

The immigrant population from Mozambique in Lisbon: updated mitochondrial DNA portrait

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Introduction

Since the end of the 1970s Portugal had a role in the migratory movements, becoming a destiny for immigrants of a wide range of nationalities, especially from the African continent⁽¹⁾. According to statistical data, until the end of 2015, there were approximately 3000 Mozambican immigrants living in Portugal and from those, more than a half living in Lisbon metropolitan region⁽²⁾.

Mitochondrial DNA identical sequences are shared by matrilineal inheritance. Along with the lack of recombination, it enables to trace the ancestral origin of each population and its evolutionary history. However, not only in evolutionary and population studies but also in forensic genetics, mtDNA is an important tool^(3,4).

The aim of our study is the genetic characterization of Mozambican immigrants living in Lisbon in order to emphasize their genetic variability contribution to Lisbon population.

Materials and Methods

Blood samples were collected from 83 Mozambican immigrants residing in Lisbon. DNA extraction was performed using Chelex® 100 method⁽⁵⁾. The Control region of mtDNA was amplified using two pairs of primers: L15971/H016 and L16555/H639. The amplified products were sequenced by BigDye® Terminator v.3.1 Cycle Sequence (AB) and the sequenced products were detected in a sequencer Genetic Analyzer 3130 (AB). Finally, the results were analysed by Sequencing Analysis v.5.2 software and also compared with rCRS^(6,7) using SeqScape v.3 (AB) software. The haplogroups were determined based on Phylotree, build 17⁽⁸⁾.

Results

In order to define haplotypes, we compared our sequences with the Revised Cambridge Reference Sequence (rCRS). Among the 83 analysed individuals, 74 different haplotypes were identified, 68 of which are unique. The remaining 6 haplotypes were shared by more than one individual. Regarding to the 68 haplotypes, we ascertained 50 different haplogroups. The L haplogroup was the most common haplogroup with 67 sequences followed by H haplogroup (6 sequences), U haplogroup (4 sequences) and K haplogroup (2 sequences). The haplogroups J, M, R and T appear only once.

References

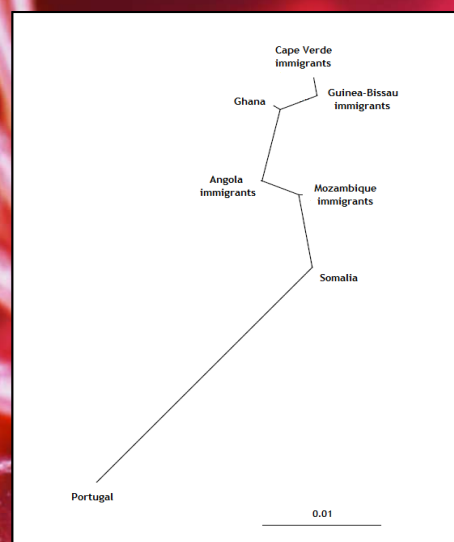
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Discussion and Conclusion

Figure 1 represents the genetic distances between the studied population and other selected populations. It's possible to verify the establishment of two distinct groups: one composed by the Portuguese population and another, more distant, by the African populations. The population under study is genetically closer to the Angolan immigrants living in Lisbon and furthest to Portuguese population. Comparing the different immigrant populations living in Lisbon, the genetically closest community of Portuguese population is Mozambique and the furthest is Cape Verde. Regarding to Portuguese population, the genetically closest population is Somalia population, from the Eastern Africa.

The obtained results display a high haplotypic diversity level of Mozambican immigrants, due to the high frequency of unique haplotypes, which make us believe that their integration among Lisbon population is going to lead to an increase of genetic variability in this region.

The majority of haplotypes fit into the L macrohaplogroup, characteristic of Sub-Saharan regions, where Mozambique is framed. This result evidences the importance of studying immigrant communities currently living in Lisbon.



Populations	Mozambique Immigrants	Angola Immigrants	Cape Verde Immigrants	Guinea-Bissau	Somalia	Ghana	Portugal
Mozambique Immigrants	-	0.0000±0.0000	0.0000±0.0000	0.0000±0.0000	0.0000±0.0000	0.0000±0.0000	0.0000±0.0000
Angola Immigrants	0.01273	-	0.0000±0.0000	0.0000±0.0000	0.0000±0.0000	0.0000±0.0000	0.0000±0.0000
Cape Verde Immigrants	0.02223	0.01268	-	0.0000±0.0000	0.0000±0.0000	0.0000±0.0000	0.0000±0.0000
Guinea-Bissau	0.04113	0.03422	0.00090	-	0.0000±0.0000	0.0000±0.0000	0.0000±0.0000
Somalia	0.02327	0.03572	0.06119	0.01452	-	0.0000±0.0000	0.0000±0.0000
Ghana	0.04070	0.03604	0.01911	0.01055	0.05110	-	0.0000±0.0000
Portugal	0.11815	0.13053	0.15929	0.16957	0.03812	0.16977	-

Figure 1 – Graphical representation of genetic distances between Mozambican immigrant population and other selected populations. The pairwise distances among different populations are also represented.

