
Scientific Dissenting
Opinion In Support Of
Ronnell Bey's
Status Correction

Indigenous peoples and individuals have the right not to be subjected to forced assimilation or destruction of their culture. (UN Declaration on the Rights of Indigenous Peoples. Article 8(1). 2007)

Prepared by: Tyrone Cannon



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SC Court of Appeals

'Jura sanguinis nullo jure civili dirimi possunt.' - The right of blood and kindred cannot be destroyed by any civil law.¹

American

AMER'ICAN, *noun* A native of America; originally applied to the aboriginals, or copper-colored races, found here by the Europeans; but now applied to the descendants of Europeans born in America.²

Aboriginal

ABORIG'INAL, *adjective* [Latin ab = from and origine = the beginning].

Of or relating to the people who have been in a region from the earliest time : of or relating to aborigines.³

ABORIG'INAL, *adjective* an original or primitive inhabitant. The first settlers in a country are called aboriginals; as the Celts in Europe, and Indians in America.⁴

Autochthon

AUTOCHTHON, *noun* [Gr.] One who rises or grows out of the earth.⁵

¹ Bouvier, Dictionary of Law (1856), Dig. 50, 17, 9; Bacon's Max. Reg. 11.

² Noah Webster, American Dictionary of the English Language (1828).

³ Merriam-Webster, Dictionary by Merriam-Webster (1828).

⁴ Webster, above n 2.

⁵ Ibid.

'Malaria of the Genus Plasmodium was established in the New World at Least 15 Million Years Ago'

One of the most comprehensive analyses yet done of the ancient history of insect-borne disease concludes for the first time that malaria is not only native to the New World, but it has been present long before humans existed and has evolved through birds and monkeys.⁶

Mosquitoes carrying malaria of the genus Plasmodium, the type that causes human illness, were established in the New World at least 15 million years ago, long before modern humans existed. At that time, the disease infected various types of birds.⁷

This information should cause a re-think in relation to how direct-to-consumer genetic testing companies assign so called Sub-Saharan African ancestry. It's currently believed the Duffy Null allele (FY*0 and SNP rs2814778 C allele) has a frequency of almost 100% in Sub-Saharan Africans, but occurs very infrequently in populations outside of this region, and that a person having this allele is thus more likely to have Sub-Saharan African ancestors. However, in my dissenting opinion I disagree, as the National Tree of Peru is in the genus Cinchona. Cinchona is a genus of flowering plants in the family Rubiaceae containing at least 23 species of trees and shrubs. They are native to the tropical Andean forests of western South America. The medicinal properties of the cinchona tree were originally discovered by the Quechua peoples of Peru, Bolivia, and Ecuador. The bark from the cinchona tree was used to treat the symptoms caused by the malaria parasite, which contained quinine, a drug that is still recommended for the treatment of Malaria.

Natural selection is the differential survival and reproduction of individuals due to differences in phenotype. Phenotypic variation (due to underlying heritable genetic variation) is a fundamental prerequisite for evolution by natural selection.⁸

Protection against Plasmodium vivax malaria (P. vivax malaria) is conferred by the Duffy Null Allele or the Duffy Negative Antigen. Of particular note, the Duffy blood group wasn't discovered until 1950. Then, in 1955 many so called African-Americans were found to be resistant to P. vivax malaria, via a paper, titled, "*Experimental testing of the immunity of Negroes to Plasmodium vivax.*" These so called Negroes were Americans! The first paragraph in the paper states, one of the first observations made after this laboratory was established in 1931 was that American Negroes are relatively insusceptible to Plasmodium vivax.⁹

⁶ Oregon State University. "Analysis reveals malaria, other diseases as ancient, adaptive and persistent foes." ScienceDaily. ScienceDaily, 4 November 2011.

<www.sciencedaily.com/releases/2011/11/1111102125650.htm>.

⁷ Ibid.

⁸ R. C. Lewontin, Annual Review of Ecology and Systematics, Vol. 1 (1970), pp. 1-18.

⁹ Martin D. Young, Don E. Eyles, Robert W. Burgess and Geoffrey M. Jeffery, "Experimental Testing of the Immunity of Negroes to Plasmodium vivax", The Journal of Parasitology Vol. 41, No. 3 (Jun., 1955), pp. 315-318.

In the following depiction, Peru is seen offering to Science, via a little dark skinned American aborigine child, a branch from the Cinchona tree, the source of Peruvian bark and an early remedy against malaria. Other Europeans are in the background helping themselves to a cinchona tree.

'Peru offers a branch of cinchona to Science (from a 17th-century engraving) Cinchona, the source of Peruvian bark, is an early remedy against malaria'¹⁰



¹⁰ Rassegna Medica, March-April (No.2) 1955 issue.

Natural selection is the differential survival and reproduction of individuals due to differences in phenotype. Phenotypic variation (due to underlying heritable genetic variation) is a fundamental prerequisite for evolution by natural selection.¹¹

The anthropological genetics of the Black Caribs "Garifuna" of Central America and the Caribbean' states the following: "Blood genetic analyses reveal that the St. Vincent Black Caribs' gene pool contains the highest proportion of Amerindian genes "approximately 50%", while the coastal communities exhibit a more African ancestry "up to 80%". This apparent discrepancy can be explained in one of three ways: "1" the original Black Caribs of St. Vincent had a higher proportion of Amerindian genes. However, gene flow and incorporation of African populations residing along the coast into the Black Carib gene pool resulted in more African coastal groups; "2" those Black Caribs displaying African phenotypes were selectively deported; "3" that natural selection, in a malarial environment, operated in favour of those individuals with the more African phenotypes and resistance to Plasmodium falciparum.¹²

In *'Saint Vincent and The Grenadines - The Mysterious Garifuna'*, the following is stated: 17th and 18th century British sources state that "Black Caribs" had practically exterminated the "Yellow" or "Red" Caribs. French sources advise that the people populating the island are simply Caribs, although there are a small number of people referred to as so called "Black Caribs" who act like other Caribs, but assumed to have some African characteristics in their ancestry largely due to their phenotype. French sources mention them as harder to get along with, but are useful allies in war. To European invaders there was an obvious strain of African appearance among the residents of St. Vincent. There is no legitimate documentation or accounts substantiating SSA introgression by way of a wrecked slave ship in the 1600s. Europeans had nothing to go on but appearance since they agreed that all the islanders behaved in much the same way. The British were in St. Vincent to produce sugar, with the aid of slaves from Africa, so if there were people who acted like Caribs, but had a complexion much darker than the British did, they were assumed to obviously be escaped slaves who needed to be restored to their "proper place". **They tended to see more "Black Caribs" than "Yellow" Caribs.**¹³

So called Black Caribs (Garinagu) are not the descendants of Africans from some shipwreck, they are American aborigines, the descendants of Paleoamericans, serving as perfect examples of natural selection, in a malarial environment, operated in favor of individuals with ancestral phenotypes, misnomered as negroes. The approx. 50% Amerindian genes is evidence of mongoloid introgression.

If *P. vivax* malaria resistance was born in Africa, the scientists would have been studying Africans for resistance to *P. vivax* malaria, not Americans. In my dissenting opinion the resistance to *P. vivax* malaria was born in the Americas, in American aborigines, not Africa, or Africans.

¹¹ Lewontin, above n 8.

¹² M. H. Crawford, *The anthropological genetics of the Black Caribs "Garifuna" of Central America and the Caribbean*, *American Journal of Physical Anthropology* (1983).

¹³ Karl Eklund, *The Mysterious Garifuna, Saint Vincent and the Grenadines* (9 April 2005).

I posit due to the establishment of the genus Plasmodium parasite in the Americas at least 15 million years ago, anatomical modern humans evolved with malaria in situ for their entire existence, and that in fact, if one possess the Duffy Null Allele/Duffy Negative Antigen, he or she is evidence of "Natural Selection", in practice and that the Duffy Null Allele/Duffy Negative Antigen should be reconsidered as an ancestry informative marker (AIM) for American aborigine ancestry.

The percentage of the C (SNP rs2814778; C allele [Duffy null allele]) has been recorded to be much higher amongst some Africans, but not isolated to only Africans.¹⁴

The C allele found in so called African Americans should be reconsidered and viewed as natural selection in situ, and not evidence of Sub-Saharan African (SSA) introgression. There have been reports that the Duffy null allele is under strong selection amongst SSA, but less so amongst other populations, and such a strong positive selection for one population, but not another, whilst experiencing the same environmental pressures is evidence of a link between SSA ancestry and the Duffy null allele. The impact of that conclusion is the over assigning of SSA ancestry by direct-to-consumer genetic testing companies, particularly based on the rs2814778 C allele AIM.

The incidence of rs2814778 C allele being nearly monomorphic amongst SSA and so called African Americans, but not isolated to only the two aforementioned groups is because the subject SNP is relative to pigmentation. In this instance, rs2814778 serves as a phenotypic marker that is associated with pigmentation. This is evidenced by the rs2814778 T allele being dominant amongst European Americans and throughout Europe, possibly due to the absence of selective pressure. Also, it's noteworthy to mention that all populations, from all countries in SSA have not been tested. With that said, it's actually scientifically incorrect to consider rs2814778 C allele to be even "nearly" monomorphic amongst SSA.

Generally speaking, evidence of SSA introgression into the Southeastern states of North America is lacking; unless much assumption, impossible to prove conclusions, "fill in the blank and terribly stretched theory" are being employed. In many instances, genealogical records/documentation does not correlate to the results being issued by direct-to-consumer genetic testing companies. This is a discrepancy that requires further examination. I believe "all" direct-to-consumer genetic testing companies are not only over assigning SSA ancestry, but incorrectly terming it SSA, based on the subject AIM, as well as other pigmentation phenotypical related AIMS.

The Duffy Null allele is under strong selection amongst SSA, but less so amongst other populations due to rs2814778 also being relative to pigmentation. One may ask why rs2814778 isn't prevalent in the tested Papua New Guinean and Melanesian (Oceania) populations. Simple answer, due to α^+ thalassemia . In Papua New Guinea, the risk of severe malaria was found to be reduced by 60% in children who were homozygous for α^+ thalassemia... the Southeast Asian HbE allele confers P. vivax malaria resistance.¹⁵

¹⁴ U. S. National Science Foundation, The Allele Frequency Database (2017).

¹⁵ Dominic P. Kwiatkowski, Am J Hum Genet, How Malaria Has Affected the Human Genome and What Human Genetics Can Teach Us about Malaria, (August 2005), 77(2): 171–192. Published online 2005 Jul 6.

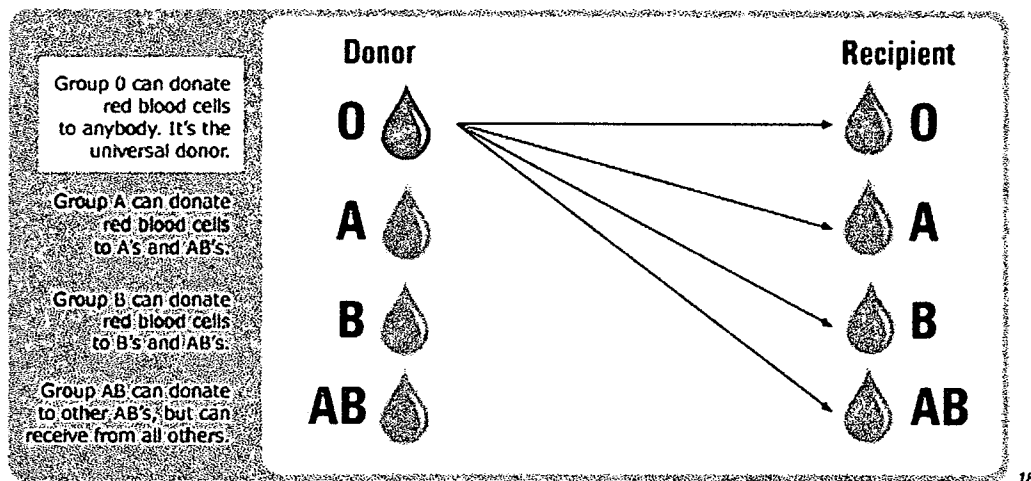
Different populations have developed independent evolutionary responses to malaria, and this is seen at both the global and the local levels. The most striking example is the HBB gene, in which three different coding SNPs confer protection against malaria: Glu6Val (HbS), Glu6Lys (HbC), and Glu26Lys (HbE). The HbS allele is common in Africa but rare in Southeast Asia, whereas the opposite is true for the HbE allele.¹⁶

Blood Group O and Malaria

It has long been known that people with blood type O are protected from dying of severe malaria. In a study published in Nature Medicine, a team of Scandinavian scientists explains the mechanisms behind the protection that blood type O provides, and suggest that the selective pressure imposed by malaria may contribute to the variable global distribution of ABO blood groups in the human population.

A team of scientists led from Karolinska Institutet in Sweden have now identified a new and important piece of the puzzle by describing the key part played by the RIFIN protein. Using data from different kinds of experiment on cell cultures and animals, they show how the Plasmodium falciparum parasite secretes RIFIN, and how the protein makes its way to the surface of the blood cell, where it acts like glue. The team also demonstrates how it bonds strongly with the surface of type A blood cells, but only weakly to type O.

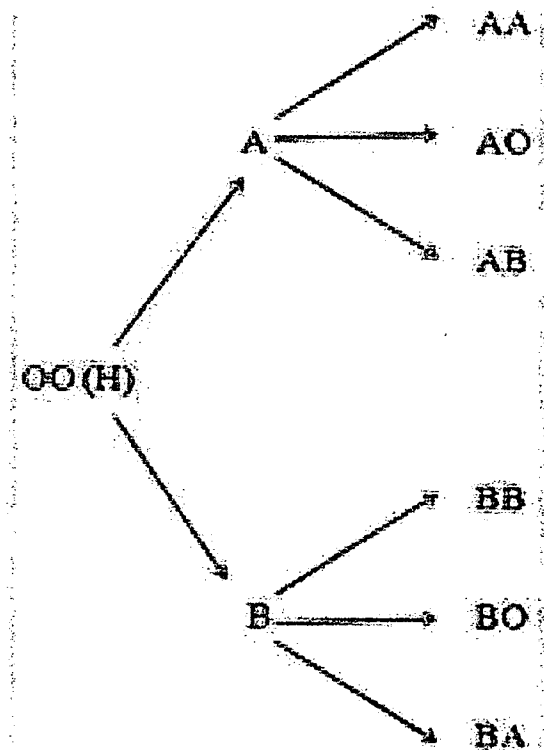
It has long been known that people with blood type O are protected against severe malaria, while those with other types, such as A, often fall into a coma and die.¹⁷



¹⁶ Kwiatkowski, Genet, above n 15.

¹⁷ Karolinska Institute, "How blood group O protects against malaria." ScienceDaily. ScienceDaily, (9 March 2015). <www.sciencedaily.com/releases/2015/03/150309124113.htm>.

¹⁸ American Red Cross, Blood Types, The ABO Blood Group System (2017).



In "A Brief History of Human Blood Groups" the following is stated, ...the emergence of all blood groups A and B and their subgroups, are resulted from successive mutations, from a basic and common blood group, which is the O group, and have been branched over millions of years. According to this hypothesis, the emergence of all blood groups is resulted from successive mutations, from the O group. Based on this theory, the old races have O blood group, such as Red Indians of South America, and Eskimos that among them the frequency of O blood group is between 75–100%. While in most of recent ethnic groups A and B blood groups are dominant...perhaps a few million years ago all people have had type O blood only, which is more resistant against many infectious diseases.¹⁹

Due to malaria of the Genus Plasmodium being established in the new world, at least 15 million years ago, blood type O's protection against severe malaria is evidence of the process of natural selection against environmental factors, such as malaria. As a result of successive mutations, from this basic and common blood type, blood type O can donate red blood cells to any recipient, as it's the universal donor, reflecting how anatomical modern humans evolved with malaria in situ. *The original colonists of North America were a small group of apparently O+ founders...*²⁰

¹⁹ Dariush D Farhud, Marjan Zarif Yeganeh, A Brief History of Human Blood Groups, Iran J Public Health. 2013; 42(1): 1–6. Published online 2013 Jan 1.

²⁰ Jones and Bartlett Publishers, LLC (2011).

Manipulations and Distortions ~ the "Out of Africa" (OOA) Concept

In *Reconsideration of the "Out of Africa" Concept as Not Having Enough Proof*, the following is stated:

- ✚ The OOA concept is based upon experimental data that has been interpreted by OOA concept proponents in a one-sided manner, which is to "prove" the OOA concept, by way of confirmation bias.
- ✚ The evolution (Y-chromosomal) tree produced at least five waves of migrants to Africa (haplogroups A00, A0, A1a, A1b1 and B).
- ✚ Four non-African (by origin) haplogroups are A0-T, A1, A1b and BT.
- ✚ A similar pattern is observed with the mtDNA haplogroup tree, which shows a deep split between African L0 and non-African (by origin) haplogroup L1 – L6.
- ✚ Biased interpretations have been employed to artificially "prove" the OOA concept. The same data can be interpreted as incompatible with the OOA concept and giving support for a "into Africa" concept.
- ✚ Haplogroups A and BT diverged from the same haplogroup, this does not mean that the younger lineage descended from the older. Research shows that they parallel to each other such as two teeth in the proverbial fork. They descend not from each other, but from a common ancestor.
- ✚ Most Europeans and Asians descended from BT, and have not descended from "African" A1b1.
- ✚ Haplogroups BT is very remote time wise from haplogroups A and their subgroups. From the haplotypes analysis it seems that a whole series of haplogroups, namely A00, A0, A1a and A1b1 have moved to Africa from non-African regions, locations of which remain unknown.
- ✚ There have been at least four "into Africa" migrations since some 200,000 years ago (ya) (haplogroup A00), then about 180,000 ya (haplogroup A0), then about 160,000 ya (haplogroup A1a) and then about 70,000 ya (haplogroup A1b1).
- ✚ African and non-African DNA lineages split about 160,000 ya, and there is a large corresponding "genetic" (mutational) distance between them.
- ✚ Non-African DNA lineages did not descend from "African" haplogroups A00, A0 A1a, and A1b1.
- ✚ Haplogroups A1, A1b, and BT did not come "Out of Africa".

- ✚ Perceived weaknesses of the “Cann et al. Study” is as follows: **it used an indirect method of comparing mtDNAs by using a small sample made up largely of African Americans to represent Native African mtDNAs.**
- ✚ The paper designed a new, upgraded African haplogroup/subclade tree with a transition to the non-African part of the tree, that is to CT haplogroup.
- ✚ CT does not come from haplogroup B. B and CT haplogroups have a common ancestor, which is haplogroup BT.
- ✚ Neither BT nor CT descended from “African” haplogroups. However, since the branching points (fork haplogroups) are designated by the authors as “A” (A1a-T, A2-T), the authors consider them as default, the “African” haplogroups, hence, “Out of Africa”.
- ✚ Haplogroup B did not descend from the “African” haplogroups. It descended from their common ancestor.
- ✚ **A recent paper in Nature (Hayden, 2013) presented data regarding two migrations from Eurasia to Khoisan tribes, one 3000 ya to East Africa, another 900 – 1800 ya to South Africa.**
The author did not report which haplogroups were brought to Africa by the migrants. However, there is no doubt that those migrations have increased the “genetic diversity” among Khoisans, which is believed to be the highest in Africa.
- ✚ Sarah Tishkoff, one of the most active proponents of the “Out of Africa” concept, has greeted the “into Africa” new data and called them “making sense”, since archaeological and linguistic studies support it.
- ✚ By definition, anatomical modern humans (AMH) were Homo sapiens who did not have noticeable archaic skeletal features. All African excavated skeletal remains dated before 36,000 ya possess noticeable archaic features. Unfortunately, radiocarbon dating practically do not work on times more than 40,000 years.
- ✚ Some dating discrepancies are as follows: A dating by Professor Reiner Protsch of 36,000 ya turned out to be 7500 ya. Another dating 21,300 ya occurred in fact 3300 ya, and a skeleton dated by Protsch by 29,400 ya happened to be that of a man who died in 1750, 225 years before.
- ✚ All announcements on discoveries of skeletal remains of AMH older than 50 kya, and more so, older than 150 kya, in the sub-Saharan area, are distorted or incorrect in the first place. All of them expose rather noticeable archaic features. A good overview of this issue was recently published in ‘Advances in Anthropology’ by Australian anthropologist Robert Bednarik. A number of studies tell of absence of such findings from south of the Sahara (e.g., Grine et al., 2007; Grine et al., 2010).

- ✚ All known oldest fossils, such as Omo Kibish 1 (195 kya, Ethiopia, fragments of skull with the face, very incomplete), Omo-2 (having a number of primitive features), Herto (the Middle Awash region, 160 – 154 kya, very robust and thus distinguishable from AMH), dated between 200 – 100 kya, possess archaic features (Rightmire, 2009) and cannot be considered AMH.
- ✚ Neither the Herto hominins, nor others from Late Pleistocene sites such as Klasies River in southern Africa and Skhu_1/Qafzeh in Israel, can be matched in living populations. Skulls are quite robust, and it is only after ~35,000 years ago that people with more gracile, fully modern morphology make their appearance.
- ✚ Hominins with a combination of archaic and modern features persist in the fossil record across sub-Saharan Africa and the Middle East until after ~35 kya. In other words, multiple references by proponents of the “Out of Africa” concept that many fossils of AMH were found in Africa with dates between 200 and 160 kya, are at least questionable, if not untrue.
- ✚ **Many loose ends remain. Yet one thing is clear: the roots of modern humans trace back to not just a single ancestral population in Africa but to populations throughout the Old World.**
- ✚ **The most alarming is the fact that the concept did not have any proof, it was based on lies, fantasies, conjectures and wishful thinking.**
- ✚ **Overall, there is not any anthropological or archaeological proof of appearance of anatomically modern human in Africa, or the “Out of Africa” migration.**²¹

In *'The Making of the African mtDNA Landscape'*, the following is stated:

“...L1c, is estimated at 60,000 years old... Haplogroup L1c is less starlike than L1a and L1b, with three major well-defined subclades and high internal diversity. The geographic distribution of L1c is especially interesting. More than one-third of L1c haplotypes in our database belong to African Americans, and few of them show matches with continental Africans...”

In *'Certain Aboriginal Remains of the Alabama River; Classics in Southeastern Archaeology, pg 135'*, the following is stated: “Crania were so badly decayed, crushed or penetrated by roots that but two were preserved. These two, found near together, close to the bluff, belonged to singularly well-preserved skeletons. One, of a male (Collection Academy of Natural Sciences, No. 2,168) seems to partake strongly of the negro type. Its companion, however (Collection Academy of Natural Sciences, No. 2,169), shows marked artificial flattening. Adair tells us that the Choctaws practised flattening of the skull...”

²¹ Anatole A. Klyosov, Reconsideration of the “Out of Africa” Concept as Not Having Enough Proof, The Academy of DNA Genealogy, Newton, USA, Advances in Anthropology (2014). Vol.4, No.1, 18-37, Published Online February 2014.

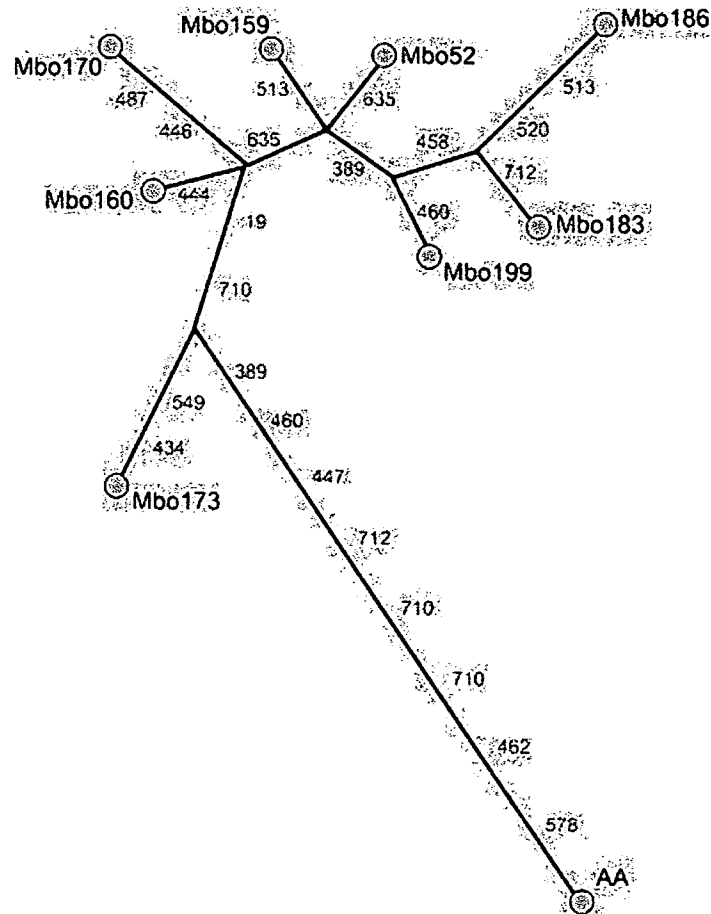
'An African American Paternal Lineage Adds an Extremely Ancient Root to the Human Y Chromosome Phylogenetic Tree'

"We report the discovery of an African American Y chromosome that carries the ancestral state of all SNPs that defined the basal portion of the Y chromosome phylogenetic tree."

"The A00 lineage was discovered in a large database of consumer samples of African Americans and *has not been identified in traditional hunter-gatherer populations from sub-Saharan Africa.*"

"A median-joining network shows that the African American A00 lineage is 11 mutational steps from the nearest Mbo and that the maximum difference between any pair of Mbo is nine steps"

"We also estimated the level of variation among nine A00 lineages (i.e., including one additional Mbo individual) by using a battery of 95 Y-STRs for which all individuals had no missing data. A median-joining network shows that the African American A00 lineage is 11 mutational steps from the nearest Mbo and that the maximum difference between any pair of Mbo is nine steps."



The above illustration shows how genetically distant the American's A00 is in comparison to the Mbo's A00, by way of an 11 step mutational difference.

"Genotyping of a DNA sample that was submitted to a commercial genetic-testing facility demonstrated that the Y chromosome of this African American individual carried the ancestral state of all known Y chromosome SNPs."

"We identified 11 Y chromosomes that were invariant and identical to the A00 chromosome at five of the six Y-STRs (2 of the 11 chromosomes carried DYS19-16, whereas the others carried DYS19-15)."

"These 11 chromosomes were all found in a sample of 174 (~6.3%) Mbo individuals from western Cameroon. Seven of these Mbo chromosomes were available for further testing, and the genotypes were found to be identical at 37 of 39 SNPs known to be derived on the A00 chromosome"

"Although we identified the A00 lineage in an African American, the unusual Y-STR profile associated with this individual's Y chromosome allowed us to identify the same divergent lineage in a single ethnic group living in a small region of western Cameroon. Interestingly, contrary to previous Y chromosome and mtDNA studies, we did not identify the most basal lineage in a traditional hunter-gatherer population, such as the Khoisan or Pygmies." (ScienceDirect, 'An African American Paternal Lineage Adds an Extremely Ancient Root to the Human Y Chromosome Phylogenetic Tree' (Volume 92, Issue 3, 7 March 2013, Pages 454-459).

The Y chromosome of this American carries the ancestral state of all known Y chromosome SNPs. It didn't say the Mbo's Y chromosomes carries the ancestral state of all known Y chromosomes, it said the American individual carries the ancestral state of all known Y chromosome SNPs. This is evidence of what was thought to be the oldest populations in the world (Khoisan and Pygmies) are in fact predated by the American's A00. To reiterate, "the unusual Y-STR profile associated with this individual's Y chromosome allowed us to identify the same divergent lineage in a single ethnic group living in a small region of western Cameroon." If A00 is Mbo derived Y-DNA lineage, it should be that the Mbo's Y chromosome allowed them to identify the same divergent lineage in an American. The American A00 allowed them to identify "similarities" in a small region of western Cameroon. This is representative of this being an American lineage.

When researchers found that Albert Perry's Y-chromosome carries the ancestral state of all SNPs that defined the basal portion of the Y chromosome phylogenetic tree, Mike Hammer of the University of Arizona was contacted, he subsequently contacted some colleagues in the UK, who searched their huge database of African samples, to see if any of them matched the American A00 sample. They found similarities, all from Cameroon. It's reported that allegedly the STR haplotype of A00 is extremely unusual; therefore, very easy to see that the Mbo samples were matches to the Perry sample. However, there were never matches, just similarities, evidenced by 11 step mutational difference and matches at 37 of 39 SNPs known to be derived on the A00 chromosome.

Identifying chromosomes at five of the six Y-STRs, particularly when 9 of the 11 chromosomes didn't match at allele 'DYS19', is not a match at all. Also, only six Y-STRs is not a sufficient haplotype. Twelve is a better number of short tandem repeats for a more informational haplotype. They had samples from 174 Mbo individuals, but were only able to identify similarities in 11 chromosomes,

respectively 11 out of 174, which is only 6.3% of the Mbo samples. If A00 origins were in fact with the Mbo people, A00 would more than likely be endemic to the Mbo, but it's not. Then it goes on to state, "Seven of these Mbo chromosomes were available for further testing, and the genotypes were found to be identical at 37 of 39 SNPs known to be derived on the A00 chromosome". This actually means that only 7 out of the 174 Mbo samples were identical at 37 of 39 SNPs. This does not denote that the American A00 and the Mbo A00 are the same or that they are the same people and surely doesn't equate to the American A00 deriving from the Mbo. In fact, the evidence equally suggests the opposite.

The ancestor of Albert Perry and the ancestor of the Mbo men split up a long time ago; however, Perry's ancestor must have split up before the Mbo men. Perry's Y-chromosome is the most basal lineage of A00.

The lack of dense sampling in so called African Americans has contributed to the failure to identify more A00 positive samples in North America.

New Evidence Puts Man in North America 50,000 Years Ago

"Radiocarbon tests of carbonized plant remains where artifacts were unearthed last May along the Savannah River in Allendale County by University of South Carolina archaeologist Dr. Albert Goodyear indicate that the sediments containing these artifacts are at least 50,000 years old, meaning that humans inhabited North American long before the last ice age."

"Topper is the oldest radiocarbon dated site in North America," Goodyear says. "However, other early sites in Brazil and Chile, as well as a site in Oklahoma also suggest that humans were in the Western Hemisphere as early as 30,000 years ago to perhaps 60,000."

"Three radiocarbon dates were obtained from deep in the terrace at Topper with two dates of 50,300 and 51,700 on burnt plant remains. One modern date related to an intrusion," Stafford says. "The two 50,000 dates indicate that they are at least 50,300 years. The absolute age is not known."

"The dates could actually be older," Goodyear says. "Fifty-thousand should be a minimum age since there may be little detectable activity left."²²

The Topper excavation site is in the central Savannah River Valley of Allendale County, South Carolina. A popular assumption in some scientific circles is anatomically modern humans (AMH) evolved in Africa between 60,000 and 80,000 years ago. Evidence of AMH migration out of the African continent has been documented in Australia and Central Asia at 50,000 years and in Europe

²² Science Daily, 'New Evidence Puts Man In North America 50,000 Years Ago' (18 November 2004). <<https://www.sciencedaily.com/releases/2004/11/041118104010.htm>>.

at 40,000 years. The fact that AMH were also in North America at or near the same time highlights the fallacy of the OOA concept.

In *Lapa Vermelha IV Hominid 1: Morphological Affinities of The Earliest known American*, by Walter A. Neves, Joseph F. Powell, Andre Prous, Erik G. Ozolins and Max Blum, the following is stated:

- ❖ “In this work the extra-continental morphological affinities of a Paleo-American skeleton well dated between 11,000 and 11,500 years before present (Lapa Vermelha IV Hominid 1, or “Luzia”) is investigated.”
- ❖ “The first South Americans show a clear resemblance to modern South Pacific and African populations, while the first North Americans seem to be at an unresolved morphological position between modern South Pacific and Europeans. In none of these analyses the first Americans show any resemblance to either northeast Asians or modern native Americans.”
- ❖ “In the first case, Lapa Vermelha IV Hominid 1 exhibited an undisputed morphological affinity firstly with Africans and secondly with South Pacific populations.”
- ❖ “The results obtained clearly confirm the idea that the Americas were first colonized by a generalized Homo sapiens population which inhabited East Asia in the Late Pleistocene, before the definition of classic Mongoloid morphology.”
- ❖ “The analysis allows us to conclude that Lapa Vermelha IV Hominid 1 presents a strong similarity firstly with Africans and secondly with South Pacific populations. No resemblance was found between Lapa Vermelha IV Hominid 1 and either Asians or Late Holocene American Indians.”
- ❖ “The results obtained in this work confirm our previous findings that the first Americans have no special biological resemblance to modern northern Asians. The oldest human skeleton of the Americas ***shows a strong similarity*** with modern Africans and Australians.”



Lapa Vermelha IV Hominid 1 ("Luzia") was morphologically reconstructed by Richard Neave, University of Manchester (One of the world's leading forensic artists.) He had this to say about the reconstruction:

"That to me is a Negroid face. It has all the features that you associate with a Negroid face."



Professor Constantine Samuel Rafinesque the Primitive Black Nations of America. 1832

By Professor C. S. Rafinesque
Atlantic Journal and Friend of Knowledge
1833 Indians

The Society of Geography having offered a reward for the best memoir on the Origin of the Asiatic Negroes, I sent them last year two Mémoires; one on those Asiatic Negroes, wherein I demonstrated the affinities of their languages with the African and Polynesian Negroes, as well as with the Hindus and Chinese, and renders it probable that all the Negroes originated in the Southern Slopes of the Himalaya Mountains, as they did once exist all over India, South China, Japan, Persia and Arabia.

My second Memoir was on the Negro or Black Nations, found in America before Columbus, wherein I proved their existence and connection by language with the Negroes of Africa and Polynesia. These Memoirs have been rewarded by the learned Society of Geography, with a gold medal of 100 Francs, which was lately communicated to me by Messrs Warden, our former Consul in Paris, and Jomard member of the Institute. This gratifying intelligence will be acceptable to all my friends, and furnish another proof of my ability to unravel at last, the origins of all the American Nations and Tribes, in pursuing the path which I have opened, by comparing all the Languages mathematically and numerically with each other.

To many, this fact of old Black Nations in America will be new, yet it is an important feature of American History, as well as the existence of primitive White Nations there still more numerous. To furnish a kind of insight into this subject. I will here merely enumerate the Black tribes of which I have found evident traces and remains in North and South America."The Native American Negroes or black Indians have been seen in Brazil, Guyana, Caraccas, Popayan, Choco, North California and etc:

- ✠ The Aroras or Caroras of Cumana, were black, but with fine features and long hair, like the Jolofs and Gallas of Africa.
- ✠ The Esteros latitude 32, are like the Hottentots and the Numuquas, Tambukis, and many other Nigritian tribes, not black, but dark brown, yet complete Negroes, with large thick lips, broad flat noses, and very ugly, with hair crisped or curly. All these tribes live in New California. The Aroras or Caroras of Cumana, were black, but with fine features and long hair, like the Jolofs and Gallas of Africa.
- ✠ The American Negroes of Quarenqua, in Choco, (the great level plain 900 miles long, 90 wide, separating the Andes of South America from the mountains of Panama,) were black and with woolly heads in 1506. They are mentioned by Dangleria, and all the early accurate writers.
- ✠ The Yemasees or Jamasi were remarkably Black people Notices of Florida and the Campaigns;
- ✠ The Ancient Caracoles of Hayti, represented as a Nation of Beasts by the Historical Songs.

- ✚ The Califurnams of the Carib Islands, called Black Caribs or Guauini by others, are a black branch of Caribs.
- ✚ The Arquahos of Cutara mentioned by Garcias in the West Indies, quite black.
- ✚ The Aroras of Raleigh or Yaruras of the Spaniards, ugly black or brown Negroes, yet existing near the Oronoco, and language known, called Monkeys by their neighbors. The Chaymas of Guyana, brown Negroes like Hottentots.
- ✚ The Manjipas and Porcigis of Nienhof, the Motayas of Knivet are all of Brazil, brown Negroes with curly hair.
- ✚ The Nigritas of Martyr in Darien, yet existing in Choco under the name of Chuanas or Gaunas or Chinos (Dariente). Ugly black or red Negroes.
- ✚ The Manabies of Popayan (in Columbia) blackish with Negro features and hair.
- ✚ The Guabas and Jaras of Tagugalpa (Tegucigalpa) near the Honduras. The Enslens or Esteros of New California, ugly blackish Negroes.
- ✚ The black Indians met by the Spaniards in Louisiana in 1543.
- ✚ The Moon-eyed Negroes, and Albinos, destroyed by the Cherokees, and seen in Panama."

In '*The Human Species*', by A. DE Quatrefages, Professor of Anthropology in the Museum of Natural History, Paris c. 1879, in part he states the following:

- ❖ "The Equatorial current of the Atlantic opens a similar route leading from Africa to America, and there are some evidences, rare it is true, showing that wrecks have been carried in this direction. It is possible, therefore, that the same may also have happened to man."
- ❖ "We shall not, therefore, be surprised at finding in the New World representatives of races which seem to belong originally to the Old World; we shall easily understand the multiplicity of American races, which is perhaps still contested by some of Morton's followers, but firmly established in the opinion of every unprejudiced person by the testimony of Humboldt and d'Orbigny's classical work on L'Homme Americain."
- ❖ "Black populations have been found in America in very small numbers only, and as isolated tribes in the midst of very different nations. Such are the Charruas of Brazil, the black Carabees of Saint Vincent in the Gulf of Mexico, the Jamassi of Florida, the dark-complexioned Californians, who are perhaps, the dark men mentioned in Quiche traditions, and by some old Spanish adventure."

"Their features are coarse, broad, and of a dark chocolate color." (Taylor, in Cal. Farmer, Nov 2, 1860.)

"Ugly, stupid and savage; otherwise they are well formed, tolerably tall, and of a dark brown complexion. The women are short and very ugly; they have much of the Negro in their countenance."

"They all have a very savage look, and are of a very dark color." (Chamisso in Kotsebie's voy., vol iii., p. 47.)

"At Santa Clara they are of a blackish color, they have flat faces, thick lips and black, coarse, straight hair." (Kotzebue's New Voy., vol. ii., p. 98)

"At Placerville they are most repulsive-looking wretches. They are nearly black, and are exceedingly ugly." (Borthwick's Three Years in Cal., p. 128)

"In Yosemite Valley they are very dark colored." (Wonders of Yosemite, p. 52)

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"And speaking of the Californian Indians, in general, they are of the middling, or rather of a low stature, and of a dark brown color, approaching to black...large projecting lips, and broad, flat, negro-like noses,...bear strong resemblance to the negroes." (Langsdorff's Voy., vol. ii., pp. 194-5, 164)

"Low foreheads and skin as black as Guinea negroes." (Domenech's Deserts, vii. i., p. 85)

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"Skin of such a deep reddish-brown that it seems almost black." (Figuier's Human Race, p. 493; Buschauen Spuren des Aztek, Sprache p. 528, Forbes' Cal., pp. 180-3, Harper's Monthly, vol. xiii., p. 538)

Found in *'The History of Hernando De Soto and Florida; Records of the Events of Fifty-Six Years, from 1512 to 1568', by Barnard Shipp* are descriptions of the American aboriginal people they first encountered along the Atlantic coast of North America.

'Chapter V' – "The Voyage of Juan Verazzani Along The Atlantic Coast of North America, 1524"

"The complexion of these people is black, not that much different from that of Ethiopians. Their hair is black and thick, and not very long; it is worn tied back upon the head in the form of a little tail. They are not very strong in body, but acute in mind, active and swift of foot, as far as we could judge by observation. In these two particulars they resemble the people of the east, especially those most remote. This is the first account of the Indians of this part of the Atlantic coast, and is much the same as that given by later voyagers. This young man remarked that these people were black, like the others; that they had shining skins, middle stature, and sharper faces, and very delicate bodies and limbs, and that they were inferior in strength, but quick in their minds."

- ❖ “It is evident that the more or less pure black elements have been brought from the Asiatic Archipelagos and from Africa through some accident at sea; they have there mixed with the local races, and have formed those small isolated groups which are distinguished by their colour from surrounding tribes.”

In *'The De Soto Chronicles: The Expedition of Hernando De Soto to North America in 1539-1543, Volume I – Concerning a Battle That The Spaniards Fought With The Indians Of The Coast'*, in part the following is stated:

- ❖ “On the last day, after noon, they saw seven canoes emerge from among some rushes and come toward them. In the first one came an Indian as large as a Philistine and as black as an Ethiopian, very different in color and appearance from those that they had left in the interior.”
- ❖ “Standing in the bow of his canoe, the Indian said to the Castilians in a gruff and haughty voice: “Thieves, vagabonds, idlers without honor or shame, who go along this shore disturbing its natives, you are to leave this place immediately by one of those two mouths of this river, if you do not want me to kill all of you and burn your boats. See that I do not find you here tonight, or not a man of you will escape with his life.”
- ❖ “Here Juan Coles adds the following words that the Indian spoke, besides those already given: “If we had large canoes like yours (he meant the ships), we would follow you to your country and take it, for we also are men like you.”

Found in *“The Native Races of the Pacific States of North America”, by Hubert Howe Bancroft (1874)* are descriptions of the phenotypes, of American aborigine people of Central California.

pg. 364 – Californians

“A nose depressed at the root and somewhat wide spreading at the nostrils, a large mouth, with thick prominent lips, teeth large and white, but not always regular, and rather large ears, is the prevailing type. Their complexion is much darker than that of the tribes farther north, often being nearly black; so that with their matted, bushy hair, which is frequently cut short, they present a very uncouth appearance.”

pg. 365 – Physical Peculiarities

“At Bodega Bay ‘they are an ugly and brutish race, many with Negro profiles.” (Id., p. 103)

“They are physically an inferior race, and have flat, unmeaning features, long, coarse, straight black hair, big mouths and very dark skin.” (Revere’s Tour., p. 120)

“Their complexion is a dark mahogany, or often nearly black, their faces round and square, with features approximating nearer to the African than the Indian.”

Skin pigmentation as an Ancestry Informative Marker (AIM)

99.9% of everyone's DNA is identical. Everything that makes us unique is concentrated in less than one one-thousandth of our genes. Only a small handful of genetic signatures are more common in some human populations than in others. This information is used to predict what geographic location people's ancestors come from. These predictions are *statistical guesses*.²³

SNP rs1426654 influences skin pigmentation. The allele, A111T, rs1426654(A), indicates light-skinned European ancestry.²⁴ It appears as if this SNP is a relatively new one in human evolution; one estimate is that the rs1426654(A) allele, in other words, light skin pigmentation, spread through the European population around 6,000 - 12,000 years ago. Prior to that, "European ancestors" were most likely relatively brown-skinned.²⁵ Another study has concluded that almost all individuals carrying the A111T [rs1426654(A) / light-skinned European ancestry] variant can trace ancestry back to a single person who most likely lived at least 10,000 years ago.²⁶ This SNP is one of three from the SLC24A5 gene that can be analyzed to categorize the ancestry of a person as European, African, or Asian, based on a 2009 study.²⁷ SNP rs1426654 (A;A) denotes probably light-skinned, European ancestry. SNP rs1426654 (A;G) denotes mixed European + (African or Asian) ancestry possible. SNP rs1426654 (G;G) denotes probably darker-skinned, Asian or African ancestry.²⁸

SNP rs1426654 (G;G) probably denoting darker-skinned, Asian or African ancestry is evidence that direct-to-consumer genetic testing companies using this SNP as an AIM for African ancestry is flawed and requires rethinking because at the subject SNP, it is currently not clear if it represents dark skin in Africans or Asians. SNP rs1426654 should not be utilized as an AIM for African ancestry. The aforementioned further supports, that possessing dark skin is being used to classify American aborigines, ancestrally as African. Africa does not have a patent on phenotype and Africa surely is not the only geographical location that is home to dark skinned people that were in situ from the earliest of times.

"Variations in human pigmentation are the most obvious phenotypes to distinguish individuals. It has been recently shown that the variation of a G in an A allele of the coding single-nucleotide polymorphism (SNP) rs1426654 within SLC24A5 gene varies in frequency among several population samples according to skin pigmentation. Because of these observations, the SLC24A5 locus has been

²³ Science NetLinks, 'Genes and Geography' (2017). <<http://sciencenetlinks.com/science-news/science-updates/genes-and-geography/>>.

²⁴ NCBI, 'Population differences of two coding SNPs in pigmentation-related genes SLC24A5 and SLC45A2' (18 July 2006). <<https://www.ncbi.nlm.nih.gov/pubmed/16847698?dopt=Abstract>>; NCBI, 'SLC24A5, a putative cation exchanger, affects pigmentation in zebrafish and humans' (16 December 2005). <<https://www.ncbi.nlm.nih.gov/pubmed/16357253?dopt=Abstract>>.

²⁵ NCBI, 'Genetic evidence for the convergent evolution of light skin in Europeans and East Asians' (2007). <<https://www.ncbi.nlm.nih.gov/pubmed/17182896?dopt=Abstract>>.

²⁶ NCBI, 'Molecular phylogeography of a human autosomal skin color locus under natural selection' (2013). <<https://www.ncbi.nlm.nih.gov/pubmed/24048645?dopt=Abstract>>.

²⁷ NCBI, 'Haplotypes in SLC24A5 Gene as Ancestry Informative Markers in Different Populations' (2008). <<https://www.ncbi.nlm.nih.gov/pubmed/19440451?dopt=Abstract>>.

²⁸ SNPedia, 'rs1426654' (3 September 2017). <<https://www.snpedia.com/index.php/Rs1426654>>.

evaluated as Ancestry Informative Region (AIR) by typing rs1426654 together with two additional intragenic markers (rs2555364 and rs16960620) in 471 unrelated individuals originating from three different continents (Africa, Asia and Europe). This study further supports the role of human SLC24A5 gene in skin pigmentation suggesting that variations in SLC24A5 haplotypes can correlate with human migration and ancestry. Furthermore, our data do reveal the utility of haplotype and combined unphased genotype analysis of SLC24A5 in predicting ancestry and provide a good example of usefulness of genetic characterization of larger regions, in addition to single polymorphisms, as candidates for population-specific sweeps in the ancestral population.”(<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2674805/>)

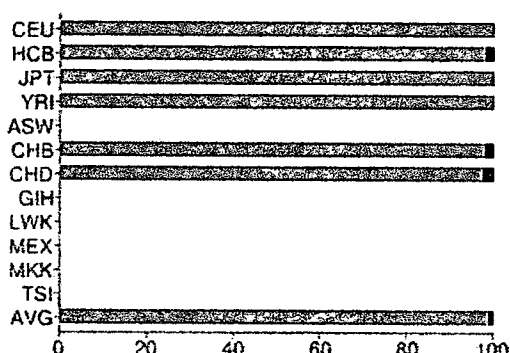
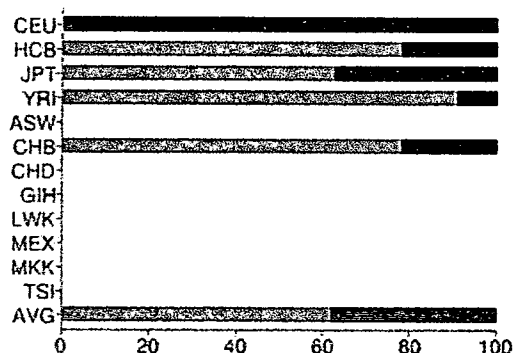
“An ancestry informative marker (AIM) is a human polymorphism that exhibits substantially different frequencies among populations. The data arising from single SNP approach demonstrated a **non-full effectiveness of rs1426654 as ancestry informative marker because of its inability to well discriminate between Asians and other populations.**”
 (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2674805/>)

“In order to improve the effectiveness of rs1426654 also in discrimination of Asian population we decided to type two new informative flanking SNPs (rs2555364 and rs16960620) other than the rs1426654 in 471 unrelated individuals originating from three different continents (Africa, Asia and Europe).”(<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2674805/>)

As previously stated, SNP rs1426654 should not be utilized as an AIM for African ancestry, due to its inability to well discriminate between Asians, Africans and other populations in general. To overcome this non-full effectiveness of rs1429954 as an AIM, scientists decided to type two new informative flanking SNPs (rs2555364 and rs16960620). Both SNPs rs2555364 and rs16960620 are used to categorize the ancestry of a person as European, African, or Asian. However, the discriminatory power of these two new informative flanking SNPs also represent non-full effectiveness, as seen in the following population diversity boxes (*snpedia.com*), they too are unable to accurately predict the ancestral backgrounds of samples, which results in further **statistical guesses.**

rs2555364 (C;C) (C;G) (G;G)

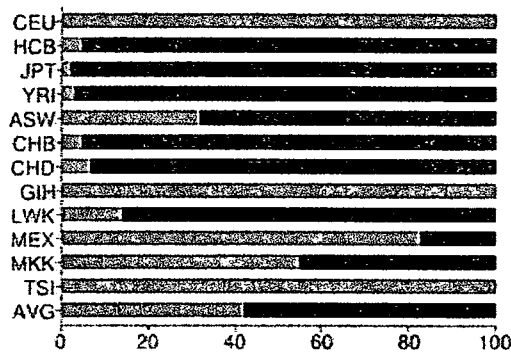
rs16960620 (A;A) (A;G) (G;G)



The interpretation of the content found in the population diversity boxes are as follows: In the population diversity box representing the frequency of SNP rs2555364 across different populations, the first line indicates 100% of the 180 samples from Utah residents with Northern and Western European ancestry have the (G;G) genotype. The second line indicates approximately (approx.) 25% of the 90 samples from Han Chinese in Beijing, China have the (C;C) genotype, approx. 53% have the (C;G) genotype and approx. 22% have the (G;G) genotype. The third line indicates 20% of the 91 samples from Japanese in Tokyo, Japan have the (C;C) genotype, 40% have the (C;G) genotype and 60% have the (G;G) genotype. The fourth line indicates that 50% of the 180 samples from Yoruba in Ibadan, Nigeria have the (C;C) genotype, 40% have the (C;G) genotype and 10% have the (G;G) genotype. The fifth line indicates African ancestry in Southwest USA population did not report data. The sixth line indicates the same data as the second line, HCB and CHB are the same thing. Lines seven to twelve indicate those populations did not report data.

In the population diversity box representing the frequency of SNP rs16960620 across different populations, the first line indicates 100% of the 180 samples from Utah residents with Northern and Western European ancestry have the (A;A) genotype. The second line indicates 70% of the 90 samples from Han Chinese in Beijing, China have the (A;A) genotype, approx. 28% have the (A;G) genotype and approx. 2% have the (G;G) genotype. The third line indicates 75% of the 91 samples from Japanese in Tokyo, Japan have the (A;A) genotype and 25% have the (A;G) genotype. The fourth line indicates that 95% of the 180 samples from Yoruba in Ibadan, Nigeria have the (A;A) genotype and 5% have the (A;G) genotype. The fifth line indicates African ancestry in Southwest USA population did not report data. The sixth line indicates the same data as the second line, as HCB and CHB are the same thing. Lines seven to twelve indicate those populations did not report data. The seventh line indicates 75% of the 100 samples from Chinese in Metropolitan Denver, Colorado have the (A;A) genotype, 20% have the (A;G) genotype and 5% have the (G;G) genotype. Lines eight to twelve indicate those populations did not report data.

rs1426654 (A;A) (A;G) (G;G)



In the population diversity box representing the frequency of SNP rs1426654 across different populations, the first line indicates 100% of the 180 samples from Utah residents with Northern and Western European ancestry have the (A;A) genotype. The second line indicates 3% of the 90 samples from Han Chinese in Beijing, China have the (A;G) genotype and 97% have the (G;G) genotype. The third line indicates approx. 2% of the 91 samples from Japanese in Tokyo, Japan have the (A;G) genotype and approx. 98% have the (G;G) genotype. The fourth line indicates that 5% of the 180 samples from Yoruba in Ibadan, Nigeria have the (A;G) genotype and 95% have the (G;G) genotype. The fifth line indicates approx. 33% of the 90 samples of African ancestry in the Southwest USA have the (A;G) genotype and approx. 67% have the (G;G) genotype. The sixth line indicates the same data as the second line, HCB and CHB are the same thing. The seventh line indicates approx. 7% of the 100 samples from Chinese in Metropolitan Denver, Colorado have the (A;G) genotype and approx. 93% have the (G;G) genotype.

The mathematical average of all samples, across different populations for SNP rs2555364, for the (C;C) genotype is approx. 25%, approx. 35% for the (C;G) genotype and approx. 40% for the (G;G) genotype. This explains that across the given populations, there is quite a variance and the frequencies do not provide great explanatory power for predicting ancestry, with the exception being 100% of the 180 samples from Utah residents with Northern and Western European ancestry have the (A;A) genotype. SNP rs2555364 (G) allele is monomorphic amongst the 180 people sampled, which supports the use of rs2555364 (G) allele as an AIM for predicting Northern and Western European ancestry, but certainly not for predicting Asian and American aborigine ancestry.

The mathematical average of all samples, across different populations for SNP rs16960620, for the (A;A) genotype is approx. 82%, approx. 19% for the (A;G) genotype and approx. 1% for the (G;G) genotype. SNP rs16960620 (A) allele is nearly monomorphic across all populations. Although 100% of the 180 samples from Utah residents with Northern and Western European ancestry have the (A;A) genotype, other populations possess in excess of 70% for the (A;A) genotype, particularly the 180 samples from Yoruba in Ibadan, Nigeria, which is approx. in excess of 95%.

The mathematical average of all samples, across different populations for SNP rs1426654, for the (A;A) genotype is approx. 25%, approx. 20% for the (A;G) genotype and approx. 55% for the (G;G) genotype. 58% of the samples across different populations for SNP rs1426654, the (G;G) genotype is at over an 80% occurrence.

In order to improve the effectiveness of rs1426654's ancestry predicting power, two new informative flanking SNPs (rs2555364 and rs16960620) were typed with rs1426654. However, the combination study of the three aforementioned SNPs as AIMs have failed to discriminate between Asians, Africans and other populations in general; therefore, cannot be relied upon to provide the level of explanatory power that is required to accurately predict a person's ancestry as African and correlate with human migration.

*“Although many efforts have been made first with STRs markers and then with SNPs, **currently used AIMs are not 100% accurate for predicting ancestral background of samples** especially for individuals with a mixed ancestral background.”* (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2674805/>). This is particularly applicable for American aborigines.

Emigration from the United States Corporation to Sierra Leone and Liberia (West Africa)

Largely speaking, American aborigines are being erroneously classified as predominately West African, by direct-to-consumer genetic testing companies. As an example of this major fallacy in practice, please find below the control populations utilized by 23andMe to represent West African ancestry.

Population	Source	Sample Size
Sierra Leone	23andMe	173
Luhya	1000 Genomes	97
Yoruba	1000 Genomes	24
Yoruba	HGDP	24
Mandenka	HGDP	24
Bantu	HGDP	20
Nigeria	23andMe	11
Ghana	23andMe	11
Ivory Coast	23andMe	2
Cameroon	23andMe	1
Liberia	23andMe	1

In relation to the aforementioned control populations having similar allele frequencies to so called African Americans, this highlights the so called introgression of West African ancestry into the genomes of so called African Americans. However, I posit that at least 63% of the samples in the control populations are in fact, ancestrally American, not African, with the remaining 37% showing similar allele frequencies due to having similar skin pigment and hair color. As an example, Luhya in Webuye, Kenya are classified as a Niger-Congo population and are Bantu-speaking. The Coriell Institute states "It may be scientifically appropriate to pool data from these samples with data from other ancestrally related groups, when the data show that the groups have similar allele frequencies." In this instance, the similar allele frequencies are due to having similar skin pigment, not because of being ancestrally related, as there is no significant amount of genealogical records to substantiate an ancestral link between American aborigines and Luhya in Webuye, Kenya.

Further evidence of the generality around American aborigines having allele frequencies in common with 23andMe's West African controls is the population, "Bantu". Bantu is a general term for over 400 different ethnic groups. They inhabit a geographical area stretching east and southward from Central Africa across the African Great Lakes region down to Southern Africa

1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities. It emphasizes that this is essential for ensuring transparency and accountability in the organization's operations.

2. The second part of the document outlines the various methods and tools used to collect and analyze data. It highlights the need for consistent data collection procedures and the use of advanced analytical techniques to derive meaningful insights from the data.

3. The third part of the document focuses on the role of technology in data management and analysis. It discusses how modern software solutions can streamline data collection, storage, and processing, thereby improving efficiency and reducing the risk of errors.

4. The fourth part of the document addresses the challenges associated with data security and privacy. It stresses the importance of implementing robust security measures to protect sensitive information and ensure compliance with relevant regulations.

5. The fifth part of the document provides a detailed overview of the data analysis process, from data cleaning and preprocessing to the final interpretation of results. It includes several examples of common data analysis techniques and their applications.

6. The sixth part of the document discusses the importance of data visualization in communicating complex information. It explores various visualization tools and techniques, such as charts, graphs, and dashboards, and provides guidance on how to design effective and user-friendly visualizations.

7. The seventh part of the document concludes by summarizing the key findings and recommendations of the study. It emphasizes the need for ongoing monitoring and evaluation of data management practices to ensure their continued effectiveness and relevance.

In 1791, Thomas Peters, a so called African American who had served in the Black Pioneers, went to England to report the grievances of the so called black population in Nova Scotia. Some of these so called African Americans were ex-slaves who had escaped to the British forces who had been given their freedom and resettled there by the Crown after the American Revolution. During his visit, Peters met with the directors of the Sierra Leone Company and learned of proposals for a new settlement at Sierra Leone. Despite the collapse of the 1787 colony, the directors were eager to recruit settlers to Sierra Leone. Lieutenant John Clarkson, RN, who was an abolitionist, was sent to Nova Scotia in British North America to register immigrants to take to Sierra Leone for a new settlement. In close proximity to Nova Scotia is Newfoundland, which at a point in the past, was termed Terranova. Nova Scotia once was part of the Terranova region.

In *Africans and Native Americans, the Language of Race and the Evolution of Red-Black Peoples*, by Jack D Forbes, he states the following: "In 1501, Miguel Corte Real sailed back to the Terranova region, where he disappeared. One of his ships returned to Portugal, with 'certain men and women whom he found'. In 1503 the Portuguese sent out two ships and thereafter the Newfoundland area was visited regularly, so much so that in 1506 a royal tax was imposed on the fishing catch. Slaves from Terranova show up in the slave-markets of Seville and Valencia very soon after 1500. In Valencia during the period to 1516, we find in 1503 Miguel (age 20) and Manne (age 10); in 1505 Juan (16) and Pedro (16); in 1507 Antonio (8) and Juan Amarco (18); in 1515 Ali, now Melchor (20); in 1516 Catalina (28). These eight slaves were, with one exception, all obtained from Portuguese sources. **They were all classified as negros** with the exception of Juan and Pedro, called simply slaves. In Seville, between 1510 and 1515, some 13 Terranova slaves were registered and sold, including: in 1510 Isabel (age 20), Cristobal (age 20), Virgida (17); in 1511 Pedro (20), Anton (25), Felipa (14); in 1512 Pedro (25), Catalina (18), Anton (25); in 1513 Fernando (20) and Maria (25); in 1514 Francisca (14), and in 1515 Maria (20). **Two of these slaves were categorized as negro**, one as loro, and ten as slaves only. In 1525 a Spaniard, Esteban Gomez, made a voyage up the Atlantic coast of North America, bringing back 'many Indians' as slaves. Interestingly, between 1548 and 1560, some 20 slaves from Terranova appeared in Peru (out of 256 who can be identified geographically in the records). Between 1560 and 1650 about 143 slaves from Terranova showed up in Peru, coming by way of Iberia probably. An additional 11 were classified as bozales (a slave, recently brought to a colony from Africa). The location of Terranova has heretofore been a matter of debate, with writers generally placing it somewhere on the west coast of Africa. On the other hand, there is very strong evidence that Terranova was, at least in the first half of the sixteenth century, Newfoundland.

Tired of the harsh weather and racial discrimination in Nova Scotia, more than 1,100 former American slaves chose to go to Sierra Leone. They sailed in 15 ships and arrived in St. George Bay between February 26 – March 9, 1792. The Nova Scotians were to build Freetown on the former site of the first Granville Town, where jungle had taken over since its destruction in 1789. Its surviving Old Settlers had relocated to Fourah Bay in 1791. At Freetown, the women remained in the ships while the men worked to clear the land. Lt. Clarkson told the men to clear the land until they reached a large cotton tree. After the work had been done and the land cleared, all the Nova Scotians, men and women, disembarked and marched towards the thick forest and to the cotton tree, and their preachers (all so called African Americans) began singing "Awake and Sing of Moses and the Lamb."

In 1800, the Nova Scotians rebelled. The British authorities used the arrival of 500 Jamaican Maroons to suppress the insurrection. Thirty-four Nova Scotians were banished and sent to either the Sherbro or a penal colony at Gore. Some of the Nova Scotians were eventually allowed back into Freetown. After the Maroons captured the Nova Scotian rebels, they were granted their land. Eventually the Maroons had their own district, which came to be known as Maroon Town. European forces were yet again playing different types of American aborigines against one another. (https://en.wikipedia.org/wiki/Sierra_Leone.2016)

Liberia

In the United States, there was a movement to resettle free-born so called blacks and freed slaves who faced legislated limits in the U.S. corporation with the belief that so called blacks would face better chances for freedom in Africa than in the U.S. corporation. The American Colonization Society (ACS) was founded in 1816 in Washington, DC for this purpose, by a group of prominent politicians and slaveholders; however, its membership grew to include mostly people who supported abolition of slavery. Slaveholders wanted free people of color to leave the South, where they were thought to threaten the stability of the slave societies. Some abolitionists collaborated on relocation of free so called blacks, as they believed they would never be accepted in the larger society. Most so called African Americans, who were native-born (*aborigines*) by this time, wanted to work toward justice in the U. S. corporation rather than emigrate. In turn, some free so called blacks were ready to try a different environment.

In 1822, the ACS began sending so called African American volunteers to the Pepper Coast to establish a colony for freed so called African Americans. By 1867, the ACS assisted in the migration of more than 13,000 so called African Americans to Liberia. These free so called African Americans and their descendants married within their community and came to identify as Americo-Liberians. Many were educated in American culture. The Americo-Liberian settlers did not identify with the indigenous peoples they encountered, especially those in communities of the more isolated "bush." They knew nothing of their cultures, languages or animist religion. Encounters with tribal Africans in the bush often developed as violent confrontations. The colonial settlements were raided by the Kru and Grebo from their inland chiefdoms. Because of feeling set apart and superior by their culture and education to the indigenous peoples, the Americo-Liberians developed as a small elite that held on to political power. Because of ethnocentrism and the cultural gap, the Americo-Liberians envisioned creating a western-style state to which the tribesmen should assimilate. They encouraged religious organizations to set up missions and schools to educate the indigenous peoples. (<https://en.wikipedia.org/wiki/Liberia>.2016)

The aforementioned supports that it is very likely at least 48% of the samples in the West African control populations are in fact ancestrally American, not African, with the remaining 52% showing similar allele frequencies, due to having similar skin pigment and hair color.

Yoruba

Yoruba, a group located in Nigeria, West Africa, has long been used as a proxy for Sub-Saharan African ancestry, and more specifically West African ancestry. Found in an article, titled 'Nigerian Man Connects with African American and Caribbean Cousins Through AncestryDNA', the following is stated by the author: "...After some time, he was reminded of the missing stories in his family history when he began to ponder on why family members on his mother's side had foreign surnames such as Da Rocha, Haastrup, and Doherty." "I remember asking my mother why they had such names. Much later, though, I found out that Ilesha [the capital city of my home region in Nigeria] was significantly impacted by the slave trade especially in the late 1700s and early 1800s. I remember her saying that they were Saro and that we had Saro families. I didn't know much about what that meant until much later. Saro is Yoruba for Sierra Leone. They must have been returning family members who were captives released by the British via Sierra Leone."

As documented, 'Saro' is Yoruba for Sierra Leone and per evidence, 'Saro' were freed slaves who emigrated to Nigeria, from North America, via Sierra Leone, in the beginning of the 1830s. As previously shown, Sierra Leone was first settled in 1787 by 400 formerly enslaved dark skinned people, sent from London, England, under the auspices of the "Committee for the Relief of the Black Poor", an organisation set up by Jonah Hanway and the British abolitionist, Granville Sharp. These dark skinned people were largely Americans from North America and the Caribbean. Those born in Britain are very likely the descendants of more recent Americans, freed from bondage in North America, and more historically, Americans that were kidnapped in the 15th and 16th centuries, and subsequently sold into slavery, appearing in European slave markets, listed as "Negroes" (Africans and Native Americans, *The Language of Race and the Evolution of Red-Black Peoples*). Saros also settled in other West African countries such as Ghana.

The very widely used sample population known as 'Yoruba in Ibadan, Nigeria [YRI]' were prepared from blood samples collected in a particular community in Ibadan, Nigeria. (catalog. Coriell.org.2017) The Saro mostly resided in the Lagos Colony, with substantial populations in Abeokuta and Ibadan. (Lorand Matory: *The English Professors of Brazil: On the Diasporic Roots of the Yoruba Nation*, *Comparative Studies in Society and History*, Vol. 41, No. 1, Jan., 1999, p 89.) If 'YRI' is actually or largely composed of 'Saro' ancestry, this should not be a proxy for so-called Sub-Saharan African ancestry, but moreover, it should be considered a proxy for American aborigine ancestry.

The aforementioned supports that it is very likely at least 82% of the samples in the West African control populations are in fact ancestrally American, not African, with the remaining 18% showing similar allele frequencies, due to having similar skin pigment and hair color.

Ronnell Bey's Genetic Analysis in Support of American Aborigine Status

Mosquitoes carrying malaria of the genus *Plasmodium*, the type that causes human illness, were established in the New World at least 15 million years ago. The Duffy blood group was discovered in 1950. In 1955 many so called African-Americans were found to be resistant to *P. vivax* malaria, via a paper, titled, "*Experimental testing of the immunity of Negroes to Plasmodium vivax.*" These so called Negroes were Americans! It is believed the Duffy Null allele has an alleged frequency of almost 100% in some Sub-Saharan populations, but occurs very infrequently in populations outside of this region, and that a person having this allele is thus more likely to have Sub-Saharan African ancestors. *P. vivax* malaria resistance was not born in Africa. Scientists weren't studying Africans for resistance to *P. vivax* malaria, they were studying American aborigines. The resistance to *P. vivax* malaria was born in the Americas, in American aborigines, not Africa, or Africans.

Populations	Ronnell
● Sub-Saharan African	87.9%
● West African	86.5%
● Central & South African	0.6%
● Broadly Sub-Saharan African	0.9%

American aborigine ancestry, misnomered 'Sub-Saharan African', represented as 87.9% of Ronnell Bey's genome, reflects the original groups that populated the Americas.

*American aborigine ancestry,
misnomered 'West African',
represented as 86.5% of
Ronnell Bey's genome, reflects
the original groups that
populated the Americas.*

Due to the establishment of the genus Plasmodium parasite in the Americas at least 15 million years ago, anatomical modern humans evolved with malaria in situ for their entire existence, and that in fact, if one possess the Duffy Null Allele with signals of introgression from Austronesians, Mongoloids and contemporary Europeans, he or she is evidence of "Natural Selection", in practice and that the Duffy Null Allele should be reconsidered as an ancestry informative marker (AIM) for American aborigine ancestry.

*American aborigine ancestry,
misnomered 'Central & South
African', represented as 0.6%
of Ronnell Bey's genome,
reflects the original groups that
populated the Americas.*

Central Africa extends from the Central African Republic at its north to Angola at its south. Southern Africa encompasses Namibia, South Africa, Botswana and Zimbabwe. While the majority of its population is now composed of Bantu peoples, Central Africa is also home to many Pygmy populations. Southern Africa was first peopled by Pygmies, San and Khoisan. These hunter-gatherer populations still live in this region today.²⁹ There are no genealogical records, oral family history or stories that would substantiate an ancestral link between Ronnell Bey and any of the aforementioned African groups. This statistical guesswork is derived from allele frequencies in common, due to skin and hair color similarity.

American aborigine ancestry, misnomered 'Broadly Sub-Saharan African', represented as 0.9% of Ronnell Bey's genome, reflects the original groups that populated the Americas.

²⁹ Ancestry Composition Reports, 23andme (2017).

Ronnell Bey's Genetic Analysis in Support of Austronesian and Mongoloid Introgression

In 'The first great seafarers: DNA from ancient skeletons reveals the Polynesians may have come from Taiwan 5,000 years ago'³⁰, the following is stated:

"The scientists say there was almost no Papuan ancestry in the genomes of the four ancient remains they analysed. This suggests that the Papuan people must have arrived on the islands at a later date and mixed with the people who were already living there around 500 to 1,100 years ago."

^	● East Asian & Native American	0.4%
	● Southeast Asian	0.1%
	● Native American	0.3%
	● Broadly East Asian & Native American	0.0%

Per autosomal genetic analysis, conducted by 23andme, Ronnell Bey broadly speaking possesses 0.4% East Asian & Native American ancestry.

Ronnell Bey more specifically possesses 0.1% Southeast Asian ancestry, 0.3% Native American ancestry and 0.0% Broadly East Asian & Native American ancestry.

The Southeast Asian and Native American ancestry in Ronnell Bey's genome serves as signals for ancient seafaring Austronesian and Mongoloid introgression. This suggests that Mongoloids and ancient seafaring Austronesians must have arrived in the Americas at a later date and interbred with Ronnell Bey's ancestors who were already living in the Americas. Introgression from Austronesians represented as 0.4% Southeast Asian is reflective of this ancestry appearing in Ronnell Bey's genome, "longer ago", but clearly after his American aborigine ancestors were already living in the Americas.

³⁰ Daily Mail Australia, 'The first great seafarers: DNA from ancient skeletons reveals the Polynesians may have come from Taiwan 5,000 years ago' (4 October 2016). < <http://www.dailymail.co.uk/sciencetech/article-3819651/The-great-seafarers-DNA-ancient-skeletons-reveals-Polynesians-come-Taiwan-5-000-years-ago.html>>.

East Asian and Native American ancestry, represented as 0.4% of Ronnell Bey's genome, reflects Austronesian introgression.

According to sound genomic data, the following information and trends have been captured. (Tyrone Lewis Cannon.2017)

- ❖ 318 out of 351 so called African American genomes possess Southeast Asian ancestry, **90.5%**.
- ❖ 309 out of 351 so called African American genomes possess Native American ancestry, **88%**.
- ❖ 350 out of 351 so called African American genomes possess East Asian and Native American ancestry, **99.7%**.
- ❖ 347 out of 351 so called African American genomes possess Nonspecific East Asian and Native American ancestry, **98.8%**.

The National Geographic Genographic Project states the following:

- ❖ 'Native American and Southeast Asian ancestry' – "The mixture of regions reflected here is due to the original groups that populated the Americas."
- ❖ Bougainville-Nasioi (Oceania) possesses Southeast Asian ancestry. "The Southeast Asian component was introduced over the past several thousand years by seafaring Austronesians, who hailed from Southeast Asia. These are believed to be the ancestors of the Polynesians, who settled in Bougainville before heading out into the open waters of the Pacific."
- ❖ Malagasy (Madagascar) possesses Southeast Asian ancestry. "The Southeast Asian ancestry reflects migratory groups arriving by boat from Austronesia."
- ❖ Mexican-Americans possess Southeast Asian ancestry. "The Southeast Asian ancestry here reflects original groups that populated the Americas."

- ❖ Ni-Vanuatu (Vanuatu) possesses Southeast Asian ancestry. “The Southeast Asian component was introduced over the past several thousand years by seafaring Austronesians, who hailed from Southeast Asia. These are believed to be the ancestors of the Polynesians, who settled in Vanuatu before heading out into the open waters of the Pacific.”
- ❖ Papuan (Papua New Guinea) possesses Southeast Asian ancestry. “The Southeast Asian component was introduced over the past several thousand years by seafaring Austronesians, who hailed from Southeast Asia. These are believed to be the ancestors of the Polynesians, who settled on the northern coast of New Guinea before heading out into the open waters of the Pacific.”

Denisovan and African Ancestry

The Denisovan hominin is an extinct species of human in the genus Homo. In March 2010, scientists announced the discovery of a finger bone fragment of a juvenile female who lived about 41,000 years ago. The remains were found in the remote Denisova Cave in the Altai Mountains in Siberia. This cave also shows evidence of being inhabited by Neanderthals and anatomical modern humans. In November 2015, a tooth fossil containing DNA was reported to have been found and studied. A bone needle dated to 50,000 years ago was discovered at the archaeological site in 2016 and is described as the most ancient needle known. Excavations have since revealed human artefacts showing an intermittent presence going back 125,000 years.

The following depictions are outputs from Gedmatch of a Denisovan ancestry composition. As seen in all three programs, the output shows substantial amounts of African ancestry. This is very interesting when one takes into account the timeframe captured by ancestry composition (approx. 500 to 1,100 years ago) and zero evidence of Denisovans ever being in Africa or a part of Africa’s fossil record.

The “World9 Admixture Proportions” program, show African ancestry predicted as high as 96%! This is very interesting, because Denisovans were never in Africa.

The “World9 Oracle Results” have used ‘modern’ populations to show single population sharing between these groups and the Denisovan sample. The genetic distance ranges from 3 generations to 75 generations. Three generations for the very broad grouping, “Bantu” and 75 generations for the very specified group, “Ethiopian Jews”.

World9 Admixture Proportions

The World9 admixture calculator is courtesy of Dienekes Pontikos and was developed as part of the Dodecad/Ancestry Project. [more](#)

Kit Number: F999903 Iteration: 1000 Delta-Q: 1.225931e-02 Elapsed Time: 59.49 seconds

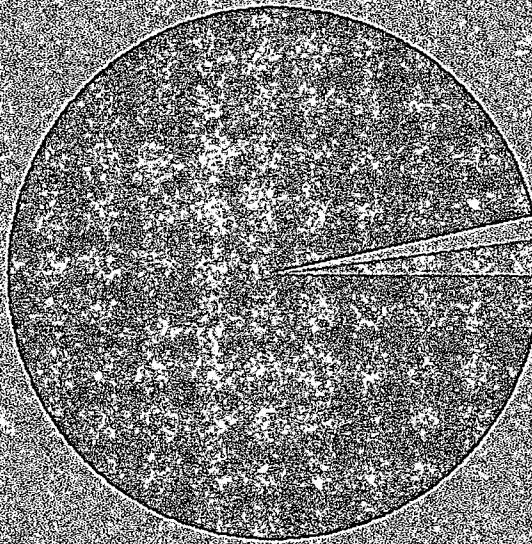
Population	
Amerindian	0.13%
East_Asian	0.08%
African	96.46%
Atlantic_Baltic	1.31%
Australasian	1.92%
Siberian	0.08%
Caucasus_Gedrosia	-
Southern	-
South_Asian	-

Oracle

Oracle-4

Oracle-x.Type 1

Oracle-x.Type 2



World9
F999903

African
Atlantic_Baltic
Australasian

GEDmatch.com

"Genetic analysis of the fossil revealed it apparently belonged to a little girl with dark skin, brown hair and brown eyes..."³¹

"The researchers will only conclude that Denisovans likely had dark skin. They also note that there are alleles "consistent" with those known to call for brown hair and brown eyes."³²

"A higher quality Denisovan genome published in 2012 reveals variants of genes in humans that are associated with dark skin, brown hair and brown eyes - consistent with features found with Melanesians today."³³

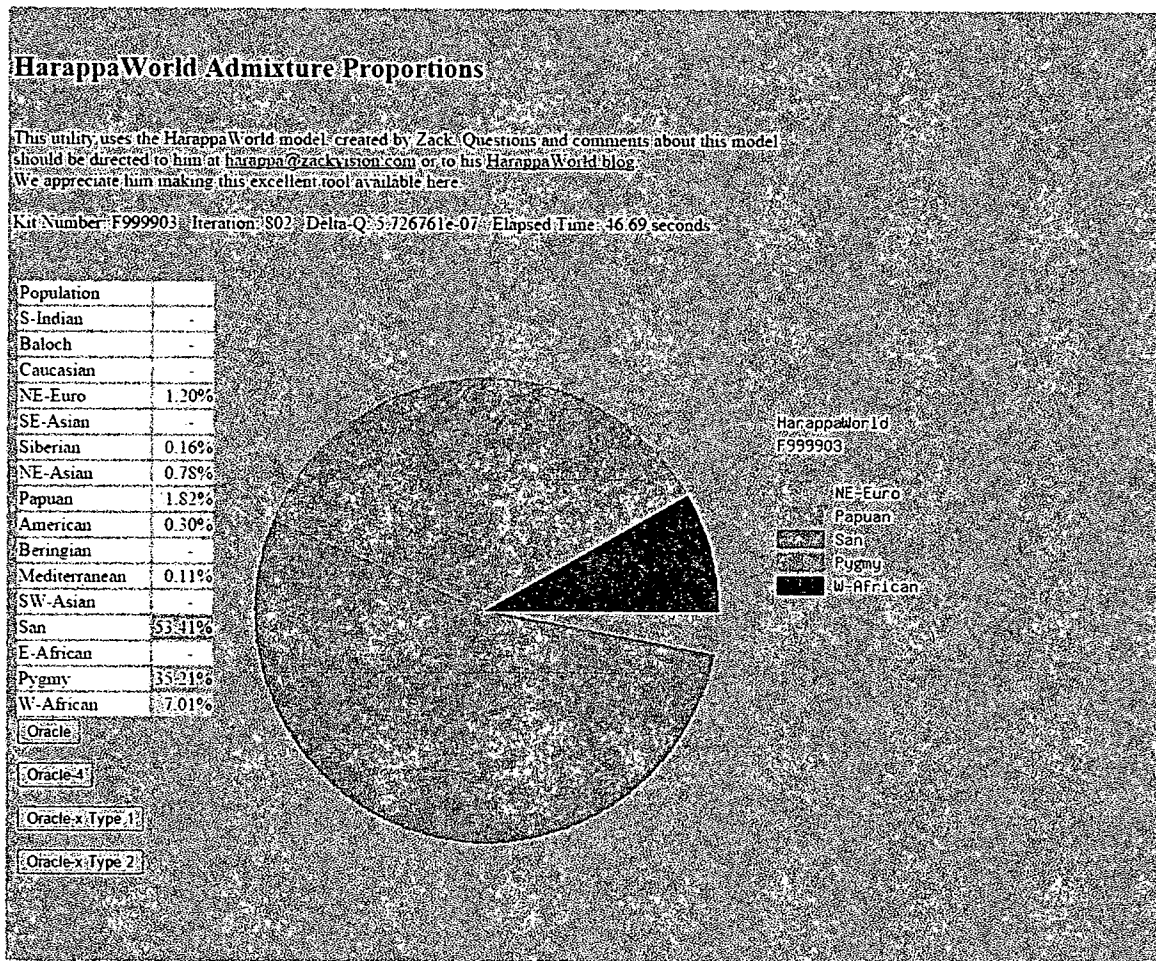
³¹ Live Science, 'Genome of Mysterious Extinct Human Reveals Brown-Eyed Girl' (30 August 2012).

<<https://www.livescience.com/22836-genome-extinct-humans-denisovans.html>>.

³² Scientific American, 'New DNA Analysis Shows Ancient Humans Interbred with Denisovans' (30 August 2012).

³³ Marshall, Michael (2014), op cit, p.38.

The "Harrappa World Admixture Proportions" program, show African ancestry predicted as high as 96%, distributed as follows: San – 53.41%, Pygmy – 35.21% and West African – 7.01%.



GEDmatch.com

"The analysis also provided details about the populations' physical features, confirming previous research that indicated that Denisovans had dark skin, brown hair and brown eyes."³⁴

"This question has been addressed by analysing the Neandertal and Denisovan genome sequences for all of the mutations known to be associated with lighter skin pigmentation in modern non-Africans. None of these mutations have been found, which has led to the inference that Neandertals and Denisovans had dark skin pigmentation." (Cerqueira et al. 2012).

"...the Denisovan individual carried alleles that in present-day humans are associated with dark skin, brown hair, and brown eyes."³⁵

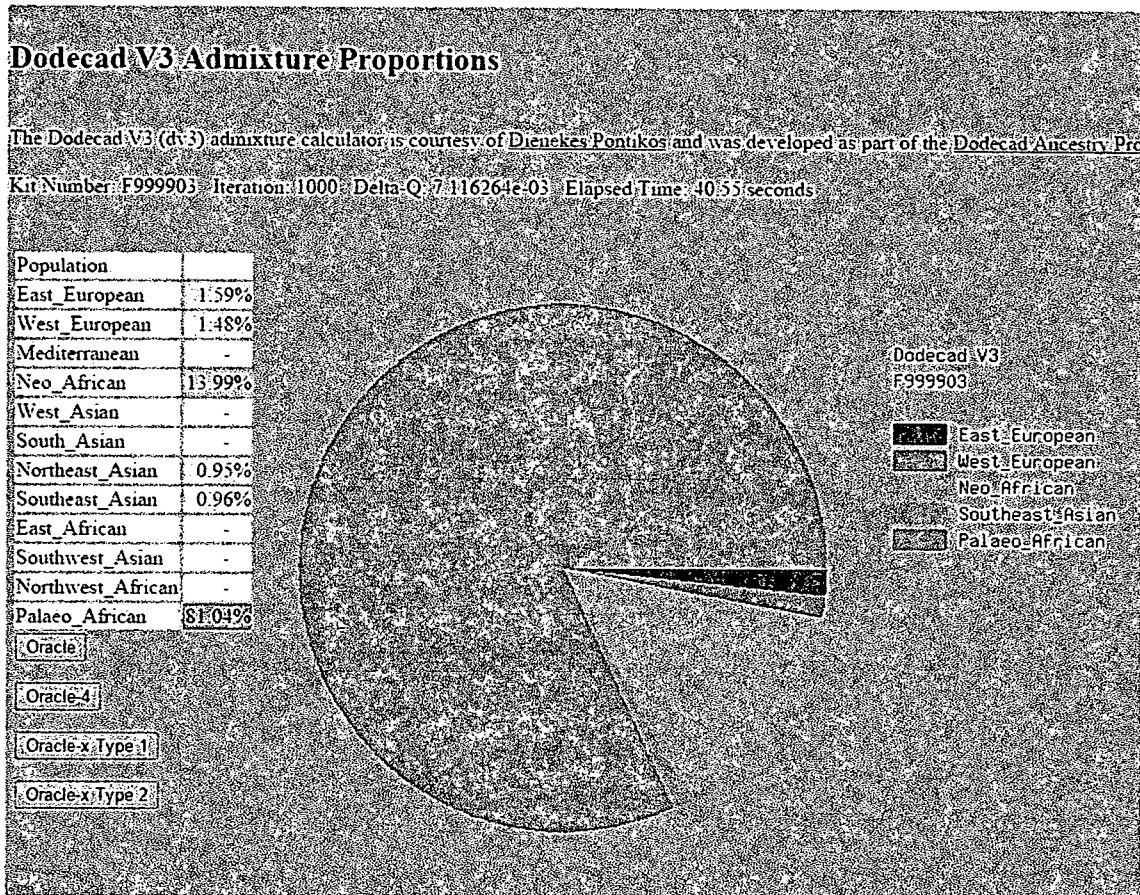
³⁴ ABC Science, 'Ancient genome offers clues to human waves' (31 August 2012).

<<http://www.abc.net.au/science/articles/2012/08/31/3580500.htm>>.

³⁵ Science, 'A High-Coverage Genome Sequence from an Archaic Denisovan Individual' (12 October 2012).

<http://www.eva.mpg.de/documents/AAAS/Meyer_High-coverage_Science_2012_1563678.pdf>.

The “Dodecad V3 Admixture Proportions” program, show African ancestry predicted to be 95%, comprised of 14% Neo African and 81% Paleo African.



GEDmatch.com

“...based on the genome, the Denisovans had dark skin, eyes, and hair.”³⁶

“In the scientific paper discussing the history of her population, Pääbo and his colleagues did mention, almost in passing, a few facts about her that they had gleaned from that library: She probably had dark hair, dark eyes, and dark skin.”³⁷

“Our knowledge of the Denisovans comes mostly from genomic studies, which revealed that the Denisovan individual sequenced probably had dark skin, brown hair, and brown eyes.”³⁸

³⁶ Ars Technica, ‘High Quality Denisovan Genome Sheds Light on Human Evolution’ (2012).

<<https://arstechnica.com/science/2012/08/high-quality-denisovan-genome-sheds-light-on-human-evolution/>>.

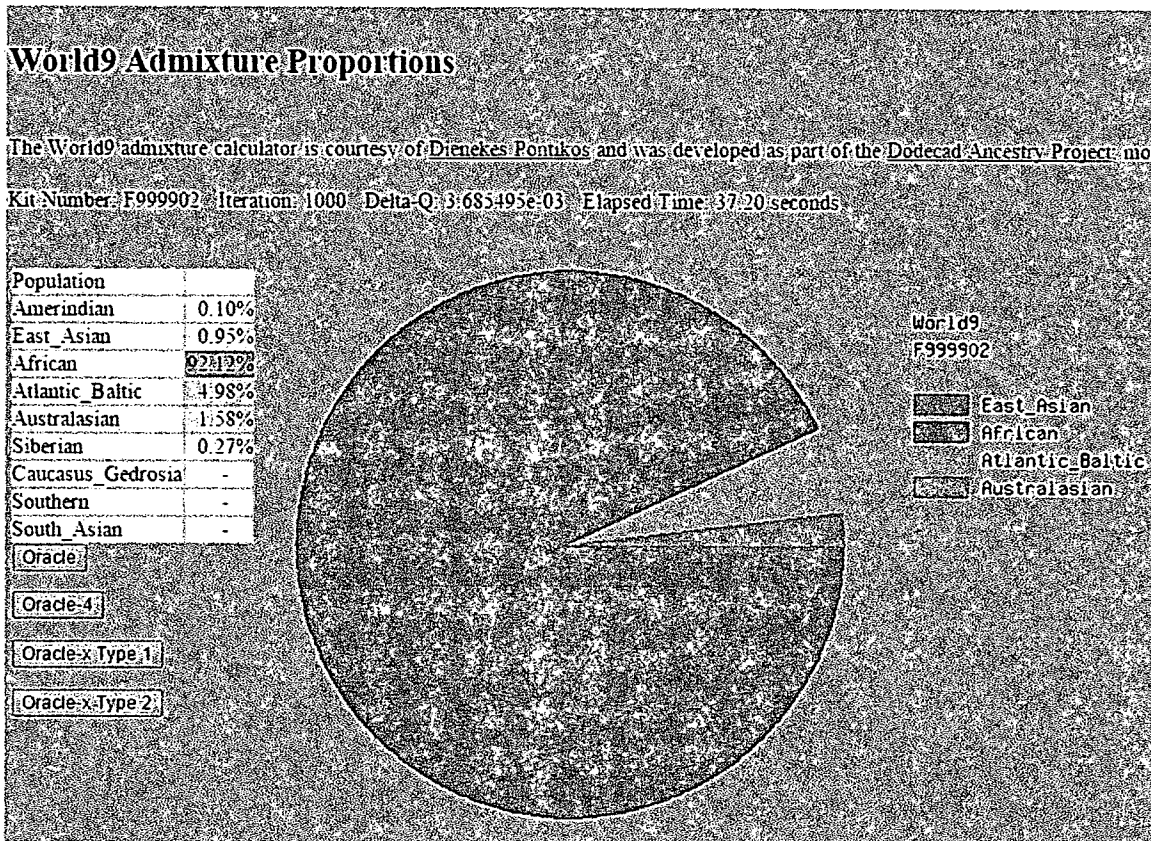
³⁷ National Geographic, ‘Missing Human Ancestor’ (2013). <<http://ngm.nationalgeographic.com/2013/07/125-missing-human-ancestor/shreeve-text>>.

³⁸ P. Gluckman, A. Beedle, T. Buklijas, F. Low, Mark Hanson (2017). Principles of Evolutionary Medicine.

Neanderthal and African Ancestry

Neanderthals were a species of archaic human, in the genus Homo. According to, "Complete Neanderthal genome sequenced: DNA signatures found in present-day Europeans and Asians, but not in Africans", they were closely related to modern humans, sharing 99.7% of DNA. The people activity left by Neanderthals include stone tools and bones, which have been found in Eurasia, from Western Europe to Central and Northern Asia, but nowhere on the African continent and does not appear in Africa's fossil record.

The following depiction is an output from Gedmatch of a Neanderthal ancestry composition. The output shows a substantial amount of African ancestry. This is very interesting when one takes into account the habitat and range of Neanderthals, which did not include the African continent.



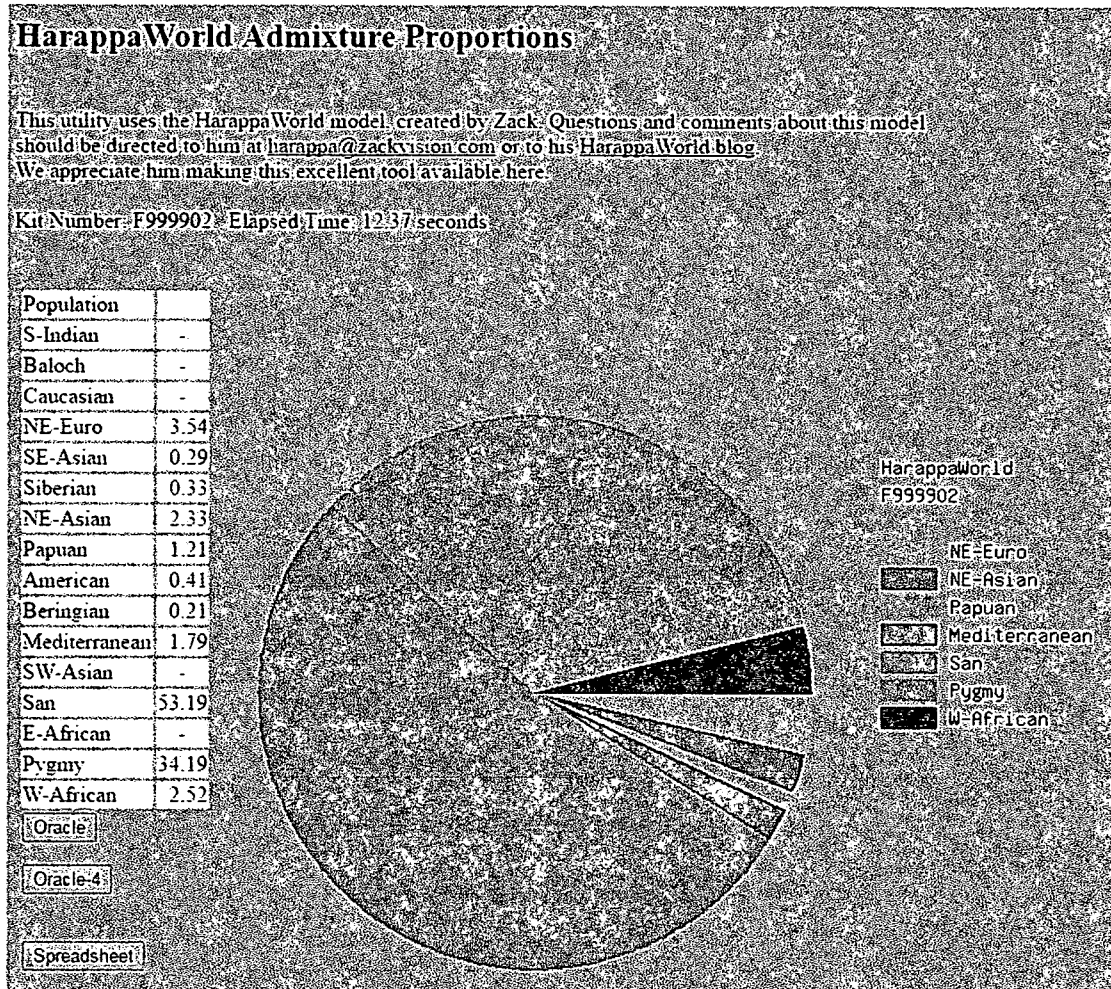
GEDmatch.com

The "World9 Admixture Proportions" program, show African ancestry as high as 92%! This is very interesting due to zero evidence supporting Neanderthals ever occupying Africa. The Neanderthal habitat was Eurasia, from Western Europe to Central and Northern Asia.

The "World9 Oracle Results" have used 'modern' populations to show single population and mixed population sharing between these groups and the Neanderthal sample. The genetic distance ranges from 5.7 generations to 71.72 generations. 5.7 generations for the population referred to as "African Caribbean" (ACB30) and 71.72 generations for the very specific group, "Ethiopian Jews".

The "Harrappa World Admixture Proportions" program show African ancestry as high as 90%, distributed as follows: San – 53.19%, Pygmy – 34.19% and West African – 2.52%.

The "Harrappa World Oracle Results" have used 'modern' populations to show single population and mixed population sharing between these groups and the Neanderthal sample. The genetic distance ranges from 46.95 generations to 84.79 generations.



GEDmatch.com

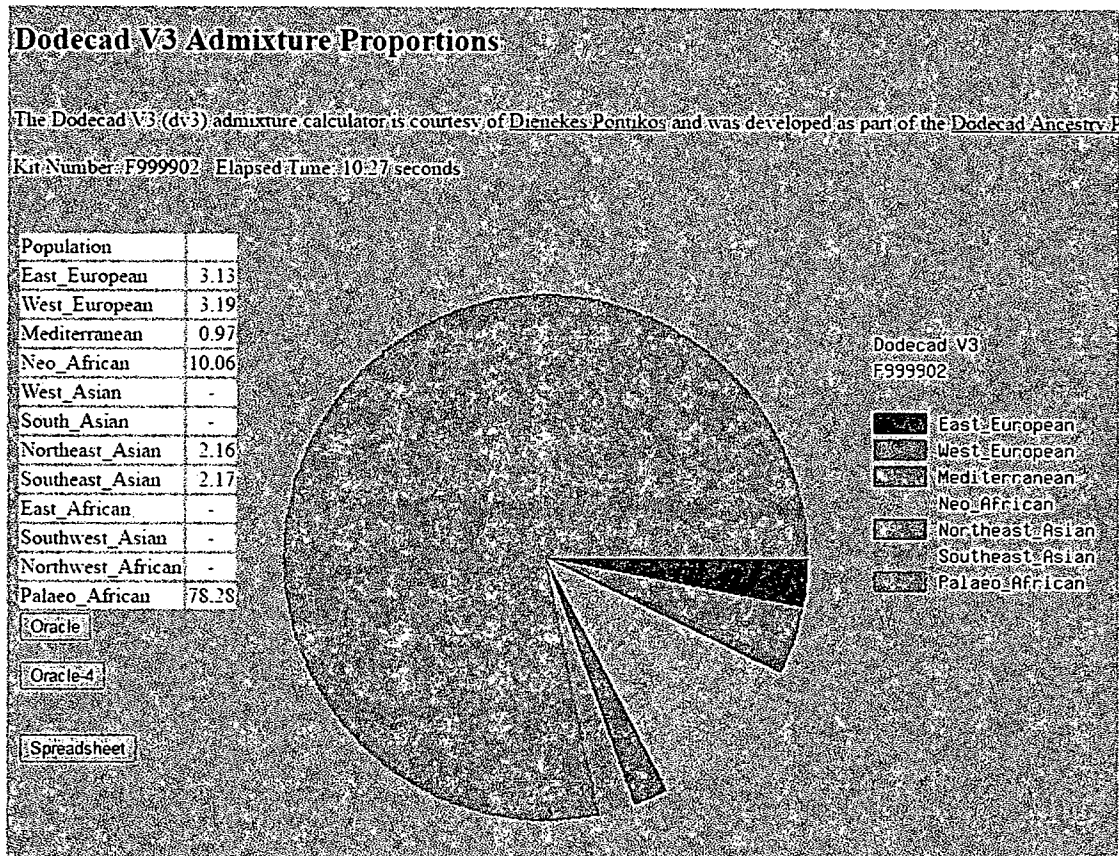
"This question has been addressed by analysing the Neanderthal and Denisovan genome sequences for all of the mutations known to be associated with lighter skin pigmentation in modern non-Africans. None of these mutations have been found, which has led to the inference that Neanderthals and Denisovans had dark skin pigmentation." (Cerqueira et al. 2012).

"...Neanderthals may have had darker skins..."; "a study earlier this year of ancient DNA suggested that Neanderthals living in what is now Croatia had dark skin and brown hair."³⁹

³⁹ New Scientist, 'Europeans did not inherit pale skins from Neanderthals' (2012).

The “Dodecad V3 Admixture Proportions” program, show African ancestry predicted to be 88%, comprised of 10.06% Neo African and 78.28% Paleo African.

The “Dodecad V3 Oracle Results” have used ‘modern’ populations to show single population and mixed population sharing between these groups and the Neanderthal sample. The genetic distance ranges from 14.55 generations to 77.91 generations.



GEDmatch.com

The aforementioned serves as a superb example of incorrect assignment of African ancestry. The timeframe captured by ancestry composition may not be broad enough to correctly predict the ancestry of a hominin that may be at least 50,000 to several hundred thousand years old. Both the Denisovan and the Neanderthal genomes reveal variants of genes in humans that are associated with dark skin, brown hair and brown eyes. Because of the variants of genes that are associated with dark skin, brown hair and brown eyes we see such high percentage predictions of African ancestry for Denisovan and Neanderthal samples. Yet again, we see an example of African ancestry predicted due to skin pigment, hair and eye color. It should be consistently acknowledged that Africa has no patent on phenotype.

Conclusion

Indigenous peoples and individuals have the right not to be subjected to forced assimilation or destruction of their culture. [UN Declaration on the Rights of Indigenous Peoples. Article 8(1)].

Indigenous peoples have the right to maintain, control, protect and develop their cultural heritage, traditional knowledge and traditional cultural expressions, as well as the manifestations of their sciences, technologies and cultures, *including human and genetic resources*, seeds, medicines, knowledge of the properties of fauna and flora, oral traditions, literatures, designs, sports and traditional games and visual and performing arts. They also have the right to maintain, control, protect and develop their intellectual property over such cultural heritage, traditional knowledge, and traditional cultural expressions. [UN Declaration on the Rights of Indigenous Peoples. Article 31(1)].

GEDmatch uses a subset of SNPs that are found to vary in the modern human populations, i.e. not comparison of an entire genome. It seems that for this subset of SNPs, the closest genetic match to archaics is found in American aborigines, misnomered Sub-Saharan Africans, largely due to dark skin being an ancestral trait, and that genomes belonging to people lacking eumelanin are more derived. In other words, ancestral archaic alleles have persisted in modern populations, due to ancient traits such as dark hair, skin and eyes.

Ancient seafaring Austronesians arrived in the Americas and interbred with Ronnell Bey's aboriginal ancestors, who were already living in the Americas. This is also the case with European introgression, which occurred at an even later date. In 'A History of Slavery and Genocide Is Hidden in Modern DNA', it states, "But one of the most amazing things about the state of modern genetics is that it also allows scientists to draw chronological conclusions about human migration, because blocks of these SNPs shorten over time at a generally consistent rate. "You can essentially break the genome up into European chunks, Native American chunks and African chunks," Martin says. "If each of these regions is longer, it suggests they arrived in the gene pool more recently, because time tends to break up the genome. If these chunks are shorter, it suggests there's been a lot of recombination and mixing up of the genome, which suggests the events were longer ago." The Austronesian signals in Ronnell Bey's genome represented as Southeast Asian is expressed as short blocks of SNPs. This suggests millennium ago, ancient seafaring Austronesians interbred with Ronnell Bey's in situ ancestors.

If 'Yoruba in Ibadan, Nigeria' [YRI] is actually or largely composed of 'Saro' ancestry, this should not be a proxy for so called Sub-Saharan African ancestry, but moreover, it should be considered a proxy for American aborigine ancestry. Saro, which is Yoruba for Sierra Leone and per evidence, 'Saro' were freed slaves who emigrated to Nigeria, from North America, via Sierra Leone, in the beginning of the 1830s. As previously shown, Sierra Leone was first settled in 1787 by 400 formerly enslaved dark skinned people, sent from London, England, under the auspices of the "Committee for the Relief of the Black Poor", an organisation set up by Jonah Hanway and the British abolitionist, Granville Sharp. These dark skinned people were largely Americans from North America and the Caribbean. Those born in Britain are very likely the descendants of more recent Americans, freed

from bondage in North America, and more historically, Americans that were kidnapped in the 15th and 16th centuries, and subsequently sold into slavery, appearing in European slave markets, listed as "Negroes" (Africans and Native Americans, *The Language of Race and the Evolution of Red-Black Peoples*).

The documented evidence in relation to emigration from the United States Corporation to Sierra Leone and Liberia (West Africa), along with the evidence showing YRI is actually or largely composed of Saro ancestry supports that it is very likely at least 82% of the samples in the West African control populations are ancestrally American, not African, with the remaining 18% showing similar allele frequencies, due to having similar skin pigment and hair color.

Mosquitoes carrying malaria of the genus *Plasmodium*, the type that causes human illness, were established in the New World at least 15 million years ago. The Duffy blood group was discovered in 1950. In 1955 many so called African-Americans were found to be resistant to *P. vivax* malaria, via a paper, titled, "Experimental testing of the immunity of Negroes to *Plasmodium vivax*." These so called Negroes were Americans! It is believed the Duffy Null allele has an alleged frequency of almost 100% in some Sub-Saharan populations, but occurs very infrequently in populations outside of this region, and that a person having this allele is thus more likely to have Sub-Saharan African ancestors. *P. vivax* malaria resistance was not born in Africa. Scientists were not studying Africans for resistance to *P. vivax* malaria, they were studying American aborigines. The resistance to *P. vivax* malaria was born in the Americas, in American aborigines, not Africa, or Africans.

Due to the establishment of the genus *Plasmodium* parasite in the Americas at least 15 million years ago, anatomical modern humans evolved with malaria in situ for their entire existence, and that if one possess the Duffy Null Allele, with signals of introgression from Austronesians, Mongoloids and contemporary Europeans, he or she is evidence of "Natural Selection", in practice and that the Duffy Null Allele should be reconsidered as an ancestry informative marker (AIM) for American aborigine ancestry.

The assignment of so called Sub-Saharan African ancestry to American aborigines, misnomered as African-American is statistical guesswork derived from allele frequencies in common, due to being Duffy negative, and possessing skin and hair color similarity.

On the Cover:

'Weasel Tail Piegan'

Weasel Tail Piegan was a Blackfoot American aborigine.



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The population codes found in the population diversity boxes are as follows:

CEU - European - 180 samples of Utah residents with Northern and Western European ancestry from the CEPH collection (originally 30 mother-father-child trios)

CHB - Han Chinese - 90 samples of Han Chinese in Beijing, China (previously called HCB, originally 45 unrelated samples)

JPT - Japanese Tokyo - 91 samples of Japanese in Tokyo, Japan (originally 44 unrelated samples)

YRI - Yoruba African - 180 samples of Yoruba in Ibadan, Nigeria (originally 30 Yoruba mother-father-child trios)

ASW - 90 samples of African ancestry in Southwest USA

CHD - 100 samples of Chinese in Metropolitan Denver, Colorado

GIH - 100 samples of Gujarati Indians in Houston, Texas

LWK - 100 samples of Luhya in Webuye, Kenya

MEX - 90 samples of Mexican ancestry in Los Angeles, California

MKK - 180 samples of Maasai in Kinyawa, Kenya

TSI - 100 samples of Toscani in Italia

AVG - Mathematical average of all samples from above groups