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GENETIC ANALYSIS OF DXS10074 SHORT TANDEM REPEAT (X-STR) IN SAMPLES OF ARAB IRAQI MALE POPULATION

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ABSTRACT

X-chromosomal short tandem repeats (X-STRs) have proven to be informative and particular role in complex relationship testing. In this present study demonstrates and investigate the allele frequency and forensic efficiency parameters for 200 healthy unrelated Arabic, Iraqi males for the microsatellite marker DXS10074 this marker located within a 280-kb region at Xq12 and provide stable allele useful for forensic application.

***Keywords*:** short tandem repeat, X-chromosome, kinship testing

Introduction

In recent years, X-chromosome microsatellites have appeared in forensic science and other forensic cases as an effective technique (Szibor *et al*., 2003). Because fathers pass on the same X-chromosome to all their children, in cases of deficiency, these markers are of significant benefit (Zarrabeitia *et al*., 2006). That is because of the unusual nature of inheritance of the X-chromosome. Females inherit one of two X-chromosomes from their mother, the other from their father, while males inherit the only X-chromosome from their mother (Ott, 1999). In assessing relationships and kinship testing between fathers and daughters, the use of STRs in the X chromosome (X-STR) application is highly effective because it enhances the power of discrimination and the possibility of exclusion from paternity as long as autosomal STR is evaluated alone (Prieto-Fernández *et al*., 2015).

Material and Methods

Genomic DNA extraction from blood samples from 200 healthy unrelated Arabic from Baghdad city, Iraqi males was carried out by commercial kit ReliaPrep™ Blood gDNA Miniprep System (Promega, Madison, USA). The PCR reaction mix (12.5 ml reaction volume) contained besides the primers GoTaq® Green Master Mix, 2X: GoTaq® (Promega, Madison, USA). DNA Polymerase is supplied in 2X Green GoTaq® Reaction Buffer (pH 8.5), 400µM dATP, 400µM dGTP, 400µM dCTP, 400µM dTTP and 3mM MgCl2. DNA concentration was 1-10 ng/ µl. and the final concentration of primer was 5pmol. X-STR was amplified at an annealing temperature of 58 ℃. The following PCR protocol was used: an initial denaturation and activation step of 12 min at 95°C was followed by 30 cycles of 1 min at 95 °C, 1 min on the annealing temperature and1 min at 72 °C, and a 30 min final elongation. Twelve microliters Hi-Di formamide (Applied Biosystems) and 0.5 µl GeneScan-500 LIZ internal size standard were added to each 1 µl PCR product. Electrophoresis was performed using the ABI PRIZM 310 Genetic Analyzer (Applied Biosystems). Fragment sizes were automatically determined using the Genes Scan Analysis software 3.1 (Applied Biosystems), and results were analyzed using the Geneious Prime software. PCR amplification was performed using the following primer DXS10074 locus. F ACTTCCTACTGCCCCACCTT NED

R GTTTCCCCTCAGAGAGCTGACACA

Statistical analysis

The polymorphism information content (PIC) and as suggested by Botstein *et al*. (1980). The power of discrimination in male (PD) and mean exclusion (MEC) was calculated according to Krüger *et al*. (1968). and Kishida *et al*. (1997). The alleles frequencies were calculated by *SPSS* Statistics 20.0 software. Power of Exclusion (PE), Polymorphism Information Content (PIC), Mean Exclusion Chance (MEC) and Power of Discrimination (PD) calculations were performed using http://www.chrx-str.org/.

Results

Fig.1.shows the DXS10074 allele frequencies of 200 healthy unrelated Arabic, Iraqi male sample calculated separately for males whereby 11alleles were identified with length variation which increased in size by 4 bp-increments ranging from 171-227 bp while in previous studies perform on male Germany mention by Hering *et al*. (2006) suggest this marker have 14 allele and rang length ranging from 165-227pb. The polymorphic region is formed by one block

consisting of variable numbers of tetranucleotide repeat motifs, i.e. (AAGA).

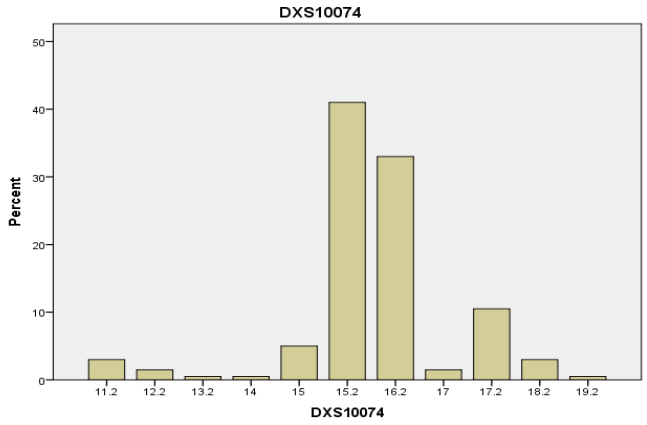

Fig. 1 : The percent distribution of alleles of DXS10074marker

Forensic efficiency parameter of DXS10074 power discrimination (PD) was 0.70715, Polymorphism Information Content (PIC) was 0.661635 Power of Exclusion (PE) was 0.439408.

Discussion

DXS10074 is located in located within a 280-kb region at Xq12 other studies mention this marker located with (DXS10079 and DXS10075) on the same region on X-chromosome mention by Castañeda *et al*. (2012) suggest that DXS10074 marker inherited as cluster with other two markers and stability towards mutation and haplotype stability make this marker appropriate for forensic application especially in complex kinship testing.

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