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The Y-Chromosome Haplotype Reference Database

– Directions for Use –

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Endorsed by International Society of Forensic Genetics (ISFG).

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<https://yhrd.org>

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1 Introduction

The Y-Chromosome Haplotype Reference Database (YHRD) (Figure 1) aims to help with the interpretation of results from comparisons of evidentiary samples typed with Y-STRs and reference samples, and to formulate conclusions. Since Y-STRs are located on the non-recombining part of the Y chromosome, the profile generated by Y-STR analysis should be considered as one trait coded by one locus (a haplotype). Consequently, the YHRD provides allele and haplotype (>1 locus typed per sample) frequencies for common marker sets consisting of up to 29 loci (Figure 2). The database is explained in detail in the article "The new Y Chromosome Haplotype Reference Database" by Willuweit and Roewer (2015).



Figure 1: YHRD homepage

Name	Description	Loci
Minimal	YHRD Core Loci	DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385
PowerPlex Y	Promega PowerPlex® Y	DYS391, DYS389I, DYS439, DYS389II, DYS438, DYS437, DYS19, DYS392, DYS393, DYS390, DYS385
Yfiler	Applied Biosystems AmpFLSTR® Yfiler®	DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385, DYS393, DYS391, DYS439, DYS635, DYS392, YGATAH4, DYS437, DYS438, DYS448
PowerPlex Y23	Promega PowerPlex® Y23	DYS576, DYS389I, DYS448, DYS389II, DYS19, DYS391, DYS481, DYS549, DYS533, DYS438, DYS437, DYS570, DYS635, DYS390, DYS439, DYS392, DYS643, DYS393, DYS458, DYS385, DYS456, YGATAH4
Yfiler Plus	Applied Biosystems AmpFLSTR® Yfiler® Plus	DYS576, DYS389I, DYS635, DYS389II, DYS627, DYS460, DYS458, DYS19, YGATAH4, DYS448, DYS391, DYS456, DYS390, DYS438, DYS392, DYS518, DYS570, DYS437, DYS385, DYS449, DYS393, DYS439, DYS481, DYF387S1, DYS533
Maximal	YHRD Max Loci	DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385, DYS438, DYS439, DYS437, DYS448, DYS456, DYS458, DYS635, YGATAH4, DYS481, DYS533, DYS549, DYS570, DYS576, DYS643, DYF387S1, DYS449, DYS460, DYS518, DYS627

Figure 2: Available marker sets (locus information)

2 Current state of the database

By June 2019, when YHRD release 61 was launched, more than 285,000 haplotypes from 1,308 sampling locations in 135 countries were submitted by more than 450 institutes and laboratories worldwide. In geographic terms, about 47% of the YHRD samples are from Asia, 23% from Europe, 11% from Latin America, 14% from North America, 3% from Africa, 1% from Oceania and less than 1% from the Arctic (Figure 3). The YHRD continuously receives new data from submitters which will be validated and used to create updates about three to four times a year (Figures 4 + 5). Four insertion methods are available for selection: **New** (a completely new dataset), **Append** (a dataset which enlarges a previous submission), **Replace** (a dataset which is inserted to replace a previous dataset) and **Merge** (a dataset which adds new haplotypes to previous haplotypes and/or includes previous haplotypes retyped for additional loci). The selection of the appropriate insertion method, which is selected by authors and approved by curators, is crucial to guarantee that no haplotype is inserted unintentionally more than once. Since new releases replace the previous ones, the release number and date is an important part of the results report (Figure 6). The release notes are included in the footer of all printable documents.

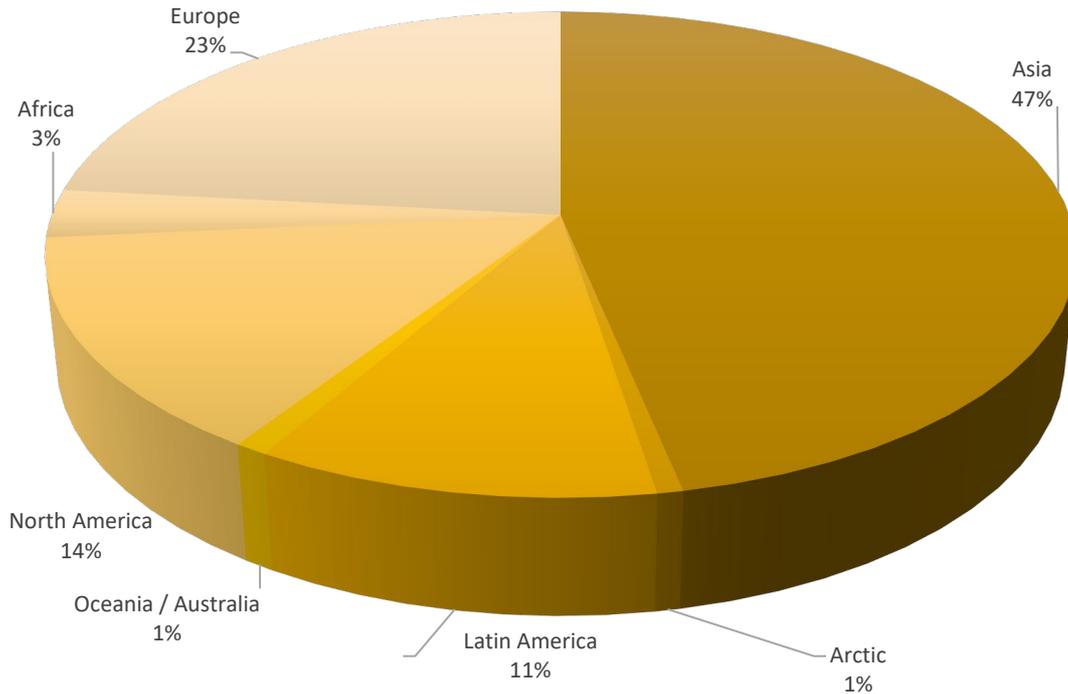


Figure 3: Continental distribution of haplotypes

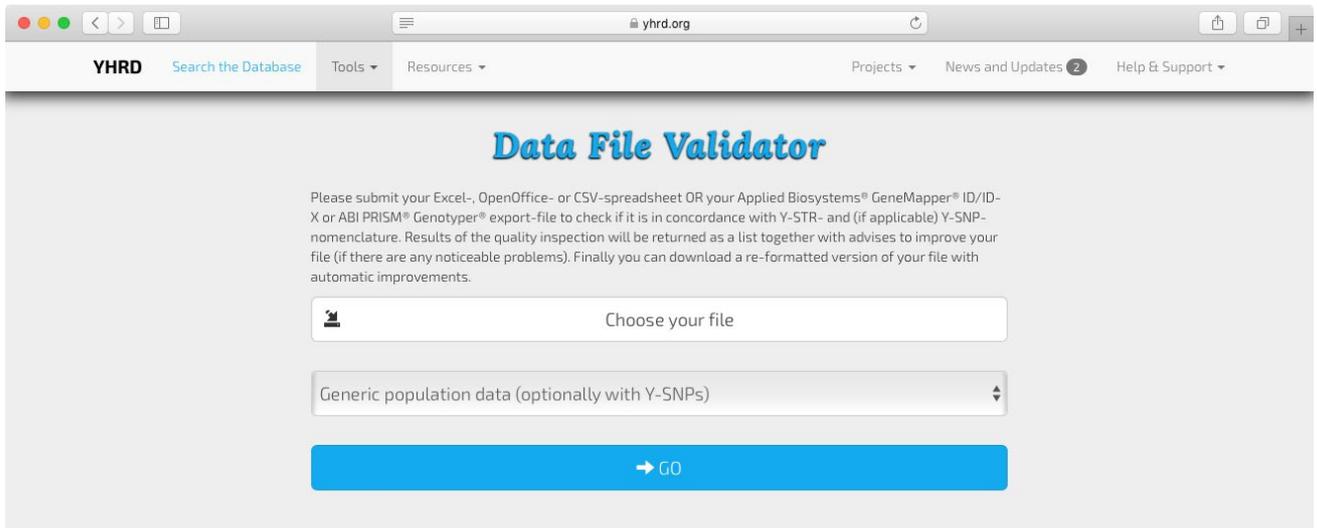


Figure 4: Data file validator (file upload)

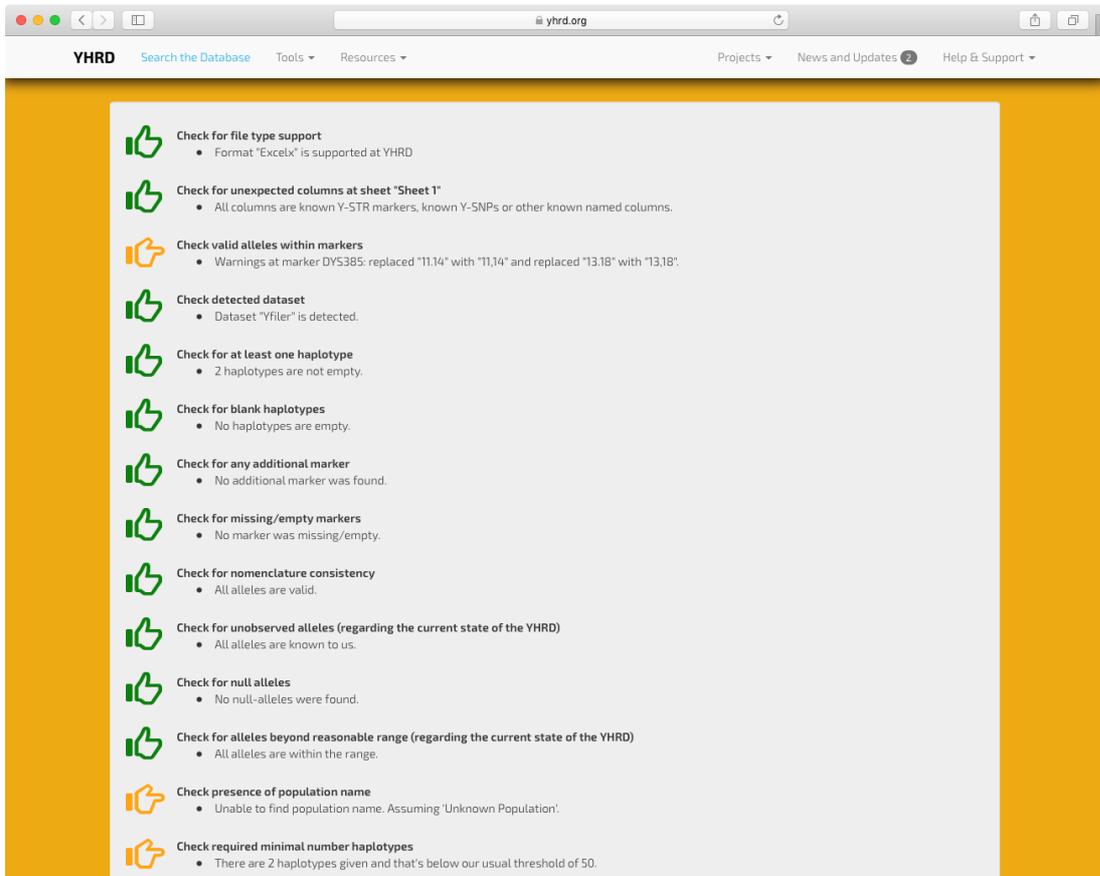


Figure 5: Data file validator (results)

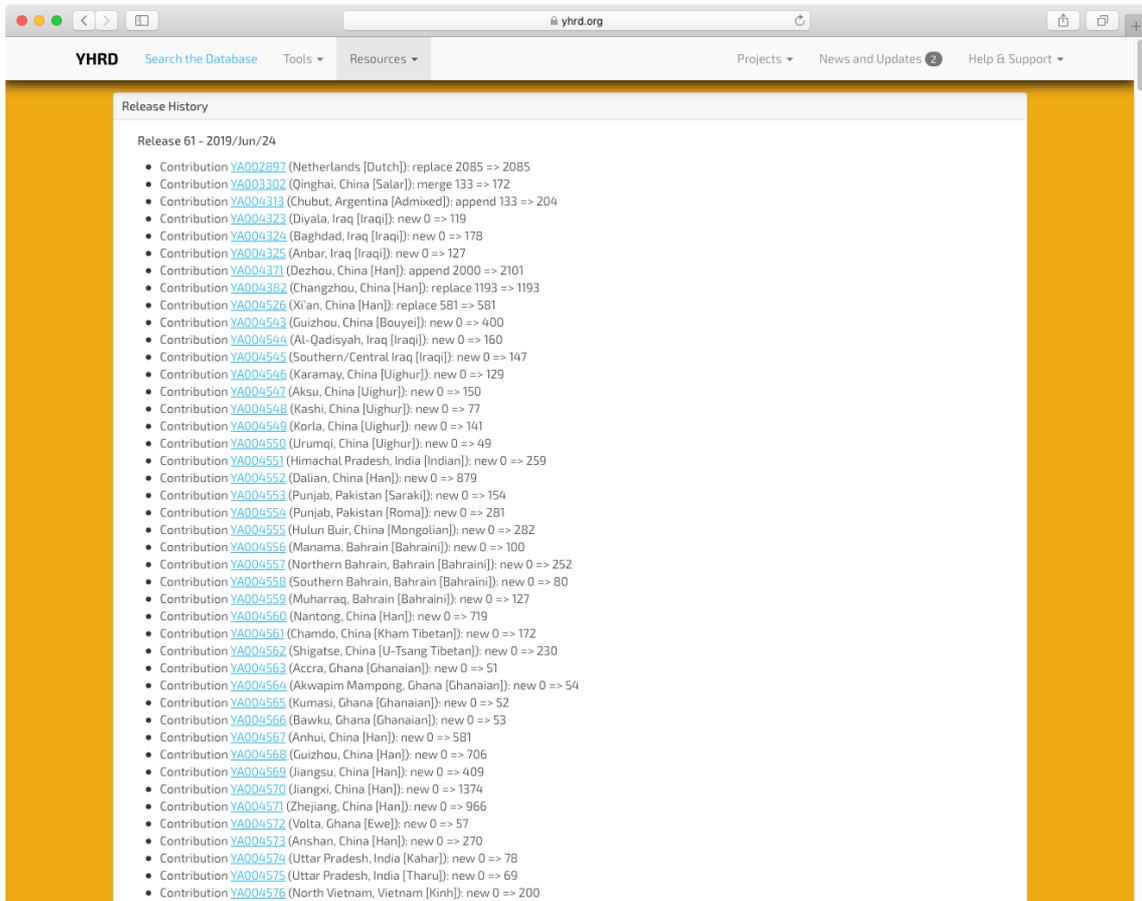
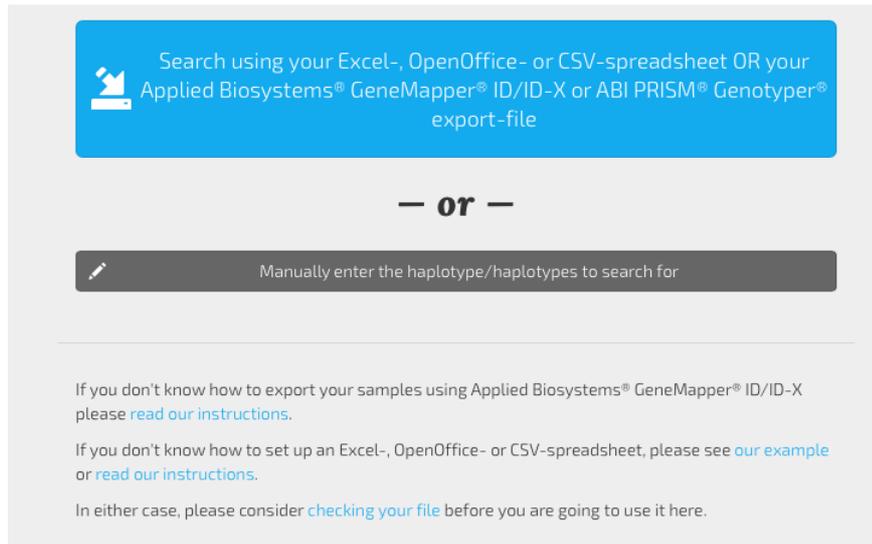


Figure 6: Release history

3 Navigation through the website

3.1 Search the database

The database can be searched either using manual input or by uploading files, including GeneMapper/GenoTyper export files (Figure 7).



The screenshot shows a search interface with two main options. The top option is a blue button with a file icon and the text: "Search using your Excel-, OpenOffice- or CSV-spreadsheet OR your Applied Biosystems® GeneMapper® ID/ID-X or ABI PRISM® Genotyper® export-file". Below this is a separator "— or —". The second option is a dark grey button with a pencil icon and the text: "Manually enter the haplotype/haplotypes to search for". Below the buttons is a horizontal line, followed by three lines of text providing instructions and links for users who need help with file exports or manual input.

Search using your Excel-, OpenOffice- or CSV-spreadsheet OR your Applied Biosystems® GeneMapper® ID/ID-X or ABI PRISM® Genotyper® export-file

— or —

Manually enter the haplotype/haplotypes to search for

If you don't know how to export your samples using Applied Biosystems® GeneMapper® ID/ID-X please [read our instructions](#).

If you don't know how to set up an Excel-, OpenOffice- or CSV-spreadsheet, please see [our example](#) or [read our instructions](#).

In either case, please consider [checking your file](#) before you are going to use it here.

Figure 7: Search database

Without registration and limitations, the YHRD database can be searched for all single alleles, partial haplotypes and full haplotypes in different formats. Nomenclature for all loci follows the ISFG recommendations (Gusmão et al. 2006). The database supports the most frequently used haplotype formats which need to be selected from the “kit” bar at the top, i.e., **Minimal (9 loci)**, **PowerPlex® Y12 (12)**, **YFiler® (17)**, **PowerPlex® Y23 (23)**, **YFiler® Plus (27)** and **Maximal (29)** (Figure 8). For each of these six panels different-sized databases exist. Note that smaller-sized panels are included in the next larger panels; for example, the YFiler is part of the PPY23 and YFilerPlus. Therefore, a PPY23 analysis in a reference sample will contribute to the three databases with lesser loci. One exception: the two loci **DYS549** and **DYS643** are not part of the higher resolution panel YFilerPlus, but all loci of PPY23 and YFilerPlus are included in the maximal panel with 29 loci. It is possible to switch from a higher-resolution to a lower-resolution haplotype format, e.g., from PPY23 to YFiler thus enlarging the database in use (~63k to ~225k in release 61) (Figure 11).

The screenshot shows the YHRD search interface. At the top, there is a navigation bar with 'YHRD' and 'Search the Database' (highlighted in blue), followed by 'Tools' and 'Resources' dropdown menus. On the right, there are links for 'Projects', 'News and Updates' (with a '2' notification), and 'Help & Support' dropdown. Below the navigation bar, there is a 'kit' selection bar with buttons for 'Minimal', 'PowerPlex Y', 'Yfiler' (selected and highlighted in blue), 'PowerPlex Y23', 'Yfiler Plus', and 'Maximal'. Underneath, there is a 'Haplotype' section with a checked checkbox. Below this, a row of 17 loci names is displayed: **DYS456**, **DYS389I**, **DYS390**, **DYS389II**, **DYS458**, **DYS19**, **DYS385**, **DYS393**, **DYS391**, **DYS439**, **DYS635**, **DYS392**, **YGATAH4**, **DYS437**, **DYS438**, and **DYS448**. Below the loci names is a row of 17 input fields, each containing a number: 15, 14, 25, 31, 15, 17, 13, 17, 13, 10, 12, 21, 11, 11, 14, 10, and 19. At the bottom of the form is a large blue 'Search' button.

Figure 8: Search database (default panel selection is “YFiler”)

At each position of the mask, the respective allele must be entered manually. Alternatively, haplotype lists can be downloaded for search. The file needs to be prepared according to the example file found at the bottom of the search page. The file is checked using the validator software and issues, e.g., an invalid file format, are highlighted. By using the function "search using the export file" all haplotypes in the file will be displayed as a list. Individual haplotypes need to be selected by clicking the checkbox for search. To avoid clerical errors, wrongly named alleles turn red. For loci which are mandatorily multi-copied (DYS385, DYS387S1) at least two alleles need to be entered. For Null alleles (caused by mutation, not by drop-out due to insufficient DNA quality) a "0" must be entered as a placeholder. Boxes for alleles which dropped or are regarded uncertain due to low DNA amount and/or degradation need to be empty. All alleles need to be called according to their repeat numbers; placeholders for off-ladder alleles like "99" are not allowed. Duplications or higher-order multi-copying events are possible for all Y chromosome sequences. If the sample is not a mixture, all true alleles need to be entered separated by a decimal point. The number of duplications, triplications, quadruplications and other rare intermediate, off-ladder or Null alleles can be viewed at the "Locus Information" page. Note that the allele spectra per locus are based on the full validated YHRD dataset and therefore often include more variants than commercial allelic ladders (Figure 9). You may choose the option "logarithmic axis" and "treat multi-copy alleles (e.g., duplications) as one observation" to get the most information on the variants spectrum.

Locus Information on DYS19

External resources/links

- [DYS19 at STRBase](#) (John M. Butler, NIST)
- [DYS19 at Human Y chromosome cosmids library Homo sapiens STS genomic sequence tagged site \(NCBI\)](#)
- [DYS19 at Yhr5STS \(NCBI\)](#)

Mutation rate

2.20e-03 (37 in 16801) based on Pontzen2007, Sanchez-Diz2008, Turrina2006, Bergey2005, Tsai2002, Goedbloed2009, Hohoff2007, Lee2007, Domingues2007, Decker2008, Bailard2005a, Kurihara2010, Guimao2005, Kavser2000, Hevar1997, Dunay2004, Bianchi1998, Budowle2005, Dunay2003, Paston1999, Ge2009, Adnan2018, Laouina2013, Buroyo2018, Petrovic2018, Mergelju2018, Serpey-Bravchenko11, Ludmila A. Livshits 11, Svetlana A. Limborska1 2, Gerhard Baessler, Tina West, Andrea Betz, Werner Pflug, Maria Gouquet, Josephine Purns, Patricia Enfo, Carmen Kruger, Petra Dremba, Marion Nagy, Lutz Roewer, Ghazi Tahir-Smith, Wei Wei, Xue-Yi Ayubi, D. Mahvudien A. Dumar, R. Zerial, T. Haldjapou A. Idahbi, S9, Staila Marie, Tabu Jona Anguata

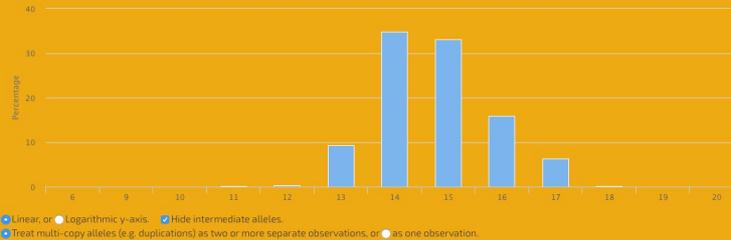
Observed alleles

6, 9, 10, 11, 12, 13, 13.2, 13.3, 14, 14.1, 14.2, 14.3, 15, 15.2, 16, 16.2, 17, 18, 19, 20

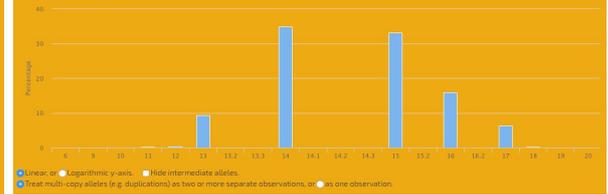
NULL alleles

34 NULL allele observations

Allelic distribution



Allelic distribution



Allelic distribution

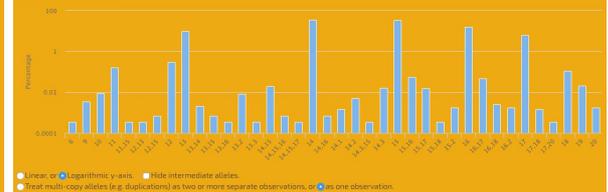


Figure 9: Locus information (DYS 19, multiple graphical options used)

After clicking on the “Search” button, a printable report for the respective sample is generated (Figure 10). It includes two main types of frequency estimates. First is the **observed value** i.e., the number of observations in the worldwide database for the selected panel accompanied by a confidence interval (CI) calculated according to Clopper and Pearson (Clopper and Pearson 1934; see [Glossary: Confidence Intervals](#) for more information on different types of CI). Second is the **expected values** calculated by (1) the Discrete Laplace Method, (2) augmented counting ($(n+1)/(N+1)$) and (3) the Kappa method (see [Glossary: Frequency estimation methods](#) for more details on each calculation method).

YHRD Search the Database Tools Resources Projects News and Updates 2 Help & Support

Minimal PowerPlex Y **Yfiler** PowerPlex Y23 Yfiler Plus Maximal

Report for Sample #1

Sample Name: Haplotype

DYS456 15
 DYS389I 14
 DYS390 25
 DYS389II 31
 DYS458 15
 DYS19 17
 DYS385 13,17
 DYS393 13
 DYS391 10
 DYS439 12
 DYS635 21
 DYS392 11
 YGATAH4 11
 DYS437 14
 DYS438 10
 DYS448 19

+ Add feature to this Report

Worldwide

Observed

Found 34 matches in 225,098 Haplotypes. This is approx. 1 match in 6,621 Haplotypes (95% CI: 1 in 9,560 — 1 in 4,738).

Expected

DL (Yfiler) Approx. 1 match in 810 Haplotypes, emerging mostly from East Asian - Japanese Metapopulation. Please note, this value is an average over the DL values of all *nested feasible metapopulations*.

n+1/N+1 Approx. 1 match in 6,431 Haplotypes (95% CI: 1 in 9,233 — 1 in 4,625)

Kappa Approx. 1 match in 14,754 Haplotypes

Results are based upon Release R61 valid as per 2019-06-24 09:01:40 UTC. This query was sent at 2019-07-03 14:45:41 UTC.

Figure 10: Search result

To switch between different panels click the panel bar at the top (Figure 11).

The screenshot shows the YHRD database interface. At the top, there is a navigation bar with 'YHRD', 'Search the Database', 'Tools', and 'Resources'. On the right, there are links for 'Projects', 'News and Updates', and 'Help & Support'. Below the navigation bar, there are several filter buttons: 'Minimal' (highlighted in blue), 'PowerPlex Y', 'Yfiler', 'PowerPlex Y23', 'Yfiler Plus', and 'Maximal'. The main heading is 'Report for Sample #1'. Below this, a green box contains 'Sample Name: Haplotype'. A white box displays the following haplotype data:

DYS19	DYS389I	DYS389II	DYS390	DYS391	DYS392	DYS393	DYS385
17	14	31	25	10	11	13	13, 17

Below the data is a blue button with a plus sign and the text '+ Add feature to this Report'. Underneath is a 'Worldwide' panel with a close button. It contains two sections: 'Observed' and 'Expected'. The 'Observed' section states: 'Found 87 matches in 285,406 Haplotypes. This is approx. 1 match in 3,281 Haplotypes (95% CI: 1 in 4,096 – 1 in 2,660)'. The 'Expected' section lists three metrics: 'DL (Minimal)' with an approx. 1 match in 288 Haplotypes; 'n+1/N+1' with an approx. 1 match in 3,243 Haplotypes; and 'Kappa' with an approx. 1 match in 3,745 Haplotypes. At the bottom, a blue-bordered box contains the text: 'Results are based upon Release R61 valid as per 2019-06-24 09:01:40 UTC. This query was sent at 2019-07-03 15:02:48 UTC.'

Figure 11: Search result with “kit” switched to “Minimal Haplotype”

Using the button “+ Add feature to this report”, the search result can be further adapted to the needs of the user (Figure 12). The first button **Metapopulation** allows selecting a match statistic within metapopulations (Figure 13), the second button **National** for political entities (countries) (Figure 14), and the third button **National databases with subpopulations** for searches within countries with predefined subpopulations. The next three buttons **Ancestry information (minimal haplotype)**, **Ancestry information (YFiler)** and **Ancestry Information 1-step Neighbors** (haplotype counts with +/- one step-allele per locus) provide access to relevant information on the biogeographical ancestry of the searched haplotype (Figure 15). At the bottom of the “Result page” you will find a release note with the date and number of the current version of the database, and the time of the query.

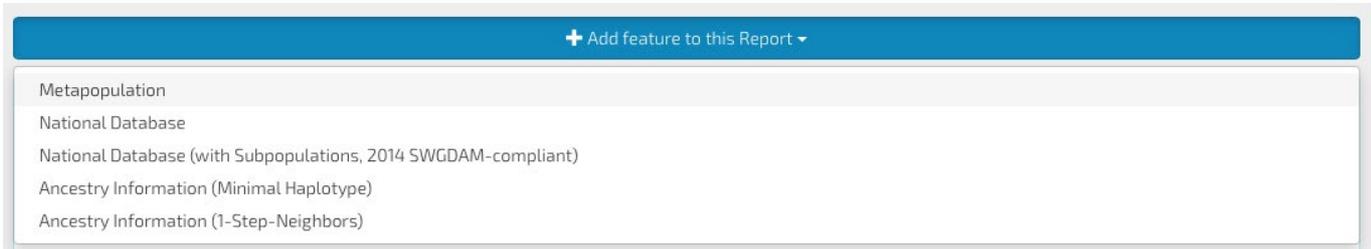


Figure 12: Search result: Add feature to this report

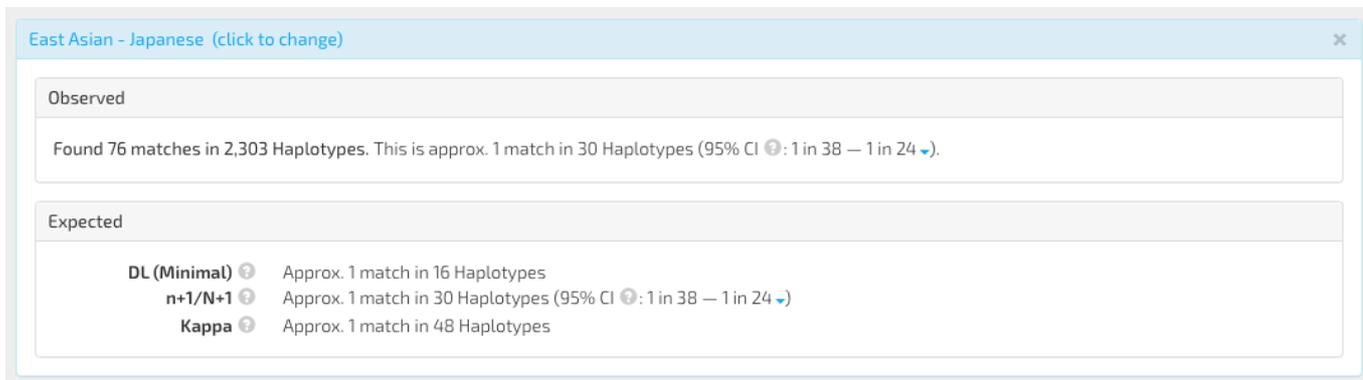


Figure 13: Search result: Add “metapopulation” feature to this report (*East Asian-Japanese*)

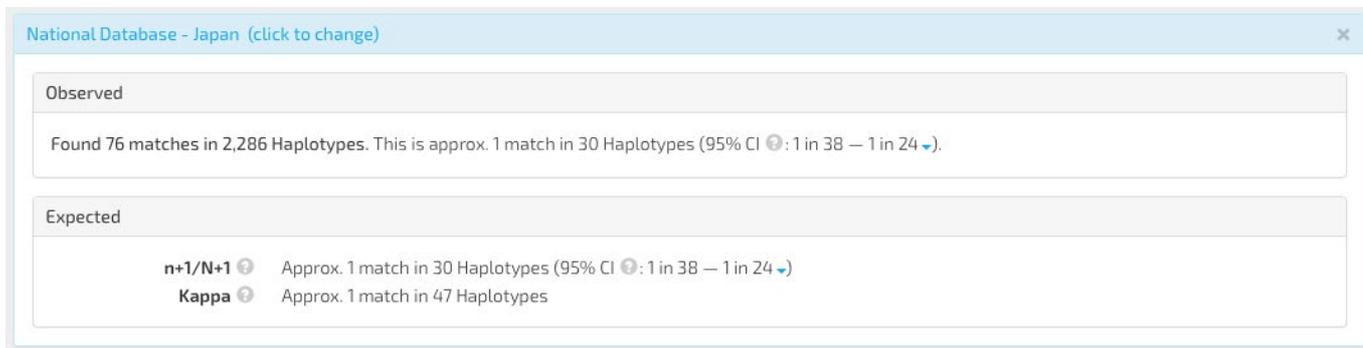


Figure 14: Search result: Add “National Database - Japan” feature to this report

The selected features will be added one after another to the general search report. Note that the computer IP is used to select the default metapopulation and national database, e.g., a user in Japan will see the “East Asian - Japanese metapopulation” and the national database “Japan” as default. The evaluation of the haplotype frequency using the DL method is restricted to the Yfiler database which incorporates the 17 loci analyzed using higher-resolution panels. Haplotypes with intermediate, duplicated or missing alleles within the Yfiler panel cannot be evaluated using DL. It is advisable to calculate the DL value in a pre-selected metapopulation, since the worldwide DL value is an average estimate over the DL values of all nested metapopulations.

If the feature ancestry information is selected, the database provides a movable and scalable world map with the relative proportion of haplotype matches shown in red/blue for each geoposition. The more matches per population occur, the larger is the red-colored symbol of the population sample. Clicking the population symbol provides information on the number of matches and the population size. Please note that, at a given geoposition, more than one population could have been sampled. Furthermore, the feature presents absolute and relative frequencies of the concerned haplotype in countries and the number of matches with SNP-typed chromosomes (haplogroups) collected in the YHRD (Figure 15).

3.2 Resources

3.2.1 Database details

Enter names of population samples, countries, contributors, accession number, etc. Choose from a list of found items for further information (Figures 16-19).

Need database details? Just type ... We'll search for all the details of the underlying database like database samples, geositions, populations, contributions, contributors, accession numbers etc. Click on an item to get more information.



The screenshot shows a search bar with the text "Japan" and a magnifying glass icon. Below the search bar, a list of search results is displayed, each representing a population from Japan with its corresponding YP accession number, number of haplotypes, and number of contributions.

Population	YP Accession	Haplotypes	Contributions
Population "Aomori, Japan [Japanese]"	YP000011	95	1
Population "Chiba, Japan [Japanese]"	YP000092	37	1
Population "Ehime, Japan [Japanese]"	YP000131	103	1
Population "Fukuoka, Japan [Japanese]"	YP000150	53	1
Population "Gunma, Japan [Japanese]"	YP000162	110	1
Population "Hiroshima, Japan [Japanese]"	YP000171	14	1
Population "Hokkaido, Japan [Japanese]"	YP000172	50	1

Figure 16: Detail results when typing “Japan”

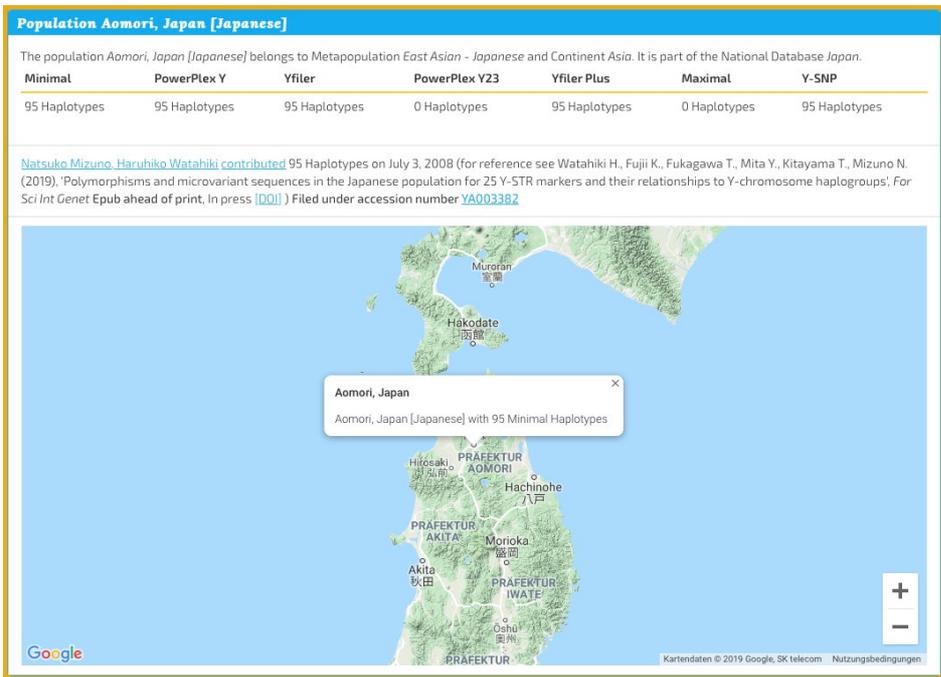


Figure 17: Details on the population sample “Aomori, Japan [Japanese]”

Contributor Natsuko Mizuno, Haruhiko Watahiki (YC000143)

The contributor can be reached using mizuno@nrrips.go.jp using +81-471-35-8001 (Phone) or using +81-471-33-9159 (Fax) or at
Fourth Biology Section
Department of first forensic science
National Research Institute of Police Science
6-3-1, Kashiwanoha, Kashiwa, Chiba, 277-0882
Japan

The contributor has successfully passed the [Quality Control Exercise](#) on April 17, 2007.

[Natsuko Mizuno, Haruhiko Watahiki contributed](#) 50 Haplotypes on July 3, 2008 to the population [Hokkaido, Japan \[Japanese\]](#) (for reference see Watahiki H., Fujii K., Fukagawa T., Mita Y., Kitayama T., Mizuno N. (2019), 'Polymorphisms and microvariant sequences in the Japanese population for 25 Y-STR markers and their relationships to Y-chromosome haplogroups', *For Sci Int Genet Epub ahead of print*, In press [\[DOI\]](#)).

[Natsuko Mizuno, Haruhiko Watahiki contributed](#) 95 Haplotypes on July 3, 2008 to the population [Aomori, Japan \[Japanese\]](#) (for reference see Watahiki H., Fujii K., Fukagawa T., Mita Y., Kitayama T., Mizuno N. (2019), 'Polymorphisms and microvariant sequences in the Japanese population for 25 Y-STR markers and their relationships to Y-chromosome haplogroups', *For Sci Int Genet Epub ahead of print*, In press [\[DOI\]](#)).

[Natsuko Mizuno, Haruhiko Watahiki contributed](#) 37 Haplotypes on July 3, 2008 to the population [Chiba, Japan \[Japanese\]](#) (for reference see Watahiki H., Fujii K., Fukagawa T., Mita Y., Kitayama T., Mizuno N. (2019), 'Polymorphisms and microvariant sequences in the Japanese population for 25 Y-STR markers and their relationships to Y-chromosome haplogroups', *For Sci Int Genet Epub ahead of print*, In press [\[DOI\]](#)).

[Natsuko Mizuno, Haruhiko Watahiki contributed](#) 103 Haplotypes on July 3, 2008 to the population [Ehime, Japan \[Japanese\]](#) (for reference see Watahiki H., Fujii K., Fukagawa T., Mita Y., Kitayama T., Mizuno N. (2019), 'Polymorphisms and microvariant sequences in the Japanese population for 25 Y-STR markers and their relationships to Y-chromosome haplogroups', *For Sci Int Genet Epub ahead of print*, In press [\[DOI\]](#)).

[Natsuko Mizuno, Haruhiko Watahiki contributed](#) 53 Haplotypes on July 3, 2008 to the population [Fukuoka, Japan \[Japanese\]](#) (for reference see Watahiki H., Fujii K., Fukagawa T., Mita Y., Kitayama T., Mizuno N. (2019), 'Polymorphisms and microvariant sequences in the Japanese population for 25 Y-STR markers and their relationships to Y-chromosome haplogroups', *For Sci Int Genet Epub ahead of print*, In press [\[DOI\]](#)).

[Natsuko Mizuno, Haruhiko Watahiki contributed](#) 110 Haplotypes on July 3, 2008 to the population [Gunma, Japan \[Japanese\]](#) (for reference see Watahiki H., Fujii K., Fukagawa T., Mita Y., Kitayama T., Mizuno N. (2019), 'Polymorphisms and microvariant sequences in the Japanese population for 25 Y-STR markers and their relationships to Y-chromosome haplogroups', *For Sci Int Genet Epub ahead of print*, In press [\[DOI\]](#)).

[Natsuko Mizuno, Haruhiko Watahiki contributed](#) 14 Haplotypes on July 3, 2008 to the population [Hiroshima, Japan \[Japanese\]](#) (for reference see Watahiki H., Fujii K.,

Figure 18: Details on the contributor YC000143

Contribution with the Accession Number YA003381

[Natsuko Mizuno, Haruhiko Watahiki](#) contributed 50 Haplotypes on July 3, 2008 to the population [Hokkaido, Japan \[Japanese\]](#) (for reference see Watahiki H., Fujii K., Fukagawa T., Mita Y., Kitayama T., Mizuno N. (2019), 'Polymorphisms and microvariant sequences in the Japanese population for 25 Y-STR markers and their relationships to Y-chromosome haplogroups', *For Sci Int Genet Epub ahead of print, In press* [[DOI](#)]).

Submission accession number	State	Accepted at	Release	Insertion method	Minimal Haplotypes	PowerPlex Y Haplotypes	Yfiler Haplotypes	PowerPlex Y23 Haplotypes	Yfiler Plus Haplotypes	Maximal Haplotypes	Y-SNP Haplotypes
YA003381-2	active submission	Sat, 28 Jul 2018 12:43:08 +0200	58	merge	50	50	50	0	50	0	50
YA003381-1	former submission	Tue, 25 Oct 2016 10:05:44 +0200	51	new	50	50	50	0	0	0	50

Figure 19: Details on submissions building the population sample YA003381

Note that each submitted population sample goes through a validation and receives a unique accession number. A further prerequisite is the laboratory accreditation certificate.

3.2.2 Database statistics

Dataset	Y-STR loci	Number of haplotypes	Number of population samples	Number of national databases	Number of metapopulations
Minimal	DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385	285,406	1308	135	33
PowerPlex Y	DYS391, DYS389I, DYS439, DYS389II, DYS438, DYS437, DYS19, DYS392, DYS393, DYS390, DYS385	244,777	1084	126	32
Yfiler	DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385, DYS393, DYS391, DYS439, DYS635, DYS392, YGATAH4, DYS437, DYS438, DYS448	225,098	999	119	32
PowerPlex Y23	DYS576, DYS389I, DYS448, DYS389II, DYS19, DYS391, DYS481, DYS549, DYS533, DYS438, DYS437, DYS570, DYS635, DYS390, DYS439, DYS392, DYS643, DYS393, DYS458, DYS385, DYS456, YGATAH4	62,737	338	67	28
Yfiler Plus	DYS576, DYS389I, DYS635, DYS389II, DYS627, DYS460, DYS458, DYS19, YGATAH4, DYS448, DYS391, DYS456, DYS390, DYS438, DYS392, DYS518, DYS570, DYS437, DYS385, DYS449, DYS393, DYS439, DYS481, DYS387S1, DYS533	56,114	250	52	30
Maximal	DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393, DYS385, DYS438, DYS439, DYS437, DYS448, DYS456, DYS458, DYS635, YGATAH4, DYS481, DYS533, DYS549, DYS570, DYS576, DYS643, DYS387S1, DYS449, DYS460, DYS518, DYS627	15,395	57	15	21

Figure 20: Database statistics

3.2.3 Database composition

National	Metapopulation			Y-SNPS		Loci
National Database	Minimal	PowerPlex Y	Yfiler	PowerPlex Y23	Yfiler Plus	Maximal
Afghanistan	743 Haplotypes	743 Haplotypes	743 Haplotypes	0 Haplotypes	260 Haplotypes	0 Haplotypes
Albania	494 Haplotypes	396 Haplotypes	322 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Algeria	166 Haplotypes	166 Haplotypes	166 Haplotypes	0 Haplotypes	64 Haplotypes	0 Haplotypes
Angola	309 Haplotypes	309 Haplotypes	71 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Argentina	5425 Haplotypes	3775 Haplotypes	2901 Haplotypes	1417 Haplotypes	0 Haplotypes	0 Haplotypes
Armenia	100 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Australia	2257 Haplotypes	2257 Haplotypes	2256 Haplotypes	0 Haplotypes	1136 Haplotypes	0 Haplotypes
Austria	1877 Haplotypes	1516 Haplotypes	1516 Haplotypes	259 Haplotypes	436 Haplotypes	0 Haplotypes
Azerbaijan	119 Haplotypes	47 Haplotypes	47 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Bahamas	427 Haplotypes	427 Haplotypes	427 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Bahrain	715 Haplotypes	715 Haplotypes	715 Haplotypes	0 Haplotypes	704 Haplotypes	0 Haplotypes
Bangladesh	1189 Haplotypes	1189 Haplotypes	1189 Haplotypes	132 Haplotypes	0 Haplotypes	0 Haplotypes
Belarus	489 Haplotypes	414 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Belgium	1628 Haplotypes	1503 Haplotypes	1168 Haplotypes	728 Haplotypes	169 Haplotypes	169 Haplotypes
Belize	157 Haplotypes	157 Haplotypes	157 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Benin	234 Haplotypes	234 Haplotypes	234 Haplotypes	51 Haplotypes	0 Haplotypes	0 Haplotypes
Bhutan	856 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Bolivia	457 Haplotypes	396 Haplotypes	396 Haplotypes	100 Haplotypes	0 Haplotypes	0 Haplotypes
Bosnia and Herzegovina	400 Haplotypes	300 Haplotypes	300 Haplotypes	300 Haplotypes	0 Haplotypes	0 Haplotypes
Botswana	337 Haplotypes	337 Haplotypes	337 Haplotypes	85 Haplotypes	0 Haplotypes	0 Haplotypes
Brazil	11398 Haplotypes	9758 Haplotypes	9538 Haplotypes	1096 Haplotypes	2051 Haplotypes	33 Haplotypes
Bulgaria	590 Haplotypes	326 Haplotypes	318 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
Cameron	54 Haplotypes	0 Haplotypes				

Figure 21: Database composition

3.2.4 Calculation methods

Note that the applicability of calculation methods depends on the size and structure of sampled metapopulations. For example, small-sized or very heterogeneous metapopulations are not suitable for DL calculations. For suitable metapopulations, the DL specs provide information on the central haplotypes and the methods to identify these (Figure 22a). The DL values are recalculated each time the YHRD is regularly updated. Further information on the DL estimation is given for each available dataset and metapopulation (Figure 22b).

Eurasian - European - Eastern European	C, Aug-C, K, DL (I) (DL specs)	C, Aug-C, K	C, Aug-C, K, DL (I) (DL specs)	C, Aug-C, K	C, Aug-C, K	C, Aug-C, K
Eurasian - European - South-Eastern European	C, Aug-C, K, DL (I) (DL specs)	C, Aug-C, K	C, Aug-C, K, DL (I) (DL specs)	C, Aug-C, K	E, Aug-C, K	C, Aug-C, K
Eurasian - European - Western European	C, Aug-C, K, DL (I) (DL specs)	C, Aug-C, K	C, Aug-C, K, DL (I) (DL specs)	C, Aug-C, K	C, Aug-C, K	C, Aug-C, K
Eurasian - Indian	C, Aug-C, K, DL (I) (DL specs)	C, Aug-C, K	C, Aug-C, K, DL (I) (DL specs)	C, Aug-C, K	C, Aug-C, K	C, Aug-C, K
Eurasian - Indo-Iranian	C, Aug-C, K, DL (I) (DL specs)	C, Aug-C, K	C, Aug-C, K, DL (I) (DL specs)	C, Aug-C, K	C, Aug-C, K	C, Aug-C, K
Eurasian - Uralic-Yukaghir	C, Aug-C, K, DL (I) (DL specs)	C, Aug-C, K	C, Aug-C, K, DL (I) (DL specs)	C, Aug-C, K	C, Aug-C, K	C, Aug-C, K
Native American ²	C, Aug-C, K, DL (DL specs)	C, Aug-C, K	C, Aug-C, K, DL (DL specs)	C, Aug-C, K	E, Aug-C, K	C, Aug-C, K

C
 Counting
Aug-C
 Augmented counting
K
 Kappa method
Avg-DL
 Average Discrete Laplace frequency estimates of all nested feasible metapopulations (see (I) note)
DL
 Discrete Laplace method
(I)
 Included for Discrete Laplace average frequency estimates of parent metapopulation (see Avg-DL)
1
 Discrete Laplace frequency estimates not available for reason of heterogeneity
2
 Not included for Discrete Laplace average frequency estimates for reason of heterogeneity (see Avg-DL)

Figure 22a: Calculation methods

Discrete-Laplace frequency estimation (Yfiler)

Release R61
Loci included DYS19, DYS389I, DYS389II*, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438, DYS439, DYS448, DYS456, DYS458, DYS635, YGATAH4
Central haplotypes 25
EM converged true
EM iterations 88
GLM method internal_coef
Init method pam
Per locus details [DL centers distribution \(download PDF\)](#)

[Table of haplotype centers \(click to show/hide\)](#)

	DYS19	DYS389I	DYS389II*	DYS390	DYS391	DYS392	DYS393	DYS437	DYS438	DYS439	DYS448	DYS456	DYS458	DYS635	YGATAH4
1	15	14	16	23	10	11	15	14	10	12	21	15	16	21	11
2	15	14	16	22	10	13	13	14	13	12	18	15	17	20	12
3	14	11	16	23	10	14	12	15	11	12	20	15	18	21	11
4	16	12	17	24	10	13	12	14	10	12	19	15	18	23	12
5	15	14	16	22	10	13	13	14	13	12	18	15	19	20	12
6	16	14	17	25	10	11	13	14	10	12	19	15	15	21	11

Figure 22b: Information on Yfiler DL estimation (Japanese MP)

3.2.5 Metapopulation information

The haplotype frequencies can be sensibly reported in groups of spatially distributed populations (metapopulations) sharing a common ancestry, and thus a similar pool of deep-rooting lineages (Figure 23a). To describe the hierarchy of metapopulations, YHRD uses a knowledge-based terminology, which incorporates linguistic, geographic resources and genetic parameters (genetic distance measures). YHRD provides information on each metapopulation including the assigned populations, a map, its common haplotypes (Figure 23b) and applicable calculation methods.

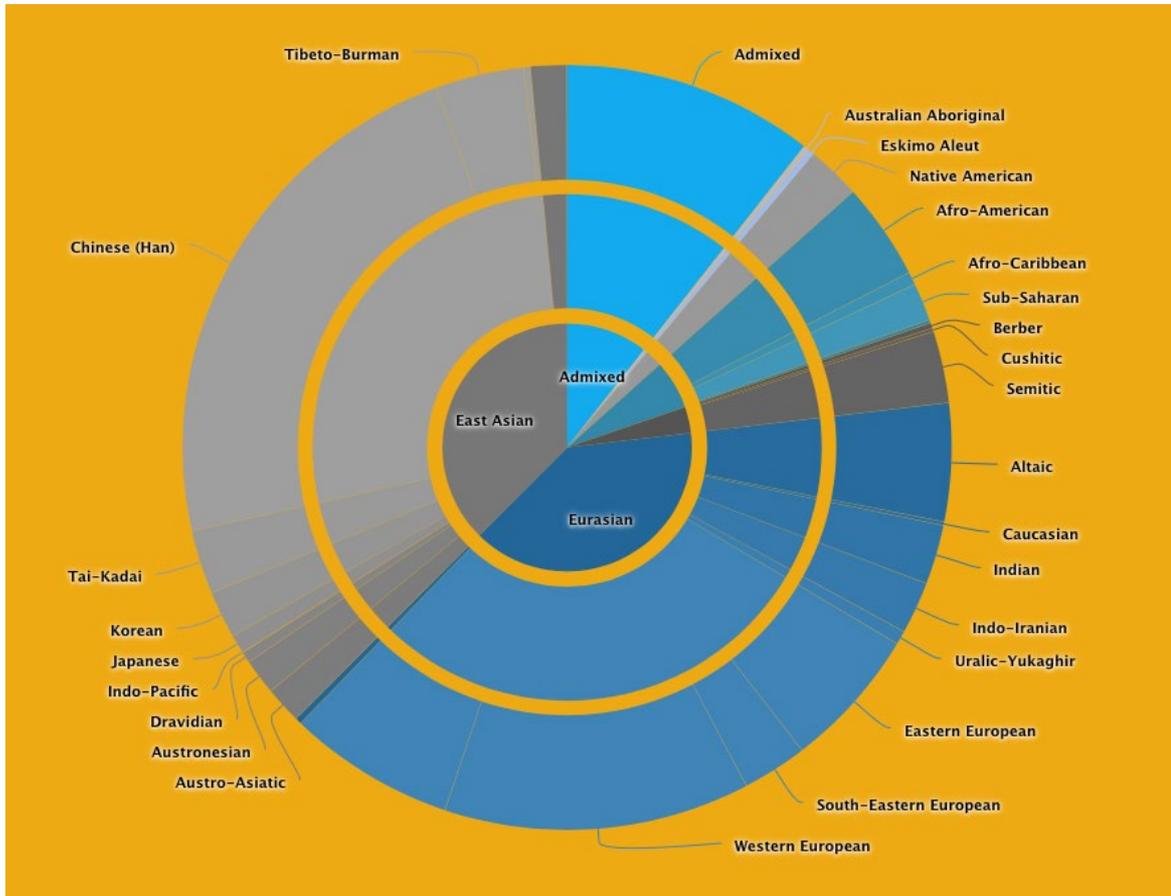


Figure 23a: Metapopulation structure

The Japanese Metapopulation (East Asian - Japanese) consists of 2303 haplotypes (at least minimal) and 26 unique population samples.

Most common haplotypes

[Minimal](#)

[PowerPlex Y](#)

Yfiler

[PowerPlex Y23](#)

[Yfiler Plus](#)

[Maximal](#)

Count	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385	DYS393	DYS391	DYS439	DYS635	DYS392	YGATAH4	DYS437	DYS438	DYS448
32	15	14	25	31	15	17	13,17	13	10	12	21	11	11	14	10	19
13	15	14	22	30	17	15	10,20	13	10	12	20	13	12	14	13	18
12	16	13	25	30	15	15	14,17	13	10	12	21	11	12	14	10	17
11	15	14	25	31	15	16	13,17	13	10	12	21	11	11	14	10	19
8	15	14	22	30	17	15	10,19	13	10	12	20	13	12	14	13	18
8	15	14	25	31	15	17	14,17	13	10	12	21	11	11	14	10	19
7	15	14	22	30	18	15	10,19	13	10	12	20	13	12	14	13	18

Figure 23b: Summary of the Japanese metapopulation

3.2.6 National databases

Each national database in the YHRD comprises all individuals sampled in a particular country regardless of the ancestry of the individuals (Figure 24). Some national databases are further structured into sub-populations (e.g., United States).

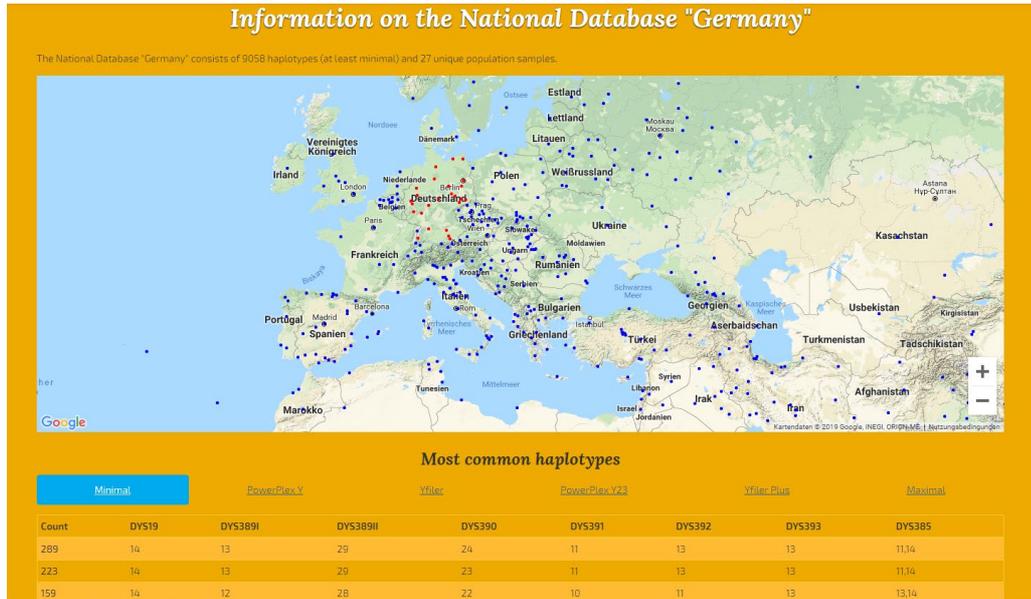


Figure 24: National database Germany

3.2.7 Y-SNP information

YHRD uses the resource *Phylotree Y* (Van Oven et al. 2014) to assign submitted SNP-analyzed haplotypes to haplogroups (Figure 25). A click on the respective haplogroup in the tree provides access to a map depicting the frequency of the selected haplogroup and to a table with the number of haplotypes typed in the current release for that haplogroup (Figure 26).

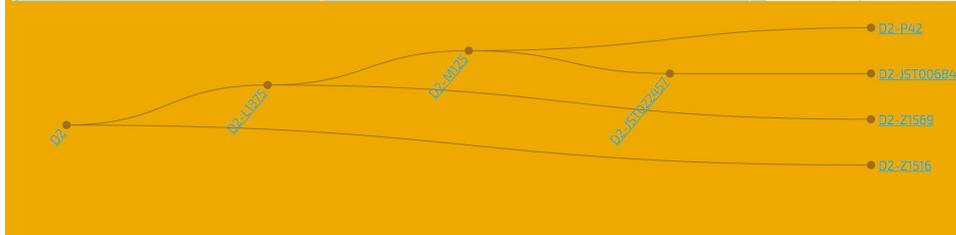
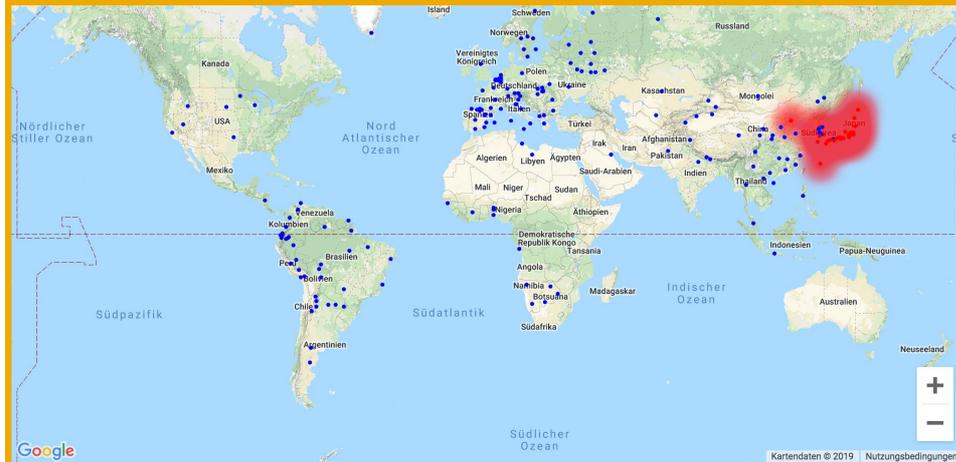
We are using [van Oven's Y-SNP tree](#) at the YHRD (Van Oven M., Geystelen V., Kayser M., Decorte R., Larmuseau MH. (2014), 'Seeing the wood for the trees: a minimal reference phylogeny for the human Y chromosome', *Hum Mutat* 35(2), 187-91 [[Pubmed](#)] [[DOI](#)]). All markers and branches are taken from the [tree](#) and/or from the set of [markers](#) published there. Please click on a branch / Y-SNP to get more information.



Figure 25: Y-SNP information

The Y-SNP branch D2 is defined by M179, M55, M57, Page31. Additionally, all downstream markers CTS2098, CTS504, CTS583, CTS7590, CTS9508, JST006841, JST022457, L1375, M116, M125, P42, Page3, Z1516, Z1520, Z1569, Z1576, Z1627 are defining this branch as well. For further information on a marker, please see [marker details](#) at [Phylotree Y](#) or consult the [Y-SNP tree](#) there.

Please note, that colours on the map only reflect a haplogroup distribution from the SNP-typed samples which were submitted to the YHRD.



Y-SNP marker	Haplogroup	Minimal	PowerPlex Y	Yfiler	PowerPlex Y23	Yfiler Plus	Maximal
CTS2098	D2-Z1516	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
CTS504	D2-Z1569	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes
CTS583	D2-Z1516	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes	0 Haplotypes

Figure 26: Description of Y-SNP branch D2

3.2.8 List of invalid Y-SNPs

Invalid Y-SNPs which are not accepted by the YHRD for various reasons, namely recurrence, are listed on a separate page (Figure 27).

List of Y-SNPs not suitable for inclusion in the YHRD

We list here all Y-SNP markers that are not suitable for inclusion in the YHRD. Please don't submit analysis results for those markers or type additional markers to support your findings.

- P25 - Invalid Recurrent within R1b. Samples with P25 as the final marker will be dropped. Downstream (e.g. M269 or M167) and/or the upstream marker (M343) need to be typed instead. See Adams SM., King TE., Bosch E., Jobling MA. (2006), 'The case of the unreliable SNP: recurrent back-mutation of Y-chromosomal marker P25 through gene conversion.', *Forensic Sci Int* 159(1), 14-20 [[PubMed](#)] [[DOI](#)]
- P41, P37, L202, and L203 - Invalid Recurrent marker with several states. This marker is completely dropped when submitted. Downstream and/or the upstream markers need to be typed instead. See Niederstätter H., Berger B., Erhart D., Willuweit S., Geppert M., Gassner C., Schennach H., Parson W., Roewer L. (2013), 'Multiple recurrent mutations at four human Y-chromosomal single nucleotide polymorphism sites in a 37 bp sequence tract on the ARSDP1 pseudogene.', *Forensic Sci Int Genet* 7, 593-600 [[PubMed](#)] [[DOI](#)]
- M35, M78, M81 and M215 are potentially recurrent. See Fernandes AT., Rosa A., Gonçalves R., Jesus J., Brehm A. (2008), 'The Y-chromosome short tandem repeats variation within haplogroup E3b: evidence of recurrent mutation in SNP.', *Am J Hum Biol* 20(2), 185-90 [[PubMed](#)] [[DOI](#)] and Cruciani F., Trombetta B., Novelletto A., Scozzari R. (2008), 'Recurrent mutation in SNPs within Y chromosome E3b (E-M215) haplogroup: a rebuttal.', *Am J Hum Biol* 20(5), 614-6 [[PubMed](#)] [[DOI](#)]

Recurrent markers with a stable/reliable branch assignment should be named according to their branch e.g. marker P203 is defining O1 with P203@O1 whereas P203 is defining I1 with P203@I1. Older recurrent markers got a trailing "1" or "2" like SRY1532.

Figure 27: List of invalid Y-SNPs

3.2.9 List of publications and references

Most population studies submitted to the YHRD for validation and upload are published in parallel in forensic journals (Forensic Science International: Genetics, International Journal of Legal Medicine and other journals). The YHRD Accession Number connects the article to the database (Figures 18, 19 + 28).

List of Publications and References

[Abban2019](#)
Kofi AE, Hakim HM, Khan HO, Ismail SA, Ghansah A, David AA, Mat NFC, Chambers GK, Edinur HA. (2019). 'Population data of 23 Y chromosome STR loci for the five major human subpopulations of Ghana', *Int J Legal Med Epub ahead of print*, In press [[DOI](#)]

[Aboukhalid2010](#)
Aboukhalid R, Bouabdellah M, Abbassi M, Bentayebi K, Elmzibri M, Squalli D, Amzazi S. (2010). 'Haplotype frequencies for 17 Y-STR loci (AmpFISTRy-filer) in a Moroccan population sample', *Forensic Sci Int Genet* 4(3), e73-4 [[PubMed](#)] [[DOI](#)]

[Achekzai2012](#)
Achekzai NM, Rahman Z, Shahzad MS, Daud S, Zar MS, Israr M, Husnain T, Willuweit S, Roewer L. (2012). 'Y-chromosomal STR analysis in the Pashtun population of Southern Afghanistan', *Forensic Sci Int Genet* 6(4), e103-5 [[PubMed](#)] [[DOI](#)]

[Adams2006](#)
Adams SM, King TE, Bosch E, Jobling MA. (2006). 'The case of the unreliable SNP: recurrent back-mutation of Y-chromosomal marker P25 through gene conversion', *Forensic Sci Int* 159(1), 14-20 [[PubMed](#)] [[DOI](#)]

[Adnan2017](#)
Adnan A, Rakha A, Noor A, Van M, Ralf A, Kayser M. (2017). 'Population data of 17 Y-STRs (Yfiler) from Punjabis and Kashmiris of Pakistan', *Int J Legal Med Epub ahead of Print*, In press [[DOI](#)]

[Adnan2018](#)
Adnan A, Rakha A, Lao O, Kayser M. (2018). 'Mutation analysis at 17 Y-STR loci (Yfiler) in father-son pairs of male pedigrees from Pakistan', *For Sci Int Genet* 36, e17-e18 [[DOI](#)]

[Adnan2019](#)
Adnan A, Rakha A, Kasim K, Noor A, Nazir S, Hadi S, Pang H. (2019). 'Genetic characterization of Y-chromosomal STRs in Hazara ethnic group of Pakistan and confirmation of DYS448 null allele', *Int J Legal Med* 133(3), 789-93 [[DOI](#)]

[Alaker2010](#)

Figure 28: List of publications and references

3.2.10 Release History

The release history provides Information about the particular submissions and how these are inserted in the current and former releases (Figures 6 + 29).

Release History
Release 61 - 2019/Jun/24
<ul style="list-style-type: none">• Contribution YA002897 (Netherlands [Dutch]): replace 2085 => 2085• Contribution YA003302 (Qinghai, China [Salar]): merge 133 => 172• Contribution YA004313 (Chubut, Argentina [Admixed]): append 133 => 204• Contribution YA004323 (Diyala, Iraq [Iraqi]): new 0 => 119• Contribution YA004324 (Baghdad, Iraq [Iraqi]): new 0 => 178• Contribution YA004325 (Anbar, Iraq [Iraqi]): new 0 => 127• Contribution YA004371 (Dezhou, China [Han]): append 2000 => 2101• Contribution YA004382 (Changzhou, China [Han]): replace 1193 => 1193• Contribution YA004526 (Xi'an, China [Han]): replace 581 => 581• Contribution YA004543 (Guizhou, China [Bouyei]): new 0 => 400• Contribution YA004544 (Al-Qadisyah, Iraq [Iraqi]): new 0 => 160• Contribution YA004545 (Southern/Central Iraq [Iraqi]): new 0 => 147• Contribution YA004546 (Karamay, China [Uighur]): new 0 => 129• Contribution YA004547 (Aksu, China [Uighur]): new 0 => 150• Contribution YA004548 (Kashi, China [Uighur]): new 0 => 177• Contribution YA004549 (Korla, China [Uighur]): new 0 => 141• Contribution YA004550 (Urumqi, China [Uighur]): new 0 => 49• Contribution YA004551 (Himachal Pradesh, India [Indian]): new 0 => 259• Contribution YA004552 (Dalian, China [Han]): new 0 => 879• Contribution YA004553 (Punjab, Pakistan [Saraki]): new 0 => 154• Contribution YA004554 (Punjab, Pakistan [Roma]): new 0 => 281• Contribution YA004555 (Hulun Buir, China [Mongolian]): new 0 => 282• Contribution YA004556 (Manama, Bahrain [Bahraini]): new 0 => 100• Contribution YA004557 (Northern Bahrain, Bahrain [Bahraini]): new 0 => 252

Figure 29: Release history

3.3 Tools

3.3.1 Data file validator

This tool can be used to validate all kinds of YHRD input files like haplotype search lists or population samples (Figures 4 + 30).

Data File Validator

Please submit your Excel-, OpenOffice- or CSV-spreadsheet OR your Applied Biosystems® GeneMapper® ID/ID-X or ABI PRISM® Genotyper® export-file to check if it is in concordance with Y-STR- and (if applicable) Y-SNP-nomenclature. Results of the quality inspection will be returned as a list together with advises to improve your file (if there are any noticeable problems). Finally you can download a re-formatted version of your file with automatic improvements.

Choose your file

Generic population data (optionally with Y-SNPs) ▾

→ GO

Figure 30: Data file validator

3.3.2 Y-STR mixture calculation

This tool can be applied when a mixed trace (≥ 2 male donors) and one person (suspect) which is included in the mixed profile should be analyzed. The trace Y-STR profile is compared to the known putative donor as well as to a number of unknown donors. The result will be a likelihood ratio of donorship vs. non-donorship of the suspect to the trace (Wolf et al. 2005) (Figures 31a – c).

Y-STR Mixture Calculation

Calculate the likelihood ratio of donorship of a given suspect versus non-donorship. The calculation requires a column named "Role" in your input file and consists of the following rows (specified at the "Role" column):

Trace	A trace (all given markers will be used for calculation)
Suspect	The profile of the suspect (or accused or defendant, or the profiles of the suspects if multiple)
Known Contributor	The profiles of additional known contributors (optional)

The only thing to enter after uploading your file is the number of unknown contributors.

Calculate Y-STR Mixture using your Excel-, OpenOffice- or CSV-spreadsheet

Figure 31a: Mixture analysis

Minimal PowerPlex Y **Yfiler** PowerPlex Y23 Yfiler Plus Maximal

Trace

DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385	DYS393	DYS391	DYS439	DYS635	DYS392	YGATAH4	DYS437	DYS438	DYS448
15, 16	13, 14	25	30, 31	15	15, 17	13, 14, 1	13	10	12	21	11	11, 12	14	10	17, 19

Suspect (XYZ123)

DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385	DYS393	DYS391	DYS439	DYS635	DYS392	YGATAH4	DYS437	DYS438	DYS448
15	14	25	31	15	17	13, 17	13	10	12	21	11	11	14	10	19

+ Add known contributor's profile

Number of unknown contributors

Use the new hierarchical approach to evaluate Y-STR mixtures (thus take all subsequent-sized datasets into consideration - instead of just using the one your profiles were typed with). Also enables the selection of metapopulation and estimation method in cases haplotypes are not observed in the database.

Reference metapopulation

 Calculate Mixture

Figure 31b: Mixture analysis – options and confirmation

Mixture Calculation Result

Congratulations! Your job has been successfully processed. It took less than a minute.

Name	Role	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385	DYS393	DYS391	DYS439
Trace A	Trace	15, 16	13, 14	25	30, 31	15	15, 17	13, 14, 17	13	10	12
XYZ123	Suspect	15	14	25	31	15	17	13, 17	13	10	12

Given the Haplotypes above and that there is 1 additional unknown contributor, the likelihood of the donorship of the suspect is approx. 15 times more likely than the non-donorship. This calculation is based on 1909 haplotypes (Yfiler) in the East Asian - Japanese Metapopulation.

Figure 31c: Mixture analysis – results

3.3.3 Kinship analysis

This tool calculates the likelihood ratio of patrilineal relationship versus non-relationship of male pairs given their Y-STR profiles (Figures 32a – d). The calculation is based on a formula adapted from Rolf et al. (Figure 32a). Calculation details can be reviewed as shown in Figure 32e.

YHRD kinship formula

L : set of loci with typed results for ancestor and offspring

s_l : allelic difference between ancestor and offspring at locus l

$\mu_{l,i}$: i -step mutation rate at loci l

$\frac{\mu_{l,i}}{2}$: probability of exactly one i -step mutation at locus l

$\left(\frac{\mu_{l,i}}{2}\right)^{s_l}$: probability of exactly one s_l i -step mutations at locus l

$1 - \mu_l$: probability of one non-mutation at locus l

$(1 - \mu_l)^{s_l}$: probability of s_l non-mutations at locus l

H_0 : hypothesis that ancestor and offspring are related

H_1 : hypothesis that ancestor and offspring are unrelated

m : number of transmission events under H_0 and H_1

$\binom{m}{s_l}$: binomial coefficient ' m choose s_l '

$$LR = \frac{P(E|H_0)}{P(E|H_1)}$$

$$LR_{\text{only 1-steps}} = \frac{\prod_{l \in L} \left[\binom{m}{s_l} \left(\left(\frac{\mu_l}{2} \right)^{s_l} (1 - \mu_l)^{m - s_l} \right) \right]}{f(\text{offspring})}$$

Figure 32a: YHRD kinship formula

Y-STR Kinship-Index Calculation

Calculate the likelihood ratio of patrilineal relationship versus non-relationship of male pairs given their Y-STR profiles. The calculation takes

- The profile of the **ancestor** ("upstream" male relative)
- The profile of the **offspring** ("downstream" male relative)
- The number of transmission events (often referred to as 'meiosis' or 'generation') between the male relatives

Please see Buckleton JS., Triggs CM., Walsh SJ. (2005), *Forensic DNA evidence interpretation*, 1st ed., CRC press and Rolf B., Keil W., Brinkmann B., Roewer L., Fimmers R. (2001), 'Paternity testing using Y-STR haplotypes: assigning a probability for paternity in cases of mutations.', *Int J Legal Med* 115(1), 12-5 [[PubMed](#)] for further details on the fundamental theory used here and [our documentation on the actual implementation at YHRD](#).

Limitation of this method

- Only one-step events are considered. E.g. it is impossible to explain a three-step difference with two transmission events.
- The relation between exactly two persons (ancestor and offspring) is calculated



Calculate Kinship-Index using your Excel-, OpenOffice- or CSV-spreadsheet file

Figure 32b: Kinship analysis

Minimal PowerPlex Y **Yfiler** PowerPlex Y23 Yfiler Plus Maximal

Ancestor Person A

DYS456 15
 DYS389I 14
 DYS390 22
 DYS389II 30
 DYS458 18
 DYS19 15
 DYS385 10, 19
 DYS393 13
 DYS391 10
 DYS439 12
 DYS635 20
 DYS392 13
 YGATAH4 12
 DYS437 14
 DYS438 13
 DYS448 18

Offspring Person B

DYS456 15
 DYS389I 14
 DYS390 22
 DYS389II 30
 DYS458 19
 DYS19 15
 DYS385 10, 18
 DYS393 13
 DYS391 10
 DYS439 12
 DYS635 20
 DYS392 13
 YGATAH4 12
 DYS437 14
 DYS438 13
 DYS448 18

Number of transmission events (often referred to as 'meiosis' or 'generation') between ancestor and offspring

Reference metapopulation used for frequency counting/estimation

Frequency counting/estimation method

Calculation method

 Calculate Kinship-Index

Figure 32c: Kinship analysis – options and confirmation

Result

The likelihood ratio of patrilineal non-relationship versus relationship (1/LR) is approx. 982.

Additional information:

- Japanese Metapopulation is used.
- Markers to consider for calculation: DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385, DYS393, DYS391, DYS439, DYS635, DYS392, YGATAH4, DYS437, DYS438, DYS448.
- There's a 1-step difference between the ancestor and the offspring at DYS458.
- There's a 1-step difference between the ancestor and the offspring at DYS385.
- Consider 1 transmission event

Figure 32d: Kinship analysis – results

[Show/Hide calculations](#)

```
 $\mu = \{\text{DYS456: } 4.408060\text{e-}03, \text{DYS389I: } 2.724252\text{e-}03, \text{DYS390: } 2.082950\text{e-}03, \text{DYS389II: } 4.327275\text{e-}03, \text{DYS458: } 6.172062\text{e-}03, \text{DYS19: } 2.086031\text{e-}03\}$   
f_offspring = n / N  
f_offspring = 7 / 1909  
f_offspring = 3.666841e-03 or 1 in 273 (using observed)  
m = 1  
s = {DYS456: 0, DHS389I: 0, DHS390: 0, DHS389II: 0, DHS458: 1, DHS19: 0, DHS385: 1, DHS393: 0, DHS391: 0, DHS439: 0, DHS635: 0}  
P(H0) = Prod_{l in L}{(m choose s_l) * ( (mu_l / 2)**s_l * (1 - mu_l)**(m - s_l) )}  
P(H0,DYS456) = (m choose s[DYS456]) * ( (mu[DYS456] / 2)**s[DYS456] * (1 - mu[DYS456])** (m - s[DYS456]) )  
P(H0,DYS456) = 1.000000e+00 * (1.000000e+00 * 9.955919e-01) = 9.955919e-01  
P(H0,DYS389I) = (m choose s[DYS389I]) * ( (mu[DYS389I] / 2)**s[DYS389I] * (1 - mu[DYS389I])** (m - s[DYS389I]) )  
P(H0,DYS389I) = 1.000000e+00 * (1.000000e+00 * 9.972757e-01) = 9.972757e-01  
P(H0,DYS390) = (m choose s[DYS390]) * ( (mu[DYS390] / 2)**s[DYS390] * (1 - mu[DYS390])** (m - s[DYS390]) )  
P(H0,DYS390) = 1.000000e+00 * (1.000000e+00 * 9.979170e-01) = 9.979170e-01  
P(H0,DYS389II) = (m choose s[DYS389II]) * ( (mu[DYS389II] / 2)**s[DYS389II] * (1 - mu[DYS389II])** (m - s[DYS389II]) )  
P(H0,DYS389II) = 1.000000e+00 * (1.000000e+00 * 9.956727e-01) = 9.956727e-01  
P(H0,DYS458) = (m choose s[DYS458]) * ( (mu[DYS458] / 2)**s[DYS458] * (1 - mu[DYS458])** (m - s[DYS458]) )  
P(H0,DYS458) = 1.000000e+00 * (3.086031e-03 * 1.000000e+00) = 3.086031e-03  
P(H0,DYS19) = (m choose s[DYS19]) * ( (mu[DYS19] / 2)**s[DYS19] * (1 - mu[DYS19])** (m - s[DYS19]) )
```

Figure 32e: Kinship analysis – calculation details

3.3.4 AMOVA and MDS

Analysis of Molecular Variance (AMOVA) is a method for analyzing genetic distances between populations using molecular data, e.g., Y-STR haplotypes (Excoffier et al. 1992). Besides the population in question, up to 10,000 haplotypes from reference populations and national databases of the YHRD can be selected. The online calculation returns as a result a CSV file (Figure 33g) with pairwise F_{ST} or R_{ST} values accompanied by p-values as a test for significance (10,000 permutations). In addition, an MDS plot is generated to illustrate the genetic distance between the analyzed populations graphically (Figure 33f). The program shows the references for the selected population studies which facilitates the correct citation. The step-by-step procedure is explained on the index page (Figures 33a – g).

Calculate AMOVA & MDS

Please perform online AMOVA as follows

1. Use your population sample(s) file (Excel) to start AMOVA. Be sure to provide haplotypes only for markers you are going to use in your AMOVA calculation. *E.g. when using a PowerPlex Y23 file, all AMOVA calculations are based on full Y23 haplotypes.*
2. Select populations and/or whole national databases from the YHRD. You can select up to 10,000 haplotypes in sum.
3. Check and adjust the calculation options/preferences as needed.

The result will consist of: a table of calculated pairwise F_{ST} or R_{ST} and p -values (as .csv file), a MDS plot (as .pdf file) and additionally, if "relaxing" was selected, a relaxation file with all the clusters built prior calculation (as .txt file).



Calculate AMOVA & MDS using your Excel-, OpenOffice- or CSV-spreadsheet population sample

Figure 33a: Calculate AMOVA and MDS

Calculate AMOVA & MDS

Please carefully check the data extracted from your file. There is 1 population sample given:

- 128 PowerPlex Y23 Haplotypes in a population sample called Berlin, Germany [German]

If the name doesn't match your expectations, please modify the appropriate column in your input file and re-submit it here.

ID	Population	DYS576	DYS389I	DYS448	DYS389II	DYS19	DYS391	DYS481	DYS549	DYS533	DYS4
TRV6L5A	Berlin, Germany [German]	17	12	20	28	15	10	27	12	12	10

→ Continue with calculate AMOVA & MDS

Figure 33b: Calculate AMOVA and MDS – confirmation

Please carefully select the populations you are going to compare your population sample to. Please note that there are only PowerPlex Y23 populations / national databases available for selection.

Filter populations ▼

Select a population to add ▾

Filter national databases ▼

Select a national database to add ▾

2732 / 10,000

- Berlin, Germany [German] (128 haplotypes)
- Freiburg, Germany [German] (260 haplotypes) ✕
- Greifswald, Germany [German] (176 haplotypes) ✕
- Berlin-Brandenburg, Germany [German] (131 haplotypes) ✕
- Leipzig, Germany [German] (303 haplotypes) ✕
- Rostock, Germany [German] (530 haplotypes) ✕
- Stuttgart, Germany [German] (1004 haplotypes) ✕
- Upper Bavaria, Germany [German] (200 haplotypes) ✕

→ Continue with calculate AMOVA & MDS

Figure 33c: Calculate AMOVA and MDS – selection

Selected populations / national databases

- Berlin, Germany [German] consists of 128 haplotypes (submitted population)
- Berlin-Brandenburg, Germany [German] consists of 131 haplotypes (YHRD provided Population)
- Freiburg, Germany [German] consists of 260 haplotypes (YHRD provided Population)
- Greifswald, Germany [German] consists of 176 haplotypes (YHRD provided Population)
- Leipzig, Germany [German] consists of 303 haplotypes (YHRD provided Population)
- Rostock, Germany [German] consists of 530 haplotypes (YHRD provided Population)
- Stuttgart, Germany [German] consists of 1004 haplotypes (YHRD provided Population)
- Upper Bavaria, Germany [German] consists of 200 haplotypes (YHRD provided Population)

- Use F_{ST} — The distance between two haplotypes is 0 if they are equal and 1 otherwise.
- Use R_{ST} — The distance between two haplotypes is the sum of the geometric distances (at each locus).
- Calculate p -values — To measure the certainty of F_{ST} or R_{ST} for any pair, the calculation will be repeated 10,000 times with a random population assignment of each haplotype each time. Thus the given value describes number of better differentiated (higher F_{ST} or R_{ST}) grouping revealed by random assignment compared to the actual F_{ST} or R_{ST} . This is **computational very intensive** — Use it with caution!
- Relax MDS calculation by clustering indistinguishable populations using the following criteria:
- Threshold F_{ST} or R_{ST} for clustering: 0.01, 0.02, 0.05 or 0.1
- Minimal size of a cluster 3, 5 or 10
- Generate output as separate CSV file.
- Generate MDS plot as separate PDF file.

Do calculate AMOVA & MDS

Figure 33d: Calculate AMOVA and MDS – options

Congratulations! Your job has been successfully processed. It took about a minute.

Below is the list of YHRD provided populations / national databases. Please cite the corresponding publications.

- 127 Haplotypes from Berlin, Germany [German]
- 127 Haplotypes from Berlin-Brandenburg, Germany [German]
 - Purps J. et al. (2014), 'A global analysis of Y-chromosomal haplotype diversity for 23 STR loci.', *Forensic Sci Int Genet* 12, 12-23 [[PubMed](#)] [[DOI](#)]
- 255 Haplotypes from Freiburg, Germany [German]
 - Schmidt U., Meier N., Lutz S. (2003), 'Y-chromosomal STR haplotypes in a population sample from southwest Germany (Freiburg area).', *Int J Legal Med* 117(4), 211-7 [[PubMed](#)] [[DOI](#)]
- 173 Haplotypes from Greifswald, Germany [German]
 - Kayser M. et al. (2005), 'Significant genetic differentiation between Poland and Germany follows present-day political borders, as revealed by Y-chromosome analysis.', *Hum Genet* 117(5), 428-43 [[PubMed](#)] [[DOI](#)]
- 296 Haplotypes from Leipzig, Germany [German]
 - Lessig R., Edelmann J. (1998), 'Y chromosome polymorphisms and haplotypes in west Saxony (Germany).', *Int J Legal Med* 111(4), 215-8 [[PubMed](#)]
- 526 Haplotypes from Rostock, Germany [German]
 - Rodig H., Grum M., Grimmecke HD. (2007), 'Population study and evaluation of 20 Y-chromosome STR loci in Germans.', *Int J Legal Med* 121(1), 24-7 [[PubMed](#)] [[DOI](#)]
- 976 Haplotypes from Stuttgart, Germany [German]
 - Roewer L. et al. (2001), 'Online reference database of European Y-chromosomal short tandem repeat (STR) haplotypes.', *Forensic Sci Int* 118(2-3), 106-13 [[PubMed](#)]
- 195 Haplotypes from Upper Bavaria, Germany [German]

⬇ Download csv-file

⬇ Download mds-file

Figure 33e: Calculate AMOVA and MDS – results

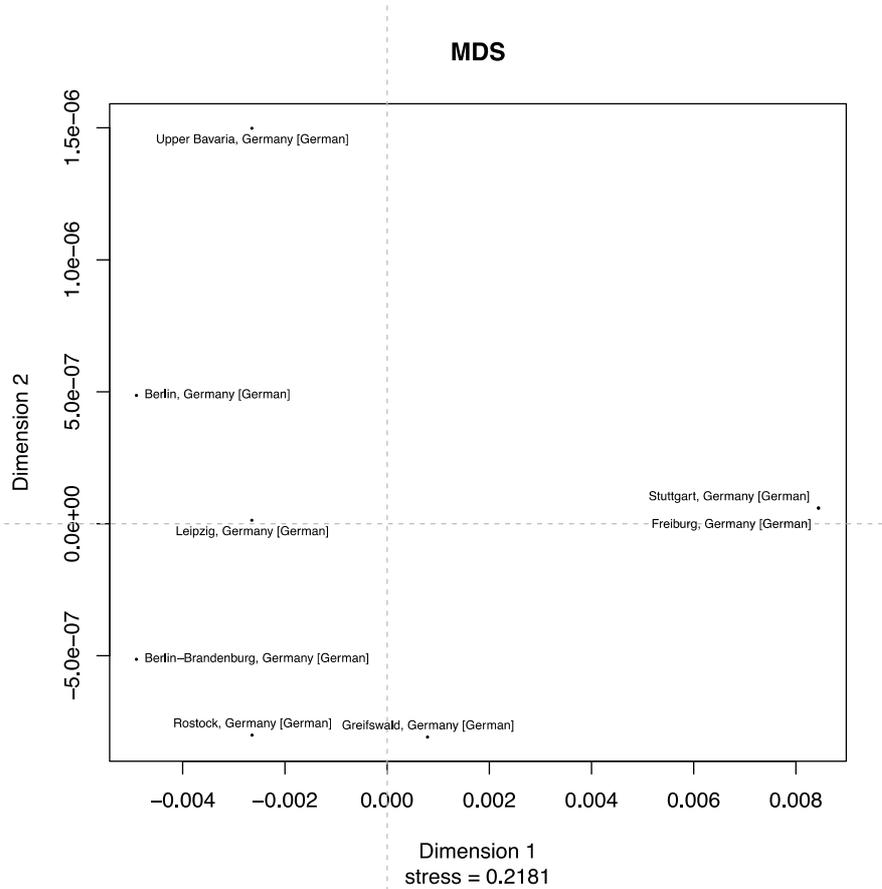


Figure 33f: Calculate AMOVA and MDS – MDS plot

	A	B	C	D	E	F	G	H	I
1	Population	Berlin, Germany [German]	Berlin-Brandenburg, Germany [German]	Freiburg, Germany [German]	Greifswald, Germany [German]	Leipzig, Germany [German]	Rostock, Germany [German]	Stuttgart, Germany [German]	Upper Bavaria, Germany [German]
2	Berlin, Germany [German]	-	10.000	0.0002	0.0175	0.2810	0.1761	0.0000	0.1877
3	Berlin-Brandenburg, Germany [German]	-0.0079	-	0.0002	0.0168	0.2752	0.1722	0.0001	0.1902
4	Freiburg, Germany [German]	0.0230	0.0230	-	0.1012	0.0002	0.0003	0.4041	0.0177
5	Greifswald, Germany [German]	0.0110	0.0110	0.0032	-	0.0625	0.2400	0.0058	0.1046
6	Leipzig, Germany [German]	0.0010	0.0010	0.0128	0.0040	-	0.6452	0.0000	0.6223
7	Rostock, Germany [German]	0.0020	0.0020	0.0116	0.0010	-0.0007	-	0.0000	0.2247
8	Stuttgart, Germany [German]	0.0256	0.0256	-0.0001	0.0073	0.0132	0.0137	-	0.0034
9	Upper Bavaria, Germany [German]	0.0024	0.0024	0.0072	0.0034	-0.0010	0.0010	0.0075	-

Figure 33g: Calculate AMOVA and MDS – R_{ST} – and p -values

3.4 Help & Support

The YHRD offers a number of help and support pages which include this manual, a screencast, FAQs, videos and links to educational webinars.

3.4.1 Contribute

This page explains in detail the submission of population samples to the YHRD and the procedure to receive an accession number (mandatory for peer-reviewed publication).

4 Glossary

4.1 Metapopulations

A metapopulation is generally considered to consist of several distinct populations. In forensic genetics the term “metapopulation” was adapted to describe an assemblage of genetic variants with shared ancestry spread over a territory (Millstein 2010; Willuweit and Roewer 2015). Population genetic analyses on different Y chromosomal marker sets show that metapopulations are stabilized over time by cultural and social factors, including a common language (Quintana-Murci et al. 2001, Baker et al. 2017), patrilocality (Oota et al. 2001) and/or geographical barriers (Rosser et al. 2000). Consequently, the YHRD was reorganized with the activation of YHRD version 4.0 in August 2014 in order to reflect Y-specific metapopulation structures and allow meaningful frequency calculations taking the cladistic structure of Y-STR haplotypes into account. Haplotype frequencies can still be reported country-wise (135 political entities are searchable) but preferably in metapopulations (MP), e.g., in the East Asian MP or the East Asian-Japanese MP (Figures 34 + 35). Frequency estimation methods such as DL use the collected samples of an MP to model the probability distribution of Y-STR haplotypes. Because these distributions differ between metapopulations, the estimated frequency of a certain haplotype also differs considerably between MPs.

Contributors to the YHRD are requested to provide metadata (geographic coordinates, ethnic ancestry and language group) on their population samples in order to assign these sensibly to a metapopulation.

It is important to state that the current metapopulation structure of the YHRD is an a-priori categorization which needs a continuous evaluation and verification by means of statistical methods to quantify the genetic similarity/dissimilarity between the samples. This research will show which groups can be abandoned, further divided or need a new definition.

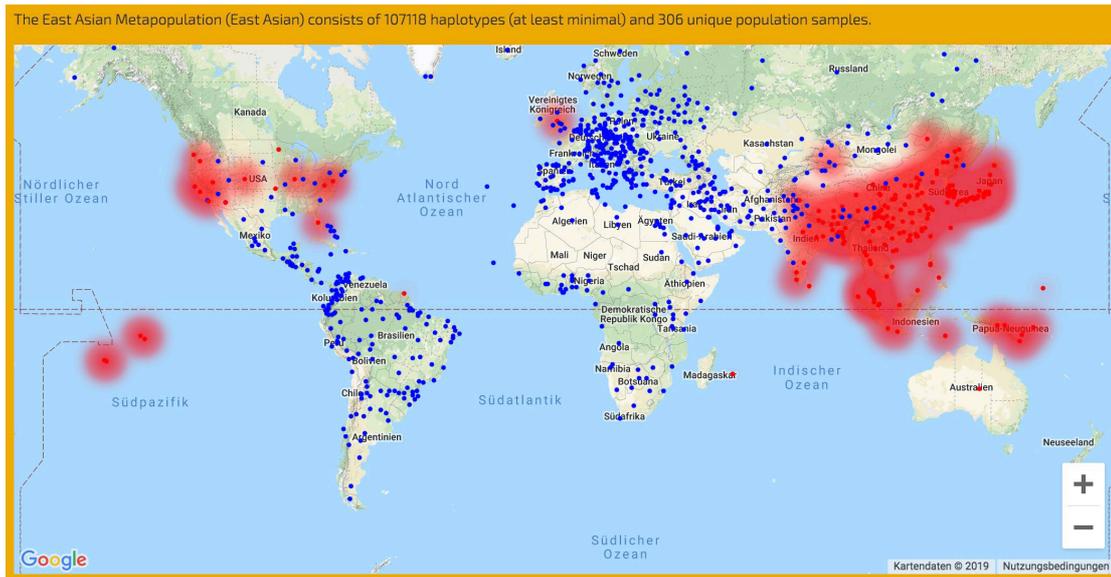


Figure 34: Distribution of the East Asian Metapopulation

The Japanese Metapopulation (East Asian - Japanese) consists of 2303 haplotypes (at least minimal) and 26 unique population samples.

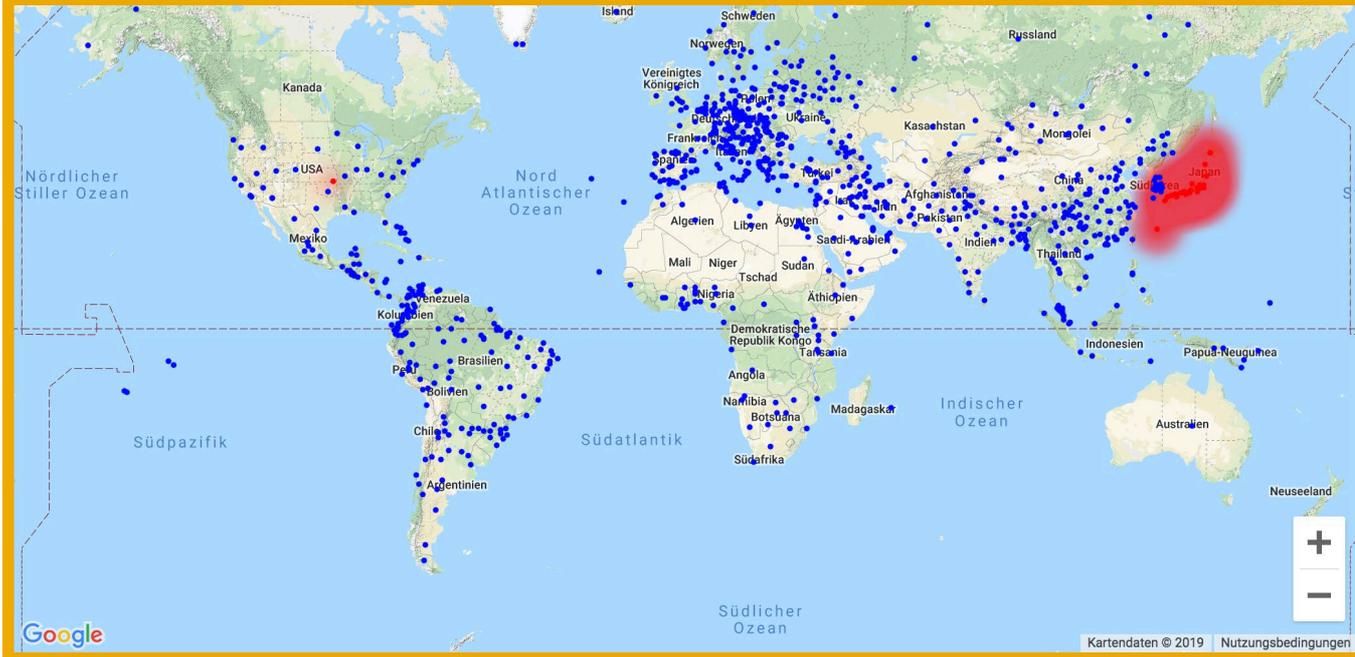


Figure 35: Distribution of the East Asian - Japanese Metapopulation

4.2 Haplogroups

The typing of Y chromosomes submitted to the YHRD is continuously extended for binary Y-SNP polymorphisms. Such “phylogenetic” Y-SNPs define a haplogroup which pertains to a single line of paternal descent. All Y chromosomes sharing a SNP mutation are related by descent, until a further mutation splits the branch. Haplogroups can be related by a single phylogeny using the principle of maximum parsimony (Jobling and Tyler-Smith 2003). The YHRD takes advantage of a consensus phylogeny used in forensic genetics (PhyloTree Y) which has a clear structure and nomenclature and captures the main Y-haplogroups of worldwide significance (van Oven et al. 2014). The YHRD submissions are prepared using the PhyloTree Y nomenclature defining Y-chromosome haplogroups by letters and the marker name, e.g., R1b-M269. The analysis of worldwide human Y-chromosome diversity has revealed a clear association of haplogroups and related haplotypes with geography and/or language (Underhill et al. 2000, Roewer et al. 2005). The Y-SNP/Y-STR typed reference samples of the YHRD can thus be used to predict the paternal ancestry of a DNA sample.

4.3 Frequency estimation methods

4.3.1 Counting

The observed match count in a database is used as the frequency estimate. The method is limited by the database size.

4.3.2 Augmented counting

The frequency of a haplotype when adding the haplotype in question once to both the database and the observations. The method is limited by the database size.

4.3.3 Discrete Laplace

The Discrete Laplace (DL) method estimates haplotype frequencies within a metapopulation by taking the phylogenetic relationship of haplotypes and its allelic distributions into account (Andersen et al. 2013). Please note that DL is calculated for minimal and YFiler haplotypes only and that the multicopy loci (DYS385ab) is excluded. Also, partial haplotypes or haplotypes with intermediate alleles or Null alleles cannot be calculated with the DL method. The method is not limited by database size but needs representatively sampled metapopulations.

4.3.4 Kappa

The Kappa method is a haplotype frequency estimation method which uses the frequency of singletons within a population sample (Brenner 2010). The method is limited by the database size.

4.3.5 Confidence Intervals

Following the correct Clopper-Pearsons (Clopper & Pearson 1934) method by evaluating the corresponding quantiles (given by $\alpha = 5\%$ in case of 95%-CI) using the beta distribution from

lower confidence interval (LCI = 2.5% in case of 95%-CI) to upper confidence interval (UCI = 97.5% in case of 95%-CI):

$$B\left(\frac{\alpha}{2}; x, n - x + 1\right) \dots B\left(1 - \frac{\alpha}{2}; x + 1, n - x\right)$$

where x is the number of successes (haplotype matches), and n is the number of trials (database size). The formula can be easily evaluated using Excel by utilizing the function "BETA.INV" and the same parameters as shown above.

Note that there are two special cases which cannot be evaluated using the initial formula:

(a) When there are no observations (successes, $x = 0$). In those cases, the LCI is 0 and the UCI is given by

$$1 - \left(\frac{\alpha}{2}\right)^{1/n}$$

(b) When all haplotypes in the database are matching (all trials are successes, $x = n$). In those cases, the LCI is given by

$$\left(\frac{\alpha}{2}\right)^{1/n}$$

and the UCI is 1.

YHRD provides four different presets for CI calculation: 95%-CI (2.5%-97.5%), 95%-UCI, 99%-CI (0.5%-99.5%) and 99%-UCI. Click the blue triangle next to the CI value to choose your appropriate CI value (see Figure 36).

Found 34 matches in 225,098 Haplotypes. This is approx. 1 match in 6,621 Haplotypes (95% UCI : 1 in 4,973 .

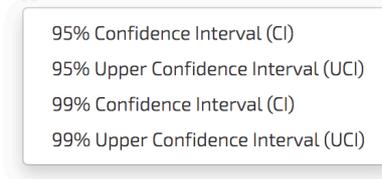


Figure 36: Choose confidence interval

4.4 AMOVA (Analysis of Molecular Variance)

4.4.1 *F*-Statistics

The values of *F*-statistics measure the correlation between genes drawn at different levels of a hierarchically subdivided population and allow the characterization of the level of genetic distinctiveness of supposedly inbred or isolated populations, and discrimination even between closely related populations; specifically the degree of (usually) a reduction in heterozygosity when compared to Hardy-Weinberg expectation.

F_{ST} describes the correlation between molecular diversity of random Haplotypes between two populations relative to random pairs of Haplotypes drawn from the whole species.

There are two different ways of dealing with a molecular distance of two Haplotypes: F_{ST} -based, where two Haplotypes are either equal ($F_{ST}=0$) or have at least one inequality ($F_{ST}=1$) and R_{ST} -based, where the sum of all squared differences between corresponding haplotype-pairs is used (Excoffier et al. 1992 and Roewer et al. 1996).

4.4.2 MDS (Multidimensional scaling)

This analysis is used to assign pair-wise similarities (or dissimilarities) to points in an *N*-dimensional space representing those similarities as distances between points. There are two major principles of MDS:

Metric MDS (M-MDS), a distance matrix *D* (similarities) into a set of coordinates such that the Euclidean distances derived from these coordinates fitting *D* as well as possible. The basic idea

of M-MDS is to transform the distance matrix into a cross-product matrix and then to find its Eigen-decomposition which gives a principal component. This requires linearity assumptions to be met.

Non-Metric MDS (N-MDS), on the other hand, uses the rank of a distance matrix Δ (dissimilarities) to iteratively assign locations to monotonic parts of Δ . In every iteration, the configuration of assigned locations is evaluated with respect to a stress criterion (how well the configuration approximates the original input dissimilarities).

5 References

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Notes

Notes
