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Original Article

Mitochondrial DNA (hypervariable region I) diversity in Basrah population – Iraq

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Abstract

In attempt to investigate the origin of Basrah, we examined the mitochondrial DNA(mt-DNA) variations by hypervariable segment 1(HVS1) Sequencing and determination of specific site haplogroups. In Basrah, no significant differences diversity among Iraqis' HVS1 compared with other countries. The values were within the range of gene diversity across the Middle East and exhibited the unimodal pattern of differences in the pairwise sequence. Given the small genetic differences between people living in this area, phylogenetic analysis showed a large variability of the communities of Basrah; they didn't cluster on the phylogenetic tree.

Introduction

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Polymorphisms of mitochondrial DNA (mt-DNA) is an important tool for study the molecular evolution and human population [34]. The maternal inheritance style of the mitochondrial genome and the high base mutation rate enable the use of mt-DNA polymorphisms to infer ancient migration patterns in different regions of the world.

Human mt-DNA is an important wellspring of information for studies on genetic diversity in a human population. Mt-DNA is transmitted maternally and described by mutation rates commonly more than most of the nuclear DNA [7]. Most polymorphic sites of mt-DNA can be found in (HV1) and (HV2) of D-loop control region [33]. HV1 and HV2 are exceptionally valuable in the Phylogenetic and Forensic Research. Haplotypes of HV1 and HV2 are divided into similar groups called mt-DNA haplogroups. The development of new technologies in molecular biology have allowed the high-throughput sequencing of mt- DNA from different human lineages. Such advances have been helpful to follow the matrilineal lineages of current people in Africa and the consequent distribute to Asia and Europe [26].

Section snippets

Population sample

Blood samples from 186 unrelated females were collected. All donors have received informed consent and informations about their ethnic background. The study included only native peoples.…

Amplification of mtDNA

Extracted Genomic DNA *via* the quick protocol of gSYNC™ DNA extraction kit by Geneaid Company. Since there are multiple copies of mt-DNA in every cell, a simple method to extra

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and measure DNA was used to amplify HV1. We utilized the accompanying PCR preliminari

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intensify these polymorphic regions…

Population differentiation and genetic structure

Table 1 illustrates the levels of diversity and neutrality test for Basrah HVS1 data and comparison with population. Value of diversity in the Basrah population was 0.9901, whereas England has the lowest genetic diversity of 0.9651. Kenya has recorded the highest genetic diversity (0.9960). Genetic diversity of controls from Failaka Island and Kuwait were 0.9886 and 0.9799, respectively; those of the neighboring populations, namely, Iran, Iraq and Saudi Arabia, were 0.9895, 0.9918 and 0.9905,…

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Conclusions

HV 1Mitochondrial DNA genetic diversity in Basrah Population is 0.9901, the nucleotide diversity is 0.07243, the mean number of pairwise differences between haplotypes 4.577, the Tajimas D tests (−1.4934) and the Fu's FS (−32.7659). The most widely recognized haplogroup among Basrah population is H (17%), followed by J (11%) and U and M haplogroups (9%)....

Ethical standards

Since all samples in this study were from Humans, all procedures performed were accordance with the ethical standards set by the committee of Ethical standards of Basrah University. All participants were willingly agreed to be part of this study, written consent form was filled by all subjects participated in the study....

Declaration of Competing Interest

The authors declare no conflict of interest....

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