INTERPOL's Approach to Missing Persons' Family Matching at an International Level: Using Population Data from Geographic Groups for Kinship Calculations

Andrea Fischer[1], Susan Hitchin[1], Willem Burgers[2], Wim Wiegerinck[2], and John Buckleton[3],[4]
[1] INTERPOL (International Criminal Police Organization), Lyon, France
[2] SMART Research BV, Nijmegen, Netherlands
[3] Environmental and Scientific Research Ltd., Auckland, New Zealand
[4] University of Washington, Seattle, USA

INTERPOL, as the world's largest international law enforcement agency, assists police in its 190 member countries by making available tools and services for the international exchange of police data including forensic DNA data.

With the ease of international travel, the rise of global migration and frequent occurrences of terrorist attacks, missing persons' cases are increasingly having cross-border dimensions. Consequently, they often cannot be resolved nationally. INTERPOL currently assists member countries by providing a platform for a direct DNA profile comparison of missing persons and unidentified human remains. For situations where a direct DNA profile of the missing person in not available, INTERPOL is working on establishing a family DNA matching service using Bonaparte software (SMART Research BV). With the ancestry of human remains most likely to be unknown, it is not obvious how to select the appropriate population data. Therefore, the level of confidence in the validity of the kinship calculations used to evaluate the searches of pedigrees against unidentified human remains is questionable. In order to make family matching feasible on an international level, a solution for determining the most appropriate population data selection had to be found.

Buckleton et al. (2016) have undertaken a world-wide analysis of allele probability variation in 446 different population studies, estimated population structure quantity Fst values and classified the data into geographic groups. Based on this work, representatives of major geographic groups have been selected and it is proposed to apply their population data in parallel and combine the results of the kinship calculations. This procedure would allow for not having to make any assumptions about the ancestry of unknown remains and allow for reporting potential associations to the source countries. The respective member countries holding the original DNA data from the missing person and the human remains can then collaborate to use further information regarding circumstances of disappearance, body recovery, ancestry, etc. to work towards a confirmed missing person identification.
This talk aims to present this approach to the forensic community to obtain their feedback on this strategy.

Reference:
Buckleton, J., Curran, J., Goudet, J., Taylor, D., Thiery, A., and Weir, B.S. (2016) Population-specific FST values for forensic STR markers: A worldwide survey. Forensic Sci Int Genet 23, 91-100.