# CHALLENGES AND EXPERIENCE IN FORENSIC MITOCHONDRIAL DNA ANALYSIS

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Mitochondrial DNA (mtDNA) analysis has become a widely used tool in forensic science to examine cases which contain old, degraded, and minute samples. The high mtDNA copy number per cell (10000 copies vs. 2 copies of nuclear genome per cell) allows great advantages in analysis of old and partially degraded samples such as bones, hair, nails, and tissue.

ReliaGene Technologies has been conducting mtDNA analysis utilizing the DYE Terminator™ Chemistry along with the ABI Prism® 310 Genetic Analyzer for approximately one year. Since beginning mtDNA casework, ReliaGene has provided results that have been used in both civil and criminal investigations and court proceedings. Due to the fact that the number of DNA laboratories performing mtDNA testing in the United States is a very small percentage of the overall forensic DNA testing facilities, it does not take a long time for an mtDNA testing laboratory to see quite an extensive variety of samples and cases. This poster will present some of the samples and challenges faced by this mtDNA testing laboratory. Included in this poster will be a brief overview of ReliaGene Technologies mtDNA QA/QC measures. These measures include, but are not limited to, a low level DNA isolation facility, disposal of used tissue grinders, positive and negative controls, sequencing of forward and reverse strands, and independent double reading of the DNA sequence. Also presented will be the laboratory's casework experience, including various sample types such as hair, bloodstains, charred remains, teeth, ancient and historical DNA sources. In addition, ReliaGene's experience with mtDNA, courtroom testimony and admissibility hearings, as well as a summary of the reasoning involved in the development of interpretation guidelines will be discussed. Finally, the use and results of various experimental approaches that have been examined and studied by ReliaGene Technologies for use on difficult samples (i.e. semi-nested PCR, mini-primer sets, alternative methods to remove unused dNTPs from sequenced product) will also be presented.