

M-FISys

Mass Fatality Identification System

Pedigree Sandbox

Kinship Likelihood: 1.5E+006
Posterior Probability: 99.3242%

Use RM...
Report
Show Equations
Reset

Sample Name	Gen	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51
V-50289-01	XY	neg	14/14	neg	neg	31.2/32.2	14/15
V-53129-01	neg	neg	neg	neg	neg	neg	neg
V-57681-01	XY	9/15	15/21	neg	9/14	28/29	neg
V-62338-01	XY	15/20	12/19	25/26	9/12	29.2/32.2	13/22
V-70593	XX	14/17	15/19	19/27	10/15	30/36	neg
V-78153-01	neg	neg	neg	neg	neg	neg	neg

Define likelihood ratios by drawing them. Say goodbye to confusing and error-prone algebraic representations.

SECURE NETWORK OPERATION

M-FISys can run standalone on a single computer or in a shared database environment that can scale to the number of samples and number of analysts you need. M-FISys utilizes password-protected logins and uses digital signatures to track changes and decisions made by individual analysts.



Gene Codes Forensics will provide all installation and training as well as customization to get your installation up and running quickly.

If you would like to see a demonstration of M-FISys or would like us to help evaluate your disaster response plan, contact us at:

Phone + 1-734-769-7249
Fax + 1-734-769-7074
e-mail info@gencodes.com
www.gencodesforensics.com



Gene Codes Forensics, Inc.
775 Technology Drive, Suite 100A
Ann Arbor, MI 48108

a division of Gene Codes Corporation

M-FISys[®]

Mass Fatality Identification System

M-FISys 8.03 - GCF Family Display

Profiles: Yun Chen Chang

RM	Gen	V-47181-01	BM-03716 #07	BF-08339 #09
37	D3S1358	15/17	15/17	15/18
46	vWA	14	14/17	14/17
56	FGA	23/24	21/24	23/24
57	D8S1179	14	10/14	13/14
66	D21S11	26/27	26/30	27/31.2
	D18S51	16/26	15/16	11/26
	D6S818	11	11	11
	D13S317	11/12	11/12	8/11
	D7S820	8/11	8/11	10/11
	D16S539	9/10	9/10	9/10
	TH01	8/9	9	7/8
	TPOX	8	8/13	8
	CSF1PO	12	12	12
	Penta D	13	13/13.2	9/13
	Penta E	13/20	14/20	13/19
	D2S1338	neg	neg	neg
	D19S433	neg	neg	neg

Likelihood: 8.0E+020
min LR to V: >99.9999%

STR SNP
Report All Races Conservative Race: Asian

Victim Remains Description
Mandible

Identification Statistics

Marker	Identified	Unidentified
D3S1358	100.00%	0.00%
vWA	100.00%	0.00%
FGA	100.00%	0.00%
D8S1179	100.00%	0.00%

Database application for managing and matching DNA profiles



M-FISys

Mass Fatality Identification System

Question: How can you handle DNA profile matching at scales both large and small?

Answer: **M-FISys**

Wherever there is the need for DNA profile matching, M-FISys (pronounced "emphasis") is uniquely able to make sense of huge quantities of data to assist in the task of human identification. Whether it be a large-scale civil incident, an airline disaster, an ongoing missing persons investigation, or management of local and national databases of DNA profiles for casework, M-FISys lets your analysts turn data into identifications. M-FISys features support:

- Extensive Missing Persons, DVI, and casework operations
- CODIS compatible file exchange
- Operation in a network environment with multiple users or as a standalone system that can be used on a common laptop
- Direct matching of DNA profiles to personal effects, with immediate access to raw electropherogram and image data for each sample
- Screening by STR/SNP or Mito with inter-assay concordance checks
- One-to-many and many-to-many searches based on user-defined thresholds for statistics or allele counts
- Automatic generation of complete match reports with statistics
- Automatic screening of all samples against exclusion profiles (e.g., laboratory personnel)
- Virtual Profiles, combining multiple test results from a single sample, with concordance & conflict reporting
- Kinship matching to family references. Samples can contribute to more than one case and M-FISys can handle complex pedigrees. Profiles can have multiple roles, allowing a direct reference or newly identified person to be used as a reference for another.

The screenshot shows the 'M-FISys 8.03 - Master List - GcfAdministrator' window. It displays a table with columns for ID, Load Date, RM, Relationship, Likelihood, I, # M Sn, Gen, D2S1328, VWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, D16S539, and TH. The table contains several rows, including a 'Direct Reference' and 'Victim' entries. Below the table are buttons for 'Expand All', 'Collapse All', 'Hide Identical Alleles', 'Exclude...', and 'Merge'. There are also checkboxes for 'Use gender in likelihood' and 'Hide Names', and buttons for 'Print' and 'Options...'. At the bottom, there are tabs for 'STR', 'Y-STR', 'mtDNA', 'SNP', 'Jobs', and 'Special'.

ID	Load Date	RM	Relationship	Likelihood	I	# M Sn	Gen	D2S1328	VWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	D16S539	TH
RM 57 (7)				8.0E+020	0		XY	15/17	14	23/24	14	26/27	16/26	11	11/12	8/11	9/10	8/8
PE-01520-01	12/13/01	57	Direct Reference	8.0E+020		16	XY	15/17	14	23/24	14	26/27	16/26	11	11/12	8/11	9/10	8/8
V-47181-01	12/13/01		Victim	8.0E+020		16	XY	15/17	14	23/24	14	26/27	16/26	11	11/12	8/11	9/10	8/8
VIRT-DM0152970			Victim	2.4E+017		14	XY	15/17	14	neg	14	26/27	16/26	11	11/12	8/11	9/10	8/8

STR view of direct match of fragmented remains to a personal effect reference

- Pedigree drawing tools to graphically specify likelihood ratio scenarios
- Graphical pedigree displays with editable relationships
- Calculation of likelihood ratios and posterior probabilities with flexible, intuitive parameters. No typing in of complex symbolic algebra!
- Calculation population statistics based on sample size. M-FISys can use any population statistics database required.
- Integration of non-DNA data, such as anthropological descriptions, location where remains were recovered including GPS or grid coordinates, and identifications made by fingerprints, dental or other methods. Annotations can include free-form text.
- Multiple levels of secure access privileges including "Administrator Only" functions
- Customizable management reports giving you insight into your data, including Administrative review tools to establish sample chain of custody
- QA tools allowing you to spot inconsistencies and errors in the data that may be the result of commingled remains, sample switches or contamination
- Data validation to reduce operator error on data entry, including automatic correction of common errors in mtDNA nomenclature (Anderson/CRS numbering)
- Extensive work lists and project management tools to help your team work effectively and efficiently
- Modular design, allowing new analysts to learn the specific parts of the program they need to contribute productively on the first day
- Data compatibility with all commercially available kits and markers and extensible for custom systems
- PM to PM kinship matching
- Annotation of failed alleles, trisomy and mixtures

M-FISys was created in response to 9/11 and was the primary software used in New York City to make the DNA identifications of the World Trade Center victims. It has been used in projects around the world, including missing persons identification in Mexico, post-war victim identification in Guatemala and the DNA Shoah Project investigating WWII deaths and family separations. It was used to make the initial DNA identifications after the Boxing Day Tsunami and was applied in response to the crash of American Airlines Flight 587. M-FISys can be used for disasters, missing persons investigations or to manage the DNA profiles in your daily casework.



Gene Codes Forensics is more than just a software company. We have practical, on-the-ground management experience at mass fatality incidents. In the event of a disaster we can put our experience at your service. Better yet, we can help you ahead of time by reviewing your current disaster response plan and making sure it addresses the likely issues. This includes the process for collecting reference samples from the families, systems and naming conventions for tracking these samples through the identification process, developing communications strategies for the families of the victims, and establishing the policies you will need to have in place in order to interpret the DNA results and translate matches into identifications.