

The Y-Short Tandem Repeat Haplotype Reference Database (YHRD) and Male Population Stratification in Europe — Impact on Forensic Genetics

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ABSTRACT: The forensic application of patrilineally transmitted Y-chromosomal markers requires knowledge of its substantial sensitivity to population substructuring. The establishment of carefully constructed, large, online-available and worldwide population databases for Y-short tandem repeat-based haplotypes illustrates the magnitude and importance of male population subdivision, which is even recognizable in the otherwise nearly indistinguishable European populations. Thus, the choice of the suitable reference population is an absolute requirement for the interpretation of haplotype matches. Based on the specific haplotype distribution in a given population, an extrapolation method has been worked out that allows the frequency estimation of very rare haplotypes. This “haplotype surveying” approach is recommended as a conservative method to assess the match probabilities in cases with non-exclusion constellations. As exemplified further, the population-specific distribution of haplotypes can help to infer the population of origin of an unknown male DNA.

KEY WORDS: Y-Chromosome, forensic DNA analysis, online population databases, population subdivision, STRs.
