PYROSEQUENCING BASED DNA ANALYSIS FOR SPECIES ID

Mirna Ghemrawi[1], Frank Fischinger[2], George Duncan[3], Bruce McCord[1]
[1]Department of Chemistry and Biochemistry, Florida International University
[2]QIAGEN
[3]Nova Southeastern Oceanographic Institute

In crime scenes, unknown biological samples are often *Human* in origin, but some of them belong to other animals. Identifying the source of a biological sample in a crime scene, as well as in wildlife forensic cases, can be critical during investigation. Yet, forensic scientists often lack appropriate standardized protocols to categorize a non-human sample. While previous studies have shown the presence of potential genetic markers to differentiate species, there is still a lack of a quick, easy, and distinct method for species identification from tissue or body fluids. Law enforcement agencies, police officers, prosecutors, and defense attorneys expect forensic personnel to have the capability to identify miscellaneous body fluids/tissue. However, no system proposed to-date achieves this end using fast, easy, and inexpensive protocols. With the immergence of novel techniques for DNA sequencing, older, less specific procedures such as the use of polyclonal/monoclonal anti-sera can be updated and replaced. In this study, *next generation sequencing methods will be* is used to analyze a short mitochondrial amplicon that is known to be hypervariable between different species of mammals, birds and fish. To do this we will utilize pyrosequencing as well as demonstrating the application on a novel massively parallel sequencer recently introduced by QIAGEN. The resultant sequences can be compared to a large database of known references for species identification. Our goal will be to provide the forensic community with a novel method that can be implemented in forensic DNA labs for a routine and user-friendly confirmatory test for *species* identification.