Enlargement of the YHRD and Accommodation of New Y-STRs to Support Court Bound Cases

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The flood of high quality population data published in forensic journals led to a continuous enlargement of the web-based Y-STR Haplotype Reference Database (YHRD) over the past 12 years. The database project organizes the external evaluation of the submitted raw data for the journals, issues YHRD accession numbers and made the annotated haplotype profiles accessible in parallel to the published study. Current release 40 from August 2012 presents about 105,000 haplotypes sampled in 775 populations from 109 countries. About 10% of these chromosomes are fully typed for phylogenetic SNPs which place the profiles in the Y chromosomal evolutionary tree and often to a restricted geographic range.

To accommodate new Y-STR multiplex kits as the PowerPlex® Y23 System the database has been reorganized. The profiles of different multiplex kits (12-23 Y-STR loci) can be pre-selected. Haplotype counts and confidence intervals are provided for the respective sub-database which is further subdivided in metapopulations, continents, countries and haplogroups. Large projects are under way around the world to enrich the YHRD with highly informative haplotypes.

The implementation of Y-STR analysis in case-sensitive forensic workflows demands methods to quantify the trace-suspect match probability. The most appropriate methods to do such calculations take the evolutionary relatedness between haplotypes into account. The major downside of these methods, namely the surveying and the coalescence-based approach consists in its enormous computational demands. Therefore, in most instances the augmented counting method is the method of choice which can be supported by very large and structured reference databases as the YHRD.