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Research Article

AFRICAN ORIGIN OF NATIVE AMERICAN R1-M173

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ABSTRACT
Controversy surrounds the origin of the y-chromosome R lineages among Native Americans in the United States. Most researchers assume that the occurrence of this gene among Native Americans is the result of European admixture. This view is not supported by the phylogeography of haplogroup R1 which does not correspond to the former territories of the European colonies with the highest population densities. The location of this paternal clade, on the other hand, does match the former centers of Black Native American occupation (and the forced migration of Mongoloid and Black Native Americans into the American Southwest), which suggest that the presence of R1 among Mongoloid Native Americans is the result of Mongoloid-Black Native American admixture. This Indian-African admixture would have been between SSA and the Black Native Americans already living here at the advent of the colonial era mating Mongoloid Native Americans. The African specific R-M173 yDNA form a Sub-Saharan African (SSA) subclade, which in association with the SSA R-M269 subclade in Africa, reveal that there was gene flow from SSA toward mongoloid people in North America, probably during the past 500 years.

Keywords: *Black Native American, Phylogeography, Clade, Mongoloid, Yamasee, Sub-Saharan African, yDNA*

INTRODUCTION
The phylogeography and origins for haplogroup R1 in the United States has been the subject of intense debate among researchers. Given the presence of R1 among Europeans, researchers have assumed that this haplogroup was introduced into North America by Europeans (Malhi *et al.*, 2008; Ripan *et al.*, 2008; Zegura *et al.*, 2004). This view is not supported by the phylogeography of haplogroup R1 which does not correspond to the former territories of the European colonies with the highest population densities.

Arnaiz-Villena *et al.*, (2006) and other researchers have suggested that SSA were among the first Americans (Alcina-France, 1985; Arnaiz-Villena *et al.*, 2006; Winters, 1977, 2011b,2013,2014,2015). Spanish explorers found Sub-Saharan Africans already in New World when they arrived (Alcina-France, 1985; Arnaiz-Villena *et al.*, 2006; Winters, 1977).

Rafinesque (1833) and Quatrafages (1899) mention a number of PreColumbian Black Native American tribes, including the Yamasee. The Black Native Americans (BNA) lived throughout the United States. They were especially prominent in the MidWest, Northeast and Southeast parts of the United States (Gallay, 2002; Winters, 2010, 2011a, 2011b).

The presence of SSA in North America suggests an African origin for the presence of y-DNA R-M173 among Native Americans. This results from the high frequency of haplogroup R1, among African populations across the African Continent, and especially in West Africa (Gonzalez *et al.*, 2012; Winters, 2010, 2011b). To evaluate this issue we will analyze the genomes belonging to the R lineages in Africa and North America.

MATERIALS AND METHODS
Methods
We analyzed three subclades of the R haplogroup. The y-chromosomes sampled, were from the Sub-Saharan African and Native American R lineages.

A database of y-Chromosome R genomes from Africa and North America was compiled. An interpopulation comparison was then conducted for the SSA and Native America (NA) R sequences following the literature survey. The data mining of the literature was used to determine haplogroup frequencies presented in this paper.

RESULTS AND DISCUSSION

Results

The most predominate y-chromosome of Native Americans in North America is R-M173. R-M173 is found in the Northeastern and Southwestern parts of the United States along with mtDNA haplogroup X (25%). Both haplogroups are found in Africa, but are absent in Siberia. There are varying frequencies of y-chromosome M-173 in Africa and Eurasia. Whereas only between 8% and 10% of M-173 is carried by Eurasians, 82% of the carriers of this y-chromosome are found in Africa (Winters, 2010, 2011b).

In Table 1, we note that R1 clades among NA populations vary. The NA populations that possess the R-M173 haplotypes are predominately found in the Northeastern and South eastern parts of the USA (see Table 2). It is important to remember that many Southwest NA population groupings originally lived in the Northeast.

This is very interesting given the presence of R-M173 is found among many American Indian groups. R-M173 among the North American Algonquian group range from Ojibwe (79%), Chipewyan (62%), Seminole (50%), Cherokee (47%), Dogrib (40%) and Papago (38%) (Malhi *et al.*, 2008).

Amerindians carry the X haplogroup (hg). Amerindians and Europeans hg X are different (Person, 2004). Haplogroup X has also been found throughout Africa (Shimada *et al.*, 2006). Shimada *et al.*, (2006) believes that X(hX) is of African origin. Amerindian X is different from European hg X, skeletons from Brazil dating between 400-7000 BP have the transition np 16223 (Martinez-Cruzado, 2001; Ribeiro-Dos-Santos *et al.*, 1996). Transition np 16223 is characteristic of African haplogroups. This suggest that Africans may have taken the X hg to the Americas in ancient times.

The African origin of this haplogroup is evident among the Seminoles who continue to show the African phenotype.

The pristine form of R1*M173 is found only in Africa (Cruciani *et al.*, 2002, 2010). The frequency of Y-chromosome R1*-M173 in Africa range between 7-95% and averages 39.5% (Coia *et al.*, 2005). The R*-M173 (haplotype 117) chromosome is found frequently in Africa, but rare to extremely low frequencies in Eurasia. The Eurasian R haplogroup is characterized by R1b3-M269. The M269 derived allele has a M207/M173 background.

This literature provides us with the data to critically examine the distribution of R1*-M173 in North America. It presents a genetic pattern of this haplogroup from Africa to Eurasia, and the dispersal of a significant African male contribution to Eurasia.

Y-chromosome V88 (R1b1a) has its highest frequency among Chadic speakers, while the carriers of V88 among Niger-Congo speakers (predominately Bantu people) range between 2-66% (Cruciani *et al.*, 2010; Bernielle-Lee *et al.*, 2009). Haplogroup V88 includes the mutations M18, V35 and V7. Cruciani *et al.*, (2010) revealed that R-V88 is also carried by Eurasians including the distinctive mutations M18, V35 and V7.

R1b1-P25 is found in Western Eurasia. Haplogroup R1b1* is found in Africa at various frequencies. In Table 3, we present the frequencies of R-M269 in Sub-Saharan Africa.

Berniell-Lee *et al.*, (2009) found in their study that 5.2% of SSA carried Rb1*. The frequency of R1b1* among the Bantu ranged from 2-20. The bearers of R1b1* among the Pygmy populations ranged from 1-25% (Berniell-Lee *et al.*, 2009). The frequency of R1b1 among Guinea-Bissau populations was 12% (Carvalho *et al.*, 2010). Y-Chromosome R1-M173 was probably spread in Western Europe first by African Roman soldiers, and later by African Muslims when they conquered Western Europe as Moors. This would explain why 60-70% French and Spanish males carry this y-haplogroup. Around 0.1 of Sub Saharan Africans carry R1b1b2. Wood *et al.*, (2005) found that Khoisan (2.2%) and Niger-Congo (0.4%) speakers carried the R-M269 y-chromosome. The Niger-Congo speakers formed a significant population in the nomes of Upper Egypt, where the founders of the 18th dynasty originated. Henn *et al.*, (2011) presents conclusive evidence that African hunter-gatherer (HG) populations share a number of ancestral lineages including B264*; although they are geographically distinct populations situated among agro-pastoral groups (Henn *et al.*, 2011)). An interesting finding of Henn *et al.*, (2011) was the discovery of the Eurasian clade R1b1b1a1a among the Khomani San of South Africa (Henn *et al.*, 2011).

Henn *et al.,* (2011) was surprised by this revelation of R-M269 among this Khoisan population. As a result, he interviewed the carries of R1b1b2a1a, and learned that no members of their families had relations with Europeans. The presence of R lineages among HG populations is not new. Wood *et al.*, reported Khoisan carriers of R-M269 (Wood *et al.*, 2005). Bernielle-Lee *et al.*, (2009), in their study of the Baka and Bakola pygmies found the the R1b1* haplogroup (Bernielle-Lee *et al.*, 2009). These researchers made it clear that the Baka samples clustered closely to Khoisan samples (Bernielle-Lee *et al.*, 2009).

The most common R haplogroup in Africa is V88. Given the interaction between hunter-gatherer (HG) groups and agro-pastoral groups they live in close proximity too, we would assume that African HG would carry the V88 lineage. Yet, as pointed out above the HG populations carry R-M269 instead of V88 (Winters, 2011b). The implications of R-M269 among HG populations, and Henn *et al.*, (2011) of shared African HG genome suggest that R-M269 may represent a HG genome thus an ancient African R lineage. The presence of R-M269 among HG human groupings fails to support a back migration of R-M269 from Europe.

In a recent article on the R1 clade, Gonzalez *et al.*, (2012), argue that R1 probably spread across Europe from Iberia to the east given the distribution of R1 in Africa.

The Gonzalez *et al.*, (2012) article further confirms the African origin for y-chromosome R1. The researchers found that 10 out of 19 subjects in the study carried R1b1-P25 or M269 as opposed to V88 in Equatoria Guinea. This is highly significant because it indicates that 53% of the R1 carriers were M269. This finding is further proof of the widespread nature of this so-called Eurasian genes in Africa among populations that have not mated with Europeans.

Myres *et al.*, (2010) argues that the neolithic European gene pool was probably influenced most, by events in Western Europe, rather than intrusive pioneer farmers from the Near East. They argue that R1b M412 lineages, phylogeographic and temperal patterns support a Central European origin for this clade and not a recent genetic heritage from Africa—not Anatolia or Southern Europe.

Myres *et al.*, (2010) note the maritime spread of neolithic farming communities using impressed cardial pottery to coastal Mediterranean populations and Crete 9kya. They interpret the phylogeography as an indication of the probable spread of M269 from Anatolia. This is contrary to the archaeological data which recognize the migration of populations around this time period from Africa, not Anatolia.

Using ancient DNA Haak *et al.*, (2010) makes it clear that during the Linearbandkeramik (LBK), Neolithic culture 5kya the predominate Eurasian haplogroup was haplogroup N (Haak *et al.*, 2010). Caramelli *et al.*, (2003) discovery of the presence of haplogroup N among hunter-gatherer Aurignacian samples suggest continuity between Western European populations from the Holocene to the Neolithic period.

The early coalescent estimate of M269*+L23 (x M412) chromosome between 8.5-12 kya (Myres *et al.*, 2010), suggest an African genesis for M269, rather than Southwest Asia, since we see not only Sub-Saharan populations entering the area around this time they also bring with them Sub-Saharan fauna (Holiday, 2000); and African groups who carry R1b are not of Middle eastern Origin (Winters, 2010).

Many of the African populations that carry R1* M173 are associated with the the Kushite people of Nubia (Winters,2010) . The African Kushites colonized Mesopotamia. As a result we find many Eurasian ethnonyms of Anatolia and Mesopotamia that indicate a Kushite presence including the Kaska tribe (Winters, 2010b); and Kings of Kish/Kush (Winters, 2010).

The archaeogenetic evidence fails to support this conclusion. The genetic, craniometric and archaeological evidence all support an African, rather than Southwest Asian or Central European origin for R1b. The skeleton associated with the civilizations of Mesopotamia are of Sub-Saharan Africans (Dieulafoy, 2004, 2010; Ricaut and Waelkens, 2008; Tomczyk *et al.*, 2010).

Haplogroup R1b1b2 was probably taken to Europe by African Roman soldiers. Africans were first recorded in the Western Europe 1800 years ago, as Roman soldiers defending Hadrian's Wall. There was a skeleton African Roman soldier recently found in Britain. Other Africans were found in Britain including the Rich African women called the bangled lady.

These SSA skeletons show how heavily integrated Africans were in western Europe. This would explain the widespread nature of y-chromosome R1-M173 in Europe. In addition to R1-M173 in western Europe, the African y-chromosome haplogroup A1 was also recently found in Britain.

Discussion

The question is where , how and when did African people carrying haplogroup R1-M173s take this haplogroup to the United States. The Black Native Americans who spread haplogroup R in North America may go back to the expedition of Mansa [King] Abubakari across the Atlantic Ocean in AD 1310

The expeditionary force of Mansa Abubakari, must have been immense, because the average boat on the Niger, could carry 80 men (Winters, 2013). Mansa Musa, the king who followed Abubakari, reports that " He [Abubakari] equipped two thousand vessels, a thousand for himself, and a thousand for water and supplies. He conferred power on me [Mansa Musa] and left with his companions on the ocean'. This means that anywhere between 25,000 to 80,000 men may have sailed from Mali along with Mansa Abubakari to the Americas (Winters, 2013).

Europeans learned about America from their travels along the West coast of Africa. Vasco da Gama, is said to have found out information concerning the West Indies from Ahmad b. Majid, of West Africa (Bazan, 1967).

The probable settlement of the Malians along the Northeastern shore of the United States, and the mounds inhabited by Black Native Americans like the Choctaw explain the presence of SSA genome: R-M173 in North America

Much of what is now Georgia was a stronghold of the Black Native Americans. These Blacks lived predominately from the Smoky Mountains in North Carolina southward as far as St. Augustine, Florida.

The vast majority of Native Black Americans lived in California, or along the Eastern seaboard in North America. They belonged to many Confederations including the Muskhoean and Algonquin. Some of their tribal names include Choctaw, Tuscarora, Secolan, Tamacraw, Nanticoke, Kashita (Kauche-te), and Yamasee to name a few. The BNA tribes mainly belonged to the Muskhogean and Algonquin Confederacies.

Due to the intimate relationship between the BNA tribes and mongoloid tribes, the BNA, given the high frequency of haplogroup R1 in Africa, probably introduced this haplogroup to Native Americans—not Europeans. This view is supported by the high frequency of R-M173 among Africans and Native Americans in North America.

One of the largest BNA tribes were the Yamasee. We know much about this tribe because of the many wars they fought against the British and Americans.

The Yamasee , was a tribe of Black Native Americans who originally lived in Florida and southern Georgia until they were forced to migrate North into South Carolina by the Spanish in the 16th Century. The Yamasee were part of the Muskhogean Confederacy. This was a Confederacy of mongoloid and Black Native Americans.

The Black Native Americans (BNA) lived on valuable farmlands during the Colonial period. The English and Americans wanted this land. This led to violent conflicts between BNAs and white Americans. In New England, the BNAs were eliminated by slaving, warfare and forced removal. The French enslaved Native Americans around the Great Lakes, Minnesota, Missouri Country and Lousiana (Gallay, 2002).

The Europeans also needed labor to work the fields. The Americans provided the Native Americans with guns and cheap goods to purchase Native American/Indian slaves. Between 1670 and 1720 many BNAs were enslaved (Bassey and Galley, 2009; Ekberg, 2007; Galley, 2002; Lauber, 1970; Newell, 2009). The BNAs were sold into slavery throughout the Thirteen Colonies, Canada and the Bristish West Indies (Gallay, 2002). The majority of BNAs sold into slavery, by white and Indian slave traders were the Choctaw (Gallay, 2002), and Yamasee and other Carolina tribes (Lauber, 1970; Newell, 2009).

A good example of the enslavement and forced removal of BNAs is the case of the Yamasee. The Yamasee , was a tribe of Black Native Americans who originally lived in Florida and southern Georgia until they forced to migrate North into South Carolina by the Spanish in the 16th Century. The Yamasee

were part of the Muskhogean Confederacy. This was a Confederacy of mongoloid and Black Native Americans.

The whites began to steal the Yamasee lands. By 1715, the Yamasee leading a Confederation of other tribes attacked the whites to drive them off their lands. The Cherokee who were part of the Muskogean Confederation broke away and formed an alliance with the British in 1718 and helped defeat the Yamasee.

The Yamasee who were not killed off were sold into slavery. Most of the Yamasee fled back into their ancestral homeland in Florida, which by this time was settled by the Creek.

The Yamasee were virtually wiped out due to protracted combat with the Creeks, who felt they were trying to take back the land they formerly owned in Florida. Some Yamasee joined the Seminole tribe. In return, the Cherokee took control of Yamasee land. If not for the break-away of the Cherokee the whites would have been defeated.

By the 18th Century Black Native Americans were divided into slave Native Americans and Free Indians. BNAs like the Choctaw had their own towns or lived on reservations. Other BNAs joined the ranks of the mongoloid Indian tribes (Winters, 2011a).

Table 1: Frequency of the R1b Sub-Clades in North America

Norm	Haplogroup	Frequency Native American Carriers	References
398	R-M17	1.5%	Hammer *et al.*,
398	R-P25*	0.3	Hammer *et al.*,
398	R-M269	21.9	Hammer *et al.*,
186	R-P25	.054	Zegura *et al.*,
186	R-M207	-----	Zegura *et al.*,
186	R-M173	-----	Zegura *et al.*,
-----	R-M173	73%	Malhi *et al.*,

- **The Zegura et al., study did not differentiate between the types of R Clades. There was only mention of the fact that 76 out of 79 Native American R lineage chromosomes belonged to R-P25.*
- ***This represents 73% of the Native American populations analyzed in Malhi et al.,*

Table 2: Native American Populations Possessing R-M173

Population	Norm	Percent
Chipewyan	48	(15) 31%
Dogrib	15	(6) 40%
Papago	-----	30%
Ojibwa	----	79%
Tanana	11	(1).09%
Apache	94	(5) .053%
Navajo	75	(2) .027%
Seminole	20	(10) 50%
TM Chippewa	34	(3) .088%
West Chippewa	29	(20) 69%
Chey/Arap	50	(8) 16%
Cherokee	30	(14) 47%
Choctaw	12	(1) .08
Creek	12	(2) 17%

Table 3: African Carriers of R-M269

African Population or Geographical area in Africa	Frequency of Haplogroup R-M269	Reference
Africa	5.2%	Berniell *et al.*, (2009)
Bantu	2-20%	Berniell *et al.*, (2009)
Pygmy	1-25%	Berniell *et al.*, (2009)
Guinea-Bissau	12%	Carvalho *et al.*, (2011)
Equatorial Guinea	53%	Gonzalez *et al.*, (2012)
Khoisan	2.2%	Wood *et al.*, (2005)
Khoisan	6.0%	Hirbo (2011)

Due to Indian slavery in North America, the Black Native American population was absorbed by the larger SSA slave population. Over time, people forgot there had been Black Native Americans and Mongoloid Native Americans. In fact, the BNA heritage and land rights were stolen by the government, as all Blacks in America, no matter their ancestry were assigned the status of former African slave. Gilio-Whitaker (2015) wrote that : "As the Indian slave trade gave way to the African slave trade by the late 1700's (by then over 300 years old) Native American women began to intermarry with imported Africans, *producing mixed-race offspring whose native identities became obscured through time. In the colonial project to eliminate the landscape of Indians, these mixed-race people simply became known as "colored" people* **through bureaucratic erasure in public records**. In some cases such as in Virginia, even when people were designated as Indians on birth or death certificates or other public records, their records were changed to reflect "colored." Census takers, determining a person's race by their looks, often recorded mixed-race people as simply black, not Indian. The result is that today there is a population of people of Native American heritage and identity (particularly in the Northeast) who are not recognized by society at large, sharing similar circumstances with the Freedmen of the Cherokee and other Five Civilized Tribes."

Conclusion

The P clade probably originated in Africa because 1) whites rarely mated with Native Americans before the Great Trek to Oklahoma, 2) R-M173 and the subclades V88 and R-M269 has its highest frequencies across Africa ; and 3) R-V88 is older than R-M269.

Researchers have found that the TMRCA of V88 was ***9200-5600 kya*** (Cruciani *et al.*, 2010). Eurasians carry the M269 (R1b1b2) mutation. The subclades of R1b1b2 include Rh1b1b2g (U106) (***TMRCA 8.3kya***) and R1b1b2h (U152) (TMRCA 7.4kya). The most recent common ancestor for R1b1b2 in Europe is probably 8kya (Balaresque *et al.*, 2010). Y-Chromosome R1b1b2 has high frequencies in England, France, Italy and Germany (Balaresque *et al.*, 2010). Clearly, R-V88 is older than R-M269.

Some of the Malian settlers probably introduced R-M173 into North America. Ancient Mali was a Confederation it was made up of many different tribes. Settling even half the 25-80,000 Malians who sail to America in 1310 on the mainland would have had a tremendous effect on the genetic and population land scape of the Americas.

It appears that Black and mongoloid Native Americans often lived side by side. They also belonged to the same Confederations. Due to the Native American slave trade many Black Native Americans owners in the West Indies other Native American were forced to work on plantations or sold into slave. Using a system of divide and rule the whites were able to get the Indians capture each other and sale their captives as slave. Since the ancestors of the Black Native Americans had originated in Africa they began to be identified as slave-Indian, freeman and finally "Colored". And then as a result of ***bureaucratic erasure*** in the public records, the former black Native Americans simply became identified as "Colored", like the former Sub-Saharan slaves, instead of Native Americans.

REFERENCES

Alcina-Franch J (1985). *Los orígenes de America* (Madrid: Editorial Alhambra).

Arnaiz-Villena A, Moscoso J and Serrano-Vela I (2006). The uniqueness of Amerindians according to HLA genes and the peopling of the Americas. Available: http://www.inmunologia.org/Upload/Articles/6/7/678.pdf.

Berniell-Lee G, Calafell F, Bosch E, Heyer E, Sica L, Mouguiama-Daouda P, Van der Veen L, Hombert JM, Quintana-Murci L and Comas D (2009). Genetic and Demographic Implications of the Bantu Expansion: Insights from Human Paternal Lineages. *Molecular Biology and Evolution* **26**(7) 1581-1589; Available: doi:10.1093/molbev/msp069.

Balaresque P, Bowden GR, Susan M Adams, Ho-Yee Leung, Turi E King, Zoë H Rosser, Jane Goodwin, Jean-Paul Moisan, Christelle Richard, Ann Millward, Andrew G Demaine and Guido Barbujani (2012). A Predominantly Neolithic Origin for European Paternal Lineages. Published: January 19, 2010 Available: DOI: 10.1371/journal.pbio.1000285. http://journals.plos.org/plosbiology/article?id=10.1371/journal.pbio.1000285.

Caramelli D, Lalueza-Fox C, Vernesi C, Lari M, Casoli A, Mallegni BC, Dupanloup I, Bertranpetit J, Barbujani G and Bertorelle G (2003). Evidence for a genetic discontinuity between Neandertals and 24,000 year-old anatomically modern Europeans. *Proceeding National Academy of Sciences U S A.* **100** (11) 6593-6597.

Carvalho M, Brito P, Bento AM, Gomes V, Antunes H, Costa HA, Lopes V, Serra A, Balsa F, Andrade L, Anjos MJ, Corte-Real F and Gusmão L (2011). Paternal and maternal lineages in Guinea-Bissau population. *Forensic Sciences International Genetic* **5**(2) 114-6.

Coia V, Destro-Bisol G, Verginelli F, Battaggia C, Boschi I, Cruciani F, Spedini G, Comas D and Calafell F (2005). Brief communication: mtDNA variation in North Cameroon: lack of Asian lineages and implications for back migration from Asia to sub-Saharan Africa. *American Journal of Physical Anthropology*, (electronically published May 13, 2005; accessed August 5, 2005). (http://www3.interscience.wiley.com/cgi-bin/fulltext/110495269/PDFSTART.

Cruciani F, Trombetta B, Sellitto D, Massaia A, destroy-Bisol G, Watson E and Colomb EB (2010). *European Journal of Human Genetics* (6 January 2010), Available: doi:10.1038/ejhg.2009.231: 1-8.

Cruciani F, Santolamazza P, Shen P, Macaulay V, Moral P and Olckers A (2002). A Back Migration from Asia to Sub-Saharan Africa is supported by High-Resolution Analysis of Human Y-chromosome Haplotypes. *American Journal of Human Genetics* **70** 1197-1214.

Dieulafoy J (2004). The Project Gutenberg EBook of Perzi, Chaldea en Susiane, by Jane Dieulafoy. Retrieved 04/04/10 http://www.gutenberg.org/files/13901/13901-h/13901-h.htm.

Dieulafoy MA (2010). L' Acropole de Suse d'après les fouilles exécutées en 1884, 1885, 1886, sous les auspices du Musée du Louvre. Retrieved 04/04/10 from: http://www.archive.org/stream/lacropoledesused01dieu#page/2/mode/2up.

Gonzalez *et al.*, (2012). The genetic landscape of Equatorial Guinea and the origin and migration routes of the Y chromosome haplogroup R-V88. *European Journal of Human Genetics*, advance online publication 15 August 2012; Available: doi: 10.1038/ejhg.2012.167.

Haak W, Balanovsky O, Sanchez JJ, Koshel S and Zaporozhchenko V *et al.*, (2010). Ancient DNA from European Early Neolithic Farmers Reveals Their Near Eastern Affinities. *PLoS Biology* **8**(11) e1000536, Available: doi:10.1371/journal.pbio.1000536.

Henn BM, Gignoux CR, Jobin M, Granka JM, Macpherson JM, Kidd JM, Rodríguez-Botigué L, Ramachandran S, Hon L, Brisbin A, Lin AA, Underhill PA, Comas D, Kidd KK, Norman PJ, Parham P, Bustamante CD, Mountain JL and Feldman MW (2011). Hunter-gatherer genomic diversity suggests a southern African origin for modern humans. *Proceedings of the National Academy of Sciences USA* **108**(13) 5154-62, Epub 2011 Mar 7, Available: http://www.pnas.org/content/108/13/5154.full.

Hammer MF, Chamberlain VF, Kearney VF, Stover D, Zhang G, Karafet T, Walsh B and Redd AJ (2005). Population structure of Y chromosome SNP haplogroups in the United States and Forensic

implications for constructing Y chromosome STR databases. *Forensic Science International*, Available: Doi:10.1016/j.forsciint.2005.11.013. http://www.sciencedirect.com.

Hirbo JB (2011). Complex Genetic History of East African Populations. PhD Dissertation, University of Maryland.

Holiday T (2000). Evolution at the Crossroads: Modern Human Emergence in Western Asia. *American Anthopologist* **102**(1).

Gilio-Whitaker D (2015). The Untold History of American Indian Slavery, Retrieved 2/24/15 http://nativeamericanhistory.about.com/od/controversies/a/The-Untold-History-Of-American-Indian-Slavery.htm.

Makoto K Shimada, Karuna Panchapakesan, Sarah A Tishkoff, Alejandro Q Nato Jr and Jody He Y (2007). Divergent Haplotypes and Human History as Revealed in a Worldwide Survey of X-Linked DNA Sequence Variation. *Molecular Biology and Evolution* **24**(3) 687-698.

Malhi RS, Gonzalez-Oliver A, Schroeder KB, Kemp BM, Greenberg JA, Dobrowski SZ and Smith DG *et al.*, (2008). Distribution of y-chromosomes among Native North Americans: A study of Athapaskan Population History. *American Journal Physical Anthropology* **137** 412-424.

Martinez-Cruzado JC, Toro-Labrador G, Ho-Fung V and Estevez-Montero MA et al., (2001). Mitochondrial DNA analysis reveals substanial Native American ancestry in Puerto Rico, Human Biology. *Human Biology* **73**(4) 491-511.

Myres N, Rootsi S and Lin A *et al.*, (2010). A major Y-chromosome haplogroup R1b Holocene era founder effect in Central and Western Europe. *European Journal of Human Genetics*, advance online publication 25 August 2010; Available: doi: 10.1038/ejhg.2010.146.

Quatrefages A de (1889). *Introduction a L'Etudes des Races Humaines*.

Ribeiro-Dos-Santos AK, Meyer D and Zago MA (1996). Multiple founder haplotypes of mitochondrial DNA in Amerindians revealed by RFLP and sequencing. *Annals of Human Genetic* **60**(Pt 4) 305-19.

Ripan S (2008). Distribution of Y Chromosomes Among Native North Americans: A Study of Athapaskan Population History. *American Journal of Physical Anthropology*, Retrieved 2010-08-27.

Ricaut FX and Waelkens (2008). Cranial Discrete Traits in a Byzatine Population and Eastern Mediterranean Population Movements. *Human Biology* **80**(5) 535-564.

Singer I (1981). Hittites and Hattians in Anatolia at the beginning of the Second Millennium B.C. *Journal of Indo-Euro Study* **9**(1-2) 119-149.

Tomczyk J, Jedrychowska-Danska K, Ploszaj T and Witas HW (2010). Anthropological analysis of the osteological material from an ancient tomb (Early Bronze Age) from the middle Euphrates valley, Terqa (Syria). *International Journal of Osteoarchaeology*, Retrieved 04/04/10 from www.interscience.wiley.com) DOI:10.1002/oa.1150.

Ricaut FX and Waelkens (2008). Cranial Discrete Traits in a Byzatine Population and Eastern Mediterranean Population Movements. *Human Biology* **80**(5) 535-564.

Winters C (1977). Islam in Early North and South America. Al-Ittihad 57-67.

Winters C (2010). The Kushite Spread of haplogroup R1*-M173 from Africa to Eurasia, *Current Research Journal of Biological Sciences* **2**(5) 294-299, Available: http://maxwellsci.com/print/crjbs/v2-294-299.pdf.

Winters C (2011a). Comment: Genetic Evidence of Early Migrations into America. Retrived 2/18/2015: http://www.plosone.org/annotation/listThread.action?root=18395.

Winters C (2011b). Is Native American R Y-Chromosome of African Origin?. *Current Research Journal of Biological Sciences* **3**(6) 555-558.

Winters C (2011c). The Gibraltar Out of Africa Exit for Anatomically Modern Humans. *Webmed Central Biology* **2**(10) WMC002319, Available: http://www.webmedcentral.com/article_view/2319.

Winters C (2013). *African Empires in Ancient America*. Createspace, Available: Amazon.com.

Winters C (2014). *History of Blacks in America from Pre-History to 1877*. Createspace, Available: Amazon.com.

Wood ET, Stover DA, Ehret C, Destro-Bisol G, Spedini G, McLeod H, Louie L, Bamshad M, Strassmann BI, Soodyall H and Hammer MF (2005). Contrasting patterns of Y-chromosome and mtDNA variation in Africa: evidence for sex-biased demographic processes. *European Journal of Human Genetic* **13** 867-876.

Zegura SL, Karafet TM, Zhivotovsky LA and Hammer MF (2004). High Resolution SNPs and Microsatellite Haplotypes point to single, Recent Entry of Native American Y Chromosomes in the Americas. *Molecular Biology and Evolution* **21**(1) 164-175.