IDENTIFICATION OF A DESAPPEARED PERSON THROUGH THE TYPING OF STRs AND miniSTRs MARKERS OF DNA EXTRACTED FROM SKELETAL REMAINS EXHUMED FROM META DEPARTMENT (COLOMBIA)

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Agreement International Organization for Migration and the general prosecution of the nation of Colombia

Based on the agreement established by the International Organization for Migration (IOM) and the general prosecution of the nation (GPN) of Colombia to support the peace and justice process of the Republic Presidency, the Genetics Group of CTI (Colombian Unit Group of Investigation) of the GPN aim to carry out DNA proofs for the human remains identification that could not have been identified totally by other scientific methodologies.

In these processes of identification it is common to have difficulty getting a genetic profile from DNA extracted of skeletal remains, due to the presence of PCR inhibitors, genetic material degradation or low quantity of DNA. These situations allow to incorporate advances in forensic genetics to achieve molecular typing from difficult samples.

In these case, DNA extraction was done in order to type based on skeletal remains; a left femur and a right tibial, and three teeth; second high left premolar, second low left premolar, and second low right premolar, belonging to a exhumed body found in META department (Colombia) from which two teeth and the same left femur were already processed without getting results.

Every skeletal remain is cut transversely in the most central part of the shaft using a pneumatic saw, periosteum and endosteum were removed from these fragments; the surface layer were removed from the teeth using a moto-tool DREMEL®. The skeletal remains and the teeth were atomized using a pulverizer MM400 RETSCH®, the powder of the skeletal remains were demineralized with EDTA according to Parsons` method (2007), DNA extraction was carried out utilizing organic solvents with the Phenol/Cloroform:Isoamilic Alcohol mix in proportion (25:24:1), the blood sample in FTA card of alleged mother was purified with the purification reagent WHATMAN™, the extracted DNA was amplified through amplification systems PowerPlex®16 System, PowerPlex®16 HS System, PowerPlex® S5 System, PowerPlex® ESI 17 System, PowerPlex® ESX 17 System, AmpFℓSTR® Minifiler™ and AmpFℓSTR® Identifiler™ plus. The fragment separation was done by using the genetic analyzer ABI 3130 XL and the allelic typing by the GENEMAPPER software.

With the amplification systems PowerPlex®16 System and PowerPlex®16 HS System obtained a profile of 10 and 11 genetic markers (included amelogenin) from the left femur and right tibial respectively. It was not obtained results for the teeth. The PowerPlex® S5 System confirmed three markers and it was obtained an additional marker, AmpFℓSTR® Minifiler™ confirmed three markers and it was obtained an additional marker, AmpFℓSTR® Identifiler™ plus confirmed twelve markers and it was

obtained an additional marker, the combined use of PowerPlex® ESI 17 System and PowerPlex® ESX 17 System confirmed nine markers and it was obtained six additional markers.

A genetic profile of 19 markers was obtained (amelogenin included). There were seven exclusions in the genetic matching between the genetics profile of sketal remains and reference sample. The genetic profile of the alleged mother was included in the "National Database of Genetics Profiles For the Application to Judicial Investigations" in the ¨missing persons¨ and ¨familiar group¨ index respectively. Matching search was not found coincidence with the alleged mother, however it was found two coincidence with the skeletal remains profile. After the analysis of various information were extended the profiles of the father, son and mother`s son of only one missing person
A probability of paternity of 99,99999% with a paternity index of 14,693,109 were obtained with the alleged father, and a probability of paternity of 99,999999999% and a paternity index of 193.227.609.846 were obtained with the alleged son. These probabilities are higher than the minimum probability required by the Colombian legislation.

These results show that the combined use of the amplification systems PowerPlex® ESI 17 System and PowerPlex® ESX 17 System allowed the increase of genetic markers to obtain a genetic profile that exceed the minimum of 14 markers (without amelogenin) to enter it to the ¨National Database of Genetics Profiles For the Application to Judicial Investigations", since the conventional amplification systems only managed to obtain a genetic profile of 13 markers (included amelogenin).