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The African Origin of mtDNA Haplogroup M1

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Abstract: The aim of this study is to determine the geographical origin of haplogroup M1. Controversy surrounds the origin and expansion of the M1 haplogroup (hg). Some researchers believe that the M1 macrohaplogroup originated in Asia and represents a backflow to Africa, while other researchers believe hg M1 is of African origin. The analysis of M1 clades in Africa and Eurasia illustrate a high frequency for hg M1 in Sub Saharan Africa instead of Asia and the Near East; and the distribution of haplogroups L3(M) and LOd across Sub Saharan Africa dating back to the Sangoan period make a 'back migration' of M1 to Africa highly unlikely.

Key words: Haplogroup, Sangoan, clade, haplotype, mtDNA, subhaplogroup

INTRODUCTION

Controversy surrounds the origin and expansion of the M1 haplogroup. Gonzalez *et al.* (2007) believe that the M1 macrogroup originated in Asia and represents a backflow to Africa. Other researchers believe that the M haplogroup originated in Africa (Sun *et al.*, 2006; Quintana-Murci *et al.*, 1999). Quintana-Murci *et al.* (1999) has suggested that M1 probably originated in Ethiopia prior to the out of Africa migration 60kya.

The M1 haplogroup is a member of the M macrohaplogroup. M1 is a sister haplogroup to Haplogroup D, one of the major Asian subgroups in Macrohaplogroup M. The M, N, and R macrogroups are found throughout East and South and Southeast Asia, the Andaman Islands and Africa (Ingman *et al.*, 2000, 2003; Macaulay *et al.*, 2005; Tanaka *et al.*, 2004). The M haplogroup was probably part of the original out of Africa event around 60,000 ya (Kivisild *et al.*, 2004; Macaulay *et al.*, 2005; Rando *et al.*, 1998; Tanaka *et al.*, 2004; Sun *et al.*, 2006), but there is controversy over wether haplogroup M1 originated in Africa, or later in Asia.

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). 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.

MATERIALS AND METHODS

We analyzed the mtDNA sequences of the M haplogroup from Africa, Asia, India, Southeast Asia and Oceania from the literatures at the Uthman dan Fodio Institute in Chicago, Illinois USA (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.*, 2006; Tambeto *et al.*, 2000; Tanaka *et al.*, 2004). This meta-analysis of mtDNA literatures allowed us to critically look at the distribution of M1 alleles across the Macrohalogroup M.

RESULTS

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.*, 2006).

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.*, 2006). The RFLP of M1, considered diagnostic in many early studies, is by MnII site loss at 12402 (an indicator of 12403T).

Gonzalez *et al.* (2007), believes that M1 originated in Asia and the most ancient M1 sublineage (called M1c by Gonzalez *et al.*, 2007), originated in Northwest Africa, though he reports that the highest frequency of M1 is found in Sub-Saharan Africa especially East Africa.

Haplotypes with HVSI transitions defining 16129-16223-16249-16278-16311-16362; and 16129-16223-16234-16249-16211-16362 have been found in Thailand and among the Han Chinese (Fucharoen *et al.*, 2001; Yao

et al., 2002) and these were originally thought to be members of Haplogroup M1. However, on the basis of currently available FGS sequences, carriers of these markers have been found to be in the D4a branch of Haplogroup D, the most widespread branch of M1 in East Asia (Fucharoen *et al*., 2001; Yao *et al*., 2002). The transitions 16129, 16189, 16249 and 16311 are known to be recurrent in various branches of Haplogroup M, especially M1 and D4.

Earlier researchers failed to fine M1 among the M lineages in India (Rajkumar *et al*., 2005; Olivieri *et al*., 2006). Gonzalez *et al*. (2007) also states that the M1 HVSI diagnostic motif has not been found among Indian M haplogroups. Gonzalez *et al*. (2007) divided M1 primarily into to subgroups which he called M1a and M1c, which are now named M1a1 positions 3705, 12346 and M1b position 13111. M1a1 may be identified when only the HVS1 data is available by its characteristic 16359C. The transitions 16260 and 16182 occur in subgroups of for M1a1, so they too may be used to identify a M1a1 sample.M1a1 lineages are frequently found in Ethiopia and East Africa. The M1a2 position 15884 (called M1b by Gonzalez *et al*., 2007) branch is identified by an HVS1 transitions at 16185, and a deletion at 16190 deletion, is common in West Africa and Jordan. Gonzalez *et al*. (2007) notes that the M1a2 (his M1c) clade is found in Northwest and West Africa.

To estimate the coalescence age of haplogroup M1 Gonzalez *et al*. (2007) analyzed 13 complete sequences of haplogroup M1. Gonzalez *et al*. (2007) claims that the M1c lineage is the oldest M1 subclade based on the coalescence age estimation of the M1 subgroup: M1a (16756 +-5997), M1b (10155 +-3590) and M1c (19040+-4916). This makes M1a and M1b the youngest clades. The available sample for M1c was complete sequences from individuals found in Jordan, Senegal, and Spain. The small data set make a precise estimation of the errors in the data uncertain.

The limited sample for M1c makes it difficult to effectively quantify the estimation error for the data, since error increases from level to level in models possessing a hierarchical structure. The small sample size makes the confidence intervals overlap. This calls into question the conclusions of Gonzalez *et al*. (2007) despite the differing levels of hierarchy. If the sample used by Gonzalez *et al*. (2007) had been larger we might expect the researchers to have paid close attention to the estimated value of the variance in the data sets. Given the extremely small size of the data set, the researchers probably has too much confidence in the predicted ages for the M1 subsets, because the sample was too small to allow the estimation errors to propagate as the data was analyzed. The failure to effectively estimate uncertainty in the limited data set probably led to estimation errors in the predicted ages for the M1 subclades, which inflated the age of M1c in relation to the other M1 subsets.

Table 1: Continental Population frequencies, Means and Standard Deviations for Haplogroups M1 and M1a based on Gonzalez *et al*. (2007)

Haplogroup Countinent	M1 Percent	M1a Percent	Mean	S D
Europe	17.9	11.0	14.5	3.45
North Africa	13.7	2.0	7.85	5.85
Africa	55.4	68.0	61.7	6.3
Asia	13.0	19.0	16	2.85

In addition to the evidence of the coalescence age estimation in support of the antiquity of M1c, Gonzalez *et al*. (2007) believe the presence of M1c among Jordanians is an important indicator for the ancient origin of this clade. The evidence of M1c in Jordan, does not really add to the hypothesis that M1c is the oldest clade because the presence of this clade in the Middle East can be explained by the thousands of West Africans who have taken the hajj to Mecca, and remained in the Middle East, instead of returning to West Africa.

The Valencia sample can also be explained by the history of Islam. There is a direct link between Senegal and Tariq ibn Ziyad's invasion of Spain in 711. This link comes from the fact that many of the followers of Tarik came from the *ribats* or 'religious schools' he had established in northern Senegal. Troops from these ribats formed the backbone of Tarik's army. These African Muslims ruled much of Spain until 1492. Since M1c is presently found in Senegal, the carrier of M1c reported by Gonzalez *et al*. (2007) in Valencia may be a descendent of these African 'Moors' that ruled Spain for over 700 years.

Sub-Saharan Africans probably spread hg M1c to Eurasia. Gonzalez *et al*. (2007) reported that the carriers of the M1c subset were from Jordan, Senegal and Valencia. It was revealed above that 1) many of the Muslim troops in Tarik's army that conquered Spain in 711 AD, came from Senegal; and 2) many West Africans after taking the Hajj, visited Jerusalem and settled in the Middle East. Even if we eliminate the Jordan sample, the evidence from Valencia and Senegal gives a 67% probability that M1c originated in Senegal, not Asia or North Africa because of the historical presence of Sub-Saharan Africans in both areas.

The results published by Gonzalez *et al*. (2007) fail to support his conclusion. In Table 1, we see the geographical ancestry of the groups used in this study. The percentage of individuals carrying this haplogroup in this study was between 13.0 and 55.4% for M1 and 11.0 and 68.0% for M1a1.

The distribution of continental populations carrying the M1 haplogroup favors Africa as the place of origin instead of Asia for both haplogroup M1 (55.4%) and haplogroup M1a1 (68.0%). The population distributions for both M1 (Fig. 1) and M1a (Fig. 2) make it clear that the most varied M1 subhaplogroups appear across Sub-Saharan Africa, not Asia or North Africa.

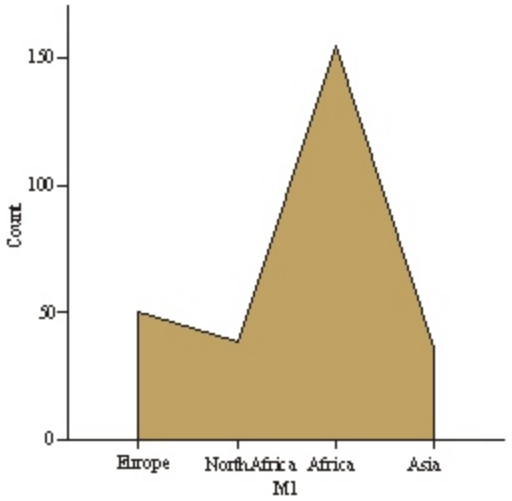

Fig. 1: Continental distribution of M1

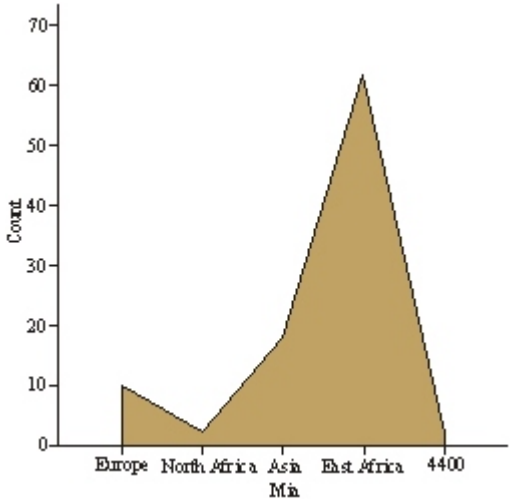

Fig. 2: Continental distribution of M1a

Gonzalez *et al.* (2007) claim that their research is supported by the research of Olivieri *et al.* (2006). Anna Olivieri *et al.* (2006) claims that M1 originated in Asia and the M1 haplogroup represents a back-migration into Ethiopia. Olivieri *et al.* (2006) based this conclusion on: 1) the absence of any distinguishing M1 root mutations in Asian M haplogroups; 2) the presence of M1only in East Africa and North Africa and 3) the lack of any Asian specific clades within M1. These conclusions by Olivieri *et al.* (2006) are incongruent with the evidence of M1 transitions in Asian M clades.

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, Uganda, Egypt and the Senegambian region (Gonzalez *et al.*, 2006; Gonder *et al.*, 2006; Winters, 2007).

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 hapotype AF24 (DQ112852), which is delineated by a DdeI site at 10394 and AluI site of np 10397. The AF-24 haplotype is a branch of the African subhaplogroup L3 (Chen, 2000). This is the same delineation of haplogroup M*. It is clear from the molecular evidence that the M1, M and N haplogroups are found not only in Northeast Africa, but across Africa from East to West (Winters, 2007).

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. Barnabas *et al.* (2005) 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 (Rosa *et al.*, 2004), East Africa and South Africa (Gonder *et al.*, 2006).

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 presences 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-Ogusu, 1973); and Cap Vert (Phillipson, 2005).

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

Table 2: Distribution of M1 Subhaplogroups, taken from Olivieri *et al.* (2006)

Haplogroup	M1a	M1a1	M1a1a	M1a1b	M1a1b1	M1a1c	M1a1d	M1a1e	M1a2a	M1a2b	M1a2	M1a3	M1a4	M1a5
Country														
Med N	-	-	4	5	30	-	-	45	24	28	-	31	-	-
Med S	-	-	7	-	-	-	-	21	24	-	-	30	-	-
Near East	-	20	4	-	-	-	-	-	-	-	-	-	-	-
Egypt	-	-	-	-	-	-	-	-	-	-	29	32	37	-
East Africa	74	33	-	-	-	21	54	-	-	53	-	-	110	79

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.

Olivieri *et al.* (2006) provide a detailed discussion of the M1 macrohaplogroup. The distribution of the M1 superhaplogroup is outlined in Table 2. Here we note that as in the Gonzalez *et al.* (2007) study, the widest distribution of M1 clades appear in Sub Saharan Africa, not the Near East or the Mediterranean region (Fig. 3).

Haplogroup M1 is found throughout Africa. The diversity haplogroup M1 on in Sub-Saharan Africa makes it clear that it could not be the result of a back migration. The predominate language spoken by carriers of M1 and M* in Africa outside of Ethiopia are Niger Congo speakers. The people in Ethiopia and Egypt that carry M1 hg speak Afro-Asiatic languages.

The fact that haplogroup M1 is found among Niger-Congo speakers and Afro-Asiatic speakers is telling given the fact that the both the Niger-Congo speakers and Afro-Asiatic speakers are associated with the Nubia. The major cultural group in Nubia during the Neolithic was the C-Group. The C-Group people of Nubia are associated with the rise of millet cultivation in Africa (Winters, 2008b), and spread of this crop and the red-and-black ceramic style from Africa to India (Singh, 1982; Winters, 2008b). Welmers (1971) explained that the Niger-Congo homeland was in the vicinity of the upper Nile valley.

In support of this theory he discusses the dogs of the Niger-Congo speakers. This is the unique barkless Basenji dogs which live in the Sudan and Uganda today, but were formerly recorded on Egyptian monuments (Welmers, 1971). According to Welmers (1971) the Basanji, is related to the Liberian Basenji breed of the Kpelle and Loma people of Liberia. Welmers believes that the Mande took these dogs with them on their migration westward. The Kpelle and Loma speak Mande languages.

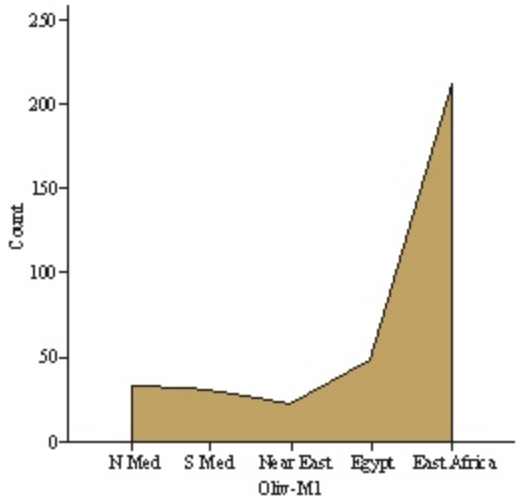

Fig. 3: Olivieri *et al*. (2006) normative M1 groups by region

Welmers (1971) proposed that the Niger-Congo speakers remained intact until 5000 years ago. This view is supported by linguistic and genetics evidence. The linguistic evidence makes it clear that the Nilo-Saharan and Niger-Congo languages are related. The genetic evidence indicates that Nilo-Saharan and Niger-Congo speakers carry the M3b*-M35 gene, an indicator for the earlier presence of speakers of this language in an original Nile Valley homeland.

The distribution of M1 in Africa is widespread. We see evidence of this haplogroup from East to West and even down into South Africa. M1 is found among many African groups especially the Niger-Congo speakers. This is very interesting because most researchers have established the origin of this linguistic family in Nubia. From here the speakers of this language family migrated in West Africa and East Africa. The numbers indicate the carriers of M1 in the various African nations

Linguistic research makes it clear that there is a close relationship between the Niger-Congo Superlanguage family and the Nilo-Saharan languages spoken in the Sudan. Heine and Nurse (2000), discuss the Nilo-Saharan connection. They note that when Westerman (1911) described African languages he used lexical evidence to

include the Nilo-Saharan and Niger-Congo languages into a Superfamily he called "Sudanic". Using Morphological and lexical similarities Gregersen (1972) indicated that these languages belonged to a macrophylum he named Kongo-Saharan. Research by Blench (1999) reached the same conclusion, and he named this Superfamily: "Niger-Saharan".

There was a close relationship between the the Niger-Congo speakers in Nubia and the Ethiopians. This view is supported by the archaeological evidence that support a close relationship between the Ethiopians and Nubians. For example, according to Fattovich (2008) the pottery from Tihama Cultural Complex and other Ethiopian sites shows similarities to the Kerma and C-Group pottery. Given this connection between Ethiopian civilizations and civilizations in Nubia, may explain the presence of the M1 haplogroup among people in East and West Africa which formerly lived in intimate contact.

In addition to M1 in Africa, we also find haplogroups M*, M23, M3 positions 482 and 16126; M30 positions 195A and 15431 and M33 position 2361. It is interesting to note that the presence of these genes, which are normally found in India are also found in Africa, is interesting given the presence of M1 in India and the existence of these genes among populations stretching from Africa into Yemen on into India along a path associated with the spread of the Tihama culture (Winters, 2008b).

The map makes it clear that M haplogroups so far found in Africa vary. They not only vary but illustrate the expansion of the Niger-Congo and Nilo-Saharan speakers. Both groups originally lived in Nubia and may have been part of the C-Group people of Nubia. Recently haplogroup M23 has been found among Afro-Americans and Malagasy. Malagasy include many Niger-Congo (Swahili) terms.This haplogroup may have formerly been found in East Africa which exported hundreds of thousands of slaves to the United States. Many parts of East Africa were depopulated as a result of the Atlantic Slave Trade

The earliest civilization in Southwest Arabia date back to the 2nd Millenium BCE. This culture is called the Tihama culture which originated in Africa (Fattovich, 2008). Keall (2008) believes that these people may have had a common ancestry and shared a common culture. The Tihama civilization probably originated in Nubia. It is characterized by the cheesecake or pillbox burial monuments which extend from Dhofar in Nubia, the Gara mountains to Adulis on the Gulf of Zula, to Hadramaut, Qataban, Ausan, Adenm, Asir, the Main area and Tihama.

Shared culture of the C-Group people (who probably included many Niger-Congo speakers would explain the affinity between the earliest Ethio-Semitic culture :Tihama and the C-Group. At Tihama and other sites in Arabia we find pottery related to the C-Group people of Nubia (Keall, 2000; 2008; Fattovich, 2008; Giumlia-Mair, 2002) The archaeological evidence indicates that C-Group people expanded from Nubia to Mesopotamia and the Indus Valley. It appears that whereas the Egyptians preferred the cultivation of wheat, many ancient C-Group people were agro-pastoral people who cultivated Millet/Sorghum and rasied cattle. Millet was the main crop of the Dravidian speakers of India and people of the Indus Valley (Possehl, 1986; Winters, 2008a).

Numerous linguists and anthropologists claim that the Dravidians originated in Africa. For example, Lal (1963), a leading Indian archaeologist made it clear that he saw a relationship between the C-Group people of Nubia and Dravidian speakers. In relation to the anthropological evidence Aravanan (1976,1979,1980), Homburger (1930,1948, 1951,1955), Sergent (1992), Sastri (1966), Lahovary, Upadhyaya (1976,1979) claim that the Niger-Congo and Dravidian languages are genetically related.

DISCUSSION

There is considerable evidence that M1 is found in Asia. Researchers have found the M1 haplogroup in the Caucasus (Bermisheva *et al*., 2004; Tambeto *et al.*, 2000) Central Asia, and East Asia (Comas *et al.*, 1998; Fucharoen *et al*., 2001). In addition, the Russian haplotype 16183c-16189, 16249, 16311 match the M1 HVSI sequence (Malyarchuk *et al*., 2004).

Olivieri *et al.* (2006) claim that East African M1 root mutations are absent in Eurasian M sister clades is not supported by the evidence. For example researchers have found that the Tanzanian M1 haplogroup cluster with people from Oceania (Gonder *et al*., 2006). And, as mentioned earlier the M1 mutations 16129, 16189, 16249 and 16311 are found in many southeast and East Asian haplogroups (Fucharoen *et al*., 2001; Yao *et al*., 2002). In addition, Roychoudhury *et al.* (2001) noted defining nucleolides shared by East African M1, and Indian M haplogroups include HG M4 at 16311 ; HG M5 at 16,129; and HG M34 at 16,249; and Sun *et al.* (2006) found that the most frequent transitions in Indian M haplogroups were 16129,16311 and 16189 (Sun *et al*., 2006). It is interesting to note that whereas 489c is found in Eastern African and Indian M mtDNA analyzed, it was not found in the non M haplogroup controls.

It is also not true that HG M1 is absent in India. Gonzalez *et al.* (2007) report the presence of one individual carrying hg M1 in the Appendix of their study. Kivisild *et al.* (1999) noted that 26 of the subjects in his study belonged to the M1 haplogroup . Kivisild *et al.* (1999) reported subcluster M1 was found mainly in Kerala and Karnataka high caste individuals (Kivisild *et al*., 1999).

Kivisild *et al*. (1999) made it clear that each Indian M lineage has its own unique star features. Kivisild *et al*. (1999) found 5 major haplogroup M subclusters in India: Haplogroup M1 transitions at 16129,16189 and

Fig. 4: Geographical distribution of M1 Haplogroup in Africa

16311 (were reported by Kivisild *et al*., 1999 in Fig. 3), Haplogroup M2 447G,1780,11083,15670, 16274 and 16319 transitions Haplogroup M3, Haplogroup M4 position 16311, and Haplogroup M5 positions 1888 and 16129 .

Chaubey *et al.* (2006) claims that the haplogroup Kivisild *et al*. (1999) identified as M1, is now HG M3. But this can not be supported by the reading Kivisild *et al.* (1999) phylogeny of Indian M haplogroups outlined in Fig. 3, makes this unlikely. A cursory examination of Fig. 3 (Kivisild *et al*., 1999) makes it clear that these researchers found different transitions for the Indian M1 and M3 subclusters as reported in their study.

Olivieri *et al.* (2006) argue that M1 was probably spread from the Levant back into Africa by the Aurignacian culture. The craniofacial and molecular evidence does not support this conclusion (Winters, 2007). There have been numerous Sub-Saharan skeletons found in the Levant and Europe (Barral and Charles, 1963; Diop, 1974, 1991; Brace *et al*., 2006; Boule, 1957; Verneaux, 1926). Moroever, the identification of Sub-Saharan craniometric features (Ehret, 1979; Haak *et al*., 2005; Holiday, 2000; Wendorf, 1968) and N haplogroup among ancient skeletons found at sites in Europe formerly occupied by Cro-Magnon people (Haak *et al*., 2005), suggest that the ancient Sub-Saharans in the Levant and Europe already possessed the N (and M) haplogroup(s) when they arrived in these areas from Africa.

CONCLUSION

In conclusion, we must reject the contention of Gonzalez *et al.* (2007) and Olivieri *et al.* (2006) that M1 originated in Asia because 1) the possible Senegalese origin of the M1c subclade; 2) the absence of the AF-24 haplotype of haplogroup LOd in Asia; and 3) the African origin of the Dravidian speakers of India.

An Asian origin for hg M1 must also be rejected because of the craniometric and genetic evidence that the Dravidian speakers who carry the Indian M haplogroups originated in Africa and spread to India within the past 4500 years (Lal, 1963; Winters, 2007, 2008b). Although Gonzalez *et al.* (2007) attempts to use Olivieri *et al.* (2006) to support their research, the latter paper fails to offer it support. The research indicates that contrary to Olivieri *et al.* (2006) view that hg M1 is only found in Africa, M1 transitions are found in many Asian M haplogroups (Fucharoen *et al*., 2001; Yao *et al*., 2002) this along with the distribution of the M1 haplogroup across Sub Saharan Africa (Fig. 4) and the greatest diversity theory support an African origin of M1, rather than an Asian origin because most diversified M1 lineages are found in Sub Saharan Africa, not Europe or Asia. Moreover the diversity of M haplogroups in Africa can not be accounted by back migrations from Asia to Africa (Fig. 5).

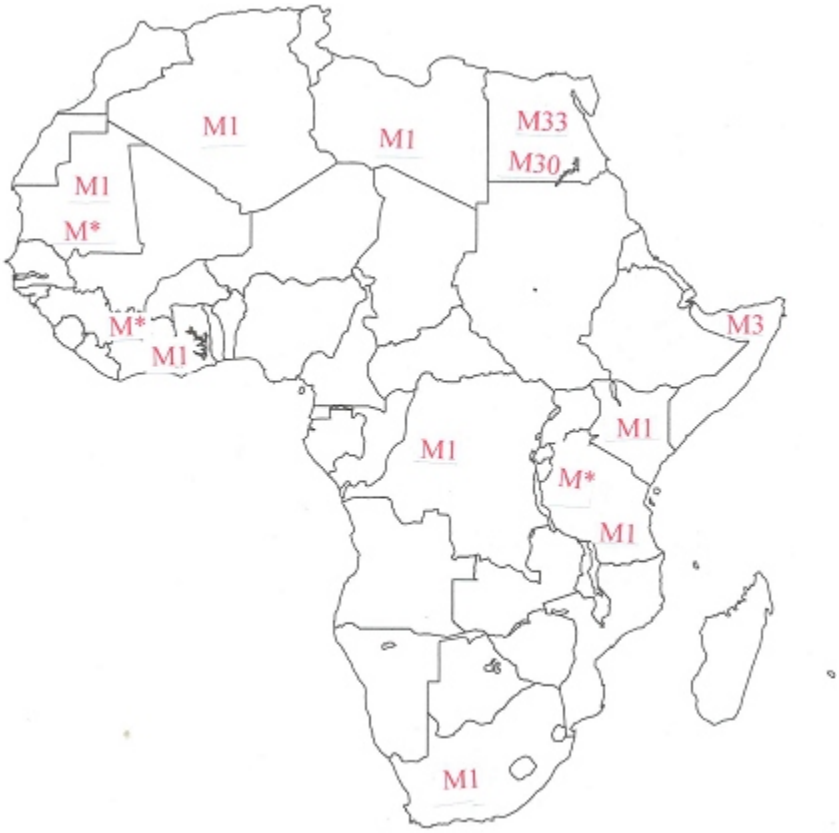

Fig. 5: M Haplogroups in Africa

The research yielded 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 acrohaplogroup 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*., 2006) 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.

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