International Congress Series 1288 (2006) 412–414

www.ics-elsevier.com

An investigation into the genetic structure of a Barbadian population

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Abstract. The male-specific inheritance of the Y chromosome and the maternal passage of mitochondrial DNA (MtDNA) allow the genetic features of a population to be investigated. In this study a total of 81 bloodstains were characterized using 29 Y-chromosome specific single nucleotide polymorphisms (SNPs) and MtDNA. The ABI PRISM® SNaPshot™ Multiplex System (Applied Biosystems) was used to genotype the Y-SNPs and enabled the paternal characteristics of the population to be assessed. Sequencing of the control region of the mitochondrial DNA loop was carried out using the BigDye® Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems). Haplogroup frequencies and genetic diversity values were calculated and compared to a less well defined UK-resident Afro-Caribbean population. It was found that the Barbados population studied was similar to other populations of African ancestry and it is proposed that further characterization may be possible using population specific SNPs. Historically, Ghana and Nigeria supplied Barbados with black labour during periods of slavery and it may be useful to first target these ancestral populations when attempting to further define the genetic features of Barbados.

Keywords: Y-chromosome single nucleotide polymorphism (SNP) haplogroup; Mitochondrial DNA haplogroup; Population frequency; Afro-Caribbean; Barbados

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0531-5131/
doi:10.1016/j.ics.2005.10.015

1. Introduction

Barbados is the most eastern of the West Indies and is an example of a relatively well defined population. Unpopulated when the British arrived in the 1620s, black slaves were forcibly brought to Barbados from West Africa in 1850. The low mortality rate in comparison with the other Caribbean islands led to a more ethnically and ancestrally defined population, in comparison with other islands that continued to import slaves [1].

2. Methods

A total of 60 males and 21 females, whose parents were both black and Barbadian by birth, provided anonymised blood samples collected onto stain cards (Whatman). 3 mm punches were extracted in duplicate from each stain using Chelex.

Using a collection of 29 validated SNPs from the SNP*for*ID consortium [2], genotyping was performed on 57 males. Target regions were amplified and treated with ExoSAP-IT (USB Corp). This was followed by single base extension with the SNaPshot Multiplex kit (Applied Biosystems), followed by clean up with CIP (New England BioLabs). SNP detection was undertaken on a 3100 Genetic Analyser (Applied Biosystems). Haplogroups were assigned using the Y-chromosome binary haplogroup tree [3].

The entire control region was amplified using a combination of six primers designed by Ward et al. [4]. PCR product clean up with ExoSAP-IT™ was followed by sequence analysis using ABI Prism BigDye Terminator v3.1 Ready Reaction kit. A combination of six sequencing reactions was undertaken using primers designed by Brandstatter et al. [5]. Sequencing products were cleaned using an ethanol–sodium acetate mix before detection on the 3100 Genetic Analyser. Sequences were compared to the Anderson reference sequence and haplogroups assigned using an African phylogeny tree [6].

3. Results

Five Y-SNP haplogroups were observed in the Barbados populations, the most frequent being E3a*m with the next most frequent being R1b* (Fig. 1A). Amongst the UK Afro-Caribbean samples tested E3a* was also the most common. Only four haplogroups were observed in this latter population but the consented sample size was only 16. Haplogroup diversity was lower in the Barbadian sample, in comparison with the UK sample (0.43 vs. 0.67) and haplogroup observations were significantly different between the two populations, $p = 0.003$.

Amongst the samples sequenced for MtDNA, 16 different haplogroups were seen in the Barbadian samples, the most common being L1b1 (15%), L2a1 (12%), L2a (9%) and L2a1a (9%), with L2 haplogroups being the most common (Fig. 1B). In comparison, in the black UK reference

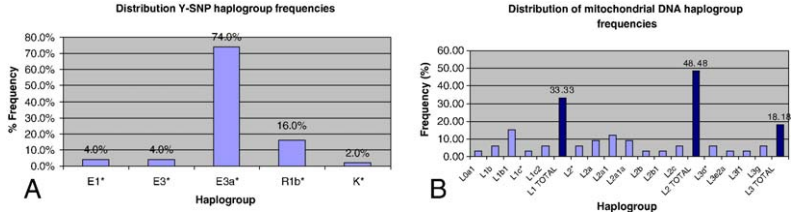

Fig. 1. Distribution of Y-SNP (A) and MtDNA haplogroups (B) in a black Bardabos population.

population, a total of 39 different haplogroups was seen amongst 124 individuals. Haplogroups of the L3 type predominate the latter population with common haplogroups L2a1 (13%), L3b* (9%), L3e2b (8%), L1b1 (7%), L1b* (6%), L2a* (6%) and L2c* (6%). Haplogroup diversity was similar in the two populations (0.947 vs. 0.954) but a significant difference was seen between the haplogroups ($p = 0.007$).

4. Discussion

Y-haplogroups of clade E are largely African in nature with E3a being commonly seen in sub-Saharan Africa. The similarity with regards to the haplogroups observed for the two populations is expected because of the activities of the Atlantic slave trade. Nevertheless E1* and E3* (at a combined frequency of 8%) was not seen in the UK population. Paternally influenced admixture, shown by clade R and K* haplogroup presence in the Barbados group, was around 18% in both populations, consistent with other literature.

Maternal contributions to the population all originated in the African L supergroup. The Barbadian population showed a significantly lower proportion of L3 types in comparison with the UK population (18% vs. 48%). While L3 contains some variations known to be exclusively African, it also includes the latter Eurasian haplogroups M and N, possibly reflecting the higher maternal admixtures amongst the UK black population. This is in accordance with the generally accepted view that very few European women migrated to Barbados during its early settlement independent of their family units.

Acknowledgements

We would like to acknowledge advice given by Juan J. Sanchez (Department of Forensic Genetics, Institute of Forensic Medicine, University of Copenhagen, Denmark) and Maria Brion (Institute of Legal Medicine, University of Santiago de Compostela, Galicia, Spain) with regard to the Y SNPs used in this study. This part of the study was completed as part of the SNP*for*ID project.

We would also like to thank the Forensic Sciences Centre, Barbados for their help in the collection and supply of samples.

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