



# Paleo-DNA Laboratory Newsletter

[www.ancientdna.com](http://www.ancientdna.com)

The Paleo-DNA Laboratory has been in operation since 1996 and fully accredited by the Standards Council of Canada under ISO 17025 since June 2004. The lab has been working on cold casework for national law enforcement organizations using mitochondrial DNA analysis since its inception. More recently the Paleo-DNA Lab has been involved with profiling hair samples for the RCMP and Provincial Police. The laboratory's extensive experience in mitochondrial DNA analysis was created through the analysis of exceptionally degraded or ancient material. Applying the techniques used on ancient material to forensic material has made the Paleo-DNA lab a leader in mitochondrial DNA analysis.

## Paleo-DNA RESEARCH

The Paleo-DNA Lab has attracted visiting researchers from around the world. Our latest guest traveled from Portugal to complete her PhD work on ancient horse. The Paleo-DNA Laboratory has also been involved in projects such as detecting the presence of tuberculosis in ancient remains, and identifying the sex of the Weerdinge Bog Bodies. Because the laboratory layout completely separates the low-copy DNA area from post-amplification areas, the chances for contamination are greatly reduced. This allows us to work on degraded samples in an optimal environment.

## MITOCHONDRIAL DNA TRAINING COURSE



This week-long training program will focus solely on mitochondrial DNA analysis and forensic applications. It will include extraction, purification, amplification, sequencing and analysis of modern samples. Laboratory sessions and lectures will be conducted by our qualified analysts.



## ANCIENT DNA TRAINING COURSE

To date, the ancient DNA Training Program has provided over 120 students with the opportunity to gain hands on experience in molecular techniques applied to degraded archaeological and forensic materials. The curriculum covers topics including extraction chemistry, Polymerase Chain Reaction (PCR), mitochondrial DNA, nuclear DNA (STR), DNA sequencing and analysis software. This year the program ran from May 8 – 27, 2006. Renowned scientists Charles Greenblatt (ancient DNA), El Molto (physical anthropologist) and Rajeev Vaidyanathan (entomologist) were the guest speakers at this year's program. Check out the website for additional details.



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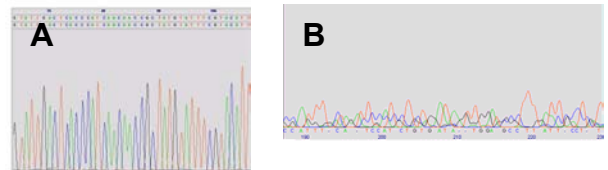
## Nuclear vs Mitochondrial DNA

Nuclear DNA consists of 46 chromosomes that inhabit the nucleus of almost every cell in the human body. These chromosomes hold the vast bulk of genetic information that you've inherited from your parents. Nuclear DNA consists of three billion base pairs of DNA and an estimated 25,000 genes. Outside the nucleus, but still within the cell, lie tiny organelles called mitochondria. Mitochondria are tiny structures that help cells in a number of ways, including producing the energy that cells need. There are about 500 to 2,000 mitochondria in every human cell. Each mitochondrion includes an identical loop of DNA approximately 16,569 base pairs long containing an estimated 37 genes.

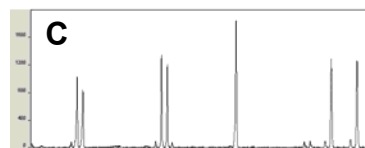
During fertilization, nuclear chromosomes from a sperm cell enter the egg and combine with the egg's nuclear DNA, producing a mixture of each parents' genetic code. The mitochondrial DNA (mtDNA) from the sperm cell, however, is not transferred to the egg. As a result, the fertilized egg contains a mixture of the father and mother's nuclear DNA and an exact copy of the mother's mtDNA, but none of the father's mtDNA. Therefore, mtDNA is passed on only along the maternal line. This means that all of the mtDNA in the cells of a person's body are copies of his/her mother's mtDNA, and all of the mother's mtDNA is a copy of her mother's, and so on. No matter how far back you go, mtDNA is always inherited maternally.

## A Low Copy Number Alternative

MtDNA is particularly well suited for low copy number (LCN) analyses because of its high cytoplasmic copy number, mode of maternal inheritance, and accelerated mutation rate over that of nuclear DNA. DNA, like any artifact, may suffer damage over time making useful interpretation difficult; however, the high copy number of mitochondrial genomes per cell (thousands), as opposed to generally two copies of a given nuclear gene, ensures that short informative sequences survive. Informative sequences can be recovered, copied, and analyzed for maternal relationships within and between groups.



A good (A) mitochondrial DNA sequence will have sharp, defined peak intensities that can distinguish individual base pairs while a poor (B) sequence will have broad, low intensity peaks that are unreadable.



Good nuclear DNA data (C) will have a low base line and very sharp defined peaks.



Heterozygous peaks should be uniform in intensity. Poor nuclear DNA data (D) may have uneven peak intensity, and a high baseline or background noise that contains high stutter or artifacts.