academicJournals

Vol. 14(15), pp. 1252-1260, 15 April, 2015
DOI: 10.5897/AJB2015.14424
Article Number: CDAAA0F52306
ISSN 1684-5315

http://www.academicjournals.org/AJB

African Journal of Biotechnology

Full Length Research Paper

Allelic frequencies for the seventeen Y-STR loci observed in Iraqi male patients with prostate cancer

Imad Hadi Hameed[1]*, Mohammed Abdullah Jebor[1] and Muhanned Abdulhasan Kareem[2]

[1]Department of Molecular Biology, Babylon University, Hilla City, Iraq.
[2]Babylon University, Centre of Environmental Research, Iraq.

Received 30 January 2015; Accepted 27 March, 2015

Prostate cancer is a significant disease in men and a large number of individuals would benefit if risk factors that increase the susceptibility to develop this neoplasia could be established, which could aid in the early detection of the disease that is crucial for successful treatment. The first objective of this study was detection of allelic frequencies of 17 Y-chromosome short tandem repeat loci from Iraqian prostate cancer patients and normal control males. The second objective was evaluating the association of these loci with the presence of prostate cancer. Blood samples were collected from 100 unrelated male patients living in Middle and South of Iraq. FTA® Technology was utilized to extract DNA from blood collected on FTA™ paper. One 1.2 mm punch from a card containing whole blood was loaded into the appropriate wells of the reaction plate. The PCR was realized with the GeneAmp® PCR System 9700 thermal cycler. Post PCR amplification was detected using an ABI Prism1 3130xl Genetic Analyzer 16-capillary array system, with POP-7™ Polymer and Data Collection Software, GeneMapper version 3.5. Six alleles (20 to 25) for DYS635, three alleles (14 to 16) for DYS437, five alleles (18 to 22) for DYS448, five alleles (13 to 17) for DYS456, seven alleles (14 to 20) for DYS458, five alleles (10 to 14) for YGATA H4, three alleles (12 to 14) for DYS389I, six alleles (28 to 33) for DYS389II, five alleles (13 to 17) for DYS19, five alleles (8 to 12) for DYS391, four alleles (9 to 12) for DYS438, five alleles (21 to 25) for DYS390, six alleles (9 to 14) for DYS439, four alleles (11 to 14) for DYS392, three alleles (13 to 15) for DYS393, eight alleles (11 to 19) for DYS385a and eight alleles (13 to 20) for DYS385b were found among the whole Iraqi subjects examined. A higher incidence of disease was found among males who had either allele 10 of DYS391 or allele 13 of DYS393. It is likely that Iraqi males who belong to Y-lineages with either allele 10 or allele 13 are more susceptible to develop prostate cancer, while those belonging to lineages with allele 9 and 14 of DYS439 or allele 15 of DYS385b are more resistant to the disease. This study shows the influence of genetic-factors on prostate cancer, and it seems that DYS391 and DYS390 loci comprising DYS635, DYS437, DYS448, DYS456, DYS458, YGATA H4, DYS389I, DYS389II, DYS19, DYS438, DYS439, DYS392, DYS393, DYS385a and DYS385b STRs have the potential to be used as a screening method for prediction of susceptibility to prostate cancer in Iraqi population.

Key words: Allele frequency, FTA™ paper, Iraq, prostate cancer, STR DNA typing, Y filer™.

INTRODUCTION

Microsatellites are a group of molecular markers chosen for a number of purposes including forensics individual identification and relatedness testing polymorphism (Kimpton et al., 1996; Gill et al., 2001; Andrea et al., 2008). There is a high genomic abundance of random distribution throughout the genome; also abundance of

polymorphism (Ellegren, 2004; Butler and Hill, 2012). The Y-chromosome is specific to the male portion of a male-female DNA mixed such as is common in sexual assault cases. These STRs can also be useful in missing person's investigations, historical investigations, some paternity testing scenarios, and genetic genealogy (Kwak et al., 2005).

Although, they are often used to suggest which haplogroup an individual matches, STR analysis typically provides a person haplotype. Most tests on the Y chromosome examine between 12 and 67 STR markers (Carolina et al., 2010; Mohammed and Imad, 2013; Muhanned et al., 2015a). The Y chromosome is less variable than the other chromosomes. Many markers are thus needed to obtain a high degree of discrimination between unrelated males' marker.

Prostate cancer is a significant disease in men accounting for approximately 33% of all male cancers and having a 9% mortality rate for men presenting with disease (Jemal et al., 2006). However, public awareness for prevention and early detection of prostate cancer is relatively low. Two classifications are used to describe prostate cancer. The Union for International Cancer Control (UICC) 2002 classifies it as tumour, node and metastasis (TNM) which is commonly used for malignant tumours (Hayes et al., 2005). The second classification system, Gleason score, is specific for grading of adeno-carcinoma of the prostate (Gleason and Mellinger, 1974).

A large number of individuals would benefit if risk factors that increase the susceptibility to develop prostate cancer could be established, which could aid in the early detection of the disease which is crucial for successful treatment (Paracchini et al., 2003; Ewis et al., 2006; Mohammed et al., 2015; Ameera et al., 2015). Numerous studies have been conducted on the molecular genetic aetiology of the disease. The incidence of prostate cancer varies considerably between people of various ethnicities (Parkin et al., 1993; Hsing et al., 2000; Jemal et al., 2006; Muhanned et al., 2015b), which suggests that in part the predisposition for developing prostate cancer is associated with alleles that are more prevalent in certain populations or groups.

In this study, we discuss the role of 17 susceptibility genes commonly debated within the field of prostate cancer research.

MATERIALS AND METHODS

Preparation of blood samples

Blood samples were collected from two hundred unrelated males patients living in middle and south of Iraq. Comprising 100 men with prostate cancer and 100 healthy male individuals as control. All patients participated in the study were males over 40 years old who had been referred to the hospital for treatment because of advanced level of cancer.

DNA extraction and amplification

DNA was extracted from all dried blood samples on FTA cards following the manufacturer's procedure as described in Whatman FTA Protocol BD01 except that the Whatman FTA purification reagent was modified to half the volume. A 1.2 mm diameter disc was punched from each FTA card with a puncher. The discs were transferred to new Eppendorf tubes and washed 3 times in 100 µl Whatman FTA purification reagent. Each wash was incubated for 5 min at room temperature with moderate manual mixing and the reagent was discarded between washing steps. The discs were then washed twice in 200 µl TE buffer (10 mM Tris-HCl, 0.1 mM EDTA, pH 8.0), the buffer was discarded and the discs were left to dry at room temperature for 1 h. A 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 was used, according to manufacturer's instructions but in a total reaction volume of 25 µl. Amplification for Y-chromosomal STR regions were carried out using sets of primers (Table 1).

The master mix was homogenized by vortex for 3 s, centrifuged briefly, then 25 µl of PCR amplification mix was pipetted into each reaction well. One 1.2 mm punch from a card containing whole blood was loaded into the appropriate wells of the reaction plate. The positive amplification control, 1 µl of 2800 M control DNA (10 ng/µl) was added to a reaction well containing 25 µl of PCR amplification mix.

The protocol used with the GeneAmp® PCR System 9700 thermal cycler is provided below. PCR program is as follows: 96°C for 1 min, then: 94°C for 10 s, 59°C for 1 min, 72°C for 30 s, for 25 cycles, then: 60°C for 20 min and soaked at 4°C. After completion of the thermal cycling protocol, the amplified samples were kept or stored at -20°C in a light-protected box.

The amplicons were visualized using the ABI Prism1 3130*x*/ 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). 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.

Statistical analysis

A. Allele diversity was calculated as (Nei, 1987).

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

*Corresponding authors. E-mail: imad_dna@yahoo.com. Tel: 009647716150716.

Abbreviation: ISFG, International society of forensic genetics.

Table 1. Primer sequence, forward (F) and reverse (R) for DYS genetic loci.

DYS loci	Primer sequence (5' - 3') (Forward; F, Reverse; R)
YGATA H4	F: 5'- ATGCTGAGGAGAATTTCCAA -3' R:5'- GCTATTCATCCATCTAATCTATCCATT -3'
DYS19	F: 5'- ACTACTGAGTTTCTGTTATAGTGTTTTT -3' R: 5'- GTCAATCTCTGCACCTGGAAAT -3'
DYS385a	F: 5'- AGCATGGGTGACAGAGCTA -3' R: 5'- GCCAATTACATAGTCCTCCTTTC -3'
DYS389I	F: 5'- CCAACTCTCATCTGTATTATCTATG -3' R: 5'- GTTATCCCTGAGTAGTAGAAGAATG -3'
DYS389II	F: 5'- CCAACTCTCATCTGTATTATCTATG -3' R: 5'- GTTATCCCTGAGTAGTAGAAGAATG -3'
DYS390	F: 5'- CCAACTCTCATCTGTATTATCTATG -3' R: 5'- GTTATCCCTGAGTAGTAGAAGAATG -3'
DYS391	F: 5'- TTCATCATACACCCATATCTGTC -3' R: 5'- GATAGAGGGATAGGTAGGCAGGC -3'
DYS392	F: 5'- TAGAGGCAGTCATCGCAGTG -3' R: 5'- GACCTACCAATCCCATTCCTT -3'
DYS393	F: 5'- GTGGTCTTCTACTTGTGTCAATAC -3' R: 5'- GAACTCAAGTCCAAAAAATGAGG -3'
DYS438	F: 5'- CCAAAATTAGTGGGGAATAGTTG -3' R: 5'- GATCACCCAGGGTCTGGAGTT -3'
DYS439	F: 5'- TCGAGTTGTTATGGTTTTAGGTCT -3' R: 5'- GTGGCTTGGAATTCTTTTACCC -3'
DYS635	F: 5'- ACCAGCCCAAATATCCATCA -3' R: 5'- TGGAATGCTCTCTTGGCTTC -3'
DYS437	F: 5'- GACTATGGGCGTGAGTGCAT -3' R: 5'- GAGACCCTGTCATTCACAGATGA -3'
DYS448	F: 5'- TGGGAGAGGCAAGGATCCAA -3' R: 5'- GTCATATTTCTGGCCGGTCTGG -3'
DYS456	F: 5'- GAGGAATCTGACACCTCTGACA -3' R: 5'- GTCCATATCATCTATCCTCTGCCTA -3'
DYS458	F: 5'- GCAACAGGAATGAAACTCCAAT -3' R: 5'- GTTCTGGCATTACAAGCATGAG -3'

Where, *n* is the sample size and *pi* is the frequency of the *i*th allele.

B. Standard error (SE): The standard error (SE) of allele frequencies was calculated as:

$$SE(p_i) = \sqrt{[(1 - p_i)\, p_i]/N},$$

Where, *pi* denotes the frequency of the *ith* allele at any given locus and N equals the total number of individuals screened at this locus.

RESULTS AND DISCUSSION

Based on Y-chromosome database (http://www.smgf.org, Sorenson Molecular Genealogy foundation), DYS19 is STR consisting 10 alleles with 7 to 15 repeats of TAGA motif, DYS385a/b is STR consisting 22 alleles with 7 to 23 repeats of GAAA motif, DYS389I is STR consisting 9 alleles with 6 to 13 repeats of TCTG motif, DYS389II is

Table 2. Allelic frequencies of (YGATA H4, DYS19, DYS385a, DYS385b, DYS389I, DYS389II, DYS390, DYS391 and DYS392) genetic loci observed in 100 Iraqi males patients with prostate cancer.

Alleles	YGATA H4		DYS19		DYS385a		DYS385b		DYS389I		DYS389II		DYS390		DYS391		DYS392	
	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	lociS.E.
8	·	·	·	·	·	·	·	·	·	·	·	·	·	·	0.09	0.03	·	·
9	·	·	·	·	·	·	·	·	·	·	·	·	·	·	0.06	0.02	·	·
10	0.15	0.04	·	·	·	·	·	·	·	·	·	·	·	·	0.66	0.08	·	·
11	0.23	0.05	·	·	0.13	0.03	·	·	·	·	·	·	·	·	0.13	0.03	0.58	0.08
12	0.41	0.06	·	·	0.03	0.02	·	·	0.15	0.04	·	·	·	·	0.06	0.02	0.16	0.04
13	0.1	0.03	0.28	0.05	0.47	0.07	0.07	0.03	0.39	0.06	·	·	·	·	·	·	0.16	0.04
14	0.11	0.03	0.11	0.03	0.09	0.03	0.31	0.06	0.46	0.07	·	·	·	·	·	·	0.1	0.03
15	·	·	0.45	0.07	0.04	0.02	0.02	0.01	·	·	·	·	·	·	·	·	·	·
16	·	·	0.11	0.03	0.09	0.03	0.1	0.03	·	·	·	·	·	·	·	·	·	·
17	·	·	0.05	0.02	0.05	0.02	0.15	0.04	·	·	·	·	·	·	·	·	·	·
18	·	·	·	·	0.1	0.03	0.1	0.03	·	·	·	·	·	·	·	·	·	·
19	·	·	·	·	0.13	0.03	0.2	0.04	·	·	·	·	·	·	·	·	·	·
20	·	·	·	·		·	0.05	0.02	·	·	·	·	·	·	·	·	·	·
21	·	·	·	·		·	·	·	·	·	·	·	0.12	0.03	·	·	·	·
22	·	·	·	·		·	·	·	·	·	·	·	0.21	0.04	·	·	·	·
23	·	·	·	·		·	·	·	·	·	·	·	0.06	0.02	·	·	·	·
24	·	·	·	·		·	·	·	·	·	·	·	0.48	0.07	·	·	·	·
25	·	·	·	·		·	·	·	·	·	·	·	0.23	0.04	·	·	·	·
28	·	·	·	·		·	·	·	·	·	0.1	0.03	·	·	·	·	·	·
29	·	·	·	·		·	·	·	·	·	0.41	0.07	·	·	·	·	·	·
30	·	·	·	·		·	·	·	·	·	0.28	0.05	·	·	·	·	·	·
31	·	·	·	·		·	·	·	·	·	0.13	0.03	·	·	·	·	·	·
32	·	·	·	·		·	·	·	·	·	0.02	0.01	·	·	·	·	·	·
33	·	·	·	·		·	·	·	·	·	0.06	0.02	·	·	·	·	·	·
D		0.991		0.99		0.971		0.99		0.98		0.99		0.991		0.991		0.989

S.E., Standard error; F., allelic frequencies.

STR consisting 11 alleles with 24 to 34 repeats of TCTG motif, DYS390 is STR consisting 12 alleles with 17 to 28 repeats of TCTG motif, DYS391 is STR consisting 9 alleles with 6 to 14 repeats of TCTA motif, DYS392 is STR consisting 11 alleles with 6 to 17 repeats of TAT motif, DYS393 is STR consisting nine alleles with 9 to 17 repeats of AGAT motif, DYS437 is STR consisting five alleles with 13 to 17 repeats of TCTA motif, DYS4 is STR consisting 9 alleles with 6 to 14 repeats of TTTTC motif, DYS439 is STR consisting 6 alleles with 9 to 14 repeats of GATA motif, DYS448 is STR consisting 10 alleles with 17 to 24 repeats of AGAGAT motif, YGATA H4 is STR consisting 6 alleles with 8 to 13 repeats of TAGA motif [18,19], DYS437 is a tetra-nucleotide STR consisting 8 alleles with 11 to 18 repeats of TCTA motif, and DYS439 is a tetra-nucleotide STR consisting 9 alleles with 8 to 16 repeats of AGAT motif (Butler et al., 2002; Gusmao et al., 2006).

Allelic frequencies involving 17 Y-STR loci have been determined with such a necessity in a representative group of Iraq population in order to make comparisons with other populations. Seventeen (17) Y-STRs have been analyzed for diversity in 200 healthy unrelated male individuals. Observed allelic or genotype frequencies of the 17 Y-STR loci have been given in Tables 2 to 5. In this study, six alleles (20 to 25) for DYS635, three alleles (14 to 16) for DYS437, five alleles (18 to 22) for DYS448, five alleles (13 to 17) for DYS456, seven alleles (14 to 20) for DYS458, five alleles (10 to 14) for YGATA H4, three alleles (12 to 14) for DYS389I, six alleles (28 to 33) for DYS389II, five alleles (13 to 17) for DYS19, five alleles (8 to 12) for DYS391, four alleles (9 to 12) for DYS438, five alleles (21 to 25) for DYS390, six alleles (9 to 14) for DYS439, four alleles (11 to 14) for DYS392, three alleles (13 to 15) for DYS393, eight alleles (11 to 19) for DYS385a and eight alleles (13 to 20) for DYS385b were found among the whole Iraqi subjects examined.

Gene diversity values for each Y-STR loci have been given in Tables 2 to 5. Allele 10 of DYS391 or allele 13 of DYS393. It is likely that Iraqi males who belong to Y-lineages with either allele 10 or allele 13 are more susceptible to develop prostate cancer, while those belonging to lineages with allele 9 and 14 of DYS439 or allele 15 of DYS385b are more resistant to the disease. As shown in Table 6, no significant differences were observed between frequency distributions of different

Table 3. Allelic frequencies of (DYS393, DYS438, DYS439, DYS635, DYS437, DYS448, DYS456 and DYS458) genetic loci observed in 100 Iraqi males patients with prostate cancer.

Alleles	DYS393		DYS438		DYS439		DYS635		DYS437		DYS448		DYS456		DYS458	
	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.
8	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·
9	·	·	0.18	0.04	0.02	0.01	·	·	·	·	·	·	·	·	·	·
10	·	·	0.54	0.07	0.46	0.07	·	·	·	·	·	·	·	·	·	·
11	·	·	0.21	0.05	0.31	0.06	·	·	·	·	·	·	·	·	·	·
12	·	·	0.07	0.02	0.05	0.02	·	·	·	·	·	·	·	·	·	·
13	0.62	0.08	·		0.15	0.04	·	·	·	·	·	·	0.09	0.03	·	·
14	0.21	0.05	·		0.01	0.01	·	·	0.42	0.06	·	·	0.06	0.02	0.04	0.02
15	0.17	0.04	·	·	·	·	·	·	0.27	0.06	·	·	0.51	0.07	0.33	0.06
16	·	·	·	·	·	·	·	·	0.31	0.06	·	·	0.23	0.05	0.11	0.03
17	·	·	·	·	·	·	·	·	·	·	·	·	0.11	0.04	0.14	0.04
18	·	·	·	·	·	·	·	·	·	·	0.29	0.06	·	·	0.08	0.042
19	·	·	·	·	·	·	·	·	·	·	0.46	0.07	·	·	0.1	0.04
20	·	·	·	·	·	·	0.1	0.03	·	·	0.1	0.03	·	·	0.2	0.05
21	·	·	·	·	·	·	0.06	0.02	·	·	0.1	0.03	·	·	·	·
22	·	·	·	·	·	·	0.04	0.02	·	·	0.05	0.02	·	·	·	·
23	·	·	·	·	·	·	0.31	0.06	·	·	·	·	·	·	·	·
24	·	·	·	·	·	·	0.39	0.06	·	·	·	·	·	·	·	·
25	·	·	·	·	·	·	0.1	0.03	·	·	·	·	·	·	·	·
26	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·
28	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·
30	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·
31	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·
33	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·
D		0.985		0.991		0.989		0.99		0.989		0.989		0.989		0.989

S.E., Standard error; F., allelic frequencies.

Table 4. Allelic frequencies of (YGATA H4, DYS19, DYS385a, DYS385b, DYS389I, DYS389II, DYS390, DYS391 and DYS392) genetic loci observed in 100 Iraqi males patients without prostate cancer.

	YGATA H4		DYS19		DYS385a		DYS385b		DYS389I		DYS389II		DYS390		DYS391		DYS392	
	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.
8	·	·	·	·	·	·	·	·	·	·	·	·	·	·	0.08	0.03	·	·
9	·	·	·	·	·	·	·	·	·	·	·	·	·	·	0.09	0.03	·	·
10	0.13	0.04	·	·	·	·	·	·	·	·	·	·	·	·	0.71	0.08	·	·
11	0.21	0.05	·	·	0.11	0.03	·	·	·	·	·	·	·	·	0.05	0.02	0.53	0.07
12	0.4	0.06	·	·	0.05	0.02	·	·	0.13	0.03	·	·	·	·	0.07	0.03	0.18	0.04
13	0.12	0.03	0.13	0.04	0.44	0.06	0.1	0.03	0.42	0.06	·	·	·	·	·	·	0.16	0.04
14	0.14	0.04	0.14	0.04	0.09	0.03	0.27	0.05	0.45	0.06	·	·	·	·	·	·	0.13	0.04
15	·	·	0.51	0.07	0.07	0.03	0.03	0.02	·	·	·	·	·	·	·	·	·	·
16	·	·	0.14	0.04	0.11	0.03	0.08	0.03	·	·	·	·	·	·	·	·	·	·
17	·	·	0.08	0.03	0.05	0.03	0.16	0.04	·	·	·	·	·	·	·	·	·	·
18	·	·	·	·	0.07	0.02	0.11	0.03	·	·	·	·	·	·	·	·	·	·
19	·	·	·	·	0.11	0.03	0.16	0.04	·	·	·	·	·	·	·	·	·	·
20	·	·	·	·		·	0.09	0.03	·	·	·	·	·	·	·	·	·	·
21	·	·	·	·		·	·	·	·	·	·	·	0.16	0.04	·	·	·	·
22	·	·	·	·		·	·	·	·	·	·	·	0.17	0.04	·	·	·	·
23	·	·	·	·		·	·	·	·	·	·	·	0.08	0.03	·	·	·	·
24	·	·	·	·		·	·	·	·	·	·	·	0.5	0.06	·	·	·	·

Table 4. Contd.

25	·	·	·	·	·	·	·	·	·	·	0.09	0.03	·	·	·	·		
28	·	·	·	·	·	·	·	·	·	0.07	0.03	·	·	·	·	·	·	
29	·	·	·	·	·	·	·	·	·	0.43	0.06	·	·	·	·	·	·	
30	·	·	·	·	·	·	·	·	·	0.31	0.06	·	·	·	·	·	·	
31	·	·	·	·	·	·	·	·	·	0.11	0.03	·	·	·	·	·	·	
32	·	·	·	·	·	·	·	·	·	0.05	0.02	·	·	·	·	·	·	
33	·	·	·	·	·	·	·	·	·	0.03	0.01	·	·	·	·	·	·	
D		0.989		0.97	0.99		0.991		0.99		0.991		0.99		0.988		0.989	

S.E., Standard error; F., allelic frequencies

Table 5. Allelic frequencies of (DYS393, DYS438, DYS439, DYS635, DYS437, DYS448, DYS456 and DYS458) genetic loci observed in 100 Iraqi males patients without prostate cancer.

Alleles	DYS393		DYS438		DYS439		DYS635		DYS437		DYS448		DYS456		DYS458	
	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.	F.	S.E.
8	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·
9	·	·	0.22	0.05	0.01	0.01	·	·	·	·	·	·	·	·	·	·
10	·	·	0.57	0.08	0.48	0.06	·	·	·	·	·	·	·	·	·	·
11	·	·	0.17	0.04	0.32	0.05	·	·	·	·	·	·	·	·	·	·
12	·	·	0.04	0.02	0.02	0.01	·	·	·	·	·	·	·	·	·	·
13	0.6	0.08	·	·	0.15	0.04	·	·	·	·	·	·	0.09	0.03	·	·
14	0.22	0.05	·	·	0.01	0.01	·	·	0.42	0.06	·	·	0.06	0.02	0.03	0.01
15	0.18	0.04	·	·	·	·	·	·	0.27	0.05	·	·	0.51	0.06	0.37	0.06
16	·	·	·	·	·	·	·	·	0.31	0.04	·	·	0.23	0.05	0.12	0.03
17	·	·	·	·	·	·	·	·	·	·	·	·	0.11	0.03	0.1	0.03
18	·	·	·	·	·	·	·	·	·	·	0.29	0.05	·	·	0.07	0.03
19	·	·	·	·	·	·	·	·	·	·	0.46	0.06	·	·	0.09	0.03
20	·	·	·	·	·	·	0.08	0.03	·	·	0.1	0.03	·	·	0.22	0.05
21	·	·	·	·	·	·	0.07	0.03	·	·	0.1	0.03	·	·	·	·
22	·	·	·	·	·	·	0.05	0.02	·	·	0.05	0.02	·	·	·	·
23	·	·	·	·	·	·	0.32	0.05	·	·	·	·	·	·	·	·
24	·	·	·	·	·	·	0.41	0.06	·	·	·	·	·	·	·	·
25	·	·	·	·	·	·	0.07	0.03	·	·	·	·	·	·	·	·
26	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·
28	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·
30	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·
31	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·
33	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·	·
D		0.989		0.98		0.991		0.99		0.992		0.991		0.991		0.99

S.E., Standard error; F., allelic frequencies.

alleles of DYS635, DYS437, DYS448, DYS456, DYS458, YGATA H4, DYS389I, DYS389II, DYS19, DYS438, DYS439, DYS392, DYS385a and DYS385b loci among cases and controls.

In another study, Y-lineages of prostate cancer patients and healthy control individuals were determined for four ethnic groups living in Hawaii and California. They found one lineage, belonging to the Japanese group in the study, associated with a statistically significant predisposition to develop prostate cancer (Paracchini et al., 2003).

On the other hand, males who had either allele 3 of DYS391 or allele 25 of DYS390 showed a significantly higher risk to develop prostate cancer. These findings are consistent with those reported by Ewis et al. (2002) and Paracchini et al. (2003) which support the hypothesis that males from different Y-chromosomal origins are different concerning their susceptibility or resistance to develop prostate cancer.

In another study conducted by the current study group on Iranian population regarding comparison of Y-haplotype

Table 6. Comparison between patients and controls based on its number and frequency.

DYS loci	Allele	Patient		Control	
		No.	Freq.	No.	Freq.
YGATA H4	10	15	0.15	13	0.13
	11	23	0.23	21	0.21
	12	41	0.41	40	0.4
	13	10	0.1	12	0.12
	14	11	0.11	14	0.14
DYS19	13	28	0.28	13	0.13
	14	11	0.11	14	0.14
	15	45	0.45	51	0.51
	16	11	0.11	14	0.14
	17	5	0.05	8	0.08
DYS385a	11	13	0.13	11	0.11
	12	3	0.03	5	0.05
	13	47	0.47	44	0.44
	14	9	0.09	9	0.09
	15	4	0.04	7	0.07
	16	9	0.09	11	0.11
	17	5	0.05	5	0.05
	19	10	0.1	7	0.07
DYS385b	13	7	0.07	10	0.1
	14	31	0.31	27	0.27
	15	2	0.02	3	0.03
	16	10	0.1	8	0.08
	17	15	0.15	16	0.16
	18	10	0.1	11	0.11
	19	20	0.2	16	0.16
	20	5	0.05	9	0.09
DYS389I	12	15	0.15	13	0.13
	13	39	0.39	42	0.42
	14	46	0.46	45	0.45
DYS389II	28	10	0.1	7	0.07
	29	41	0.41	43	0.43
	30	28	0.28	31	0.31
	31	13	0.13	11	0.11
	32	2	0.02	5	0.05
	33	6	0.06	3	0.03
DYS390	21	12	0.12	16	0.16
	22	21	0.21	17	0.17
	23	6	0.06	8	0.08
	24	48	0.48	50	0.5
	25	23	0.23	9	0.09
DYS635	20	10	0.1	8	0.08
	21	6	0.06	7	0.07
	22	4	0.04	5	0.05
	23	31	0.31	32	0.32

Table 6. Contd.

	24	39	0.39	41	0.41
	25	10	0.1	7	0.07
DYS391	8	9	0.09	8	0.08
	9	6	0.06	9	0.09
	10	66	0.66	71	0.71
	11	13	0.13	5	0.05
	12	6	0.06	7	0.07
DYS392	11	58	0.58	53	0.53
	12	16	0.16	18	0.18
	13	16	0.16	16	0.16
	14	10	0.1	13	0.13
DYS393	13	62	0.62	60	0.6
	14	21	0.21	22	0.22
	15	17	0.17	18	0.18
DYS438	9	18	0.18	22	0.22
	10	54	0.54	57	0.57
	11	21	0.21	17	0.17
	12	7	0.07	4	0.04
DYS439	9	2	0.02	1	0.01
	10	46	0.46	48	0.48
	11	31	0.31	32	0.32
	12	5	0.05	2	0.02
	13	15	0.15	15	0.15
	14	1	0.01	1	0.01
DYS437	14	42	0.42	42	0.42
	15	27	0.27	27	0.27
	16	31	0.31	31	0.31
DYS448	18	29	0.29	29	0.29
	19	46	0.46	46	0.46
	20	10	0.1	10	0.1
	21	10	0.1	10	0.1
	22	5	0.05	5	0.05
DYS456	13	9	0.09	9	0.09
	14	6	0.06	6	0.06
	15	51	0.51	51	0.51
	16	23	0.23	23	0.23
	17	11	0.11	11	0.11
DYS458	14	4	0.04	3	0.03
	15	33	0.33	37	0.37
	16	11	0.11	12	0.12
	17	14	0.14	10	0.1
	18	8	0.08	7	0.07
	19	10	0.1	9	0.09
	20	20	0.2	22	0.22

lineages of prostate cancer patients and healthy control individuals comprising DYS388, DYS435, DYS437 and DYS439 loci, it was revealed that some haplotypes had higher frequency among Iranian patients than controls (unpublished data).

In a study done by Kim et al. (2007) on Korean populations of prostate cancer patients and healthy controls using Y-chromosomal binary loci, no significant difference was observed in distribution of Y-haplogroup frequencies among Korean case and control groups. Ewis et al. (2002) compared allele frequency distribution of DYS19 in Japanese prostate cancer patients and healthy controls. Based on their findings, males with allele C (194 bp) of DYS19 were more susceptible to develop prostate cancer.

Conclusion

There are some DYS lineages among Iraqi populations with significantly different allelic frequencies between prostate cancer and healthy control people, indicating that belonging to these lineages would potentially increase the level of susceptibility or resistance to prostate cancer. It is likely that Iraqi males who belong to Y-lineages with either allele 10 of DYS391 or allele 13 of DYS393 are more susceptible to develop prostate cancer.

Declaration of interest

The authors have declared that no competing interest exists.

REFERENCES

Ameera OH, Muhanned AK, Imad HH (2015). Analysis of mtDNA hypervariable region II for increasing the discrimination power from middle and south of Iraq. African J. of Biotechnology. 14(10): 843-850.

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.

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 (2002). A Novel multiplex for simultaneous amplification of 20 Y-chromosome STR markers. Forensic Sci. Int. 129:10-24.

Carolina N, Miriam B, Cecilia S, Yolanda C, Jianye G, Bruce B (2010). Reconstructing the population history of Nicaragua by means of mtDNA, Y-chromosome STRs and autosomal STR markers. Am. J. Phys. Anthropol. 143(4): 591-600.

Gill P, Brenner C, Brinkmann B, Budowle B, Carracedo A, Jobling MA (2001). DNA Commission of the International Society of Forensic Genetics: recommendations on forensic analysis using Y-chromosome STRs. Forensic Sci. Int. 124: 5-10.

Gleason DF, Mellinger GT (1974). Prediction of prognosis for prostatic adenocarcinoma by combined histological grading and clinical staging. J. Urol. 111:58-64.

Gusmao L, Butler JM, Carracedo A (2006). 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. 157:187-197.

Ellegren H (2004). Microsatellites: simple sequences with complex evolution. Nat. Rev. Genet. 5: 435-445.

Ewis AA, Lee J, Naroda T (2006). Prostate cancer incidence varies among males from different Y-chromosome lineages. Prostate Cancer. 9:303-309.

Ewis AA, Lee J, Naroda T (2002). Linkage between prostate cancer incidence and different alleles of the human Y-linked tetranucleotide polymorphism DYS19. J. Med. Invest. 49:56-60.

Hayes VM, Serveri G, Eggleton SA, Padilla EJ, Southey MCSutherland RL, Hopper JL (2005). The E11 G>A androgen receptor polymorphism is associated with a decreased risk metastatic prostate cancer and androgenic alopecia. Cancer Epidemol. Biomarkers Prev. 14: 993-6.

Jemal A, Siegel R, Ward E, Murray T, Thun MJ (2006). Cancer statistics. CA Cancer J. Clin. 56:106-30.

Kim W, Yoo TK, Kim SJ (2007). Lack of association between Y-chromosomal haplogroups and prostate cancer in the Korean population. PLOS ONE. 2(1): e172. doi:10.1371/journal.pone.0000172

Kimpton CP, Oldroyd NJ, Watson SK, Frazier RR, Johnson PE, Millican ES, Urquhart A, Sparkes BL, Gill P (1996). Validation of highly discriminating multiplex short tandem repeat amplification systems for individual identification. Electrophoresis. 17:1283-1293.

Kwak KD, Jin HJ, Shin DJ, Kim JM, Roewer L, Krawczak M (2005). Y-Chromosomal STR Haplotypes and Their Applications in Forensic and Population Studies in East Asia. Int. J. Leg. Med. 119(4):195-201.

Mohammed A, Imad H (2013). Autosomal STR: From locus information to next generation sequencing technology. Res. J. Biotechnol. 8(10):92-105.

Mohammed AJ, Imad HH, Muhanned AK (2015). Detection of New Variant “Off-ladder” at the (D12S391, D19S433 and D1S1656 loci) and Tri-allelic Pattern at the D16S539 Locus in a 21 Locus Autosomal Short Tandem Repeat Database of 400 Iraqi Individuals. Afr. J. Biotechnol. 14(5): 375-399.

Muhanned AK, Ameer IA, Imad HH, Mohammed AJ (2015a). A New Polymorphic Positions Discovered in Mitochondrial DNA Hypervariable Region HVIII From Central and North-Central of Iraq. Mitochondrial DNA. 1–5.

Muhanned AK, Mohammed AJ, Imad HH (2015b) Allele frequency present within the DYS635, DYS437, DYS448, DYS456, DYS458, YGATA H4, DYS389I, DYS389II, DYS19, DYS391, DYS438, DYS390, DYS439, DYS392, DYS393, DYS385a and DYS385b of unrelated individuals in Iraq. Afr. J. of Biotechnol. 14(10): 851-858.

Nei M (1987). Molecular Evolutionary Genetics, Columbia University Press, New York.

Paracchini S, Pearce CL, Kolonel LN (2003). A Y chromosomal influence on prostate cancer risk: the multiethnic cohort study. J. Med. Genet.40:815-819.