



Differential slave trade to Europe and Brazil from the western and eastern African coasts as registered in the mtDNA pool

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Abstract

Within historical times, the forced displacement of Mozambicans as part of the slave trade, documented as being mainly to the Americas, generated a differential input of eastern African sequences into the mtDNA pools of the Americas and of Europe, as testified by the greater number of sequences matches between Mozambique and the Americas compared to those between Mozambique and Europe.

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1. Introduction

The Atlantic slave trade began in the fifteenth century with the European overseas expansion. In the beginning, the main origin of slaves was the western African coast. Of a total of ~ 13,000,000 slaves, it is estimated that 23% were from Angola, 15% each from The Slave Coast, Benin and Senegambia, and 12% from The Gold Coast. In the eighteenth century, due to the loss of Portuguese control over some of these regions, Mozambique and Madagascar became the major source of the slaves shipped, amounting

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to a proportion of around $\sim 8\%$ of the total trade [1]. This shift in the place of origin of the slaves with time was accompanied by a change in the place to where they were exported: in that period, the majority of the European countries forbade the entry of black slaves, but the trade to the former European colonies in America, e.g., Brazil, was still expanding.

Until now, it has been impossible to investigate this issue using mtDNA, because there were few populations on the eastern coast of Africa characterised for mtDNA variation. We have screened 109 individuals from Mozambique, the main eastern source of slaves and investigated whether the contribution of Mozambican sequences to the mtDNA sequence pool of Brazil was indeed higher than to the European pool.

Table 1

Matches between Mozambican (MOZ), Brazilian, European and other African (N—north; W—west, E—East and S—South Africa) sequences for L lineages

Brazil/Europe	MOZ	Other African	HVRI sequence	Hap.
1Brazil	1	–	093 129 148 168 172 187 188 ^G 189 223 230 278 293 311 320	L1a
2Brazil	8	1N 2W 1E	129 148 168 172 187 188 ^G 189 223 230 278 293 311 320	L1a
2Brazil	–	2W 12E	129 148 168 172 187 188 ^G 189 223 230 311 320	L1a
1Sardinia				
1Brazil	6	1E	148 172 187 188 ^G 189 223 230 311 320	L1a
1Canary	–	7W	093 126 187 189 223 264 270 278 293 311	L1b
1Brazil	–	1W	111 126 187 189 223 239 270 278 293 311	L1b
1Portugal	1	5W	126 145 187 189 223 264 270 278 293 311	L1b
1Brazil	–	2N 20W 2E	126 187 189 223 264 270 278 293 311	L1b
2Canary	–	3N 5W 1S	126 187 189 223 264 270 278 311	L1b
2Brazil	1	1S	129 163 187 189 209 223 278 293 294 311 360	L1c
1Portugal	–	2W	093 189 192 223 278 294 309	L2a
2Brazil	–	3N 10W 2E 3S	189 192 223 278 294 309	L2a
1Brazil	–	1N 4W 2E	189 223 278 294 309	L2a
1Brazil	–	4W	223 278 294	L2a
1Italy	10	1W 1E	223 278 286 294 309	L2a
1Brazil	2	1N 7W 4E	223 278 294 309	L2a
1Portugal				
2Canary				
1Brazil	1	2S	114 ^A 129 213 223 278 354	L2b
1Switzerland	–	1E	176 188 209 223 234 311 355	L3*
2Portugal	–	1N 1W 1E	209 223 311	L3*
1Canary				
2Portugal	–	Widespread	223	L3*
1Basque	–	Widespread	223 311	L3*
1Galicia	1	–	093 124 223 278 362	L3b
1Spain	–	1N	124 223 234 278 362	L3b
1Brazil	–	1S	185 223 311	L3e*
3Brazil	2	1S	176 223 327	L3e1*
1Brazil	1	–	223 327	L3e1*
1Brazil	3	1S	185 223 327	L3e1a
3Brazil	2	2N 3W 5S	172 189 223 320	L3e2b

2. Material and methods

A total of 109 unrelated Mozambican individuals was scored for HVRI and HVRII diversity (sequences can be provided upon request to <http://lpereira@ipatimup.pt>). Individuals belonged to different ethnic groups (Changana 35, Ronga 21, Chope 12, Bitonga 8 and Matsua 8 and 25 to various other groups), but all were Bantu speakers (<http://www.sil.org/ethnologue/countries/Moza.html>). Sequence matches with Brazil [2] and large databases for Europe and Africa were sought.

3. Results

Table 1 displays all the sequences of African haplogroups observed in Brazil and Europe for which there was a match with an African population.

There was a considerable number of sequence matches between Mozambique and Brazil, representing 10 shared sequences in a total of 55 different haplotypes from African haplogroups in the Brazilian pool. Two of these matches correspond to sequences that until now have been observed only in Mozambique, five have not been detected in western Africa, while three have been also observed in western Africa. All the Mozambique–Brazil matches for haplogroup L3e1 were not shared elsewhere, except with the southern Khoisan-speaking populations. With respect to the 45 Brazilian sequences with no match with Mozambique, there were seven matches with the African database, from which two were restricted to western African populations.

For sequences observed in the European pool from African haplogroups, in a total of 48 different haplotypes, four matches were detected with Mozambique, but three of those sequences were also detected in western African populations. Besides those, nine further were detected, of which two were western African specific, one was northern African, two were eastern and four were widespread.

4. Discussion

MtDNA reflects a high proportion of matches between Mozambique and America, in accordance with the historical documentation. This is particularly striking since other documented factors would have tended to weaken this signal. Firstly, the female/male proportion of slaves taken to Europe was much higher than to America, and secondly, slave reproduction (particularly from female slave and white owner) was tolerated in Europe (especially after the ban on the importation of slaves after the middle of the eighteenth century) but repressed in America.

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