



Paleo-DNA Laboratory Newsletter

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Mitochondrial DNA

Mitochondria are energy-producing organelles that are abundant in every living cell. They are present in the hundreds to thousands per cell. Because of the large number of mitochondria present, mitochondrial DNA (mtDNA) seems an easier target over the more popular nuclear DNA. MtDNA is particularly well suited for ancient DNA analysis because of its abundance, mode of maternal inheritance, and accelerated mutation rate over that of nuclear DNA. Ancient DNA, like any artifact, suffers damage over time making useful interpretation difficult; however, the abundance of mitochondrial genomes per cell (1,000's), as opposed to generally two copies of a given nuclear gene, ensures that short informative sequences survive through time. Informative sequences can be recovered, copied, and analyzed for maternal relationships within, and between groups. The Paleo-DNA Laboratory has developed methods for amplifying mtDNA regions from 100 to 1000 base pairs (a unit of measurement) in a single reaction to reduce the amount of sample extract used.

Identification of Unknown Samples

Samples of unknown origin can be identified by targeting short, specific regions of DNA shared throughout all living organisms. These regions of DNA can usually be found in the mitochondria of a cell. Copying or amplifying these regions produces a DNA sequence that is fairly specific to that particular organism. By searching DNA databases, the Paleo-DNA Laboratory can compare and contrast characteristics in the DNA leading to the identity of unknown samples down to the species level. Very little sample is used in this process. It is possible to distinguish between animal and human DNA. Also, plant material can be identified by targeting the DNA located in the chloroplast, an organelle that carries out photosynthesis.



Animal Detection at Lakehead University

Collaborative efforts have been made between Lakehead University and other agencies to identify animal remains, detect predators in a specific region, or confirm sightings of a particular species of animal. Sample types have included hair, scat, tissue, blood and Bones. This research is carried out by the experienced staff at the Paleo-DNA Laboratory. Reference samples are recommended but not compulsory to the DNA analysis.



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Treatment of Archaeological Remains

Prior to submitting remains for DNA analysis, handling should be kept to a minimum with gloves being worn. Any modern DNA can be transferred to a sample causing false positive results. To ensure a high quality of results when analyzing DNA from archaeological or degraded samples containing very little DNA, the samples should be prepared and handled in a limited quantity DNA lab area. The surface area of these samples should be decontaminated as well. DNA samples containing large amounts of genetic material should be worked on in a separate area from DNA samples that are degraded or have a minimal amount of genetic material. Laboratory areas should be monitored for contamination on a regular basis. When working with human remains it is also recommended to submit reference samples from those who have been in contact with the sample so they can be excluded as a possible source of any data obtained. Cross contamination is a big issue in DNA research so the Paleo-DNA Laboratory takes extra precautions when handling precious DNA material.



DNA Barcoding

DNA Barcoding is a molecular technique that utilizes short regions of DNA as a means to identify species. This area of DNA occurs in the mitochondrial DNA. The term “barcode” refers to the specific mutations present in the DNA sequence. The barcode of a specimen is compared to a reference database of DNA barcodes. The result is a positive identification of an organism down to the species level.

Analysis of Bog Bodies

The Weerdinge bog bodies were discovered in 1904 and have been dated back to the late Iron Age or Roman Era. It was thought that the bog all but destroyed any remnants of DNA in the remains. Successful mitochondrial DNA analysis of Hypervariable Regions I and II were achieved. This allowed for genetic characterization of the individuals. Determination of the sex followed, but mixed results were obtained due to the degradation of the nuclear DNA. Mitochondrial DNA analysis is the preferred target for ancient samples due to its abundance and high success rate for preserved specimens.

