



The Demic expansion of the M-Haplogroup from East Africa to the Senegambia

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Received: 26 November 2010 / **Accepted:** 05 December 2010 / **Published online:** 02 September 2011

Abstract

The M haplogroup was carried to Asia by anatomically modern humans (amh) 60kya. The spatial distribution of haplogroup L3(M) and LOd across Sub-Saharan Africa suggest significant demic expansion of carriers of the haplogroup M. The basal L3(M) motif is characterized by the Ddel site np 10394 and Alul site np 10397 in haplotype AF-24 which is at the base of the M haplogroups. Haplotype AF-24 belongs to haplogroup LOd which is not found in Asia, and suggest a human migration from East Africa to the Senegambia by amh using the Sangoan industry 80-50kya.

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Article citation:

Clyde Winters.2011. The Demic Expansion of the M Haplogroup from East Africa to the Senegambia. *Bioresearch Bulletin* 4: 217-220.



INTRODUCTION

Many researchers assume that the M haplogroup was probably part of the original out of Africa event around 60kya (Kivisild et al, 2004; Macaulay et al, 2005; Rando et al, 1998; Tanaka et al, 2004; Sun et al, 2006). Much has been written about the spread of M haplogroups in Asia, but nothing has been written about the demic diffusion of the M haplogroup across Africa. In this paper we discuss this migration.

MATERIALS AND METHOD

We analyzed the mtDNA sequences of the M haplogroup from Africa, Asia, India, Southeast Asia and Oceania from the literatures (Gonzalez et al, 2006,2007; Ingman et al, 2000, 2003; Kivisild et al, 1999, 2004; Macaulay et al, 2005; Rajkumar et al, 2005; Sun et al, 2005; Tambeto et al, 2000; Tanaka et al, 2004). This review of prior literature on haplogroup M allowed us to critically look at the distribution of the Macrohaplogroup M across Africa.

RESULTS

The transitions 489T>C,10400C>T, and 15043G>A define Haplogroup M, though in the early studies membership in Haplogroup M was usually determined from the results of an RFLP test—an AluI site of np 10397 (an indicator of 10400T). The DdeI site np 10394 and AluI site np 10397 in haplotype AF24 (DQ112852) are at the base of the M macrohaplogroup

All members of haplogroup M also have other well known differences. From CRS, namely 10398G and 10873C, which are the ancestral states, compared to the mutation 10398G>A and 10873C>T that occurred in Haplogroups N and R on the line to CRS, and the HVR1 mutation 16223T>C, which also occurred in haplogroup R, also on the line to CRS. Haplogroup M originated from an African Haplogroup L3 background.

The M1 macrohaplogroup is found throughout Africa and Asia. But the basal M1 lineage has not been found outside Africa (Kivisild et al, 2004; Rajkumar et al, 2005;Sun et al, 2005).

The Haplogroup M1 branch is defined by several mutations, including 195T>C, 16129G>A, 16249T>C and 16311 T>C, in the control region, and 6446G>A,6680T>C,12403A>C and 14110T>C (Sun et al, 2005). The RFLP of M1, considered diagnostic in many early studies, is by MnlI site loss at 12402 (an indicator of 12403T).

Gonzalez et al (2007), reports that the highest frequency of M1 is found in Sub-Saharan Africa especially East Africa. The molecular evidence makes it clear that haplogroup M1 is not confined solely to Ethiopia as maintained by Olivieri et al (2006). This haplogroup along with HGs N and M*, are also found in Tanzania

In Tanzania the predominate M1 clades are M1, M1a1 and M1a5. In Senegal the predominate M1 lineage is M1c1.

In addition to haplogroups M1, M* and N in Sub-Saharan Africa we also find among the Senegambians haplotype AF24 (DQ112852. Gonder et al (2006) maintains that LOd is “the most basal branch of the gene tree”. The TMRCA for LOd is 106kya. This makes haplotype AF-24 much older than L3a.

Haplotype AF-24 is an ancient African haplotype.This haplotype is also found among the Khwe, a Khoisan speaking group of South Africa (Chen et al, 2000). AF-24 is aligned to the Asian M macrohaplogroup. Makes it clear that the M nodal (032,MA13) characterizing the Indian M haplogroups comprises haplotype AF-24.

The Senegalese haplotype AF-24 (DQ112852) belongs to the rare ancient mtDNA haplogroups LOd (Kivisild et al, 2006). The LOd haplogroup is limited only to West Africa, East Africa and South Africa (Gonder et al, 2006).

The majority of carriers of Haplogroup LOd live in East (and South Africa) and speak Khoisan. Haplogroup LOd probably originated in east Africa (Gonder et al, 2006).

Haplogroup LOd is the most ancient genome. The LOd transitions include 14381,4232,6815,8113A, 8152,8251, 12121, 15466, 15930, 15941, 16243.

Haplogroup LOd predicts a significant period of time for anatomically modern humans (amh) living in Africa to spread across the continent. The existence of the LOd haplotype AF-24 among Senegalese supports this view. AF-24 is an ancient haplotype associated with LOd.

Haplogroup LOd is found at the root of human mtDNA. Gonder et al (2006) maintains that LOd is “the most basal branch of the gene tree”. The TMRCA for LOd is 106kya. This makes haplotype AF-24 much older than L3a and probably explains why this haplotype is found among the Khwe (Chen et al,2000).

The TMRCA of LOd dates to 106kya. As a result, anatomically modern humans (amh) had



plenty of time to spread this haplogroup to Senegal. In West Africa the presence of amh date to the Upper Palaeolithic (Giresse,2008). The archaeological evidence makes it clear that amh had ample opportunity to spread LOd and L3(M,N) which has an affinity to AF-24 (Chen,2000), to West Africa during this early period of demic diffusion.

The earliest evidence of human activity in West Africa is typified by the Sangoan industry (Phillipson,2005). The amh associated with the Sangoan culture may have deposited Hg LOd and haplotype AF-24 in Senegal thousands of years before the exit of amh from Africa. This is because it was not until 65kya that the TMRCA of non-African L3(M,N) exited Africa (Kivisild et al, 2006).

Anatomically modern humans arrived in Senegal during the Sangoan period. Sangoan artifacts spread from East Africa to West Africa between 100-80kya. In Senegal Sangoan material has been found near Cap Manuel (Giresse, 2008), Gambia River in Senegal (Davies,1967; Wai-Ogussu,1973); and Cap Vert (Phillipson,2005).

DISCUSSION

Gonder et al (2006) argues that the TMRCA of mtDNA L3(M,N) and their derivatives is around 94.3kya. It was not until 65kya that the TMRCA of non-African L3(M,N) exited Africa. This was over 30,000 years after the rise of L3 and LOd and predicts a significant period of time for anatomically modern humans (amh) living in Africa to spread L3(M) haplogroups across the continent. The existence of the basal L3a(M) motif and the LOd haplotype AF-24 among Senegalese supports this view.

Gonder et al (2006) claimed that LOd is exclusive to the southern African Khoisan (SAK) population. The presence of the ancient AF-24 haplotype among the Senegalese (Chen et al, 2000), that is absent in other parts of Africa, suggest a long-term population in the Senegambia that preserved this rare haplotype—that originated early in the history of amh.

Moreover, the existence of the L3a(M) motif in the Senegambia characterized by the DdeI site np 10394 and AluI site np 10397 in haplotype AF24 (DQ112852) make a 'back migration of M1 to Africa highly unlikely, since this haplotype is associated with LOd (Kivisild et al, 2006). The first amh to reach Senegal belonged to the Sangoan

culture which spread from East Africa to West Africa probably between 100-80kya.

The reality that AF-24 is a haplotype of haplogroup LOd makes it clear that this haplotype is not only an ancient human genome, it is also evidence that AF-24 probably did not originate in Asia, since it was found among the Senegalese and Khoisan, and reflects an early migration from East Africa to West Africa. The presence of basal nucleotides characteristic of macrohaplogroup L3 (M) in West Africa and the reality that M1 does not descend from an Asian M macrohaplogroup because of the absence of AF24 in Asia (Sun et al, 2005) and its presence among the Khoisan and Senegalese suggest that expansion of M1 was probably from Africa to Eurasia. The existence of haplotype AF-24 and basal L3(M) lineage in East and West Africa suggest the probable existence of the Proto-M1 lineage in Africa, not Eurasia since we find an earlier spread of amh to West Africa, than Eurasia.

ACKNOWLEDGEMENT

I would like to thank those researchers who have read earlier versions of this paper and made comments relating to how it could be improved. This paper was not funded by any organizations.

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