B75 Identification of Panamanian Victims: Mitochondrial DNA Analysis

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The goal of this presentation is to present to the forensic scientists the mitochondrial DNA analysis methods for over 25-year-old and degraded bone samples.

Mitochondrial DNA analysis has been utilized in many forensic cases for the identification of victims whose bodies have been subjected to harsh and severe environments such as extremely high temperatures, humidity, and burials in shallow graves. This environment, which leads to the extreme degradation of the DNA from the bodies, has made mtDNA the method of choice for analysis of these cases.

Hundreds of individuals in Panama have been victimized during the decades of military dictatorship that ended in 1989 with the ousting of Manuel Noriega. Today, Panama is a democracy, and the country has formed a "Comision de la Verdad" (a "Truth Commission") to locate and identify the missing bodies. Extensive efforts in Panama involving canine and anthropology disciplines led to the excavation of numerous remains. Early in 2002, ReliaGene received 52 remains, including teeth and bone fragments and 28 known saliva samples, to be analyzed for mtDNA. The saliva samples were obtained from maternal relatives of the missing individuals. An attempt to isolate DNA from each sample was made and compared to DNA from known reference saliva samples. Samples analyzed by ReliaGene included remains mixed with cement and discovered in the walls and foundations of old army barracks, remains found in creek beds in the Panamanian rainforest, and remains embedded in the bark of a tree.

Sample processing techniques used to overcome PCR inhibitors will also be discussed. These include the use of an ultrasonic cleaner to remove any contaminating surface debris, the determination of DNA quantities and any protein contaminants or inhibitors in the sample, and the subsequent Qiagen column cleaning procedure used to rid the samples of inhibitors. Alternate PCR approaches, such as the use of mini primer sets, will be presented. Success rates of the remains will be discussed as well as rare mtDNA sequences that had never been observed in the available database beforehand. Identical sequences between remains obtained from different physical locations, and the implications of this finding, will be analyzed. Positive identifications made to date will also be discussed.

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