A167 YHRD 3.0 – An Improved Version of the YSTR Haplotype Reference Database

for the Calculation of Match Probabilities

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The goals of this presentation are to access/query contribution by accession numbers, search the database with a given haplotype, interpret matches and frequency calculations, build/query a custom reference database, and perform an online AMOVA analysis

This presentation will impact the forensic community by demonstrating the calculation and interpretation of match probabilities, demonstrating further sampling of Y-chromosomal STRs and population genetics.

The successful implementation of Y-STR analysis in forensic practice led to the establishment of large web-based population databases which facilitate the assessment of match probabilities for haplotypic profiles. Thanks to international collaboration the current release 24 of the Y-STR Haplotype Reference Database (YHRD)[1] consists of nearly 59,000 haplotypes from 499 population samples. The database has been online for 8 years with regular updates to meet the requirements of a broad community of users. However, recent developments in the forensic field and a still growing number of users made it necessary to rework the database for its next major version: YHRD 3.0.[2]

New capabilities, new features to improve usability and the enhancements of the existing functional range will be presented. Major changes originate from the inclusion of all types of mutation and the expansion of the set of markers available through the new underlying database. This expansion includes both Y-STR Loci (e.g., full Y-Filer coverage) and Y-SNP haplogroups (see SNPY nomenclature[3]).

The implementation of an AMOVA module (pairwise Φ_{ST} values and MDS plot are calculated) enables the user to study genetic distances between population samples from the YHRD and those submitted by the user. A reprogrammed mapping module to visualize the geographic distribution, the possibility to submit batch queries and a new export functionality, make the database an even more powerful scientific tool.

Another improvement is a module called "Custom Search", which enables the user to search in an own reference set of population samples. This is done by creating a new "Custom Database" by picking appropriate populations from the YHRD database set. There are pre-defined

databases (e.g., countries) which enable the forensic user to search the YHRD like a national reference database.

References:

1   Willuweit S, Roewer L, on behalf of the International Forensic Y Chromosome User Group (2007) Y chromosome haplotype reference database (YHRD): Update, Forensic Science International: Genetics 1(2) 83-87
2   http://www.yhrd.org
3   http://www.snp-y.org

Y-Cromosomal STRs, Forensic Reference Database, Population Genetics