FORENSICS TTA PROGRAM

DNA Basics: Understanding the Science and Tools Behind DNA Kinship Analysis

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Michelle Halsing earned her degree in Biological Sciences from California Polytechnic State University in San Luis Obispo, California.

She joined the California Department of Justice in 2001 as a Criminalist with the California State Offender DNA Database. In 2007, she was qualified as a casework analyst for the Missing Persons DNA Program (MPDP), where she has since advanced to a supervisory role while maintaining active qualifications in both short tandem repeat (STR) and mitochondrial DNA (mtDNA) casework.

In her current capacity, Michelle oversees complex case management and conducts in-depth research to identify cases suitable for forensic genetic genealogy (FGG) analysis. She has also served as a qualified ANSI National Accreditation Board/Quality Assurance Standards (ANAB/QAS) assessor since 2012, contributing her expertise to quality assurance and accreditation efforts within forensic laboratories.

Disclaimer

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DNA Basics: Understanding the Science and Tools Behind DNA Kinship Analysis

Michelle Halsing – Missing Persons DNA Program

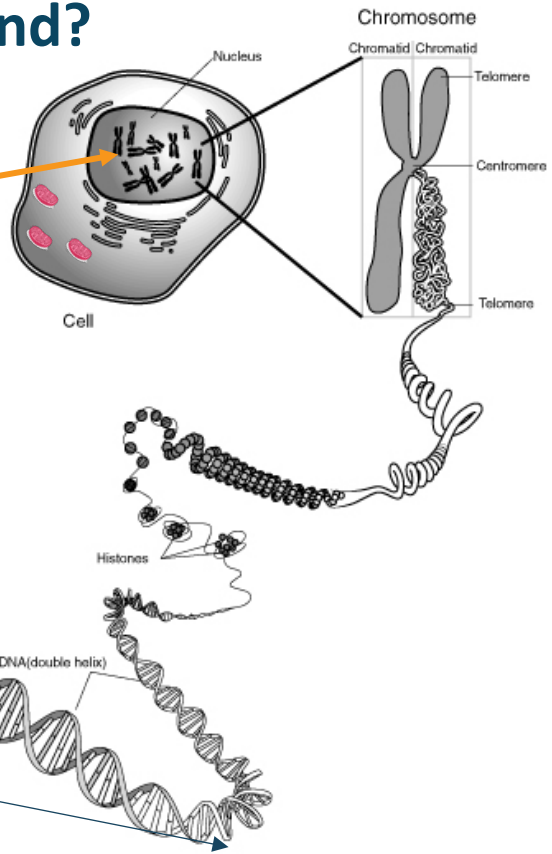
State of California Department of Justice Bureau of Forensic Services
Jan Bashinski DNA Laboratory

Outline

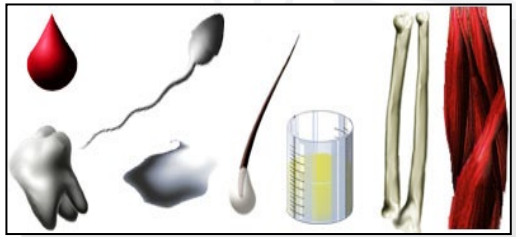
- Part One: Introduction
  - DNA 101
  - Application of CODIS
- Part Two: Kinship Analysis
  - Kinship Basics
  - The Kinship Testing Process at the Lab
  - Kinship Report Interpretation
- Part Three: Case Examples

DNA 101 – What is DNA and where is it found?

- Deoxyribonucleic Acid
  - The building blocks of life
  - ½ from Mom and ½ from Dad
  - Found in the nucleus of a cell or in the mitochondria

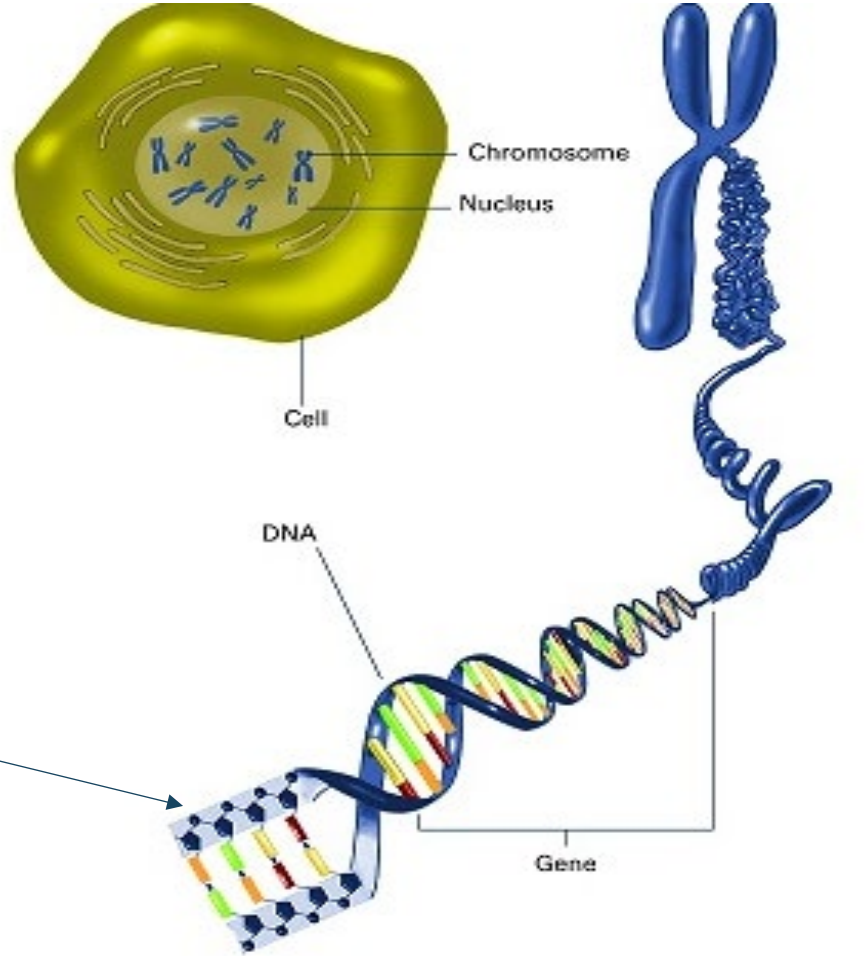


- Some types of evidence containing DNA:
  - Semen, bone, saliva, muscle tissue, hair, and blood (white blood cells only).



DNA Basics: Understanding the Science and Tools Behind DNA Kinship Analysis

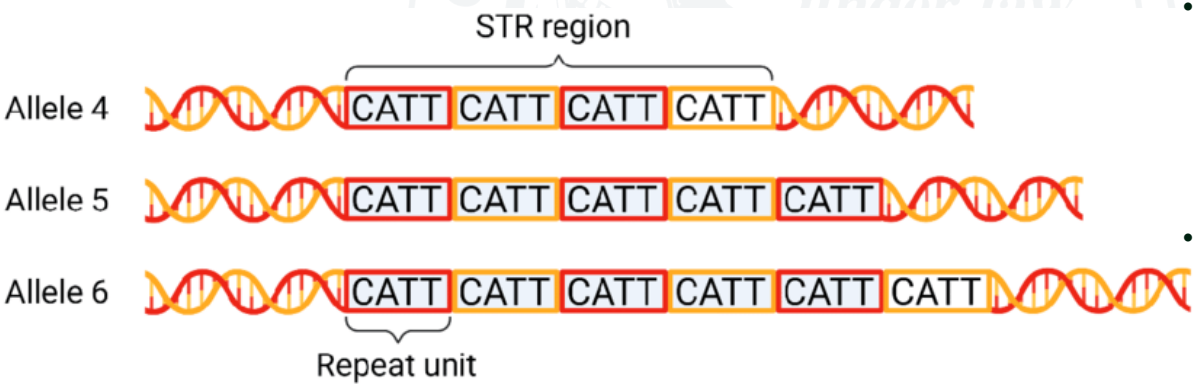
DNA, as the genetic instructions for our body's function, is a very long molecule. To be able to fit DNA in our cells, it is packaged into chromosomes. But if we unwind the chromosomes, we find that it is made of two strands that twist together to form a double helix like a twisted ladder. This double helix, or ladder, is held together by chemical bonds between four different building blocks or bases. These are the rungs of the ladder. It is the order of these bases that encodes genetic information.
For example: ATCG ATCG ATCG



What types of DNA testing are there?

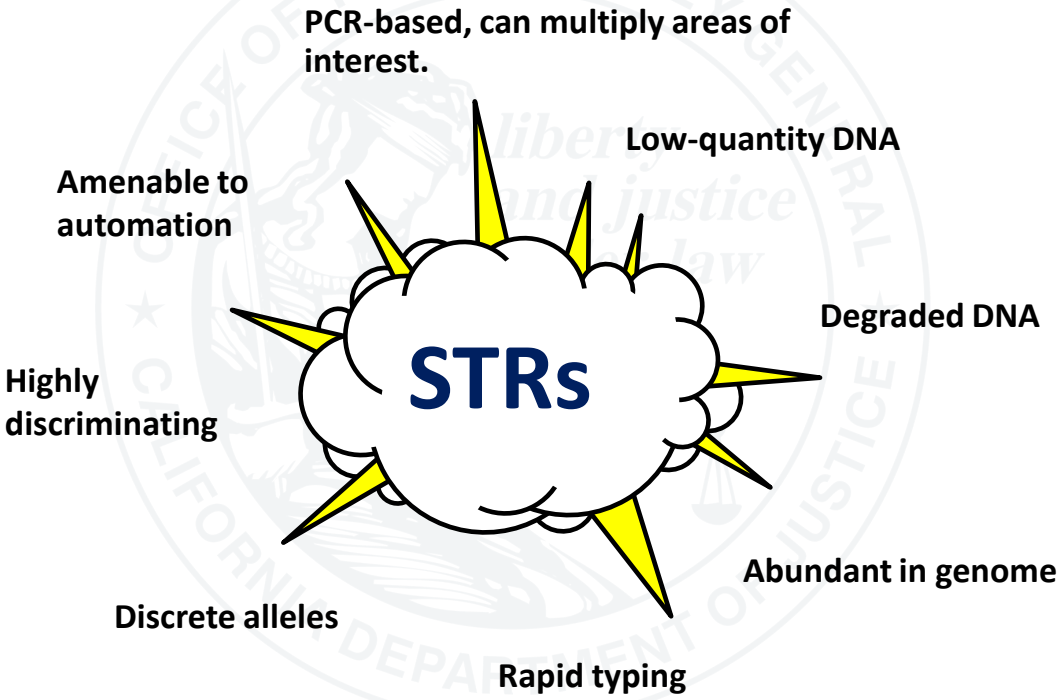
Short Tandem Repeat (STR) DNA Testing

- The gold standard in DNA testing, DNA found in the nucleus of the cell.
- In forensics, we look at 4-base repeat sequences on the DNA. It is the number of those repeats that make up the allele number.



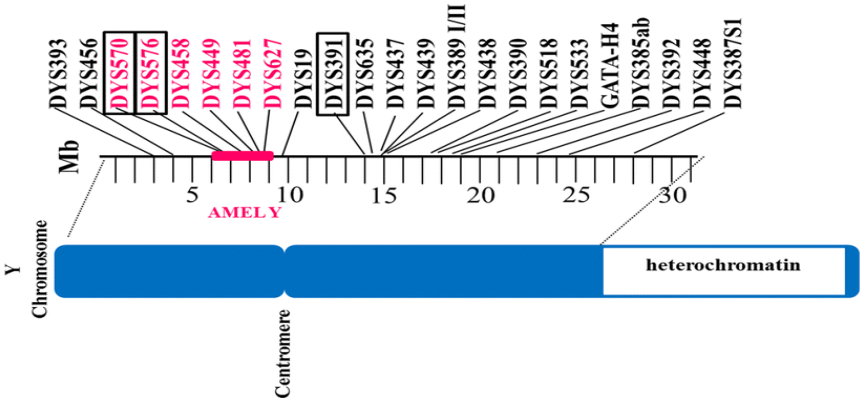
- With the number of repeats varying significantly between individuals, this makes it a useful genetic test for identification purposes, particularly in forensic science.
- A specific set of locations that have an STR have been chosen in the forensic community to produce a highly unique pattern per person that provides no useful information other than identity.

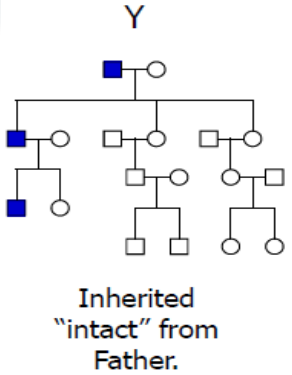
Why are STRs useful in forensics?



Y-STR testing and its usefulness in forensics

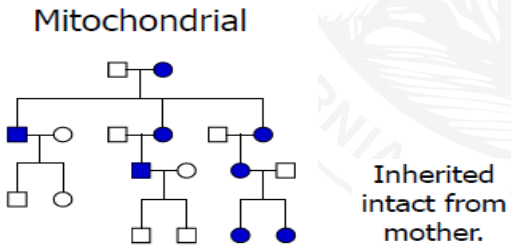
- Y-STR DNA refers to "Y-chromosome short tandem repeat" DNA, which means a specific sequence of repeating DNA nucleotides located on the male Y chromosome.
- Used primarily in forensic analysis to identify male lineage, it has a unique inheritance pattern from father to son only.
- Y-STR testing can be particularly useful in cases like sexual assault where there might be a mixture of male and female DNA, allowing identification of the male contributor.

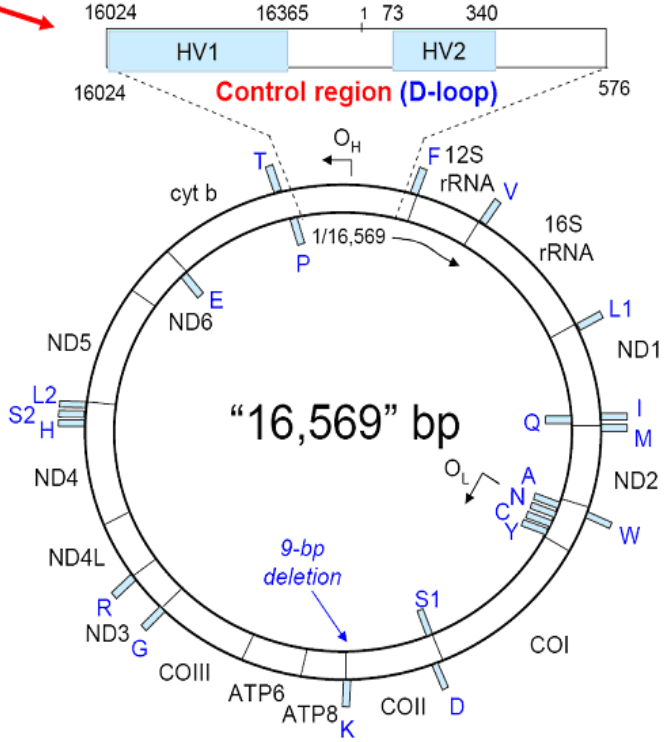




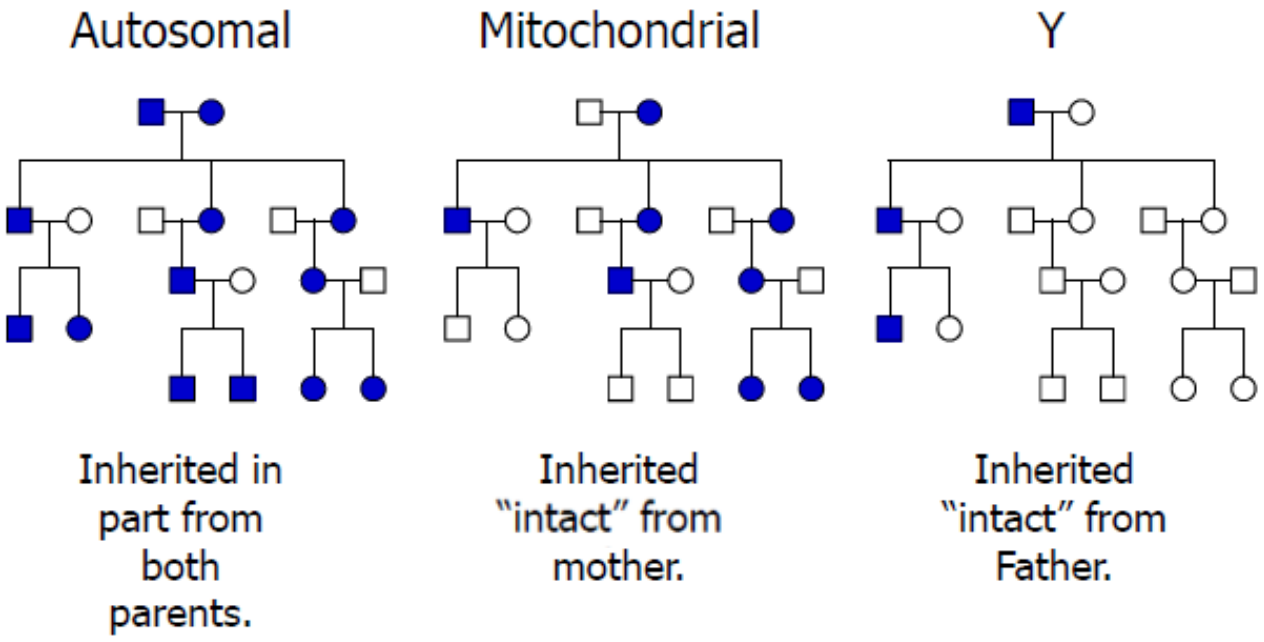
Mitochondrial DNA (mtDNA) testing and its usefulness in forensics

- There are many copies of the mtDNA genome in one cell (instead of just two for nuclear) allowing for analysis of small amount of biological material.
- Mitochondrial DNA is inherited from mother to child intact (barring mutation). This makes mtDNA useful for identifying familial relationships even when relatives are separated by multiple generations.
- Historically, forensic testing of mtDNA only used a small section called the non-coding or control region. Now with newer technology we can sequence the whole mtGenome.

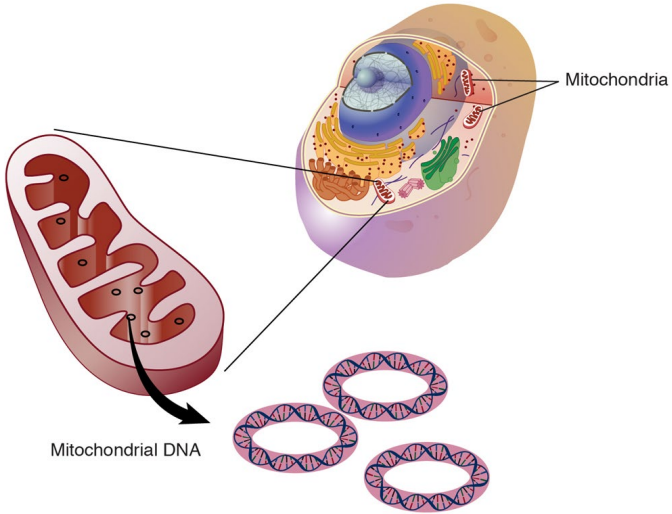


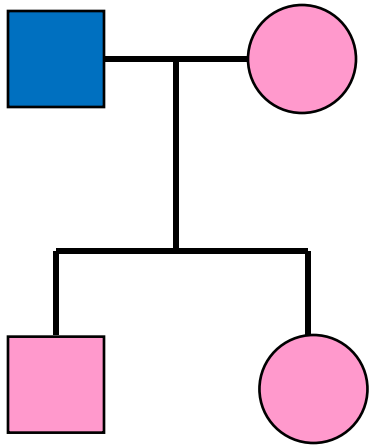


Nuclear (autosomal), mtDNA, and Y-STR Inheritance Patterns



Mitochondrial DNA (mtDNA)



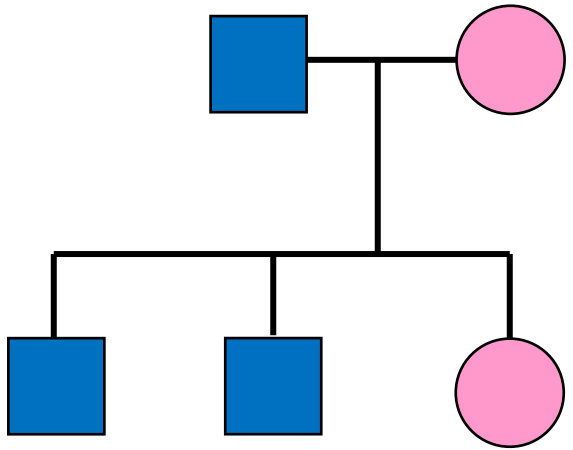


- Mitochondria have their own DNA
- Inherited maternally (passed down from mother to child)

Diagram from National Human Genome Research Institute

Y Chromosome

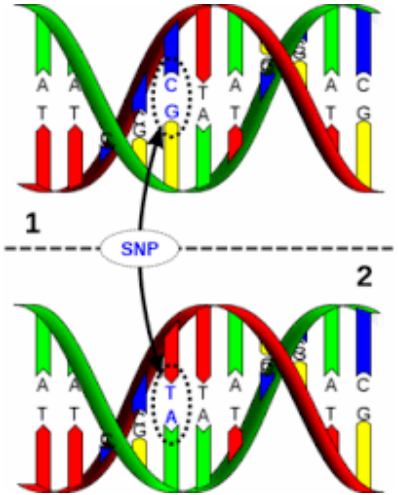
- Causes development of male sex characteristics
- Inherited paternally (passed down from father to son)



Single Nucleotide Polymorphisms (SNP)

A single nucleotide substitution at a specific location on the chromosome.

An example of a SNP is the substitution of a C for a G in the nucleotide sequence AAC**G**AT, thereby producing the sequence AAC**C**AT. The DNA of humans contains many SNPs, since these variations occur at a rate of one in every 100–300 nucleotides in the human genome.



Types of SNPs used in Forensic Science:

- Identity Informative – iiSNPs – Identity SNPs (Comparable to STRs)
- Phenotypic Informative – piSNPs – Eye, skin, hair color estimations
- Ancestry Informative – aiSNPs – Ancestry
- Kinship Informative – kiSNPs – Relationship testing
- X-SNP and Y-SNPs – Specific SNPs on X and Y chromosome- Lineage

Single Nucleotide Polymorphisms (SNP) – Genealogy

Genealogy searches utilize a large SNP profile to create associations. SNP typing methods:

Microarray Genotyping - Used by direct-to-consumer companies

- Array chips can vary in number of SNPs targeted.
- Works best with high input and quality DNA with no microbial co-extraction.

Targeted Sequencing - Massive Parallel Sequencing (MPS)

- Kintelligence, Kintelligence HT, or FORCE Panel
- A targeted number of SNPs specific for investigative genetic genealogy are sequenced.
- Avoids medical information.
- This is a great tool for degraded samples with high microbial content.

Whole Genome Sequencing - Massive Parallel Sequencing (MPS)

- An attempt at sequencing the whole human genome.
- The results are not in the standard genealogy database format and need to be converted, which is an involved process.
- Uses large scale instruments with a high price tag for most public laboratory systems.
- Can process DNA fragments of very small sizes which makes it a great tool for degraded samples.

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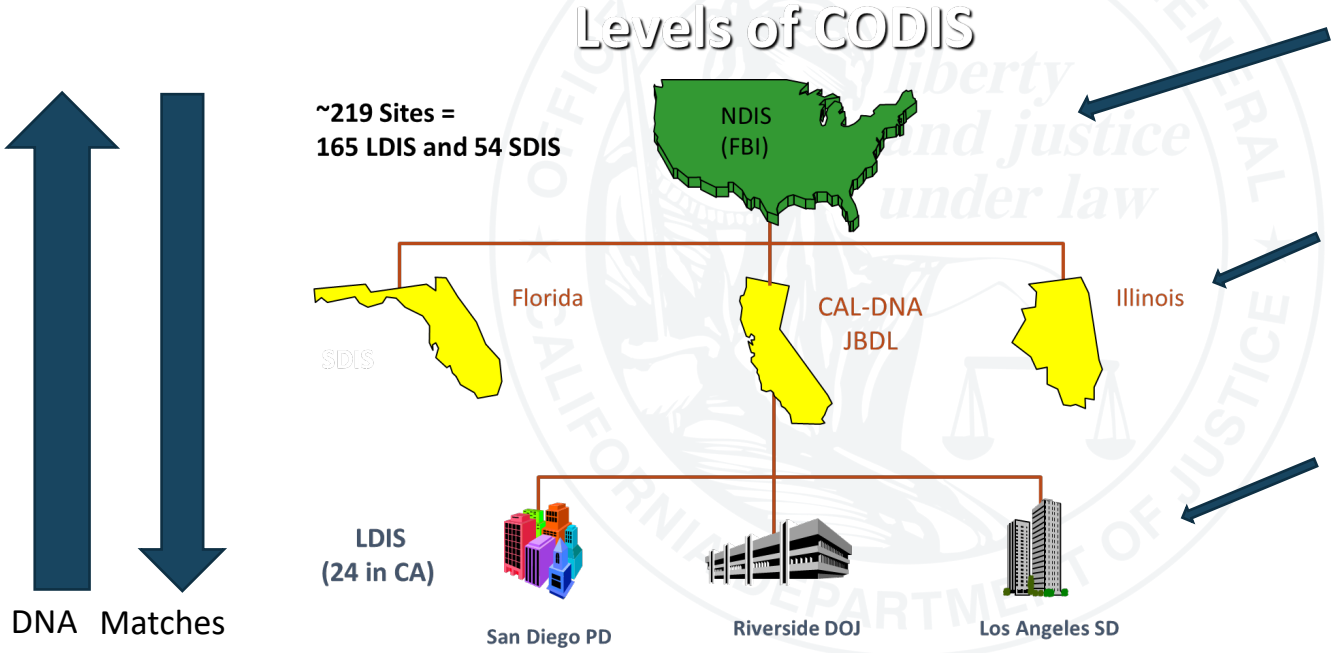
Combined DNA Index System (CODIS)

CODIS is the name of the software that runs the DNA database.

The **software** is used to conduct searches between specified indexes (types) of DNA records the goal of identifying matching profiles.

The use of CODIS enhances public safety by providing investigative leads that help identify criminals, and it helps to bring closure to victims of crimes and families of victims and missing persons by aiding in the identification of an individual or human remains.

CODIS System Structure



NDIS – The National DNA Index System (operated by the Federal Bureau of Investigation)

SDIS – A State DNA Index System (operated by a state agency such as attorney general, state police or department of forensic sciences)

LDIS – A Local DNA Index System (operated by a city or county law enforcement or government agency)

CODIS Laboratory Requirements

Laboratory	Standards	Laws
• Government • Public	• FBI QAS • Accrediting (ANAB Stds.) • ISO/IEC 17025:2017	• Federal • State

Memorandum of Understanding *(contract)*

Different searches done within CODIS

NDIS Searchable Indexes

Index	Forensic[32]	Offender[33]	Unidentified Human (Remains)	Missing Person	Relatives of Missing Person and Pedigree Tree
Forensic[24]	X	X	X	X	
Offender[25]	X		X	X	
Missing Person	X	X	X		
Relatives of Missing Person and Pedigree Tree			X		
Unidentified Human (Remains)	X	X	X	X	X

Please note family of missing person samples are NOT searched against any other database other than the Unidentified Human Remains Index.

CODIS MPDP Searches

SDIS (MPDP Searches)

- Weekly searches (4)
  - Identity Search (Direct Match)
  - Pedigree Search (Indirect Match)
  - mtDNA only
  - Y-STR only

NDIS (National)

- Weekly Search
  - Identity Search (Direct Match)
- Monthly Search
  - Pedigree Searches (2 types)
- Quarterly Search
  - mtDNA only
  - Y-STR only

https://www.fbi.gov/services/laboratory/biometric-analysis/codis/codis-and-ndis-fact-sheet

CODIS HIT - Direct

Unidentified Remains

D3S1358	15,16
vWA	14,16
D16S539	9,10
CSF1PO	11,12
TPOX	8,8
Y indel	2
Amel	X,Y
D8S1179	12,13
D21S11	28,31
D18S51	12,15
DYS391	11
D2S441	14,15
D19S433	14,15
TH01	7,9.3
FGA	24,26
D22S1045	11,16
D5S818	11,11
D13S317	11,11
D7S820	7,12
SE33	17,25.2
D10S1248	12,15
D1S1656	13,16
D12S391	18,19
D2S1338	20,23

=

D3S1358	15,16
vWA	14,16
D16S539	9,10
CSF1PO	11,12
TPOX	8,8
Y indel	2
Amel	X,Y
D8S1179	12,13
D21S11	28,31
D18S51	12,15
DYS391	11
D2S441	14,15
D19S433	14,15
TH01	7,9.3
FGA	24,26
D22S1045	11,16
D5S818	11,11
D13S317	11,11
D7S820	7,12
SE33	17,25.2
D10S1248	12,15
D1S1656	13,16
D12S391	18,19
D2S1338	20,23

Offender Sample

Personal effect from Missing Person

Other human remains

CODIS HIT - Indirect

Unidentified Remains

Marker	Item JH-3
	Femur
D3S1358	15,16
vWA	14,16
D16S539	9,10
CSF1PO	11,12
TPOX	8,8
Y indel	2
Amel	X,Y
D8S1179	12,13
D21S11	28,31
D18S51	12,15
DYS391	11
D2S441	14,15
D19S433	14,15
TH01	7,9.3
FGA	24,26
D22S1045	11,16
D5S818	11,11
D13S317	11,11
D7S820	7,12
SE33	17,25.2
D10S1248	12,15
D1S1656	13,16
D12S391	18,19
D2S1338	20,23

Marker	MP-18-0126A
	Bio Mom
D3S1358	15,17
vWA	14,18
D16S539	9,12
CSF1PO	10,12
TPOX	8,8
Y indel	ND
Amel	X,X
D8S1179	12,16
D21S11	29,31
D18S51	10,15
DYS391	ND
D2S441	12,15
D19S433	14,16
TH01	6,9.3
FGA	24,27
D22S1045	11,15
D5S818	11,11
D13S317	11,13
D7S820	9,12
SE33	17,26
D10S1248	12,14
D1S1656	12,16
D12S391	16,19
D2S1338	20,24

Looking for DNA that is shared in common between remains profile and profiles from relatives.

For a parent/child relationship DNA must be shared at each marker.

What to do if the comparison results (requested comparison or CODIS search) are inconclusive?

- Additional DNA analysis (UHR and/or MP relatives)
- Collect DNA samples from more and closer relatives
- Mitochondrial DNA analysis (must be maternally related)
- Y-chromosome analysis (must be paternally related)
- Compare other metadata (physical characteristics, case circumstances, etc.)

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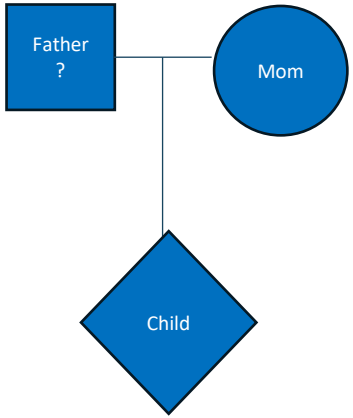
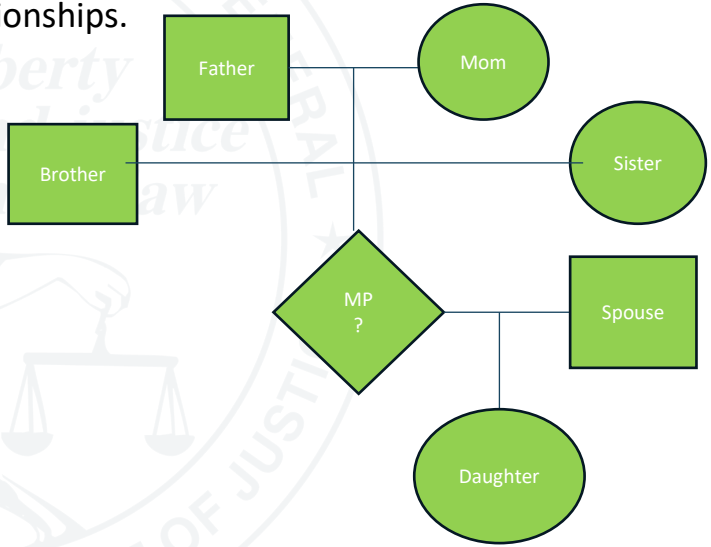
Kinship Basics

Kinship DNA testing determines the biological relationships between individuals by analyzing their genetic markers. It's often used to establish paternity, maternity, or to identify sibling relationships, including full siblings (shared both parents) and half-siblings (sharing only one parent). This type of testing can also be used to identify a broader range of family relationships.



References include biological mom, child(ren), and possible father.

Paternity Testing



References can include any combination of biological mom, biological father, siblings, and/or biological children.

Kinship Testing

Kinship Basics – Solving Cases

Unidentified Remains – Kinship Testing

DNA profiles obtained from both unknown human remains, and family reference standards are uploaded to CODIS and are then routinely searched against the appropriate DNA databases. Alternatively, a law enforcement agency may request a direct comparison of the remains profile and a family reference sample. Kinship testing is done when an association is made to potential family members.

Missing Person / Family DNA

Analyzing the DNA from a direct reference from the missing person (such as a toothbrush or newborn bloodspot) or known family. DNA profiles are entered into CODIS and are searched against the appropriate DNA Database(s). Kinship testing is done when an association is made to a potential unidentified human remains case.

Product of Conception – Reverse Paternity Testing – Father not available

By analyzing the DNA from the fetal tissue (products of conception), scientists can identify the alleles (genetic variations) present in the fetus, then compare those to the known alleles of the mother to deduce the possible alleles that must have come from the father.

Analysis Results – DNA Profile Obtained

21 DNA markers
Amelogenin (sex determination)
2 Y chromosome markers

So now what to do with the profile?

Marker / Type	
D3S1358	15,16
vWA	14,16
D16S539	9,10
CSF1PO	11,12
TPOX	8,8
Y indel	2
Amel	X,Y
D8S1179	12,13
D21S11	28,31
D18S51	12,15
DYS391	11
D2S441	14,15
D19S433	14,15
TH01	7,9.3
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D5S818	11,11
D13S317	11,11
D7S820	7,12
SE33	17,25.2
D10S1248	12,15
D1S1656	13,16
D12S391	18,19
D2S1338	20,23

What to do with a DNA profile from a decedent? – Request a Comparison

- Coroner/Law Enforcement has an idea who the decedent is based on case circumstances.
- Profile for remains is compared to profiles from family (or personal effects from missing person if family cannot be found)
- Important to note on submission paperwork that you are requesting a comparison!

What to do with profile? – Search CODIS

Direct Match

- The DNA profile from the uploaded unidentified remains matches a DNA profile from the personal effects of a missing person or convicted offender in CODIS.
- These DNA profiles must match exactly at all genetic markers.

Indirect Match (association)

- The DNA profile from the uploaded unidentified remains doesn't directly match another profile but instead shows a strong genetic similarity to the DNA profiles of one or more of the missing person's relatives.
- This happens because family members share a significant amount of DNA.

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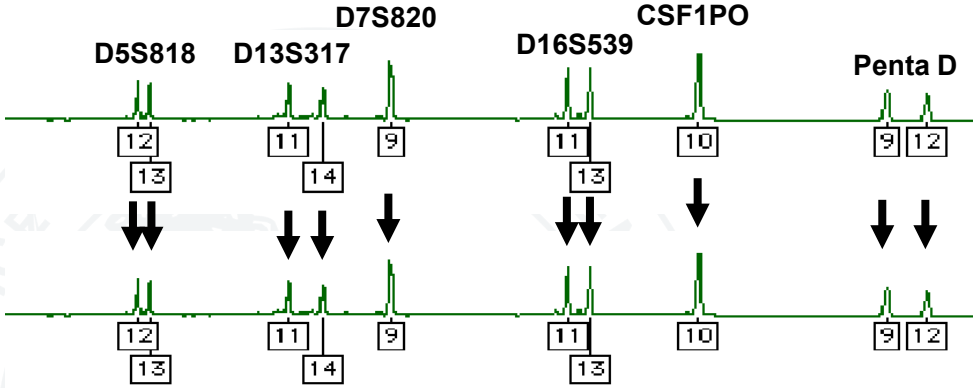
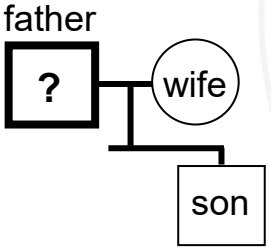
(A) Direct comparison

DNA profile from **Decedent**

DNA profile from **direct reference** (toothbrush believed to have belonged to the missing father)



(B) Kinship analysis (Indirect comparison)



	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D	
	11,13	8,12	8,12	8,9	10,12	8,10	wife
	11,13	8,14	8,9	9,13	10,10	9,10	son
Possible decedent profile	11,**?** *or* **?**,13	**?**,14	9,**?**	**?**,13	**?**,10	9,**?**	father
Decedent profile	12,13	11,14	9,9	11,13	10,10	9,12	actual profile

Figure 24.1, J.M. Butler (2005) *Forensic DNA Typing*, 2nd Edition © 2005 Elsevier Academic Press

Collect samples from additional relatives

- Best choices to collect from are first order relatives (parent/child and siblings).
- When the MP is a father or mother it is important to collect DNA from all children AND the other parent.
- Make sure to verify relationship between the relative and the MP (e.g., full sibling vs. half sibling).
- Consider possible non-paternity (may need to conduct interviews of relatives separately)

Collection of Family Reference Samples – Who to Collect?

When it comes to collecting family references, it can be confusing not only with who to collect but also how many relatives to collect DNA from.

The California DOJ requests submission of two family reference samples per missing person as available. These family reference samples should be from the closest relations to the missing person as possible. This is due to how DNA is shared though family members.

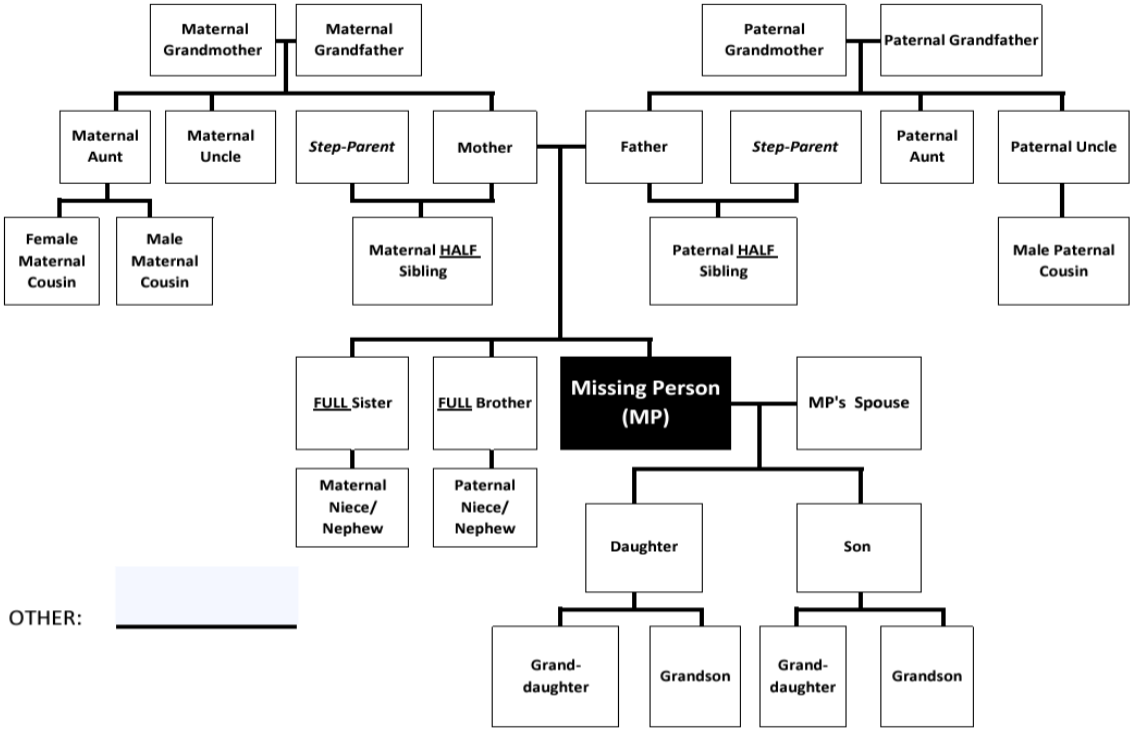
The missing person gets half their DNA from their Mom and Half from their Dad. Therefore, they share about a **50%** of their DNA with their siblings. Half-siblings, Aunt/Uncle, Grandparents, Niece/Nephews all share approx. **25%** of their DNA. The amount of shared DNA keeps dropping approximately by half the further you get away from the missing person.

Diagram of the amount of DNA shared between relatives

Relationship	Average % DNA Shared	Range
Identical Twin	100%	N/A
Parent / Child	50%	N/A
Full Sibling	50%	38% - 61%
Grandparent / Grandchild Aunt / Uncle Niece / Nephew Half Sibling	25%	17% - 34%
1st Cousin Great-grandparent Great-grandchild Great-Uncle / Aunt Great Nephew / Niece	12.5%	4% - 23%

Table adapted from 23andMe website

Collection of Family Reference Samples – Who to Collect?



Collection of Family Reference Samples Important Note: Documentation of Consent from the Donor is a Must

A reference sample collected with the intention of entering the profile into CODIS, **must** be accompanied by a form showing consent. A sample cannot be taken under duress and must be voluntarily provided.

The reference sample must also be collected by a member of the Law Enforcement community and submitted to the DNA lab by a Law Enforcement Agency.

There are different versions of these consent forms based on the DNA testing Laboratory involved.

Collection of Reference Samples – Consent (continued)

Excerpt from CALDOJ Form (donor signature required):
Please carefully read the donor information sheet. I have reviewed and understand the procedures as explained in the "Donor Information Sheet." I voluntarily agree to provide a sample for DNA analysis and no incentive or coercion has been used to compel me to provide a DNA sample. I understand this DNA sample will be entered into CODIS to be used onl for the purpose of identifying the missing person.

Excerpt from NamUs Form:
I understand that the answers provided on this form are correct to the best of my knowledge. I fully understand that my answers are critical to the process of identifying my missing family member. I freely and voluntarily consent to provide my sample(s) for DNA analysis, entry into the Relatives of Missing Persons Index of the Combined DNA Index System (CODIS) and searching against the Unidentified Persons Index of CODIS. CODIS is maintained by the FBI under authority of Title 34, United States Code, Section 12592.

Kinship Testing – How it Occurs

- An association is made in CODIS.
  - Laboratory with the unidentified remains will do a likelihood calculation based on the family relationship reported for the family reference sample in which it Hit in CODIS.
- An agency requests a comparison.
  - Laboratory will compare the unidentified and the family samples requested, then report the likelihood calculation.

A sample of our report language – Note that these will vary between laboratories.

"A comparison of the STR DNA profile obtained from the femur was compared to the STR DNA profile from the family reference sample for John Doe, obtained as part of case RM-25-000001. A statistical calculation provided the approximated kinship indices as follows: 4.0 million for African Americans, 20 million for Caucasians, and 500,000 for Hispanics. In other words, the STR DNA profile obtained from the femur is approximately 500,000 to 20 million times more likely if the decedent is a biological sister of John Doe than if she is unrelated."

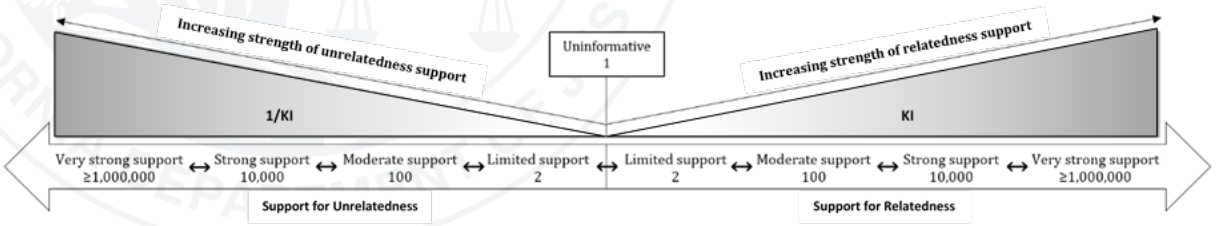
Kinship Testing – Report Language

Sample of our report language – KI < 1 - Note that these will vary between laboratories.

"A comparison of this STR DNA profile obtained from the femur was compared to the STR DNA profile from the family reference sample for John Doe, obtained as part of case RM-25-00000. This comparison provides moderate support that the decedent is NOT a biological sister of John Doe. A statistical calculation provided approximated kinship indices as follows: 0.0046 for African Americans, 0.00036 for Caucasians, and 0.00044 for Hispanics. A kinship index of less than 1 means that the DNA profile is more likely to occur if the femur is from an unrelated person than from a biological sister of John Doe."

Please Note: As a general principle, a KI above 1 provides support for a proposition of relatedness, while a KI below 1 provides support for a proposition of unrelatedness. When a KI is below 1, the inverse value of the KI (i.e., 1/KI) is used to ascertain the proper verbal qualifier for the proposition of unrelatedness.

KI for Relatedness Support or 1/KI for Unrelatedness Support	Verbal Qualifier
1	Uninformative
2-99	Limited Support
100-9,999	Moderate Support
10,000-999,999	Strong Support
≥ 1,000,000	Very Strong Support



What is the Significance of a Match (or rank)? – We need statistics

- Direct Comparison – Calculate the Random Match Probability (the chance of randomly selecting an unrelated person from the population who happens to have the exact same DNA profile as the evidence profile - UHR).

- Indirect Comparison – Calculate a Kinship Index (KI) (aka Likelihood Ratio) – Ratio of two probabilities – Probability that UHR and family have these profiles if the UHR is related / Probability that UHR and family have these profiles if the UHR is unrelated.

Kinship Basics – Concerns / Issues

No Immediate Family Available for References – What testing can be done?

Maternal Relatives Available - mtDNA testing
Paternal Relatives Available – YSTR testing
Distant Relatives Available – Genealogy Testing / Extended Kinship

Wrong Biological Relationship Reported – What happens?

Example: Son and Daughter entered into CODIS for a missing Father

- No hits in CODIS to remains
- Genealogy done and points to a family already in CODIS
  - Why did it not hit years earlier?
- Turns out, the son is not a biological child of the Father which was causing an exclusion in CODIS.

Kinship Basics – Concerns / Issues

Wrong Biological Relationship Reported – What happens?

Example: Two biological siblings entered into CODIS for a missing 3rd sibling

- No hits in CODIS to any remains
- Genealogy done and points to the family already in CODIS
  - Why did this not hit in CODIS?
- Turns out, one of the siblings is a half-sibling while the remains and 2nd sibling are full biological siblings

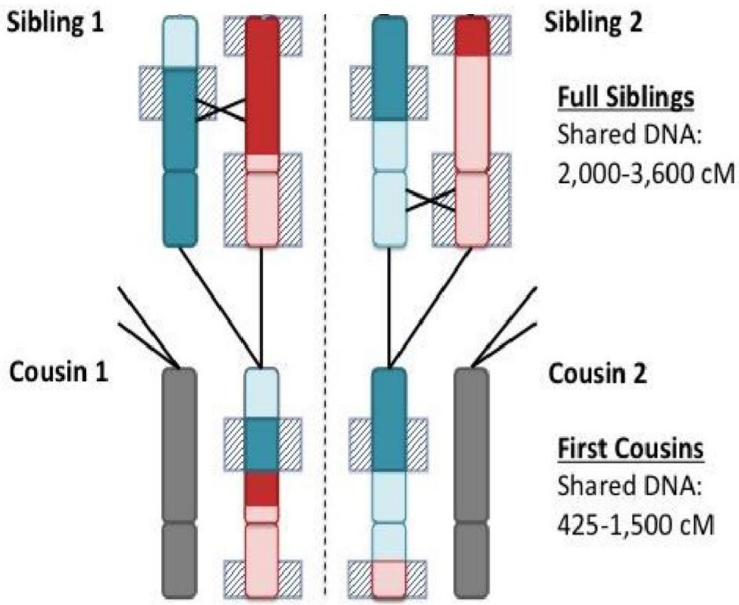
These scenarios are happening more and more and with genealogy testing.

- We need to make sure we are asking that donors are positive the relationship they are reporting is true (to the best of their knowledge)
- In the cases we have seen, the sibling or family member had no idea the relationship they reported was not the true relationship
- Side note, siblings can share a wide range of DNA between each other and tests that use more sections of DNA, like SNPs, can be better at detecting those relationships

Forensic Investigative Genetic Genealogy (FIGG)

What is Genetic Genealogy?

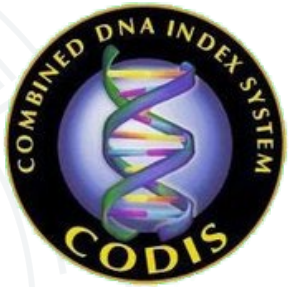
The use of DNA analysis and genealogy database searches in combination with traditional genealogical and historical records analysis to infer relationships between relatives and an unknown DNA sample from a crime scene or a missing person.



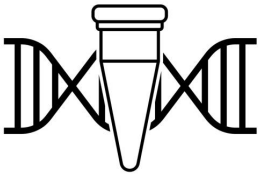
Traditional STR typing and FIGG – How the paths cross

Unidentified

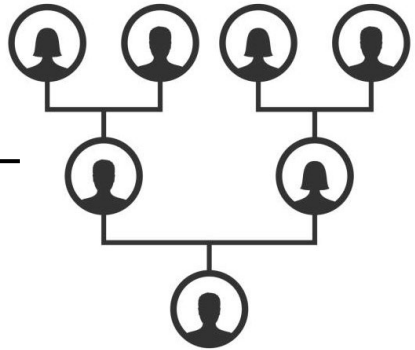
Obtain STR DNA profile



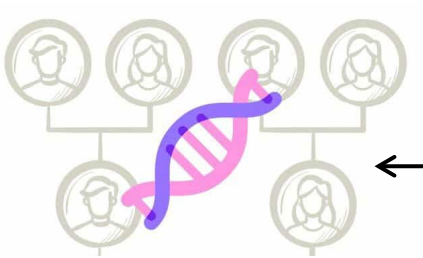
No Hits in CODIS



Send extract to genealogy to obtain a SNP DNA profile



Possible family Identified



Confirmation of lead with STR testing

Forensic Investigative Genetic Genealogy (FIGG)

Kit	1:1	Name	Email	Largest Seg	Total cM	Gen	Overlap	Date Compared	Testing Company
[redacted]	A	[redacted]	[redacted]	146.4	2112.7	1.4	324455	2021-01-05	23andMe
	A			149.9	1464.3	1.6	320747	2021-01-05	23andMe
	A			106.6	1039.5	1.9	64798	2021-01-05	Ancestry
	A			93.5	760.4	2.1	318712	2021-02-10	23andMe
	A			53.9	232.9	3.0	315779	2021-01-05	23andMe
	A			53.2	161.6	3.2	314796	2021-01-05	23andMe
	A			24.6	125.1	3.4	78287	2021-01-05	Migration - V3 - M
	A			24.5	116.8	3.5	70202	2021-01-05	Migration - F2 - A
	A			18.1	109.7	3.5	69904	2021-01-05	Migration - F2 - T
	A			23.9	105.5	3.5	69835	2021-01-05	Migration - F2 - F
	A			20.7	102.4	3.6	70340	2021-01-05	Migration - F2 - T
	A			19.0	101.3	3.6	64834	2021-01-05	Ancestry
	A			15.6	95.8	3.6	50019	2021-01-05	Migration - F2 - A
	A			17.5	95.2	3.6	67486	2021-01-05	Migration - F2 - T
	A			15.7	94.6	3.6	66131	2021-01-05	Ancestry
	A			14.2	94.6	3.6	50709	2021-01-05	Migration - F2 - A
	A			22.6	94.5	3.6	68678	2021-01-05	Migration - F2 - H
	A			25.2	93.0	3.6	315431	2021-01-05	23andMe
	A			22.9	91.6	3.6	49526	2021-01-05	Migration - F2 - A
	A			16.4	87.5	3.7	68354	2021-01-05	Migration - F2 - A
	A			34.3	87.4	3.7	49437	2021-01-05	Migration - F2 - A
	A			17.7	84.9	3.7	46448	2021-01-05	Migration - V4 - M
	A			31.3	84.9	3.7	67434	2021-01-05	Migration - F2 - H
	A			15.7	84.6	3.7	50031	2021-01-05	Migration - F2 - G
A336767	A	Gloria Martha Morales Treviño	victor.manuel@notariapublica108.com	15.2	84.6	3.7	49718	2021-01-05	Migration - F2 - A

Forensic Investigative Genetic Genealogy (FIGG)

The Shared cM Project – **Version 4.0** (March 2020)

Blaine T. Bettinger
www.TheGeneticGenealogist.com
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How to read this chart:
Aunt/Uncle
1741
1201 - 2282
Relationship
Average
Range (min-max)

							Great-Great-Great-Grandparent		GGGG-Aunt/Uncle	
						Great-Great-Grandparent		GGG-Aunt/Uncle		
Half GG-Aunt/Uncle 208 103 – 284	Great-Grandparent 887 485 – 1486						Great-Great Aunt/Uncle 420 186 – 713	1C3R 117 25 – 238	2c3R 51 0 – 154	Other Relationships
Half 1C2R 125 16 – 269	Half Great-Aunt/Uncle 431 184 – 668	Grandparent 1754 984 – 2462				Great Aunt/Uncle 850 330 – 1467	1C2R 221 33 – 471	2c2R 71 0– 244	3C2R 36 0 – 166	6C 18 0 – 71
Half 2c1R 66 0 – 190	Half 1C1R 224 62 – 469	Half Aunt/Uncle 871 492 – 1315	Parent 3485 2376 - 3720		Aunt/Uncle 1741 1201 - 2282	1C1R 433 102 – 980	2c1R 122 14 – 353	3C1R 48 0 – 192	4C1R 28 0 – 126	6C1R 15 0 – 56
Half 3c 48 0 – 168	Half 2c 120 10 – 325	Half 1C 449 156 – 979	Half-Sibling 1759 1160 – 2436	Sibling 2613 1613 – 3488	SELF	1C 866 396 – 1397	2c 229 41 – 592	3c 73 0 – 234	4c 35 0 – 139	5c 25 0 – 117	6C2R 13 0 – 45
Half 3c1R 37 0 – 139	Half 2c1R 66 0 – 190	Half 1C1R 224 62 – 469	Half Niece/Nephew 871 492 – 1315	Niece/Nephew 1740 1201 - 2282	Child 3487 2376 – 3720	1C1R 433 102 – 980	2c1R 122 14 – 353	3C1R 48 0 – 192	4C1R 28 0 – 126	5C1R 21 0 – 80	7C 14 0 – 57
Half 3c2R 27 0 – 78	Half 2c2R 48 0 – 144	Half 1C2R 125 16 – 269	Half Great Niece/Nephew 431 184 – 668	Great-Niece/Nephew 850 330 – 1467	Grandchild 1754 984 – 2462	1C2R 221 33 – 471	2c2R 71 0– 244	3C2R 36 0 – 166	4C2R 22 0 – 93	5C2R 18 0 – 65	7C1R 12 0 – 50
Half 3c3R	Half 2c3R	Half 1C3R 60 0 – 120	Half GG Niece/Nephew 208 103 – 284	Great-Great-Niece/Nephew 420 186 – 713	Great-Grandchild 887 485 – 1486	1C3R 117 25 – 238	2c3R 51 0 – 154	3C3R 27 0 – 98	4C3R 19 0 – 60	5C3R 13 0 – 30	8C 11 0 – 42

Minimum was automatically set to 0 cM for relationships more distant than Half 2C, and averages were determined only for submissions in which DNA was shared

Shared cM Relationship Chart with the average and range (min-max) shared cMs for each relationship type. Image credit—Blaine T. Bettinger.

Forensic Investigative Genetic Genealogy (FIGG)

Associations based on how much DNA is shared between the unknown DNA profile and entries in the genealogy database are used provide an investigative lead to law enforcement.

- Use of open source and law enforcement accessible databases in conjunction with DNA matches to create family trees. Birth, death and marriage certificates, obituaries and grave records, and other sources
- A match at 3rd cousin or closer allows for best advancement of case

If a “close” match is not found:

- A targeted kinship sample might be used
- DNA from a person not related to the case can be obtained to test kinship theories or eliminate branches of a family tree
- Y-STRs, mtDNA and phenotypic information can further assist this process

Forensic Investigative Genetic Genealogy (FIGG)

WARNING

FIGG is an **investigative lead**, it should not be considered the end of the DNA testing.

Per USDOJ's Interim Policy for Forensic Genetic Genealogy, traditional STR testing should be done to confirm the FIGG lead.

It is the traditional DNA analysis in conjunction with kinship testing results that should be taken to court NOT the investigative lead.

DNA Basics: Understanding the Science and Tools Behind DNA Kinship Analysis

CA DOJ MPDP uses an SDIS Database Kinship Search:

- Uses the highly regarded familial searching tool to identify potential close relatives of missing persons
- Searches the MP's DNA profile against the state's CODIS database of Convicted Offenders (the state's Arrestee database is not searched)

Kinship Search	Familial Search
Unidentified Human Remains (UHR)	Crime scene evidence, originating from the perpetrator
Submitted by Missing Persons DNA Program (MPDP)	Submitted by investigating Law Enforcement Agency (LEA)
No Memorandum of Understanding (MOU) needed	Memorandum of Understanding (MOU) with investigating LEA, prosecuting agency, and CA DOJ
Point of Contact – MPDP Supervisor	Point of Contact for agency – Familial Search unit Supervisor
If case has a suitable DNA profile for submission, then it will be submitted by a MPDP Supervisor (me)	Familial Search Committee: Oversees Familial Search Program, votes to accept cases and release information to the LEA. Includes representatives from CA DOJ's scientific, legal, and investigative branches

CA DOJ Kinship Database Search Success - Case Stats

Kinship Cases Submitted

- 38 cases
  - 21 Male UHRs
  - 17 Female UHRs
- ~19 currently searches in progress

Kinship has aided in

- 4 case investigations
  - 3 identified potential male relatives
  - 1 identified potential female relative

Outline

- Part One: Introduction
  - DNA 101
  - Application of CODIS
- Part Two: Kinship Analysis
  - Kinship Basics
  - The Kinship Testing Process at the Lab
  - Kinship Report Interpretation
- Part Three: Case Examples

The following slides contain graphic images that are sensitive in nature which may be considered triggering to some audiences

Kinship Database Search Success - Case Studies

March 29, 2007: A bow fisherman retrieves metal cooler from the Conway Canal in Yolo County, CA.

Contents included plastic sheet, brick, metal car parts, “Winnie the Pooh” baby blanket, booties, and a diaper containing skeletal remains of an infant.

Kinship Database Search Success - Case Studies

Kinship Database Search Success - Case Studies

Forensic Anthropology

- Male
- 1-3 months old, approximately 1 year since death
- Likely Native American, Hispanic or Asian
- Multiple broken bones, including healed fractures to multiple ribs suggesting possible abuse

DNA Analysis

- Both femurs were submitted in April 2007
- Partial profile obtained, entered into CODIS in December 2007

Femur

No Identification for almost 10 years…

- June 2017: Yolo County DA's Office requested "Kinship Search"
- CA DOJ Policy: Familial Search restricted to profiles in the Forensic Unknown specimen category
- The process was reimagined and accepted in 2017 as first Kinship search.

Original DNA profile obtained required additional testing. Kinship Requirements:

- If male decedent, need a nearly complete STR profile and a Y-STR profile
  - Profile considered complete with 15 STR markers (loci).

- If female, we want tested with an extended STR kit (21 or more loci) and it can only be missing 2 STR loci.

- For this case, since we had a partial STR profile, we went back and did:
  - Mini-STRs (MiniFiler)(useful for degraded DNA) - now had 14 of 15 loci
  - Y-STRs (YFiler) - got all but 2 Y-STR loci
  - Our current technology for autosomal STRs (GlobalFiler) – we were able to get 18 of 21 loci

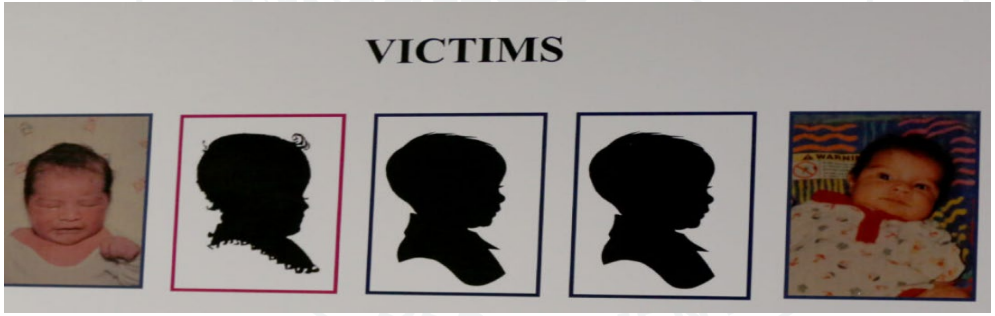
Kinship Database Search Success - Case Studies

Kinship Searching Started

- "Ratiometer" tool compares unknown profile to convicted offenders either as a Parent/Child or Sibling/Sibling
- Arrestee database is not searched
- Evaluate both 13-locus and 15-locus to account for composition of database.
  - Back in the day a complete profile was 13 loci
- Rank candidates by Likelihood Ratio
- The top 168 male candidates were screened using Y-STRs
  - Y-STRs are inherited through the paternal lineage, so a male shares the same Y-STR profile with all of his patrilineally-related male relatives (i.e., his biological father and brothers, paternal grandfather, uncles, nephews, sons, and male cousins)
- Using publicly available information, CA DOJ investigates any candidate with a matching Y-STR profile to locate a close relative who might be related to this UHR.

Possible Biological Father Identified

- One convicted offender from the top candidates had a matching Y-STR profile
- Was currently incarcerated
- A new evidentiary sample was obtained for the decedent – confirmed all results – California Department of Public Health
- The convicted offender, the possible biological father of the deceased infant, was not incarcerated during time frame required to have fathered this child



- Now charged with murdering 5 of his infant children and there maybe more. He is still awaiting trial!

Genealogy Case via Riverside Sheriff-Coroner's Office – Confirmation by CADOJ

Unidentified human remains were submitted to CA DOJ in 2011

Multiple attempts were made to get a searchable profile for CODIS

- Entered into CODIS in 2018
- Technologies provided by CA DOJ – Identifiler, MiniFiler, Globalfiler
- No Hits in CODIS

Riverside Sheriff Coroner asked if there was DNA extract remaining for FIGG testing

The FIGG lab tested the DNA extract, performed a genealogy search, and identified a possible family member

Riverside County Sheriff obtained a DNA reference sample and sent it to the MPDP for confirmation testing

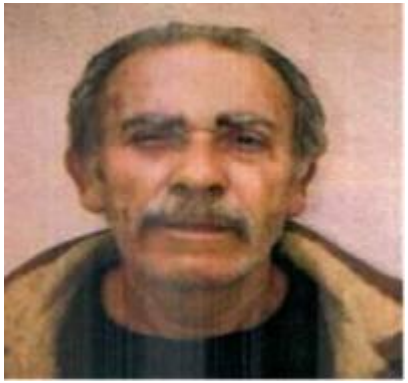
The UHR was ID'd as Kathryn Coffey

Genealogy Case via Riverside Sheriff-Coroner's Office – Confirmation by CADOJ

- Kathryn's remains were found in a wash area at the base of a hill on January 22, 1991
- Only bones were found, and they appeared to have been in the desert for a while
- Kathryn's Date of Last Contact (DLC) was 1989
- In 2022, the Riverside County cold case team began a forensic genealogy investigation and obtained a reference DNA sample from Kathryn's sister. The MPDP confirmed Kathryn's identification on August 8, 2022, and her family was informed of the positive identification.
- Kathryn's remains were finally identified after 31 years

Genealogy Case via Orange County Sheriff-Coroner's Office – Confirmation by CALDOJ

The case of Donald Raymond Loar:



On Aug. 29, 1998, a research biologist for the Rancho Mission Viejo Company discovered what he believed to be human remains in a remote area of southeastern Orange County.

In September 1998, an additional search of the remote area was conducted where the remains were initially discovered. The search resulted in what was believed to be a shallow grave, additional human remains and additional clothing.

In April 2003, the Orange County Sheriff-Coroner's Office submitted a tooth and femur to the Jan Bashinski DNA Laboratory's Missing Persons DNA Program (MPDP).

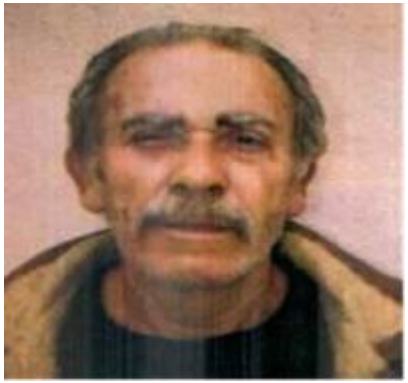
In 2004, the MPDP reported a male DNA profile obtained from the tooth and uploaded the profile to CODIS.

Family reference samples (FRS) from a reported biological daughter and son of Raymond Loar were submitted to MPDP in March 2010. The FRS samples from Diana McGee (daughter) and Donald Raymond Loar Jr (son) were entered into CODIS June 2010.

We would have expected the FRS samples to have hit the remains in CODIS submitted in 2004, but that did not occur.

Genealogy Case via Orange County Sheriff-Coroner's Office – Confirmation by CALDOJ

The case of Donald Raymond Loar:



In October 2022, at the request of the Orange County Sheriff-Coroner's Office, the MPDP submitted pulverized tooth powder for genealogy testing.

November 2023 it was reported to MPDP that Donald Raymond Loar may be the source of the remains. The Orange County Sheriff's Office investigated and located possible biological children of Loar and stated they were already in CODIS as part of BK-10-000274.

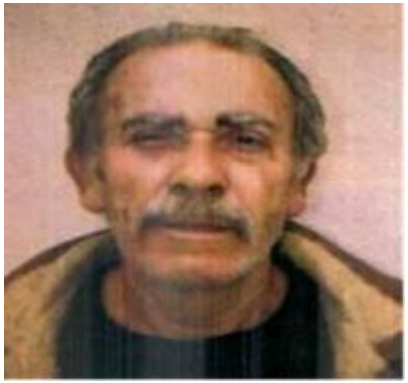
Why would this case not hit in CODIS?

When looking at the DNA profiles from the reported biological daughter and son of Mr. Loar, the daughter shared genetic information at every marker tested however the son did not. Since they were entered into CODIS as the biological children of Mr. Loar and the son does not share enough genetic information consistent with being a biological son, no match occurred in CODIS.

I contacted the lead investigator on the case and explained why these had not hit in CODIS. He was able to get a FRS from Rosalie Pearman, reported as the biological sister of Mr. Loar.

Genealogy Case via Orange County Sheriff-Coroner's Office – Confirmation by CALDOJ

The case of Donald Raymond Loar:



The sample was processed and the DNA profiles from Diana McGee (daughter), Donald Raymond Loar Jr (son), Rosalie Pearman (sister) were compared to the unidentified remains thought to be Mr. Loar. The comparison provided very strong support that the decedent is related to Diana McGee and Rosalie Pearman as reported and was excluded from being the biological father of Donald Loar Jr.

MPDP reported this association, and on January 2024, 25 years after his remains were found, the Orange County Sheriff-Coroner's Office accepted the identification of the remains as those of Donald Raymond Loar.

Lesson learned: CODIS searches are only as good as the information entered into it. Even with existing true relationships it took only one incorrectly reported relationship on the CODIS pedigree tree to miss an identification. It took genealogy and MPDP taking a closer look at the profiles to solve the mystery. This beautifully illustrates the importance of investigating and reporting true Kinship relationships.

CODIS HIT - Monterey County Sheriff-Coroner's Office – Kinship by CADOJ

The case of Richard Andrew Rader

Richard was last seen August 13, 2001, in the Pacific Ocean South of the Golden Gate Bridge fishing.

Family reference samples were collected from Richard's mother and father of Sonoma County and submitted to MPDP October 2003.

Family STR DNA was uploaded to CODIS in 2005 and mtDNA added in 2008.

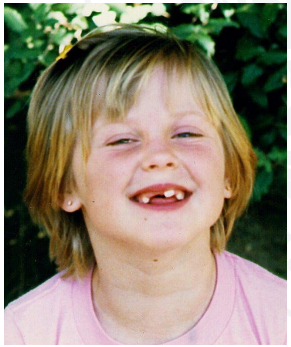
In May 2003, a fisherman in Monterey County found a skull caught up in his fishing net.

The skull was not submitted to MPDP until June 2023. It was submitted once a cold case team started researching unidentified doe cases to send out for genealogy.

A profile was obtained from the skull and uploaded into CODIS September 2023 and hit the following week.

In October 2023, the results of the CODIS hit was reported and Richard Andrew was ID'd 22 years after he disappeared.

This is why we do what we do… Help bring them home!



The Missing Persons DNA Program (MPDP) Team

Outreach – Crime Analyst
Kathryn (Kay) Clarke x 3553

Email: DNAMissingpersons@doj.ca.gov
Phone: 510-620-3300

MPDP Management

Jennie Smythe – Manager
Michelle Halsing – Supervisor and Case Management Lead
Sandra Sheehan – Supervisor and DNA Technical Leader

MPDP DNA Lab Staff

Jessica Battaglia and Amy Hoover – MPDP Day # 1
Jonathan Schell – CODIS Administrator
Carolyn Weigand
Karen Tsai
Ruben Carlos
Daniela Cuenca
MaryJo Olegario
Rachel Gordon
John Tonkyn

The absence of a family member causes a void in people's lives; it is our job to help fill that void and give them peace in their hearts.

Thank you

Contact Information

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Questions or Feedback?

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