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SHORT COMMUNICATION

Mitochondrial control region sequences from a Vietnamese population sample

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Abstract Entire mitochondrial control region data were generated for 187 individuals from Vietnam. These samples have been previously typed for 16 autosomal short-tandem repeats (STRs) [1].

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Introduction

The value of mitochondrial DNA (mtDNA) evidence is based largely on the relative rarity of the questioned profile in appropriate population databases. However, forensic mtDNA databases that adhere to strict guidelines in terms of their generation and maintenance are not available for many populations. In this paper, we present a population database of northern Vietnamese for use in forensic mtDNA testing.

Materials and methods

Oral swab samples were collected from 187 unrelated individuals, primarily from Northern Vietnam (Hanoi area). Cotton swabs were extracted using the Qiagen QIAmp DNA kit on a Qiagen 9604 robotic platform, using a custom automated protocol. Polymerase chain reaction (PCR) set-up was performed on a Corbett CAS-1200 robotic liquid handler using primers F15971/R16400, F16190/R285, F15/R599, as described in Brandstätter et al. [2]. Sequencing reactions were prepared on a Tecan Genesis workstation, and sequencing products were separated on an Applied Biosystems 3100. Sequencher version 4.1.4Fb19 was used to align electropherograms and trim data to control region positions 16024–576. Sequences were numbered according to the Cambridge Reference Sequence [3, 4]. The guidelines of Wilson et al. [5, 6] were largely followed for the consistent placement of gaps, although novel length variants were designated with nomenclature based on phylogenetic information [7]. A

Table 1 Diversity measures for control region data from a Vietnamese population sample

Population statistic	Vietnam (n=187)
Random match prob.	
Empirical	0.40%
Sum of squares	0.90%
Haplotypes	153 (19 shared)
Polymorphic positions	165
Mean pairwise differences	12.83
Genetic diversity	0.9964

Statistics are based on entire control region sequences (16024–576). Insertions at 16193, 309, and 573 were ignored.

redundant approach to data generation and data analysis was used to ensure data quality. Additional details of the approach can be found in Brandstätter et al. [2]. Sequence data in electronic form are available from the authors upon request. Data are also available under GenBank accession numbers: DQ535903–DQ536089 and have been submitted to the EMPOP database (www.empop.org).

Summary statistics were either calculated by hand or generated by the software package Laboratory Information Systems Applications (LISA, Future Technologies, Fairfax, VA, USA). For the calculation of random match probabilities, point heteroplasmies were considered to be consistent with either of the component bases at the heteroplasmic position. Point heteroplasmies were denoted by the appropriate International Union of Pure and Applied Chemistry (IUPAC) code and evaluated for the relative proportion of minor vs major component molecule. A lower apparent threshold of approximately 10% minor to major component was set to designate a site heteroplasmic. Observed length heteroplasmies were treated consistently, with the predominant molecule described.

To better understand these data and the mtDNA composition of this particular population in the context of described global mtDNA variation, sequences were assigned to haplogroups on the basis of polymorphisms or constellations of polymorphisms reported to be associated with particular haplogroups ([8–30]).

Results and discussion

Mitochondrial control region haplotypes were determined for a northern Vietnamese population. The haplotype summary is listed in Table S1 and summary statistics are presented in Table 1. The Vietnamese population sample presented in this paper possessed a very low random match probability, high genetic diversity and a large number of unique haplotypes. Of 159 total haplotypes, 15 were shared in the database of 187 individuals. Samples were polymorphic at a total of 165 positions, with any two samples differing at an average of 12.99 sites.

Length heteroplasmies and point heteroplasmies were observed in this dataset. Point heteroplasmies were identified in 28 individuals (15% of the database), at 19 different positions. Twenty-three percent of all point heteroplasmies occurred at position 16,093, with multiple instances also occurring at positions 204, 214, and 215. Positions were called heteroplasmic only if they showed clear, reproducible evidence of mixture in sequence data from both strands, in the absence of significant background.

These data should help provide a framework within which to evaluate the relative rarity of mtDNA types in the Vietnamese population.

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