

## mtDNA Variation in the South African Kung and Khwe—and Their Genetic Relationships to Other African Populations

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The mtDNA variation of 74 Khoisan-speaking individuals (Kung and Khwe) from Schmidtsdrift, in the Northern Cape Province of South Africa, was examined by high-resolution RFLP analysis and control region (CR) sequencing. The resulting data were combined with published RFLP haplotype and CR sequence data from sub-Saharan African populations and then were subjected to phylogenetic analysis to deduce the evolutionary relationships among them. More than 77% of the Kung and Khwe mtDNA samples were found to belong to the major mtDNA lineage, macrohaplogroup L\* (defined by a *HpaI* site at nucleotide position 3592), which is prevalent in sub-Saharan African populations. Additional sets of RFLPs subdivided macrohaplogroup L\* into two extended haplogroups—L1 and L2—both of which appeared in the Kung and Khwe. Besides revealing the significant substructure of macrohaplogroup L\* in African populations, these data showed that the Biaka Pygmies have one of the most ancient RFLP sublineages observed in African mtDNA and, thus, that they could represent one of the oldest human populations. In addition, the Kung exhibited a set of related haplotypes that were positioned closest to the root of the human mtDNA phylogeny, suggesting that they, too, represent one of the most ancient African populations. Comparison of Kung and Khwe CR sequences with those from other African populations confirmed the genetic association of the Kung with other Khoisan-speaking peoples, whereas the Khwe were more closely linked to non-Khoisan-speaking (Bantu) populations. Finally, the overall sequence divergence of 214 African RFLP haplotypes defined in both this and an earlier study was 0.364%, giving an estimated age, for all African mtDNAs, of 125,500–165,500 years before the present, a date that is concordant with all previous estimates derived from mtDNA and other genetic data, for the time of origin of modern humans in Africa.

### Introduction

The South African Kung San were among the first human groups in which mtDNA variation was analyzed by restriction analysis (Denaro et al. 1981; Johnson et al. 1983). In these studies, the mtDNA sequences of the Kung were surveyed for variation, by means of six rare-cutting restriction endonucleases (*AvaII*, *BamHI*, *HaeII*, *HincII*, *HpaI*, and *MspI*) and Southern blotting. Although this procedure screened only 2%–3% of the mtDNA sequence for variation, it revealed that ~90%–

95% of the Kung mtDNAs were characterized by a *HpaI* site gain at nucleotide position (np) 3592. This marker was subsequently found at very high frequencies in mtDNAs of other sub-Saharan African populations (Scozzari et al. 1988, 1994; Soodyall and Jenkins 1992, 1993; Chen et al. 1995) but was not observed in populations of non-African origin, with a few exceptions (Cann et al. 1987; Soodyall 1993). Furthermore, the African mtDNAs defined by the *HpaI* np-3592 site gain formed a group of related mtDNA haplotypes (originally defined as haplogroup “L” and here redefined as “L\*”), which was found to be the most divergent of those identified in human populations from around the world (Chen et al. 1995). These findings contributed to the hypothesis of an African origin of modern human mtDNAs (Johnson et al. 1983; Cann et al. 1987; Chen et al. 1995), although other interpretations of these data have also been put forward (Excoffier and Langaney 1989; Templeton 1992).

Since 1981, relatively limited data have been collected on the RFLP variation in Kung or related Khoisan-speaking populations. Those studies that were conducted on Khoisan-speaking populations continued to

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use low-resolution (LR)-RFLP analysis with only the six rare-cutting restriction endonucleases listed above (Soodyall and Jenkins 1992, 1993). As a consequence, these data provided additional information about Khoisan groups but could not be entirely integrated with those obtained, on other populations, by high-resolution (HR)-RFLP analysis (Cann et al. 1987; Torroni et al. 1992).

The value of using HR-RFLP analysis with African mtDNAs, for phylogenetic reconstructions of human mtDNA, has been shown primarily by two studies of African populations (Cann et al. 1987; Chen et al. 1995). In the first study, Cann et al. (1987) conducted genomic digestions of mtDNAs, by 12 enzymes (*AluI*, *AvaII*, *DdeI*, *FnuDII*, *HaeIII*, *HhaI*, *HinfI*, *HpaI*, *HpaII*, *MboI*, *RsaI*, and *TaqI*), with the resulting restriction fragments being resolved by PAGE. In the later study, the entire genome of African mtDNAs was PCR amplified in nine overlapping fragments, which were then subjected to digestion by 14 enzymes (*AluI*, *AvaII*, *BamHI*, *DdeI*, *HaeII*, *HaeIII*, *HhaI*, *HincII*, *HinfI*, *HpaI*, *HpaII*, *MboI*, *RsaI*, and *TaqI*), with the resulting restriction fragments being resolved by agarose gel electrophoresis. Both of these studies revealed that African haplotypes form the deepest branches of the human mtDNA phylogeny and that African groups are the most divergent of all world populations.

Several additional aspects of mtDNA variation in African populations were shown in the Chen et al. (1995) study. First, two types of length polymorphisms were observed in some of the central-African mtDNAs (Mbuti [eastern] and Biaka [western] Pygmies), one of which was the COII/tRNA<sup>Lys</sup> intergenic 9-bp deletion that formerly had been thought to occur only in Asian populations. This length polymorphism had previously been noted in African individuals but had not been assigned to a particular haplogroup or mtDNA lineage (Cann and Wilson 1983). In addition, western-African populations from Senegal were found to have haplotypes that lacked the *HpaI* np-3592 site gain and, thus, appeared not to belong to haplogroup L\*. Because nearly all of these "non-L" haplotypes had the *DdeI* np-10394 site gain, a polymorphism that was also present in almost every haplogroup L\* mtDNA, the data suggested that the former haplotypes derived from the latter, although the exact subhaplogroup (L1 or L2) from which these non-L haplotypes originated was not clear. Alternatively, non-L mtDNAs could have evolved from haplotypes observed in Europeans, such as those belonging to haplogroups I-K (Torroni et al. 1994a), and could have been spread into Africa through population contractions/expansions since their origin. Such ambiguities clearly indicated that further analysis of non-L haplotypes was necessary in order to understand

their phylogenetic relationships to other African and non-African mtDNAs.

Similarly, until very recently, only a limited number of Kung mtDNAs had been surveyed for control region (CR) sequence variation. In earlier studies (Vigilant et al. 1989, 1991), mtDNAs from Kung individuals consistently clustered at the deepest nodes of the phylogenies constructed from CR sequences, a result that indicated that they are some of the most divergent—hence, oldest—mtDNAs present in human populations. Soodyall et al. (1996) also studied CR sequence variation in southern-African populations and found that the COII/tRNA<sup>Lys</sup> intergenic 9-bp deletion had occurred multiple times in African populations, independent of those appearing in Asian mtDNAs, a trend first noted by Vigilant (1990). Interestingly, deletion mtDNAs were not observed in Khoisan-speaking populations and were rare in western- and southwestern-African groups, whereas they occurred frequently in Pygmy and so-called Negroid populations from central Africa and in Bantu-speaking peoples of southern Africa (Soodyall et al. 1996). This distribution suggested that deletion mtDNAs arose in central Africa and were disseminated into southern Africa via the recent Bantu expansion.

Although studies using HR-RFLP methods of analysis have provided new insights into the mtDNA variation of African populations, there has been almost no effort to relate the data sets generated by RFLP to those generated by a CR sequence analyses. To date, only the western-African Mandelaku (Mandenka) have been subjected to both LR-RFLP and CR sequencing analyses (Graven et al. 1995), whereas the linkage between the HR-RFLP data and the CR sequence data for the African samples analyzed by Cann et al. (1987) and Vigilant et al. (1989, 1991) has not been made explicitly clear. Thus, the relationship between HR-RFLP haplotypes and CR sequences in African populations has yet to be adequately addressed. In addition, because of the different methods of RFLP haplotyping used in the Cann et al. (1987) and Chen et al. (1995) studies, there were some inconsistencies in the positioning of certain polymorphisms that were critical for phylogenetic reconstructions of the haplotypes defined in each study. Consequently, a more complete characterization of the distribution of genetic variation in coding (i.e., RFLP) versus noncoding (i.e., CR) regions of the mtDNA genome was needed.

Both to increase our knowledge of the genetic relationships between Khoisan (Kung San and Khoi) populations and other African peoples, and to better define the relationship between RFLP and CR sequence variation within these groups, we conducted HR-RFLP and CR sequence analyses of 74 Kung San and Khwe individuals from southern Africa and then compared the

resulting data to those obtained for African populations in previous studies. This comparison revealed that many of the Kung mtDNAs clustered within a distinct sublineage (L1a<sub>2</sub>) of subhaplogroup L1a and that the Khwe are more closely genetically related to western-African (Bantu-speaking) populations than they are to the Kung San. Furthermore, the genetic relationships deduced from HR-RFLP analysis were found to be completely consistent with—and sometimes more detailed than—those obtained from CR sequencing alone. These findings implied the need for studies combining the two methods of analysis, in order to more fully understand the genetic relationships among human populations.

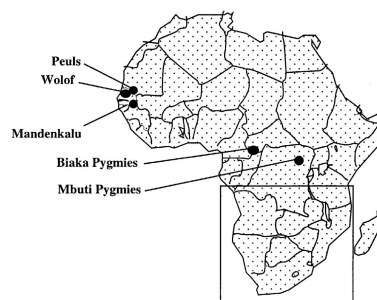
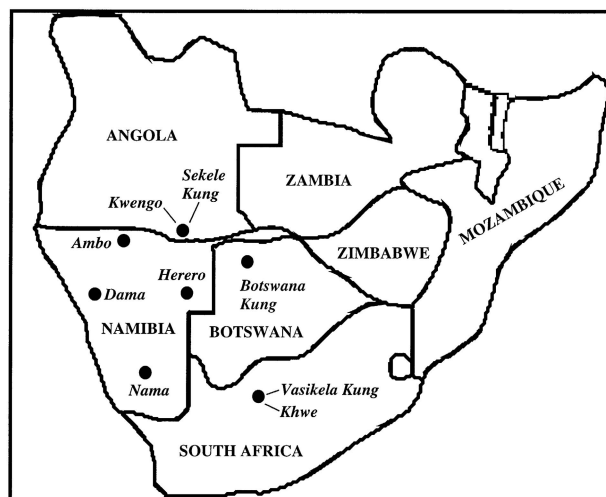
## Subjects and Methods

### Subjects

Khoisan-speaking populations can generally be divided into two distinct groups, the San and the Khoi. San populations consist of 10 different Kung groups (“!Xu” is pronounced “Kung”), as well as the //au//en, Nharo, G/wi, G//ana, !Xo and G!aokxite, who also speak click-languages. The Khoi consist of five populations—two Topanaar groups and the Kede, Hei//om, and Nama. A third set of southern-African populations, which coexist with Khoisan-speaking groups, are the so-called Negroids, who are largely Bantu-speakers. These include the Kwisi, Kwadi, Cimba, Dama, Kgalagadi, and Denasena (Nurse et al. 1985). Although the two Khwe (Kwengo) groups physically appear to be “Negroid,” they speak a Khoisan language (de Almeida 1965). Consequently, they have been called “black Bushmen.” The geographic locations of the populations analyzed in this study, as well as the populations to which they are compared, are shown in figure 1.

A total of 181 Khoisan-speaking individuals of the northwestern Kalahari Desert in southern Africa formed the sample group for this study. Of this group, 144 were identified as Kung (Vasikela Kung), 37 as Khwe (also known as “Barakwena”). Of the 181 southern-African mtDNA samples, 74 (43 Kung and 31 Khwe) were analyzed for mtDNA sequence variation.

The individuals involved in this study were classified according to the ethnicity listed on either their identity documents or birth certificates. In the few rare cases in which this information was not available, both parents were independently questioned about their own ancestry before their child was classified as belonging to either of the two groups. Fortunately, in all cases, the family history furnished by both parents was identical, simplifying the classification of their children. Interpreters were used in the interviews and counseling sessions, and care was taken to verify the data and information gathered. Even though these two groups have been known to in-



**Figure 1** Map of southern Africa, and geographic locations of Khoisan and non-Khoisan populations surveyed for mtDNA variation.

termarry, no such instance was recorded for these particular individuals.

### Sample Acquisition and Preparation

After informed consent was obtained, two 10-ml tubes of blood were collected from Kung and Khwe individuals, by venipuncture, in acid citrate–dextrose vacutainer tubes and then were stored at 4°C until they were shipped to Emory University. At Emory University, the blood samples from each individual were separated into their constituent cellular fractions, by low-speed centrifugation. The platelets were subsequently collected from the plasmas by centrifugation in 15-ml Corning tubes, at 5,000 *g* and 10°C for 20 min; all the mtDNAs used in the RFLP and CR sequence analyses were then extracted from these platelet pellets (Torrioni et al. 1992).

### Molecular Genetic Analysis

The entire mtDNA of each sample was subjected to HR-RFLP analysis using the primer pairs and PCR amplification conditions described by Torrioni et al. (1992, 1993). This HR-RFLP analysis defined the *complete haplotype* for each individual. The evolutionary rela-

**Table 1**  
**HR mtDNA Haplotypes in Southern-African Populations**

HR HAPLOTYPE <sup>a</sup>	STATUS <sup>b</sup>		No.		
	<i>Hpa</i> I	<i>Dde</i> I	Kung	Khwe	Total
AF46	+	+		2	2
AF80	-	+		1	1
AF81	-	+		1	1
AF82	-	+	2		2
AF83	-	+		6	6
AF84	-	-		1	1
AF85	-	+	4	1	5
AF86	-	+	1		1
AF87	+	+	6		6
AF88	+	+	3		3
AF89	+	+	5		5
AF90	+	+	2		2
AF91	+	-	2		2
AF92	+	-		5	5
AF93	+	+	2		2
AF94	+	+	1		1
AF95	+	+	1		1
AF96	+	+	1		1
AF97	+	+	2		2
AF98	+	+		1	1
AF99	+	+	1	6	7
AF100	+	+	4		4
AF101	+	+	4		4
AF102	+	+		2	2
AF103	+	+		1	1
AF104	+	+		1	1
AF105	+	+		3	3
AF106	+	+	1		1
AF107	+	+	1		1
Total			43	31	74

<sup>a</sup> As defined by the polymorphic restriction sites shown in Appendix A.

<sup>b</sup> A plus sign (+) denotes presence, and a minus sign (-) denotes absence.

tionships among the Kung and Khwe mtDNAs were further differentiated by the sequencing of both hypervariable segments (HVS-I and HVS-II) of the CR of each individual, by methods described by Schurr et al. (1999). Both hypervariable segments were PCR amplified by use of heavy-strand primer H15704 (np 15704–15723) and light-strand primer L770 (np 770–751), whereas two different sets of primers—H15978 (np 15978–15997) and reverse primer L16501 (np 16501–16483) for HVS-I, H1 (np 1–19) and L429 (np 429–412), for HVS-II—were used for sequencing. The resulting data were analyzed by SEQUENCHER 3.0 software (Gene Codes).

*Phylogenetic Analyses*

The phylogenetic relationships between the mtDNA haplotypes observed in the Kung and Khwe and those previously reported in the other sub-Saharan African populations (Chen et al. 1995) were inferred by parsimony analysis with PAUP 3.1.1 (Swofford 1994) and PAUP 4.0.2b (Swofford 1998).

The samples included complete haplotypes of 62 Senegalese (AF01–AF24, AF26–AF36, AF45–AF59, AF64–AF65, and AF70–AF79), 17 Pygmy (AF25, AF37–AF44, AF60–AF63 and AF66–AF69), and 29 Kung and Khwe (AF46, AF80–AF107). All dendrograms were rooted from a chimpanzee haplotype that was extrapolated from the whole mitochondrial genome sequence presented by Horai et al. (1995), by identification of all recognition sequences of the 14 enzymes used in the HR-RFLP analyses. The African haplotypes were also midpoint rooted without an outgroup.

Maximum parsimony (MP) trees were generated via random addition of sequences, by the tree-bisection and-reconnection (TBR) algorithm, with ≤10 MP trees being saved for each replication. Because of the numerous terminal taxa in this data set, a large number of MP trees were obtained, with 3,000 MP trees being generated after 1,388 replications. Although shorter trees could exist, none were observed in this analysis. Strict and 50%-majority-rule consensus trees encompassing all MP trees were also obtained, to test the consistency of the branching order in the MP trees. Similarly, the data were subjected to bootstrap analysis to test the statistical support for the branch structure of the MP trees. All RFLP haplotypes were bootstrapped through 10–500 replications, with resampling of characters (i.e., RFLPs) by the TBR algorithm, with a 50%-majority-rule bootstrap consensus tree being generated from the best trees saved after each independent analysis. Genetic distance/neighbor-joining (NJ) trees were also generated by PAUP 4.0.2b, on the basis of the mean character differences of the haplotypes. These were also subjected to bootstrap analysis (Swofford 1998).

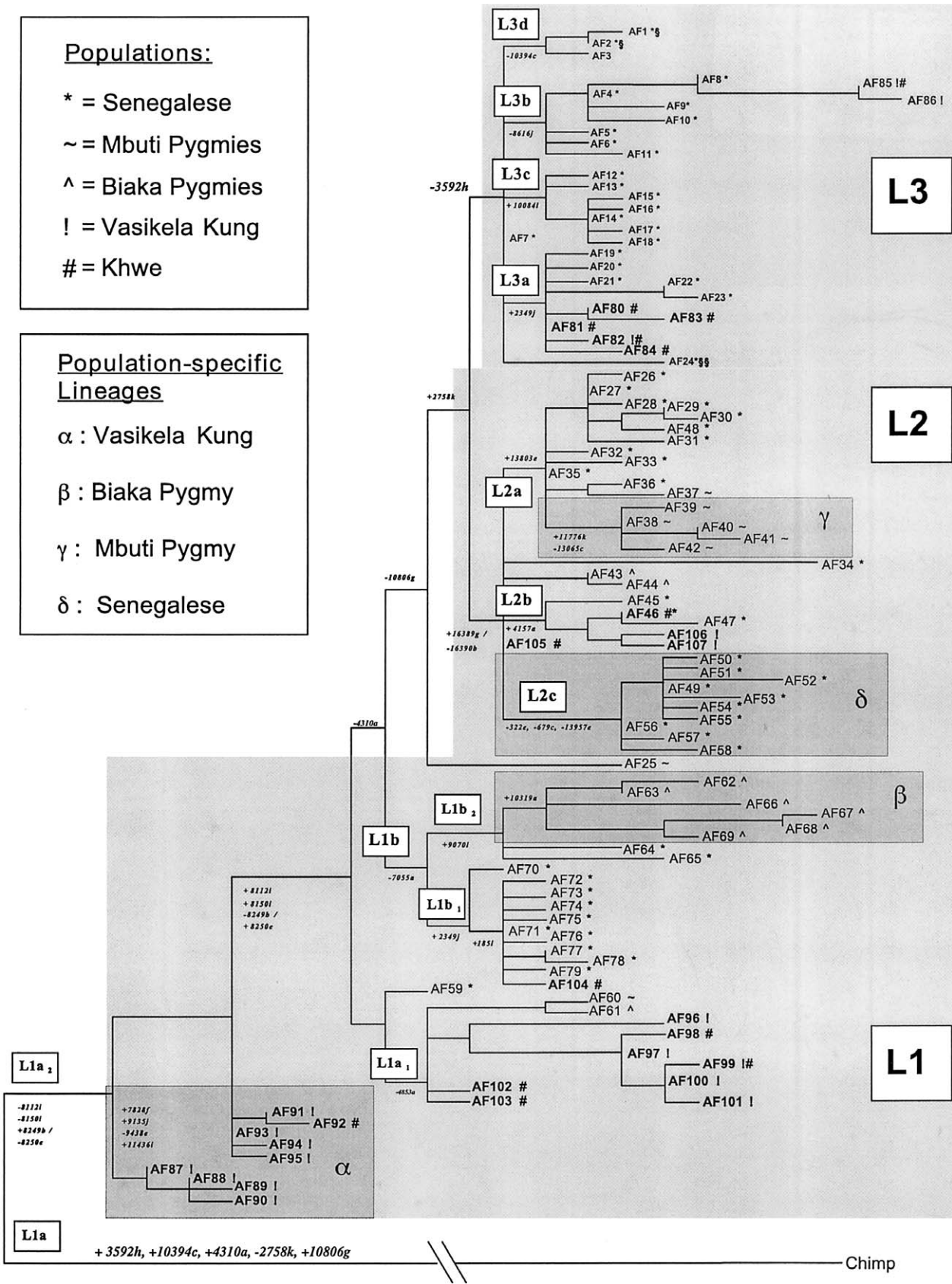
In addition, the CR sequences obtained from the 43 Kung and 31 Khwe samples were combined with the 11 distinct CR sequences from the Botswana Kung (sequences 1, 5–9, and 11–15) reported by Vigilant et al. (1989) and were subjected to phylogenetic analysis. To distinguish between the CR sequences belonging to the two different Kung San groups, the population samples described in this study were called the “Vasikela Kung,” and those analyzed by Vigilant et al. (1989) were called the “Botswana Kung.” Phylogenies of these sequences were obtained with the NJ (Saitou and Nei 1987) method present in the MEGA 1.01 statistical package (Kumar et al. 1993). The evolutionary distance between pairs of CR sequences were estimated as *p* distances, the proportion (*p*) of nucleotide sites at which the pair of sequences being compared differed, as calculated by dividing the number of nucleotide differences (*n<sub>d</sub>*) by the total number of nucleotides compared (*n*). Similar genetic distances were obtained with the other algorithms available in MEGA, but they are not presented here.

Populations:

- \* = Senegalese
- ~ = Mbuti Pygmies
- ^ = Biaka Pygmies
- ! = Vasikela Kung
- # = Khwe

Population-specific Lineages

- $\alpha$  : Vasikela Kung
- $\beta$  : Biaka Pygmy
- $\gamma$  : Mbuti Pygmy
- $\delta$  : Senegalese



All  $p$  distances were used with the NJ method, to produce phylogenetic trees. The NJ trees generated from HVS-I sequences were rooted by use of either a chimpanzee (Horai et al. 1995) or the Neanderthal (Krings et al. 1997) sequence, and those generated from both HVS-I and HVS-II data were rooted from only the chimpanzee sequence, because no HVS-II data were available for the Neanderthal mtDNA. Unrooted NJ trees were midpoint rooted without an outgroup sequence. The branching structure of these NJ trees was, in turn, tested by bootstrap analysis, which produced bootstrap confidence-level estimates for each interior branch.

### Sequence-Divergence Estimates

To calculate the genetic divergence of the southern-African populations, as well as the divergence within specific haplogroups and their sublineages, we used the iterative maximum likelihood (ML) method of Nei and Tajima (1983). The interpopulation ML estimates were obtained by taking a weighted average of the number of individuals in each population. "Corrected" interpopulation values (Corr) were obtained by taking an average of two intrapopulation estimates and subtracting that value from the uncorrected interpopulation value—that is,  $\text{Corr} = \delta_{xy} - [(\delta_x + \delta_y)/2]$ , where  $x$  and  $y$  are the two populations being analyzed. The same method was used for estimation of the divergence of haplogroups and their sublineages. When calculating the divergence times of these haplogroups and of their sublineages, we used the mtDNA evolutionary rate of 2.2%–2.9%/1 million years (Torroni et al. 1994c).

## Results

### Southern-African RFLP Haplotypes

A total of 29 haplotypes (AF46 and AF80–AF107) defined by 47 restriction-site polymorphisms were observed among the 74 South African individuals analyzed (Appendix A). One of these haplotypes, AF46, was described in our previous study of African mtDNA (Chen et al. 1995), whereas haplotypes AF80–AF107 were observed for the first time in African populations. A total of 18 haplotypes were detected in the Vasikela Kung, and 13 haplotypes were found in the Khwe, only 2 of which (i.e., AF85 and AF99) were shared between them (table 1). Of these southern-African haplotypes, 77% clustered into haplogroup L\*, including 84% of the Vasikela Kung mtDNAs and 68% of the Khwe mtDNAs.

Haplotypes belonging to haplogroup L\* have previously been observed in the western-African Senegalese (Chen et al. 1995; Graven et al. 1995) and Biaka and Mbuti Pygmy (Chen et al. 1995) populations, at very high frequencies, as well as at similar frequencies in the Bamileke of Cameroon (Scozzari et al. 1994) and in various southern-African groups (Soodyall and Jenkins 1992, 1993). However, no comparable haplotypes have been observed in European, Middle Eastern, or Asian populations (Ballinger et al. 1992; Torroni et al. 1994a, 1994b, 1994c, 1996), with the exception of those groups with a history of contact with African populations (Bonné-Tamir et al. 1986; De Benedictis et al. 1989; Semino et al. 1989; Ritte et al. 1993). Thus, these results substantiate the African origin of this mtDNA lineage,

**Figure 2** MP tree showing evolutionary relationships among 107 haplotypes (AF1–AF107) observed in 214 sub-Saharan Africans (Chen et al. 1995; present study). The tree is 200 steps in length, has consistency and retention indices (CI and RI) of .745 and .893, respectively, and is one of 3,000 MP trees generated by the TBR algorithm. It was rooted from a chimpanzee haplotype defined by sequence analysis (Horai et al. 1995) (see text). The RFLPs that define each of the major branches of the MP tree are indicated by the number of the first nucleotide of the respective recognition sites, according to the CR sequence (Anderson et al. 1981), with the restriction enzymes being indicated by single-letter codes as given in Appendix A. The length of the horizontal branches is proportional to the number of mutations that separate the haplotypes. The three major haplogroups are denoted by the light-gray shading, whereas the subhaplotype clusters, defined in table 2, are indicated by the smaller unshaded boxes. The "AF"-prefixed numbers at the end of each branch denote the individual haplotypes, and the population(s) in which the individual haplotypes were detected are indicated by symbols as defined in the key. All population-specific lineages are encompassed by dark-gray shading and are also denoted by Greek letters as defined in the key. Haplotypes AF1 and AF2, which are aligned with European haplogroup U, are located in L3d and are indicated by a section symbol (§). Haplotype AF24, which is aligned with Asian macrohaplogroup M, is indicated by a double section symbol (§§). The bootstrap values for the major branches of the MP tree were calculated by use of 100 replicates, with resampling by the TBR algorithm. L1a<sub>2</sub> cluster AF87–AF90 has a bootstrap value of 92%; subcluster AF88–AF90 has a bootstrap value of 100%. L1a<sub>2</sub> cluster AF91–AF92 has a bootstrap value of 95%; but AF93 and AF94 were not resolved at bootstrap values >50%. L1a<sub>1</sub> cluster AF97–AF101 has a bootstrap value of 100%; and subclusters AF99–AF101 and AF60–AF61 have bootstrap values of 52% and 60%, respectively; but AF60 and AF61 were not resolved at bootstrap values >50%. L1b, cluster AF70–AF71/AF77–AF78 has a bootstrap value of 100%, as does subcluster AF71/AF77/AF78. L1b, cluster AF62–AF69 has a bootstrap value of 100%, as do subclusters AF62–AF63 and AF67–AF69, whereas subcluster AF62–AF64/AF66–AF69 has a bootstrap value of 55%. L2 cluster AF26–AF38/AF40–AF50/AF52–AF53/AF55–AF58/AF105–AF107 has a bootstrap value of 52%. L2a cluster AF26–AF38/AF40–AF42 has a bootstrap value of 58%. L2b cluster AF46–AF47 has a bootstrap value of 100%. L2c cluster AF49–AF50/AF52–AF53/AF55–AF58 has a bootstrap value of 100%, and cluster AF106–AF107 has a bootstrap value of 52%. L3a cluster AF22–AF23 has a bootstrap value of 100%, whereas subclusters AF19–AF21/AF24 and AF80–AF84 were not resolved at bootstrap values >50%. L3b cluster AF8/AF85–AF86 has a bootstrap value of 100%, as does subcluster AF85–AF86, but cluster AF4/AF6/AF9/AF11 was not resolved at a bootstrap value of 50%. L3c cluster AF12/AF14–AF18 has a bootstrap value of 100%, as does subcluster AF14–AF18. L3d cluster AF1–AF3 has a bootstrap value of 97%.

as well as its widespread distribution, albeit at varying frequencies, in all African populations.

Consistent with a previous study of Khoisan mtDNA variation (Soodyall et al. 1996), none of the Vasikela Kung or the Khwe haplotypes exhibited any length polymorphisms in the COII/tRNA<sup>Lys</sup> intergenic region. These results support the conclusion that deletion haplotypes from haplogroup L\* originated not in Khoisan populations but, instead, in Bantu-speaking and/or Pygmy groups of western and central Africa.

#### Phylogenetic Analysis of RFLP Haplotypes

The phylogenetic relationships among the mtDNA haplotypes observed in the Vasikela Kung and Khwe and those previously reported in the other sub-Saharan African populations were assessed by both MP and genetic-distance/NJ analysis. The MP tree of African mtDNAs is presented in figure 2. The statistical robustness of the branches and subbranches of this tree are demonstrated by their preservation in 50%-majority-rule and strict consensus trees.

From the MP tree, it is clear that the African mtDNA phylogeny forms a successive series of branches, each one occupied by clusters of related mtDNA haplotypes (fig. 2 and table 2), consistent with our previous report (Chen et al. 1995). The overall phylogeny is divided into two major parts, the lower two-thirds having the *HpaI* site at np 3593 and the upper one-third lacking this site. We had previously designated the mtDNAs that have the *HpaI* np-3592 site as “haplogroup L” (Chen et al.

1995) and had reported that it subdivides into two major branches—L1, having a *HinfI* site at np 10806, and L2, having a combined *HinfI* site gain at np 16389 and an *AvaII* site loss at np 16390. The expanded phylogeny in figure 2 shows that L1 is further subdivided into L1a and L1b, on the basis of the presence or absence of an *AluI* site at np 4310. L2 is subdivided into L2a, L2b, and L2c, on the basis of the presence of a *HaeIII* site at np 13803, for L2a; the presence of an *AluI* site at np 4157, for L2b; and the absence of *HaeIII* sites at np 322 and 13957 and of a *DdeI* site at np 69, for L2c. L1a is further subdivided into L1a<sub>1</sub>, by an *AluI* site loss at np 4853, and L1a<sub>2</sub>, by *MspI* site losses at np 8112 and 8150 and by a combined *AvaII* np-8249 site gain and *HaeIII* np-8250 site loss. L1b is also subdivided into L1b<sub>1</sub>, by a *MboI* np-2349 site gain, and L1b<sub>2</sub>, by a *TaqI* np-9070 site gain (fig. 2 and table 2).

The upper one-third of the mtDNA phylogeny encompasses mtDNAs that lack the np-3592 *HpaI* site, which, in our previous study, we had designated “non-L” (Chen et al. 1995). This was subsequently redefined as “L3,” by Watson et al. (1997). When this nomenclature is adopted, L3 is subdivided into four haplogroups: L3a, associated with a *MboI* np-2349 site gain; L3b, associated with a *MboI* np-8616 site loss; L3c, associated with a *TaqI* np-10084 site gain; and L3d, associated with a *DdeI* np-10394 site loss (fig. 2 and table 2).

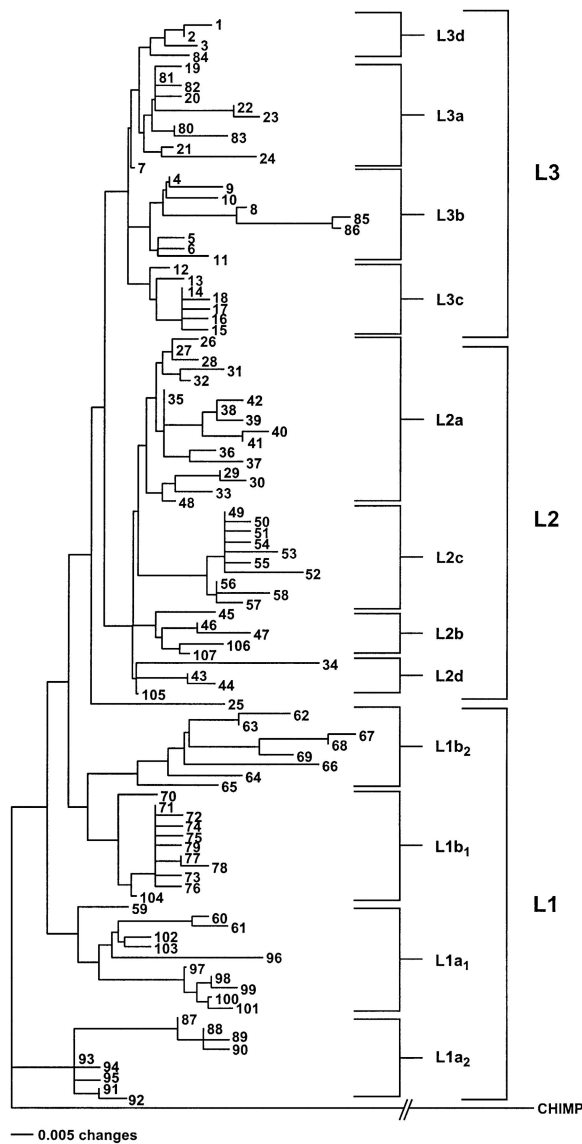
L1, L2, and L3 each encompass a sequence diversity that is approximately equivalent to those of other continent-specific haplogroups (Ballinger et al. 1992; Tor-

**Table 2**

**mtDNA Haplogroup Distribution in African Populations**

HAPLOGROUP	DEFINING POLYMORPHISMS	NO. (%) IN					
		Kung (N = 43)	Khwe (N = 31)	Mandenkalu (N = 60) <sup>a</sup>	Wolof (N = 20) <sup>a</sup>	Mbuti Pygmies (N = 22) <sup>a</sup>	Biaka Pygmies (N = 17) <sup>a</sup>
L	+ <i>HpaI</i> 3592, + <i>DdeI</i> 10394	36 (84)	21 (68)	44 (73)	14 (70)	22 (100)	17 (100)
L1	+ <i>HinfI</i> 10806, – <i>RsaI</i> 2758	34 (79)	16 (52)	17 (28)	4 (20)	8 (36)	15 (88)
L1a	+ <i>AluI</i> 4310	34 (79)	15 (48)	1 (2)	...	6 (27)	4 (23)
L1a <sub>1</sub>	– <i>AluI</i> 4853	12 (28)	10 (32)	1 (2)	...	6 (27)	4 (23)
L1a <sub>2</sub>	– <i>MspI</i> 8112, – <i>MspI</i> 8150, + <i>AvaII</i> 8249, – <i>HaeIII</i> 8250	22 (51)	5 (16)	...	...	...	...
L1b	– <i>AluI</i> 7055	...	1 (3)	16 (27)	4 (20)	...	11 (65)
L1b <sub>1</sub>	+ <i>MboI</i> 2349	...	1 (3)	13 (22)	4 (20)	...	...
L1b <sub>2</sub>	+ <i>TaqI</i> 9070	...	...	3 (5)	...	...	11 (65)
L2	+ <i>HinfI</i> 16389/– <i>AvaII</i> 16390	2 (5)	5 (16)	27 (45)	10 (50)	14 (64)	2 (12)
L2a	+ <i>HaeIII</i> 13803	...	...	10 (17)	5 (25)	14 (64)	...
L2b	+ <i>AluI</i> 4157	2 (5)	5 (16)	...	3 (15)	...	...
L2c	– <i>HaeIII</i> 322, – <i>DdeI</i> 679, – <i>HaeIII</i> 13957	...	...	17 (28)	2 (10)	...	...
L3	– <i>HpaI</i> 3592	7 (16)	10 (32)	16 (27)	6 (30)	...	...
L3a	+ <i>MboI</i> 2349	2 (5)	9 (29)	4 (7)	1 (5)	...	...
L3b	– <i>MboI</i> 8616	5 (12)	1 (3)	7 (12)	2 (10)	...	...
L3c	+ <i>TaqI</i> 10084	...	...	4 (7)	3 (15)	...	...
L3d	– <i>DdeI</i> 10394	...	...	1 (2)	...	...	...

<sup>a</sup> Data are from Chen et al. (1995).



**Figure 3** NJ tree constructed on the basis of mean character genetic differences of the RFLP haplotypes. The numbers represent the AF haplotype numbers shown in figure 2. The bootstrap values for various haplotype clusters of the NJ tree were calculated by use of 500 replicates, with resampling. The L1a<sub>2</sub> cluster of haplotypes separated from all other African haplotypes, with a bootstrap value of 55%. L1a<sub>2</sub> cluster AF87–AF88/AF90–AF93 has a bootstrap value of 54%; subcluster AF91–AF93 has a bootstrap value of 59%; subsubcluster AF91–AF92 has a bootstrap value of 65%; subcluster AF87–AF88/AF90 has a bootstrap value of 99%; and subsubcluster AF88–AF90 has a bootstrap value of 75%. L1b<sub>1</sub>+L1b<sub>2</sub> cluster AF62–AF65/AF67–AF68/AF70–AF72/AF78 has a bootstrap value of 56%. L1b<sub>1</sub> cluster AF70–AF72/AF78 has a bootstrap value of 94%; subcluster AF71–AF72/AF78 has a bootstrap value of 67%; and subsubcluster AF71, 72 has a bootstrap value of 60%. L1b<sub>2</sub> cluster AF62–AF65/AF67–AF68 has a bootstrap value of 70%; subcluster AF67–AF68 has a bootstrap value of 100%; and subcluster

roni et al. 1994a, 1994b; Chen et al. 1995). Therefore, it is reasonable to delineate these as haplogroups and to delineate the combination of L1 and L2, delineated by the presence of the *HpaI* site at np 3592, as a macrohaplogroup, “L\*.” This then relegates L1a, L1b, L2a–L2c, and L3a–L3d to the level of subhaplogroups. Of our L3 subhaplogroups (i.e., L3a–L3d), L3a and L3b are identical to similarly named groupings recognized by Watson et al. (1997).

Within the African MP phylogeny (fig. 2), the southern-African Kung and Khwe samples cluster together in L1a. Within L1a, L1a<sub>2</sub> is predominantly Kung, L1a<sub>1</sub> is Kung and Khwe, L2b includes Kung and Khwe, and L3a is predominantly Khwe. This asymmetric distribution of haplotypes is also seen for the Biaka Pygmies, L1b<sub>2</sub>; and the Mbuti Pygmies, L2a (fig. 2).

To establish the reliability of the major branches of our African mtDNA MP tree, we subjected the MP tree to a bootstrap analysis. Because of the large number of taxa (haplotypes) and character states (restriction-site variants) in our data set, the 50%-majority-rule bootstrap tree was unable to provide confidence values for a number of the internal branches. To facilitate the analysis, we reduced the number of taxa from each of the major clusters seen in figure 2, eliminating most of the haplotype-specific restriction-site variants. This gave confidence values, for the major branches, that were in the 55%–85% range (fig. 2, legend). However, confidence values could not be obtained for a few of the subhaplogroup clusters, a common problem when boot-

AF62–AF63 has a bootstrap value of 69%. L1a<sub>1</sub> cluster AF59–AF61/AF96–AF98/AF100–AF101/AF103 has a bootstrap value of 60%; subcluster AF60–AF61 has a bootstrap value of 90%; subcluster AF97–AF98/AF100–AF101 has a bootstrap value of 96%; subsubcluster AF97–AF98 has a bootstrap value of 72%; and subsubcluster AF100–AF101 has a bootstrap value of 67%. L2c cluster AF49–AF53/AF56/AF58 has a bootstrap value of 83%; subcluster AF49–AF53 has a bootstrap value of 53%; and subcluster AF56–AF58 of 63%. L2b cluster AF45–AF47/AF105 has a bootstrap value of 53%; subcluster AF46–AF47/AF105 has a bootstrap value of 74%; and subcluster AF46–AF47 has a bootstrap value of 76%. L2 cluster AF43–AF44 has a bootstrap value of 87%. L2a subcluster AF38–AF41 has a bootstrap value of 84%; subsubcluster AF38–AF39 has a bootstrap value of 66%; and subsubcluster AF40–AF41 has a bootstrap value of 70%. L2a subcluster AF36–AF37 has a bootstrap value of 69%; subcluster AF29–AF30 has a bootstrap value of 84%, whereas subclusters AF26–AF28 and AF33–AF35 were not resolved at bootstrap values >50%. L3d subcluster AF1–AF2 has a bootstrap value of 69%, whereas AF3 was not resolved at a bootstrap value >50%. L3c subcluster AF14–AF16 has a bootstrap value of 51%, although AF12 and AF13 were not resolved at a value of 50%. L3b cluster AF8/AF85–AF86 has a bootstrap value of 88%; and subcluster AF85–AF86 has a bootstrap value of 96%; however, clusters AF4–AF7 and AF9–AF11 were not resolved at a value of 50%. L3 cluster AF24–AF25 and L3a cluster AF80–AF83 were not resolved at a value of 50%.



strap analysis is applied to large data sets containing similar taxa.

To further define the African mtDNA phylogeny, we performed a genetic distance/NJ analysis on the same data set, using PAUP 4.0.2b. The resulting NJ tree (fig. 3) is virtually identical to the MP tree shown in figure 2. The only exception is the position of haplotypes AF34, AF43, AF44, and AF105. In the MP tree, these mtDNAs are dispensed between L2a, L2b, and L2c. However, in the NJ tree, they form a distinct cluster, which could be designated “L2d.”

To test the robustness of the African NJ phylogeny, we applied bootstrap analysis using PAUP 4.0.2b. Since the genetic distances used to construct the NJ trees represent single summaries of the genetic relationships among taxa (Saitou and Nei 1987), the number and complexity of the taxa were reduced. Consequently, bootstrap analysis of the NJ-tree genetic-distance data gave confidence values, for most branches, that were in the 51%–94% range. Again, however, some branches could not be assigned numerical values (fig. 3, *legend*).

Since both the MP and the genetic distance/NJ methods produced nearly identical trees, with the major branches having high bootstrap values, it is apparent that the African mtDNA phylogenies shown in figures 2 and 3 provide a reasonable representation of the phylogenetic relationships of African mtDNAs. Hence, the macrohaplogroups, haplogroups, and subhaplogroups shown in figures 2 and 3 can be used to further investigate the mtDNA genetic history of African populations.

At present, the relationship of the African mtDNA phylogeny to the mtDNA phylogenies of Europe and Asia can only partially be deduced. If included in the African phylogenetic analysis, all European mtDNAs would cluster outside haplogroups L1 and L2 and would form separate branches within haplogroup L3. This is because all European haplogroups are defined by distinct sets of RFLPs not usually present in African haplogroups (Torroni et al. 1996, 1998). Many of the L3 mtDNAs have the *DdeI* site at np 10394, a characteristic also seen in European haplogroups I–K; others, such as AF01, AF02, and AF03 of L3d, lack the *DdeI* np-10394 site, which is characteristic of European haplogroups H and T–X. Among the African mtDNAs lacking the *DdeI* 10394 site, haplotypes AF01 and AF02 from the Senegalese have a *HinfI* site at np 12308, which characterizes haplogroup U in European populations (Torroni et al. 1996). This raises the possibility that the L3d lineage may have given rise to several of the European haplogroups; however, it is also possible that the haplogroup U mtDNAs observed in these African samples may be the product of back-migrations into Africa from Europe.

The Asian mtDNA phylogeny is subdivided into two macrohaplogroups, one of which is M. M is delineated

by a *DdeI* site at np 10394 and an *AluI* site of np 10397. The only African mtDNA found to have both of these sites is the Senegalese haplotype AF24. This haplotype branches off African subhaplogroup L3a (figs. 2 and 3), suggesting that haplogroup M mtDNAs might have been derived from this African mtDNA lineage; however, it is also possible that this particular haplotype is present in Africa because of back-migration from Asia.

Interestingly, the *MboI* np-2349 site gain is shared by the haplogroup L3a mtDNAs in the Vasikela Kung and the Khwe populations and a subset of subhaplogroup L1b mtDNAs from Senegalese populations, implying a possible linkage between these population groups. Unlike subhaplogroup L1b mtDNAs, however, these L3a mtDNAs do not have either the *HinfI* np-10806 site gain or the *AluI* np-7055 and *RsaI* np-2758 site losses that define haplogroup L1b. Thus, it appears that the haplogroup L3a mtDNAs acquired the *MboI* np-2349 site independently of the subhaplogroup L1b mtDNAs.

#### Haplogroup Distribution in African Populations

The overall distribution of mtDNA haplogroups in African populations, including the Vasikela Kung and the Khwe, is shown in table 2. Both the Mbuti and Biaka Pygmy populations have 100% macrohaplogroup L\* mtDNAs. In addition, macrohaplogroup L\* haplotypes constitute the large majority of the mtDNAs of the Vasikela Kung, Khwe, and Senegalese groups. However, these groups also encompass significant frequencies of L3 haplotypes, with subhaplogroups L3a–L3d being nonuniformly distributed among these populations. Furthermore, there is some degree of geographic partitioning of the clusters within macrohaplogroup L\* (table 2), a trend also noted by Watson et al. (1997). The distribution of haplogroups among these African populations implies that they have experienced quite different genetic histories and that macrohaplogroup L\* has undergone considerable regional diversification in Africa.

The Vasikela Kung and the Khwe encompass different arrays of mtDNA haplotypes. Of those present in the Vasikela Kung, 79% and 5% are found in haplogroups L1 and L2, respectively, with these haplotypes belonging to subhaplogroups L1a and L2b (table 2). In addition, Vasikela Kung subhaplogroup L1a mtDNAs segregate into two distinct lineages: L1a<sub>2</sub>, which encompass >51% of their mtDNAs (AF87–AF91 and AF93–AF95), and L1a<sub>1</sub>, which encompass 28% of their mtDNAs (AF96–AF97 and AF99–AF101) (figs. 2 and 3 and table 2). L1a<sub>2</sub> is found almost exclusively in the Vasikela Kung, while lineage L1a<sub>1</sub> includes Mbuti and Biaka Pygmy mtDNAs (haplotypes AF60–AF61), as well as Khwe mtDNAs; thus L1a<sub>1</sub> is not Kung specific.

Among the Khwe, 52% and 16% of the mtDNAs are found in haplogroups L1 and L2, respectively (table 2).

**Table 3**  
**Sequence Divergence and Divergence Time of Population-Specific Lineages**

Population-Specific Haplogroup	Primary Defining Polymorphism(s) <sup>a</sup>	Haplotypes	No. of (%) Subjects	Sequence Divergence (%)	Divergence Time (YBP)
Kung: $\alpha$	-8112 <i>MspI</i> , -8150 <i>MspI</i> , +8249 <i>AvaII</i> , -8250 <i>HaeIII</i>	AF87–AF95 <sup>b</sup>	26 (59) <sup>b</sup>	.119	41,000–54,100
Biaka Pygmies: $\beta$	+10319 <i>AluI</i>	AF62–63, AF66–AF69	11 (65)	.225	77,600–102,000
Mbuti Pygmies: $\gamma$	+11776 <i>RsaI</i> , -13065 <i>DdeI</i>	AF38–AF42	10 (45)	.042	14,500–19,100
Senegalese: $\delta$	-322 <i>HaeIII</i> , -679 <i>DdeI</i> , -13957 <i>HaeIII</i>	AF49–AF58	22 (22)	.052	17,900–23,200

<sup>a</sup> All population-specific lineages listed are also defined by *HpaI* 3592 and *DdeI* 10394 site gains.

<sup>b</sup> Haplotype AF92 was the only haplotype  $\alpha$  lineage that was observed in the Khwe; its presence in the Khwe is attributed to genetic admixture with the Vasikela Kung, since five other Vasikela Kung individuals also have AF92 mtDNAs.

With the exception of AF104, which is located in sub-haplogroup L1b, within a cluster of related western-African mtDNAs, all the Khwe mtDNAs from haplogroup L1 cluster within subhaplogroup L1a. Within L1a, 32% of the Khwe mtDNAs (AF98–AF99 and AF102–AF103) belong to lineage L1a<sub>1</sub>, and only 16% occur in lineage L1a<sub>2</sub>. Lineage L1a<sub>1</sub> is also present in the Vasikela Kung and Biaka Pygmies, but L1a<sub>2</sub> is found almost exclusively in the Vasikela Kung, with only one Khwe haplotype (AF92) being found in this cluster. Hence, the presence of a Khwe haplotype in lineage L1a<sub>2</sub> is most likely due to admixture with Khoisan-speakers.

Both the Vasikela Kung and the Khwe possess haplotypes belonging to subhaplogroup L2b (table 2). The two Vasikela Kung haplotypes from this subhaplogroup (i.e., AF106 and AF107) are closely related. The two Khwe haplotypes include one (AF46) that is the same as that occurring in three Wolof from Senegal (Chen et al. 1995) and another (AF105) that is found in three Khwe and that occupies the nodal position in the haplogroup L2; hence, AF105 could be the founding haplotype for this subhaplogroup. This distribution raises the possibility that the L2b haplotypes found in the Vasikela Kung were acquired by admixture with the Khwe.

Both southern-African populations also have haplogroup L3 mtDNAs (table 2). Two of the L3 haplotypes in the Kung (i.e., AF85 and AF86) are quite distinctive and cluster on a distant branch of haplogroup L3b, haplotype AF85 also occurring in the Khwe. Khwe haplotypes AF80–AF84 all cluster together within haplogroup L3a, with AF82 being shared with the Kung. This pattern of haplotype sharing suggests that the L3 haplotypes in the Vasikela Kung and the Khwe are probably of Khwe origin. Hence, it seems probable that lineage L1a<sub>2</sub> mtDNAs originated in the Vasikela Kung and were disseminated into the Khwe, whereas the L2 and L3 mtDNAs originated in the Khwe and were passed on to the Vasikela Kung.

HR-RFLP analysis also reveals several distinct sublineages that appear to be population specific (figs. 2 and 3 and table 3). Among Khoisan-speakers, the Vasikela

Kung have sublineage  $\alpha$  within subhaplogroup L1a, the Biaka Pygmies have sublineage  $\beta$  within subhaplogroup L1b, the Mbuti Pygmies have sublineage  $\gamma$  within subhaplogroup L2a, and the Senegalese have sublineage  $\delta$  within subhaplogroup L2c (fig. 2 and table 3). The presence of such population-specific sublineages within macrohaplogroup L\* further demonstrates the extensive regional sequence divergence of African mtDNAs.

*Sequence Divergence of African Haplogroups*

On the basis of intrapopulation ML calculations, we estimated the divergence times for all major clusters of mtDNAs thus far observed in African populations (table 4 and Appendix B). The sequence-divergence value for all African HR haplotypes is 0.364%, an estimate that gives a maximum age, for the most recent common ancestor (MRCA), of ~126,000–166,000 years

**Table 4**  
**Sequence Divergence and Divergence Time of African mtDNA Haplogroups**

Haplogroup	No. of Haplotypes	No. of Subjects	Sequence Divergence (%)	Divergence Time (YBP)
All African	107	214	.364	125,500–165,500
L	76	164	.356	122,800–161,800
L1	40	98	.328	113,100–149,100
L1a	20	60	.265	91,400–120,500
L1a <sub>1</sub>	10	32	.166	57,200–75,500
L1a <sub>2</sub>	9	27	.119	41,000–18,600
L1b	19	36	.214	73,800–97,300
L1b <sub>1</sub>	11	21	.041	14,100–18,600
L1b <sub>2</sub>	8	15	.246	84,800–111,800
L2	36	66	.171	59,000–77,700
L2a	17	29	.113	39,000–51,400
L2b	5	9	.072	24,800–32,700
L2c	10	22	.052	17,900–23,600
L3	31	50	.227	78,300–103,200
L3a	10	17	.120	41,400–54,500
L3b	9	17	.225	77,600–102,300
L3c	7	9	.082	28,300–37,300
L3d	3	5	.051	17,600–23,200

**Table 5**  
**Sequence Divergence Within and Between African Populations**

	SEQUENCE DIVERGENCE (%)					
	Kung (N = 43)	Khwe (N = 31)	Mandenkalu (N = 60)	Wolof (N = 20)	Mbuti Pygmies (N = 22)	Biaka Pygmies (N = 17)
Kung	<u>.320</u>	.334	.366	.368	.378	.400
Khwe	.036	<u>.277</u>	.300	.298	.315	.353
Mandenkalu	.069	.024	<u>.274</u>	.275	.294	.332
Wolof	.076	.028	.007	<u>.263</u>	.283	.369
Mbuti Pygmies	.098	.056	.036	<u>.032</u>	<u>.241</u>	.371
Biaka Pygmies	.068	.043	.024	.067	.080	<u>.342</u>

NOTE.—Intrapopulation sequence-divergence values are on the diagonal (*underlined*), whereas the raw and corrected interpopulation sequence-divergence values are above and below the diagonal, respectively.

before the present (YBP). Similarly, macrohaplogroup L\* shows a sequence divergence of 0.356%, which gives a divergence time of 123,000–162,000 YBP. These findings are concordant with earlier estimates of African mtDNA divergence, which gave coalescence values of 110,000–160,000 YBP (Chen et al. 1995; Graven et al. 1995; Horai et al. 1995; Vigilant et al. 1989, 1991; Watson et al. 1997), and confirm that macrohaplogroup L\* is the most divergent of all haplogroups in human populations (Chen et al. 1995). These data further support the hypothesis that, in being the oldest mtDNAs in human populations, these African haplotypes form the root of the modern human mtDNA phylogeny (figs. 2 and 3).

Within macrohaplogroup L\*, the major clusters of African mtDNAs show varying levels of sequence diversity (table 4). Haplogroup L1 is nearly as diverse as macrohaplogroup L\*, whereas haplogroup L2 is half as diverse. This indicates that haplogroup L1 originated well before the emergence of haplogroup L2. Among the smaller haplotype clusters within macrohaplogroup L\*, subhaplogroup L1a has the largest divergence value, whereas subhaplogroup L2c has the smallest value, implying that there are considerable differences in times of origin for these haplotype clusters within African populations. Haplogroup L3 is less divergent than L1, and the subhaplogroups of L3 are generally less divergent than those of L1. Only haplogroup L3b is comparable, in terms of sequence diversity, to the oldest subhaplogroups of L1 and L2; however, the L3b value could be inflated, because of the inclusion of the highly divergent haplotypes AF85 and AF86, since these southern-African haplotypes are at least five mutations different from any other haplotypes (AF04–AF06 and AF08–AF11) of this Senegalese-specific subhaplogroup (Chen et al. 1995). Therefore, it appears that the L3 subhaplogroups arose long after the radiation of haplogroup L1 and

approximately at the time that haplogroup L2 split from haplogroup L1.

Sequence-divergence estimates were also calculated for each of the population-specific sublineages (table 3). These results show that sublineages found in the Mbuti Pygmies ( $\gamma$ ) and the Senegalese ( $\delta$ ) have approximately comparable divergence values (0.042%–0.052%). By contrast, the Vasikela Kung lineage ( $\alpha$ ) is twice as diverse (0.119%), and the Biaka Pygmy ( $\beta$ ) is four times as diverse (0.225%), as the Mbuti Pygmies and Senegalese.

These diversity levels suggest that the Biaka Pygmies of sublineage  $\beta$  may be one of the oldest distinct African populations and, hence, one of the oldest human populations in the world, although other demographic factors could have contributed to this level of diversity. The Vasikela Kung sublineage  $\alpha$  may be the other truly ancient African mtDNA cluster. Not only is sublineage  $\alpha$  of the Kung the second most diverse, but it is positioned at the deepest root of the African phylogenetic tree (figs. 2 and 3), suggesting that the Kung San became differentiated very early during human radiation.

#### Genetic Divergence of African Populations

The intra- and interpopulation sequence divergences within and between African populations are shown in table 5. The Biaka Pygmies have the highest intrapopulation sequence divergence (0.342%), followed by the Vasikela Kung (0.320%) and then the Khwe (0.277%). In addition, all the interpopulation sequence-divergence values between Vasikela Kung and other African populations are higher than those between the Khwe and other African populations. Thus, the Vasikela Kung are more divergent from other African populations than are the Khwe. This finding is consistent both with the Vasikela Kung being genetically distinct from the Khwe (Nurse et al. 1977) and with the Khwe being more closely related to the Negroid populations of South Af-

rica, who, in turn, show greater affinities with populations from western and central Africa.

These same relationships are seen quite clearly in the NJ tree based on these ML estimates (fig. 4 and Appendix B). In this tree, the Khwe clearly cluster more closely to other Bantu-speaking Senegalese groups—the Mandelaku and Wolof—than to the Vasikela Kung. The Vasikela Kung, on the other hand, form a distant outlier between the Biaka and Mbuti Pygmy populations. In addition, the Mbuti Pygmies are closer to western-African Bantu-speaking groups than to the Biaka Pygmies, a relationship that reflects the considerably different haplotype compositions of the two populations. The marked divergence between the two Pygmy groups raises the possibility that these two Pygmy populations had independent origins.

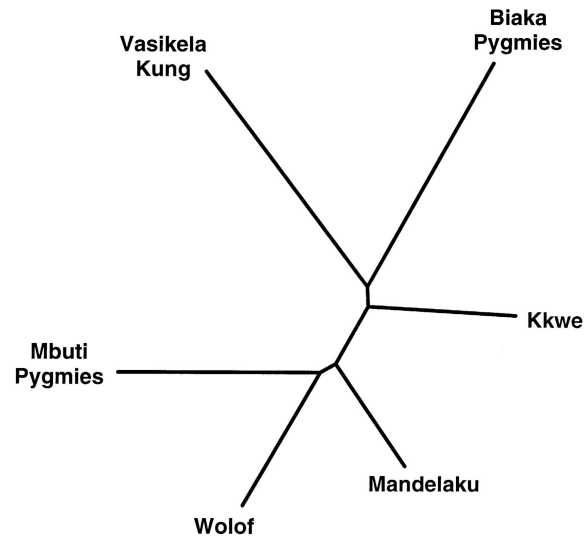
#### *Distribution of CR Sequences in Southern-African Populations*

A total of 640 nucleotides from HVS-I and HVS-II of the CRs for all 74 southern-African individuals were sequenced. The sequence data from the Vasikela Kung and Khwe are shown in table 6. A total of 24 distinct CR sequences based on 65 variable nucleotides were detected. Of the 65 variable nucleotides found in this study, only 31 had previously been reported in the study of CR sequence variation in the Botswana Kung (Vigilant et al. 1989). The vast majority (84%) of these nucleotide substitutions are transitions, both in the HVS-I and in the HVS-II, a result that is consistent with patterns of variation observed in previous CR-sequencing studies of human populations (Horai and Hayasaka 1990; Vigilant et al. 1991).

The distribution of CR sequences in the Vasikela Kung and the Khwe show them to be quite distinctive from each other; indeed, there is virtually no overlap of their CR sequences (table 6). Therefore, each CR sequence has been given a two-letter prefix indicating its probable population of origin, as shown in figure 5. The only CR sequence that the Vasikela Kung and the Khwe populations have in common is CR 17, which is associated with haplotype AF99. Since this mtDNA is found in seven Khwe but in only one Vasikela Kung, we have given it a Khwe designation, “KW17.” Similarly, two very similar CR sequences—10 and 11—share the same haplotype, AF85, that is found in five Kung but in only one Khwe. Hence, the AF85 CR sequence 11 that appears in the Khwe is most likely of Vasikela Kung origin and therefore has been given the designation “VK11.”

#### *Phylogenetic Analysis of CR Sequences*

The phylogenetic relationships among the CR sequences of the Vasikela Kung, Khwe, and Botswana Kung (Vigilant et al. 1989) are shown in figure 5 and



**Figure 4** NJ tree of ML genetic distances for major African populations (table 5).

table 6. In general, there is a very good correspondence between the groupings identified by CR sequences and those identified by HR-RFLP haplotypes (figs. 2 and 3). A similar correlation between CR sequences and LR-RFLP types was seen, by Graven et al. (1995), in the Mandenka of Senegal. This correspondence is strongest when only HVS-I sequences are used in the comparison, since the addition of HVS-II sequences creates minor difficulties in the resolution of certain branching relationships among these mtDNAs, a trend noted in previous studies of CR sequence variation (Horai and Hayasaka 1990; Vigilant et al. 1991). In addition, when only HVS-I sequences are compared, there is no major difference, in the branching order or structure of the NJ tree, irrespective of whether the chimpanzee or Neanderthal mtDNA is used to root the tree, or whether mid-point rooting is used to construct the tree.

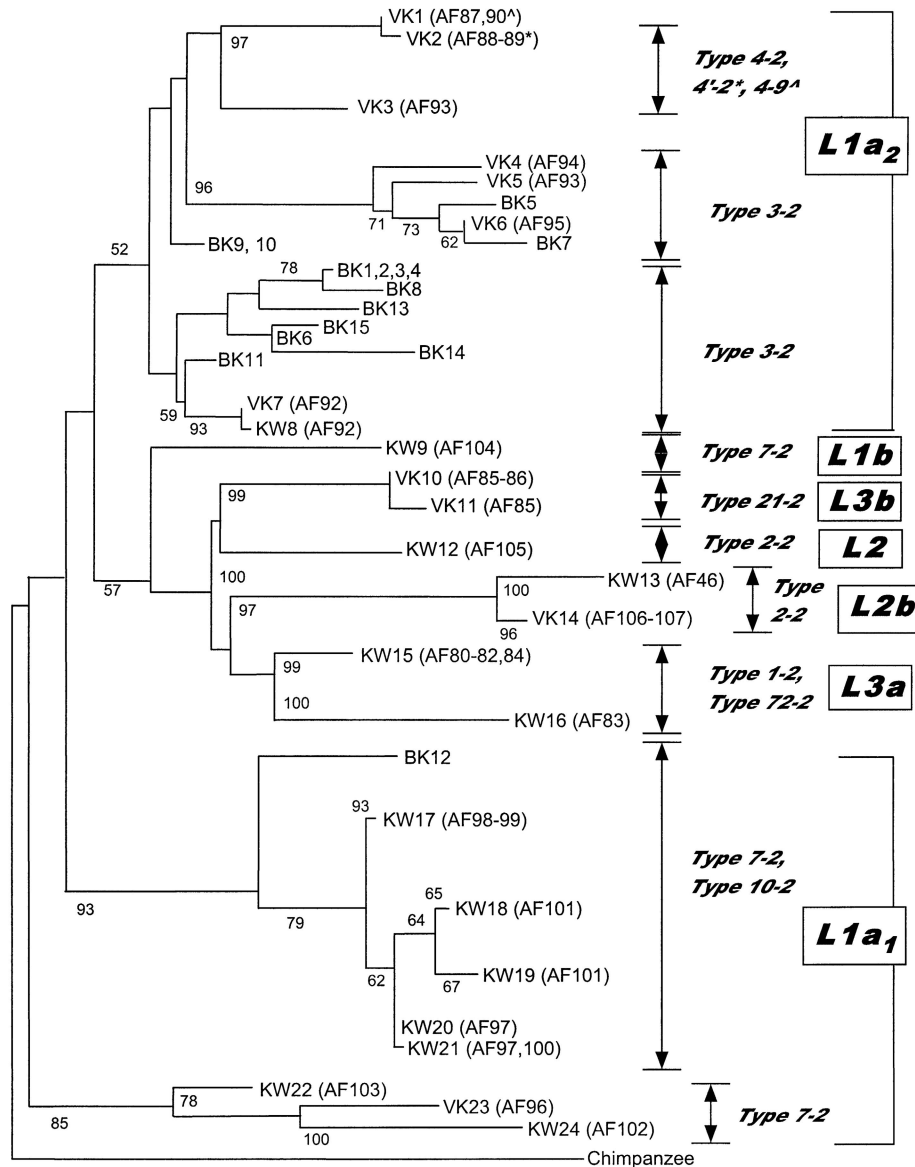
The CR sequences of all L1a subhaplogroup sequences—both those in L1a<sub>1</sub> and those in L1a<sub>2</sub>—cluster together with one another and apart from those belonging to haplogroups L2 and L3 (fig. 5). The CR sequences also split lineages L1a<sub>1</sub> and L1a<sub>2</sub> into distinct branches, encompassing distinct subclusters, including ones that are constituted almost solely of population-specific mtDNAs. By contrast, the CR sequences of haplogroups L2 and L3 cluster closer to each other, as they do in the RFLP phylogeny (figs. 2 and 3), while also showing some degree of genetic substructure.

Although there is a good correspondence between the RFLP haplotypes and CR sequences, specific RFLP haplotypes have multiple CR sequences associated with them (e.g., AF93 and CR sequences VK3 and VK5). In other cases, the same CR sequence is associated with

**Table 6**

**Kung and Khwe CR Sequences**

CR	HAPLOTYPE(S) (HAPLOGROUP)	No. IN		POSITIONS IN	
		Kung	Khwe	HVS-1	HVS-2
1	AF87, AF90 (L1a)	8	...	16167T, 16187T, 16189C, 16223T, 16230G, 16234T, 16242T, 16243C, 16311C	73G, 146C, 152C, 195C, 198T, 247A, 315C+
2	AF88-AF89 (L1a)	8	...	16167T, 16187T, 16189C, 16223T, 16230G, 16234T, 16242T, 16243C, 16311C	73G, 146C, 152C, 195C, 198T, 247A, 309C+, 315C+
3	AF93 (L1a)	1	...	16153A, 16187T, 16189C, 16223T, 16230G, 16243C, 16294T, 16311C	73G, 146C, 152C, 195C, 247A, 315C+
4	AF94 (L1a)	1	...	16129A, 16187T, 16189C, 16230G, 16234T, 16243C, 16266A, 16311C	73G, 146C, 152C, 199C, 247A, 315C+
5	AF93 (L1a)	1	...	16129A, 16187T, 16189C, 16230G, 16234T, 16243C, 16264T, 16266G, 16311C	73G, 146C, 152C, 195C, 199C, 247A, 315C+
6	AF95 (L1a)	1	...	16093C, 16129A, 16187T, 16189C, 16230G, 16234T, 16243C, 16266G, 16311C	73G, 146C, 152C, 195C, 199C, 247A, 315C+
7	AF91 (L1a)	2	...	16129A, 16179T, 16187T, 16189C, 16223T, 16230G, 16243C, 16311C	73G, 146C, 152C, 188G, 195C, 247A, 315C+
8	AF92 (L1a)	5	...	16129A, 16179T, 16187T, 16189C, 16223T, 16230G, 16243C, 16311C	73G, 146C, 152C, 188G, 195C, 247A, 309C+, 315C+
9	AF104 (L1b)	...	1	16126C, 16187T, 16189C, 16223T, 16264T, 16270T, 16278T, 16311C	73G, 151T, 195C, 247A, 263A, 315C+
10	AF85-AF86 (L3b)	5	...	16124C, 16183C, 16189C, 16193C+, 16223T, 16278T, 16304C, 16311C	73G, 152C, 195C, 263G, 309C+, 315C+
11	AF85 (L3b)	1	...	16124C, 16183C, 16189C, 16193C+, 16223T, 16278T, 16304C, 16311C	73G, 152C, 263G, 315C+
12	AF105 (L2)	...	3	16189C, 16192T, 16223C, 16278T, 16294T, 16309G, 16390A	73G, 146C, 152C, 195C, 263G, 309C+, 315C+
13	AF46 (L2b)	...	2	16114A, 16129A, 16213A, 16223T, 16278T, 16284C, 16355T, 16362C, 16390A	73G, 150T, 151T, 152C, 182T, 195C, 198T, 204C, 263G
14	AF106-107 (L2b)	2	...	16114A, 16129A, 16213A, 16223T, 16278T, 16354T, 16390A	73G, 150T, 151T, 152C, 182T, 195C, 198T, 204C, 263G
15	AF80-AF82, AF84	2	3	16172C, 16189C, 16223T, 16320T	73G, 150T, 152C, 195C, 263G, 315C+
16	AF83 (L3a)	...	6	16185T, 16209C, 16223T, 16327T	73G, 150T, 152C, 189G, 195C, 200G, 207A, 263G, 309C+, 315C+
17	AF98-AF99 (L1a)	1	7	16166C, 16172C, 16187T, 16189C, 16209C, 16214T, 16223T, 16230G, 16278T, 16291G, 16311C	73G, 146C, 152C, 189G, 195C, 198T, 247A, 315C+
18	AF101 (L1a)	2	...	16166C, 16172C, 16187T, 16189C, 16209C, 16214T, 16223T, 16230G, 16278T, 16291G, 16311C	73G, 146C, 152C, 189G, 195C, 198T, 204C, 207A, 247A, 309C+, 315C+
19	AF101 (L1a)	2	...	16166C, 16172C, 16189C, 16209C, 16214T, 16223T, 16230G, 16278T, 16291G, 16311C	73G, 146C, 152C, 189G, 195C, 198T, 204C, 207A, 247A, 309C+, 315C+
20	AF97 (L1a)	1	...	16166C, 16172C, 16187T, 16189C, 16209C, 16214T, 16223T, 16230G, 16278T, 16291G, 16311C	73G, 146C, 152C, 189G, 195C, 198T, 207A, 247A, 309C+, 315C+
21	AF97, AF100 (L1a)	5	...	16166C, 16172C, 16187T, 16189C, 16209C, 16214T, 16223T, 16230G, 16278T, 16291G, 16311C	73G, 146C, 152C, 189G, 195C, 198T, 207A, 247A, 315C+
22	AF103 (L1a)	...	1	16129A, 16148T, 16172C, 16187T, 16188G, 16189C, 16223T, 16230G, 16311C, 16320T	73G, 95C, 152C, 189G, 207A, 236C, 247A, 263G, 309C+, 315C+
23	AF96 (L1a)	1	...	16129A, 16148T, 16169T, 16172C, 16187T, 16188G, 16189C, 16223T, 16230G, 16278T, 16311C	93G, 146C, 152C, 185A, 189G, 195C, 198T, 207A, 236C, 247A, 263G, 315C+
24	AF102 (L1a)	...	2	16129A, 16148T, 16168T, 16172C, 16187T, 16188G, 16189C, 16223T, 16230G, 16278T, 16293G, 16311C, 16320T, 16344T	93G, 95C, 185A, 189G, 236C, 247A, 263G, 315C+



**Figure 5** NJ tree based on HVS-I and HVS-II sequences from Vasikela Kung and Khwe (present study) and Botswana Kung (Vigilant et al. 1989). The CR sequence numbers are positioned at the end of each branch; VK = Vasikela Kung sequence, KW = Khwe sequence, and BK = Botswana Kung sequences; and the associated HR haplotypes are in parentheses. LR types are indicated in boldface italic, and the square brackets indicate all CR sequences associated with them. The major haplogroups and subhaplogroups to which these mtDNAs belong are shown within the boxes. Bootstrap values for each major branch of the tree are shown at their corresponding positions. This tree was rooted from a chimpanzee CR sequence (Horai et al. 1995).

multiple RFLP haplotypes (e.g., CR sequence KW15 with AF80–82 and AF84). These observations indicate that both HR-RFLP and CR sequence data provide valuable phylogenetic information about human mtDNAs and are more valuable when used together than when employed separately.

With regard to the population-specific clusters, the CR sequences for the Kung San populations generally segregate into distinct clusters of related types. With one

exception (BK12), all the Botswana Kung CR sequences (BK01–BK11 and BK13–BK15) cluster together within lineage L1a<sub>2</sub> (fig. 5), along with similar Vasikela Kung CR sequences (VK01–VK07). The large majority of the CR sequences in the Botswana Kung cluster within a single group to which virtually no Vasikela Kung mtDNAs belong. The remainder cluster more closely with CR sequences in the Vasikela Kung that correspond to sublineage α. This pattern of CR sequence diversity

within subhaplogroup L1a, for both the Botswana Kung and the Vasikela Kung, suggests a significant degree of genetic differentiation of the Kung San populations, although the perceived difference between the Botswana Kung and Vasikela Kung could simply reflect limited or regional sampling (Vigilant et al. 1989, 1991).

## Discussion

### *The Origins of African Populations*

Studies of African mtDNA sequence variation that have used HR-RFLP analysis (Chen et al. 1995; present study) have confirmed the ubiquity of macrohaplogroup L\* in African populations. Moreover, we have documented that macrohaplogroup L\* is the oldest African and human mitochondrial lineage, encompassing a sequence diversity of 0.364% and having an estimated age ~126,000–165,000 YBP; as such, it must be considered the root of the human mtDNA phylogeny, from which all other haplogroups evolved. Macrohaplogroup L\* is further subdivided into two major haplogroups: L1 and L2 (figs. 2 and 3 and table 2). Haplogroup L1 is the most ancient of African haplogroups, and it is further subdivided into subhaplogroups L1a and L1b, with L1a being the older of the two (table 4). L1a is further subdivided into lineages L1a<sub>1</sub> and L1a<sub>2</sub> (table 2). Lineage L1a<sub>2</sub> contains the core population-specific haplotypes ( $\alpha$ ) of the Vasikela Kung, and lineage L1b<sub>2</sub> contains the population-specific haplotypes ( $\beta$ ) of the Biaka Pygmies, the two most ancient and distinct African populations known (figs. 2 and 3 and tables 2 and 3).

Haplogroup L2 is considerably younger than haplogroup L1, being approximately half the age of the latter. It is subdivided into three subhaplogroups: L2a, L2b, and L2c. L2a contains the core population-specific haplotypes ( $\gamma$ ) of the Mbuti Pygmies, whereas L2c contains the core haplotypes ( $\delta$ ) of the Bantu-speaking Senegalese (figs. 2 and 3 and tables 2 and 3).

The existence of four distinct L3 subhaplogroups (Chen et al. 1995) also has been confirmed. Of these, L3a and L3b are the oldest, whereas L3c and L3d are of more recent origin. In addition, L3 mtDNAs have been found to be much more closely related to those from L2 than either is to L1, by both RFLP and CR sequence analysis (figs. 2 and 3 and table 2). These findings suggest that haplogroups L2 and L3 have a more recent origin than does haplogroup L1 and that the split of L3 from L2 happened relatively soon after L2 split from L1 (figs. 2 and 3 and table 4).

An unexpected result is the marked difference, in haplotype distribution, between the Mbuti and Biaka Pygmy populations. Not only do the mtDNAs of these two populations form distinct clusters by parsimony analysis (figs. 2 and 3), but they branch separately in the NJ tree

of RFLP genetic distances (fig. 4). The distinction between the two Pygmy populations is further demonstrated by the significantly greater sequence diversity of the Biaka Pygmies (0.342%) relative to that of the Mbuti Pygmies (0.241%). This difference suggests that the Biaka Pygmies arose before the Mbuti Pygmies (table 3) and represent one of the oldest African populations, whereas the Mbuti Pygmies appear to have arisen independently and more recently. This conclusion is consistent with the nuclear genetic data reported by Cavalli-Sforza et al. (1994) and with the different linguistic affiliations of the two populations, with the Mbuti speaking a Nilo-Saharan language and with the Biaka speaking a Niger-Kordofarian language (Greenberg 1963).

The Vasikela Kung mtDNA data also suggest a relatively ancient origin for the Kung San. The population-specific haplotypes of the Biaka Pygmies ( $\beta$ ) and the Vasikela Kung ( $\alpha$ ) are both located in the ancient African haplogroup L1. Moreover, the Vasikela Kung sublineage  $\alpha$  haplotypes form the deepest root of the African tree, relative to the chimpanzee outgroup haplotype (figs. 2 and 3). Thus, the Kung must also represent one of the most ancient modern human populations. The antiquity of the Vasikela Kung is further emphasized by the high intragroup sequence diversity, 0.320%, of this population, a value only slightly smaller than that of the Biaka Pygmies (0.342%) (table 5). Thus, our data suggest that the Biaka Pygmies and the Vasikela Kung represent the earliest modern human populations, whereas the Mbuti Pygmies and the Bantu-derived Senegalese have emerged more recently.

### *The Relationship between the Kung and the Khwe*

The Vasikela Kung and the Khwe both speak Khoisan languages. However, the Khwe have a physical appearance that is more similar to that seen in many Bantu-derived populations than to that of the Vasikela Kung. Therefore, the Khwe may have originated from the Bantu migration into southern Africa and subsequently may have adopted the Khoisan language. This possibility is supported both by the striking differences between the population-specific haplotypes of the Kung San ( $\alpha$ ) and those of the Bantu-speaking Senegalese ( $\delta$ ) and by the greater similarities between the Khwe and Senegalese haplotypes than between the Kung and the Khwe haplotypes.

To most effectively address this question, we have compared the mtDNA variation in all of the southern-African populations that have been studied thus far. However, with the exception of our current and previous (Chen et al. 1995) studies, all African mtDNA RFLP variation has been analyzed by LR-RFLP methods rather than by HR-RFLP methods. As noted above, LR-RFLP

analysis typically employs the five rare-cutting restriction endonucleases—*HpaI*, *BamHI*, *HaeII*, *MspI*, and *AvaII*—and, in some instances, *HincII* also has been included (Johnson et al. 1983; Scozzari et al. 1988; Soodyall and Jenkins 1992, 1993). Fortunately, the most informative restriction-site polymorphisms for African mtDNAs are recognized by *HpaI*, *MspI*, and *AvaII*, which are included in both LR- and HR-RFLP analysis. Hence, once nomenclatural differences between LR- and HR-RFLP haplotypes have been resolved, a constructive population comparison can be made for African populations, by use of both types of data.

LR-RFLP analysis involves examination of restriction-fragment patterns by use of Southern blot analysis, with a unique restriction-endonuclease pattern being called a *morph* and being given a specific morph number. The sum of all of the individual morphs for a particular mtDNA is defined as its mtDNA *type*. The LR-RFLP types are numbered and described by listing the morph numbers of the five restriction endonucleases, in the order *HpaI*-*BamHI*-*HaeII*-*MspI*/*HpaII*-*AvaII*. Thus, type 1 is defined by morph-2 for *HpaI*, morph-1 for *BamHI*, morph-1 for *HaeII*, morph-1 for *MspI*/*HpaII*, and morph-1 for *AvaII*, which can be written, in shorthand form, as “2-1-1-1-1.” Later, when *HincII* was added to the enzyme set, its morph was appended to the type number, such that a type 1 mtDNA with a *HincII* morph-2 became type 1-2. Most of the variation represented by these morphs can now be equated with the presence or absence of specific restriction sites identified by HR-RFLP analysis. Thus, the LR-RFLP types can be equated with HR-RFLP haplogroups, at the restriction site—and, thus, at the nucleotide level. These associations can be further refined by use of CR sequence data.

*HpaI* morph-3 is the most common African *HpaI* restriction pattern. By contrast, *HpaI* morph-2 delineates all L3 African mtDNAs and is found in all European and Asian mtDNAs. *HpaI* morph-3 differs from morph-2 by having the *HpaI* site gain at np 3592. Thus *HpaI* np-3592 morph 3 defines macrohaplogroup L\*, and distinguishes L\* from L3 and the remaining global mtDNAs. Accordingly, all African LR-RFLP types that start with a 3 (e.g., 3-1-1-1-1-2 or type 7-2) can be considered L\*(L1 or L2) mtDNAs, while those which start with a 2 (e.g., 2-1-1-1-1-2 or Type 1-2) can be considered L3 mtDNAs (table 7).

Similarly, the *MspI*/*HpaII* morphs delineate major subsets of African mtDNAs. These are represented by the fourth number in the LR-RFLP type designation (table 7). *MspI*-2 is defined by site losses at np 8112 and np 8150. These are the primary site changes that define the HR-RFLP lineage L1a<sub>2</sub> and the Kung San-specific sublineage  $\alpha$  (figs. 2 and 3). Similarly, *MspI*-3 is defined by the site losses of *MspI*-2, as well as by an additional site gain at np 11436. This new polymorphic site further

subdivides lineage L1a<sub>2</sub>, into two major subgroups (figs. 2 and 3). Finally, *MspI* -3' has the same site changes as does *MspI*-3, together with an additional site gain at np 16494. This further subdivides sublineage- $\alpha$  mtDNAs. Thus, all mtDNA types having *MspI* morphs 2, 3, and 3' correspond to the Vasikela Kung-specific sublineage  $\alpha$  in L1a<sub>2</sub> (figs. 2 and 3 and table 7).

Several of the *AvaII* morphs also correspond to RFLPs that define major sublineages of the African phylogeny. The first is *AvaII*-2, which is defined by a site gain at np 8249. This site appears in haplotypes from lineage L1a<sub>2</sub> and from the Vasikela Kung-specific sublineage  $\alpha$  (figs. 2 and 3 and table 7). *AvaII*-3 is defined by a site loss at np 16390, and *AvaII*-5 is defined by both a site gain at np 8249 and a site loss at np 16390. Thus, *AvaII*-5 could derive from either *AvaII*-2 or *AvaII*-3.

Therefore, the LR-RFLP sites for *HpaI*-3, for *MspI* -2, -3, and -3', and for *AvaII*-2 all help to define the lineage L1a<sub>2</sub>, which encompasses the Kung-specific mtDNA sublineage  $\alpha$ . Consequently, mtDNA types 3-2, 4-2, 4-9, 4'-2, 5-2, 14-2, and 32-2 (all *HpaI*-3 and *MspI*-2 or 3) can be considered to be of Kung San origin (table 7). As a result, these mtDNA types can be used to determine the relative representation of Kung San-derived mtDNAs in other African populations that have been analyzed by LR-RFLP analyses (table 7).

By contrast, mtDNAs that are *HpaI*-2 and *MspI*-1 belong to haplogroup L3, with type 1-2 (i.e., 2-1-1-1-1-2) belonging to subhaplogroup L3a and with type 21-2 (i.e., 2-1-1-1-2-2) belonging to subhaplogroup L3b. Since the Senegalese have a much higher frequency of L3 types than does the Kung population, the presence of these mtDNAs are more indicative of a Bantu origin than of a Kung origin (table 7).

Using these distinctions, we can now compare our current data on the Vasikela Kung and Khwe with those from other LR-RFLP studies of the Kung San and Bantu populations (table 7). The three Kung San groups that have been studied are the Vasikela Kung, the Botswana Kung, and the Sekele Kung. The single Khoi group that has been examined is the Nama, whereas the Bantu-speaking groups that have been analyzed include the Bantu, Herero, Dama, and Ambo.

The Kung-associated mtDNA types (3-2, 4-2, 4-9, 4'-2, 5-2, 14-2, and 32-2) constitute 51% of the Vasikela, 88% of the Botswana, and 59% of the Sekele Kung mtDNAs (table 7). Of these, types 4-2, 4-9, and 4'-2 are Kung specific, whereas types 3-2 and 7-2 are present in all southern-African populations, although at generally higher frequencies in the Kung and Khoi (Nama) (table 7). By contrast, the Khwe lack virtually all the Kung San-specific L1a<sub>2</sub> types and, instead, exhibit 29% of the Bantu-associated types 1-2 and 21-2 of haplogroup L3. This frequency of L3 mtDNAs in the Khwe is comparable to the 18%–83% seen in the Bantu-derived groups



Table 7

## Distribution of LR-RFLP Types in Khoisan Populations and in Neighboring Groups

LR TYPE (DESIGNATION) [HR HAPLOGROUP] <sup>a</sup>	NO. IN								
	Vasikela Kung (N = 43)	Botswana Kung <sup>b</sup> (N = 34)	Sekele Kung <sup>c</sup> (N = 49)	Nama <sup>d</sup> (N = 46)	Khwe <sup>e</sup> (N = 41)	Bantu <sup>b</sup> (N = 40)	Herero <sup>c</sup> (N = 54)	Dama <sup>c</sup> (N = 43)	Ambo <sup>c</sup> (N = 22)
2-1-1-1-2 (1-2) [L3a]	...	2.9	2.0	6.5	26.8	25.0	33.3	20.9	13.6
2-1-1-1-2-2 (21-2) [L3b]	11.6	...	4.1	13.0	2.4	...	50.0	32.6	4.5
2-1-1-1-12-2 (72-2) [L3a]	4.6	...	...	...	...	...	...	...	...
3-1-1-1-3-2 (2-2) [L2]	4.7	2.9	...	...	17.1	32.5	...	...	13.6
3-1-1-2-2-2 (3-2) [L1a <sub>2</sub> ]	14.0	26.5	14.3	54.3	17.1	7.5	5.6	2.3	4.5
3-1-1-3-2-2 (4-2) [L1a <sub>2</sub> ]	20.9	26.5	40.8	...	...	...	...	...	...
3-1-1-3-2-9 (4-9) [L1a <sub>2</sub> ]	4.7	...	2.0	...	...	...	...	...	...
3-1-1-3'-2-2 (4'-2) [L1a <sub>2</sub> ]	11.6	...	...	...	...	...	...	...	...
3-1-1-2-5-2 (5-2) [L1a <sub>2</sub> ]	...	20.6	2.0	6.5	...	...	...	...	...
3-1-1-1-1-2 (7-2) [L1]	18.6	5.9	20.4	6.5	36.6	10.0	...	2.3	54.5
3-1-1-1-2-2 (10-2) [L1a <sub>1</sub> ]	9.3	5.9	12.2	6.5	...	5.0	1.9	...	...
3-1-1-2-4-2 (14-2) [L1]	...	5.9	...	...	...	...	...	...	...
3-1-1-5-1-2 (32-2) [L1]	...	2.9	...	...	...	2.5	...	...	...
3-1-1-12-1-2 (113-2) [L1]	...	...	2.0	...	...	...	...	...	...
3-1-1-1-6-2 (140-2) [L1]	...	...	...	2.2	...	...	...	...	...
7-1-6-13-1-2 (139-2) [?]	...	...	...	4.3	...	...	...	...	...

<sup>a</sup> HR haplogroups were assigned to LR types according to the RFLPs that define these types. The LR designations are according to the nomenclature that was developed by Johnson et al. (1983) and that subsequently was elaborated in many subsequent studies (Bonné-Tamir et al. 1986; De Benedictis et al. 1989; Scozzari et al. 1988, 1994; Semino et al. 1989; Soodyall and Jenkins 1992, 1993; Graven et al. 1995). The LR haplotypes are defined by restriction-endonuclease morphs, in the order *HpaI-BamHI-HaeII-MspI-AvaII-HincII*; those types defined by Johnson et al. (1983) would have an “#” in place of the *HincII* morph number, since this enzyme was not used to characterize mtDNA variation; however, since the vast majority of mtDNAs from various world populations have *HincII* morph-2, it is assumed to be the default morph for this enzyme unless additional data show otherwise (see text). The following restriction-site polymorphisms identify each LR-RFLP haplotype: 1 = no polymorphisms relative to CR sequence; 2 = +3592h, -16390b; 3 = +3592h, -8112i, -8150i, +8249b; 4 = +3592h, -8112i, -8150i, +8249b, +11436i; 4-9 = +3592h, -8112i, -8150i, +8249b, +11436i, +13259o; 4'-2 = +3592h, -8112i, -8150i, +8249b, +11436i, +16494i; 5 = +3592h, -8112i, -8150i, +8249b; 7 = +3592h; 10 = +3592h, +8249b; 14 = +3592h, -8112i, -8150i, +8249b, +15890b; 21-2 = +8249b; 32 = +3592h, -8112i, -8150i, +13070i, +8249b; 72-2 = -12629b; 113-2 = +3592h, +8469i; 140-2 = +3592h, +15882b; and 139-2 = -12406h, +9250n, +11164i.

<sup>b</sup> Data are from Johnson et al. (1983).

<sup>c</sup> Data are from Soodyall and Jenkins (1992).

<sup>d</sup> Data are from Soodyall and Jenkins (1993).

<sup>e</sup> The data obtained in the present study were combined with those reported, by Soodyall and Jenkins (1992), for the related Kwengo.

but is quite different from the 3%–12% seen in the Kung San populations (table 7). Thus, on the basis of these data, as well as on the basis of genetic-distance analysis (fig. 4 and table 5), the Khwe appear to be much more closely related to Bantu-derived populations than to the other Khoisan-speaking populations (Nurse et al. 1985).

Since nearly all of the haplotypes in Bantu-speaking populations from western Africa and in the Pygmy populations from eastern and central Africa are *MspI*-1 (Chen et al. 1995; Graven et al. 1995; authors' unpublished data), *MspI*-2 must be of Khoisan origin. This further supports the conclusion that the *MspI*-2 mtDNAs in the Bantu-speaking populations have been acquired through genetic admixture with Khoisan-speaking populations since the Bantu expansion into southern Africa.

The population distribution of the individual LR-RFLP morphs can also permit deduction of their inter-relatedness; for example, *AvaII*-5 is defined by the np-8249 site gain of *AvaII*-2 and by the np-16390 site loss

of *AvaII*-3. Therefore, it could have derived from either of these morphs. However, both *AvaII*-2 and *AvaII*-5 occur primarily in the Kung San, whereas *AvaII*-3 does not. Therefore, it is most likely that *AvaII*-5 derived from *AvaII*-2 within the Kung population, through the loss of the np-16390 site. A parallel and independent mutation must then have created the np-16390 site loss seen in *AvaII*-3. This conclusion is supported by the fact that the np-16390 site is located in the hypervariable CR at the very end of HVSI and, thus, is prone to repeated mutational events.

#### Correlation between RFLP and CR Sequence Data

In most respects, the phylogenetic relationships between the CR sequences of the Kung and Khwe correlated well with those seen for the combined LR- and HR-RFLP haplotype data (fig. 5 and table 7). The CR sequences of haplogroup L1 mtDNAs were clearly delineated from those of L2 and L3, and the four subhap-

logroups of L3 were also distinctive. In a number of cases, the CR sequence provided more information than did HR-RFLP analysis. Indeed, the CR sequence data revealed several distinct subdivisions within these RFLP groupings; for example, lineage L1a<sub>1</sub> was divided into two major subbranches by CR sequences (AF97–AF99 and AF100–AF101 in one branch and AF96, AF102, and AF103 in a distinct second branch) (fig. 5). Moreover, some HR-RFLP haplotypes have more than one CR sequence (AF93 with VK3 and VK5). By contrast, in other instances the CR sequences provided less resolution. CR sequences were unable to clearly distinguish between L2 and L3, such that, in the absence of supporting RFLP data, the L2 and L3 CR sequences could be interpreted as belonging to the same haplogroup (fig. 5). Furthermore, certain CR sequences were found to be present in several different RFLP haplotypes (CR 15 is common to haplotypes AF80–AF82 and AF84) (table 6). Only when both RFLP and CR sequence data are used can the optimal phylogenetic relationships between African mtDNAs be resolved.

The conclusion that the deepest root of the African mtDNA tree occurs at the Vasikela Kung sublineage  $\alpha$ —and that the Kung and the Biaka and Mbuti Pygmies harbor distinctive groups of mtDNA types—is supported by both RFLP and CR sequence data (figs. 2, 3, and 5). This result is fully consistent with earlier analyses, by Vigilant et al. (1989, 1991), of African and non-African CR sequences and with our own RFLP data (Chen et al. 1995). Thus, all of these studies place the Kung San among the oldest African and extant human populations.

The importance of macrohaplogroup L\*, with its component haplogroups L1 and L2, as opposed to haplogroup L3 (non-L), was also confirmed in another study, by Watson et al. (1997), of African mtDNA CR sequence variation. In that study, a total of 407 African samples, including Kung San, Mbuti and Biaka Pygmies, and multiple Bantu-derived populations, were analyzed, by CR sequencing and screening, for both the presence of the *HpaI* np-3592 site (delineating L\*) and the absence of the *AvaII* np-16390 site (equal to the presence of the *HinfI* site at np 16389 and delineating L2) (figs. 2 and 3 and table 2). This analysis confirmed the distinctive nature of haplogroups L1–L3, which we previously had described (Chen et al. 1995), and also revealed that haplogroup L3 has three distinct sublineages: L3a, L3b, and L3c (Watson et al. 1997).

The primary question addressed by Watson et al. (1997) is the number and nature of African population expansions. To address this question, they examined the sequence diversity of these samples, partitioning their CR sequences into those which were observed in more than one population (87%) versus those which were found in only one population (13%). The multipopu-

lation CR sequences were then used to construct a median network, which resulted in the separation of these sequences into haplogroups L1 (a and b), L2, and L3 (a–c). Estimation of the distribution of pairwise differences of and between haplogroups L1a, L1b, L2, L3a, and L3b revealed all of them to have unimodal distributions, a finding that is consistent with each haplogroup being associated with a different population expansion. The remaining population-specific CR sequences (termed “isolated lineages”) were then combined into a new category termed “L1i.” A median network of the L1i sequences converged on a MCRA having CR transition mutations at np 16129, 16187, 16189, 16223, 16230, 16278, and 16311; however, this L1i network was not starlike, and the pairwise distribution of CR sequences was not unimodal.

The nature of Watson et al. (1997)’s L1i haplogroup can be more fully explained if it is compared with our data (Chen et al. 1995; present study). By placing all of the population-specific CR sequences into L1i, Watson et al. (1997) combined mtDNAs from the Kung San-specific sublineage  $\alpha$  from L1a, the Biaka Pygmy sublineage  $\beta$  from L1b, the Mbuti Pygmy sublineage  $\gamma$  from L2a, and the Senegalese sublineage  $\delta$  from L2a. In addition, a comparison of the variant sites of their MRCA with the data from our study shows that it has the greatest similarities to our CR sequences 4, 5, 7, and 8 of lineage L1a<sub>2</sub>, sequence 9 of subhaplogroup L1b, and sequences 22–24 of lineage L1a<sub>1</sub> (fig. 5 and table 6). Not surprisingly, therefore, L1i coalesces to the deepest root of the African phylogeny, at subhaplogroup L1a, because it encompasses widely different clusters of haplotypes from both haplogroup L1 and haplogroup L2; for this same reason, it follows that L1i is not starlike or unimodal, since it subsumes several different population-specific sublineages.

Our estimates of the age of the African population and its haplogroups are also comparable to estimates made by other investigators. In our studies, the antiquity of African mtDNAs has been demonstrated by means of a sequence-divergence time of 125,500–165,500 YBP (Chen et al. 1995; present study). Similarly, the coalescence time for the MRCA, as calculated by Watson et al. (1997) on the basis of their L1i cluster, was  $111,000 \pm 5,700$  YBP; that estimated by Horai et al. (1995) on the basis of whole mtDNA sequences was  $143,000 \pm 18,000$  YBP; and that estimated by Cann et al. (1987) on the basis of RFLP haplotype data was 120,000 YBP. By contrast, the age of haplogroup L2 was much younger, being 59,000–77,700 YBP by our analysis,  $56,000 \pm 3,000$  YBP according to Watson et al. (1997), and  $70,333 \pm 25,710$  YBP according to Graven et al. (1995). Finally, the age of haplogroup L3 is 78,300–103,200 YBP by our analysis,  $60,000 \pm 2,400$  YBP according to Watson et al. (1997), and  $66,321 \pm$

24,965 YBP according to Graven et al. (1995). Thus, all of the most recent studies show consistent trends in the diversity and ages of the major clusters of mtDNAs in African populations.

The other interesting question raised both by our analyses (Chen et al. 1995; present study) and by that of Watson et al. (1997) is the origin and dispersal of haplogroup L3 mtDNAs. These haplotypes are widely dispersed in eastern Africa but are less prevalent in western and southern Africa (table 2; also see Watson et al. 1997; Passarino et al. 1998). Moreover, there are several different subhaplogroups within L3 (figs. 2 and 4), and these appear to be differentially distributed in these populations (table 2). On the basis of the continental distribution and age that they reported, Watson et al. (1997) proposed that a subset of L2 and L3 mtDNAs moved out of eastern Africa to found the Eurasian populations ~60,000 YBP.

Since the subhaplogroups of L3 are the most likely precursors of modern European and Asian mtDNA haplotypes (Chen et al. 1995; Watson et al. 1997), their sequence variation and age are of considerable importance in the determination of the timing and process by which these mtDNAs were dispersed out of Africa. In this regard, subhaplogroups L3a and L3b appear to be the oldest of the L3 subhaplogroups, dating to 41,400–54,500 YBP and 77,600–102,300 YBP, respectively. These estimates are somewhat similar to the  $60,000 \pm 3,200$  YBP and  $44,000 \pm 3,000$  YBP coalescence times that Watson et al. (1997) calculated for the analogous subhaplogroups. In contrast, subhaplogroups L3c and L3d have somewhat younger divergence times—28,300–37,300 YBP and 17,600–23,200 YBP, respectively (table 4)—suggesting that they emerged after the evolution of L3a and L3b.

We have also observed that subhaplogroup L3d lacks the *DdeI* np-10394 site, a polymorphism that it has in common with the vast majority of European haplogroups (H and T-X). Although our estimate of the age of subhaplogroup L3d is younger than those of most European haplogroups (Torroni et al. 1994a, 1996, 1998), the relatively young age of L3d in the present study might be due to the limited number of L3d mtDNAs that we sampled. Since two of the L3d haplotypes (i.e., AF01 and AF02) identified in our study possess the *HinfI* np-12308 site-gain marker for haplogroup U (Torroni et al. 1996), haplotype U could have arisen in Africa and migrated into Europe. Consistent with this hypothesis, the third haplotype in this sub-

haplogroup (i.e., AF03) lacks this haplogroup U marker but clusters with the haplogroup U mtDNAs. Hence, AF03 could be an African precursor to haplogroup U; alternatively, the haplogroup U mtDNAs in our sample may have been introduced into Africa by a back-migration/flow of European mtDNAs. Additional L3d mtDNAs, from other African populations, will need to be analyzed to further clarify the relationship of African haplogroup L3 and L3d mtDNAs to European mtDNA haplogroups.

Similarly, L3a was found to have a close affinity to haplotype AF24, a mtDNA that has the *DdeI* np-10394 and *AluI* np-10397 site gains characteristic of Asian macrohaplogroup M (figs. 2 and 3). Therefore, it is possible that subhaplogroup L3a was the progenitor of Asian mtDNAs belonging to M. Although the age of subhaplogroup L3a is somewhat less than our estimate for the age of Asian haplogroup M (Torroni et al. 1994b; Chen et al. 1995), the differences could be due to the limited number of L3a mtDNAs in our African sample. Alternatively, AF24 may have been introduced from Asia into Africa more recently.

On the basis of these observations, it is possible that mtDNA subhaplogroups L3a and L3d arose in sub-Saharan Africa and then moved upward into eastern Africa and out of eastern Africa into the Middle East, to yield Asian macrohaplogroup M and European haplogroup U. Such a hypothesis is supported by recent studies of eastern-African populations, which have revealed an unusually high percentage of L3 mtDNAs (Watson et al. 1997; Passarino et al. 1998). Interestingly, a number of these mtDNAs also have the *DdeI* np-10394 and *AluI* np-10397 site gains characteristic of “Asian” macrohaplogroup M (Passarino et al. 1998). Therefore, it is possible that subhaplogroups L3a and L3d radiated out of eastern Africa, to give rise to European and Asian mtDNAs. If so, then eastern Africa may still harbor the progenitor haplotypes from which European and Asian mtDNAs were derived.

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Appendix A

Table A1

Polymorphic Sites Defining RFLP Haplotypes in Southern-African Populations

	HAPLOTYPE (AF) <sup>b</sup>
POLYMORPHIC SITE <sup>a</sup>	0000000000000000000111111111 4888888888889999999990000000 60123456789012345678901234567
102e	00000000000000000000100000
185l	00000000000000000000001000
762k	00000000000000000000000100
1715c	1111110011111101111111111111
2349j	011111000000000000000010000
2758k	11111110000000000000000111
3592h	11000000111111111111111111
4157a	10000000000000000000000011
4310a	111111111111111111111110000
4341g	1111111111111111011111111111
4464k	1111111111111111011111111111
4583a	111111111111111000000001111
4769a*	00000000000000000000000000
4901j	0000000000000000010000000000
5164k	0000000000000000100000000000
5176a	1111110011111111111111111111
5811g	0000000000000000011111000000
6610g	000000000000000000000000011
7025a*	1111111111111111111111111111
7055a	1111111111111111111111110111
7828f	0000000011110000000000000000
7967c	0000000001110000000000000000
8112i	1111111100000000011111111111
8150i	1111111100000000011111111111
8249b/8250e	0000001111111111000001000000
8519g	0000000000000000010000000000
8587k	1111111111111111111111011111
8616j	1111110011111111111111111111
8858f*	1111111111111111111111111111
8921k	0000000000000000001100000000
8994e	1111111111111111111100011111
9135j	0000000011110000000000000000
9246e	0000100000000000000000000000
9438e	1111111100001111111111111111
10394c	1111101111110011111111111111

Table A1 Continued

	HAPLOTYPE (AF) <sup>b</sup>
POLYMORPHIC SITE <sup>a</sup>	0000000000000000000011111111 4888888888889999999990000000 60123456789012345678901234567
10806g	000001001111111111111111000
11436i	0000000011110000000000000000
11641e	00000000000000000100000110000
12629b, j	1110111111111111111111111111
12802a	0000000000000000100000000000
13259o	1111111111011111111111111111
13702e*	0000000000000000000000000000
14149o*	0000000000000000000000000000
14268g*	1111111111111111111111111111
14368g*	0000000000000000000000000000
14406c	0000000000000000000000000010
15208k	0000001100000000000000000000
15357j	1111110011111111111111111111
16208k	111101001111111111100000111111
16208k	11110100111111111100000111111
16275k	0000001100000000000000000000
16373e	0000000000000001000000000000
16389g/16390b	1000000000000000000000000111
16501i	0000000001000000000000000000
16517e	0011010111111111011111111101

<sup>a</sup> Restriction enzymes used in the analysis are designated by single-letter code, as follows: a = *AluI*; b = *AvaII*; c = *DdeI*; e = *HaeIII*, *HhaI*; g = *HinfI*; h = *HpaII*; i = *MspI*; j = *MboI*; k = *RsaI*; l = *TaqI*; m = *BamHI*; n = *HaellI*; and o = *HincII*. Sites separated by a slash (/) indicate either (a) simultaneous site gains or site losses for two different enzymes or (b) a site gain for one enzyme and a site loss for another, because of a single inferred nucleotide substitution; in the parsimony analysis and sequence-divergence calculations, these sites are considered to be only one restriction-site polymorphism. Sites marked with an asterisk (\*) were found to be present or absent in all samples, contrary to the published sequence.

<sup>b</sup> A “1” indicates the presence of a site; and a “0” indicates the absence of a site. Sites are numbered from the first nucleotide of the recognition sequence, according to the sequence published by Anderson et al. (1981).

## Appendix B

Table B1

## Percent Sequence Divergence Within and Between African Haplogroups

	SEQUENCE DIVERGENCE <sup>a</sup>																
	(%)																
	L	L1	L2	L3	L1a	L1b	L2a	L2b	L2c	L3a	L3b	L3c	L3d	L1a1	L1a2	L1b1	L1b2
L	<u>.356</u>	.360	.331	.362	.357	.355	.343	.353	.351	.355	.373	.357	.356	.348	.365	.343	.370
L1	.018	<u>.328</u>	.357	.362	.315	.322	.352	.343	.364	.341	.369	.339	.334	.309	.322	.305	.347
L2	.068	.108	<u>.171</u>	.264	.335	.288	.165	.172	.163	.214	.251	.199	.185	.277	.310	.231	.274
L3	.071	.084	.065	<u>.227</u>	.350	.306	.262	.249	.270	.213	.243	.221	.220	.309	.336	.254	.320
L1a	.047	.019	.118	.104	<u>.265</u>	.323	.328	.305	.341	.315	.347	.300	.286	.252	.252	.281	.337
L1b	.070	.051	.096	.086	.083	<u>.214</u>	.289	.272	.303	.260	.333	.259	.243	.279	.313	.165	.249
L2a	.108	.132	.023	.092	.139	.125	<u>.113</u>	.141	.162	.204	.266	.180	.155	.271	.311	.214	.301
L2b	.140	.144	.051	.100	.137	.129	.099	<u>.072</u>	.120	.196	.286	.193	.160	.243	.267	.175	.343
L2c	.147	.174	.051	.130	.182	.170	.100	.101	<u>.052</u>	.206	.274	.176	.128	.283	.325	.221	.320
L3a	.117	.117	.069	.039	.122	.093	.197	.147	.138	<u>.120</u>	.134	.119	.071	.259	.294	.163	.321
L3b	.082	.092	.053	.017	.102	.114	.155	.132	.101	.239	<u>.225</u>	.248	.052	.318	.333	.271	.401
L3c	.138	.134	.073	.067	.127	.111	.148	.183	.146	.158	.104	<u>.082</u>	.098	.239	.253	.161	.320
L3d	.152	.144	.074	.081	.128	.111	.093	.140	.127	.140	.226	.128	<u>.051</u>	.215	.208	.125	.309
L1a1	.088	.063	.108	.113	.037	.090	.218	.149	.169	.214	.259	.155	.101	<u>.166</u>	.267	.215	.298
L1a2	.127	.099	.165	.163	.060	.146	.305	.220	.258	.293	.228	.216	.141	.221	<u>.119</u>	.239	.329
L1b1	.144	.120	.126	.120	.128	.038	.141	.144	.210	.084	.087	.120	.114	.090	.161	<u>.041</u>	.217
L1b2	.069	.060	.065	.084	.081	.019	.168	.169	.125	.195	.380	.156	.114	.218	.202	<u>.012</u>	<u>.246</u>

<sup>a</sup> Intra-haplogroup sequence-divergence values are shown on the diagonal (*underlined*), whereas the raw and corrected interhaplogroup values are shown above and below the diagonal, respectively.

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