B123 I-FAMILIA: An Innovative Service Offering International DNA Kinship Matching Capacity for Missing Persons Identifications

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Learning Overview: The goal of this presentation is to present the innovative service INTERPOL Family Associated Matching to Identify Lost Individuals Abroad (I-FAMILIA), which will bring an international DNA kinship-matching capacity to all member countries for their missing persons investigations.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by helping ongoing and future missing persons investigations by facilitating international DNA kinship matching and data exchange between police worldwide

In light of the ease of international travel, an increased global migration, and the consequences of international crime and human trafficking that results in a vulnerability of migrants and refugees, many Missing Persons (MPs) investigations exhibit a cross-border dimension. When national MP DNA programs have exhausted all possible leads, an international DNA comparison needs to be adequately considered.

The International Criminal Police Organization (INTERPOL), is the world's largest international police organization, connecting 194 member countries and provides the legal framework and technical infrastructure for a secure exchange of police information. INTERPOL's international DNA sharing platform provides a structured means for member countries to send antemortem DNA profiles (conventionally obtained from personal items of the missing person) and postmortem DNA profiles (obtained from Unidentified Human Remains [UHR]) for an automated comparison in the INTERPOL DNA database against data previously entered by member countries.

In many cases, antemortem DNA profiles from MPs are either unavailable or of insufficient quality to confirm the identity of the MP. Consequently, antemortem DNA data can only be obtained through biological relatives and the fit of an MP for any given pedigree (e.g., parent, child, sibling of the MP) is estimated by the computation of Likelihood Ratios (LR) using specific allele frequencies from the reference population.[1] Although kinship DNA matching is relatively easy to implement nationally, where the MP and UHR are reported within the same country, many challenges need to be resolved before applying this method to an international configuration. First, ancestry is very often unknown or inaccurately reported and the use of allele frequencies from the wrong reference population could lead to erroneous conclusions as rare alleles in one population may not be as rare in another population. Second, while kinship DNA analysis is performing well with full DNA profiles, many DNA profiles are partials, due to the nature of degraded DNA from UHR samples. Also, the heterogeneity of analytical Short Tandem Repeat (STR) kits used by different laboratories leads to a reduced number of common STR markers and can give rise to weak LR values. Third, arbitrary LR thresholds are often used to determine whether or not a match should be reported but are not accurate for several types of pedigree and/or partial DNA matches.

Considering that international DNA kinship matching would positively impact international police cooperation for MP investigations, INTERPOL has launched I-FAMILIA, an innovative service aiming to facilitate and standardize the international DNA sharing and comparison of UHRs, MPs, and their relatives' profiles.

I-FAMILIA consists of three components: a dedicated database to host the anonymized DNA profiles from the biological relatives of reported missing persons; the DNA matching software, called Bonaparte™, developed by SMART Research BV to perform kinship calculations; and new accompanying interpretation guidelines to efficiently identify and report potential matches between UHR samples and family pedigrees in an international context.[2]

The developmental validation of the service was based on LR calculations using worldwide allele frequencies, allowing kinship analysis in an ancestry-neutral manner.[3] Tailor-made determination of optimal LR thresholds, based on data simulation of related and unrelated pedigrees, were calculated for nine common scenarios found in MP investigations and for a common number of STR markers between 7 and 24 to mimic partial DNA profiles often transmitted by member countries. Streamlined interpretation tables are then used to interpret the LR values for each specific case to make an informed decision of rejection or confirmation of the potential association. In case of a positive hit, a potential match report will be sent to both countries who will then be able to compare, in accordance with their national procedures, antemortem data and postmortem data by using additional means of identification to officially identify the MP and ultimately bring closure to families expecting news of their loved ones.

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