

Full Length Research Paper

Genetic variation of 17 Y-chromosomal short tandem repeats (STRs) loci from unrelated individuals in Iraq

Imad H.^{1*}, Cheah Q.¹, Mohammad J.² and Aamera O.³

¹Department of Molecular Biology, Putra University, Kuala Lumpur City,

Malaysia. ²Department of Molecular Biology, Babylon University, Hilla City,

Iraq. ³Institute of Medico-legal in Baghdad, Ministry of Health of Iraq, Iraq.

Accepted 28 November, 2013

Analysis of 17 Y chromosomal STR loci in a population sample of 400 unrelated male living in the middle and south of Iraq was done to evaluate allele frequencies and gene diversity for each Y-STR locus of the Y filer™ PCR amplification kit. The seventeen loci include DYS635, DYS437, DYS448, DYS456, DYS458, YGATA H4, DYS389I, DYS389II, DYS19, DYS391, DYS438, DYS390, DYS439, DYS392, DYS393, DYS385a and DYS385b. Total DNA from blood cells was extracted using the FTA™ paper DNA extraction. A total of 361 unique haplotypes were identified among the four hundred individuals studied. The DYS385b had the highest diversity ($GD = 0.8392$), while loci DYS392 had the lowest ($D = 0.2695$).

Key words: Allele frequency, gene diversity, Iraq, Y filer™.

INTRODUCTION

Microsatellites (Ellegren et al., 2004) are DNA regions with repeat units that are 2 to 7 bp in length or most generally short tandem repeats (STRs) or simple sequence repeats (SSRs). The classification of the DNA sequences is determined by the length of the core repeat unit and the number of adjacent repeat units. It may contain several hundred to thousands (Butler et al., 2012; Andrea et al., 2008) of them. Length and sequence polymorphisms (Silvia et al., 2009) may be found within the DNA.

DNA can be used to study human evolution. Besides, information from DNA typing are important for medico-legal matters with polymorphisms leading to more biological studies (Walkinshaw et al., 1996). Since the STR markers are important for human identification purposes (Carolina et al., 2010), the number of repeats can be highly variable among individuals and can be used for identification purposes.

Chromosome Y microsatellites or STRs seem to be ideal markers to delineate differences between human

populations for several reasons: (a) They are transmitted in uniparental (paternal) fashion without recombination, (b) They are very sensitive for genetic drift, and (c) They allow a simple highly informative haplotype construction. Also, for forensic applications this ability to differentiate distinct Y chromosomes makes Y-STR's an advantageous addition to the well characterized autosomal STRs. For a number of forensic applications, Y-STRs could be superior to autosomal STRs. Especially in rape cases where (1) the differential lysis was unsuccessful, (2) the number of sperm cells is very low, (3) to vasectomy epithelial cells instead of sperm cells from the ejaculate of the perpetrator have to be analysed, and (4) the perpetrator, due to a familial relationship shares many autosomal bands with the victim, Y-STR's could provide crucial evidence. Also, in the case of male-male rape or rape cases with multiple perpetrators, Y-STRs could lead to essential qualitative evidence. In all such cases Y-STRs facilitates a simple and reliable exclusion of suspects (Park et al., 2007; Parson et al.,

*Corresponding author. E-mail: imad_dna@yahoo.com. Tel: 006-017-3642869.

2003; Butler et al., 2002).

Multiplex polymerase chain reaction (PCR) is defined as the simultaneous amplification of multiple regions of DNA templates by adding more than one primer pair to the amplification reaction mixture. Since its first description in 1988, PCR multiplexing has been applied in many areas of DNA testing including the analysis of deletions, mutations and STRs (Chamberlain et al., 1988; Henegariu et al., 1994; Kimpton et al., 1996). Furthermore, the wide availability of genetic information due to the publishing of the sequence of the human genome makes the demand for multiplex PCR even greater (Venter et al., 2000; Lander et al., 2001). For example, more than 1.4 million single nucleotide polymorphisms (SNPs) have been identified in the human genome (Venter et al., 2001; Lander et al., 2001). Multiplex PCR primer sets have been used for linkage studies to track genetic diseases (Evans et al., 2001; Kwak et al., 2005). Eukaryotic genomes are full of repeated DNA sequences.

The use of the Y chromosome for forensic purposes was until recently restricted by a lack of polymorphic markers (Kayser et al., 1997). The Y chromosome is less variable than the other chromosomes. The majority of Y STRs including the ones presented here are located within its non-recombining region and are passed without recombination. Thus, results from individual markers cannot be combined using the product rule. Many markers are thus needed to obtain a high degree of discrimination between unrelated males (Kuppareddi et al., 2010; Hanson and Ballantyne, 2007).

The first aim of this study was to determine the genetic structure of Iraq population. The second one was to evaluate the importance of these loci for forensic genetic purposes.

MATERIALS AND METHODS

Population

Four hundred unrelated healthy males from the middle and south of Iraq provinces (Figure 1) were used.

DNA extraction

Total DNA from blood cells was extracted using the FTA™ paper DNA extraction (Dobbs et al., 2002).

PCR

PCR is the process used to amplify a specific region of DNA. It is possible to create multiple copies from the small amount of template DNA using this process. 12Plex amplification was performed by the commercial kit Y filer™ PCR amplification kit (Applied Biosystems, Foster City, CA) that amplifies 17 Y-STR loci (DYS635, DYS437, DYS448, DYS456, DYS458, YGATA H4, DYS389I, DYS389II, DYS19, DYS391, DYS438, DYS390, DYS439, DYS392, DYS393, DYS385a and DYS385b) and a segment of the

amelogenin gene, according to manufacturer's instructions but in a total reaction volume of 25 ml.

Typing

The ABI Prism1 3730xl Genetic Analyzer 16-capillary array system (Applied Biosystems, Foster City, CA, USA) following manufacturer's protocols, with POP-7™ Polymer and Data Collection Software, GeneMapper version 3.5 software (Applied Biosystems) were used. The allele designations were determined by comparison of the PCR products with those of allelic ladders provided with the kit. Nomenclature of loci and alleles is according to the International Society of Forensic Genetics (ISFG) guidelines reported in Gill et al. (2001). By comparison of the size of a sample's alleles to size of alleles in allelic ladders for the same loci being tested in the sample, the STR genotyping was conducted.

Quality control

Allelic ladders, male DNA (positive internal control), female DNA (negative control) and the amelogenin (internal control), provided by Applied Biosystems, were used in each reaction with the Y filer™ kit.

Statistical data analysis

Allele frequencies were calculated by direct counting. Allele diversity was calculated as per Nei (1987):

$$D = \frac{n}{n-1} \left(1 - \sum_{i=1}^n p_i^2 \right)$$

where n is the sample size and p_i is the frequency of the i th allele.

RESULTS AND DISCUSSION

We identified 317 different haplotypes in our study sample (Table 2). 216 of which (82.3%) were unique, 15 were found twice (4.7%) and 13 were found in three individuals (4.1%). The most frequent haplotype was haplotype number 77 (Table 1). Haplotype 77 seems to be specific to Iraq. This is to be corroborated by future investigations. The DYS385b and DYS458 had the highest diversity ($GD = 0.8392$ and 0.806 , respectively), while loci DYS392 and DYS439 had the lowest ($D = 0.2695$ and 0.2991 , respectively).

Data comparison between our samples and a previously published sample from the Iraqi population (Nadia et al., 2011) was performed for markers which are common to both studies using the exact test for population differentiation implemented in GENEPOL (Raymond and Rousset, 1995).

In another study on 17 Y-STR Y-chromosomal short tandem repeat loci from the Cukurova region of Turkey, the DYS391 recorded lowest gene diversity in this region to be 0.51 and the highest 0.95 for DYS385a/b and no significant differences were found when comparing this

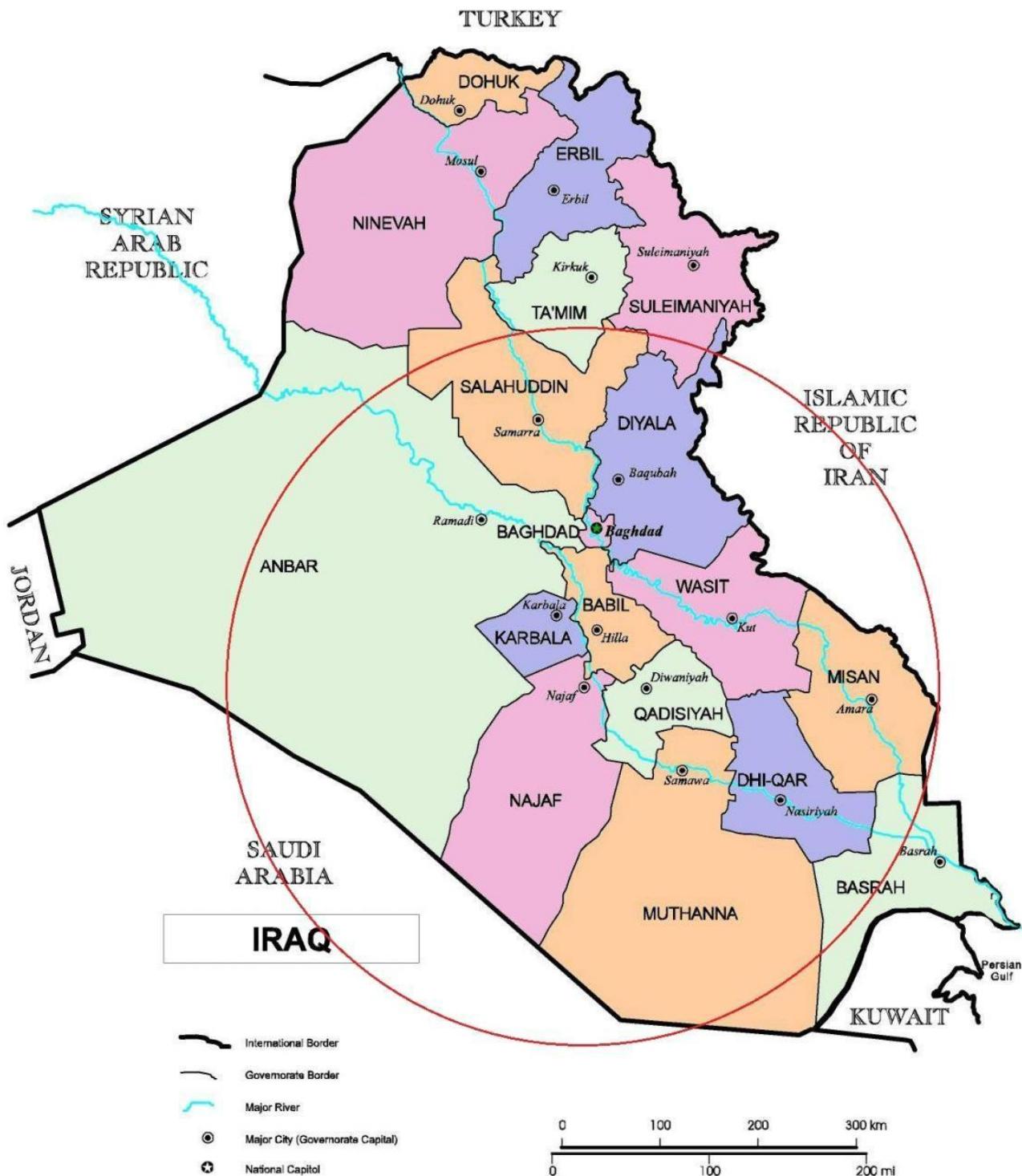


Figure 1. An Iraq administrative map showing the population and the central governorates where our samples came from (areas included in the red circle) (Source: UNOSAT, www.unosat.org, United Nations).

data with haplotype data of other Turkish populations (Ayse et al., 2011). In Northern Greece, the haplotype diversity was 0.9992 in seventeen Y STR loci typed in a population sample of unrelated male individuals.

Haplotypes are presented for the following loci: DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385a/b, DYS393, DYS391, DYS439, DYS635, DYS392, Y GATA H4, DYS437, DYS438 and DYS448

Table 1. Allele frequencies of 17 Y-STR loci in 400 Iraq males.

Alleles	DYS6 35	DYS4 37	DYS4 48	DYS4 56	DYS4 58	YGAT AH4	DYS1 9	DYS3 85a	DYS3 85b	DYS3 89I	DYS3 89II	DYS3 90	DYS3 91
8	-	-	-	-	-	-	-	-	-	-	-	-	0.0563
9	-	-	-	-	-	-	-	-	-	-	-	-	0.2188
10	-	-	-	-	-	0.1030	-	-	-	-	-	-	0.4969
11	-	-	-	-	-	0.2030	-	0.1625	-	-	-	-	0.1250 0.8
12	-	-	-	-	-	0.4981	-	0.0438	-	0.2750	-	-	0.1031 0.0
13	-	-	-	0.0982	-	0.0901	0.3594	0.5219	0.0625	0.3406	-	-	0.0
14	-	0.4881	-	0.0880	0.0531	0.1000	0.4219	0.1719	0.2500	0.3844	-	-	0.0
15	-	0.2500	-	0.5031	0.3300	-	0.1625	0.0094	0.1063	-	-	-	-
16	-	0.2601	-	0.2380	0.1882	-	0.0343	0.0188	0.1438	-	-	-	-
17	-	-	-	0.0450	0.1001	-	0.0218	0.0563	0.0438	-	-	-	-
18	-	-	0.1300	-	0.0730	-	-	-	0.1688	-	-	-	-
19	-	-	0.5032	-	0.1030	-	-	0.0156	0.1719	-	-	-	-
20	0.0781	-	0.2430	-	0.1431	-	-	-	0.0531	-	-	-	-
21	0.1650	-	0.1003	-	-	-	-	-	-	-	-	0.0500	-
22	0.0530	-	0.1000	-	-	-	-	-	-	-	-	0.0594	-
23	0.2880	-	-	-	-	-	-	-	-	-	-	0.4406	-
24	0.3781	-	-	-	-	-	-	-	-	-	-	0.3688	-
25	0.0301	-	-	-	-	-	-	-	-	-	-	0.0813	-
28	-	-	-	-	-	-	-	-	-	-	0.0906	-	-
29	-	-	-	-	-	-	-	-	-	-	0.4125	-	-
30	-	-	-	-	-	-	-	-	-	-	0.2938	-	-
31	-	-	-	-	-	-	-	-	-	-	0.1188	-	-
32	-	-	-	-	-	-	-	-	-	-	0.0500	-	-
33	-	-	-	-	-	-	-	-	-	-	0.0344	-	-
GD*	0.737	0.631	0.651	0.671	0.806	0.682	0.6650	0.6547	0.8392	0.6606	0.7140	0.6573	0.5802

GD*: Genetic diversity; In **bold** are the most common allele for each locus.

This database study provides additional information for the application of Y chromosomal STRs to forensic identification efforts in Greece (Leda et al., 2008).

This paper follows the guidelines for publication of population data requested by Lincoln et al.

(2000).

Conclusions

Power of discrimination values for all tested loci

means that the based database across the popu was DYS392 diversity was D statistical param

Table 2. Haplotypes for the 17 Y-STR loci observed 400 Iraqi males.

Haplotype	<i>DYS635</i>	<i>DYS437</i>	<i>DYS448</i>	<i>DYS456</i>	<i>DYS458</i>	<i>YGATA H4</i>	<i>DYS19</i>	<i>DYS385a</i>	<i>DYS385b</i>	<i>DYS389I</i>	<i>DYS389II</i>	<i>DYS390</i>	<i>DYS391</i>	<i>DYS392</i>	<i>DYS393</i>	<i>V1343</i>	<i>DYS439</i>	N	F
H1	24	15	20	15	14	12	13	11	16	12	30	23	10	11	13	10	13	1	0.0025
H2	24	15	18	15	14	13	13	11	16	12	30	23	8	11	13	9	13	1	0.0025
H3	24	15	20	15	15	12	13	11	16	12	31	23	8	11	12	9	10	1	0.0025
H4	24	15	19	15	15	11	13	11	14	12	31	23	8	11	13	11	10	1	0.0025
H5	24	15	19	16	15	10	13	13	14	12	31	23	10	11	13	10	10	1	0.0025
H6	24	15	19	16	17	12	13	13	14	12	28	23	10	11	13	10	13	1	0.0025
H7	24	15	19	14	17	12	13	13	14	12	28	23	9	11	14	12	13	1	0.0025
H8	24	15	19	16	17	11	13	13	14	12	28	23	10	11	13	12	10	1	0.0025
H9	24	15	20	16	17	14	13	13	14	12	29	23	10	11	13	12	10	5	0.0125
H10	24	15	19	16	15	14	13	13	14	12	29	23	8	11	14	12	11	1	0.0025
H11	24	15	19	13	15	11	13	13	14	12	29	23	9	11	14	10	11	1	0.0025
H12	24	15	21	13	15	10	13	13	14	14	29	23	10	11	12	11	11	1	0.0025
H13	24	15	21	15	15	13	13	13	14	14	29	23	10	11	13	10	11	1	0.0025
H14	24	15	22	15	15	12	13	13	14	13	29	23	10	11	14	10	10	1	0.0025
H15	24	15	19	15	20	12	13	13	18	13	29	23	10	11	14	12	10	1	0.0025
H16	24	15	19	15	16	12	13	13	18	13	28	23	8	11	13	12	13	1	0.0025
H17	24	15	19	15	18	12	13	13	18	13	28	23	8	11	13	12	10	1	0.0025
H18	24	15	19	14	18	13	13	13	16	13	28	23	10	11	13	12	10	1	0.0025
H19	24	15	19	16	18	12	13	14	16	13	31	23	10	11	13	10	10	1	0.0025
H20	24	15	21	16	15	12	13	14	16	12	31	23	10	11	13	10	10	1	0.0025
H21	24	14	21	16	16	12	13	11	16	12	31	23	10	11	12	10	10	1	0.0025
H22	24	14	19	15	15	12	13	11	13	12	28	23	10	11	12	10	10	1	0.0025
H23	24	14	19	15	20	12	13	11	13	12	28	23	10	11	14	9	10	1	0.0025
H24	24	14	19	13	15	12	13	11	13	12	30	23	10	11	14	10	10	1	0.0025
H25	24	14	20	15	15	12	13	11	18	12	30	23	10	11	13	10	10	3	0.0075
H26	24	16	18	15	19	12	13	11	14	12	30	25	10	11	13	10	10	3	0.0075
H27	24	16	18	16	15	12	13	11	14	12	32	23	10	11	13	10	10	1	0.0025
H28	24	14	19	13	15	12	13	11	18	12	33	23	10	11	13	10	10	1	0.0025
H29	24	14	19	15	20	12	13	13	18	14	30	21	10	11	13	10	10	1	0.0025
H30	24	14	20	15	19	12	13	13	18	14	29	24	10	11	13	10	10	1	0.0025
H31	24	14	20	16	15	12	13	13	18	13	29	24	10	11	12	10	11	1	0.0025
H32	24	14	20	13	15	11	13	13	18	14	29	25	10	11	13	10	11	1	0.0025
H33	24	16	20	15	15	10	13	13	18	14	29	21	10	11	13	10	11	1	0.0025
H34	24	15	20	15	16	12	13	13	18	14	29	23	10	11	13	10	11	1	0.0025
H35	24	15	21	15	16	10	13	13	18	13	29	23	10	11	13	10	11	1	0.0025
H36	24	15	21	14	16	13	13	13	18	12	29	23	10	11	14	10	11	1	0.0025
H37	24	15	19	15	16	11	13	13	18	14	29	24	10	11	13	10	11	1	0.0025
H38	24	14	20	15	15	14	13	13	16	13	30	23	10	11	13	10	11	1	0.0025
H39	24	14	19	15	15	10	13	13	19	13	28	23	10	11	13	10	11	1	0.0025
H40	24	14	19	14	15	12	13	13	19	13	30	24	10	11	13	10	11	1	0.0025
H41	24	14	19	13	15	12	13	13	19	13	32	21	10	11	13	10	11	1	0.0025
H42	24	14	19	16	15	12	13	13	19	13	32	25	10	11	12	10	11	1	0.0025
H43	24	14	19	15	16	12	13	13	14	13	28	25	10	11	12	10	11	1	0.0025
H44	24	14	19	15	20	12	13	13	14	13	29	25	10	11	12	10	11	1	0.0025
H45	24	14	19	15	19	12	13	12	14	13	32	25	10	11	13	10	12	1	0.0025
H46	24	14	21	15	16	12	13	12	14	13	30	25	10	11	13	10	12	1	0.0025
H47	24	14	18	15	16	11	13	12	14	13	28	23	10	11	12	10	12	1	0.0025

Table 2. Contd.

H48	23	14	19	15	16	13	13	12	14	13	28	23	10	11	14	10	12	1	0.0025
H49	23	14	19	13	15	12	13	12	14	12	28	24	10	11	13	10	12	1	0.0025
H50	23	14	19	16	15	14	13	12	14	12	30	24	10	11	12	10	10	1	0.0025
H51	23	14	21	16	15	11	13	11	14	14	30	24	10	11	12	9	10	1	0.0025
H52	23	14	20	15	15	11	13	11	14	14	30	25	10	11	12	10	13	2	0.0050
H53	22	14	20	15	16	11	13	11	14	13	30	23	10	11	12	10	14	1	0.0025
H54	22	14	18	15	20	11	13	11	14	12	30	23	10	11	13	10	10	1	0.0025
H55	23	14	20	15	19	11	13	11	14	14	30	24	11	11	13	10	13	1	0.0025
H56	23	14	20	15	18	12	13	11	19	13	30	24	11	11	13	10	12	1	0.0025
H57	23	14	20	14	18	11	13	11	16	12	30	24	11	11	14	11	10	1	0.0025
H58	23	14	20	15	17	12	13	11	16	14	30	24	11	11	13	9	10	1	0.0025

Table 2. Contd.

Haplotype e	DYS635	DYS437	DYS448	DYS456	DYS458	Y _{GATA} H4	DYS19	DYS385a	DYS385b	DYS389I	DYS389II	DYS390	DYS399 ₁	DYS392	DYS393	DYS438	DYS439	N	F
H59	23	14	19	17	17	11	13	11	15	13	32	22	8	11	14	10	10	1	0.0025
H60	23	16	19	15	17	14	13	11	15	13	32	24	10	11	13	10	10	1	0.0025
H61	23	14	19	16	17	13	13	11	15	13	30	25	10	11	13	12	10	1	0.0025
H62	23	14	18	16	17	11	13	11	15	12	30	25	10	11	13	11	10	1	0.0025
H63	23	15	19	13	17	11	13	11	15	14	30	25	9	11	14	11	9	1	0.0025
H64	23	15	19	14	17	12	13	11	15	14	32	25	10	11	14	11	10	1	0.0025
H65	23	15	19	17	20	12	13	11	15	14	29	25	10	11	13	10	9	3	0.0075
H66	23	14	20	17	19	12	13	11	15	14	30	23	8	11	13	10	9	1	0.0025
H67	23	14	20	15	19	11	13	11	15	14	30	23	10	11	12	10	14	1	0.0025
H68	23	14	21	16	19	13	13	11	15	14	30	24	9	11	13	10	13	1	0.0025
H69	23	14	21	16	20	12	13	11	18	13	30	24	9	11	13	9	10	1	0.0025
H70	23	14	19	16	18	12	13	11	18	14	29	24	9	11	13	12	10	1	0.0025
H71	23	14	19	15	20	12	13	11	18	12	29	24	9	11	13	11	10	1	0.0025
H72	23	14	20	16	17	12	13	11	18	12	29	23	12	11	13	11	10	1	0.0025
H73	23	14	21	16	17	10	13	11	19	12	29	23	10	11	13	11	10	1	0.0025
H74	23	14	19	16	15	11	13	11	19	12	29	22	10	11	13	11	11	1	0.0025
H75	23	14	19	14	15	14	13	11	19	12	29	23	9	11	13	11	11	1	0.0025
H76	23	14	19	15	15	12	13	11	14	12	29	23	9	11	13	10	11	1	0.0025
H77	23	14	18	15	15	13	13	11	14	12	29	24	11	11	13	10	11	7	0.0175
H78	23	16	18	15	15	12	13	11	14	13	29	24	10	11	13	12	11	1	0.0025
H79	23	15	18	15	20	12	13	11	14	12	30	24	10	11	13	10	11	1	0.0025
H80	23	16	18	13	20	11	13	11	14	14	30	24	9	11	13	10	14	1	0.0025
H81	23	16	19	13	19	11	13	11	14	14	30	23	11	11	13	10	14	1	0.0025
H82	23	16	19	15	19	12	13	16	13	14	30	25	10	11	13	10	10	1	0.0025
H83	23	16	19	15	16	12	13	16	13	12	30	25	10	11	13	9	10	1	0.0025
H84	23	14	19	15	15	12	13	16	13	12	30	25	10	11	13	10	10	1	0.0025
H85	23	16	20	15	15	11	13	14	13	12	30	24	9	11	13	10	10	1	0.0025
H86	23	16	20	16	16	13	13	14	17	12	30	24	11	11	13	10	14	1	0.0025
H87	23	14	21	15	16	11	13	14	17	12	29	24	12	11	13	10	14	1	0.0025
H88	23	15	21	15	19	12	13	14	20	12	29	24	11	11	13	11	12	1	0.0025
H89	23	14	21	15	20	12	13	14	20	12	29	25	9	11	13	11	13	1	0.0025
H90	20	16	21	15	18	12	13	14	20	12	29	24	10	11	13	9	13	3	0.0075
H91	20	16	21	15	17	12	13	14	18	12	29	24	10	11	13	10	13	3	0.0075
H92	20	16	21	13	17	11	13	14	19	12	29	24	12	11	13	12	13	1	0.0025
H93	20	16	19	16	17	12	13	14	19	12	29	24	10	11	13	10	13	1	0.0025
H94	20	15	19	15	15	12	13	14	16	12	29	23	10	11	13	11	13	1	0.0025
H95	20	14	19	15	20	12	13	14	16	12	29	23	9	11	13	10	13	1	0.0025
H96	20	14	19	17	15	12	13	14	16	12	29	23	8	11	13	10	14	1	0.0025
H97	20	14	19	14	15	14	13	14	16	12	29	23	12	11	13	10	10	1	0.0025

Table 2. Contd.

H98	24	14	19	13	15	13	13	14	16	14	29	21	12	11	13	11	10	1	0.0025
H99	24	14	19	16	15	10	13	14	16	14	29	22	8	11	13	11	11	1	0.0025
H100	24	14	19	17	15	12	13	13	16	14	29	22	10	11	13	11	13	1	0.0025
H101	21	14	19	17	16	12	13	13	16	14	29	25	10	11	13	11	12	1	0.0025
H102	21	14	19	15	16	11	13	13	16	14	32	23	10	11	13	10	12	1	0.0025
H103	21	14	20	15	16	12	14	13	16	14	28	22	10	13	13	10	12	1	0.0025
H104	21	14	20	15	19	12	14	13	16	14	33	23	10	13	13	10	11	1	0.0025
H105	21	14	18	14	19	10	14	13	16	14	28	25	10	11	13	10	11	1	0.0025
H106	21	14	18	15	19	11	14	13	19	14	28	25	10	11	13	10	14	1	0.0025
H107	21	14	21	15	19	10	14	13	15	14	28	23	10	11	13	10	14	1	0.0025
H108	21	14	22	15	19	12	14	13	19	14	28	23	10	11	13	10	14	1	0.0025
H109	21	14	22	15	20	12	14	13	20	14	32	23	10	12	13	10	11	5	0.0125
H110	21	14	19	15	15	12	14	13	20	13	32	23	10	11	13	10	11	1	0.0025
H111	21	14	20	15	16	12	14	14	20	13	29	23	10	11	13	10	11	1	0.0025
H112	21	14	22	15	16	11	14	14	13	13	29	23	10	11	13	10	11	1	0.0025
H113	21	14	19	15	15	11	14	14	13	13	29	25	10	13	13	10	11	1	0.0025
H114	22	14	19	16	15	10	14	14	13	13	31	23	10	13	13	10	11	1	0.0025
H115	23	14	22	16	15	13	14	14	13	12	31	24	10	13	13	10	11	1	0.0025
H116	22	14	18	16	15	12	14	14	13	13	31	25	10	12	13	10	11	1	0.0025

Table 2. Contd.

Haplotype pe	DYS635	DYS437	DYS448	DYS456	DYS458	Y ^{GATA} H4	DYS19	DYS385a	DYS385b	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS438	N	F	
	H117	21	14	19	16	20	12	14	14	19	14	30	23	10	11	13	12	10	1
H118	21	14	19	15	16	12	14	14	18	12	30	23	10	11	13	9	10	1	0.0025
H119	21	16	19	15	16	11	14	14	16	12	30	23	10	11	13	9	13	1	0.0025
H120	21	15	19	15	18	12	14	14	18	12	30	23	10	12	13	10	11	2	0.0050
H121	21	14	19	16	18	14	14	14	18	12	30	23	9	11	14	10	11	3	0.0075
H122	21	14	19	13	17	14	14	14	18	12	30	23	11	11	12	10	11	1	0.0025
H123	21	16	19	15	15	14	14	14	18	14	30	23	11	11	14	10	11	1	0.0025
H124	21	15	19	15	15	12	14	14	18	13	30	23	11	12	14	10	11	1	0.0025
H125	21	16	19	15	20	12	14	14	18	13	30	23	10	14	14	10	13	1	0.0025
H126	21	16	19	16	20	12	14	14	14	13	28	23	10	11	13	10	10	1	0.0025
H127	21	14	19	16	19	12	14	14	14	13	29	23	10	14	13	9	10	1	0.0025
H128	24	14	22	16	19	11	14	14	14	13	30	24	12	11	13	9	10	1	0.0025
H129	24	14	20	16	19	13	14	14	14	14	28	24	12	11	12	9	10	1	0.0025
H130	24	14	20	14	15	13	14	14	14	14	28	25	12	13	13	9	12	1	0.0025
H131	24	14	20	13	15	12	14	14	14	12	28	24	11	13	13	9	13	1	0.0025
H132	24	14	20	13	16	12	14	14	14	14	31	24	11	14	13	12	10	1	0.0025
H133	24	15	20	15	14	12	14	14	14	14	31	22	11	11	14	10	10	1	0.0025
H134	24	16	20	15	17	12	14	14	14	14	28	22	9	11	12	10	10	2	0.0050
H135	22	16	20	15	18	12	14	14	14	13	28	23	9	11	12	12	11	2	0.0050
H136	24	16	18	15	17	11	14	14	14	13	29	24	9	11	12	11	11	1	0.0025
H137	24	16	19	15	15	11	14	16	14	13	29	24	10	11	12	10	11	1	0.0025
H138	24	15	19	16	15	13	14	16	14	13	29	24	9	11	12	10	10	1	0.0025
H139	24	14	19	16	16	12	14	16	13	13	29	24	9	11	14	10	10	1	0.0025
H140	24	16	19	16	14	12	14	16	13	13	29	24	11	11	13	10	10	1	0.0025
H141	21	16	19	13	14	12	14	15	17	13	29	24	12	11	13	10	11	1	0.0025
H142	21	15	19	16	15	12	14	14	17	12	30	24	12	12	13	10	11	1	0.0025
H143	23	15	22	16	19	12	14	14	19	12	30	24	12	11	13	10	11	1	0.0025
H144	23	14	18	16	19	11	14	14	19	12	30	23	12	11	14	10	11	5	0.0125

Table 2. Contd.

Haplotype	DYS635	DYS437	DYS448	DYS456	DYS458	YGATA H4	DYS19	DYS385a	DYS385b	DYS389I	DYS389II	DYS391	DYS390	DYS392	DYS393	DYS438	DYS439	N	F
H145	23	16	18	16	15	11	14	14	19	14	30	24	11	11	13	10	11	1	0.0025
H146	23	16	21	16	15	13	14	14	19	14	30	22	10	13	14	10	11	1	0.0025
H147	23	16	19	15	15	12	14	14	19	14	28	23	10	11	12	12	10	1	0.0025
H148	23	16	22	15	15	10	14	12	19	14	28	22	10	11	12	9	10	4	0.0100
H149	23	14	22	14	15	10	14	12	16	14	29	23	10	11	13	9	11	1	0.0025
H150	23	14	19	15	16	10	14	17	16	14	29	21	10	11	13	11	11	1	0.0025
H151	23	14	20	15	16	12	14	17	16	14	29	24	10	12	12	11	11	2	0.0050
H152	23	14	20	13	16	12	14	17	16	13	29	24	10	11	14	11	11	2	0.0050
H153	23	16	20	14	17	12	14	17	19	13	29	24	10	11	13	11	11	1	0.0025
H154	23	16	21	15	14	12	14	13	19	13	29	24	10	13	13	10	10	1	0.0025
H155	23	15	20	15	14	11	14	13	19	13	28	24	10	11	12	10	10	1	0.0025
H156	23	14	20	15	16	11	14	13	15	13	29	25	10	11	12	10	11	1	0.0025
H157	23	15	20	16	17	11	14	13	15	13	33	25	10	13	13	10	11	1	0.0025
H158	20	15	20	13	15	11	14	13	15	13	33	25	10	11	12	10	11	1	0.0025
H159	20	15	18	15	15	13	14	13	15	14	33	24	11	11	13	10	11	1	0.0025
H160	20	15	22	15	15	12	14	13	15	14	33	21	11	14	13	10	11	1	0.0025
H161	20	16	21	15	15	12	14	12	15	12	33	23	11	11	13	9	11	1	0.0025
H162	20	16	19	15	15	10	14	13	15	12	33	23	11	11	13	12	11	1	0.0025
H163	20	14	19	15	16	12	14	13	18	12	28	23	11	11	13	12	14	1	0.0025
H164	20	14	19	16	16	10	14	13	20	12	32	23	11	11	13	10	10	1	0.0025
H165	21	14	19	16	20	12	14	13	18	12	32	23	11	11	13	10	12	1	0.0025
H166	21	16	20	15	15	12	14	12	14	12	28	23	11	11	13	9	12	1	0.0025
H167	21	16	20	14	15	11	14	13	14	12	30	23	10	11	13	10	10	1	0.0025
H168	24	16	20	14	16	11	14	13	14	14	30	23	9	12	13	10	10	1	0.0025
H169	24	15	20	15	16	11	14	13	14	13	30	23	12	12	12	10	10	1	0.0025
H170	24	14	20	15	20	11	14	13	14	13	30	21	11	13	12	10	10	1	0.0025
H171	24	14	20	16	16	11	14	13	14	13	30	21	12	11	12	10	13	3	0.0075
H172	24	14	19	16	15	12	14	13	19	13	30	23	12	11	12	11	11	2	0.0050
H173	24	16	19	13	15	12	14	13	19	14	30	23	10	11	12	10	11	1	0.0025
H174	24	15	19	15	15	10	14	19	17	14	30	23	9	11	12	10	11	1	0.0025

Table 2. Contd.

Haplotype	DYS635	DYS437	DYS448	DYS456	DYS458	YGATA H4	DYS19	DYS385a	DYS385b	DYS389I	DYS389II	DYS391	DYS390	DYS392	DYS393	DYS438	DYS439	N	F
H175	25	15	19	15	17	12	14	13	17	14	31	23	11	11	13	10	10	1	0.0025
H176	25	15	19	15	20	12	14	12	19	14	33	23	11	11	13	10	11	4	0.0100
H177	25	14	19	15	19	12	14	13	19	14	29	23	9	11	13	10	11	1	0.0025
H178	25	14	20	15	17	12	14	13	20	14	30	23	9	11	13	12	10	1	0.0025
H179	23	14	20	15	14	12	14	13	20	14	31	24	10	11	13	10	13	1	0.0025
H180	23	15	20	15	15	10	14	13	18	14	31	24	10	11	13	10	14	1	0.0025
H181	23	15	19	15	15	12	14	13	15	14	31	24	10	11	13	9	11	1	0.0025
H182	23	14	19	15	16	12	14	16	18	14	31	24	12	11	13	9	11	1	0.0025
H183	23	16	19	15	20	11	14	17	18	14	28	24	9	11	13	10	11	1	0.0025
H184	23	16	22	15	20	13	14	17	18	14	29	24	11	11	13	10	10	1	0.0025
H185	24	16	21	15	20	14	14	13	18	14	29	24	10	11	13	10	10	1	0.0025
H186	24	14	21	15	18	12	14	13	16	14	32	24	10	11	13	10	10	1	0.0025
H187	24	14	19	15	19	14	14	13	16	14	29	24	10	11	13	10	13	1	0.0025
H188	24	14	19	15	16	12	14	13	19	14	29	24	10	11	13	10	11	1	0.0025
H189	24	14	19	15	16	11	14	13	19	14	30	24	9	11	13	10	10	5	0.0125
H190	24	14	19	15	16	13	14	13	14	14	30	24	9	11	13	11	12	1	0.0025
H191	24	14	20	15	16	10	14	16	14	14	29	24	9	11	13	11	11	1	0.0025

Table 2. Contd.

H192	24	14	20	15	15	12	14	13	14	14	29	24	9	11	13	9	10	1	0.0025
H193	24	16	18	15	15	10	14	13	14	14	33	24	9	11	13	9	10	1	0.0025
H194	24	15	18	15	19	12	14	17	14	14	29	24	11	11	13	9	10	1	0.0025
H195	24	14	18	15	20	12	14	13	14	14	29	24	12	11	13	9	10	1	0.0025
H196	24	16	18	15	20	14	14	13	14	13	28	23	8	11	13	10	10	1	0.0025
H197	24	16	20	15	20	12	14	13	14	13	28	23	10	11	13	10	10	1	0.0025
H198	25	16	20	14	20	11	14	13	14	13	32	22	9	11	13	10	10	1	0.0025
H199	21	16	20	16	15	12	14	13	14	13	30	22	9	11	13	9	10	1	0.0025
H200	21	14	20	16	16	12	14	13	14	13	30	24	11	11	13	9	11	3	0.0075
H201	21	14	22	16	15	12	14	13	17	13	30	24	11	11	13	11	11	3	0.0075
H201	21	15	22	13	15	12	14	13	15	13	29	24	10	11	13	11	11	1	0.0025
H202	21	16	22	13	14	12	14	13	15	13	29	23	9	11	13	11	11	1	0.0025
H203	22	16	18	15	14	10	14	13	18	13	29	23	9	11	13	10	13	1	0.0025
H204	24	16	19	15	14	12	14	13	18	13	29	21	11	11	13	10	13	1	0.0025
H205	24	15	19	16	16	12	14	19	13	13	29	24	11	11	13	11	13	1	0.0025
H206	24	14	19	14	16	11	14	13	13	14	30	24	11	11	13	12	13	1	0.0025
H207	24	15	19	15	16	11	14	13	13	14	30	22	9	11	13	12	13	1	0.0025
H208	24	15	20	15	20	11	14	13	19	12	30	22	9	11	12	10	13	1	0.0025
H209	24	15	21	15	15	14	14	13	19	12	30	24	10	11	12	10	10	2	0.0050
H210	24	16	21	15	18	14	14	13	16	12	28	24	10	11	12	10	10	2	0.0050
H211	24	16	18	15	18	12	14	13	19	12	30	24	10	11	12	12	12	2	0.0050
H212	24	14	18	16	16	12	14	13	19	14	29	22	10	11	12	9	12	1	0.0025
H213	24	14	19	16	16	13	14	13	19	14	30	23	10	11	12	11	11	1	0.0025
H214	24	14	20	16	16	14	14	13	17	13	30	23	10	11	12	12	12	1	0.0025
H215	24	16	19	16	19	12	14	13	19	13	30	23	9	11	12	12	12	1	0.0025
H216	24	16	19	15	20	12	14	17	19	13	29	23	11	11	12	12	10	1	0.0025
H217	24	15	19	13	15	12	14	13	15	13	29	23	8	11	12	12	10	1	0.0025
H218	24	15	22	15	15	11	14	13	15	13	31	23	9	11	12	11	10	1	0.0025
H219	24	15	18	15	15	10	14	13	15	14	29	23	9	11	12	11	13	1	0.0025
H220	24	15	21	15	17	12	15	17	18	14	29	23	9	11	12	11	10	1	0.0025
H221	24	15	19	15	16	12	15	17	18	14	29	24	10	11	12	11	14	1	0.0025
H222	24	14	19	13	16	14	15	13	18	14	29	24	10	11	12	11	11	1	0.0025
H223	24	14	20	14	16	11	15	13	18	14	31	23	12	11	14	10	11	1	0.0025
H224	22	16	20	13	15	11	15	13	18	14	31	21	12	11	13	10	11	6	0.0150
H225	21	15	20	15	14	11	15	13	18	14	31	24	9	11	14	10	11	1	0.0025
H226	21	15	19	15	14	10	15	13	14	14	29	24	9	11	13	9	14	1	0.0025
H227	21	15	18	15	14	14	15	19	19	14	29	24	9	11	13	10	13	4	0.0100
H228	21	16	19	16	15	12	15	13	19	12	29	24	10	11	13	10	10	1	0.0025
H229	23	14	19	14	15	10	15	13	16	12	30	22	11	11	13	10	10	1	0.0025
H230	23	15	19	16	20	12	15	13	16	12	30	23	10	11	13	10	10	1	0.0025
H231	23	15	22	16	17	12	15	17	20	12	28	23	10	11	13	9	10	3	0.0075

Table 2. Contd.

Haplotype	DYS635	DYS437	DYS448	DYS456	DYS458	YGATA H4	DYS19	DYS385a	DYS385b	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS438	DYS439	N	F
H232	21	16	20	15	17	12	15	17	16	13	29	23	9	11	12	12	11	2	0.0050
H233	21	16	19	16	16	12	15	13	16	13	29	23	9	14	12	12	10	1	0.0025
H234	25	14	19	15	16	11	15	13	16	12	29	23	8	14	12	10	11	1	0.0025
H235	25	16	19	14	16	11	15	13	16	12	29	24	8	13	12	10	11	1	0.0025
H236	25	16	22	14	15	14	15	13	16	12	29	23	9	11	13	10	13	1	0.0025
H237	25	14	19	13	15	13	15	13	16	13	29	23	9	13	13	9	14	1	0.0025
H238	21	14	18	15	15	13	15	13	16	12	29	23	9	13	13	11	10	1	0.0025
H239	21	15	18	15	20	12	15	13	13	14	29	23	10	11	13	11	10	3	0.0075
H240	22	16	18	16	20	12	15	12	13	13	29	23	10	11	14	11	10	1	0.0025

Table 2. Contd.

H241	22	16	19	16	19	12	15	12	13	14	29	23	12	11	13	10	12	3	0.0075
H242	22	14	19	16	15	13	15	12	20	14	29	23	12	11	13	10	11	1	0.0025
H243	24	14	19	14	15	11	15	13	19	14	29	23	12	13	12	10	10	1	0.0025
H244	24	15	19	15	15	11	15	13	19	14	31	23	12	13	14	10	10	1	0.0025
H245	24	14	20	15	19	11	15	13	15	14	31	23	9	11	13	10	10	1	0.0025
H246	20	16	20	15	18	14	15	13	18	14	31	21	9	12	13	10	10	1	0.0025
H247	20	16	21	15	18	12	15	13	18	14	31	23	9	11	12	10	14	1	0.0025
H248	20	14	21	13	18	12	15	13	18	14	31	24	9	12	13	10	10	1	0.0025
H249	20	14	18	15	15	12	15	13	18	12	29	24	9	12	13	10	11	1	0.0025
H250	20	14	22	15	20	11	15	13	18	13	28	24	9	11	13	10	10	1	0.0025
H251	20	14	22	16	15	13	15	15	18	14	28	24	9	11	13	10	13	1	0.0025
H252	20	15	22	14	15	11	15	13	18	14	30	24	9	11	14	10	13	1	0.0025
H253	20	15	19	15	16	11	15	13	14	14	31	24	9	12	13	10	10	1	0.0025
H254	20	14	19	15	19	11	15	13	14	13	31	22	9	12	13	10	10	1	0.0025
H255	20	16	19	15	18	10	15	13	17	13	31	22	11	11	13	10	10	1	0.0025
H256	20	14	19	16	18	10	15	15	20	13	31	23	8	11	13	10	10	1	0.0025
H257	24	14	22	16	20	12	15	13	19	13	29	23	10	11	13	10	10	1	0.0025
H258	24	16	22	14	20	12	15	13	19	13	29	24	9	11	13	10	10	2	0.0050
H259	24	16	19	14	16	12	15	13	17	13	29	24	9	11	13	10	10	2	0.0050
H260	24	16	20	13	16	12	15	13	19	13	31	24	9	11	13	10	10	1	0.0025
H261	24	16	21	15	19	12	15	13	15	13	29	24	12	11	13	10	10	1	0.0025
H262	24	15	21	15	20	12	15	19	15	13	30	24	10	11	13	10	10	1	0.0025
H263	24	14	21	15	15	12	16	13	15	13	29	24	10	11	14	10	10	1	0.0025
H264	24	14	19	15	18	12	16	13	15	12	30	24	10	11	12	10	11	1	0.0025
H265	23	14	19	16	15	10	16	13	15	14	30	24	10	11	13	10	11	1	0.0025
H266	23	15	19	14	15	10	16	13	15	14	30	23	10	11	12	10	11	1	0.0025
H267	23	16	19	14	16	12	16	17	15	14	28	23	10	11	13	10	11	1	0.0025
H268	23	16	20	15	16	12	16	17	15	14	28	21	10	11	12	10	13	1	0.0025
H269	23	14	20	14	19	12	16	17	19	14	29	24	10	11	13	10	10	1	0.0025
H270	23	16	21	14	20	13	16	17	19	14	29	22	10	11	13	10	10	1	0.0025
H271	23	14	21	16	20	13	16	13	16	14	29	24	10	11	13	10	10	3	0.0075
H272	23	14	18	16	16	13	16	13	16	13	29	24	10	11	14	10	10	1	0.0025
H273	23	15	18	15	15	11	16	13	14	13	30	24	10	11	13	10	10	1	0.0025
H274	23	14	19	15	18	11	17	13	18	13	30	24	10	11	13	10	10	1	0.0025
H275	23	16	19	13	15	11	17	13	20	13	29	24	10	14	13	10	14	1	0.0025
H276	23	15	19	16	15	12	17	19	14	13	29	24	10	14	13	10	14	2	0.0050
H277	23	14	19	17	15	12	17	13	17	13	31	21	9	13	13	10	11	1	0.0025
H278	23	15	19	17	18	12	17	14	17	13	30	24	9	12	13	9	10	1	0.0025
H279	23	14	19	15	15	11	13	14	17	13	32	23	9	11	13	11	13	1	0.0025
H280	24	14	19	16	15	10	13	14	19	13	30	22	9	11	14	10	12	1	0.0025
H281	24	14	20	16	20	11	13	12	19	15	30	25	9	11	12	12	13	1	0.0025
H282	20	14	22	15	20	12	13	17	13	15	30	23	10	12	14	10	12	1	0.0025
H283	20	14	18	15	16	12	13	17	16	13	30	21	8	14	12	9	13	1	0.0025
H284	20	16	18	17	16	14	13	13	13	15	32	25	11	12	14	9	10	1	0.0025
H285	20	16	19	16	19	14	14	13	20	13	31	21	12	13	13	9	11	1	0.0025
H286	24	16	20	17	15	14	14	11	20	15	28	22	8	12	12	11	10	1	0.0025
H287	24	15	20	15	15	11	16	17	20	13	30	25	10	12	14	9	10	1	0.0025
H288	23	15	20	14	15	12	16	11	16	13	29	25	12	11	12	10	11	1	0.0025

Table 2. Contd.

Haplotype	DYS635	DYS437	DYS448	DYS456	DYS458	H4YGATA	DYS19	DYS385a	DYS385b	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS434	DYS439	N	F
H289	21	15	20	15	14	12	16	13	16	12	28	21	11	14	13	9	10	1	0.0025
H290	21	15	20	15	20	12	17	13	16	13	28	24	12	11	13	12	13	1	0.0025
H291	22	15	19	15	19	12	13	13	18	12	30	24	8	13	13	9	13	1	0.0025
H292	22	14	19	15	16	12	13	17	16	12	28	21	9	12	13	9	10	1	0.0025
H293	24	14	19	13	15	12	13	17	15	14	29	25	10	12	14	9	12	4	0.0100
H294	24	16	19	14	15	10	13	12	18	12	31	22	9	11	14	9	10	1	0.0025
H295	23	16	19	16	15	14	13	13	14	14	30	23	11	11	12	10	10	1	0.0025
H296	23	14	19	16	19	10	16	13	14	14	33	23	10	11	13	12	10	4	0.0100
H297	20	14	22	16	20	10	14	13	18	14	28	23	8	12	13	11	10	1	0.0025
H298	23	14	18	17	16	10	14	19	18	12	31	23	9	13	13	10	10	1	0.0025
H299	23	15	18	14	16	13	14	16	18	13	29	23	9	13	12	10	13	1	0.0025
H300	23	15	20	17	16	12	14	17	16	13	30	24	9	14	14	10	13	1	0.0025
H301	24	14	20	14	16	11	14	12	16	14	30	22	9	12	14	10	11	1	0.0025
H302	21	14	19	17	16	14	14	11	16	13	28	21	10	11	14	10	11	1	0.0025
H303	24	14	18	13	17	12	14	13	13	12	29	24	10	12	12	12	11	1	0.0025
H304	24	14	22	15	17	14	15	13	15	12	32	24	10	13	12	11	12	1	0.0025
H305	24	16	22	15	19	12	13	13	16	12	28	24	12	11	12	9	10	1	0.0025
H306	21	16	19	17	14	14	13	16	16	13	31	24	11	11	14	9	10	1	0.0025
H307	22	16	19	15	14	12	15	13	20	13	33	24	12	13	13	10	13	1	0.0025
H308	24	16	18	15	15	12	13	11	17	13	28	24	8	12	13	12	13	1	0.0025
H309	24	16	20	16	15	10	13	16	13	15	29	24	11	14	13	9	13	1	0.0025
H310	24	14	20	15	15	12	15	13	15	15	29	21	8	11	13	9	11	1	0.0025
H311	23	14	20	15	17	11	13	13	13	13	33	23	11	13	14	9	11	1	0.0025
H312	23	15	20	17	17	11	14	13	15	13	30	22	10	11	14	10	10	1	0.0025
H313	23	14	22	15	16	11	14	11	15	12	29	22	12	14	13	11	10	1	0.0025
H314	20	14	22	14	16	14	14	16	16	14	28	21	12	11	12	12	10	1	0.0025
H315	21	14	18	15	20	10	14	19	20	12	32	23	11	11	12	11	10	2	0.0050
H316	21	16	19	17	19	13	14	17	20	15	29	24	10	11	14	9	13	1	0.0025
H317	21	15	20	15	14	14	14	12	20	13	28	24	8	11	13	10	11	1	0.0025

N: Number of males observed for each haplotype. F: frequency of each haplotype in the sample of 105 males.

use this 17 STR loci as a vital tool for forensic identification and paternity testing.

REFERENCES

- Andrea V, Nicoletta C, Fausta G, Anna P, Elena M, Francesco DF (2008) . Population Data for 15 Autosomal STRs Loci and 12 Y Chromosome STRs Loci in a Population Sample from the Sardinia Island (Italy), Leg. Med. 11(1):37-40.
- Ayse S, Husniye C, Behnan A, Yasar S (2011). Haplotype frequencies of 17 Y-chromosomal short tandem repeat loci from the Cukurova region of Turkey, Croat Med. J. 52(6):703-708.
- Butler JM, Hill CR (2012). Biology and genetics of new autosomal STR loci useful for forensic DNA analysis. Forensic Sci. Rev. 24(1):15-26.
- Butler JM, Schoske R, Vallone PM, Kline MC, Redd AJ, Hammer MF (2002) . A Novel Multiplex for Simultaneous Amplification of 20 Y-Chromosome STR Markers, Forensic Sci. Int., 129(1):10-24.
- Carolina N, Miriam B, Cecilia S, Yolanda C, Jianye G, Bruce B, et al.,(2010). Reconstructing the Population History of Nicaragua by means of mtDNA, Y-Chromosome STRs, and Autosomal STR Markers, Am. J. of physical anthropology, 143(4), 591-600.
- Chamberlain JS, Gibbs RA, Rainer JE, Nguyen PN, Casey CT (1988). Deletion screening of the Duchenne muscular dystrophy locus via multiplex DNA amplification. Nucleic Acids Res. 16:11141-11156.
- Dobbs LJ, Madigan MN, Carter AB, Earls L (2002). Use of FTA gene guard filter paper for the storage and transportation of tumor cells for molecular testing, Arch. Pathol Lab Med., 126 (1):56-63.
- Ellegren H (2004). Microsatellites: simple sequences with complex evolution. Nat. Rev. Genet. 5:435-445.
- Evans JC, Frayling TM, Cassell PG, Saker PJ, Hitman GA, Walker M, Levy JC, O'Rahilly S, Rao PV, Bennett AJ, Jones EC, Menzel S, Prestwich P, Simecek N, Wishart M., Dhillon R., Fletcher C., Milward A., Demaine A., Wilkin T., Horikawa Y., Cox NJ, Bell GI, Ellard S, McCarthy MI, Hattersley AT (2001). Studies of association between the gene for calpain-10 and type 2 diabetes mellitus in the United Kingdom. Am. J. Hum. Genet. 69:544-552.
- Gill P, Brenner C, Brinkmann B, Budowle B, Carracedo A, Jobling MA et al. (2001). DNA Commission of the International Society of Forensic Genetics: recommendations on forensic analysis using Y-chromosome STRs, Forensic Sci. Int. 124:5-10.

- Hanson EK, Ballantyne J (2007). An Ultra-High Discrimination Y Chromosome Short Tandem Repeat Multiplex DNA Typing System, PLoS ONE, 2(8):e688.
- Henegariu O, Hirschman P, Killian K, Kirsch C, Lengauer R, Maiwald K (1994). Rapid screening of the Y chromosome in idiopathic sterile men, diagnostic for deletions in AZF, a genetic Y factor expressed during spermatogenesis. Andrologia 26:97-106.
- Kayser M, Caglia A, Corach D, Fretwell N, Gehrig C, Graziosi G et al. (1997). Evaluation of Y-chromosomal STRs: a multicenter study. Int. J. Legal Med. 110:125-133.
- Kimpton CP, Oldroyd NJ, Watson SK, Frazier RRE, Johnson PE, Millican ES, Urquhart A, Sparkes BL, Gill P (1996) Validation of highly discriminating multiplex short tandem repeat amplification systems for individual identification. Electrophor. 17:1283-1293.
- Kuppareddi B, Suhasini G, Vijaya M, Kanthimathi S, Nicole M, Martin T et al. (2010). Y Chromosome STR Allelic and Haplotype Diversity in Five Ethnic Tamil Populations from Tamil Nadu, India, Leg. Med. 12:265-269.
- Kwak KD, Jin HJ, Shin DJ, Kim JM, Roewer L, Krawczak M et al. (2005). Y-Chromosomal STR Haplotypes and Their Applications in Forensic and Population Studies in East Asia, Int. J. Leg. Med. 119(4):195-201.
- Lander ES, Linton LM, Birren B, Nusbaum C, Zody MC, Baldwin J, Devon K, Dewar K, Doyle M, Fitz HW et al. (2001) Initial sequencing and analysis of the human genome . Nat. 409:8-921.
- Leda K, Jessica L, Jodi A (2008). Population genetics of Y-chromosome STRs in a population of Northern Greeks, Forensic Sci. Int. 175(2-3):250-255.
- M Nei (1987). Molecular Evolutionary Genetics, Columbia University Press, New York,.
- Nadia Al-Zahery, Maria P, Vincenza B, Viola G, Mohammed A, Baharak H (2011). In search of the genetic footprints of Sumerians: a survey of Y-chromosome and mtDNA variation in the Marsh Arabs of Iraq. BMC Evol. Biol. 11:288.
- Park MJ, Lee HY, Chang U, Kang SC, Shin KJ (2007) .Y-STR Analysis of Degraded DNA Using Reduced-Size Amplicons, Int. J. Leg. Med. 121(2):152-157.
- Parson W, Niederstätter H, Brandstätter A, Berger B (2003). Improved Specificity of Y-STR Typing in DNA Mixture Samples, Int. J. Leg. Med. 117(2):109-114.
- Raymond M, Rousset F (1995). GENEPOP (version 1.2). Population genetics software for exact tests and ecumenicism, J. Heredity 86:248-249.
- Silvia B, Marta CD, Andrea Z, Dario B, Tatiana G (2009). Integration of Genomic and Gene Expression Data of Childhood ALL Without Known Aberrations Identifies Subgroups with Specific Genetic Hallmarks. Genes Chromosomes Cancer 48:22-38.
- Venter JC, Adams MD, Myers EW, Li PW, Mural RJ, Sutton GG, Smith HO, Yandell M et al. (2001). The sequence of the human genome. Science 291(5507):1304-1351.
- Walkinshaw M, Strickland L, Hamilton H, Denning K, Gayley T (1996). DNA Profiling in two Alaskan Native Populations Using HLA-DQA1, PM, and D1S80 Loci. J. of Forensic Sci., 41:47Rui P., Christopher P. , Críntia A. , Anto' nio A. , A' ngel, C. and Leonor G.,. A new multiplex for human identification using insertion/deletion polymorphisms . Electrophor. 30:3682-3690.