

FORENSIC BIOLOGY PROTOCOLS FOR FORENSIC STR ANALYSIS

Usage of the “Y-Mix Database Filter”

Status:Published

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DATE EFFECTIVE
07/16/2021

APPROVED BY
Nuclear DNA Technical Leader

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Usage of the “Y-Mix Database Filter”

1 Procedure

1.1 Open the [Y mixture database](#) filter

1.2 Excel window will open. Enable the content by choosing Options→ Enable this content→ OK

The screenshot displays the 'Y-Mix Database Filter 3.0.1' application running within a Microsoft Excel window. The application interface includes a menu bar (Home, Insert, Page Layout, Formulas, Data, Review, View) and a ribbon with various toolbars. A 'Security Alert - Macro' dialog box is prominently displayed in the center, with the following text:

Security Alert - Macro

Macro
Macros have been disabled. Macros might contain viruses or other security hazards. Do not enable this content unless you trust the source of this file.

Warning: It is not possible to determine that this content came from a trustworthy source. You should leave this content disabled unless the content provides critical functionality and you trust its source.

More information
File Path: M:\..._Y_MAIN\Validations\Y STR mixture tool\Testing\CADOY-MixTool.xlsm

Help protect me from unknown content (recommended)
 Enable this content

Buttons: OK, Cancel

The background spreadsheet shows a 'Y-STR Profile' section with columns for markers: DYS 387S1, 19, 385, 388I, 388II, 390, 391, 392, 393, 437, 438, 439, 446, 445, 456, 458, 460, 461, 518, 533, 549, 570, 576, 627, 636, 643, 14. Rows list alleles 1 through 15. Below this is a 'New Variant' section with 'Observed Alleles' and a grid of numerical values representing frequencies or counts for each marker across different allele variants.

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1.3 Using drop-down menu, enter all of the alleles of the single source, deconvoluted donor, or mixture into the loci columns within the “Profile” worksheet.

Note: The order of loci in the Y-STR Mixture Tool is different from the Y-STR kit order. Please carefully enter these loci as they cannot be copied and pasted.

1.3.1 Null allele: A sample believed to contain a legitimate null allele due to mutation will be represented by a “0” allele at that locus. To include haplotypes with “0” alleles, you must manually enter “0” as an allele at that locus.

1.3.2 Drop Out: If drop out is suspected at any locus in the profile (i.e., there are visible peaks below analytical threshold that are unambiguously attributable to a contributor), the locus should be left blank.

1.3.2.1 This applies to the DYS385a/b locus with a single peak below stochastic threshold

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1.3.3 If an allele in the evidence profile is not present in the list below the table, enter it as a “New Variant” prior to entering it into the table (see red arrow below or the Instructions tab).

Y-Mix Database Filter 3.0.1
BETA 10/15/2011

Database Source: www.usisfdbase.org
Release 4.1 (Sept. 20, 2015)

Upper Confidence Interval:
Clopper and Pearson approach
(Biometrika 1934)

Database: x N x/N 1 in... 95% UCI 1 in...

Limit database to samples with all the Joci entered above?
Treat this profile as a single source sample?
Yes No Desired UCI 95.0%

This is a BETA vers
Filter spreadsheet.
been performed to a
results, there is no r
accuracy. Prior to its
case matters, users
own validation,
independently confir
case basis. The a
assumes no res
associated with
performance. U
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steven m

Y-STR Profile	DyF 38751	DyS 19	DyS 385	DyS 389	DyS 389b	DyS 390	DyS 391	DyS 392	DyS 393	DyS 437	DyS 438	DyS 439	DyS 448	DyS 449	DyS 458	DyS 458	DyS 460	DyS 481	DyS 518	DyS 533	YGATA 543	DyS 570	DyS 578	DyS 627	DyS 635	DyS 643	YGATA HA	
Allele 1	33			10																								
Allele 2	36			12																								
Allele 3																												

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1.4 In the center of the screen, ensure the following options are selected (see red arrows in diagram below):

1.4.1 Where it says: “Limit database to samples with all the loci entered above”, choose **YES**

1.4.2 Where it says: “Treat this profile as a single source sample”:

1.4.2.1 For a single source sample or deconvoluted donor profile: choose **YES**

1.4.2.2 For a mixed profile: choose **NO**

1.4.3 The desired Upper Confidence Interval (Desired UCI) should be set to **95%**.

1.4.4 Where it says: Use $(x+1) / (N+1)$, choose **NO**

Y-Mix Database Filter 3.1
BETA 041017spm

Database Source: www.usysdbdatabase.org
Release 4.2 (Feb. 18, 2017)

Upper Confidence Interval:
Clopper and Pearson approach
(Biometrika 1934)

Database	x	N	x/N	1 in...	95% UCI	1 in...
African American						
Asian						
Caucasian						
Hispanic						
Native American						
Combined						

Limit database to samples with all the loci entered above? **Yes**

Treat this profile as a single source sample? **No**

Desired UCI **95.0%**

Use $(x+1) / (N+1)$? **No**

This is a BETA version Filter spreadsheet. It has not been fully tested. If you use it, you assume no responsibility for any results. There is no accuracy. Prior to its use, users must perform their own validation independently on a case basis. The accuracy of the results is not guaranteed. Steven M. O'Connor, Director of Forensic Biology, New York State Office of Chief Medical Examiner.

New Variant:

Observed Alleles:	23	6	7	9	10	12	13	14	15	16	17	18	19	20	21	22	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	
32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
33	<10	8	10	25	19	6	8	10	12	<8	6	15	26	12	11	11	16	24	9	9	12	11	15	17	8	<8							
34	10	9	11	26	20	<7	9	11	<13	6	9	<16	27	<13	12	12	17	34.2	10	10	13	12	16	18	9	9							
35	11	10	12	27	20.1	7	10	12	13	8.2	10	16	28	13	13	13	18	35	10.1	11	14	13	17	<19	10	9							
36	12	10.2	13	28	21	8	10.2	13	14	9	10.1	16.2	29	14	<14	18	36	11	11.1	15	14	18	19	11	10								
37	13	11	14	28.3	21.1	9	11	14	14.3	10	11	<17	30	14.3	14	20	37	12	12	16	15	19.2	<20	11	11								
37.2	13.2	11.2	15	29	22	10	11.1	15	15	11	12	17	31	15	14.1	21	37.1	13	13	17	16	19	20	12	12								
38	14	11.3	16	30	23	11	12	16	16	12	13	17.2	32	16	14.2	22	37.2	14	14	17.3	17	19.2	21	13	13								
39	14.1	12		31	24	12	13	17	17	13	14	17.4	33	17	15	23	38	15	15	18	17.2	20	21.3	14	>13								

1.5 Click on the macro button “Compare the profile to the database.” (see green arrow below). This will filter the database, leaving only those haplotype(s) that would be included as possible contributors to your evidence.

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- 1.6 Summary of results. The website reports the number of times the haplotype was observed in the database (x), the database size (N), sample frequencies (x/N), and the upper bound of the 95% confidence interval (UCIs). See screenshot below.

Y-Mix Database Filter 3.1
BETA 04/07/20m

Database	x	N	x/N	1 in...	95% UCI	1 in...
African American	0	560	0		0.005335239	187
Asian	0	332	0		0.000982702	111
Caucasian	0	576	0		0.005187423	193
Hispanic	0	387	0		0.007711027	130
Native American	0	239	0		0.012456216	80
Combined	0	2,094	0		0.001429604	699

Limit database to samples with all the loci entered above? Yes No
Treat this profile as a single source sample? Yes No
Desired UCI Use (x+1)/(N+1)? 95.0% No

- 1.7 Print the screen by selecting “Print” from the printer menu at the top of the page and selecting a printer.
- 1.8 Verify on the printout that the Y-haplotype alleles were correctly entered into the website.
- 1.9 Report the 95% upper-bound confidence statistic from the African American, Asian, Caucasian, and Hispanic ethnic groups, **and truncate to three significant figures** (the “1 in...” column furthest to the right)
- 1.10 If both autosomal and Y-STRs are typed, the results are reported separately.

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