Forensic Science International: Genetics 5 (2011) 561–562

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Letter to the editor

Y-chromosomal STRs in two populations from Israel and the Palestinian Authority Area: Christian and Muslim Arabs

Keywords:
Y-chromosomal STRs
Haplotypes
Muslim Arabs
Christian Arabs
Israel
Population database

Dear Editor,

We determined the allele frequencies for the 17 Y-chromosomal STR loci (DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385a/b, DYS393, DYS391, DYS439, DYS635, DYS392, Y GATA H4, DYS437, DYS438 and DYS448), in a total of 163 individuals unrelated at the great-grandfather paternal level: 44 Christian Arabs (CA) from Israel and 119 Muslim Arabs (MA) from Israel and the Palestinian Authority Area (PAA). They represent a subset of samples previously typed for 13 Y-chromosomal binary and 6 STR loci [1,2]. Informed consent and information about birthplace, parents and grandparents were received from all individuals prior to enrollment.

The DNA samples of MA were prepared from peripheral blood and DNA samples of CA were extracted from buccal swabs using standard phenol/chloroform protocols [1,2]. DNA was amplified using the AmpFISTR® YFiler™ PCR Amplification Kit (Applied Biosystems, Darmstadt, Germany), according to the manufacturer's instructions. Genotyping was performed using ABI PRISM 310 Genetic Analyser (Applied Biosystems). The allele typing was performed according to the published nomenclatures and the ISFG guidelines for STR analysis [3] except in the GATA H4 locus where the nomenclature applied is the same in use by the YHRD (which is the same used by Applied Biosysytems). Proficiency testing was performed following the guidelines of the GHEP-ISFG Working Group. The data have been submitted to the Y-chromosomal haplotype reference database (YHRD: http://www.yhrd.org) and have received the following accession number: YA003643. Allele and haplotype frequencies were estimated by gene/haplotype counting. Haplotype diversity (h) was calculated according to Nei [4] as $h = n(1 - \Sigma pi^2)/(n - 1)$, where n represents the population size and p_i is the frequency of the ith haplotype. Interpopulation comparison was performed using the analysis of molecular variance (AMOVA), included in the Arlequin software package 3.1, with the sum of the squared allele size differences (Rst) used as a measure of microsatellite haplotype distance [5,6]. The system DYS385 was excluded from the analysis.

The allele frequencies distribution of the 17-loci Y-STR haplotypes from a total of 163 individuals from two populations in Israel and the PAA are presented in Supplementary Table 1. A total of 154 different haplotypes ($n = 40$ in CA and $n = 115$ in MA) was observed when the two groups where considered together, with 146 of them being singletons. Only one haplotype (H129) was found to be shared by the Christian and Muslim Arabs. Haplotypes H9, H14, H25, H34, H96, H109 and H129 were observed twice and H32 was observed in triplicate. Two of the 17-loci haplotypes (H62 and H81), have also been identified in a population of Jordan (YA003523) among 26,136 haplotypes in the YHRD (release 33 March 2010) [7]. However, once there are in the YHRD database much more individuals typed to the minimal 9 loci haplotypes (DYS19–DYS389I–DYS389II–DYS390–DYS391–DYS392–DYS393–DYS385a/b) we also analyzed our populations considering only this minimal haplotype. We found a total of 136 different haplotypes in the CA and MA populations, 66 of which were not observed in the YHRD (48.5%), while 1311 matches among 84,771 minimal YHRD-haplotypes were detected, 308 being from the metapopulation of Afro-Asian Semitic. The two most frequent minimal haplotypes in the MA population were found in five individuals (H40–H44) and in seven individuals (H45–H51). Among 84,771 minimal haplotypes accessed at the YHRD, these two haplotypes were observed in two and five individuals, respectively, 5 of them being from two populations from Yemen (YA003082 and YA003571), classified as Afro-Asian Semitic. In the CA population the two most frequent minimal haplotypes were found in three individuals (H14/H15 and H32) and none of them was found among 84,771 minimal haplotypes accessed at the YHRD.

A high-haplotype diversity ($h = 0.9993$ with a mean expected heterozygosity of 0.6460, SD 0.3267) was observed when both CA and MA populations are considered together. In the CA population, haplotype diversity was calculated as 0.9958 (with an expected heterozygosity of 0.6178, SD 0.3213) and in the MA group – as 0.9994 (with an expected heterozygosity of 0.6158, SD 0.3156). The genetic affinities between the CA and MA populations were assessed by AMOVA, and the two groups have been found to be significantly different ($Rst = 0.02078$, $P = 0.01802 \pm 0.0121$) with 4.4% of the differences being attributed to the variation ng the populations and 95.6% to the variation within the populations.

This paper follows the guidelines for publication of population data requested by the journal [8].

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.fsigen.2010.08.005.

1872-4973/$ – see front matter © 2010 Published by Elsevier Ireland Ltd.
doi:10.1016/j.fsigen.2010.08.005

References

[1] A. Nebel, D. Filon, B. Brinkman, P. Majumder, M. Faerman, A. Oppenheim, The Y chromosome pool of Jews as part of the genetic landscape of the Middle East, Am. J. Hum. Genet. 69 (2001) 1095–1112.
[2] A. Nebel, D. Filon, A. Oppenheim, M. Faerman, The genetic history of populations in the Southern Levant as revealed by Y chromosome polymorphisms, in: M. Faerman, L.K. Horwitz, T. Kahana, U. Zilberman (Eds.), Faces from the Past: Diachronic Patterns in the Biology and Health Status of Human Populations in the Eastern Mediterranean. Papers in honour of Patricia Smith, BAR International Series 1603, Oxford, 2007, pp. 257–270.
[3] L. Gusmao, J.M. Butler, A. Carracedo, P. Gill, M. Kayser, W.R. Mayr, N. Morling, M. Prinz, L. Roewer, C. Tyler-Smith, P.M. Schneider, DNA Commission of the International Society of Forensic Genetics (ISFG): an update of the recommendations on the use of Y-STRs in forensic analysis, Forensic Sci. Int. 157 (2006) 187–197.
[4] M. Nei, Molecular Evolutionary Genetics, Columbia University Press, New York, 1987, 178.
[5] S. Schneider, D. Roessli, L. Excoffier, Arlequin ver. 3.1: A Software for Population Genetics Data Analysis, Genetics and Biometry Laboratory, University of Geneva, Switzerland, 2000.
[6] L. Roewer, M. Kayser, P. Dieltjes, M. Nagy, E. Bakker, M. Krawczak, P. de Knijff, Analysis of molecular variance (AMOVA) of Y-chromosome-specific microsatellites in two closely related human populations, Hum. Mol. Genet. 7 (1996) 1029–1033; L. Roewer, M. Kayser, P. Dieltjes, M. Nagy, E. Bakker, M. Krawczak, P. de Knijff, Hum. Mol. Genet. 6 (1997) 828, erratum.
[7] S. Willuweit, L. Roewer, The International Forensic Y Chromosome User Group Y chromosome haplotype reference database (YHRD): update, Forensic Sci. Int. Genet. 1 (2) (2007) 83–87.
[8] A. Carracedo, J.M. Butler, L. Gusmão, W. Parson, L. Roewer, P.M. Schneider, Publication of population data for forensic purposes, Forensic Sci. Int. Genet. 4 (2010) 145–147.

Ana Teresa Fernandes
Rita Gonçalves
Sara Gomes
Human Genetics Laboratory, University of Madeira, Funchal, Portugal

Dvora Filon
Department of Hematology, Hadassah-Hebrew University Medical Center, Jerusalem, Israel

Almut Nebel
Institute of Clinical Molecular Biology, Christian-Albrechts-University, Kiel, Germany

Marina Faerman
Laboratory of Biological Anthropology and Ancient DNA, Faculty of Dental Medicine, Hebrew University of Jerusalem, Jerusalem, Israel

António Brehm*
Human Genetics Laboratory, University of Madeira, Funchal 9000-390, Portugal

*Corresponding author
E-mail address: brehm@uma.pt (A. Brehm)

28 April 2010