Population genetics and medical sciences resources can be found in the human mitochondrial genome database.

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Abstract

A small number of peptides essential for cellular energy production are encoded by the mitochondrial genome, which is found in the subcellular mitochondrial network. The cataloguing of existing variation is of importance to medical researchers working to identify mutations causing mitochondrial malfunction as well as population genetics studies because mitochondrial genes are highly polymorphic. Database of the Human Mitochondrial Genome (mtDB).

Keywords: Peptides, Mitochondrial genome, Polymorphic.

Introduction

It was now necessary to offer a web-based database of human entire genome and complete coding region sequences due to an increase in the number of published complete human mitochondrial genome sequences. In this database, there are 2104 sequences (1544 whole genomes and 560 coding regions) that may be downloaded or searched for a particular polymorphism as of August 2005. A detailed list of the (now 3311) mitochondrial polymorphisms among these sequences is of particular importance to medical researchers and population geneticists examining certain places. A haplotype search capability and the ability to locate and download sequences bearing certain variations are recent additions to mtDB's capabilities [1].

The mitochondrial genome uses a set of five multiple-subunit enzymes present in the mitochondrial inner membrane to provide components of the protein machinery required for oxidative phosphorylation (OXPHOS). Both nuclear and mitochondrial genes encode the intricate components. Therefore, a genetic flaw could result from gene mutations in any system. Since mitochondrial DNA (mtDNA) mutations are more commonly introduced into the mitochondrial genome, a higher percentage of mitochondrial malfunction is brought on by mtDNA mutations. Numerous human disorders, including Leber's hereditary optic neuropathy (LHON) (1) and neurogenetic muscular weakness, ataxia, and retinitis pigmentosa (NARP), have been demonstrated to be brought on by mitochondrial abnormalities (2). In assessing a potential functional impact of a mitochondrial variation discovered in [2].

Most metazoan species, including humans, inherit their mtDNA mostly from their mothers (3). Because of this clonal inheritance and a substitution rate in vertebrates that is typically 5–10 times higher than that of nuclear DNA (4), mitochondria have become a desirable source of DNA polymorphism data for population genetics investigations in a variety of species. It is possible to trace a direct genetic line where all variability is caused by mutation, and the high substitution rate makes it easy to investigate variance across closely related people. The maternal and paternal mitochondrial genomes do not recombinate (i.e., within species). Numerous studies of the evolution of humans have used mtDNA sequences as their primary data source. These are stored in the Human Mitochondrial Genome Database (mtDB) [3].

Based on the donor's demographic origin, the sequences are divided into 10 major geographic regions (Table 1). The sequences are categorised according to the ancestry of their donors when the donors' geographic origin differs from their purported historical background. African American, European American, and Asian American sequences, for instance, are included under the headings of Africa, Europe, and Asia, respectively, rather than North America. The same population's large sets are available as collections of individual files. All sequences have cross references to both their original publications and, if available, their Gen Bank accession numbers. At the moment, 2104 mitochondrial sequences are available at mtDB [4].

Using the donor's population as a guide, the sequences are divided into 10 major geographic areas (Table 1). The sequences are reported under the heading that most closely matches the donors' ancestry when the donors' geographic origin differs from their purported historical background. As an illustration, the sequences for African Americans, European Americans, and Asian Americans are listed under the headings of Africa, Europe, and Asia, respectively, rather than North America. Batches of individual files representing

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large sets from the same population are accessible. Any available Gen Bank accession numbers are cross-referenced with each sequence's original publications. 2104 mitochondrial sequences are available at the moment on [5].

Conclusion

There are predetermined haplotypes (haplogroups) that certain population genetics researchers use to indicate particular mitochondrial lineages. This page provides a link to a haplogroup tree, which works in conjunction with our search function by displaying a list of all sequences that are members of each specific haplogroup by just clicking on its individual letters.

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