H15 Analysis of an Additional Nine Short Tandem Repeat (STR) Loci to 15 STR Loci and the Detection of Allele Frequencies in a Cukurova Population of Turkey

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After attending this presentation, attendees will better understand the effect of the number of STR loci to the kinship analysis.

This presentation will impact the forensic science community by illustrating how the number of STR loci could be critical for the evaluation of relatives, especially close relatives.

In this presentation, discrimination power will be calculated with allele frequency distribution in nine STR loci of people who live in the Cukurova region of Turkey and the statistical significance for forensic identification and kinship analysis will be detected. The results obtained from this study will be used as a database to calculate the match probability of the individualization and kinship analysis in a statistical evaluation in a Cukurova population.

STRs are the structures with two to six base pairs in length that repeat like the heads and tails in the human genome.[1] Since the number of these structures differ among individuals, they are used in forensic individualization and kinship analysis.[2] Allele frequencies of STR loci show differences among populations. Therefore, before the use of STR loci in individualization and kinship analysis, allele frequency distribution related to the population of that locus must be determined. In an attempt to specify identification and kinship, analyses of 15 STR loci are routinely made; however, when the population number in a DNA database increases more and more in time, these standard STR loci that are determined in studies, especially between close relatives, may become inadequate.[3] In such circumstances, the usage of different STR loci in addition to this set could increase discrimination power and may possibly make forensic cases more accurate and qualified.

For the United States national database, 13 STR loci were determined as Combined DNA Index System (CODIS) markers in 1997.[4,5] With later studies in 2001, a commercial kit named Identifiler®, which consists of 15 STR loci, was produced.[5] Next, the VeriFiler™ kit, which consists of additional STR loci, was released as a commercial kit in 2013. Both commercial kits share three autosomal STR loci (D2S1338, D19S433, and THO1) and sex typing locus Amelogenin (AMEL) as internal genes.[6,7] In circumstances where the discrimination power is inadequate, additional STR loci in addition to 15 STR loci are studied.

In this study, genomic DNA samples prepared from whole blood and oral swabs taken from 100 unrelated healthy volunteers who applied for kinship analysis to the Cukurova University Department of Forensic Medicine were used to determine the allele frequencies of nine STR loci. The analysis of nine autosomal STR loci (D6S1043, D1S1656, D2S441, D10S1248, D12S391, D22S1045, THO1, D2S1338, and D19S433) and the sex typing marker AMEL within a commercial kit in addition to 15 STR loci within another commercial kit used in routine forensic cases was performed. The allele frequency 0.3 for D10S1248 with allele 14, 0.17 for D1S1656 with allele 16, 0.185 for D2S1338 with allele 17, 0.415 for D22S1045 with allele 15, 0.315 for D19S433 with allele 14, 0.25 for THO1 with allele 6, 0.345 for D2S441 with allele 11, 0.275 for D6S1043 with allele 12, and 0.19 for D12S391 with allele 19 were identified as being the most frequent. Combined power of discrimination was found to be 0.9998.

In routine cases, the paternity index remains below 10,000 with 15 STR loci. It was observed that the paternity index could be increased to more than 10,000 by an additional six new STR loci.

In conclusion, this study shows that additional STR loci provides accurate and qualified results to identify people when the discrimination power is inadequate. With this study, allele frequencies of six new (three over again) STR loci were determined in a Cukurova population for the first time.

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Allele Frequency, Cukurova Population, STR Analysis