

B38 Short Tandem Repeat (STR) Profiles and Ethnic Affiliation — Chemometric Evaluation

Patryk Wlasiuk, MSc, Dept of Analytical Chemistry, Jagellonian Univers, ul.Golebia 24, Krakow 31007, POLAND; Eugenio Alladio, PhD*, Centro Regionale Antidoping "A. Bertinaria," Regione Gonzole 10/1, Orbassano (Turin) 10043, ITALY; Monica Omedei, PhD, Centro Regionale Antidoping "A. Bertinaria," Regione Gonzole 10/1, Orbassano 10043, ITALY; Giuseppina D'amico, Regione Gonzole 10/1, Orbassano, ITALY; Denise Caneparo, MS, Regione Gonzole 10/1, Orbassano, ITALY; Marco Vincenti, MS, Centro Regionale Antidoping, Regione Gonzole 10/1, Orbassano, Torino 10043, ITALY; Roberto Testi, MD, PhD, ASL Torino, Via Lessona 54/12, Torino 10145, ITALY; Paolo Garofano, MD, PhD, Laboratorio Genetica Forense - CAD, Regione Gonzole 10/1, Orbassano (TO) 10043, ITALY; and Grzegorz Zadora, Institute of Forensic Research, Westerplatte 9, Krakow 31033, POLAND

After attending this presentation, attendees will better understand an alternative approach for the interpretation of ethnic affiliation from unknown DNA trace evidence.

This presentation will impact the forensic science community by providing an alternative method for the estimation of ethnic affiliation with a proposition stemming from the chemometric evaluation of the data.

The issue of ethnic affiliation may arise in a forensic context. For instance, the determination of the race of a donor of a stain, left at the crime scene, may be thought to ease the investigation by contrasting such evidence with an eyewitness account. The DNA typing is a powerful tool in the determination of the identity since the majority of genetic variation is ascribed to inter-individual differences. Although the contribution of population differences is quite small to the overall variability, the genetic profiles have been used to infer the population of origin.^{1,2} As the Short Tandem Repeat (STR) microsatellites are still intrinsic to the forensic domain, the present study focuses on the use of STR profiles as the basis for inferring ethnic affiliation. In the course of the past two decades, a few approaches have been presented. The methods implemented in the population genetics software usually follow the profile frequency approach, procedures based on the genetic distance, or the approaches that use tools derived from the multivariate data analysis methods. The latter two are said to be free of considering the Hardy-Weinberg (HW) and Linkage (L) equilibriums.

The goal of this study is to contrast those ethnic affiliation approaches with the proposition stemming from the chemometric evaluation of the data. For the purposes of the present study, the STR profiles were generated from the allele frequency tables available for different populations. As the derivation of the STR profile depends on the set of markers, this study inspects the usefulness of different, used-in-daily-practice sets (e.g., the Combined DNA Index System (CODIS), the European Standard Set (ESS), and the International Society for the Study of the Origin of Life (ISSOL)). For a fair comparison of models, the test set of profiles was held out for testing models developed on the training data. The ethnic affiliation methodology for each approach was to be set in the Bayesian framework to enable the forensic weight of the evidence assessment. Different chemometric approaches were inspected and evaluated.

Reference(s):

1. Ogden R., and Linacre A. Wildlife forensic science: A review of genetic geographic origin assignment. *Forensic Science International: Genetics*. 18 (2015): 152-159.
2. Klintschar M., Füredi S., Egyed B., Reichenpfader B., and Kleiber M. Estimating the ethnic origin (EEO) of individuals using short tandem repeat loci of forensic relevance. *International Congress. Series* 1239 (2003): 53-56.

Ethnic Affiliation, Chemometrics, Unknown DNA Trace Evidence