

MITOCHONDRIAL DNA CHARACTERIZATION OF Brazilian IMMIGRANT POPULATION LIVING IN LISBOA



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Introduction

Migration is one of the main factors for genetic variability within populations. Currently, the Portuguese population, and particularly the population from Lisboa, welcomes a considerable number of immigrants. Brazilian immigrants are the main foreign community in Portugal, with about 184 000 individuals in 2020.

Mitochondrial DNA (mtDNA), due to its unique characteristics such as being exclusively maternal inheritance and suffering no recombination, which results in its slow evolution, is a useful genetic marker to study the evolution of populations.

In this study mtDNA sequencing analysis of 64 Brazilian immigrants who currently live in Lisboa were carried out in order to assess the impact of this population on the Portuguese gene pool.

The mtDNA control region were amplified using two pairs of primers - L15971 / H016 and L16555 / H639. The amplified products were then sequenced using BigDye® Terminator v.3.1 Cycle Sequence (AB) and detected in the SeqStudio™ Genetic Analyzer (AB). The results were analysed with the Sequencing Analysis v7. and SeqScape v4. (AB) softwares, where the obtained sequences were compared with the rCRS in order to obtain haplotypes that, with Phylotree, build 17, can be converted in haplogroups.

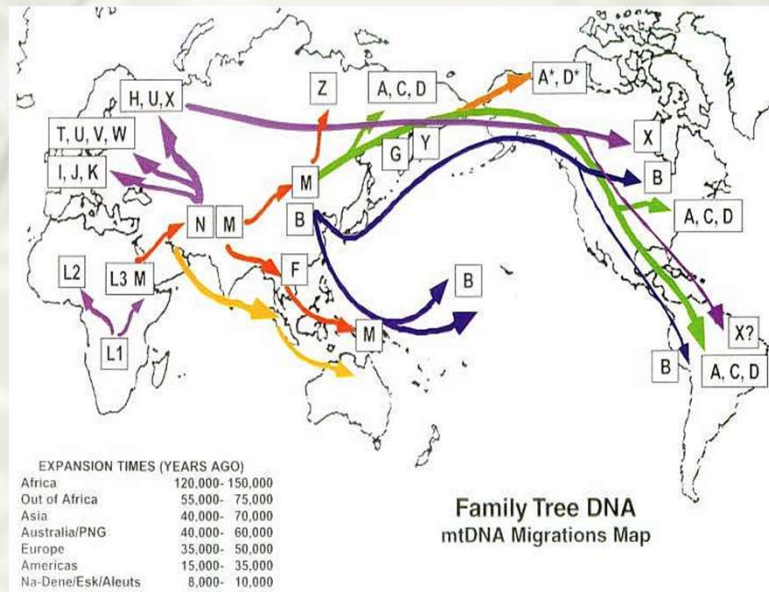
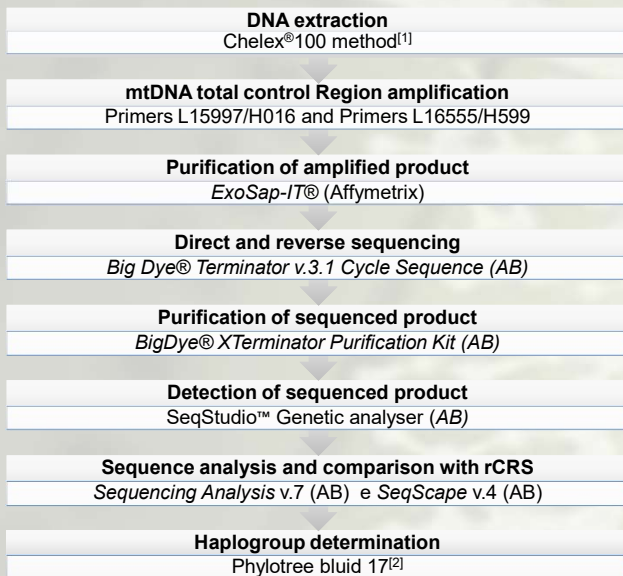


Figure 1: Distribution of mtDNA Haplogroups

Material and methods



Conclusions

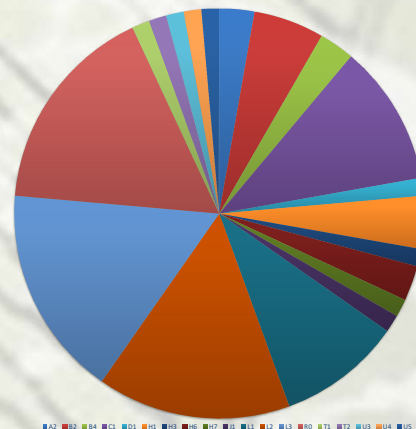
The heterogeneity of the obtained haplogroups shown improves the diversity of the Brazilian population. This results demonstrate the importance of determining the haplotypes of Brazilian immigrants in Lisboa, who now belong to Portuguese population and therefore, increase the genetic diversity of Lisboa population.

References

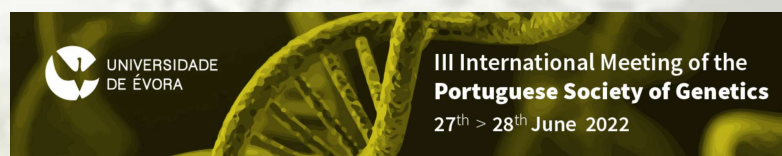
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- ⁽²⁾ van Oven M, Kayser M. 2009. Updated comprehensive phylogenetic tree of global human mitochondrial DNA variation. *Hum Mutat* 30(2):E386-E394
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Results

For each sample were obtained both amplification segments which included hypervariable regions HV1, HVII and HVIII, with reverse and forward primers, resulting in total control regions sequencing.



From our results, it is possible to confirm that this Brazilian population living in Lisboa presents a high number of unique haplotypes, most of them had no coincidence on EMPOP Forensic data. It's an extremely heterogeneous population with half of the studied haplotypes belonging to macrohaplogroup L, characteristic mainly of Sub-Saharan region of Africa, and a quarter of the studied haplotypes belonging to South American population and the other quarter belonging to Euro Asiatic population.





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Miguel Marcelino

has presented the following **Poster**

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held in Évora, Portugal.

On behalf of the Organising Committee,

Leonor Cancela

Leonor Cancela
Director of SPG



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