Genetics and Molecular Biology, 36, 2, 167-176 (2013)
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Research Article

Reconstruction of major maternal and paternal lineages of the Cape Muslim population

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Abstract

The earliest Cape Muslims were brought to the Cape (Cape Town - South Africa) from Africa and Asia from 1652 to 1834. They were part of an involuntary migration of slaves, political prisoners and convicts, and they contributed to the ethnic diversity of the present Cape Muslim population of South Africa. The history of the Cape Muslims has been well documented and researched however no in-depth genetic studies have been undertaken. The aim of the present study was to determine the respective African, Asian and European contributions to the mtDNA (maternal) and Y-chromosomal (paternal) gene pool of the Cape Muslim population, by analyzing DNA samples of 100 unrelated Muslim males born in the Cape Metropolitan area. A panel of six mtDNA and eight Y-chromosome SNP markers were screened using polymerase chain reaction-restriction fragment length polymorphisms (PCR-RFLP). Overall admixture estimates for the maternal line indicated Asian (0.4168) and African mtDNA (0.4005) as the main contributors. The admixture estimates for the paternal line, however, showed a predominance of the Asian contribution (0.7852). The findings are in accordance with historical data on the origins of the early Cape Muslims.

Keywords: PCR-RFLP, genetic polymorphism, mitochondrial DNA, population genetic structure, chromosome variations.

Received: November 13, 2012; Accepted: March 12, 2013.

Introduction

In 1652, the first Dutch settlers arrived in Cape Town, South Africa, to establish a refreshment station for the Dutch East India Company (DEIC) ships en route to and from the East (Du Pre, 1994). The importation of slaves shortly began after the establishment of the refreshment station serving as the major labour force at the Cape, following failed attempts to enslave the indigenous Khoisan people (Da Costa and Davids, 1994; Shell, 2000). The DEIC imported slaves from the East Coast of Africa, India, Madagascar, Sri Lanka and the Indonesian Archipelago. (Bradlow and Cairns, 1978; Davids, 1980; Mahida, 1993; Da Costa and Davids, 1994; Shell, 2000). The importation of slaves remained a common practice at the Cape even after the transfer of the colony to British Empire in 1795 and again in 1806 (Giliomee, 2003). Alongside the slaves, convicts and political exiles (mainly from Indonesia) were also sent to the Cape, some of whom were prominent Muslim clerics (adherents of the faith Islam) who later became known as the Vryezwarten or Free Blacks (Bradlow and Cairns, 1978; Davids, 1980; Mahida, 1993; Shell, 2000). It is estimated that 63,000 slaves were brought to South Africa between 1652 and 1807, when the British abolished the oceanic slave trade (Shell, 2000). The major proportion of slaves, however, was not imported but were Cape-born (Bradlow and Cairns, 1978). These slaves were of mixed parentage due to the mixed relations among early White settlers, the Khoisan, slaves, and the so-called Bantu-speaking people (Pickel, 1997). In the early 18th century the slave population exceeded the settler population, with males outweighing the number of females in both the slave and free populations (Shell, 2000). Marriage between European men and women, who were either Khoisan, manumitted (freed) slaves or of mixed parentage (Keegan, 1996), and between Khoisan and slaves were thus not uncommon and were socially acceptable, but already from the 18th century, offspring of such mixed marriages and liaisons mainly were assimilated into the growing population group known as 'Coloured', after race-based restrictions were imposed by the British (Mountain, 2003). These periods also proved extremely fertile for the spread of Islam, which was mainly attributed to the growing number of Free Blacks who were well schooled in Islam and eager to convert slaves. Furthermore, Dutch colonist encouraged slaves to embrace Islam fearing the loss of their property after a Placaaten (Law) was issued that prevented the sale of baptised Christian slaves. Islam became a flourishing religion after the emancipation of slaves in 1834, and by 1840 they represented a third of the total Colony population, which had then become a more cohesive group later to be known as Cape Malay (Davids, 1980). This distinct ethnic identity was later

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re-enforced by the apartheid government Population Registration Act of 1950, which classified Cape Malay as a subgroup of the Coloured classification (Da Costa Y 1990, PhD thesis. University of South Africa, Pretoria). The term Malay was initially introduced by whites to describe Muslims and subsequently became synonymous with being Muslim (Bickford-Smith, 1994). Terms such as Coloured Muslim, Javaan, and Mohammedan were also used to reflect the religious and diverse ethnic identity of Muslims, later to be used interchangeably by Muslims themselves (Adihikari, 1989). In recent times the term Cape Muslim has become a more socially acceptable term to describe the Muslim community residing in the Cape Metropolitan region, which consists of diverse ethnic subgroups the majority being the descendants of early Cape Muslims (who mainly self-identify as Cape Coloured Muslim and Cape Malay Muslim) and the descendants of Indian immigrants (Cape Indian Muslims). The history of the Cape Muslims has been well documented and researched, however no significant genetic studies have been undertaken. To date only one genetic study using Y-STR markers has attempted to analyze the parental contributions made to this community (Cloete *et al.*, 2010). In the study, nine Y-STR loci (DYS19, DYS389-I, DYS389-II, DYS390, DYS391, DYS392, DYS393) were used to characterize the minimal haplotype, and the duplicated locus DYS385) as well as eight widely used loci of DYS449, DYS481, DYS518, DYS557, DYS570, DYS607, DYS612 and DYS614. Factorial Correspondence Analysis was used to establish genetic relations between the Cape Muslim population using published data from three South African populations namely Asian Indian, European English and Xhosa. The results indicated that the Cape Muslim population was more closely related to the Asian Indian population, followed by the European English in the second place, and more distantly related to the Xhosa (Cloete *et al.*, 2010). In the present study, mitochondrial DNA (mtDNA) and the non-recombining Y chromosome (NRY) were screened using PCR-RFLP analysis with the aim of determining the African, Asian and European contributions to the mtDNA (maternal) and NRY (paternal) of the Cape Muslim population, thereby providing some insight into the genetic ancestry of this population.

Material and Methods

Sample collection and DNA extraction

Buccal swab samples were collected from a 100 anonymous, unrelated Muslim males born in the Cape Town Metropolitan area. Information pertaining to donor's languages spoken, familial birthplaces, and a short genealogy of two generations for maternal and paternal family members to establish regional ancestry were also obtained. This was done to draw more conclusive answers regarding the population history and explore past demographic events of this population. The self-perceived ethnic identity listed by donors and the number of individuals in each Cape Muslim subgroup were: Cape Coloured Muslim (n = 34), Cape Indian Muslim (n = 29), Cape Malay Muslim (n = 27) and Cape Other Muslim (n = 10). The term 'Other' refers to individuals that were reluctant to indicate an ethnicity or formed part of a Cape Muslim minority subgroup. The question of identity in the Cape Muslim community has always been a point of interest. A study conducted by Da Costa (1994) considered the problem of identity amongst Muslims, post-apartheid. His research suggested that many Muslims chose a religious identity over other forms of identity such as national origin or ethnicity. All samples were obtained with informed consent, and ethical clearance for the study was approved by the Senate Research Committee of the University of the Western Cape, South Africa. DNA was extracted from buccal swabs using the BuccalAmpTM DNA extraction kit (Epicentre Technologies) according to the manufacturer's instructions. Extracted DNA was further purified with a standard phenol chloroform protocol to improve the quality of the DNA as well as the sensitivity of the PCR.

Mitochondrial DNA

A total of six restriction sites and one insertion/deletion polymorphism (IDP) were analyzed in the study according to published PCR-RFLP protocols. The markers included an *Alu*I loss at np 7025 (denotes haplogroup H), *BstO*I loss at np 13704 (denotes haplogroup J), *Hpa*I gain at np 3592 (denotes haplogroup L), *Dde*I gain at np10394 and *Alu*I gain at np 10397 (denotes haplogroup M) (Santos *et al.*, 2004). The IDP screened was the COII/tRNA^{Lys} intergenic 9-bp deletion (denotes haplogroup B) (Martinez-Cruzado *et al.*, 2001) which has routinely been used to assess Asian and Asian-derived origins in populations (Edwin *et al.*, 2002). This was done following a hierarchical approach to differentiate haplogroups firstly by their DdeI 10394/*Alu*I 10397 motif (designated as +/+, +/- and -/-) then testing for the haplogroup specific marker reducing the potential to which an unknown mtDNA might belong.

Y-Chromosome

Y-chromosomal binary markers consisting of seven SNPs: M2, M35, M52, M170, M9, M175, M173 and one Alu insertion/deletion (YAP) polymorphism were used to screen DNA samples. The markers allowed the identification, of haplogroups E1b1a, E1b1b1, H1, I, K, O, R1 and DE according to methods described by (Hammer and Horai, 1995; Underhill *et al.*, 1997, 2000; Flores *et al.*, 2003; Kayser *et al.*, 2005) with only minor modifications. The nomenclature used to assign haplogroups was done according to the Y Chromosome Consortium, 2002.

Restriction digestion

The restriction digestion reactions were performed using 10 μL of the unpurified amplified product, incubated with the haplogroup specific restriction enzyme according to conditions specified by the manufacturer. The digested fragments were run alongside an undigested simile in a 3% agarose gel, previously stained with ethidium bromide and photodocumentated under UV light.

Statistical analyses

The frequencies and the number of mtDNA and NRY haplogroups were calculated by direct counting, and the admixture proportions of the maternal (mtDNA) and paternal (NRY) lines were estimated by ADMIX 95 software based on the gene identity method (Chakraborty, 1985). Principal component analysis (PCA) was done based on haplogroup frequencies using the XLSTAT program implemented in Excel (Agresti, 1990). The populations hypothesized to have contributed to the Cape Muslim admixture were chosen from published data representing three major groups namely (1) African (Khoisan), (2) Asian (Indian and South-East populations) and (3) European. Sample sizes of African, Asian and European populations were respectively n = 74 (Chen *et al.*, 2000), n = 378 (Kivisild *et al.*, 1999; Sudoyo *et al.*, 2002), and n = 956 (Byrne *et al.*, 2008) for mtDNA, and n = 129 (Underhill *et al.*, 2001, Cruciani *et al.*, 2002), n = 398 (Kayser *et al.*, 2003; Cordaux *et al.*, 2004; Tajima *et al.*, 2004), and n = 66 (Semino *et al.*, 2000) for NRY.

Results

PCR-RFLP analysis

Most of the markers used in the study were screened using PCR-RFLP analysis (Figure 1) with the exception of the 9 bp deletion for haplogroup B and the YAP element defining haplogroup DE. These markers were characterized by either an insertion or deletion polymorphism thereby rendering restriction digestion non-essential. The banding pattern of the amplified fragment was therefore sufficient to discern a genotype. None of the donors harboured the 9 bp deletion while three individuals harboured the YAP element. Haplogroup markers defined by the absence of cleaved digested fragments were verified using both positive and negative controls (Figure 2).

Maternal lineages of the Cape Muslims

The mtDNA haplogroups observed in the study are reported in Table 1. Their ancestry has phylogenetically been established (Torroni *et al.*, 1996, 2006; Wallace *et al.*, 1999; Van Oven and Kayser, 2008). Cape Muslims maternal lineages mainly belonged to haplogroups L and M (Figure 3). Haplogroup L is an African specific lineage that is distributed throughout the African continent with an increased frequency in Sub-Saharan African populations

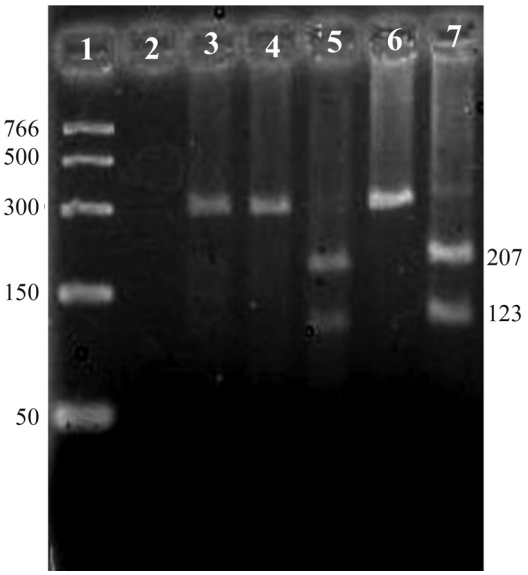

Figure 1 - RFLP screening for the 3592 *Hpa*I site (mtDNA haplogroup L). Lane 1 shows the PCR marker and lanes 5 and 7 individuals harbouring the polymorphism (207 bp and 123 bp).

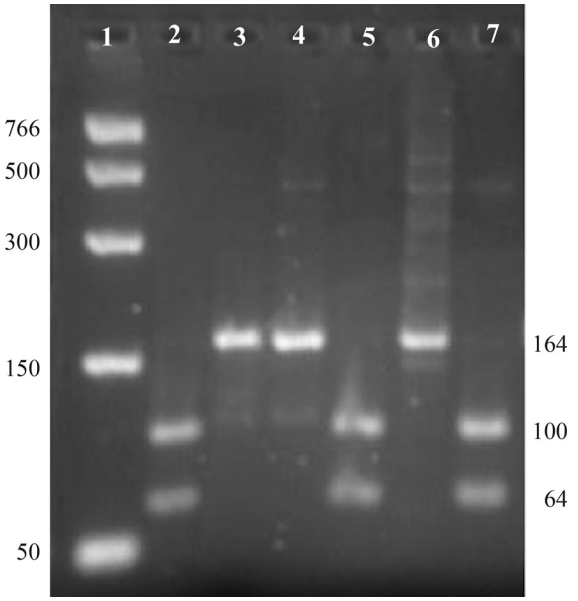

Figure 2 - RFLP screening for M9 (Y chromosome haplogroup K). Lane 1 shows the PCR marker and lane 2 and 3 the negative (100 bp, 64 bp) and positive control (164 bp) respectively. Lanes 4 and 6 show individuals harbouring the polymorphism (164 bp).

(Mishmar *et al.*, 2003; Underhill and Kivisild, 2007; Maji *et al.*, 2009).

The haplogroup distribution differed among the self-perceived subgroups, with Cape Coloured Muslims (47%) and Cape Malay Muslims (44%) showing the highest frequencies while Cape Other Muslims (20%) and Cape Indian Muslims (14%) had the lowest. The Cape Indian Muslims' mtDNA mainly belonged to an Asian lineage, haplogroup M which has the most frequent and diverse dis-

Table 1 - mtDNA and Y chromosome haplogroup distribution in the Cape Muslim population and in each self-perceived subgroup.

Haplogroup	Population				
mtDNA	Cape Coloured Muslim *n* = 34	Cape Malay Muslim *n* = 27	Cape Indian Muslim *n* = 29	Cape Other Muslim *n* = 27	Total *n* = 100
B	0	0	0	0	0
H	9 (3)	19 (5)	38 (11)	50 (5)	24 (24)
J	12 (4)	15 (4)	3 (1)	0	9 (9)
L	47 (16)	44 (12)	14 (4)	20 (2)	34 (34)
M	32 (11)	22 (6)	45 (13)	30 (3)	33 (33)
Y chromosome DE	6 (2)	0	0	10 (1)	3 (3)
E1b1a	0	0	1 (1)	0	1 (1)
E1b1b	0	0	0	10 (1)	1 (1)
H1	3 (1)	11 (3)	17 (5)	20 (2)	10 (1)
I	17 (6)	8 (2)	0	0	8 (8)
K	35 (12)	52 (14)	41 (12)	5 (5)	43 (43)
O	18 (6)	15 (4)	38 (11)	10 (1)	22 (22)
R 1	6 (2)	7 (2)	0	10 (1)	5 (5)
Others	15 (5)	7 (2)	0	0	7 (7)

Numbers outside parentheses are counts (n) and numbers inside the parentheses are percentages.

tribution in Asia, Melanesia and Native American populations (Kivisild *et al.*, 1999; Bermisheva *et al.*, 2002; Maji *et al.*, 2009). Furthermore, it represents the most dominant mtDNA haplogroup in India (Kivisild *et al.*, 1999; Roychoudhury *et al.*, 2000; Schurr and Wallace, 2002; Edwin *et al.*, 2002; Cordaux *et al.*, 2003; Tripathy *et al.*, 2008, Maji *et al.*, 2009).

The European mtDNA lineages H and J were both observed in the study albeit at different frequencies. Haplogroup H was the third most frequent mtDNA haplogroup (24%) in the study. Cape Other Muslim displayed the highest frequency (50%) followed by Cape Indian Muslims (38%). Haplogroup H is the most prevalent mtDNA in Europe with the highest frequency (40-50%) in western and northern Europe. In southern, southwestern and eastern Europe, North Africa and Turkey an intermediate frequency (20-40%) is observed. The lowest frequency for haplogroup H is reported in the Middle East, India, and Siberia (Wallace *et al.*, 1999; Alves-Silva *et al.*, 2000; Bermisheva *et al.*, 2002; Cordaux *et al.*, 2003). Haplogroup J was mainly prevalent among the Cape Malay Muslims (15%) and Cape Coloured Muslims (12%). Cape Indian Muslims had the lowest frequency (3%), while Cape Other Muslims harboured no J mtDNA. Haplogroup J represents 11.3% of European mtDNA (Wallace *et al.*, 1999) with an appreciable frequency in the Near East (Wells, 2007). The admixture estimates for the maternal line (Table 2) indicate Asian (0.4168) and African mtDNA (0.4005) as the main contributors. The PCA plot for Cape Muslim subgroups (Figure 5b) corresponded with these finding. However when the population was analysed as a group, the Cape Muslims (Figure 5a) clustered with Europeans. This could possibly

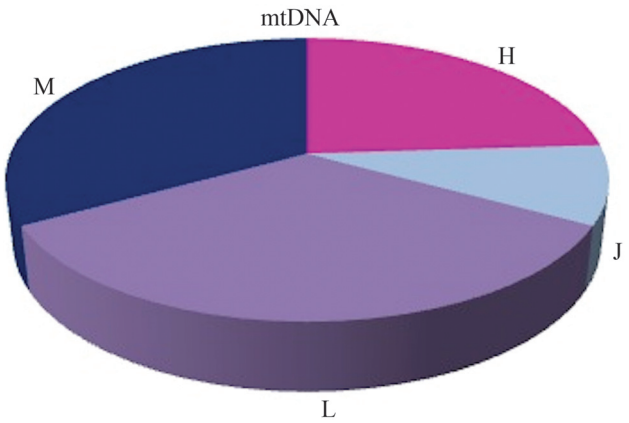

Figure 3 - mtDNA haplogroup variation in the Cape Muslim population.

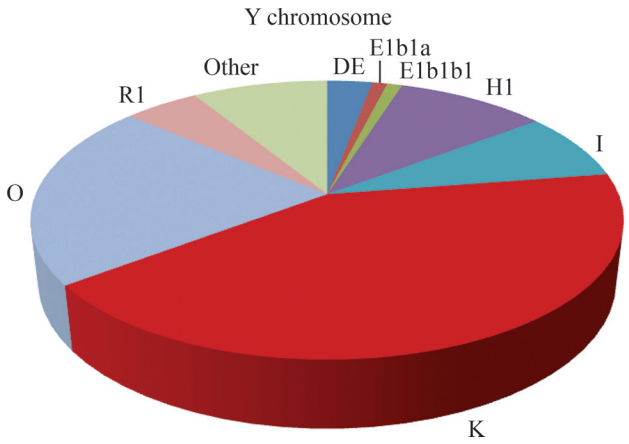

Figure 4 - Y-chromosome haplogroup variation in the Cape Muslim population.

Table 2 - Estimated admixture proportions of mtDNA lineages.

Hybrid population	African % (±SE)	Asian % (±SE)	European % (±SE)
Cape Coloured Muslim	0.5838 (0.0779)	0.4578 (0.1641)	-0.0416 (0.1667)
Cape Malay Muslim	0.5431 (0.0758)	0.2505 (0.1607)	0.2064 (0.1632)
Cape Indian Muslim	0.1208 (0.1342)	0.5705 (0.2846)	0.3087 (0.1342)
Cape Other Muslim	0.1986 (0.1365)	0.2479 (0.2895)	0.5535 (0.2941)
Total	0.4005 (0.0991)	0.4168 (0.2102)	0.1826 (0.2135)

be due to Western Eurasian haplogroups (H and J) being shared among Indian and European populations.

Paternal lineages of the Cape Muslims

Cape Muslim paternal lineages were classified into eight different haplogroups (Figure 4) mainly belonging to haplogroups H1, K and O (Table 1), with only a small percentage of paternal lineages remaining unresolved. Cape Malay Muslims displayed the highest frequency (52%) for haplogroup K, while Cape Indian Muslims demonstrated a high frequency for haplogroup O (38%) and H1 (17%). Haplogroup K is distributed throughout Asia having a substantial presence in East Asia (Basu *et al*.; 2003; Kumar *et al.*, 2007). Haplogroup O characterises a major Y-chromosome lineage in East Asia and represents 80-90% of Y-chromosomes in Southeast and East Asia, with high frequencies observed in Indian populations (Underhill, 2004; Wells, 2007; Debnath *et al.*, 2011). Haplogroup H1 is restricted to India and is frequently found among tribal and lower caste population groups (Krithika *et al.*, 2007; Karafet *et al.*, 2008).

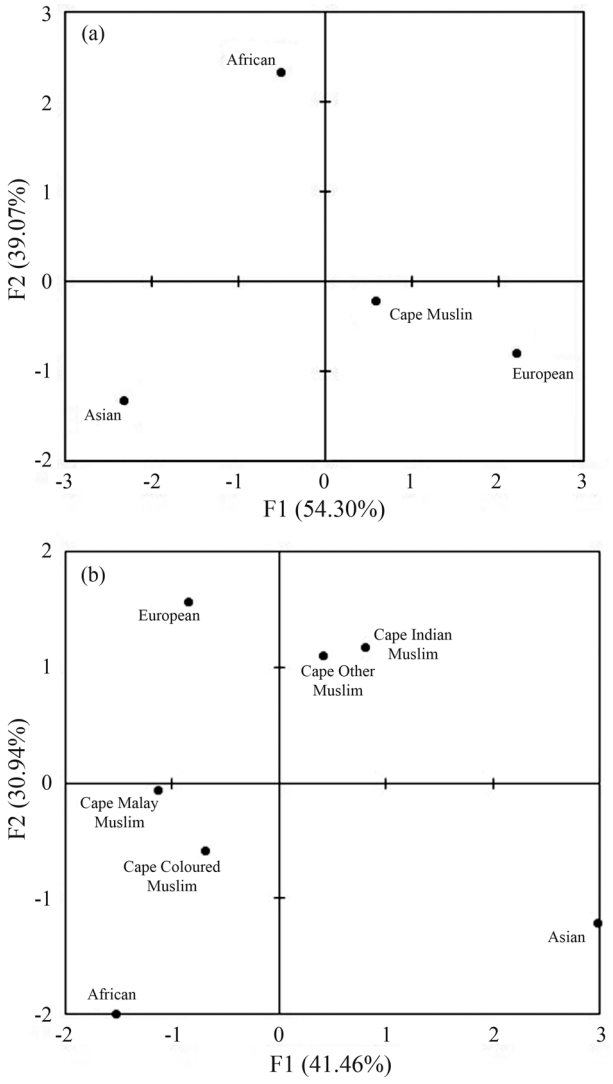

Figure 5 - Principal component analysis based on mtDNA haplogroup frequency data. (a) Cape Muslim population, (b) Cape Muslim subgroups.

The European lineages observed in the study were haplogroups R1 and I. These haplogroups are widespread across Europe and are found at high frequencies in western Europe (Cavalli-Sforza and Feldman, 2003; Rootsi *et al.*, 2004; Fregel *et al.*, 2009). Haplogroup I was the most frequent in the study it observes its highest frequency in Cape Coloured Muslims (17%), while R1 in Cape Other Muslims (10%). These haplogroups were however, absent in Cape Indian Muslims.

Haplogroups DE, E1b1a and E1b1b1 make up the remaining paternal lineages. These haplogroups had the lowest frequencies in the study and are mainly prevalent among African populations (Underhill *et al.*, 2001). The YAP element defining haplogroup DE was observed only in Cape Coloured Muslims (6%) and Cape Other Muslims (10%). This haplogroup defines both Asian (haplogroup D) and African (haplogroup E) Y-chromosome lineages. Nonetheless, its greatest frequency is observed in Sub Saharan populations (Hammer and Horai, 1995; Agrawal *et al.*, 2005). Haplogroup E1b1a is common in Sub Saharan populations and is used to trace Bantu migrations (Hammer and Zegura 2002; Beleza *et al.*, 2005; Fregel *et al.*, 2009). The haplogroup was observed in a Cape Indian Muslim while haplogroup E1b1b1 was present in a Cape Other Muslim. The haplogroup is frequent among East and North African populations (Hammer and Zegura, 2002; Beleza *et al.*, 2005). Estimates for admixture through the paternal lineage (Table 3) indicate a predominance of the Asian contribution (0.7852), which is reflected in the PCA analysis of the Cape Muslims (Figure 6a) and the self-perceived subgroups (Figure 6b).

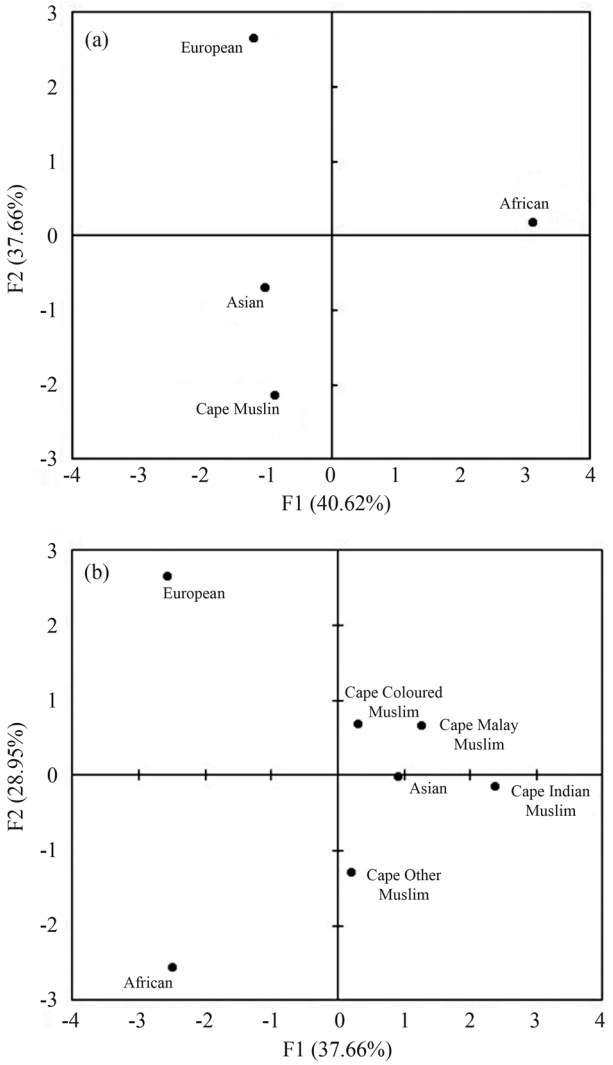

Figure 6 - Principal component analysis based on NRY haplogroup frequency data. (a) Cape Muslim population, (b) Cape Muslim subgroups.

Discussion

The data from the mtDNA haplogroups (Figure 3) and admixture estimates (Table 2) suggest a strong African contribution to the maternal gene pool of the Cape Muslim population, particularly for the Cape Coloured Muslim and Cape Malay Muslim. Cape Other Muslim (20%) and Cape Indian Muslim (14%) showed a reduced frequency (Table 1).

Haplogroup L is widely distributed among African populations especially in Sub-Saharan Africa (Wallace *et al.*, 1999; Gonder *et al.*, 2007). The presence of this haplogroup suggests Khoisan and Bantu females as likely contributors of this lineage. However, African slaves originating from Mozambique and Madagascar may also have been contributors, as haplogroup L represents a common mtDNA among the Malagasy population (Hurles *et al.*, 2005). In Cape Indian Muslims, however, haplogroup L accounts for 14% of their mtDNA, which could possibly be attributed to geneflow with the Siddis, as the genealogical survey indicated that maternal grandmothers were recent immigrants from India. The Siddis are tribal groups in India that were brought as slaves during the 16th and 17th century to India from East Africa and other regions in Africa such as Mozambique (Lodhi 1992; Gauniyal *et al.*, 2008; Shah *et al.*, 2011). Analysis of the genealogical survey indicated that maternal grandmothers were recent immigrants from India. These results also suggest that the remaining L mtDNA was mainly derived through recent admixture with either the Cape Coloured Muslim or Cape Malay Muslim.

Haplogroup M was the second most frequent haplogroup in the study. It is common among Asian populations and is the most dominant mtDNA haplogroup in India (Kivisild *et al.*, 1999; Roychoudhury *et al.*, 2000; Edwin *et al.*, 2002; Schurr and Wallace 2002; Cordaux *et al.*, 2003; Tripathy *et al.*, 2008, Maji *et al.*, 2009). A study by Cordaux *et al.* (2003) reported the haplogroup's frequency among northeastern tribes as being 51% while eastern, central and southern tribes had an equal share in the frequency of 76%. This result was consistent with findings in our study as the Cape Indian Muslims displayed the highest frequency (45%) for haplogroup M. A moderate frequency for haplogroup M was observed among the Cape Coloured Muslims (32%), Cape Malay Muslims (22%), and Cape Other Muslims (30%). The origin of their mtDNA was likely mainly derived from female slaves originating from India and South East Asia, as a significant number of Asian slaves originated from India and the Indonesian Archipelago (Bradlow and Cairns, 1978; Davids, 1980; Da Costa and Davids, 1994). Haplogroup M may even have been introduced via slaves from Madagascar due to their mixed In-

Table 3 - Estimated admixture proportions of NRY lineages.

Hybrid population	African % (±SE)	Asian % (±SE)	European % (±SE)
Cape Coloured Muslim	0.1461 (0.0920)	0.6641 (0.0925)	0.1898 (0.0264)
Cape Malay Muslim		0.8559 (0.0129)	0.1441 (0.0219)
Cape Indian Muslim	0.0954 (0.0111)	0.9046 (0.0111)	
Cape Other Muslim	0.1829 (0.0013)	0.6726 (0.0013)	0.1445 (0.0004)
Total	0.1008 (0.0376)	0.7852 (0.0378)	0.1445 (0.0004)

The empty cells correspond to unsupported parental populations that were not used in admixture calculations.

donesian ancestry and recently through admixture with Indian and other Asian populations (Hurles *et al.*, 2005).

Haplogroup H was the third most frequent mtDNA (24%) in our study. In the self-perceived subgroups, Cape Other Muslim displayed the highest frequency (50%) followed by Cape Indian Muslim (38%). A lower frequency for haplogroup J was observed, this being mainly prevalent among the Cape Malay Muslim (15%) and Cape Coloured Muslim (12%). The Cape Indian Muslim had the lowest frequency (3%), while the Cape Other Muslim harboured no J mtDNA. Haplogroup H and J may have been introduced via recent and historical admixture with European and Indian populations, as haplogroup H represents nearly 50% of European mtDna, while haplogroup J represents 11.3% of European mtDNA (Torroni *et al.*, 1996; Lell and Wallace, 2000; Bermisheva *et al.*, 2002; Loogväli *et al.*, 2004; Piechota *et al.*, 2004; Alzualde *et al.*, 2005; Manwaring *et al.*, 2006). Furthermore, West Eurasian haplogroups make up 20% to 30% of Indian mtDNA, with northern Indians possessing a higher frequency of West Eurasian mtDNA than southern Indians (Roychoudury *et al.*, 2000; Tripathy *et al.*, 2008).

Haplogroup B was the only mtDNA not observed in the study. The 9 bp deletion defining this haplogroup is routinely used to infer Asian and Polynesian ancestry (Ballinger *et al.*, 1992; Stone and Stoneking, 1998; Edwin *et al.*, 2002; Berniell-Lee *et al.*, 2008). Haplogroup B has a high to moderate frequency among East Indonesians and Malays (Stone and Stoneking, 1998; Merriwether *et al.*, 1999; Schurr and Wallace, 2002). Therefore, the absence of this haplogroup was unexpected, as a number of slaves had originated from the Indonesian Archipelago (Bradlow and Cairns, 1978; Davids, 1980; Da Costa and Davids, 1994).

To further characterise the genetic variability of the Cape Muslim population and to analyse their maternal origin in greater detail, admixture analysis and PCA analyses were carried out. Table 3 indicates the African, Asian and European maternal ancestry present in the Cape Muslim population and subgroups. Admixture estimates indicated that the Cape Muslim mtDNA is mainly of African and less so Asian and European ancestry. The PCA analysis (Figure 4) indicated that Cape Coloured Muslim and Cape Malay Muslim are more closely related to African populations, while the Cape Indian Muslim and Cape Other Muslim are so to Indian populations.

A comparison of mtDNA and NRY lineages present in the Coloured population of the Western Cape

A number of researchers have recently investigated the mixed ancestry of the Coloured population in the Western Cape (Tishkoff *et al.*, 2009; De Wit *et a*l., 2010; Patterson *et al.*, 2010; Quintana-Murci *et al.*, 2010). This is largely due to the unique opportunities this population provides for studies related to population history, natural selection, and admixture mapping. The study by Tishkoff *et al.* (2009) analyzed 1,327 nuclear microsatellite and insertion/deletion markers in a large panel of African populations and found that the Coloured population has equal levels of four ancestries: Southern African Khoisan, Bantu speaking, Indian, and European. The second study conducted by Patterson *et al.* (2010) genotyped 20 Coloured individuals using genome wide analysis of almost 900,000 markers and concluded that the Coloured population has a substantial genetic contribution from at least four population groups, *viz*. African (genetically close to isiXhosa), Indonesian, European, and South Asian. Genome wide analysis performed by De Wit *et al.* (2010) genotyped 959 self-identified Coloured individuals with nearly 500,000 markers using a linkage and admixture model. Their study revealed that the major ancestral contributions were Khoisan (32-43%), Bantu speaking Africans (20-36%), European (21-28%), and to a lesser extent Asian (9-11%), this depending on the model used. The study by Quintana-Murci *et al.* (2010) analysed mtDNA and NRY lineages of 590 individuals which indicated that the maternal pool was mainly Sub-Saharan African (79%), with a lower frequency for South/South East Asian (16%) and West Eurasian/European lineages (4.6%). The NRY haplogroups revealed that the paternal pool was predominately African (45.2%) than West Eurasian/European (37.72), and with fewer South/South East Asian paternal lineages (17.11%). These findings (De Wit *et al.*, 2010; Quintana-Murci *et al.*, 2010) were particularly interesting as they excluded Cape Muslims from their studies, focusing only on Christian Coloured individuals. The selection criteria for donors in other studies (Tishkoff *et al.*, 2009; Patterson *et al.*, 2010) were not as clearly specified and may have included Cape Muslims, as suggested by De Wit *et al.* (2010) on commenting the findings of Tishkoff *et al.* (2009) given the high Asian and European ancestry found in their study. This seems plausible given the results of the present study (Table 1), particularly when one only examines the ancestry of the oldest Cape Muslim subgroups (Cape Coloured Muslims and Cape Malay Muslims). Even though their mtDNA lineages were primarily African, considerable frequencies for Asian and European lineages were also observed. Furthermore, their paternal lineages showed a significant contribution of Asian and European lineages, with only minor African contributions. The studies regarding the ancestry of the Coloured population, particularly the one by Quintana-Murci *et al.* (2010) indicate that both Cape Muslims and the Coloured population share the same parental populations, even though the mtDNA and NRY distributions of African, Asian and European lineages may vary between these two population groups.

Conclusion

The results of this study showed a clear difference in the contribution of major continent-specific haplogroups to the maternal and paternal lineages of the contemporary

Cape Muslim population. Overall admixture estimates for the maternal line indicated Asian (0.4168) and African mtDNA (0.4005) as the main contributors. The admixture estimates for the paternal line however showed a predominance of Asian contribution (0.7852). It should be interesting to further investigate the contribution of other local small communities to the Cape Muslim populations throughout the Western Cape Province of South Africa. The study of the genetic diversity of local communities sharing the same residential areas, such as the Coloured Christian and Muslim communities living in the Kensington-Factreton residential area in the Cape Peninsula, can give genetic evidence of their origins, migration histories, and their relatedness to each other, and especially so the contribution of these communities to each other's gene pool, through intermarriages, conversion and blending.

Acknowledgments

We would like to thank all the donors who participated in the study, as well as everyone who assisted in the collection of samples. We are also grateful to Prof Yusuf Da Costa, Mr. Ebrahim Rhoda, Mr. Ebrahim Salie, Mr. Ebrahim Manual, Prof. Rob Shell, Dr Yassin Mohamed and Dr Mohamed Haron for their valuable contributions. Special thanks to Moulana Igsaan Hendricks, the president of the Muslim Judicial Council of South Africa, for his support for the study. The present study was supported by the National Research Foundation (South Africa).

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Internet Resources

ADMIX 95 Software, http://www.genetica.fmed.edu.uy/software.htm (February 17, 2013).

Associate Editor: Francisco M. Salzano

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