



B23 Genetic Variation at 15 Forensic Informative STR Loci in Upper (Southern) Egyptians

Ghada Omran, MPhil, and Guy Rutty, MD, University of Leicester, Forensic Pathology Unit, Leicester Royal Infirmary, Robert Kilpatrick Clinical Sciences Building, Leicester, Leicestershire LE2 7LX, United Kingdom; and Mark Jobling, PhD, University of Leicester, Department of Genetics, University Road, Leicester, Leicestershire LE1 7RH, United Kingdom*

The goal of this presentation is to present the forensic genetic characters of fifteen autosomal short tandem repeat loci (STRs) in a population sample from Upper (south) Egypt. Allele frequency distribution of the used loci along with application of other forensic indices and population differentiation tests in this ethnic group will be addressed. Furthermore, comparison of the yielded data to other related populations either in local or global level is another important goal. The questions considered are: 1) how could the examined loci help in estimation of DNA profile frequency in forensic situations in relation to that population? and 2) could the data differentiate Upper Egyptians from Lower, other geographically and historically relevant populations?

This presentation will impact the forensic community and/or humanity through building up and developing a forensic population database for different ethnic groups and regions in Egypt, which can be implemented in medico-legal practice at both personal identification and ethnic affiliation levels.

Forensic databases had been established for several populations all over the world however, they are still lacking in Middle Eastern countries including Egypt. From the earliest times of history, Egyptians always referred to their country as "Two Lands," meaning the land of the North (Lower Egypt) and the land of the South (Upper Egypt). This ancient classification has led to the persistent ethnic division of Egyptians into two main groups: Lower (Northern) and Upper (Southern) groups. The present study is focused on the southern ethnic group residing in an area extending from south of Cairo to Aswan along the narrow River Nile valley. The residents are Arabic language speakers with a dialect distinguishable from the Northern population.

A sample of 265 unrelated individuals inhabiting south Egypt for at least up to the third generation in a subset of that area's governorates (a total of five) were collected after signing informed consents. Afterwards, the samples were subjected to DNA extraction by a silica-based method, quantitation and multiplex PCR amplification using the AMPF[®]STR Identifiler kit (containing 15 loci: D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818 and FGA). PCR products were genotyped subsequent to capillary electrophoresis. Statistical analysis of the generated data aimed at estimating allele frequencies for each locus, followed by testing for suitability of the used loci in determination of random match probabilities in forensic practice. This was achieved through testing for Hardy-Weinberg equilibrium (HWE) for alleles' independence and linkage equilibrium (LE) for loci independence. Furthermore, important forensic indices such as the values of heterozygosity (H), polymorphic information content (PIC), power of discrimination (PD), power of exclusion (PE), paternity index (PI) and matching probability (MP) were considered for each locus. Population differentiation tests e.g. Fst genetic distances and pair-wise analysis of molecular variance (AMOVA) are other useful parameters for comparative study of the present population data to other related ones. Preliminary results indicated neither departure from expectation of the HWE in most of the tested loci nor dependence of alleles between loci, allowing multiple locus profile frequency estimation in forensic situations using the product rule. All tested loci were polymorphic; the most discriminating is D18S51 while the least is TPOX.

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