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The Phylogeography of Mitochondrial DNA Haplogroup L3g in Africa and the Atlantic Slave Trade

To the Editor:

From the 16th to the 19th century, ~4 million slaves were transported from sub-Saharan Africa to Brazil. With the use of historical records, it is possible to estimate that ~65% of them were Bantus from west-central Africa, ~30% originated from western Africa, and ~5% came from southeastern Africa (Klein 2002).

Salas et al. (2004) have compared the phylogeography of mtDNA haplogroups in Africa with available data on Brazilians and have concluded that their results agree with these historical estimates. However, they were careful to point out that the west-central African contribution to Brazil, signaled by a high frequency of haplogroups L1c and L3e (Bortolini et al. 1997; Alves-Silva et al. 2000; Bandelt et al. 2001), derives largely from an area (the Congo basin) that, thus far, has not been thoroughly analyzed for mtDNA variation. Also, Salas et al. (2002, 2004) called attention to the presence of the haplogroup L3g—which they had only encountered in eastern African populations—in three Brazilians (among the 92 African mtDNA haplotypes that were characterized), one Colombian, and one African American individual. On the basis of this observation, they proposed the occurrence of either direct slave trade from eastern Africa to America or hitherto undetected gene flow from eastern Africa into western or southeastern Africa and then into America.

Intrigued by this proposal, we tried to identify historical evidence of direct slave trade from eastern Africa to Brazil and, indeed, found some anecdotal reports but certainly not enough to explain the significant frequency of L3g seen among African mtDNA haplogroups in Brazil (proportion, 3.3%; 95% CI, 0.7%–9.2%). We then tried to identify other potential sources for the Brazilian L3g mtDNAs. While studying the mtDNA haplotypes of 10 individuals from Cameroon (described in Da Silva

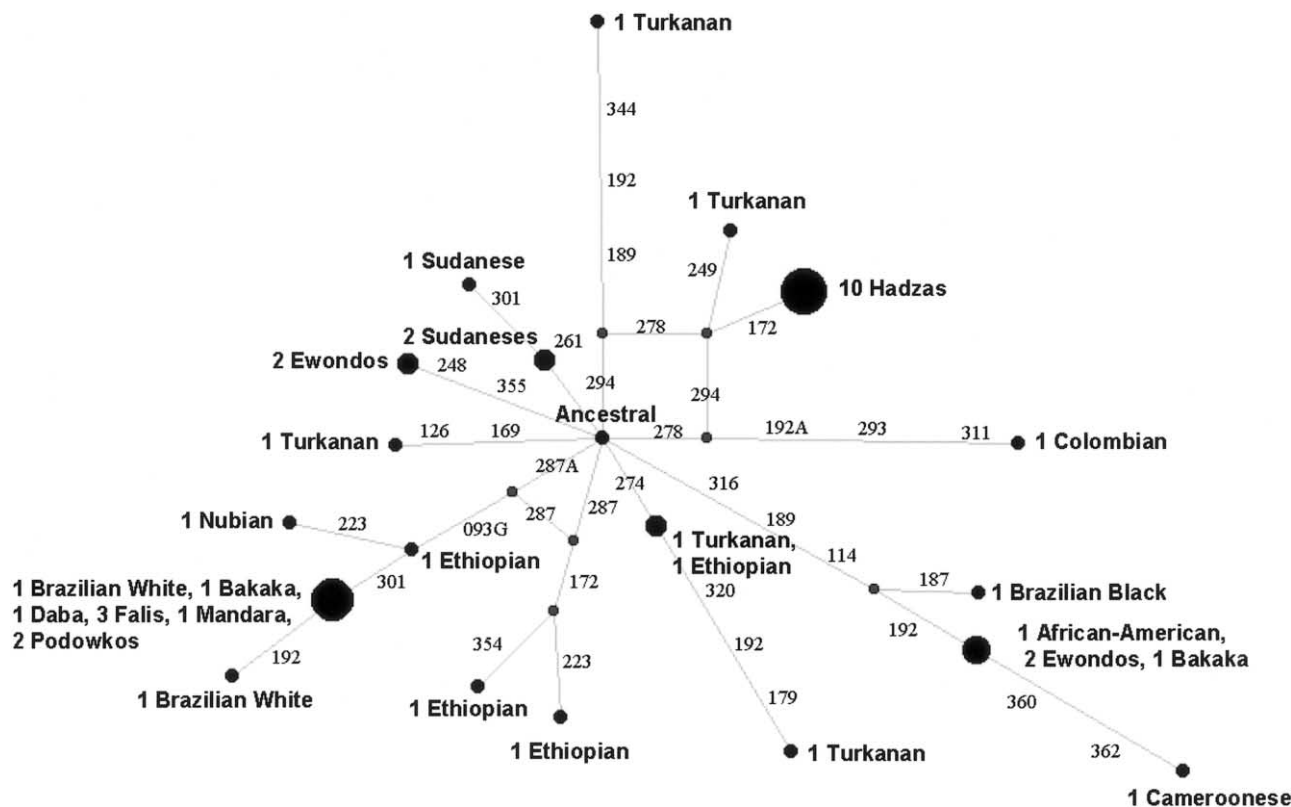


Figure 1 Median network of 20 different L3g lineages identified in populations from sub-Saharan Africa and America. The ancestral haplotype (16223T-16293T-16311C-16355T-16362C) was identified in a single Sudanese individual by Salas et al. (2002). The branches of the network show the additional mutations that identify each haplotype. Positions are indicated as variants from the reference sequence, minus 16,000; a letter next to the position indicates a transversion. The data were compiled from the following groups: Ethiopians, Colombians, and African Americans (Salas et al. 2002); Hadzas (Vigilant et al. 1991); Turkanans (Watson et al. 1997); Nubians (Krings et al. 1999); Ewondos (Destro-Bisol et al. 2004); Bakaka, Bassa, Daba, Falis, Podowkos, and Mandara (see Web site of the Laboratory of Molecular Anthropology, University of Rome “La Sapienza”); Brazilian whites (Alves-Silva et al. 2000); Brazilian blacks (Bortolini et al. 1997); and Camerooneese (present study).

et al. 1999), we identified 1 individual of undisclosed ethnic origin whose mtDNA unequivocally belonged to the L3g haplogroup (fig. 1). This finding stimulated us to search for further mtDNA data from Cameroon, and we came across an article by Destro-Bisol et al. (2004) in which they reported 4 instances of the L3g haplogroup among 53 Ewondo individuals. Moreover, the same authors described (on the Laboratory of Molecular Anthropology Web site) another 11 instances of the L3g haplogroup in several ethnic groups (Bakaka, Bassa, Ewondo, Daba, Fali, Podowko, and Mandara) from different geographical regions of Cameroon. The 14 mtDNA sequences from Cameroon belonged to only four different haplotypes.

We incorporated the four L3g lineages from Cameroon with those from eastern Africa and obtained the median-joining network shown in figure 1. One Brazilian haplotype was identical to the most common Cam-

erooneese haplotype (seen in 8 of the 14 cases), whereas another was closely related. Both the third Brazilian and the single African American haplotype also clustered with Camerooneese sequences. A noteworthy feature of the network was that there did not appear to exist any clear segregation of the Camerooneese L3g haplotypes from the eastern African counterparts. This feature, plus the fact that the putative ancestral haplotype was seen in an individual from Sudan and that there is a much smaller haplotype diversity in Cameroon (0.602) as compared with eastern Africa (0.911, excluding the Hadza), suggests that the Camerooneese L3g lineages might have originated from eastern Africa by transcontinental gene flow, as put forward by Salas et al. (2004) in one of their two possible scenarios. At any rate, it appears that the L3g lineages seen in America probably have their immediate origin in Cameroon or in neighboring regions and not in eastern Africa.

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Electronic-Database Information

The URL for data presented herein is as follows:

Laboratory of Molecular Anthropology, University of Rome "La Sapienza," <http://www.scienzemfn.uniroma1.it/labantro/>

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Reply to Bortolini et al.

To the Editor:

The availability of new mtDNA data from central Africa has allowed Bortolini et al. (2004 [in this issue]) to evaluate two alternative scenarios, formulated by Salas et al. (2004), regarding the source of the L3g mtDNAs carried from Africa to America by the Atlantic slave trade. Bortolini et al. proposed that the American L3g haplotypes have an Atlantic African provenance, rather than a direct eastern African origin, and that their most likely source was Cameroon or the neighboring regions.

On the basis of the extensive amount of new data that can be added to the L3g phylogeny (fig. 1), we are wholeheartedly in favor of this scenario. Of particular interest are three mtDNA sequences belonging to the L3g1 haplogroup that we observed in southwestern Africa (Angola and Cabinda), this region being the second most important source for the Atlantic slave trade (Thomas 1997), with an important demographic impact in Bra-