Forensic Science International: Genetics Supplement Series 2 (2009) 419–420

Contents lists available at ScienceDirect

Forensic Science International: Genetics Supplement Series

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

Research article

Evaluating Y-chromosome STRs mutation rates: A collaborative study of the Ge.F.I.-ISFG Italian Group

Valerio Onofri *, Loredana Buscemi, Adriano Tagliabracci

the Ge.F.I. Group

Institute of Legal Medicine, Università Politecnica delle Marche, Via Conca - Torrette, 60126, Ancona, Italy

ARTICLE INFO

Article history:
Received 24 August 2009
Accepted 27 August 2009

Keywords:
Y chromosome haplotypes
STRs
AmpFlSTR Yfiler kit
PowerPlex Y System kit
Mutation rates

ABSTRACT

A collaborative study was carried out by the Italian ISFG Working Group in order to improve the data on Y-STR mutations at the loci mostly used in forensic analysis, following recommendations of the ISFG DNA Commission.

The knowledge on Y-STR mutation rates needs to be considered in the paternity probabilities, especially in deficiency cases of disputed paternity involving male offspring where the alleged father is not available for DNA analysis. Furthermore, the mutation rate represents a precious tool to estimate the local and temporal origin of a given Y-SNP based haplogroup.

The sample consisted of 433 father/son pairs from paternity cases in 15 different laboratories from Italy. The biological relationship of all father/son pairs was previously confirmed by using autosomal microsatellites. The laboratories used AmpFlSTR YFiler kit (AB) and PowerPlex Y System (Promega); DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385, DYS437, DYS438, DYS439, DYS448, DYS456, DYS458, GATA C4, and GATA H4.1 data were collected. The participants were also asked to provide the age of the biological father and, if possible, male descendants beyond the first generation.

20 mutations were observed among all of the allele transfers in the sample (19 single step and 1 double step), and mutations in the same father/son pair were found in three cases. Locus-specific mutation rates were calculated. Forensic implication of the average age of the father as well as the number of locus deletions and amplifications were discussed.

1. Introduction

Y chromosome STRs are inherited along the paternal lineage and have been widely used as a useful tool to complete autosomal markers data. Over 200 Y-microsatellites have been discovered and most of them will be probably incorporated in multiplex kits for forensic applications in the next future, increasing the discrimination power of Y analyses. The possibility to distinguish between relatives belonging to the same paternal lineage will be increased due to the accumulation of mutations from one generation to the next. So the knowledge on Y-STR mutation rates begin pivotal and needs to be considered in the paternity probabilities, especially in deficiency cases of disputed paternity involving male offspring where the alleged father is not available for DNA analysis but is replaced by someone of the paternal lineage.

Furthermore, the mutation rate represents a precious tool to estimate the local and temporal origin of a given Y-SNP based haplogroup, but has been demonstrated the dating severely changed when different rates were used [1].

For this reason the ISFG DNA Commission encourage the forensic laboratories to collect data [2] and some larger dataset has been produced [3].

The study increased the existing data on mutation rates by the results of 433 independent father–son pairs collected from 15 laboratories of the Italian ISFG Working Group.

2. Materials and methods

The laboratories were asked to collect data on paternity tests involving male subjects and confirmed by autosomal STRs, possibly providing the age of the father at the time of son's birth. This study included 866 DNA samples (433 meiosis) from routine paternity testing in Italy.

The origin of the father was largely from Italy, but some lineages came from different geographical areas (Afghanistan (2), Albania

* Corresponding author. Tel.: +39 071 596 5044; fax: +39 071 596 4723.
E-mail address: v.onofri@univpm.it (V. Onofri).

1875-1768/$ – see front matter © 2009 Elsevier Ireland Ltd. All rights reserved.
doi:10.1016/j.fsigss.2009.08.167

Table 1
Results of the allele transmissions and observed mutation per Y-STR locus.

Marker	No. of mutation	Allele transmission	Freq. ($\times 10^{-3}$)	95% CI ($\times 10^{-3}$)
DYS19	3	431	6.961	1.4–20.2
DYS389I	1	432	2.315	0.1–12.8
DYS389II	2	432	4.630	0.6–16.6
DYS390	1	432	2.315	0.1–12.8
DYS391	0	432	0.000	0–8.5
DYS392	0	424	0.000	0–8.7
DYS393	1	432	2.315	0.1–12.8
DYS385	4	864	4.630	1.3–11.8
DYS438	1	430	2.326	0.1–12.9
DYS439	1	432	2.315	0.1–12.8
DYS437	0	432	0.000	0–8.5
DYS448	0	432	0.000	0–8.5
DYS456	2	291	6.873	0.8–24.6
DYS458	1	291	3.436	0.1–19
Y GATA C4	3	291	1.031	2.1–29.8
Y GATA H4.1	0	291	0.000	0–12.6
Total	20	6769	2.955	1.8–4.6

(3), Canada, Egypt, Eritrea, Ghana (2), India, Iraq (2), Lebanon, Macedonia, Morocco (3), Pakistan, Philippines, Romania (4), Somalia, Tunisia and Ukraine).

Samples were amplified using the 17 loci AB AmpFlSTR Yfiler kit (291 cases) or the 12 loci Promega PowerPlex Y System kit (142).

Alleles from GATA H4.1 locus were named according to the ISFG recommendations (+9 repeats to the kit allele calling).

3. Results and discussion

20 mutations were observed among all of the allele transfers in the sample, 19 single step (12 repeat gains and 7 repeat losses) and 1 double step repeat loss (see Table 1).

Two mutations in the same father/son pair were found in three cases involving DYS389I and DYS389II in two cases, DYS19 and DYS456 in the third pair.

In forensic caseworks, any additional allele at one Y-locus (duplication or triplication) is normally interpreted as multiple contributors profile, thus the knowledge of the frequency of this phenomenon is considered necessary. In this study we observed one duplication at DYS19 locus and triplication of DYS385 in three cases. Also a null allele at DYS448 was observed.

In 377 of the 433 father/son pair we could collect the age of the father at the time of the son's birth. The mean age of fathers with mutations (33.22 years) quite similar than that of the fathers without mutations (35.67 years).

The observed locus-specific mutation rate ranged between 0 of DYS391, DYS392, DYS437, DYS448, GATA H4.1 and 6.961×10^{-3} (95% CI $1.4–20.0 \times 10^{-3}$) of DYS19 locus. The average mutation rate in this study was 2.955×10^{-3} (95% CI $1.8–4.6 \times 10^{-3}$), higher than some previously studies [4,5] but more similar to other ones [1,6].

This study showed preliminary results, nevertheless it could confirm the relevant heterogeneity of the mutation rate across different Y-STRs loci. In the next part of the exercise, a second laboratory will confirm the observed mutations and relevant allele variants by sequence analysis; data of further 23 cases of multi-generation pedigrees will be included, as it has been demonstrated to be a reliable tool for the estimation of mutation rate [7].

Conflict of interest

None.

Acknowledgements

On behalf of the Ge.F.I. Group laboratories participating to the collaborative exercise: M. Alù, Department of Diagnostic and Laboratory Service and Legal Medicine, Section of Legal Medicine, University of Modena and Reggio Emilia, Italy; S.L. Baldassarra, Section of Legal Medicine, University of Bari, Italy; A. Barbaro, Department of Forensic Genetics, Studio Indagini Mediche e Forensi (SIMEF), Reggio Calabria, Italy; L. Caenazzo, Department of Environmental Medicine and Public Health, University of Padova, Italy; E. Carnevali, Department of Surgery and Forensic Sciences, University of Perugia and Section of Legal Medicine, Hospital of Terni, Italy; N. Cerri, Department of Surgery, Radiology and Forensic Medicine, University of Brescia, Italy; G. Peloso, Department of Environmental Medicine and Public Health, University of Pavia, Italy; S. Pelotti, Department of Medicine and Public Health, Section of Legal Medicine, University of Bologna, Italy; N. Resta, Dipartimento di Biomedicina dell'Età Evolutiva, Sezione di Genetica Medica, Università di Bari, Italy; U. Ricci, Medical Genetic Unit, Azienda Ospedaliero Universitaria "A. Meyer", Firenze, Italy; C. Robino, Department of Anatomy, Pharmacology and Legal Medicine, University of Torino, Italy; F. Scarnicci, Institute of Legal Medicine, Università Cattolica Sacro Cuore, Roma, Italy; C. Vecchiotti, Institute of Legal Medicine, Università La Sapienza, Roma, Italy; M. Venturi, Department of Biomedical Sciences, Section of Legal Medicine, University of Ferrara, Italy.

References

[1] M. Kayser, L. Roewer, M. Hedman, L. Henke, J. Henke, S. Brauer, C. Kruger, M. Krawczak, M. Nagy, T. Dobosz, R. Szibor, P. de Knijff, M. Stoneking, A. Sajantila, Characteristics and frequency of germline mutations at microsatellite loci from the human Y chromosome, as revealed by direct observation in father/son pairs, Am. J. Hum. Genet. 66 (2000) 1580–1588.

[2] 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, Int. J. Leg. Med. 120 (4) (2006) 191–200.

[3] L. Gusmao, P. Sanchez-Diz, F. Calafell, P. Martin, C.A. Alonso, F. Alvarez-Fernandez, C. Alves, L. Borjas-Fajardo, W.R. Bozzo, M.L. Bravo, J.J. Builes, J. Capilla, M. Carvalho, C. Castillo, C.I. Catanesi, D. Corach, A.M. Di Lonardo, R. Espinheira, E. Fagundes de Carvalho, M.J. Farfán, H.P. Figueiredo, I. Gomes, M.M. Lojo, M. Marino, M.F. Pinheiro, M.L. Pontes, V. Prieto, E. Ramos-Luis, J.A. Riancho, A.C. Souza Góes, O.A. Santapa, D.R. Sumita, G. Vallejo, L. Vidal Rioja, M.C. Vide, C.I. Vieira da Silva, M.R. Whittle, W. Zabala, M.T. Zarrabeitia, A. Alonso, A. Carracedo, A. Amorim, Mutation rates at Y chromosome specific microsatellites, Hum. Mutat. 26 (6) (2005) 520–528.

[4] P. P Sánchez-Diz, C. Alves, E. Carvalho, M. Carvalho, R. Espinheira, O. García, M.F. Pinheiro, L. Pontes, M. João Porto, O. Santapa, C. Silva, D. Sumita, S. Valente, M. Whittle, I. Yurrebaso, A. Carracedo, A. Amorim, L. Gusmão, GEP-ISFG (The Spanish and PortugueseWorking Group of the International Society for Forensic Genetics), population and segregation data on 17 Y-STRs: results of a GEP-ISFG collaborative study, Int. J. Legal Med. 122 (6) (2008) 529–533.

[5] B.M. Dupuy, M. Stenersen, T. Egeland, B. Olaisen, Y-chromosomal microsatellite mutation rates: differences in mutation rate between and within loci, Hum. Mutat. 23 (2004) 117–124.

[6] M. Goedbloed, M. Vermeulen, R.N. Fang, M. Lembring, A. Wollstein, K. Ballantyne, O. Lao, S. Brauer, C. Krüger, L. Roewer, R. Lessig, R. Ploski, T. Dobosz, L. Henke, J. Henke, M.R. Furtado, M. Kayser, Comprehensive mutation analysis of 17 Y-chromosomal short tandem repeat polymorphisms included in the AmpFlSTR® Yfiler® PCR amplification kit, Int. J. Legal Med. (2009), doi:10.1007/s00414-009-0342-y.

[7] E. Heyer, J. Puymirat, P. Dieltjes, E. Bakker, P. de Knijff, Estimating Y chromosome specific microsatellite mutation frequencies using deep rooting pedigrees, Hum. Mol. Genet. 6 (1997) 799–803.