

Haplotype Analysis of Three Combined Y-Chromosomal STR Loci in Eastern Austria

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In criminal investigations of sexual assaults and body violence crimes, as well as in paternity testing, the *polymerase chain reaction* (PCR) approach has become the method of choice since its first publication in 1987. Generally, PCR systems focus on loci located on autosomal chromosomes where genotype frequencies in human population (probability of identity, W , likelihood ratio, L , or paternity index, P_i) can be calculated by multiplying allele frequencies if genetically unlinked loci are involved. However, in special cases, e.g. mixed stains in sexual crime or deficiencies in paternity testing, the use of Y-chromosomal PCR systems may represent an alternative approach.

Up to 14 *short tandem repeat* (STR) loci on the human Y-chromosome have been investigated in a multicentre study to evaluate their use in the elucidation of sexual crimes and specific cases of paternity testing (Kayser *et al.*, Int. J. Legal Med. 110 (1997): 125-133). For the interpretation of Y STR typing results the specific mode of inheritance of the Y-chromosome has to be considered. Y-linked loci do not recombine in mitosis or meiosis and establish patrilineages. Since these loci are genetically linked, allele frequencies can not easily be multiplied to calculate genotype frequencies. One possibility to interpret Y-specific data is to determine haplotype frequencies in the human population of combined Y-linked loci.

Here we present haplotype analysis of three combined Y-chromosomal STR loci (DYS19, DYS385 and DYS390) on 291 human male DNAs originating from eastern Austria. Of 92 different DYS19/DYS385-haplotypes observed, 54 were found only once and 6 haplotypes more than 10 times (>3.4%). For further discrimination, DNAs having one of these frequent haplotypes were subsequently typed using DYS390. These population data allow efficient use of Y-STR analysis in forensic medicine in our district and will be available for the European database.