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Short communication

Population Genetic data for 15 Autosomal STR markers in Eastern Turkey

Mehmet Tokdemir [a,*], Ferhat Turgut Tunçez [a], Nazif Harun Vicdanli [b]

[a] Firat University, Department of Forensic Medicine, 23119 Elazig, Turkey
[b] Council of Forensic Medicine, Ministry of Justice, 23100 Elazig, Turkey

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ABSTRACT

The allelic frequency distribution and statistical genetic parameters of forensic relevance for 15 STR loci (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818 and FGA) in a population sample of 802 unrelated individuals in Eastern Turkey. The expected performance of these loci for personal identification and paternity testing in this population was estimated. Eastern Turkey and other 12 country population data were compared using allele frequencies.

1. Introduction

In the human genome, there are repeated sequenced and generally non-functional series with a certain base index with a length of 2–7 base pair. These series are termed microsatellites or STR (short tandem repeat). As STR loci have a high heterozygosity, the variability in these loci is particularly useful in population genetics, chromosome mapping and forensic studies (Butler, 2006; Demirçin and Serdar, 2010).

Eastern Anatolia Region, is one of Turkey's seven geographical regions. Turkey's population density is a region in the least. To the large surface area is this one of the main factors. It covers 21% of Turkey's land in terms of surface area. According to the census in 2014 the population of the region is 5.9 million people. There are 14 cities in the Eastern Anatolis Region (Fig. 1). In this study, we have investigated allele frequencies for the 15 autosomal STR loci included in the AmpF/STR® Identifiler™ PCR Amplification Kit panel D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818 and FGA.

2. Materials and methods

Blood samples were collected along with signed informed consent from 802 unrelated and healthy volunteers from Eastern Turkey. Volunteers were randomly selected. All the samples were used with permission of the ethical committee of the Firat University for research purposes. DNA was extracted from 2 ml blood samples by using QIAamp DNA Mini Kit (Qiagen) according to the manufacturer's instructions.

A multiplex PCR using 1 ng of genomic DNA was amplified for the 15 autosomal STR loci (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, THO1, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818 and FGA. The AmpF/STR^R Identifiler™ PCR Amplification Kit (Applied Biosystems, Foster City, CA, USA) is used as per manufacturer's recommendations (Applied Biosystems, 2006). PCR fragments were separated by capillary electrophoresis following the manufacturer's recommendations using a 310 Genetic Analyzer (Applied Biosystems) and sized with GeneScan500-LIZ internal lane size standard (Applied Biosystems, USA) following manufacturer's protocols. Allelic calls and genotyping were carried out by comparison to the reference allelic ladder included in the kit using GeneMapper ID1 v3.2 (Applied Biosystems).

Analysis of data: Allelic frequency data (Table 1) and key statistical parameters of forensic interest [Power of Discrimination (PD), Matching Probability (pM), Polymorphic Information Content (PIC), Power of Exclusion (PE), and Typical Paternity Index (TPI)] (Table 2) were calculated using the PowerStats v1.2 Microsoft Excel spreadsheet (Promega Corporation, Madison, WI, USA) (Power Stats V12.xls software). Arlequin software version 3.5 was used to calculate Expected Heterozygosity (He)/Observed Heterozygosity (Ho) and to evaluate Hardy–Weinberg equilibrium (P value of exact test) using a modified version of the Markov chain random walk algorithm (Excoffier and Lischer, 2010) (Table 2). Allele frequencies from the tested population were compared with data for other populations with P value of exact test for Hardy–Weinberg

* Corresponding author.
E-mail addresses: mehtokdemir@yahoo.com (M. Tokdemir), ftuncez@hotmail.com (F.T. Tunçez), drharun83@gmail.com (N.H. Vicdanli).

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Abbreviations

A	adenosine
A	absorbance (1 cm)
aa	amino acid(s)
Ab	antibody(ies)
Ad	adenovirus
AdoMet (or SAM)	*S*-adenosylmethionine
AMV	avian myeloblastosis virus
Ap	ampicillin
βGal	β-galactosidase
bp	base pair(s)
BSA	bovine serum albumin
C	cytidine
cAMP	cyclic adenosine 3′,5′-monophosphate
CAT	Cm acetyltransferase
cat	gene encoding CAT
ccc	covalently closed circular
cDNA	DNA complementary to RNA
CHO	Chinese hamster ovary
CIAP	calf intestinal alkaline phosphatase
Cm	chloramphenicol
cp	chloroplast
cpm	counts per minute
d	deoxyribo
Δ	deletion
dd	dideoxyribo
DMSO	dimethylsulfoxide
DNase	deoxyribonuclease
dNTP	deoxyribonucleoside triphosphate
ds	double strand(ed)
DTT	dithiothreitol
EF	elongation factor
ELISA	enzyme-linked immunosorbent assay
ENase (or R·)	restriction endonuclease
Er	erythromycin
EtdBr	ethidium bromide
G	guanosine
Gm	gentamicin
G418	Geneticin
HIV	human immunodeficiency virus
HPLC	high-performance liquid chromatography
HPRT	hypoxanthine-guanine phosphoribosyl transferase
HSV	Herpes simplex virus
Hy	hygromycin
IF	initiation factor
IFN	Interferon
Ig	immunoglobulin(s)
IL	interleukin
IPTG	isopropyl β-D-thiogalactopyranoside
IS	insertion sequence(s)
kb	kilobase(s) or 1000 bp
kDa	kilodalton(s)
Km	kanamycin
lacZpo	lac promoter-operator
LB	Luria-Bertani (medium)
LTR	long terminal repeat(s)
m^6A	N^6-methyladenosine
mAb	monoclonal Ab
MCS	multiple cloning site(s)
moi	multiplicity of infection
M_r	relative molecular mass (dimensionless)
mt	mitochondria(l)
MTase (or M·)	DNA methyltransferase
Myr	million years
N	any nucleoside
$\left.\begin{matrix}NAD\\NADH\end{matrix}\right\}$	nicotinamide-adenine dinucleotide and its reduced form
Nm	neomycin
nt	nucleotide(s)
o, *O*	operator
oligo	oligodeoxyribonucleotide
ONPG	o-nitrophenyl β-D-galactopyranoside
ORF	open reading frame
ori	origin(s) of DNA replication
p	plasmid
p, *P*	promoter
PA	polyacrylamide
PAGE	PA-gel electrophoresis
PEG	poly(ethylene glycol)
pfu	plaque-forming unit(s)
P_i	inorganic phosphate
Pipes	1,4-piperazinediethanesulfonic acid
PMSF	phenylmethylsulfonyl fluoride
Pollk	Klenow (large) fragment of *E. coli* DNA polymerase I
PP_i	inorganic pyrophospate
PPO	2,5-diphenyloxazole
^{R}	(superscript) resistance/resistant
R	purine (or restriction)
RBS	ribosome-binding site(s)
rDNA	DNA coding for rRNA
re-	recombinant
RFLP	restriction-fragment length polymorphism
Rif	rifampicin
RNase	ribonuclease
rRNA	ribosomal RNA
^{s}	(superscript) sensitivity/sensitive
S	sedimentation constant
SD	Shine-Dalgarno (sequence)
SDS	sodium dodecyl sulfate
Sm	streptomycin
ss	single strand(ed)
SSC	0.15 M NaCl/0.015 M Na_3·citrate pH 7.6
T	thymidine
t, *T*	terminator of transcription
Tc	tetracycline
Th	thiostrepton
TK	thymidine kinase
TMV	tobacco mosaic virus
Tn	transposon
tsp	transcription start point(s)
u	unit(s)
U	uridine
URF	unidentified open reading frame
UTR	unstranslated region(s)
UV	ultraviolet
wt	wild type
Xgal	5-bromo-4-chloro-3-indolyl β-D-galactopyranoside
Y	pyrimidine
[]	denotes plasmid-carrier state
()	denotes prophage (lysogenic) state
::	novel junction (fusion or insertion)
′ (prime)	denotes a truncated gene at the indicated side

Nucleotide symbol combinations

Pairs	K = G/T; M = A/C; R = A/G; S = C/G; W = A/T; Y = C/T.
Triples	B = C/G/T; D = A/G/T; H = A/C/T; V = A/C/G; N = A/C/G/T.