Fire Investigator Strike Force Training: Forensic Biology and DNA

RYAN PAULSEN

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About me

Ryan Paulsen

Title: DNA Group Supervisor

Employment: ISP FSC-C since May 2004

Education: Bachelor's degree in Biology and Chemistry from Lake Forest College

About ISP Bio/DNA section

ISP has 6 labs that have Bio/DNA sections

- Chicago, Rockford, Joliet, Springfield, Belleville, Decatur
- 62 analysts, 10 evidence technicians

Caseload in 2023:

- 14,868 case reports (103 Arson Cases)

Indexing lab in Springfield

- 4 analysts, 3 evidence technicians

Northeastern Illinois Regional Crime Lab and DuPage County Crime Lab round out CODIS eligible labs in Illinois

Goal of the Forensic Biology and DNA section

Suspects

Crime scene

Victims

Case Acceptance Policy – Tier 1

Homicides
- Up to 5 most probative items
- Appropriate DNA standards

Sexual Crimes
- Sexual Assault kit
- If no kit or most probative item not in kit, the 2 most probative items

All other Crimes Against Persons
- Up to 3 most probative items
- Appropriate DNA standards

Property Crimes

Up to 2 most probative items

Appropriate DNA standards

Case Acceptance Policy – Tier 2

Homicides
- Up to 5 additional items after consultation with the lab

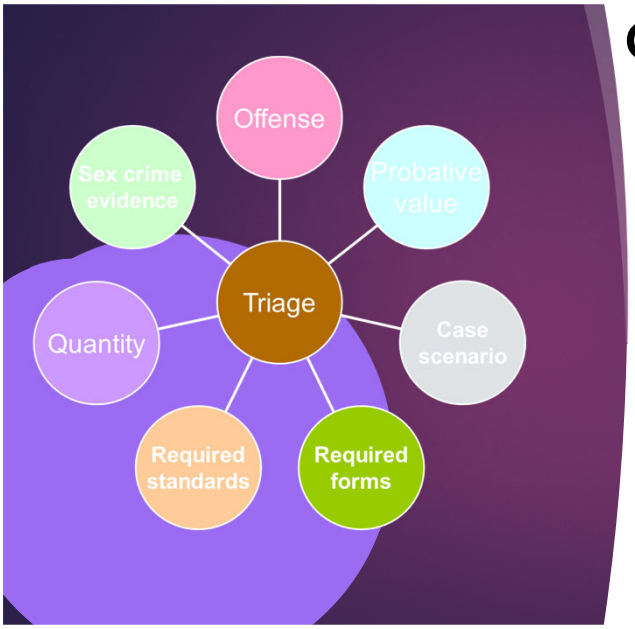
Sexual Crimes
- Up to 2 additional items after consultation with the lab

All other Crimes Against Persons
- Up to 2 additional items after consultation with the lab

Property Crimes

Up to 2 additional items after consultation with the lab

Case Evaluation



A FEW IMPORTANT NOTES:

- **MUST BE A CRIMINAL CASE**
- **BRIEF CASE SYNOPSIS IN LIMS**
- **IS THE EVIDENCE PROBATIVE**
- **VICTIM AND/OR SUSPECT NAMES**
- **CERTIFY SEXUAL ASSAULT CASES**
- **CODIS ELIGIBILITY**

Forensic Biology analysis

- **Routinely conducted:**
  - **Blood**
  - **Semen**
  - **Saliva**
  - **Swabbing for cellular material (wearer's, handler's, sweat)**
- **Not conducted:**
  - **Species testing**
  - **Vaginal secretion**
  - **Urine**
  - **Feces**
  - **Blood spatter**

Blood testing

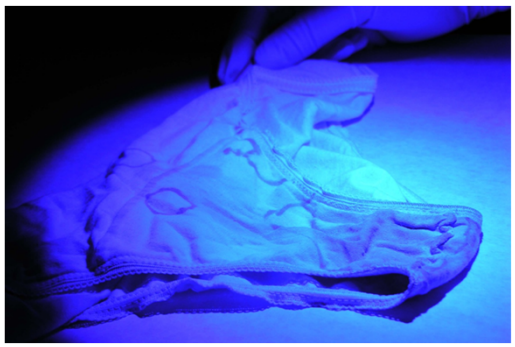
- Kastle-Meyer test
  - Indicates presence of blood, does not identify presence of blood
  - Color change test
  - Not species specific
  - Common items tested for blood: knives, clothing, scene swabs

Blood testing in the field

- BLUESTAR and Leucomalachite Green are most popular
- We *strongly* encourage that you don't do this unless absolutely necessary
  - Once tested, it can not be retested
  - If stain is not marked, we will not know where to swab
- If you must…
  - Swab the glowing stain and submit the swabs
  - Circle the glowing stain before submitting to the lab

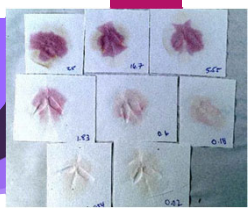
Semen testing

- Common items tested for semen: clothing, bedding, tampons, condoms
- Clothing, bedding, or similar items are first analyzed under ALS (alternate light source)
  - Glowing stains are circled and tested



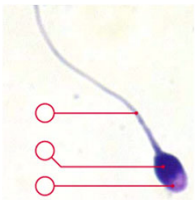
- Orifice swabs are not routinely tested
  - D2D approach discussed shortly
  - Can be requested

Semen testing



- AP - Acid Phosphatase
  - Indicates presence of semen, does not identify presence of semen
  - Color change test

- p30 (PSA - prostate specific antigen)
  - Indicates presence of semen, does not identify presence of semen
  - Cartridge test



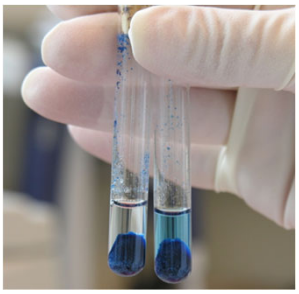
- KPIC – Kernechtrot PicroIndigoCarmine stain
  - Identifies the presence of semen
  - Microscope slide

To semen test…or not to semen test

- Direct to DNA (D2D) approach for orifice swabs
  - Swabs are not tested for the presence of semen but instead sent directly onto DNA analysis
  - More efficient and better turnaround times
  - Quantitation is a better indicator of sample information than biology analysis
  - No separate biology report
- Samples from kit are chosen based on case scenario
  - Generally, half of each probative sample is preserved for DNA
- If case question is not answered in the first round of D2D analysis, additional kit swabs or clothing may be sent for biology analysis and/or DNA
  - This will be reflected in the report

Saliva testing

- Phadebas test
  - Indicates the presence of saliva, does not identify presence of saliva
  - Color change test
  - Not species specific
  - Most common item tested for saliva: clothing in sexual assault cases based on scenario



- Testing is almost always not done on items thought to have saliva on them such as bottles, cups, cigarettes
  - These items are swabbed/preserved and sent directly to DNA
  - Saliva testing will be taken into consideration if request is made up front, prior to analysis

Cellular material

- Handler's DNA
  - Common items: knife handles, guns, crowbars
- Wearer's DNA
  - Common items: gloves, clothing, face masks, hats, ski masks, shoes
- Airbags
  - Analyzed for the presence of blood and/or glowing stains under ALS
  - If neither, we will swab entire front of airbag
    - Orientation of curtain airbags is impossible to determine
- Bottles, cans, cups
  - Agency encouraged to swab these items, especially if request for additional sections (LP)

Collection and storage of samples

- Ensure Clean Technique is used during collection
  - Gloves, masks, sterile swabs/water
- Concentrate sample onto as few swabs as possible
  - 1 swab for most items, can use 2 if area to be swabbed is large
- Allow swabs to dry completely
  - Store in paper, not plastic
  - Room temperature
  - Out of direct sunlight
- Ensure location collected/ownership properly documented
  - Location collected
  - Owner (if known)
  - Elimination standards

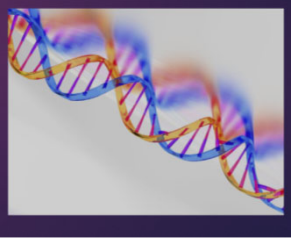
Scene swabs

- Car swabs
  - Limit submission to best evidence: steering wheel, gear shift, driver compartment
- Building/residence swabs
  - Point of entry of private residence, items touched for a decent amount of time, blood
- Swabs not routinely accepted:
  - Items touched once for access or to be moved (door pulls, cords)
  - Drug packaging
  - Items taken from person if that's whose profile you are looking for
    - This includes their car and residence, unless additional information is provided
  - Public area items (store door handles, counter tops, common housing areas)

Consumption policy (Permission to consume)

- Some samples have a higher chance of having low amounts of DNA
  - Touch DNA, fingernail swabs, external body swabs,
- Granted through LIMS
- Approval by agency or State's Attorney's office
  - If no suspect charged, agency can grant PTC
  - If suspect charged, approval must come through the State's Attorney's Office
- If PTC not approved, cancellation report will be written

DNA ANALYSIS



What is DNA

- DNA stands for deoxyribonucleic acid
- Found in all cells of the body except red blood cells
- Blueprint of life and is necessary for all functions of the body
- Does not differ from cell to cell within your body
- Does differ from person to person except for identical siblings
- You obtain half from your father and half from your mother

What are the steps for DNA analysis

- 1 – Extraction
  - Get the DNA off the sample
- 2 – Quantitation
  - How much DNA is present
- 3 – Amplification
  - Making copies of the DNA
- 4 – Capillary Electrophoresis
  - Separate the DNA to create a profile

1 - Extraction

- The sample is soaked in a master mix of chemicals and exposed to heat
- This releases the cells from the samples and breaks the cell walls open
- The sample is "cleaned up" so that you end with a purified liquid DNA sample
- We use 3 main methods to complete extraction:
  - PCI
  - Maxwell robot
  - Tecan robot

1 – Extraction - PCI

- The "gold standard"
- Very hands on
  - Limited batch size
- Requires an overnight incubation
- Use of a toxic chemical
  - Must be done in a fume hood
- Now used mostly for hair extractions only

1 – Extraction – Maxwell robot

- Samples are preprocessed to release the cells off the substrate and into a liquid
- This liquid is added to a cartridge and placed onto the instrument
- The instrument utilizes DNA IQ technology which uses magnetic beads that attract the DNA
- These beads move through the wells of the cartridge into a series of lysis and washes
- 26 minutes later, you have a purified DNA sample
- Each instrument can process 48 samples
  - Chicago has 6 Maxwell 48s

1 – Extraction – Tecan robot

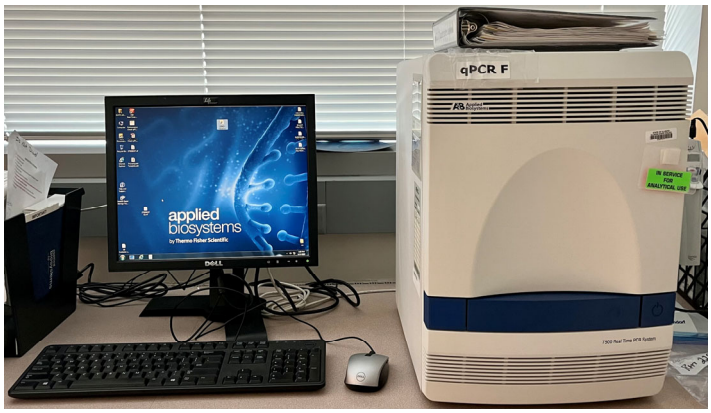
- Like the Maxwell robot:
  - Samples are preprocessed prior to putting on the instrument
  - Uses DNA IQ technology
- Unlike the Maxwell robot:
  - Tecan moves the liquid from step to step, not the beads
  - Runs up to 96 samples per batch
  - Also used to set up the next two steps in DNA analysis: quant and amp
- Utilizing Tecans has greatly reduced our backlog

1 – Extraction of semen samples

- Sperm heads are more difficult to break open so we take advantage of this
  - First, break open the non-sperm cells and separate them out (F1 or non-sperm fraction)
  - Next, add an additional chemical that breaks open sperm cells (F2 or sperm fraction)
  - In the past, an additional extraction of the substrate was done as a last ditch effort (F3 or mixed fraction)
- We do our best but it's not a perfect method
- Only process the F1 and F2 at this time (F3 saved for consumed sample)

2 - Quantitation

- qPCR (quantitative PCR)
- Tells us:
  - How much human DNA is present
  - How much male DNA is present
    - Use both to calculate MTFR
  - How degraded the DNA is (quality of the sample)
- All this information is used to determine how to proceed with the sample



Examples of qPCR results

Well	Sample Name	Dilution	Target Name	Task	CT	Quantity(ng/µl)	MTFR	DI
G4	DFS22[redacted]		Autosomal	UNKNOWN	32.6401	0.0112	0.9649	2.7317
G4	DFS22[redacted]		Degradation	UNKNOWN	34.2318	0.0041		
G4	DFS22[redacted]		IPC	UNKNOWN	20.3866			
G4	DFS22[redacted]		Y	UNKNOWN	33.4417	0.0057		
B2	DFS22[redacted]		Autosomal	UNKNOWN	Undetermined	0.0000		
B2	DFS22[redacted]		Degradation	UNKNOWN	Undetermined	0.0000		
B2	DFS22[redacted]		IPC	UNKNOWN	20.2806			
B2	DFS22[redacted]		Y	UNKNOWN	Undetermined	0.0000		
G6	DFS21[redacted]		Autosomal	UNKNOWN	34.9151	0.0023		3.8333
G6	DFS21[redacted]		Degradation	UNKNOWN	37.0301	0.0006		
G6	DFS21[redacted]		IPC	UNKNOWN	20.3819			
G6	DFS21[redacted]		Y	UNKNOWN	Undetermined	0.0000		

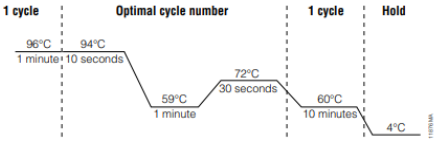
G4 – A sample that is ~1:1 MTFR with good quality

B2 – A sample with no human DNA detected

G6 – A sample with only female DNA with good quality

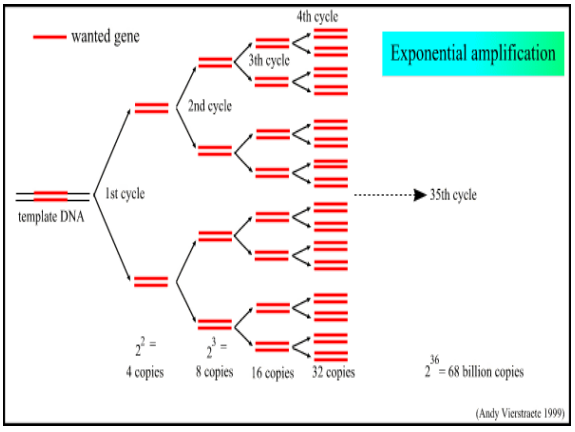
3 - Amplification

- Goal: to make billions of copies of specific locations within the DNA that together create a forensic DNA profile
  - Short tandem repeats or STR
- How: a portion, or all, of the sample is added to a mixture of chemicals and subjected to 29 cycles of temperature changes
  - Polymerase chain reaction or PCR



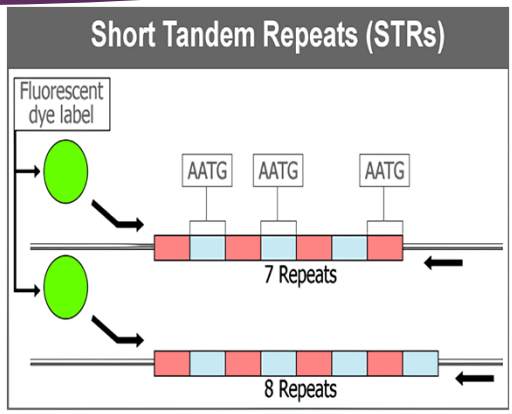
3 – Amplification - PCR

- Polymerase chain reaction
- Master mix chemicals contain "primers"
  - Know exactly where to bind to the DNA to create the fragments we need
  - Uses forward and backwards primers to get precise length
  - Also contain a specific fluorescent dye which is important for the next step



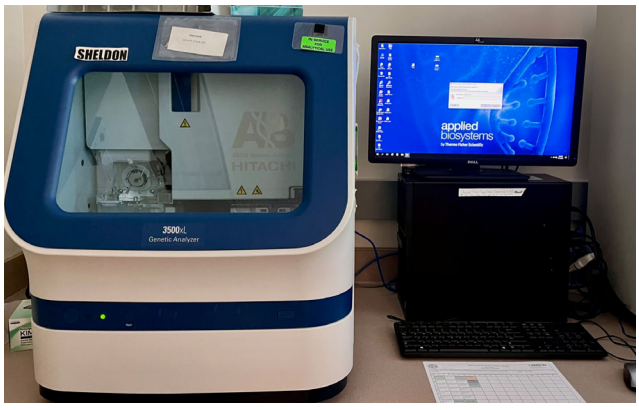
3 – Amplification - STR

- Short tandem repeats
- DNA genome is made of 4 nucleobases: adenine, cytosine, guanine, thymine
- STRs are repeats of the same sequence of these bases
  - The number of repeats directly determines how we refer to information in a person's DNA profile
- Found in "junk DNA" which is located In between important genes
  - Loci or locations
- Our current profiling kit uses 23 STR loci plus a sex-determining location

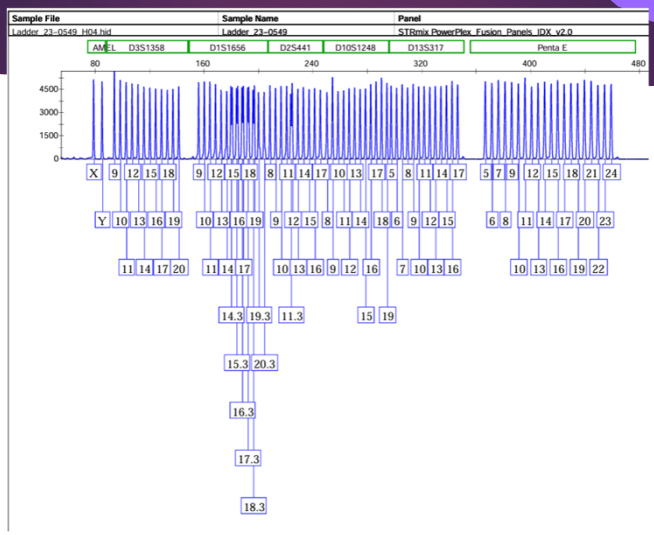


4 – Capillary electrophoresis

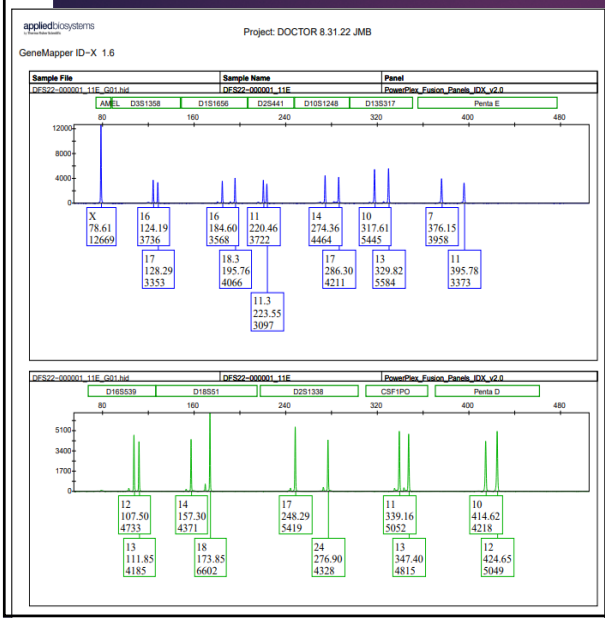
- Amplified product is loaded into the instrument
- DNA is injected into extremely thin tubes via electric charge – 36 cm long
- Tubes (aka capillaries) are filled with polymer
- As DNA moves through the polymer, it naturally separates out by size
  - Smaller fragments navigate through the polymer faster
- At the end, the DNA passes by a very small area containing a window, a laser, and a camera. The laser excites the fluorescent tag attached during amp and this is captured by a camera.
- Combination of the size of the DNA fragment and the color of the fluorescent tag helps put together a DNA profile

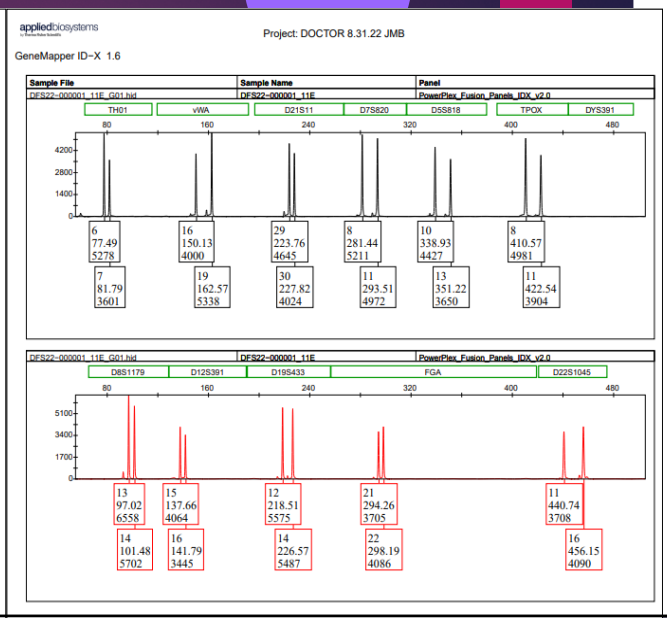


Fusion 5C ladder used to size alleles



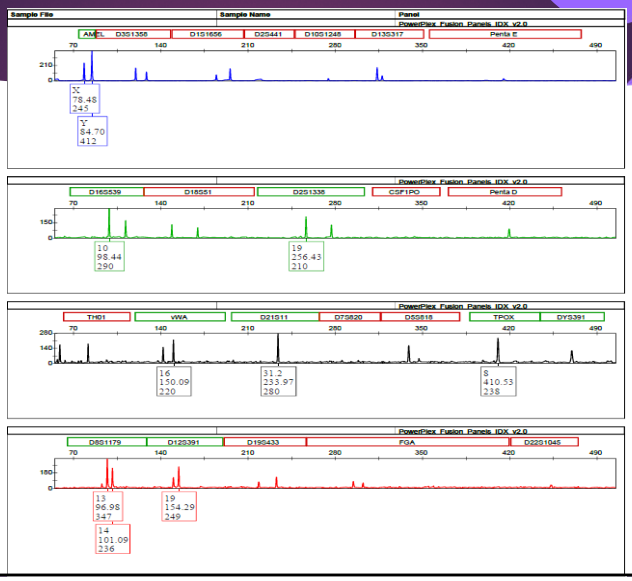
A DNA profile



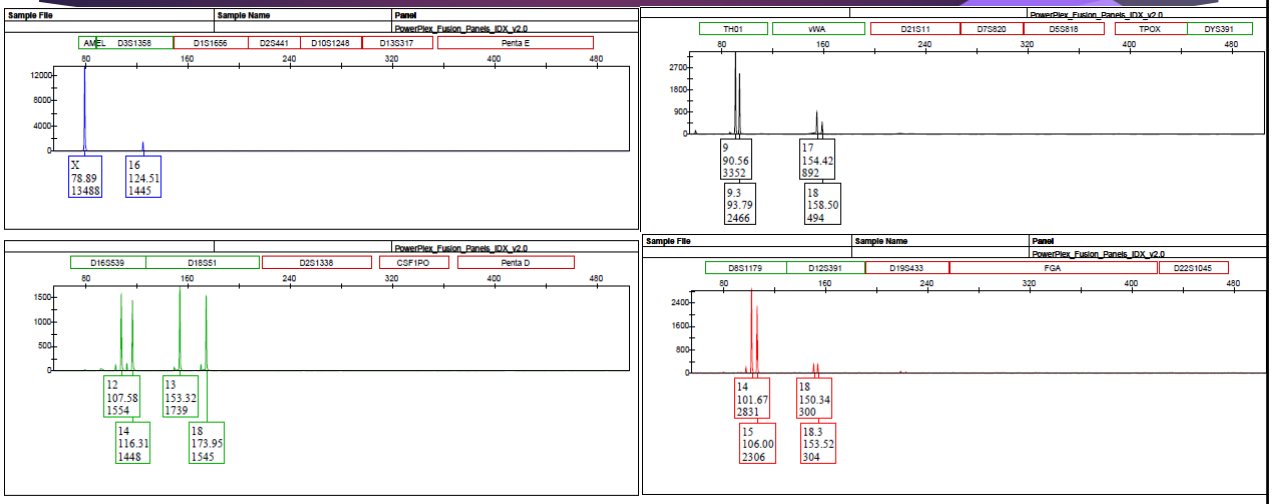


"Flatline" – No profile identified

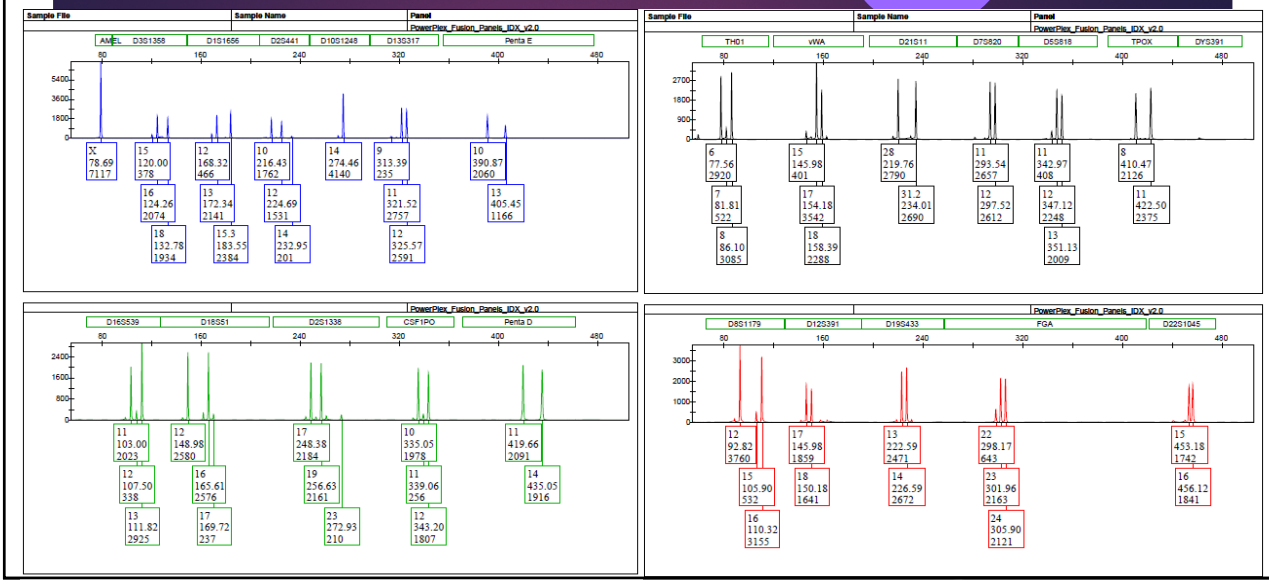
Low level single source with dropout



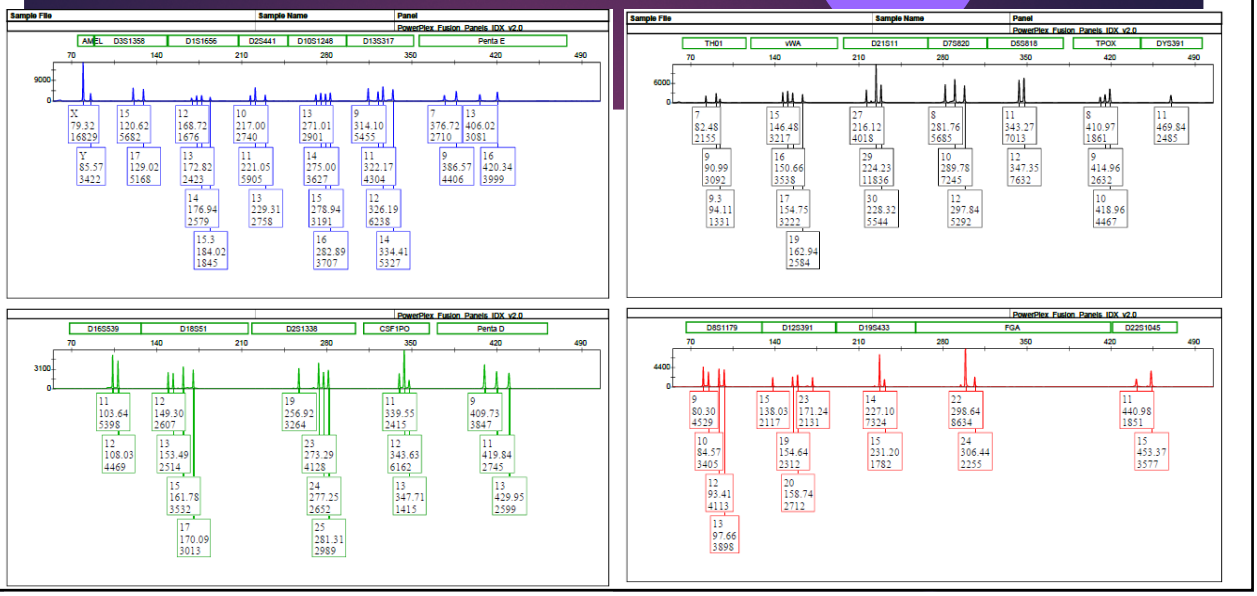
Single source with dropout due to degradation



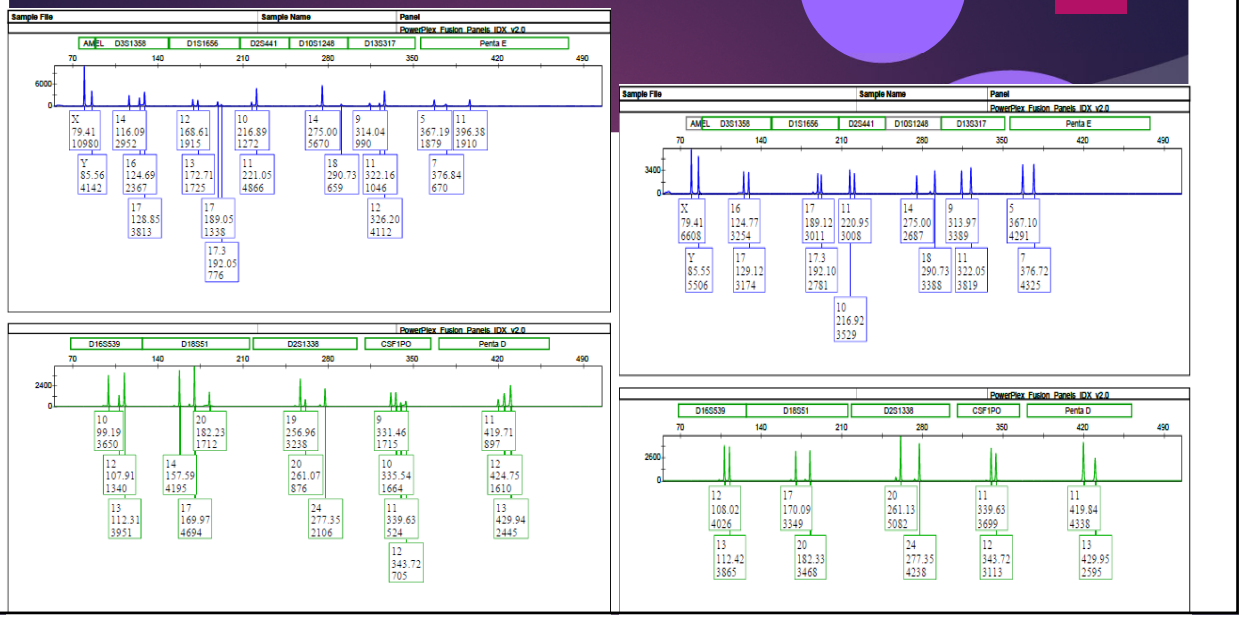
Two person mixture with major and minor



Two person mixture with 1:1 ratio



Assuming a contributor



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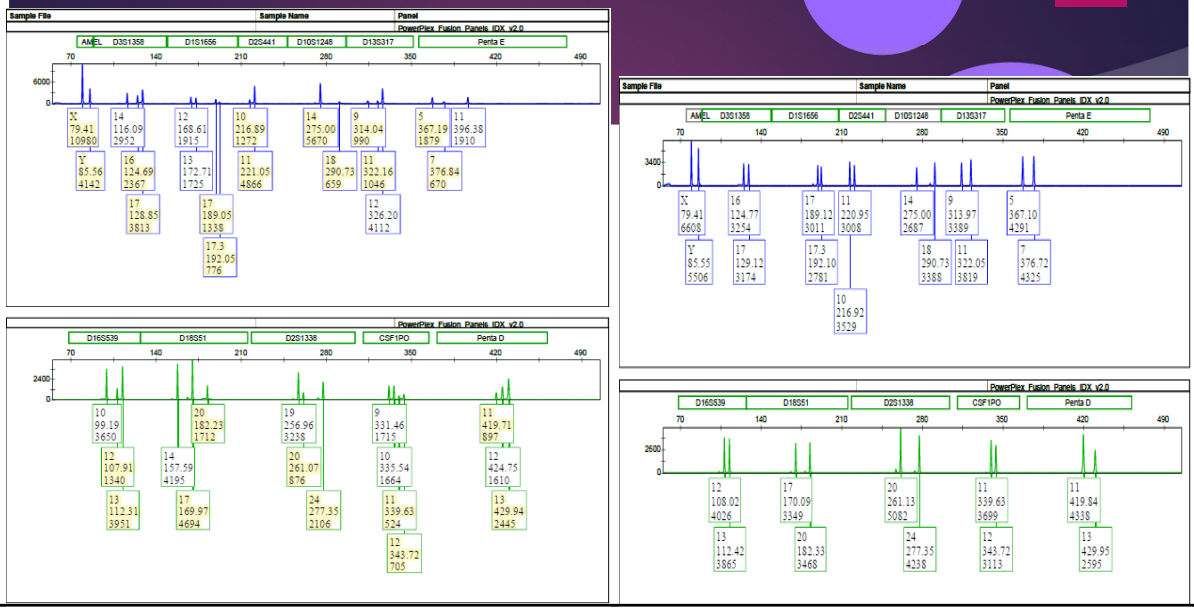

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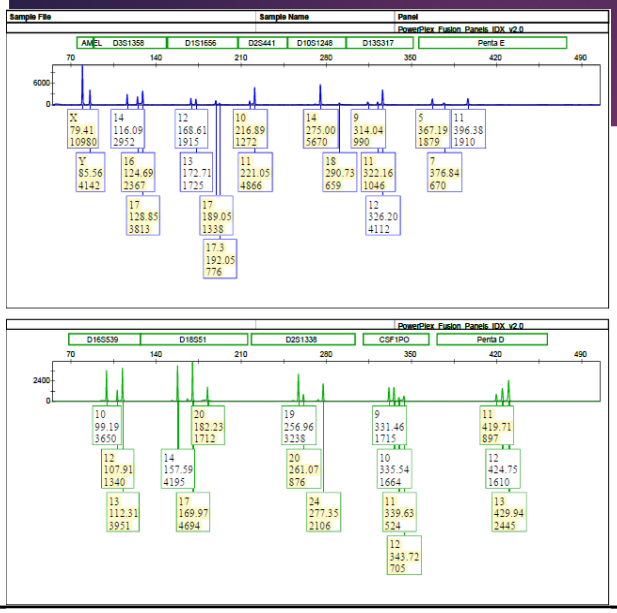


Deduced contributor:

Amelo: X,X

D3: 14,17

D1: 12,13

D2: 11,11

D10: 14,14

D13: 12,12

Penta E: 5,11

D16: 10,13

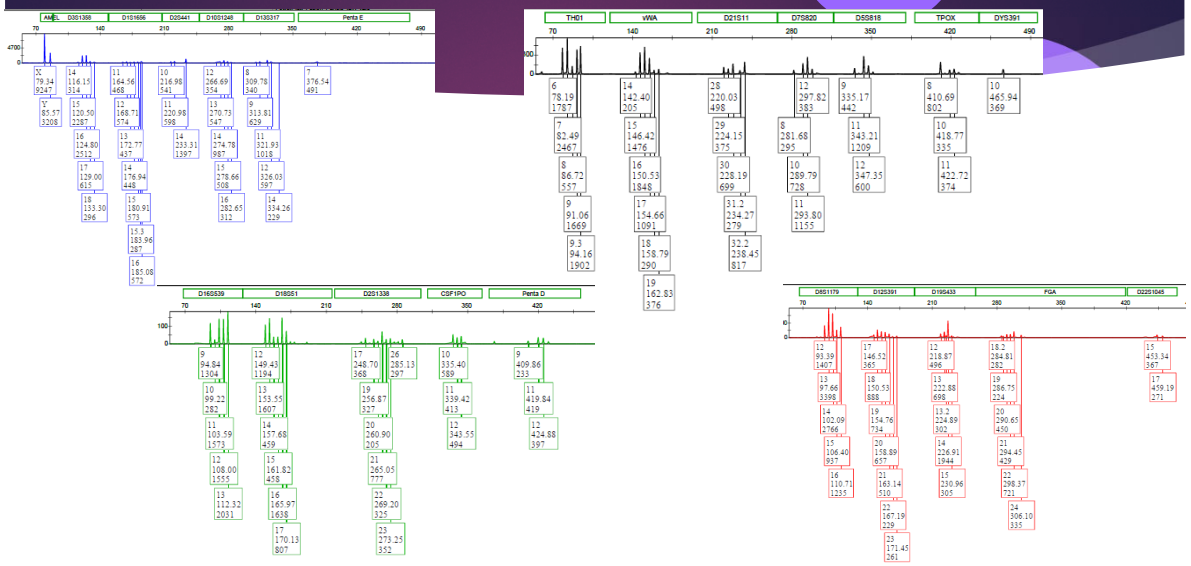
D18: 14,17

D2: 19,24

CSF: 9,10

Penta D: 12,13

Complex mixtures with three or more contributors



STRmix™ EMPOWERING FORENSIC SCIENCE.

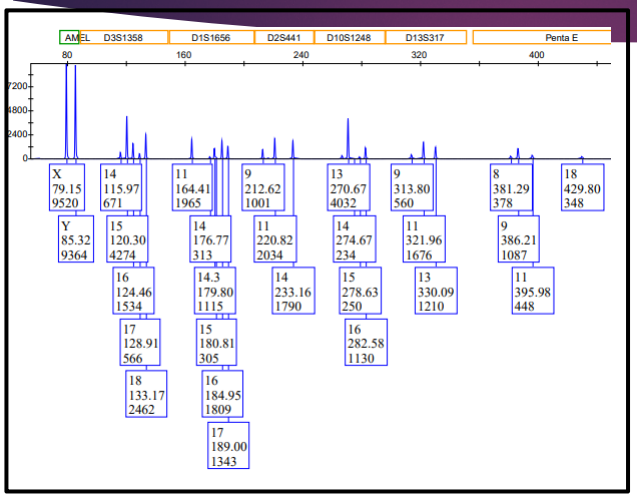
STRMIX™ TO THE RESCUE!

- STRmix™ is a probabilistic genotyping computer program that aids in interpretation of complex mixtures and also performs statistical calculations based on comparisons to reference profiles
- Created by the New Zealand Institute of Environmental Science and Research (ESR) and Forensic Science South Australia (FSSA)
- First used by ESR in casework in 2012.

How does STRmix™ work?

- The number of contributors is assigned by the analyst
  - Can be used on mixtures of up to 4 contributors
- STRmix™ uses what we know about biological modeling to propose genotype combinations that best explain the DNA profile
- STRmix™ creates up to billions of these genotype proposals to best explain the DNA profile
  - Markov Chain Monte Carlo (MCMC)
- If a proposal is a "good fit" it is accepted by the software. Most "bad fits" are rejected, though a few slip through
  - Hot cold game

Traditional interpretation vs STRmix™ interpretation



- Traditional (Binary) and report writing
  - Number of Contributors: At least 3
  - Profile inconclusive*
  - *DNA results are unsuitable for comparison to reference standards and/or unknown evidentiary profiles. The DNA analyst is unable to provide any information (Inclusion OR Exclusion) to the court.
- STRmix™ and report writing
  - Number of Contributors: 3
  - Proportion of Contributors: 61%, 35%, 4%
  - CODIS: 61%, 35%, 4%

The realities of STRmix™

Advantages

- STRmix™ can quickly and easily analyze complex mixtures
- The software reduces variability in interpretation.
- Using more data enhances the ability to distinguish between true donors and non-donors

Limitations

- STRmix™ analysis cannot be done on all DNA samples. Samples not suitable for STRmix™ include:
  - Very low level profiles including those with data at only one location.
  - Samples in which the number of contributors cannot be determined.
  - Samples which have more than 4 contributors.

Statistical weight to a positive association

- **Random Match Probability (RMP)**
  - Estimates how often we expect to find someone in the general population who could have the evidence profile.
  - Expressed as a frequency.
    - "The profile is estimated to occur once in # of unrelated individuals."
  - Value is *COMPLETELY INDEPENDENT* of any reference profiles.

Item 1A: Sample from Condom (Previously profiled)
Fraction: Non-Sperm[9]
Number of Contributors[16]: 1
Male: 23 STR loci
Cannot be excluded (is included): CARLOS DASONSECA (DAFONSECA)
Statistical Frequency[19]: 1 in 5.6E30 (5.6 Nonillion) at 23 STR loci

- **Likelihood Ratio (LR)**
  - Estimates how likely the DNA profile is given two different hypothesis.
  - Value is *ENTIRELY DEPENDENT* upon the possible contributors and specific propositions being considered.

Item 1B1: Sample from Vaginal Swab(s)
Fraction: Sperm[9]
STRmix™[28]
Proposition Set: 1
Number of Contributors[16]: 2
Proportion of Contributors[29]: 92%, 8%
Assumed[31]: DEZIRAY SIMMONS (92% Contributor)

H_1: The DNA profile originated from DEZIRAY SIMMONS and DEVIN HEMPHILL.

H_2: The DNA profile originated from DEZIRAY SIMMONS and an unknown unrelated individual.

The DNA profile is approximately 2.3E+5 (230 thousand) times more likely if it originated from DEZIRAY SIMMONS and DEVIN HEMPHILL than if it originated from DEZIRAY SIMMONS and an unknown unrelated individual.

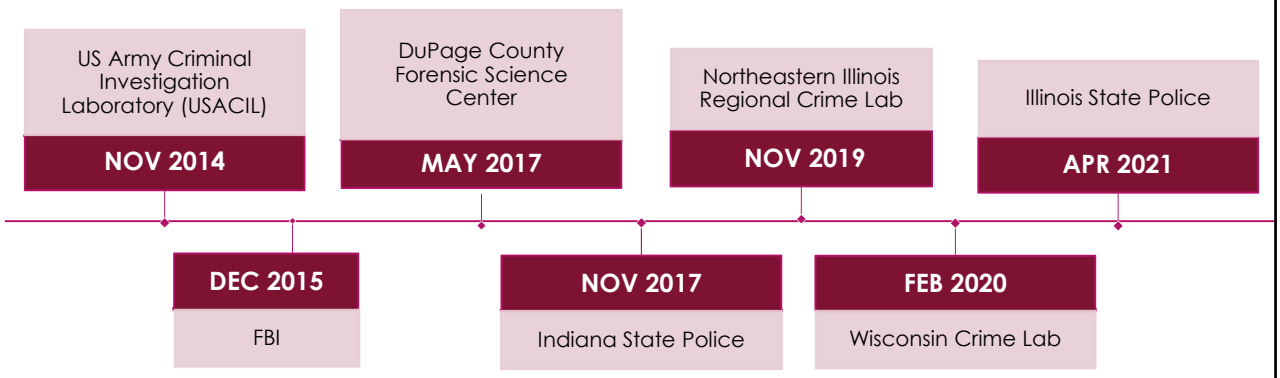
This analysis provides *Strong Support*[30] for the proposition that DEVIN HEMPHILL is a contributor to the DNA profile.

Likelihood verbal scale

- To help understand the magnitude of the numbers…

Likelihood Ratio	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

STRmix™ timeline throughout the USA



State of Illinois v Dwright Doty

- 9 year old boy killed in an alley while playing basketball in 2015
- Evidence included a basketball, two guns, car swabs
  - Basketball was swabbed in quadrants that were profiled separately
- CCSAO requested STRmix be used
  - ESR helped with ISP validation
  - Data was sent to ESR for analysis
- Frye hearing was held to gain admissibility
  - Multiple "big names" came in to testify

State of Illinois v Dwright Doty

Traditional (Binary) interpretation

- Quadrants of basketball:
  - Mix of at least 3 – major matches victim
  - Mix of at least 2 – major matches victim
  - Mix of at least 3
  - Mix of at least 2
- Various car swabs – Dwright Doty included in 2 sets of swabs

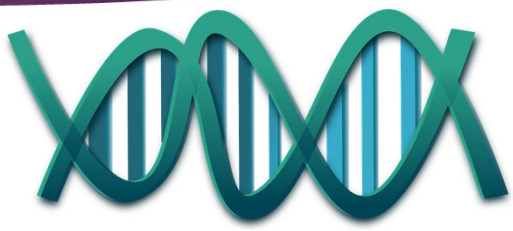
STRmix interpretation

- Quadrants of basketball:
  - The DNA profiles on the basketball are at least $6x10^5$, $3x10^{12}$, $1x10^{16}$, $1x10^6$ times more likely if Mr. Doty is a donor than if he is not.
- Various car swabs – Both inclusions corroborated by STRmix

What else can DNA offer you?

….SO MUCH MORE

Rapid DNA analysis



- Fully automated, hands off approach to DNA
  - "Swab in – profile out"
- Modified rapid
  - Human intervention needed for interpretation
- Buccal standards are eligible for CODIS entry
- Not approved for crime scene samples, therefore you must have a database for comparisons
- Rapid DNA Act of 2017
  - Modified the DNA Identification Act of 1994 DNA to include standards and procedures for Rapid DNA

NDIS (CODIS) approved Rapid DNA Instruments

ANDE 6C

- NDIS approval for lab use in June 2018
- NDIS approval for booking stations in February 2021
- 5 samples at a time
- 27 STR loci
- ~90 minute run time
- 85% first run passing rate reported
- ISP had 65% passing rate in 632 samples
  - February 2020 – May 2021

Applied Biosystems RapidHIT

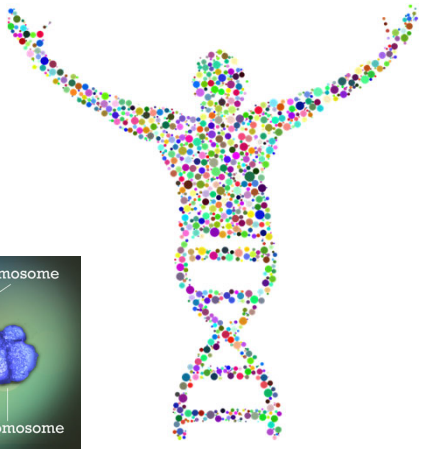
- NDIS approval for lab us in September 2020
- NDIS approval for booking stations in July 2021
- 1 sample at a time
- 23 STR loci
- ~90 minute run time
- 85% first run pass rate reported
- ISP has 76% passing rate in 441 samples
  - August 2022 – Current

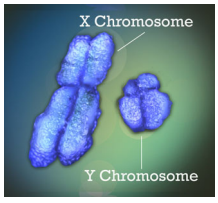
Bone extractions

- When nothing else remains
- Requires a clean bone from the ME's office
  - Whole bone is absolute best, we request the ME does not cut it in half
  - Prefer a femur
- A portion of the bone is sawed into dust, purified, and extracted
- Unidentified human remains

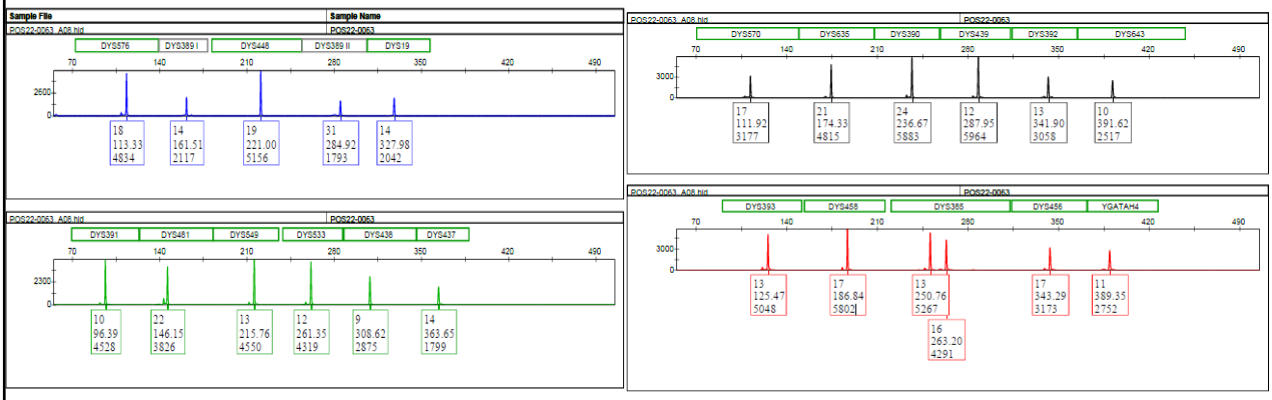
Y-STR analysis

- Focuses on the male contributor
- Passed on through the male lineage: father to son
- Most applicable in sexual assault cases
  - Typically utilized when the ratio between female and male is too high for autosomal DNA
- 23 loci kit
  - All locations on the Y chromosome
- Last resort to find a probative link
  - Best possible statistic = 1 in 2800
  - Not as discriminating as autosomal DNA





Y-STR profile



Parentage analysis

- Criminal paternity/maternity or identification of human remains
- To be evaluated at ISP, all three samples are required.
  - Alleged mother, alleged father, child
  - Two of three must be from reference standards
- If only two samples are available, results are forwarded to an accredited parentage laboratory for evaluation
  - ISP can report out exclusions
- Report wording "John Doe cannot be excluded as the biological father of Child. It is XXX more likely to see these genetic results if John Doe is the biological father of Child than if an untested, unrelated man is the father."

Familial analysis

- A search of CODIS to determine if a close biological relative of a convicted offender (in the Illinois DNA Index) could be the source of the DNA profile from an unsolved case
- Non-routine and must meet strict criteria to be considered
  - Approval needed from FSC Familial Search Committee
- Two pedigree trees are created to represent a parent/offspring relationship or a full sibling relationship
- The profile to be searched is associated to each tree as a known relative and candidates from each search will be ranked from highest to lowest
- Important to remember: THESE NAMES ARE NOT THE PERSON THAT LEFT DNA BEHIND AT THE SCENE, they are possible relatives. Deeper agency investigation is needed.

Fired cartridge casing analysis

- FCCs (or DCCs) historically have not been accepted for DNA analysis
  - Thought that heat from discharge did all the damage
  - Would go straight to LP before FA
- ATF published a paper highlighting a new method for swabbing FCCs in *Forensic Science International: Genetics*
  - Reasoned that it's actually the copper in brass that damages DNA
  - Proposed a new swabbing master mix and swabbing technique to neutralize the effects of copper
- ISP traveled to the ATF in December 2021

An improved process for the collection and DNA analysis of fired cartridge cases

Todd W. Bille*, Glenn Fahrig, Steven M. Weitz, Greg A. Peiffer

United States Bureau of Alcohol, Tobacco, Firearms, and Explosives, National Laboratory Center, 6000 Ammendale Road, Beltsville, MD, 20705, United States

CODIS – the end game to all of our work (mostly)

- Combined DNA Index System
  - Created and maintained by the FBI
- Houses several databases
  - Local, State, and National level databases
  - Convicted offender, arrestee, forensic, forensic mixture, forensic partial, suspect standards, homicide victim standards (legal), unidentified human remains, staff, etc
- Goal of casework is to get a profile suitable for entering and searching in CODIS
- Samples need to meet certain criteria and level of completeness to be eligible
  - Must be criminal case, thought to be offender's profile, not found on offender's person
  - At least 6 loci for SDIS and 10 for NDIS as well as meet rarity threshold
  - Elimination standards are HIGHLY recommended and must be at least requested before entry

CODIS database sizes as of 12/12/23

Local (LDIS)

Forensic: 20,118

Forensic mixture: 4,786

Forensic partial: 6,774

Legal: 8,247

Missing person: 7

Unidentified human remains: 32

Staff: 882

Suspect: 9,215

State (SDIS)

Arrestee: 914

Forensic: 47,603

Legal: 12,181

Missing person: 55

Offender: 696,178

Staff: 881

Suspect: 29,549

National (NDIS)

Arrestee: 5,303,917

Convicted offender: 14,502,179

Detainee: 1,484,033

Forensic: 874,621

Forensic mixture: 154,738

Forensic partial: 206,602

Legal: 134,522

NDIS stats as of June 2022

Latest NDIS Statistics

NDIS Searchable Profiles As Of Jun 2022

- Forensic: 1,196,661
- Arrestee: 4,745,783
- Convicted Offender: 14,707,834
- Total: 20,650,278

CODIS Hits Graph Stats

Period	Investigations Aided	Forensic	Intrastate Offender Hits	Interstate Offender Hits
Jun	605,028	98,388	450,908	69,798
May	601,467	97,830	448,354	69,400
Apr	597,287	97,038	445,444	68,905
Mar	592,944	96,243	442,334	68,348
Feb	589,095	95,539	439,719	67,846
Jan	585,151	94,837	436,731	67,365

In 2021, FSC-C had 2439 positive associations. We're at 2140 associations as of 9/21/22 and counting.

Case Examples

ARSON CASES SUBMITTED FOR DNA ANALYSIS

Case 1
Office of the Illinois State Fire Marshal Arson Division

- Door handle assembly from POE submitted for DNA
- Swabs collected from both sides of knob and deadbolt plates
- Swabs listed as "black stained" possibly from fire/smoke damage
- Quant results indicate low level, degraded

Item 4A: Sample from Door Knob(s) and deadbolt key and latch plates
No DNA Profile Identified

Item 4B: Sample from Door Knob(s) and deadbolt key and latch plates
No DNA Profile Identified

Item 4C: Sample from Door Knob(s) and deadbolt key and latch plates
No DNA Profile Identified

Item 4D: Sample from Door Knob(s) and deadbolt key and latch plates
Not Amplified[13]: No human DNA was detected

Case 2
Office of the Illinois State Fire Marshal Arson Division

- Gasoline Can from scene for DNA
- Mattress, box spring and clothing positive for gasoline and acetone
- Handle of gas can swabbed for DNA

Case 2
Office of the Illinois State Fire Marshal Arson Division

- 2 contributor
- 93% contributor entered into CODIS
- 7% contributor not suitable for CODIS eligible for direct comparisons
- Sample consumed in analysis

Item 1: Gasoline Can
STRmix™[28] Number of Contributors[16]: 2 Proportion of Contributors[29]: 93%, 7% CODIS[23]: 93%

Remarks:

Please submit standards for comparison to the profile(s) identified in Item(s) 1.[7]
Consumed: Item(s) 1. No extract remains: Item(s) 1.

Case 3
CPD Unit 603
Bomb and Arson Section

- Lighter and nitrile gloves found next to burned vehicle
- Swabbed lighter
- Swabbed inner/outer sides of gloves
- LP analyst revealed no suitable prints

Case 3
CPD Unit 603
Bomb and Arson Section

- Lighter
  - 2 contributors
  - 83% to CODIS
  - 17% Suitable for comparison
- Gloves
  - 2 contributors
  - 98% to CODIS
  - 2% Suitable for comparison

Item 1: One (1) lighter

STRmix™[28]
Number of Contributors[16]: 2
Proportion of Contributors[29]: 83%, 17%
CODIS[23]: 83%

Item 2: Two (2) Nitrile gloves

STRmix™[28]
Proportion of Contributors[29]: 98%, 2%
CODIS[23]: 98%

Remarks:

Please submit standards for comparison to the DNA profiles identified in Items 1 and 2.[7]
Consumed: Items 1A, 2A and 2B. No extract remains.

Case 3
CPD Unit 603
Bomb and Arson Section

- CODIS Hit to Convicted Offender
- CODIS Hits are issued as separate reports from the DNA analysis

LABORATORY REPORT
DNA-CODIS HIT

Hit # 27073

DFS Item #	1
Agency Item #	15097629-11805977
Description	One (1) lighter

Your agency is being notified of a CODIS association with the following case(s) and/or individual(s)

Name:	Janaiya Cail
DOB:	09-29-1988
SID:	IL34990141
IL DOC #:	Information Not Available

Case 4
CPD Unit 603
Bomb and Arson Section

- Vehicle stolen, used in shooting, then burned
- 2 possible blood samples recovered from interior of car for DNA analysis

DESCRIPTION	TEST RESULT
1 - BLOOD-LIKE STAIN FROM DOOR FRAME	Blood indicated.[6]

1 - BLOOD-LIKE STAIN FROM SEAT BACKREST	Blood indicated.[6]

Case 4
CPD Unit 603
Bomb and Arson Section

- Single source profile from 1A
- Single source profile from 2A
- 1A and 2A consistent with common donor-only 2A entered into CODIS

Item 1A: Sample from 1 - BLOOD-LIKE STAIN FROM DOOR FRAME
Number of Contributors[16]: 1 Male: 23 STR loci

Item 2A: Sample from 1 - BLOOD-LIKE STAIN FROM SEAT BACKREST
Number of Contributors[16]: 1 Male: 23 STR loci CODIS[23]

Remarks:

DNA profiles from the following items were compared and determined to be consistent with having originated from a common donor: Items 1A and 2A.
Please submit standards for comparison to the profiles identified in Items 1A and 2A.[7]

Case 4
CPD Unit 603
Bomb and Arson Section

- CODIS Hit to Convicted Offender
- CODIS Hit to another CPD case

LABORATORY REPORT
DNA-CODIS HIT

Hit # 25652

DFS Item #	2A
Agency Item #	15254565-12655592
Description	1 - BLOOD SAMPLE FROM SEAT BACKREST

Your agency is being notified of a CODIS association with the following case(s) and/or individual(s)

Name:	Austin Gooden
DOB:	4/8/1995 & 9/8/1995
SID:	IL11454871
IL DOC #:	M54555

DFS Case #:	DFS20-012467
DFS Item #:	5A
Description:	Sample from "Vinter's Cruncy Kurls" bag recovered from the front driver's side door pocket
Agency:	CHICAGO PD UNIT 610
Agency Case #:	JD196739
Agency Contact:	SORIA, STEVE
Offense:	First Degree Murder

Case 4
CPD Unit 603 Bomb and Arson Section

- CODIS Hit to Lisle/DuPage Lab case

Laboratory:	DuPage County Forensic Science Center #20-01639
Agency:	Lisle Police Department #LIPC2001295
Agency Item:	#005 Swab of steering wheel
Contact:	Det. Jeremiah Arnold
Phone:	630-271-4200
Offense:	Theft

Case 5
Des Plaines Police Department

- Mask from scene
- 3 contributors
- 45%, 44%, 19% all suitable for CODIS

Item 1A: Swab from Disposable Face Mask

STRmix™[28]

Number of Contributors[16]: 3

Proportion of Contributors[29]: 45%, 36%, 19%

CODIS[23]: 45%, 36%, 19%

Case 6
Kewanee Police Department

- Explosive device found at scene
- Swabs from device submitted for DNA analysis
- Suspect standard submitted for direct comparison

Item 1A: Sample from Two swabs taken from the exterior of Ex.1

STRmix™[28]

Proposition Set: 1

Number of Contributors[16]: 2
Proportion of Contributors[29]: 58%, 42%

H_1: The DNA profile originated from Paul Carter and an unknown unrelated individual.

H_2: The DNA profile originated from two unknown unrelated individuals.

The DNA profile is approximately 2.8E+8 (280 million) times more likely if it originated from two unknown unrelated individuals than if it originated from Paul Carter and an unknown unrelated individual.

This analysis provides *Very Strong Support*[30] for the proposition that Paul Carter is not a contributor to the DNA profile.

Case 6
Kewanee Police Department

- Explosive device found at scene
- Swabs from device submitted for DNA analysis
- Suspect standard submitted for direct comparison

Item 1B: Sample from Two swabs taken from the exterior of Ex.1

STRmix™[28]

Proposition Set: 1

Number of Contributors[16]: 2
Proportion of Contributors[29]: 96%, 4%
CODIS[23]: 96%

H_1: The DNA profile originated from Paul Carter and an unknown unrelated individual.

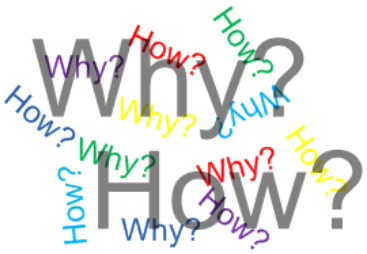
H_2: The DNA profile originated from two unknown unrelated individuals.

Paul Carter is excluded as a contributor to this DNA profile.

Forensic DNA analysis has its limitations

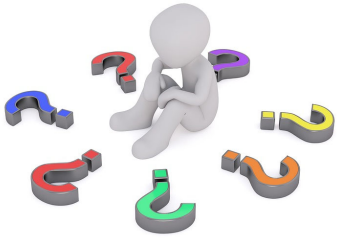
- We cannot tell you *how* a DNA profile was left at the scene
- We cannot tell you *when* a DNA profile was left at the scene
- We cannot tell you the last person to touch an object

- The process takes time
  - Rush 2-4 weeks
  - Priority 1-3 months
  - CSA up to 6 months
  - General turnaround time up to 10 months
- We cannot work every last piece of evidence collected
- We prioritize violent crimes and crimes against people



Questions?

- Section Chief:
  - Jennifer Bell-Schoon: Ext. 8368; Jennifer.Bell-Schoon@Illinois.go
- Group Supervisors:
  - Cynara Anderson: Ext. 8361; Cynara.Anderson@Illinois.gov
  - Gregory DiDomenic: Ext. 8342; Gregory.DiDomenic@Illinois.gov
  - Ryan Paulsen: 312-779-8374; Ryan.Paulsen@Illinois.gov
- CODIS Contacts:
  - Kathleen Kozak: Ext. 8378; Kathleen.Kozak@Illinois.gov
  - Karen Abbinanti: Ext. 8369; Karen.Abbinanti@Illinois.gov



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