



## Haplotype data for the 12 RM Y-STR loci in a Syrian population

Mustafa Ay<sup>a</sup>, Ayse Serin<sup>a,b,\*</sup>, Husniye Canan<sup>a</sup>, Necmi Cekin<sup>a,b</sup>

<sup>a</sup> Cukurova University, Institute of Addiction and Forensic Sciences, Department of Forensic Sciences, Adana, Turkey

<sup>b</sup> Cukurova University, Faculty of Medicine, Department of Forensic Medicine, Adana, Turkey



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### ABSTRACT

Researches with RM Y-STRs have shown that these loci provide substantially higher haplotype diversity and haplotype discrimination capacity in worldwide populations when compared with the YSTRs commonly used in genetic forensics. The aim of this study was to develop an allelic frequency database for the Syrian population living in Turkey in order to obtain population data of 12 RM Y-STRs. A total of 80 unrelated males from the Syrian population living in Turkey were typed with 12 RM Y-STRs loci: DYF387S1, DYF399S1, DYF404S1, DYS449, DYS518, DYS526a/b, DYS547, DYS570, DYS576, DYS612, DYS626 and DYS627. The highest GD was observed for the locus DYF399S1 (0.91), followed by loci DYS449 (0.86) and DYS518 (0.83). RM Y-STR haplotype diversity was found 1.00 in these samples. Based on the results of this study, the RM YSTR loci showed remarkable haplotype resolution power in the Syrian population, high genetic diversity and, therefore, demonstrating their usefulness in forensic identification cases.

### 1. Introduction

Y-chromosomal Short Tandem Repeat (Y-STR) markers have been used for forensic purposes such as kinship analysis of male-lineage and detection of a male DNA component in a mixture of male and female DNA. However, the Y-STRs generally used in forensic sciences show low haplotype diversity in some populations and cannot distinguish between closely or distantly related males [1,2]. A recently identified set of 13 rapidly mutating (RM) Y-STRs (DYF387S1, DYF399S1, DYF403S1, DYF404S1, DYS449, DYS518, DYS526, DYS547, DYS570, DYS576, DYS612, DYS626, and DYS627) provides a substantially higher discrimination between haplotypes than other commercially available Y-STR sets and enables differentiation between closely and distantly related males [3–5].

The aim of this study was to develop an allelic frequency database for the Syrian population living in Turkey in order to obtain population data of 12 RM Y-STRs.

### 2. Materials and methods

Genomic DNA was extracted from 80 unrelated Syrian males using either silica (Qiagen, Hilden, Germany) or chelex-based (InstaGene Matrix; Bio-Rad, Hercules, CA) method.

PCR amplification of the 12 RM Y-STR loci (DYF387S1, DYF399S1, DYF404S1, DYS449, DYS518, DYS526a/b, DYS547, DYS570, DYS576,

DYS612, DYS626, and DYS627) and electrophoresis were carried out as previously described elsewhere [5].

Allele frequency calculations were carried out according to Ballantyne et al. Haplotype and gene diversity values were calculated based on Nei [6]. To investigate pairwise genetic distances among RM-YSTR population dataset, an allele frequency based approach was taken whereby Nei's  $D_A$  distances were computed and visualized using Neighbour-Joining phylogenetic tree from POPTREE software [7].

### 3. Results and discussion

A total of 80 different haplotypes were identified from 80 unrelated male individuals. Since all the 80 haplotypes were unique, HD and DC values were both calculated as one.

A total of 128 alleles were detected at 12 RM Y-STR loci. The number of alleles at each locus ranged from 7 for DYF576 to 19 for DYS399. DYF387S1, DYF399S1, and DYF404S1 often show multiple alleles and are therefore categorized as multi copy loci. As expected, the RM Y-STR loci showed high genetic diversity (GD) values. The average gene diversity was high in Syrian population (0.88). The highest GD was observed for the locus DYF399S1 (0.91), followed by loci DYS449 (0.86) and DYS518 (0.83) (Table 1) in Supplementary material.

Allele frequencies of this population were compared to relatively geographically close populations previously reported (Turkey, Greece, Czech Republic, Hungary, Slovenia, Bosnia, Croatia, Ukraine) were

\* Corresponding author at: Cukurova University, Faculty of Medicine, Department of Forensic Medicine, Adana, Turkey.

E-mail address: [ayserin@yahoo.com](mailto:ayserin@yahoo.com) (A. Serin).

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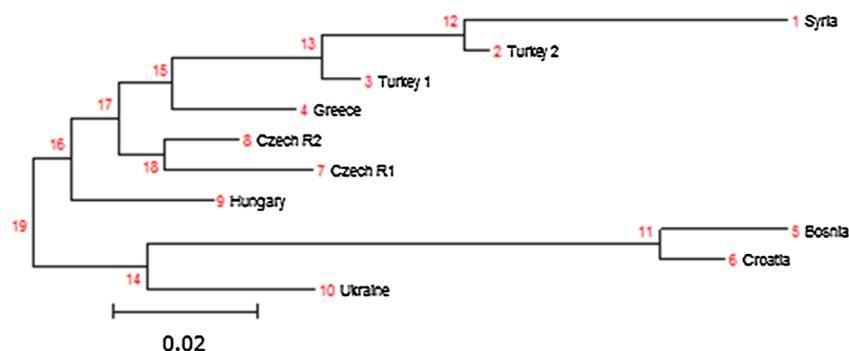


Fig. 1. Neighbor joining tree based on the population pairwise genetic distances between 10 population's data (Syria, Turkey-1 and 2, Greece, Czech Republic 1 and 2, Hungary, Bosnia, Croatia, Ukraine), generated using the POPTREE2 software.

compared for the genetic distances [3,5]. Nei's  $D_A$  genetic distances between ten populations data were estimated and visualized using Neighbor-Joining phylogenetic tree on the POPTREE software and shown at the bottom figure [7]. For these set of markers, the comparison with published data showed that the population in this study had low genetics distances values with Turkish and Greek populations that are geographically close. This figure also showed that as the geographical distance between countries increases, genetic differences also increases (Fig. 1).

#### 4. Conclusion

New RM-YSTR multiplex assay tested in this study functioned well and efficiently generated genotyping data for all 80 Syrian donors. Based on the results of this study, the RM Y-STR loci showed remarkable haplotype resolution power in the population of Syrian living in Turkey, high genetic diversity and, therefore, demonstrating their usefulness in forensic identification and parentage cases.

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#### Declaration of Competing Interest

None.

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#### Appendix A. Supplementary data

Supplementary material related to this article can be found, in the online version, at doi:10.1016/j.fsigs.2019.09.035.

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