International Congress Series 1239 (2003) 367–368

Y chromosome haplotypes in the Madeira archipelago population

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1. Introduction

The archipelago of Madeira consists of two inhabited islands, Madeira and Porto Santo, with 250,000 and 5000 inhabitants, respectively. The islands were initially populated in the 15th century by the Portuguese, but suffered many different influences throughout the centuries. In the 15th and 16th centuries, Madeira was part of the Slave Route, and received many of them for sugar cane plantations. In the early 19th century, there was some British influence with entire families settling in the island. Known for its favourable climate, people from different origins came to the islands to recover from diseases such as tuberculosis. In the 20th century, tourism certainly contributed to the settling of new waves of Europeans.

Unlike Madeira, Porto Santo was exposed to attacks by North African pirates during the early colonisation period.

Here, we present a survey on the genetics of the present day Madeira population using Y STRs (DYS19, DYS389I and II, DYS390, DYS391, DYS392 and DYS393) and 11 Y-chromosomal biallelic polymorphisms defining 10 haplogroups. Our aim is to verify the different genetic male input in the present day population of these islands.

2. Material and methods

We collected blood samples from unrelated male individuals originating from Madeira ($N = 95$) and Porto Santo ($N = 16$) with known local ancestors for at least three generations.

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PII: S0531-5131(02)00869-5

The DNA extraction was made by chelex method and the STRs were determined by PCR multiplexing, using a Perkin Elmer ABI 310 sequencer. Y biallelic markers were done by PCR with specific primers for each Y marker separated in polyacrylamide gels and visualized by silver staining.

We used restriction enzymes to digest the PCR products except in case of YAP.

3. Discussion

The haplotype frequencies of both populations were compared with other populations and the results discussed.

There is no relevant influence of Africans in the present male population in contrast to another study using mitochondrial DNA and showing a high influence of African haplotypes.

We also found that at least some influence from North Europe could have not originated in the Portuguese mainland.