

Modern molecular genetic analyses on Mexican human remains

Nuclear DNA (nDNA) analysis on the human remains of the 43 Mexican students missing resulted in one identification that was reported in December 2014. The remaining 16 specimens did not contain enough intact nDNA to allow for further identifications.

Mitochondrial DNA (mtDNA) is more abundant in the cell than nDNA. This is why mtDNA analysis is often applied in cases where nDNA fails to provide results. The quantification of mtDNA in the 16 unidentified remains was also negative.

The results suggest that the excessive heat has destroyed the nuclear and mitochondrial DNA in the remains at least to an extent, that the conventional methods applied so far cannot be used for successful analysis.

However, there is still a slight chance for positive results in this case. A novel technology termed “Massively Parallel Sequencing” (MPS) could serve as a useful tool to further investigate these remains. MPS has a couple of advantages over conventional DNA methods, including an increased success rate when analyzing severely degraded DNA. This technology is currently evaluated for its application in forensics to identify further remains.

The Institute of Legal Medicine, Medical University of Innsbruck, has over two years of experience with MPS technology and conducted numerous analyses. Experimental data on test samples demonstrate that the new sequencing method produces useful results. In a case, where conventional DNA analysis failed, application of MPS technology would be a last attempt.

Links:

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