

USE OF Y-STRs TO REUNITE FAMILIES

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The Y-STR haplotyping method can be used to detect patrilinear relationships between all members of a paternal genealogy. A genealogy forms a tree, whose roots extend many hundred years deep into the historical time and whose branches could spread around the world. Even though mutations accumulate at STR sequences over time and slightly transform the ancestral haplotypes, groups of related STR profiles (“neighbours”) can be recognized in population databases that might be used to predict the ancestral population of a male individual. People who are curious about their paternal descent are increasingly using databases available online. We will present examples as to how the use of population databases can reliably predict an ancestral paternal population of a person.

However, most questions that can be answered by Y-STR haplotyping methods are simpler but of higher relevance: Is this man my brother or cousin or grandfather? How can one identify this orphan’s burnt body? Do I belong to this family or not? Is this sperm that of the perpetrator? Do the traces at the scene stem from paternal relatives? We present casework examples mainly from kinship cases that illustrate the capability of the method to answer these questions. In one of the presented cases two questioned lineages of a genealogy could be connected to each other by a common recent ancestor whereas a third branch could be excluded from the tree. Other casework examples include the reuniting of family members that have been separated during and after World War II and lived with different names in different countries until Y-DNA analysis proved their relationship.

Approaching this kind of casework demands besides an approved lab technology precise knowledge of the frequencies and the distribution of Y-STR haplotype profiles around the world. Two major man-made forces shape the male genetic landscape of the earth: on the one hand patrilocality that stabilizes separable subpopulations and on the other migration leading to population admixture. Consequences of both forces are detectable in worldwide Y-STR haplotype population databases (www.ystr.org) if haplotype searches are conducted. These quality-approved YHRDatabases have been created to support the decision-making process for analysts working in the field of kinship or forensic casework as far as the Y-STR haplotyping method is concerned. The size of the YHRD is for some regions of the world, large enough to employ a posterior mean value of the haplotype frequency in a given population with respect to a prior distribution of haplotypes, with parameters determined by the observed haplotype counts. Ascertainment of regional variations and thus (population) statistical calculations of match probabilities are limited by the size of the population databases that are available.