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Pitout JDD, Church DL, Gregson DB, Chow BL, McCracken M, Mulvey M, Laupland KB (2007). Molecular epidemiology of CTXM-producing Escherichia coli in the Calgary Health Region: emergence of CTX-M-15-producing isolates. Antimicrob. Agents Chemother. 51: 1281-1286.

Pelczar JR, Harley JP, Klein DA (1993). Microbiology: Concepts and Applications. McGraw-Hill Inc., New York, pp. 591-603.

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Table of Contents: Volume 7 Number 6 August, 2015

ARTICLES

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Full Length Research Paper

DYS459, DYS391, DYS388 and DYS19 genetic loci have high allelic frequency in patients with prostate cancer

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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 prostate cancer could be established, which could aid in the early detection of the disease which is crucial for successful treatment. The first objective of this study was detection of allele frequencies of 12 Y-chromosome short tandem repeat loci from Iraqian prostate cancer patients and normal control males. The second objective was to evaluate the importance of these loci to develop prostate cancer. Blood samples were collected from 70 patients unrelated males living in middle and south of Iraq. FTA® Technology was utilized to extract DNA from blood collected on FTA™ paper. Post PCR amplification was detected by using ABI Prism1 3130xl Genetic Analyzer 16-capillary array system, with POP-7™ Polymer and Data Collection Software, Genemapper version 3.5 software. A higher incidence of disease was found among males who had either allele 10 of DYS391 or allele 9 of DYS459. It is likely that Iraqi males who belong to Y-lineages with either allele 10 or allele 9 are more susceptible to develop prostate cancer, while those belonging to lineages with allele 17 of DYS456 and DYS19 are more resistant to the disease. This study shows the influence of genetic elements on prostate cancer, and it seems that DYS391 and DYS459 locus comprising with other loci have the potential to be used as a screening method for prediction of susceptibility to prostate cancer in Iraqi population.

Key words: DYS459, DYS391, DYS388, DYS19, high allelic frequency, prostate cancer, STR DNA typing.

INTRODUCTION

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 aware-ness for of prostate cancer is relatively law. Two classifications are used to describe prostate cancer. The Union International Contra Cancer (UICC) 2002 tumour, node, metastasis (TNM) classification is a common classifi-cation 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

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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).

Microsatellites are a group of molecular markers chosen for a number of purposes including forensics individual identification and relatedness testing polymorphic (Kimpton et al., 1996; Gill et al., 2001; Andrea et al., 2008; Imad et al., 2015). There is a high genomic abundance of random distribution throughout the genome. There is also an abundance of polymorphism (Ellegren et al., 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 persons investigations, historical investigations, some paternity testing scenarios, and genetic genealogy (Carolina et al., 2010). 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). The Y chromosome is less variable than the other chromosomes. Many markers are thus needed to obtain a high degree of discrimination between unrelated male markers (Muhanned 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 (Jemal et al., 2006; Mohammed et al., 2015), which suggest that in part the predisposition for developing prostate cancer is asso-ciated with alleles that are more prevalent in certain populations or groups. We hypothesized that there are some DYS lineages among Iraqi populations with signi-ficant different frequencies between prostate cancer and healthy control people, indicating that belonging to these lineages would potentially increase the level of suscep-tibility or resistance to prostate cancer. 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 70 patients unrelated males living in middle and south of Iraq and sent to the genetic laboratories comprising 35 men with prostate cancer and 35 healthy male individuals as control. All patients that 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

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 preferred protocol used with the GeneAmp® PCR System 9700 thermal cycler is provided below. The estimated total cycle time was 1.5 h. 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 4°C soak. After completion of the thermal cycling protocol, the amplified samples were kept or stored at -20°C in a light-protected box.

The major application of CE in forensic biology is in the detection and analysis of short tandem repeats (STRs). STR markers are preferred because of the powerful statistical analysis that is possible with these markers and the large databases that exist for convicted offenders' profiles using the ABI Prism1 3130xl 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).

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

Where, n is the sample size and pi is the frequency of the ith 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

Allelic and haplotypic frequencies involving 12 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. Twelve Y-STRs have been analyzed for diversity in 70 healthy unrelated male individuals (Table 2) and (Table 3). Observed allele or genotype frequencies of the 12 Y-STR loci have been given in Table 4 and Table 5. In this study, three alleles (12,13 and 16) for DYS446, four alleles (23-26) for DYS447, three alleles (8-10) for DYS450, eight alleles (10-17) for DYS388, two alleles (11-12) for DYS435, three alleles (14-16) for DYS437, four alleles (28-33) for DYS452, three alleles (14-16) for DYS456, three alleles (8-11) for DYS459, four alleles (13-16) for DYS19, five alleles (21-25) for DYS390, five alleles (8-12) for

Table 1. Sets of primers for amplification of Y-chromosomal STR regions.

DYS loci	Primer sequence (5' - 3') (Forward; F, Reverse; R)	Reference
DYS446	F: 5'-TATTTTCAGTCTTGTCCTGTC-3' R:5'-AAATGTATGGCCAACATAGCAAAACCA -3'	Redd et al. (2002)
DYS447	F: 5'-GGTCACAGCATGGCTTGGTT-3' R: 5'-GGGCTTGCTTTGCGTTATCT-3'	Redd et al. (2002)
DYS450	F: 5'- CCAGTGATAATTCAGATGATATG-3' R: 5'- GCCTTTCCAATTTCAATTTCTGA-3'	Redd et al. (2002)
DYS388	F: 5'- GTG AGT TAGCCG TTT AGC GA -3' R: 5'- CAG ATC GCA ACC ACTGCG -3'	Nargesi et al (2011)
DYS435	F: 5'- AGC ATC TCC ACA CAGCAC AC -3' R: 5'- TTC TCT CTC CCC CTC CTC TC -3'	Nargesi et al (2011)
DYS437	F: 5'- GAC TAT GGG CGT GAG TGCAT -3' R: 5'- AGA CCC TGT CAT TCA CAG ATG A -3'	Nargesi et al (2011)
DYS452	F: 5'- GTGGTGTTCTGATGAGGATAAT-3' R: 5'- TTTACATGATGTAGCAAATAGGTT -3'	Redd et al. (2002)
DYS456	F: 5'-GGACCTTGTGATAATGTAAGATA -3' R: 5'-CCCATCAACTCAGCCCAAAAC -3'	Redd et al. (2002)
DYS459	F: 5'-CAGGTGAACTGGGGTAAATAAT -3' R: 5'- TTGAGCAACAGAGCAAGACTTA -3'	Redd et al. (2002)
DYS19	F: 5'- ACTACTGAGTTTCTGTTATAGTGTTTTT -3' R: 5'- GTCAATCTCTGCACCTGGAAAT -3'	Designer in lab.
DYS390	F: 5'- CCAACTCTCATCTGTATTATCTATG -3' R: 5'- GTTATCCCTGAGTAGTAGAAGAATG -3'	Designer in lab.
DYS391	F: 5'- TTCATCATACACCCATATCTGTC -3' R: 5'- GATAGAGGGATAGGTAGGCAGGC -3'	Designer in lab.

Table 2. Haplotypes for the 12 Y-STR loci observed 70 Iraqi males patient with prostate cancer.

Haplotype	DYS446	DYS447	DYS450	DYS388	DYS435	DYS437	DYS452	DYS456	DYS459	DYS19	DYS390	DYS391	N	F
1	13	26	10	10	12	15	33	16	9	13	24	10	1	0.0025
2	13	26	10	14	12	15	33	16	9	13	24	10	1	0.0025
3	13	26	10	14	12	14	33	16	9	16	23	10	1	0.0025
4	13	23	10	14	12	14	31	15	9	16	24	9	1	0.0025
5	13	24	10	12	12	16	33	16	10	16	24	10	1	0.0025
6	13	25	10	12	11	16	33	16	10	13	24	10	1	0.0025
7	13	24	10	11	11	16	30	16	10	13	25	10	1	0.0025
8	13	24	10	11	11	14	30	16	10	13	24	10	1	0.0025
9	13	24	8	12	11	14	30	14	9	13	24	10	1	0.0025
10	13	24	8	12	11	14	33	14	9	13	21	10	1	0.0025
11	13	23	8	12	12	14	33	14	9	16	21	10	1	0.0025
12	13	23	8	12	12	14	28	16	9	15	21	10	1	0.0025
13	12	23	8	12	12	15	28	16	9	15	24	10	1	0.0025
14	12	26	8	12	11	14	28	16	9	15	24	12	1	0.0025
15	12	26	8	15	11	14	33	15	9	15	24	10	1	0.0025
16	12	26	9	12	11	15	33	15	9	15	24	10	1	0.0025
17	12	26	10	12	11	15	30	16	8	15	25	10	1	0.0025
18	12	26	9	13	11	14	33	16	8	15	24	10	1	0.0025
19	12	26	9	13	11	14	33	16	8	15	24	8	1	0.0025
20	12	26	9	12	11	16	28	16	8	16	24	10	1	0.0025
21	12	26	8	14	11	14	33	16	8	13	24	10	1	0.0025
22	12	26	8	14	11	14	30	16	9	13	24	10	1	0.0025
23	12	26	8	12	11	14	30	14	9	13	21	10	1	0.0025
24	13	26	10	11	11	14	33	16	9	13	24	10	1	0.0025
25	13	26	8	12	12	15	33	16	9	16	24	10	1	0.0025
26	13	26	8	12	12	14	33	16	9	15	24	8	1	0.0025
27	12	24	8	12	12	14	31	16	9	15	24	8	1	0.0025
28	12	24	8	12	12	14	33	16	9	15	24	10	1	0.0025
29	12	23	9	12	12	14	33	14	9	15	21	10	1	0.0025
30	12	23	9	12	11	16	33	16	9	15	24	10	1	0.0025
31	12	23	8	16	11	14	30	16	8	14	24	10	1	0.0025
32	12	23	8	12	11	14	33	16	8	14	24	10	1	0.0025
33	13	23	10	12	11	14	33	16	8	15	24	10	1	0.0025
34	13	23	10	12	11	14	28	16	9	15	24	10	1	0.0025

Table 2. Contd.

35	13	23	10	12	11	15	28	16	9	15	24	10	1	0.0025
36	13	23	10	11	11	15	33	16	9	14	21	10	1	0.0025
37	13	23	8	12	11	14	30	16	8	14	25	10	1	0.0025
38	13	24	8	12	11	14	30	16	9	14	25	10	1	0.0025
39	13	23	8	17	12	16	30	16	9	14	25	10	1	0.0025
40	13	23	8	12	11	16	33	14	9	13	25	10	1	0.0025
41	12	23	10	12	11	14	33	14	9	13	21	10	1	0.0025
42	12	23	10	14	11	14	28	14	9	15	25	10	1	0.0025
43	12	23	8	12	11	14	28	14	8	15	25	10	1	0.0025
44	12	23	8	13	11	14	33	16	9	15	25	10	1	0.0025
45	16	24	8	12	11	14	33	16	9	15	24	8	1	0.0025
46	13	23	10	11	11	14	33	16	9	15	22	10	1	0.0025
47	16	23	10	11	11	14	33	14	9	15	22	10	1	0.0025
48	13	23	8	11	11	14	33	14	9	13	22	10	1	0.0025
49	13	23	8	11	12	14	33	16	9	13	22	10	1	0.0025
50	16	23	8	11	12	16	30	16	9	13	22	11	1	0.0025
51	13	26	8	11	11	14	30	16	9	15	22	11	1	0.0025
52	13	26	8	11	11	14	33	16	9	15	25	11	1	0.0025
53	13	26	10	11	11	14	28	14	9	15	25	10	1	0.0025
54	13	26	10	11	11	15	28	14	9	15	25	10	1	0.0025
55	13	26	10	11	11	14	28	14	9	15	25	10	1	0.0025
56	13	26	10	11	12	14	28	16	9	13	25	10	1	0.0025
57	13	26	10	11	12	14	33	16	9	13	22	10	1	0.0025
58	13	24	8	11	11	14	28	16	9	13	22	10	1	0.0025
59	13	26	8	11	11	14	33	16	9	15	25	11	1	0.0025
60	13	26	8	11	11	15	30	16	9	13	25	10	1	0.0025
61	13	23	8	11	11	14	33	16	9	15	25	11	1	0.0025
62	13	26	8	11	11	14	28	16	9	15	25	10	1	0.0025
63	13	23	8	11	11	15	28	16	9	15	25	10	1	0.0025
64	13	23	8	11	11	15	28	16	9	15	22	10	1	0.0025
65	13	23	8	11	11	15	28	16	9	13	22	11	1	0.0025
66	12	23	8	11	11	14	33	14	9	15	22	11	1	0.0025
67	12	23	8	11	11	14	33	16	9	15	22	11	1	0.0025
68	12	23	8	11	11	14	33	16	9	13	22	10	1	0.0025
69	16	23	8	11	11	14	33	16	9	13	22	10	1	0.0025
70	12	23	8	11	11	14	33	16	9	15	22	10	1	0.0025

Table 3. Haplotypes for the 12 Y-STR loci observed 70 Iraqi males control without prostate cancer.

Haplotype	DYS446	DYS447	DYS450	DYS388	DYS435	DYS437	DYS452	DYS456	DYS459	DYS19	DYS390	DYS391	N	F
1	13	23	8	12	12	16	33	16	9	14	23	12	1	0.0025
2	13	23	8	12	12	14	33	16	9	14	21	12	1	0.0025
3	16	23	8	12	11	14	33	16	9	14	21	9	1	0.0025
4	16	23	8	12	11	14	33	16	9	13	21	9	1	0.0025
5	13	26	9	12	11	14	33	16	9	13	21	10	1	0.0025
6	13	25	8	12	12	14	33	14	9	15	25	10	1	0.0025
7	12	25	10	14	12	14	31	14	10	15	25	10	1	0.0025
8	12	24	10	14	12	14	28	16	10	15	25	10	1	0.0025
9	12	24	10	14	12	14	28	16	9	15	24	10	1	0.0025
10	12	24	10	14	12	16	28	16	9	15	24	10	1	0.0025
11	13	24	8	12	11	16	28	16	9	15	24	10	1	0.0025
12	13	26	9	12	11	14	33	17	9	15	24	10	1	0.0025
13	13	26	8	12	12	14	33	16	9	15	23	10	1	0.0025
14	16	23	8	10	12	14	33	15	9	15	23	10	1	0.0025
15	13	26	8	10	12	15	28	15	9	15	24	9	1	0.0025
16	13	26	8	12	12	15	28	15	9	15	24	9	1	0.0025
17	13	25	8	12	12	15	28	16	9	17	24	10	1	0.0025
18	12	26	8	12	12	15	33	14	9	17	21	10	1	0.0025
19	12	26	8	13	12	15	33	16	9	15	24	10	1	0.0025
20	13	24	8	12	12	14	33	16	9	15	24	10	1	0.0025
21	13	24	9	12	12	14	30	16	9	14	24	10	1	0.0025
22	13	23	9	12	11	14	30	14	8	14	24	10	1	0.0025
23	16	23	8	12	11	14	33	16	8	14	24	10	1	0.0025
24	16	23	8	10	11	14	33	16	9	14	24	10	1	0.0025
25	16	26	8	12	12	16	28	16	9	15	24	10	1	0.0025
26	13	25	8	12	12	14	28	17	9	15	25	10	1	0.0025
27	13	26	8	17	12	14	33	16	9	15	24	10	1	0.0025
28	13	26	8	17	12	15	33	16	9	15	24	10	1	0.0025
29	12	26	8	12	12	14	33	16	9	15	24	10	1	0.0025
30	13	24	8	12	12	14	33	16	8	15	24	10	1	0.0025
31	12	24	10	12	12	14	30	16	9	15	24	10	1	0.0025
32	12	26	10	17	12	14	33	14	9	13	24	10	1	0.0025
33	12	26	10	12	12	15	33	16	9	13	24	10	1	0.0025
34	13	25	10	12	12	14	28	16	9	16	24	10	1	0.0025

Table 3. Contd.

35	13	26	10	12	12	14	33	16	9	16	24	10	1	0.0025
36	13	23	10	11	12	14	33	16	9	16	24	10	1	0.0025
37	16	23	10	12	11	14	30	16	9	16	21	10	1	0.0025
38	13	23	10	12	12	14	33	16	9	13	21	10	1	0.0025
39	13	23	8	12	11	14	33	16	9	13	21	10	1	0.0025
40	13	23	8	11	12	14	28	16	9	13	21	10	1	0.0025
41	13	23	8	11	12	14	28	16	9	13	21	10	1	0.0025
42	13	26	8	12	12	14	33	16	9	15	21	10	1	0.0025
43	13	26	8	12	12	15	33	16	9	17	21	10	1	0.0025
44	13	25	8	12	12	15	33	16	9	15	21	10	1	0.0025
45	13	26	8	17	12	14	33	16	9	15	21	10	1	0.0025
46	13	24	10	15	12	14	30	15	9	16	21	8	1	0.0025
47	13	24	10	12	12	16	30	15	9	16	21	8	1	0.0025
48	16	25	10	12	11	16	33	16	9	15	21	8	1	0.0025
49	13	25	10	12	12	14	33	16	8	15	24	10	1	0.0025
50	13	25	10	12	11	14	33	16	8	15	24	10	1	0.0025
51	13	24	8	15	12	14	33	16	8	15	24	10	1	0.0025
52	13	26	8	12	12	14	28	15	9	15	24	10	1	0.0025
53	13	26	8	12	12	14	28	15	9	15	24	10	1	0.0025
54	13	26	8	12	12	14	33	15	9	15	24	10	1	0.0025
55	12	26	8	12	12	16	33	15	9	16	24	10	1	0.0025
56	12	24	8	12	12	16	33	16	9	16	21	10	1	0.0025
57	12	24	8	12	11	16	33	16	9	16	21	10	1	0.0025
58	12	26	8	12	12	16	33	16	9	15	24	10	1	0.0025
59	12	26	8	12	12	14	33	16	9	15	24	10	1	0.0025
60	13	24	10	12	12	14	33	16	8	15	24	10	1	0.0025
61	13	26	10	12	12	14	33	16	9	15	24	10	1	0.0025
62	13	23	8	16	12	14	33	16	9	15	24	10	1	0.0025
63	13	23	8	16	12	14	33	16	9	14	24	10	1	0.0025
64	13	23	8	16	12	14	33	16	9	14	24	10	1	0.0025
65	12	23	8	12	12	14	33	16	9	16	24	10	1	0.0025
66	12	23	10	12	12	16	28	16	9	16	24	10	1	0.0025
67	13	23	10	12	12	16	28	16	9	16	21	10	1	0.0025
68	12	23	10	12	12	16	28	16	9	16	21	10	1	0.0025
69	12	23	10	12	12	16	28	16	9	16	21	10	1	0.0025
70	12	26	10	12	12	16	28	16	8	16	21	10	1	0.0025

Table 4. Allele frequencies , Standard error and Genetic diversity of for the 12 Y-STR loci observed 70 Iraqi males patients with prostate cancer.

Allele	DYS446		DYS447		DYS450		DYS388		DYS435		DYS437		DYS452		DYS456		DYS459		DYS19		DYS390		DYS391	
	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.	F.	S.E.	F.	S.E.	F.	S.E.
8	-	-	-	-	0.557	0.06	-	-	-	-	-	-	-	-	-	-	0.143	0.04	-	-	-	-	0.057	0.03
9	-	-	-	-	0.086	0.03	-	-	-	-	-	-	-	-	-	-	0.8	0.07	-	-	-	-	0.014	0.01
10	-	-	-	-	0.357	0.05	0.014	0.01	-	-	-	-	-	-	-	-	0.057	0.03	-	-	-	-	0.8	0.07
11	-	-	-	-	-	-	0.071	0.03	0.729	0.06	-	-	-	-	-	-	-	-	-	-	-	-	0.114	0.03
12	0.357	0.05	-	-	-	-	0.743	0.06	0.271	0.04	-	-	-	-	-	-	-	-	-	-	-	-	0.014	0.01
13	0.571	0.06	-	-	-	-	0.043	0.02	-	-	-	-	-	-	-	-	-	-	0.329	0.05	-	-	-	-
14	-	-	-	-	-	-	0.086	0.03	-	-	0.7	0.06	-	-	0.229	0.04	-	-	0.086	0.03	-	-	-	-
15	-	-	-	-	-	-	0.014	0.01	-	-	0.186	0.04	-	-	0.043	0.02	-	-	0.5	0.06	-	-	-	-
16	0.071	0.03	-	-	-	-	0.014	0.01	-	-	0.114	0.04	-	-	0.729	0.06	-	-	0.086	0.03	-	-	-	-
17	-	-	-	-	-	-	0.014	0.01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
21	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.1	0.03	-	-
22	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.229	0.04	-	-
23	-	-	0.471	0.05	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.014	0.01	-	-
24	-	-	0.143	0.04	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.543	0.06	-	-
25	-	-	0.014	0.01	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.257	0.04	-	-
26	-	-	0.357	0.05	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
28	-	-	-	-	-	-	-	-	-	-	-	-	0.287	0.04	-	-	-	-	-	-	-	-	-	-
30	-	-	-	-	-	-	-	-	-	-	-	-	0.186	0.04	-	-	-	-	-	-	-	-	-	-
31	-	-	-	-	-	-	-	-	-	-	-	-	0.029	0.02	-	-	-	-	-	-	-	-	-	-
33	-	-	-	-	-	-	-	-	-	-	-	-	0.529	0.06	-	-	-	-	-	-	-	-	-	-

F, Frequency; S.E, Standard Error; GD: genetic diversity.

DYS391, were found among the whole Iraqi subjects examined.

As shown in Table 6, no significant differences were observed between frequency distributions of different alleles among cases and controls. This study show the influence of genetic elements on prostate cancer, and it seems that DYS391 and DYS459 locus comprising with other loci have the potential to be used as a screening method for prediction of susceptibility to prostate cancer in Iraqi population. 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., 2004). 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) and 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 lineages of prostate cancer patients and healthy control individuals comprising DYS388, DYS435, DYS437, and DYS439 loci, it was revealed that some haplotypes had higher

Table 5. Allele frequencies and genetic diversity of for the 12 Y-STR loci observed 70 Iraqi males control without prostate cancer.

Allele	DYS446		DYS447		DYS450		DYS388		DYS435		DYS437		DYS452		DYS456		DYS459		DYS19		DYS390		DYS391	
	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.	F.	S.E.	F.	S.E.	F.	S.E.
8	-	-	-	-	0.6	0.06	-	-	-	-	-	-	-	-	-	-	0.114	0.04	-	-	-	-	0.043	0.02
9	-	-	-	-	0.057	0.03	-	-	-	-	-	-	-	-	-	-	0.857	0.07	-	-	-	-	0.057	0.03
10	-	-	-	-	0.343	0.05	0.043	-	-	-	-	-	-	-	-	-	0.029	0.02	-	-	-	-	0.871	0.07
11	-	-	-	-	-	-	0.043	-	0.814	0.07	-	-	-	-	-	-	-	-	-	-	-	-	-	
12	0.271	0.04	-	-	-	-	0.714	0.06	0.186	0.04	-	-	-	-	-	-	-	-	-	-	-	-	0.029	0.04
13	0.614	0.06	-	-	-	-	0.014	0.01	-	-	-	-	-	-	-	-	-	-	0.114	0.04	-	-	-	
14	-	-	-	-	-	-	0.057	0.03	-	-	0.657	0.06	-	-	0.071	0.03	-	-	0.129	0.04	-	-	-	
15	-	-	-	-	-	-	0.029	0.01	-	-	0.129	0.04	-	-	0.129	0.04	-	-	0.589	0.06	-	-	-	
16	0.114	0.04	-	-	-	-	0.043	0.02	-	-	0.214	0.04	-	-	0.771	0.06	-	-	0.129	0.04	-	-	-	
17	-	-	-	-	-	-	0.057	-	-	-	-	-	-	-	0.029	0.04	-	-	0.043	0.02	-	-	-	
21	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.157	0.04	-	
22	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.171	0.04	-	
23	-	-	0.414	0.05	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.043	0.02	-	
24	-	-	0.171	0.04	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.571	0.06	-	
25	-	-	0.086		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.057	0.03	-	
26	-	-	0.329	0.05	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
28	-	-	-	-	-	-	-	-	-	-	-	-	0.271	0.04	-	-	-	-	-	-	-	-	-	
30	-	-	-	-	-	-	-	-	-	-	-	-	0.129	0.04	-	-	-	-	-	-	-	-	-	
31	-	-	-	-	-	-	-	-	-	-	-	-	0.014	0.01	-	-	-	-	-	-	-	-	-	
33	-	-	-	-	-	-	-	-	-	-	-	-	0.589	0.06	-	-	-	-	-	-	-	-	-	

F, Frequency; S.E, Standard Error; GD, genetic diversity.

Table 6. Comparison between patients and controls.

DYS loci	Allele	No.	Freq.	No.	Freq.
DYS446	12	25	0.357	19	0.271
	13	40	0.571	43	0.614
	16	5	0.071	8	0.114
DYS447	23	33	0.471	29	0.414
	24	10	0.143	12	0.171
	25	1	0.014	6	0.086
	26	25	0.357	23	0.329

Table 6. Contd.

DYS loci	Allele	No.	Freq.	No.	Freq.
DYS450	8	39	0.557	42	0.6
	9	6	0.086	4	0.057
	10	25	0.357	24	0.343
DYS388	10	1	0.014	3	0.043
	11	5	0.071	3	0.043
	12	52	0.743	50	0.714
	13	3	0.043	1	0.014
	14	6	0.086	4	0.057
	15	1	0.014	2	0.029
	16	1	0.014	3	0.043
	17	1	0.014	4	0.057
DYS435	11	51	0.729	57	0.814
	12	19	0.271	13	0.186
DYS437	14	49	0.7	46	0.657
	15	13	0.186	9	0.129
	16	8	0.114	15	0.214
DYS452	28	18	0.287	19	0.271
	30	13	0.186	9	0.129
	31	2	0.029	1	0.014
	33	37	0.529	41	0.589
DYS456	14	16	0.229	5	0.071
	15	3	0.043	9	0.129
	16	51	0.729	54	0.771
	17	0	0	2	0.029
DYS459	8	10	0.143	8	0.114
	9	56	0.8	60	0.857
	10	4	0.057	2	0.029
DYS19	13	23	0.329	8	0.114
	14	6	0.086	9	0.129
	15	35	0.5	41	0.589
	16	6	0.086	9	0.129
	17	0	0	3	0.043

Table 6. Contd.

DYS loci	Allele	No.	Freq.	No.	Freq.
	21	7	0.1	11	0.157
	22	16	0.229	12	0.171
DYS390	23	1	0.014	3	0.043
	24	38	0.543	40	0.571
	25	18	0.257	4	0.057
	8	4	0.057	3	0.043
	9	1	0.014	4	0.057
DYS391	10	56	0.8	61	0.871
	11	8	0.114	0	0
	12	1	0.014	2	0.029

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

Conflict of interest

The authors have declared that no competing interest exists.

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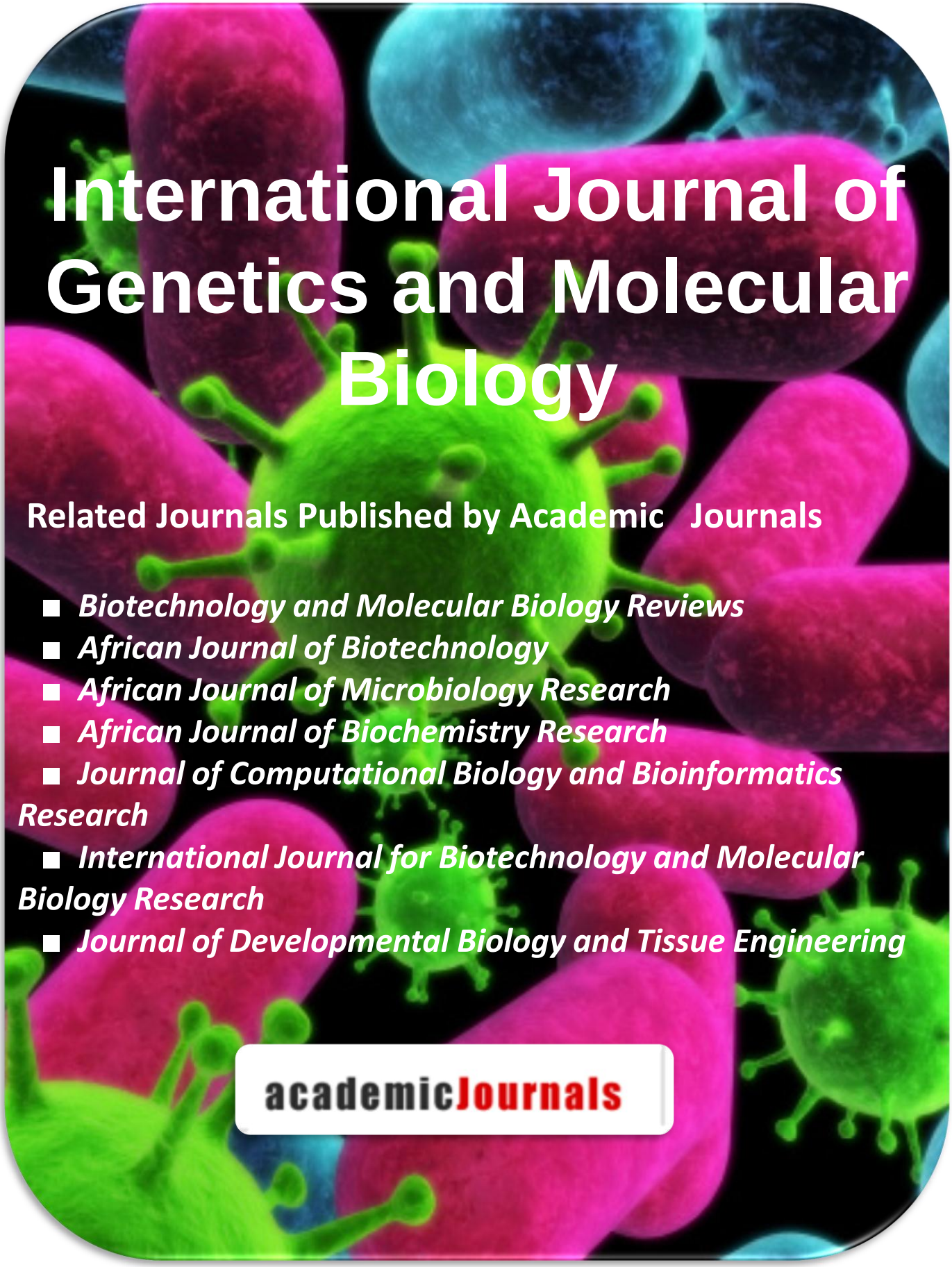

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