



Significant differences between the Leeward and Windward groups of the Cabo Verde archipelago (West African Coast)

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1. Introduction

The Cabo Verde archipelago is composed of nine islands sub-divided into the Barlavento (Windward) and Sotavento (Leeward) groups.

The archipelago was discovered in 1419 by the Portuguese and was part of the slave trade route, which flourished in the 15th and 16th centuries. Slaves originating from the West African coast (especially the coast of Guinea) were sold in Cabo Verde and then transported to Lisbon. They were also used to colonise the islands of Santiago, Fogo and Brava.

The Leeward islands were essentially populated with slaves brought from Guinea (West African Coast), the European colonisers have never been more than 10% of the total population.

The Windward islands were colonised later in the 18th century by some slaves from the Leeward and together with some deported Portuguese men.

In this study, we used five autosomal STRs (CD4, TPO, FES/FPS, TH01 and VWA31) and three Y-biallelic markers YAP, SRY₈₂₉₉ and sY81 to trace the composition of Y-related markers in the present-day population.

The YAP polymorphism is due to an Alu insertion, while SRY₈₂₉₉ and sY81 occur because of a base substitution; these markers together define three haplotypes known as 4, 21 and 8. The haplotype 8 being characteristic of the sub-saharan population and the 21, although occurring in Europe, has its highest frequency in North African populations.

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2. Materials and methods

We collected DNA from unrelated individuals whose ascendency goes back to the same island for at least three generations. Sample sizes and origins were the following: Cabo Verde Leeward ($N=120$) and Cabo Verde Windward ($N=110$).

DNA was extracted using the chelex method and PCR amplification was done using specific primers for each STR and Y marker. PCR products were separated in polyacrylamide gels and visualised by silver staining.

In the case of sY81 and SRY₈₂₉₉ markers, we used restriction enzymes *Nla*III and *Bsr*BI to digest the PCR products.

3. Discussion

The two populations were found to be in Hardy–Weinberg equilibrium. Haplotype and allele frequency values of populations were compared. Using Arlequin software we found significant differences between the two groups of islands on the basis of both STRs and Y-markers.

Full data set is available from www.uma.pt/lgh/