). The emergence of a Homin out of Sub-Saharan Africa that interbreed with Homo sapiens, Neanderthal and Denisovan to form the World 's Homin population known as the Russian Snowman, Sasquatch, Woodwose, Yeren, Yeti and Yowie. Overwhelming evidence of footprints, hand prints; video and audio along with direct sightings over centuries are validated by these findings. Artificial Intelligence (AI) through deep genome sequencing algorithms and Environmental eDNA will develop global DNA profiles that will change scientific models. The accumulative value of the DNA studies establishes a base for the scientific study of Hominology. The existence of Zana and her descendants are the living record that this Homin exists today in the modern world.

Recent DNA studies and the discovery of interbreeding by Neanderthal, Denisovan and Homo sapiens have shaped how science is looking at the early interactions of these emergent early Humans. Emergent Homin Theory envisions a third relative to the Homo sapiens genome out of Sub Saharan Africa. A MUC7 (gene unique to our mucous) study was completed in October of 2017 that identified an outlier in Sub Saharan African descendants. A presently unknown (ghost) introgression occurred, identified as MUC7E in Sub Sharan Africans. Haplo group E when compared did not group with Neanderthal or Denisovan and is its own sub group. This is significant, because we now have an unknown (Ghost) Homin out of Sub Saharan Africa and a third introgression that occurred with Homo sapiens unique to Sub Saharan Africa.

Emergent Homin theory proposes Haplo group E as the origin (Y chromosome) of the modern Russian Snowman, Sasquatch, Yeren, Yeti, Yowie and Woodwose of Europe. The theory links the Haplo Group E Homin as the (Y) male progenitor of the major Homin groups globally. The (Y) Homin emerged out of Africa and would later encounter other emergent

Homin groups through abduction, consensual or nonconsensual intercourse interbreeding occurred.

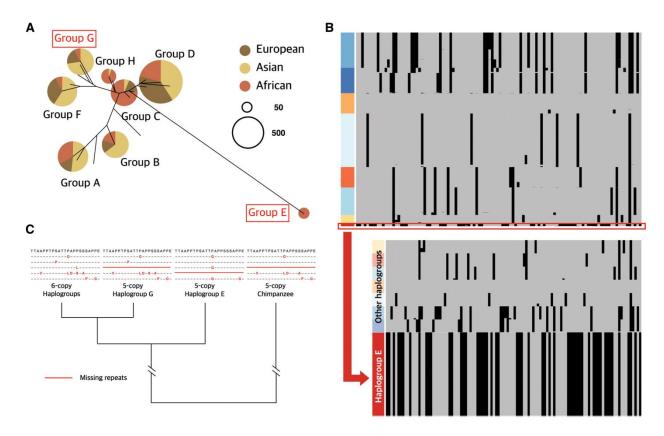
EX: The African Y Homin interbreeding with the Denisovan may represent a hypothetical "Yeren" in China. (See graphic below by Chris Murphy of global stratification)

The modern DNA will consist of variations of this genome with the Homo sapient, Neanderthal and Denisovan admixture and the "unknown" male progenitor being the (Y) Sub Saharan African Homin. This is consistent with DNA of Sub Saharan African MUC7E group introgression. The interbreeding that had occurred historically of Homo sapiens with Neanderthal and Denisovan are the norm and not outliers. Emergent Homin Theory links migration of this Haplo Group E out of Africa as the precursor to the Homo sapiens migration. Just as we have migrated throughout the world the Haplo group E Homin migrated prior to us. This may have occurred as far back as the Pangea period.

The story of Zana (Russian Snowman) is pivotal in the historical records of Emergent Homin Theory. The descendants of Zana are Sub Saharan African (Sykes Study) "Nature of the Beast". These modern descendants should have a comprehensive DNA study completed to assist in the identification of the (Y) Sub Saharan African Homin and then serve as the foundation for the study of Hominology in the scientific community.

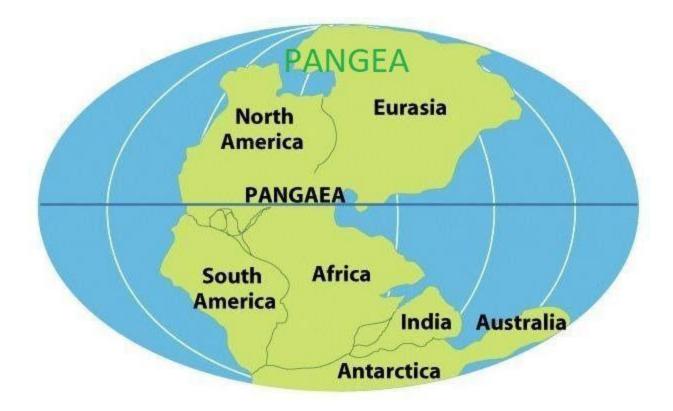


(Christopher Murphy Sasquatch Canada) map of global stratification of Homins and their regional names.



Haplo group E identified as an outlier only existing in Sub Saharan African genome.

The haplo group E (MUC7 E) did not group with Neanderthal or Denisovan and is its own unique introgression in only Sub Saharan Africa. The "Y" male progenitor of haplo group E is the proposed male ancestor of Zana and the global stratification of these Homin. This study identifies a Ghost introgression that occurred within Sub Saharan Africans and is the foundation for Emergent Homin Theory.

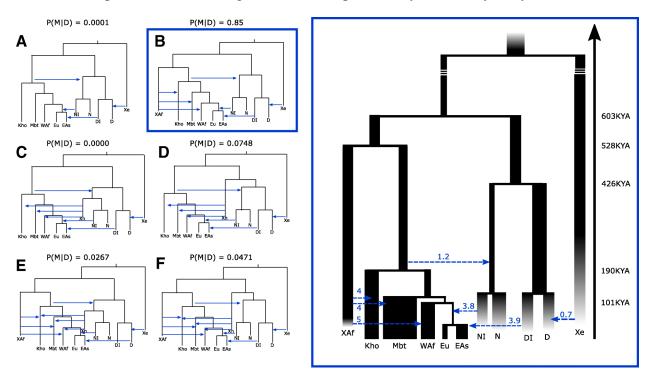


Ancient Homin ancestors 200 million years may have existed in the Pangea period inhabiting all the major continents today. (Large Homin footprints have been found alongside that of Dinosaurs). John Green "The Apes Among us"



Image of Emergent Homin XAf (Black hair) and Hybrid Xn (light haired)

I theorize the XAf Homin to be entirely black or red haired and then the Hybridized with Neanderthal Xn displaying lighter color hair and skin. The Sub Saharan African Ghost progenitor (XAf) would have traveled out of Africa and Hybridized with Neanderthal (Xn). Zana also had equally equivalent Neanderthal genome as many Europeans have. This explains an introgression taking place historically and is genetic proof of Emergent Homin Theory (EHT). The Sub Saharan African genome XAf and Xn are the genetic markers that these Homins have existed in the past and Zana is the genetic link that proves they exist today as hybrids (EHT).



Graph of XAf (slide B) introgression archiac ghost DNA to some Sub Sahran Africans. Confirmation in this new study the XAF and MUC 7E introgression are outliers and support a unknown Homin interbreeding Sub Saharan African Homo sapiens! Link to full study African DNA study Excerpt below for graph

Archaic introgression from known hominins (Excerpt of Pan African Study 2019)

Archaic introgression from either known or unknown extinct hominins has been suggested in different African populations [26, 30, 33, 34, 35, 36, 37, 38, 39]. In our data, we confirmed previous findings [28, 29, 30], as the results of the D-statistics of the form D(X = African population 1, Y = African population 2; Neanderthal/Denisova; Chimpanzee) showed that Eurasian samples as well as North African individuals exhibit a significant enrichment of Neanderthal DNA (higher in East Asia than in West Eurasia or North Africa) when compared to sub-Saharan African samples (Additional file 1: Figure S8.1). Z-score values are generally lower for signatures of Denisovan introgression than for Neanderthal, meaning that a lower proportion of gene flow is observed when admixture has taken place. Asian samples were enriched in archaic DNA from Denisovans, and the European and North African samples too, but at lower levels. This is probably due to the fact that Neanderthal and Denisova are sister groups and consequently share derived alleles that might confound their admixture signals. We found no signals of Neanderthal or Denisovan introgression in the sub-Saharan individuals, which was additionally confirmed with an F4-ratio test for the Neanderthal introgression (Additional file 1: Table S8.1).

Demographic model

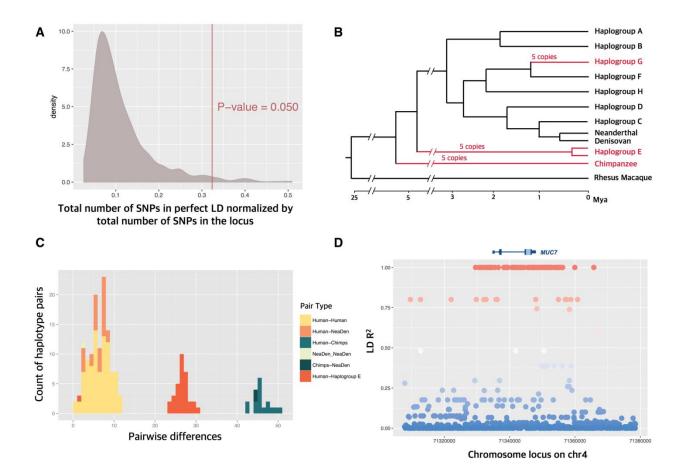
We aimed to explore the impact of recent population admixture on the genetic landscape of sub-Saharan populations in an integrative manner, as well as the presence and nature of archaic introgression from hominin populations. To this end, we conducted an Approximate Bayesian Computation (ABC) analysis coupled to a Deep Learning (DL) framework [50] (Additional file 1: Figure S9.1).

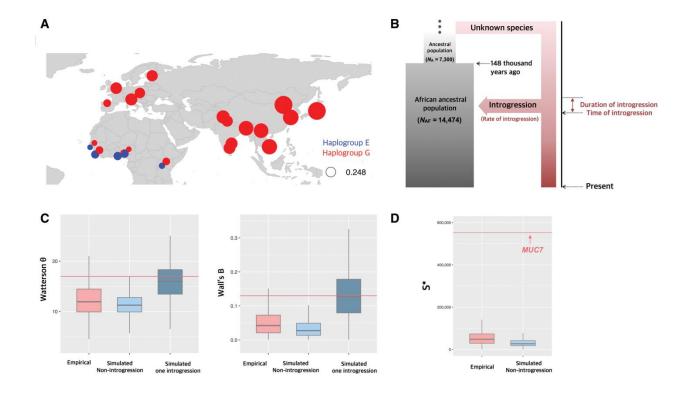
We implemented six demographic models (Fig. 4; Additional file 1: Table S9.1) of increasing complexity from a basic one (model A). Model A summarizes accepted features of human demography [65]: (i) presence of archaic populations out of the African continent, represented by the Neanderthal and Denisovans lineages, (ii) introgression from early anatomically modern humans into Neanderthal [44, 45], (iii) introgression from an extremely archaic population into Denisovans [36], (iv) Khoisans at the root of mankind [11, 14, 15, 16, 17, 18], (v) Out-of-Africa event of AMHs [3], (vi) archaic introgression of a Neanderthal-like population after the Out-of-Africa event in Eurasian populations [30], and (vii) archaic introgression from a Denisovan-like population in East Asians [31]. Furthermore, we included recent migrations between Europeans to West Africans, Europeans to Mbutis, Europeans to Khoisans, West Africans to Mbutis, West Africans to Khoisans, Mbutis to West Africans, Mbuti to Khoisans, and Khoisans to Mbutis. These last parameters, as well as the introgression of the archaic population in Denisovans, can be considered as nuisance parameters. Model B extends model A by adding a "ghost" archaic population, XAf, directly related to the lineage leading to AMHs. In this model, XAf independently inbreeds with each of the AMH African populations. Model C extends A by considering that the ghost archaic population is directly related to the Neanderthal lineage, Xn.

Model D considers that Xn appears in the archaic lineage out of Africa before the Neanderthal and Denisovan split. Model E is a mixture of model B and C. It considers two ghost archaic populations, one that directly split from the lineage that will produce the AMHs and another related to the Neanderthal lineage, both admixing with AMH populations within Africa. Finally, model F mixes the ghost features of models B and D.

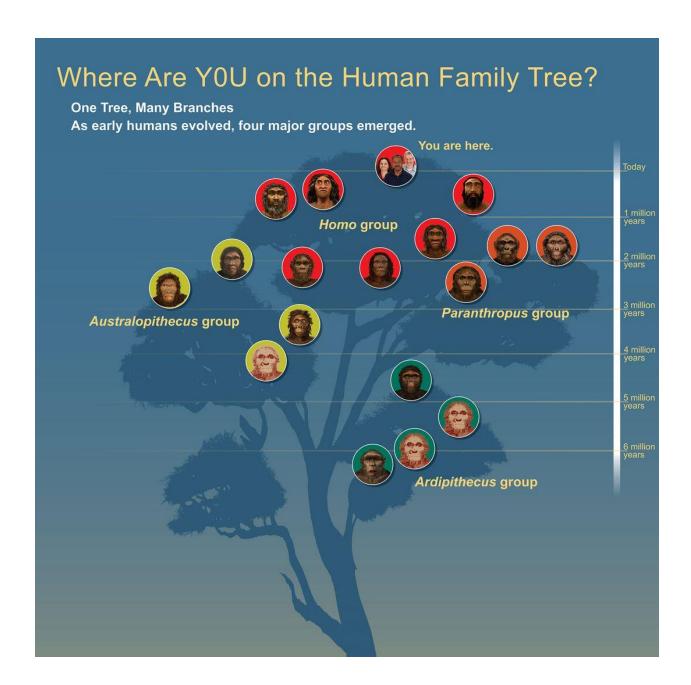
MUC7E Graphs Linked to (XAf) and (Xn) hybrid (Emergent Homin Theory).

Below graph indicates Haplo Group E (Y Male progenitor) between great Apes and Denisovan Neanderthal groups.





The A graph is Haplo Group E (Above graph) Archaic Sub Saharan African Homin Introgression unique to only Sub Saharan Africans. The B graph time line of introgression historically in Sub Saharan Africans.

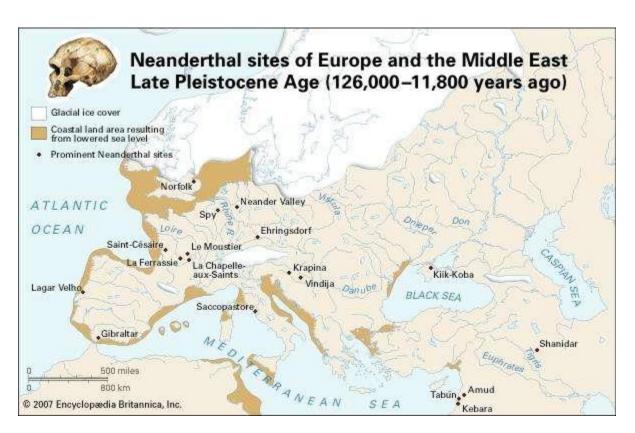


Humans, or *Homo sapiens*, are descended from a complex tree of upright walking ancestors, including species from the genera *Ardipithecus*, *Australopithecus* and *Paranthropus*. (Smithsonian's Human Origins

Program)

Emergent Homin Theory suggests that the modern hybrid Homin , Russian Snowman, Yeti, Yowie, Woodwose and Sasquatch all descend from a Sub Saharan African origin. The Y male progenitor may be one of the Homo group listed above. This previously believed instinct Homin or Ghost introgression maybe alive and well flourishing globally. DNA research using AI algorithms and Environmental eDNA will eventually uncover this connection that I have stated in Emergent Homin Theory with Sub Saharan Africa origins. Other species such as the Ceolacanth were considered extinct for 65 million years only to be found existent in modern times circa 1938.

"We cannot assume all previous animals that are considered extinct are still, they may have remained into modern times undetected by Science." Richard L. Soule



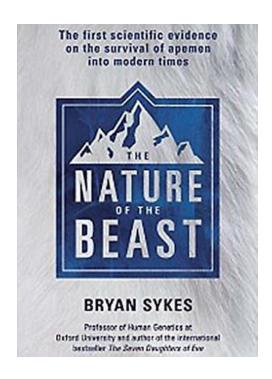
Neanderthal sites where the XAf introgression may have occurred of the Sub Saharan African Ghost genome.

The merging of these three studies provides scientific evidence of Emergent Homin interbreeding in Sub Sahara Africa and it is reflected in the genome stratification through time to the present day. Emergent Homin Theory links these studies to the Dr. Sykes study conducted with Zana and Kwhit's descendants. The genetic match of Sub Saharan Africans and the Emergent Homin that left Africa is compelling evidence that Zana is a descendant of the MUC 7E and XAf/Xn Hybrid ghost introgressions.

The work of Dr. Igor Burtsev who provided the evidence of Zana's descendants along with collaboration of Dmitri Bayanov's research historically of Zana, have bridged the test of time to see the fruition of genetic research uncover this truth. "The Making of Hominology" by Dmitri Bayanov and Christopher Murphy is the catalyst to bring this new science to the forefront of modern genetics. The three independent genetic studies together corroborate scientific proof that the existence of an emergent homin from Sub Sahara Africa is the origin of the worlds Homin's Russian Snowman, Sasquatch, Yeti, Yeren, Yowie and Woodwose.

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- 1) Dr. Bryan Sykes identified a theory that Zana may have descended from an unknown Sub Saharan African Homin. (The Nature of the Beast) Published 2015
- 2) Archaic Hominin Introgression in Africa Contributes to Functional Salivary MUC7 Genetic Variation Molecular Biology and Evolution, Volume 34, Issue 10, 1 October 2017, Pages 2704–2715, https://doi.org/10.1093/molbev/msx206 Published: 21 July 2017
- 3) Whole-genome sequence analysis of a Pan African set of samples reveals archaic gene flow from an extinct basal population of modern humans into sub-Saharan populations David Comas *Genome Biology*2019**20**:7 https://doi.org/10.1186/s13059-019-1684-5 Received: 17 August 2018 Accepted: 28 March 2019
 Published: 26 April 2019
- 4) Research of Dr. Igor Burtsev "In the Footsteps of the Russian Snowman" by Dmitri Bayanov 1996
- 5) <u>The Nox Gigas Study</u> My website that includes additional research of Emergent Homin Author Richard L. Soule