

## **DID AFRICAN SLAVES BRING THE Y-CHROMOSOMES R1 CLADES TO THE AMERICAS?**

**\*Clyde Winters**

*Department of Archaeogenetics, Uthman dan Fodio Institute, Chicago, Illinois 60643*

*\*Author for Correspondence*

### **ABSTRACT**

Previous studies of the genetic structure of Afro-Americans have observed a considerable presence of European haplotype R1, among Afro-Americans in North America and the Caribbean. Researchers have assumed that these European genetic signals were probably the result of European males mating with Sub-Saharan African (SSA) females during the Atlantic Slave Trade. Even though this is the usual explanation for the presence of European clades carried by Afro-Americans (AA), recent studies show a high frequency of R haplogroup ancestry among SSAs in West Africa. This study illustrates that the existence of Y-chromosome R1a, and R1b (M-269 and V88) among Afro-Americans may be derived from SSAs instead of Europeans.

**Keywords:** *Afro-American, Atlantic Slave Trade, Haplogroup, Haplotype, Genome, Y-Chromosome*

### **INTRODUCTION**

Afro-Americans (AA) in the United States and the Caribbean carry a high frequency of the Y-Chromosome R1.

Most researchers argue that the presence of R1 among Afro-Americans is the result of Sub-Saharan African (SSA) female slaves mating with their European Masters.

This argument was justified until researchers discovered that many SSAs carry the Y-Chromosome clades R1a, R1-V88 and R1-M269 (Berniell-Lee *et al.*, 2009; Cruciani *et al.*, 2010; Gonzalez *et al.*, 2013; Winters, 2016; Wood *et al.*, 2005).

These Y-Chromosomes in the African paternal gene pool may represent a genetic signature of some West Africans. The presence of these clades among SSAs that were sold into slavery during the Atlantic Slave Trade suggests that some of the slaves brought these Y-Chromosome clades with them when they came to the Americas.

The Caribbean Islands were occupied by Europeans shortly after Columbus found the New World. As these Islands became centers of agricultural production European planters imported Native American slaves from the United States to work the fields (Winters, 2016). In addition, Irish, Scottish and Walsh indentured servants were also an early labor force in Jamaica and the Bahamas Islands (Simms *et al.*, 2012).

From the 1500's to the late 17<sup>th</sup> Century most slaves in the British Caribbean were Native Americans (Winters, 2015).

The Native American slaves and European bond-servants were replaced by SSA slaves. For example, Jamaica had the largest slave population in the Caribbean.

During the Atlantic Slave Trade 914,902 SSAs were transported to the Islands (Henriques, 1964; Hurwitz and Hurwitz, 1971; Pepin, 2005).

The mating of SSA females and European males varied. In North America the mating of SSA and European males were sporadic.

In the French Caribbean there was widespread concubinage (Coupeau, 2008), while the rate of genetic admixture among SSA females and British males in the Caribbean was much lower (Browne, 2004; Simms *et al.*, 2012).

Simms *et al.*, (2012) believed that French concubinage may account for the high sex bias R haplotypes in Haiti. By 1789, for example, the *Affranchis* (mulattos) resulting from SSA slave females mating with European males, were just about equal to the European (Blanc) population.

## **Research Article**

### **MATERIALS AND METHODS**

This is a review article. The Y-Chromosomes sampled, were from Sub-Saharan Africans (SSA) and North American, Jamaican and Barbados Afro-American (AA) R lineages. We analyzed three subclades of the R haplogroup: R1a, R-V88 and R-M269. A database of Y-Chromosome R genomes from Africa, the Caribbean and North America was compiled. An interpopulation comparison was then conducted for the SSA and Afro-American R sequences following the literature survey.

### **RESULTS AND DISCUSSION**

#### **Results**

##### *R1 in Africa*

The pristine form of R1\*-M173 is found only in Africa (Cruciani *et al.*, 2004, 2010, 2011). The frequency of Y chromosome R1\*-M173 in Africa ranged 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 R1b1a1a2 (R-M269). The M269 derived allele has a M207 /M173 background.

The phylogeography of R1 in Africa makes it clear that this Y-chromosome is spread globally across Africa and includes the genetic structure of diverse African populations including Berber, Chadic, Cushitic, Khoisan, Pygmy, Niger-Congo, Nilo-Saharan and Semitic speaking African populations (Berniell-Lee *et al.*, 2009; Cruciani *et al.*, 2010; Winters, 2016; Wood *et al.*, 2005).

The phylogenetically deep haplogroup R1b is mainly found in West Africa and the Sahel, where the frequency ranges between 5-85% among various Niger Congo speakers (Cruciani *et al.*, 2010). The paternal record of M173 on the African continent illustrates a greater distribution of this y-chromosome among varied African populations than, in Asia.

Dravidian speakers originated in Africa (Lal, 1963; Sergent, 1992; Winters, 2007, 2008). Archaeological (Lal, 1963), genetic (Winters, 2008; 2010a), place names (Balakrishnan, 2005) and linguistic data (Aravanan, 1979, 1980; Upadhyaya and Upadhyaya, 1979) link Africans and Dravidians.

The Dravidian speakers spread into Eurasia via Iran. From here they migrated into Europe (Lahovary, 1963) and India (Sergent 1992, Winters 2007, 2008).

In addition, Dravidians and SSA share HLA, mtDNA and Y-chromosome haplogroups (Winters, 2010a, 2010c, 2012). This supports the recent demic diffusion of Sub-Saharan African and Dravidian gene flow from Africa to Eurasia.

Kivisild (2017), provides a detailed discussion of R1 in prehistoric Europe. The article is most interesting because it places R1b1a2 ( R-V88) in ancient Europe. This finding matches Turek (2012), which explains the spread of typically beaker style stamped decoration Bell Beaker culture pottery from Morocco into Iberia, and thence the rest of Europe.

Turek (2012) argued that the “Maritime tradition” of the Beaker culture style of “Copos” site on the River Tajo in Portugal, originated in Morocco. This Beaker decorated pottery was found in the cemeteries of El Keffen (c.3350-2660BC).

From Iberia the Beaker tradition migrated to the Lower Rhine, where it evolved into the Corded Ware beakers (Turek, 2012).

Gonzalez *et al.*, (2013), argued that R1 probably spread across Europe from Iberia eastward given the distribution of R1 in Africa. Gonzalez *et al.*, (2013) proposed a West to East spread for P-25 across Europe, with a possible entry of this clade via Gibraltar.

Kivisild (2017) made it clear that R-V88 is the earliest offshoot of R-M343, so it is older than R-M269. Kivisild (2017) dates R-V88 in Europe to around 18kya.

Kivisild (2017) noted that during prehistoric times in Europe, the V88 sub-clade, *had relatives in Early Neolithic samples from across a wide geographic area from Iberia, Germany to Samara. The presence of V88 in these areas correspond to the spread of “Maritime tradition” beaker style pottery from Morocco into Europe (Turek, 2012).* This would place carriers of V88 among the Yamnaya and Bell Beaker people.

### Research Article

An early colonization of Eurasia 4kya by Sub-Saharan Africans and Dravidian carriers of R1\*-M173 is the best scenario to explain the high frequency and widespread geographical distribution of this y-chromosome on the African continent (Winters, 2010c, 2016). Given the greatest diversity of R1\*-M173 in Africa, makes this explanation for R1\*-M173 in Africa, the most parsimonious model explaining the frequency of R-M173 in Africa.

Abu-Amero *et al.* (2009), revealed the fact that Dravidians carry R haplogroups. This illustrates the recent introduction of R Y-chromosomes to Eurasia because the Dravidian speakers are of African origin (Sargent, 1992). The frequency of haplotype M173 in Eurasia is as follows: Anatolia 0.19%, Iran 2.67%, Iraq 0.49% Oman 1.0%, Pakistan 0.57% and Oman 1.0%. This contrast sharply with the widespread distribution of R1 in Africa that ranges between 7- 95% in various parts of Africa, especially Cameroon (Coia *et al.*, 2005). Coia *et al.*, (2005) has revealed that no maternal Eurasian lineages have been found among Sub-Saharan Africans with a R1\*-M173 profile.



Rosa *et al.*, (2007) noted that most Niger-Congo speakers like the Mande and Balanta carry the E3a-M2 gene, whereas a number of Felupe-Djola, Papel, Fulbe, and Mande carry the M3b\*-M35 gene, the same as many people in the Sudan.

In addition to haplogroup E3, we also find some carriers of R1\*-M173 (Cruciani *et al.*, 2004, 2010, 2011). Most carriers of Y chromosome M173 in Africa speak Niger-Congo languages (Winters, 2010). For example, Scheinfeldt *et al.*, (2010) in a study on Fulani Y chromosomes found that the R1\*M173 lineage is found in high frequencies among some Fulanis.

**Research Article**

Coia *et al.*, (2005) provided substantial data that the presence of R1\*-M173 did not follow the spread of mtDNA haplogroup U6 in sub-Saharan Africa, which is found in North Africa. These authors suggest that R1\*-M173 may not be the result of back migration from Asia if this theory depends on the spread of haplogroup U6 in areas where R1\*-M173 is found.

Y-chromosome V88 (R1b1a2) has its highest frequency among Chadic speakers. The carriers of V88 among Niger-Congo speakers (predominately Bantu people) range between 2-66% (Cruciani *et al.*, 2010; Berniell-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.

**Table 1: African Carriers of R-M269**

African Geographical Area in Africa	Population or Frequency of RM269	Haplogroup	Reference*
Africa	5.2%		Berniell-Lee <i>et al.</i> , (2009)
Bantu	2-20%		Berniell-Lee <i>et al.</i> , (2009)
Pygmy	5%		Berniell-Lee <i>et al.</i> , (2009)
Guinea-Bissau	12%		Carvalho <i>et al.</i> , (2011)
Equatorial Guinea	53%		González <i>et al.</i> , (2012)
Khoisan	2.2%		Wood <i>et al.</i> , (2005)
Khoisan	6.0%		Hibro (2011)

Around 0.1 of Sub Saharan Africans carry R1b1a1a2 (Table 1). Wood *et al.*, (2009) 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 (Winters, 2016).

R1b1-P25 is found in Western Eurasia. Haplogroup R1b1\* is found in Africa at various frequencies (Table 1).

Berniell-Lee *et al.*, (2009) found in their study that 5.2% carried Rb1\*. The frequency of R1b1\* among the Bantu ranged from 2-20. The bearers of R1b1\* among the Pygmy populations ranged from 1-5% (Berniell-Lee *et al.*, 2009). The frequency of R1b1 among Guinea-Bissau populations was 12% (Carvalho *et al.*, 2011)

Gonzalez *et al.*, (2013) provided some interesting data on the Y-chromosome R1. These researchers found both R-V88 and R-M269 in a part of West Africa that was the origin of many North American and Caribbean slaves. Gonzalez *et al.*, (2013) found that 10 out of 19 subjects in the study carried R1b1-P25 or M269. This is highly significant because it indicates that 53% of the R1 carriers were M269. The finding provides further support to the widespread nature of haplogroup R ancestry in Africa among populations that have not mated with Europeans, but came to the Americas as slaves.

*Africans Carry Haplogroup R1a*

In India the Dravidian people carry the R1a haplogroup the Dravidian people of India originally lived in Middle Africa and belonged to the Proto-Saharan Civilization (Lal, 1963; Sergent, 1992; Winters, 2007, 2008, 2010a). Africans also carry haplogroup R1a (Berniell-Lee *et al.*, 2009).

The Proto-Saharan civilization was situated in the Proto-Sahara, which includes Cameroon. In Cameroon we find carriers of R1a (Berniell-Lee *et al.*, 2009). The Khoisan also carry RM343 (R1b) and M 198 (R1a1) (Naidoo *et al.*, 2010). In addition to carriers of R1a in Cameroon; the Dravidian languages are still spoken today in Cameroon see: <https://www.youtube.com/watch?v=vWyAYGIFZjk>

*North America*

It is very difficult to determine the frequency of R1 haplogroups among North American Afro-Americans because this data is usually left out of the final analysis of admixture studies (Bryc *et al.*, 2014). To

### Research Article

determine this genetic signature, you have to look at the literature of forensic scientists. Bryc *et al.*, (2014) estimated that at least 22% of AAs claim Native American ancestry.

Many Afro-Americans in the United States have oral traditions that they are descendants of Black Native Americans (Winters, 2015). Many of these Afro-Americans carry R1 genes (Table 2).

Haplogroup E-P1 is called E1b1a1. In the Hammer *et al.*, (2006) study while 63% of Afro-Americans carry this haplogroup, 1.3% Native Americans carry the same haplogroup.

It is difficult to determine the frequency of Eurasian clades carried by Afro-Americans in North America. This data is rarely collected because of the protocols of Admixture and Structure programs; and the use of research programs developed to exclude evidence of non-Africans carrying mtDNA haplogroups L, and Y-Chromosomes E and A.

The protocols of Admixture and Structure programs assume that Native Americans, Europeans and Sub-Saharan Africans only met after 1492.

And as a result, researchers assume that if Native American and Eurasian genes are found among Afro-Americans this genetic evidence should be excluded because any African admixture among these populations has to be recent, and date back to the Atlantic Slave Trade.

This analogy is false because many African populations carry the Eurasian R1 clades (Winters, 2016). But researchers argue, this evidence should be excluded because any African admixture among these populations have to be recent. Reich *et al.*, (2012) outlines the method and motivations he uses to exclude African admixture with Native Americans in his study. This data set allowed Reich *et al.*, (2012) to mask segments of Native American admixture of potentially non-Native origin.

Information on the frequency of R haplogroups carried by Afro-Americans in the United States, has mainly been recorded by Forensic scientist, rather than population geneticists. Hammer *et al.*, (2006), and Vallone and Butler (2004) presented interesting statistics on the frequency of R1 among Afro-Americans.

In the Vallone and Butler (2004) study AAs carried around 0.3% R-M207, and 23% R1b (Figure 1). The frequency of R1 among AAs in North America are similar to the frequency of this Y-chromosome in Haiti and Jamaica.

Hammer *et al.*, (2007) has also examined the frequency of R1 among AAs in North America. Hammer *et al.*, (2007) found that the second most frequent Y-chromosome among Afro-Americans is R1b. In Table 2, we see a comparison of Native American and Afro-American Y-Chromosomes.

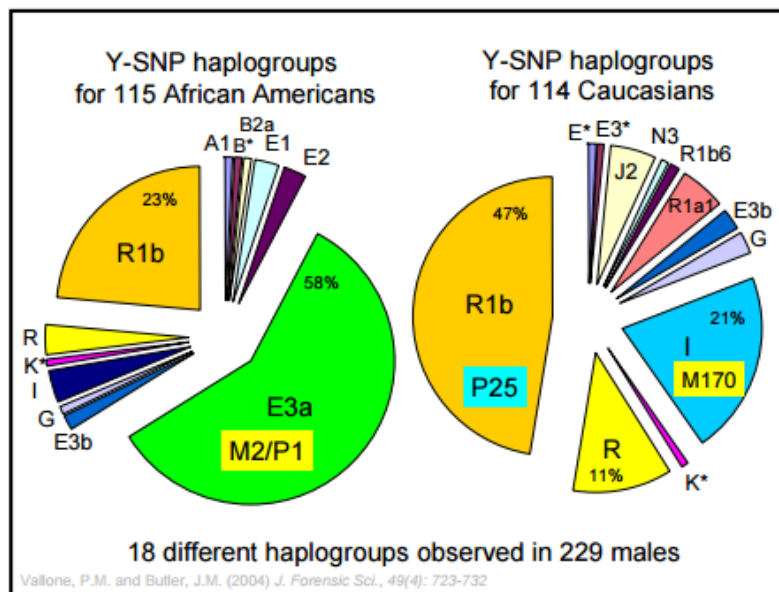


Figure 1: Afro-American and Caucasian Y-Chromosomes

**Table 2: Native American and Afro-American Y-Chromosomes**

Native American and Afro-American Y-Chromosomes Haplogroups		
Haplogroups	Native American	Afro-American
Q-P36	0.2	31.2
P-M027	0.2	0.3
R-M17	1.5	1.1
R-P25	0.2	0.3
R-M269	21.9	17.3

M.F. Hammer *et al.*, Forensic Science Intern. 164 (2006) 45-56

Miller *et al.*, (2006) did a detailed study of Afro-American and Native American (NA) Y-Chromosome. Miller *et al* (2006) revealed that NA and AAs share many R haplogroups including R-M17 and R-M207 (Table 2). It is interesting to note that in relation to R-M269, that 21% of NAs carried this haplogroup, while 17.0 of AAs carried the same haplogroup. This is interesting because there is very little statistical difference between 17% and 21%.

In a study, of the genetic ancestry of over 5269 self-described Afro-Americans who were customers of 23and Me, discovered that the frequency of Y-chromosomes carried by AAs varied across geographic locations in the US (Bryc *et al.*, 2014).

Bryc *et al.*, (2014) yielded genome-wide ancestry estimates of 24% European ancestry and 0.8% Native American ancestry among Afro-Americans.

The Bryc *et al.*, (2014), did not break down the European haplogroups carried by Afro-Americans, but given the research of Hammer *et al.*, (2006) and Vallone and Butler (2004) a majority of these AAs probably were carriers of R1.

#### Caribbean

The frequency of R haplogroups in the Caribbean vary (Figure 2). The AA clades in the Caribbean can be divided into R+, R1b (M269 ,V88) and RM306 (R (xR1a-M20 and R1a-M420) (Simms *et al.*, 2012).

Haitians and Jamaicans carry a variety of European haplogroups (Figure 2). In Haiti and Jamaica RM306 is 21.1% and 18.9% respectively. The majority of Haitians carry 14.6% M269, and the Jamaicans carry 13.2% of the same clade. In relation to R-V88 Haitians carry 4.9% of the clade and Jamaicans carry 3.8% R-V88.

The frequency of M269 and V88 in the Caribbean, are strikingly similar to those found along the Guinea coast where many AA slaves originated. Whereas, in Western and Central Africa and beyond we find V88 as the predominant R clade. Among AAs in North America and the Caribbean the major R haplogroup is R-M269 (Figure 2), like the majority of carriers of the R clade from Guinea and Guinea-Bissau (Gonzalez *et al.*, 2013) (Table 1).

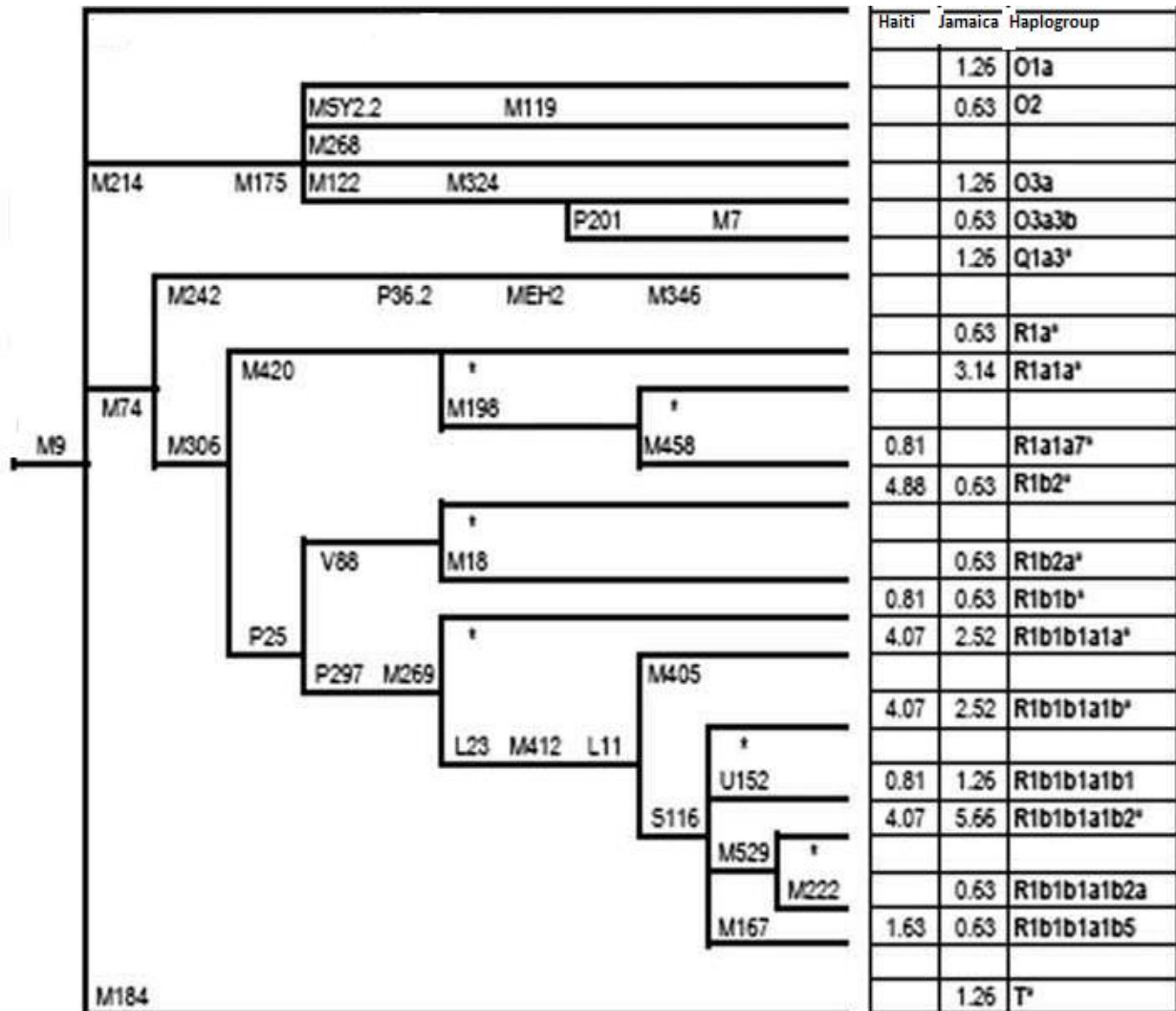
#### Discussion

The Map of Africa illustrates the global existence of the R chromosome in Africa. The frequency of Y-Chromosome R clades in Africa, supports an ancient presence of this paternal gene pool among West Africans.

The global presence of the R macrohaplogroup in Africa suggests that Africans may have took this clade into Europe, and explains why it is found in Europe.

It has always been known that the first hunter-gatherers of Europe were SSAs (Winters, 2016). Now we can declare that the carriers of haplogroup R1, that introduced the European agro-pastoral cultures to Europe, i.e., Bell Beaker and Yamnaya were probably also SSAs because they carried V88 (and M269) and Dravidians were carrying R1a.

This should not be surprising according to Turek (2012), the Bell Beaker culture probably began in Morocco, moved to Iberia and spread across Europe. Neolithic migrants into Europe from the Levant were also SSA.



Adapted from Simms et al (2012), The Paternal Structure of Haitians and Jamaicans.  
**Figure 2: Haitian and Jamaican R Clades**

Holliday (2000), tested the hypothesis that if modern Africans had dispersed into the Levant from Africa, "tropically adapted hominids" would be represented in the archaeological history of the Levant, especially, in relation to the Qafzeh-Skhul hominids. This researcher found that the Qafzeh-Skhul hominids (20,000-10,000), were assigned to the Sub-Saharan population, along with the Natufians samples (4000 BP). Holliday (2000) also found African fauna in the area. If they were Sub-Saharan Africans in the Levant some of these Africans may have carried the R-M334.

Winters (2010b) argued that the P clade originated in Africa because 1) the age of R-V88 and 2) the widespread nature of R1 in Africa and prehistoric Europe.

Researchers have found that the TMRCA of V88 was 18kya (Kivisild, 2017). Eurasians carry R- M269 mutation dates to 15kya (Kivisild, 2017). Chromosome R1b1a1a2 has high frequencies in England, France, Italy and Germany.

The Bronze Age remains of the Y-Chromosomes of Central Europe, Northern Caucasus and the Steppe belt belong to sub-clades of haplogroups: R1a-M420 and R1b-M343. Late Neolithic, Early Bronze Age and Iron Age are usually the R1b-L11, R1a1-Z283 and R1a-M417 (xZ645). The R1 samples from the Yamnaya and Samara belong to sub-clades R-V88, R1b11-Z2105 and R1a2-Z93 (Kivisild, 2017).

## **Research Article**

### **Conclusion**

It is obvious that African and Dravidian speakers could have introduced R1 into Asia, Iberia in the East and the Levant in the West. The early presence of SSAs in the Levant (Holliday, 2000), that probably migrated into the Steppes and other parts of Eurasia and the spread of the Beaker Bell culture from Morocco into Iberia and thence across Europe makes it clear that Africans probably carried the R clade into Europe. This view is supported by the genomic evidence that clearly, make R-V88 older than R-M269 and, the reality that the former haplogroup separated from R-M334 first (Kivisild, 2017).

Granted there was admixture between SSA females and European males that could have helped spread R1 among Afro-Americans. The global nature of R1 clades in Africa suggest that this macrohaplogroup originated in Africa. The presence of the diverse R1 clades in areas where African slaves originated, make it clear that RV88, R-M269 and R1a, represent a genetic signature for some SSA living in West Africa before the Atlantic Slave Trade and European colonization. This along with the antiquity of V88, whose origin was in Africa and its early separation from R-M334 indicate that when some Afro-Americans came to America they carried R1. As a result, Europeans were probably not the only source for the R1 paternal clades in North America and the Caribbean.

### **REFERENCES**

**Abu-Amero, K. K., Hellani, A., González, A. M., Larruga, J. M., Cabrera, V. M., & Underhill, P. A. (2009).** Saudi Arabian Y-Chromosome diversity and its relationship with nearby regions. *BMC Genetics*, 10, 59. <http://doi.org/10.1186/1471-2156-10-59>.

**Aravanan KP (1976).** Physical and cultural similarities between Dravidians and Africans. *Journal of Tamil Studies* 10 23–7.

**Aravanan KP (1979).** *Dravidians and Africans*, Tamil Kottam, Madras, India.

**Aravanan KP (1980).** Notable negroid elements in Dravidian India. *Journal of Tamil Studies* 17 20-45.

**Balakrishnan R (2005).** African Roots of the Dravidian -speaking Tribes: A Case Study in Onomastics. *International Journal of Dravidian Linguistics* 34(1) 153-202

**Berniell-Lee G, Calafell F, Bosch E, Heyer E, Sica L, Mougouma-Daouda P, van der Veen L, Hombert J-M, 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.

**Browne KE (2004).** *Creole Economics: Caribbean Cunning under the French Flag*, (Austin, Texas: University of Texas Press).

**Bryc K, Durand EY, Macpherson JM, Reich D and Mountain JL (2014).** The Genetic Ancestry of African Americans, Latinos, and European Americans across the United States. *The American Journal of Human Genetics* 96(1) 37 – 53.

**Butler JM (2006).** NEAFS Y-mtDNA Workshop (Butler and Coble). *Y-Chromosome: Background and Y-SNPs. Populations, Statistics, Mutations.* Available: <http://citeseerx.ist.psu.edu/viewdoc/download?doi=10.1.1.693.8705&rep=rep1&type=pdf>

**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 Science International Genetics* 5(2) 114-6.

**Coia V et al., (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* 128 678–681.

**Coupeau S (2008).** *The History of Haiti*, (Westport, Connecticut: Greenwood Press).

**Cruciani F, La Fratta R, Santolamazza P, Sellitto D, Pascone R, Moral P, Watson E, Guida V, Colomb EB, Zaharova B, Lavinha J, Vona G, Aman R, Cali F, Akar N, Richards M, Torroni A, Novelletto A and Scozzari R (2004).** Phylogeographic analysis of haplogroup E3b (E-M215) Y chromosomes reveals multiple migratory events within and out of Africa. *American Journal of Human Genetics* 74 1014–1022.



**Research Article**

**Cruciani F, Trombetta B, Massaia A, Destro-Bisol G, Sellitto D and Scozzari R (2011).** A revised root for the human Y-Chromosomal Phylogenetic Tree: the origin of patrilineal diversity in Africa. *American Journal of Human Genetics* **88** 814–818.

**Cruciani F, Trombetta B, Sellitto D, Massaia A, Destro-Bisol G, Watson E, Beraud Colomb E, Dugoujon JM, Moral P and Scozzari R (2010).** Human Y chromosome haplogroup R-V88: a paternal genetic record of early mid Holocene trans-Saharan connections and the spread of Chadic languages. *European Journal of Human Genetics* **18** 800–807.

**González M, Gomes V, López-Parra AM, Amorim A, Carracedo Á, Sánchez-Diz P and Gusmão L (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* **21**(3) 324–331. <http://doi.org/10.1038/ejhg.2012.167>

**Hammer MF et al., (2006).** Population structure of Y chromosome SNP haplogroups in the United States and forensic implications for constructing Y chromosome STR databases. *Forensic Science International* **164**(1) 45 - 55.

**Henriques F (1964).** *Jamaica: Land of Wood and Water*, (USA, New York: London House and Maxwell).

**Hirbo,JB.(2011).**Complex Genetic History of East African Human Populations. Dissertation Doctor of Philosophy.

**Holiday T (2000).** Evolution at the Crossroads: Modern Human Emergence in Western Asia. *American Anthropologist* **102**(1) 54–68.

**Hurwitz S and Hurwitz E (1971).** *Jamaica: A Historical Portrait*, (USA, New York: Praeger Publishers).

**Kivisild T (2017).** The study of human Y chromosome variation through ancient DNA. *Human Genetics* **136**(5) 529–546. Available: <https://link.springer.com/article/10.1007/s00439-017-1773-z>

**Lahovary N (1963).** *Dravidian Origins and the West*, (India, Madras: Longmans).

**Lal BB (1963).** *The Only Asian Expedition in Threatened Nubia: Work by an India Mission at Afyeh and Tumas*, (London: The Illustrated Times).

**Naidoo T, Schlebusch CM, Makkani H, Patel P, Mahabeer R, Erasmus JC and Soodyall H (2010).** Development of a single base extension method to resolve Y chromosome haplogroups in sub-Saharan African populations. *Investigative Genetics* **1** 6. Available: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2988483/>

**Pepin J (2005).** From the Old World to the New World: an ecologic study of population susceptibility to HIV infection. *Tropical Medical International Health* **10** 627–639.

**Reich D, Patterson N, Campbell D, Tandon A, Mazieres S, Ray N and Ruiz-Linares A (2012).** Reconstructing Native American Population History. *Nature* **488**(7411) 370–374. Available: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3615710/>

**Rosa A, Ornelas C, Jobling MA, Brehm A and Villems R (2007).** Y-chromosomal diversity in the population of Guinea-Bissau: A multiethnic perspective. *BMC Evolutionary Biology* **7** 124.

**Scheinfeldt LB, Soi S and Tishkoff SF (2010).** Working toward a synthesis of archaeological, linguistic, and genetic data for inferring African population history. *Proceeding National Academy of Science USA* **107**(Supplement 2) 8931–8938.

**Sergent B (1992).** *Genèse de L'Inde*, (France, Paris: Payot).

**Simms TM, Wright MR, Hernandez M, Perez OA, Ramirez EC, Martinez E and Herrera RJ (2012).** Y-chromosomal diversity in Haiti and Jamaica: Contrasting levels of sex-biased gene flow. *American Journal of Physical Anthropology* **148** 618–631.

**Turek J (2012).** Chapter 8 – “Origin of the Bell Beaker phenomenon. The Moroccan connection”, In: Fokkens, H. & F. Nicolis (edition) 2012: *Background to Beakers: Inquiries into Regional Cultural Backgrounds of the Bell Beaker Complex*, (Netherlands, Leiden: Sidestone Press). Available: [https://www.academia.edu/1988928/Turek\\_J.\\_2012\\_Chapter\\_8\\_-](https://www.academia.edu/1988928/Turek_J._2012_Chapter_8_-)

**Research Article**

**Upadhyaya P and Upadhyaya SP (1979).** Les liens entre Kerala et l’Afrique tels qu’ils ressortent des survivances culturelles et linguistiques. *Bulletin de L’Institut Fondamental d’Afrique Noire* **1** 100–32.

**Vallone PM and Butler JM (2004).** Y-SNP typing of U.S. African American and Caucasian samples using allele-specific hybridization and primer extension. *Journal of Forensic Sciences* **49** 723–732.

**Winters C (2007).** Did the Dravidian Speakers Originate in Africa? *Bio Essays* **27** 497–8.

**Winters C (2008).** Origin and spread of Dravidian speakers. *International Journal of Human Genetics* **8** 325–9.

**Winters C (2010a).** Sickle Cell Anemia in India and Africa. *International Journal of Hematology* **7**. Available: <https://print.ispub.com/api/0/ispub-article/3381>

**Winters C (2010b).** The Fulani are not from the Middle East. *Proceedings of the National Academy of Sciences of the United States of America* **107**(34) E132. <http://doi.org/10.1073/pnas.1008007107>

**Winters C (2010c).** 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 (2012).** A comparison of Fulani and Nadar HLA. *Indian Journal of Human Genetics* **18**(1) 137–138. <http://doi.org/10.4103/0971-6866.96686>

**Winters C (2015).** *We Are Not Just Africans: The Black Native Americans*. Createspace.

**Winters C (2016).** *The Phylogeography of Afro-Americans and Africans*. Createspace.

**Wood ET, Stover DA, Ehret C et al., (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.