Unraveling the Helix: Defending Against DNA Evidence

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The Power of DNA

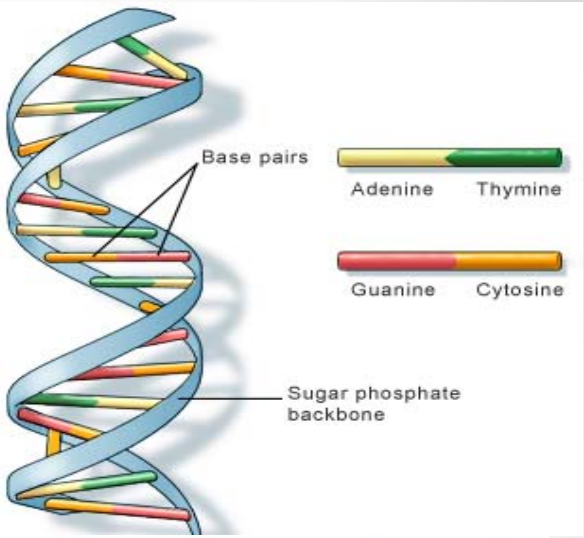
DNA evidence holds a "unique status within the criminal justice system" having a capacity to persuade the trier of fact of a defendant's guilt "unlike anything known before," and operating to shroud the prosecution's case with a "mystical aura of definitiveness" that renders it virtually "invincible."

- *People v. Wright*, 25 N.Y.3d 769, 783-84 (2015).

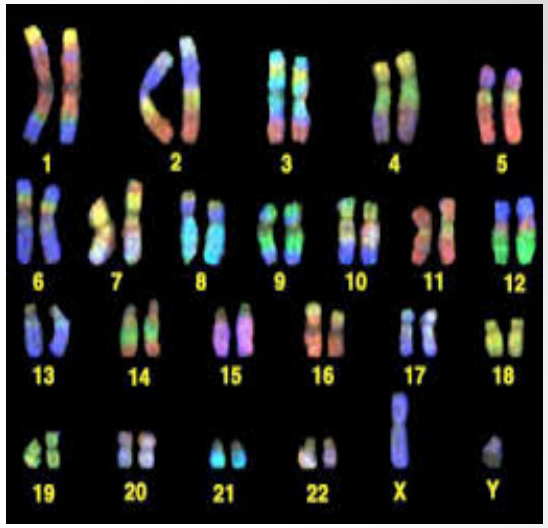
The Basics of DNA

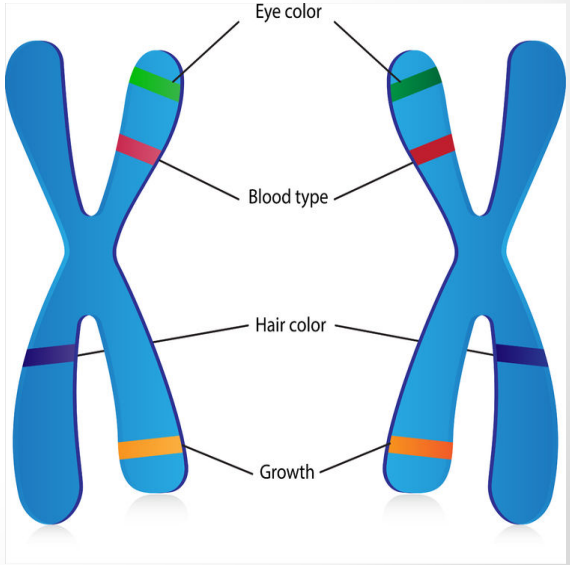
- Deoxyribonucleic Acid (“DNA”) is present in the nucleus of the cells of almost all organisms, and all nucleated cells in each organism have the same DNA.
- If stretched out, each strand of human DNA would be about 6 feet long, and 2 nanometers wide, but it is tightly bundled in the chromosomes within the nucleus, which are each 1–10 micrometers long (.001 millimeters or .000039 inches).
- Human DNA consists of about 3 billion bases, and 99.9% are the same in all people – only .1% unique.
- The order of these bases determines our unique genetic makeup.

- Information in DNA is stored as a code made up of four chemical bases: Adenine, Guanine, Cytosine, and Thymine, which pair with each other – A with T, and C with G, to form units called base pairs.
- Each base is attached to a sugar molecule and a phosphate molecule; together they make a “nucleotide.”
- Nucleotides are arranged in two long strands that form a double helix; the base pairs form the ladder’s rungs and the sugar and phosphate form the vertical sidepieces.
- DNA is designed to replicate when cells divide, so that each new cell has an exact copy of the DNA of the old cell; each strand forms a pattern for duplicating the sequence of bases.



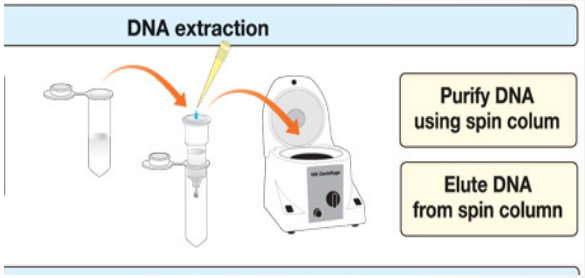
- DNA is bundled in chromosomes within the nucleus, and each cell has 23 chromosome pairs -- 46 total -- with 23 inherited from each parent.
- A “gene” is a segment of DNA at a specific locus on a chromosome that codes for certain traits. It is not an entity, but a location on the chromosome.
- An “allele” is one member of a gene pair. Humans have two alleles at each genetic locus, one inherited from each parent.
- The typical DNA report admitted at trial is a list of the alleles at 13 – 20 loci, plus the sex chromosome.

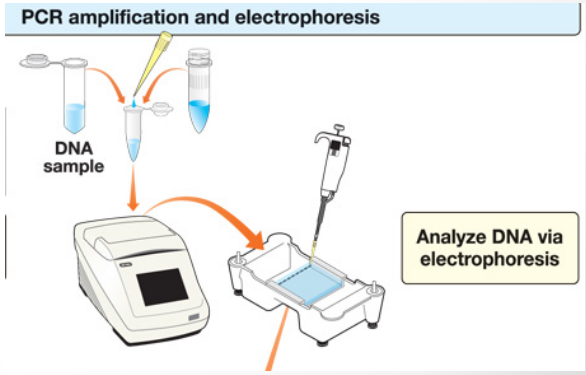


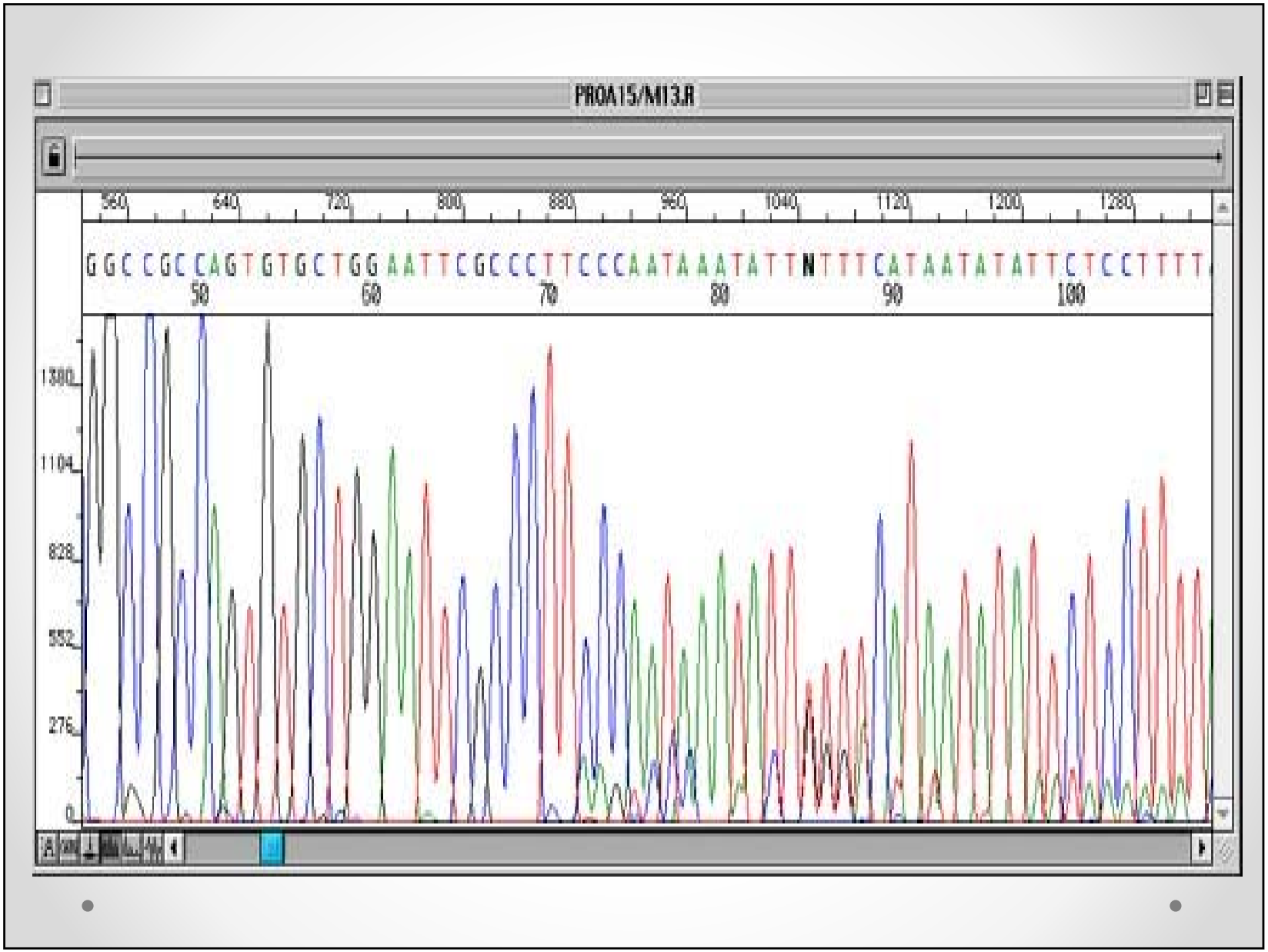


The Basics of DNA Testing

- **Collection**: area or substance is swabbed for DNA
- **Extraction**: any cells picked up on swab are broken apart, releasing DNA from their nuclei
- **Quantitation**: total amount of DNA in sample is measured to ensure sufficient quantity for testing.
- **Amplification**: DNA is copied, then copies are copied, etc.
- **Capillary Electrophoresis:** DNA molecules are separated by size and data is collected
- **Analysis:** electropherograms are read and interpreted by analyst






PROA15/M13.R
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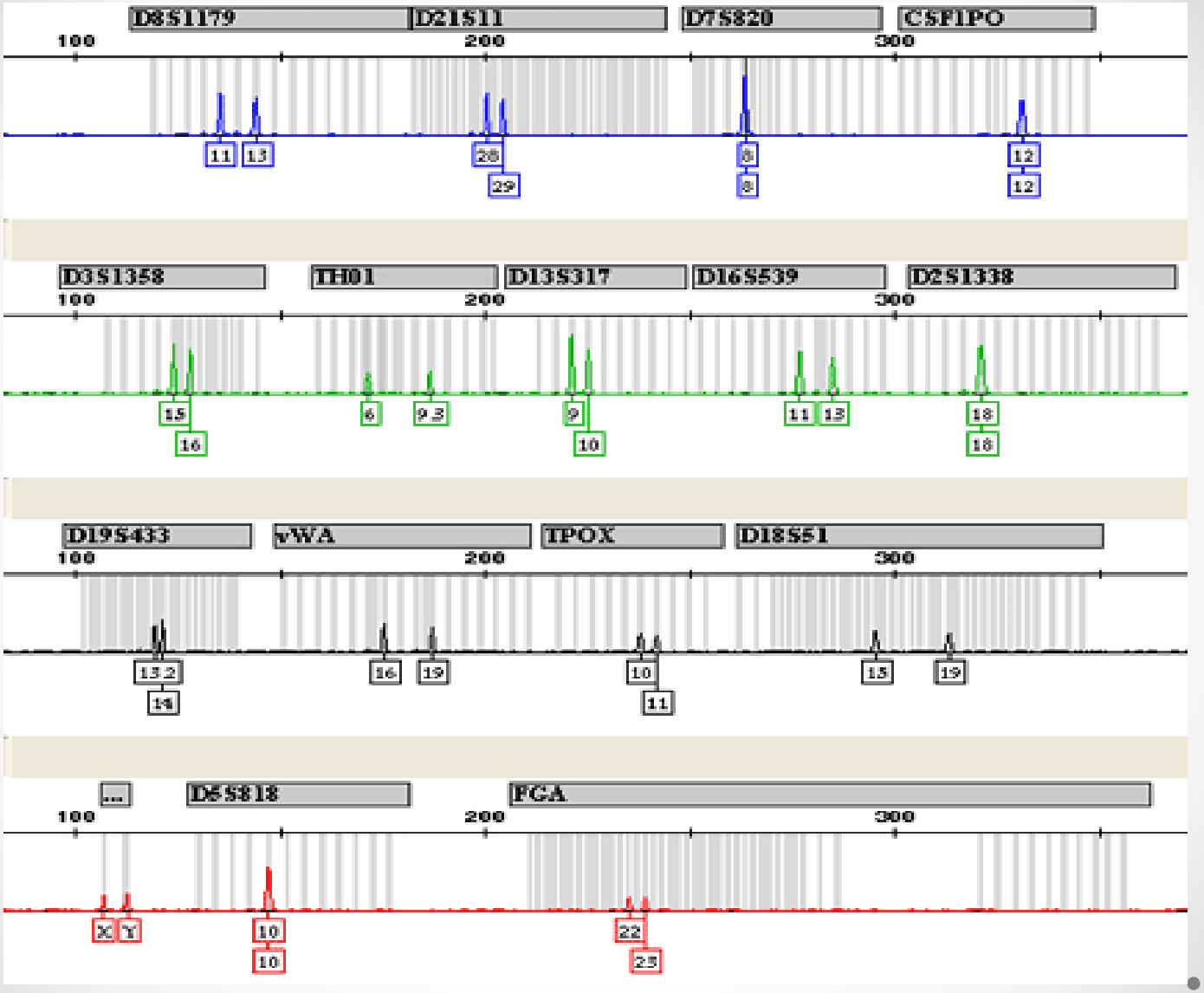
D8S1179
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D13S317
D16S539
D2S1338
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16
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9.3
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D19S433
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D18S51
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11
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19
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D5S818
FGA
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200
300
X
Y
10
10
22
25

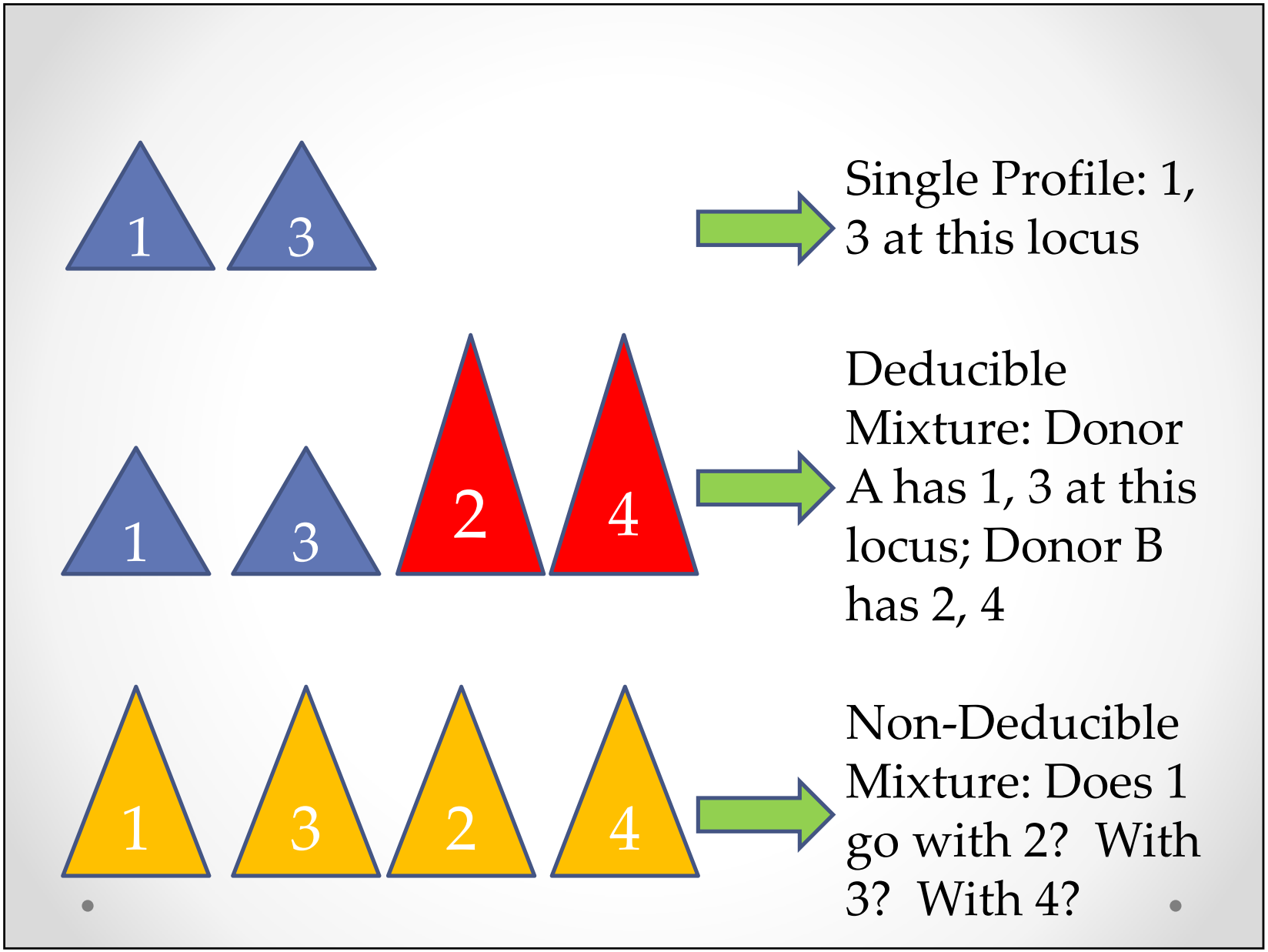
Loci	Suspect Profile	Sample
D8	13, 14	13, 14
D21	30, 32.2	30, 32.2
D7	10, 12	8, 9
CSF	11,11	11, 11
D3	16,16	6, 16
THO1	6,7	6, 7
D13	11,11	11, 11
D16	9,11	9, 11
D2	21,22	21, 22
D19	13,14	13, 14
VWA	15,19	15
TPOX	6,8	6, 8
D18	12,14	12, 12
D5	10,11	11
FGA	24,24	--
Sex	XY	XY

NO MATCH: both alleles different

NO MATCH: one allele different

NO MATCH: degraded sample, missing an allele

NO MATCH: degraded sample, missing both alleles


1
3
Single Profile: 1, 3 at this locus
1
3
2
4
Deducible Mixture: Donor A has 1, 3 at this locus; Donor B has 2, 4
1
3
2
4
Non-Deducible Mixture: Does 1 go with 2? With 3? With 4?

Loci	Victim	Susp Profile	Sample Rep 1	Sample Rep 2	Sample Rep 3	Composite
D8	13, 14	14, 14	10,12,13,14,15	10,12,13,14	13,14	10,12,13,14
D21	30, 32.2	29, 30	29,30,31,32	27,29,30,32	29,30,31,32	29,30,31,32
D7	10,10	10, 11	9,10	10	10,11	10
CSF	11,11	11, 12	8,10,11,12	11,12	11	11,12
D3	16,16	14, 14	14,15,16	14,16	14,15,16	14,15,16
THO1	6,7	9, 9.3	6,7,8,9,9.3	3,6,7,9,9.3	6,7,9,9.3	6,7,9,9.3
D13	11,11	12, 14	11,13,14	11,12	11,12,14	11,12,14
D16	9,11	11, 12	9,11,12	9,10	9,11,13	9,11
D2	21,22	17, 19	21	17,19,20,22	21,22	21,22
D19	13,14	14, 16	12,13,14,16	12,13,14	12,13,14,15,16	12,13,14,16
VWA	15,19	15,18	15, 18, 19	15,17,18,19	15,17,18,19	15,17,18,19
TPOX	6,8	8,10	6,8,10	6,8	6,8,9,10	6,8,10
D18	12,14	13,14	12,14	12,14	12,13,14	12,14
D5	10,11	11,11	10,11	10,11	10,11	10,11
FGA	24,24	21,22	21,22,24,27	21,22,24	24	21,22,24

Problems to Look For

- **Contamination**
  - Prior to the crime
  - During collection at the scene
  - During testing at the lab
- **Analyst Error**
- **Misusing Test Kits**
  - Low Copy Number / High Sensitivity Testing (LCN / HST)
  - STR Mix run outside validated threshold
- **Using Unreliable / Untested Probabilistic Software**
  - Different programs can yield different results
  - OCME's Forensic Statistical Tool (FST)
- **Overstating the Scientific Conclusion**
  - Implying a statistic is a match, or highlighting irrelevant numbers
  - Attorney exaggeration during argument or summation

Contamination

- Contamination before the crime even happens:
  - 2015 University of Indianapolis study on touch DNA
    - Person A and B shake hands, and then A handles a knife.
    - B's DNA recovered from knife in 85% of samples.
    - In 20% of those cases, B's DNA was identified as the main or only contributor
  - Phantom of Heillbronn
    - DNA of one woman found on evidence from 6 murder scenes
    - "Germany's most dangerous woman" was a worker at cotton swab factory
- Contamination during scene processing
  - Genetic material from first responders
  - Use of swabs in multiple areas
    - E.g. blood collection in People v. Cal Harris case
  - Failure to wear gloves and face masks
  - Failure to change gloves during collection of each sample
  - Improper packaging of evidence
    - E.g. rug in Harris case crumpled in a box
- Contamination during testing at lab
  - Lab technician contamination (e.g. Avery case)
  - Failure to follow lab protocols
  - Mixing samples

Contamination Cases

- People of the State of California v. Lukis Anderson (Smith, P., Scientific American 6/1/16, *When DNA Implicates the Innocent*)
  - DNA EVIDENCE: Homeless man charged with murder of Silicon Valley millionaire based on DNA found under victim's fingernails.
  - THE PROBLEM: Anderson had airtight alibi – he was at the hospital nearly comatose with BAC of .40% , under constant medical supervision
  - THE EXPLANATION: paramedics who treated Anderson earlier that day inadvertently "planted" his DNA at the crime scene more than three hours later.

- *People v. Graham*, 107 A.D.3d 1296 (3d Dept. 2013)
  - Defendant's DNA found on gun handle.
  - AD reverses conviction on weight-of-the-evidence review finding that DNA could have been deposited through "secondary transfer" when police officer "touched defendant and then [touched] the gun."

Analyst Error

- **Many parameters are set or defined by analysts**
  - Herskovic: DNA results showed 5 or more alleles at multiple locations, but analyst ran data under "assumption" that there were only 2 donors
  - Harris: analyst defined peak heights at lowest lab limit
- **Electropherograms are read by analysts**
  - Extra peaks can be discounted as "stutter" or "noise" but may be significant
  - Low peaks that are actually noise may be erroneously counted as part of a profile
  - Analysts can disagree: Theresa Caragine of OCME forced to resign in 2013 for changing colleagues results against protocol
- **Machines or software can malfunction**
  - FST software has been found to drop data from calculations, and has an admitted 30% margin of error in quantifying DNA in sample
  - FST validation studies show 163 out of 550K non-contributors with likelihood ratio greater than 1; 56>10; 14>100; 5>1000; 1>10,000

Case Law Recognizes the Importance of the Analyst to a Reliable DNA Result

- People v. John, 27 N.Y.3d 294 (2016)
  - "We will not indulge in the science fiction that DNA evidence is merely machine-generated, a concept that reduces DNA testing to an automated exercise requiring no skill set or application of expertise or judgment. Likewise, the sophisticated software programs require trained analysts who engage in skilled interpretation of the data from the electrophoresis instrument, using the computer software with its color images, particularly as to the peaks in the graphs, to construct the DNA profile."

Misuse of Test Kits Against Manufacturer's Protocols

HS (High Sensitivity)/LCN (Low Copy Number) Testing:

- Test kit: 500-1000 picograms optimal to permit "reliable results"
- 125 picograms is minimum threshold required to run test
- Sample has less than 100 picograms at quantitation stage.
  - People's expert: *"you would typically say its insufficient" to continue testing*
- *OCME "tweaks the protocols"* by running three additional amplification cycles to artificially increase the amount of DNA by creating more copies
  - "*our laboratory looked and said, we know DNA is there right? We have to say it's insufficient because no one had ever went into that realm …. So, we validate it high sensitivity testing. That will take us into that lower range of testing. We're using the same instruments. We're using the same kits. We've just tweaked the protocols…"*
- produces increase in stochastic effects (inconsistent results when different parts of the sample are tested), drop-ins (the presence of alleles that should not be there), drop-outs (the absence of alleles that should be present), and stutter (echoes of alleles) .
  - Unsuitable for upload in CODIS
  - Failed to pass Frye test in *People v. Collins & Peaks*, 49 Misc.3d 595 (Kings Co. 2015).
  - Subject of Front Page NY Times Article: *Traces of Crime: How New York's DNA Techniques Became Tainted* (9/4/17)

Misuse of Test Kits Against Manufacturer's Protocols

STRMix v. True Allele: Picking, Choosing and Tweaking

- People v. Oral Nicholas Hillary
  - Charged with murder of 12 yr old boy based on a mixed profile of DNA evidence under V's fingernails
  - Prosecutors initially used "True Allele" forensic software tool: "No statistical support for a match"
  - Prosecutors then turned to New Zealand lab using "STRMix" resulting in proffered statistics that only 80 people in the country (pop. 319 million) would match the profile, and Hillary was one (ie., roughly 1 in 4 million)
  - Defense showed that STRMix was not run at validated 30 rfu threshold – which would have excluded Hillary as a donor, but at 50 rfu threshold.
    - Ie. Twist the knobs, get different results.
  - So while STRMix is generally accepted, the trial court found that the manner in which it was used was not validated, and granted the defense Frye motion excluding the evidence. *People v. Hillary*, 2015-15 (St. Lawrence Co., 8/26/15).

Using Unreliable/Untested Probabilistic Software

- **Probabilistic Software is used for:**
  - Incomplete results due to low quantity or low quality samples
  - Complex mixtures of DNA with multiple contributors (ie., non-deducible mixtures)
- **Many Programs:**
  - STRMix, True Allele, DNA View, Lab Retriever, Like LTD, LRMIx, CEESit, Euroformix, and many more.
  - Different programs can generate different results (ie., Hillary)
    - This is because they each have their own parameters for peak heights, stutter, allele overlap, probability for drop in and drop out, databank inclusion, etc.
  - Each is only as reliable as its source code (algorithms), data bank information, and analysts
    - 2017 Report by President's Council on Science and Technology expressed concerns about use of the programs beyond scope of current validation
  - Reliability often can't be tested because source code isn't released, or validation studies are conducted in-house
    - United States v. Johnson, 1:15-Cr-00565-VEC (6/7/16) (granting defense motion to order OCME to reveal source code of FST, but granting protective order).
    - Litigation currently pending for public release

CASE IN POINT: FST

"There are three kinds of lies: lies, damned lies, and statistics" -- Mark Twain

- **The Forensic Statistical Tool (FST)**
  - Proprietary software developed by OCME to "give meaning" to "non-deducible mixtures" from which "no match" can be made
  - A "likelihood probability" is calculated for one analyst-defined scenario or another
  - Stats based on 480 mixtures obtained from only 61 contributors
  - Only 11 involved mixtures of same race; some races under-represented
  - Failed to pass Frye test in *People v. Collins & Peaks*, 49 Misc.3d 595 (Kings Co. 2015).
  - Heavily criticized and questioned (*see* NY Times Article: *Traces of Crime: How New York's DNA Techniques Became Tainted* , 9/4/17)
  - Currently pending before Appellate Division in *People v. Herskovic*

Overstating the Conclusion: Drawing Inferences the Science Doesn't Support

EXAMPLE 1: *Harris Case*

- LMG testing of spots on rug was presumptively positive for blood; DNA matching victim's recovered from swab; Prosecution concluded that spots were victim's blood.
  - WRONG:
    - **DNA test is species specific**
      - Will not provide any profile if the genetic material is not human
    - **DNA test alone cannot reveal the source of DNA**
      - Could be from saliva, skin, blood, semen, sweat, etc.
  - Analyst forced to admit on cross that stain could have been meat drippings or dog blood (LMG positive for blood), and DNA deposited separately from victim walking on rug.

Overstating Scientific Conclusions: Misuse of the Evidence on Summation

EXAMPLE 2: *Powell case*

- Victim was dating defendant's estranged wife. Defendant claimed he saw them together, sat and talked to wife in kitchen, and then left. Victim found bludgeoned to death, and victim's DNA recovered from stain on elbow of defendant's shirt.
  - People's Summation: *"That piece of evidence right there by itself … tells you that he's the killer" because "there's no explanation on earth, none, zero, that would explain why [the victim's] blood is on that shirt."*
    - *Fallacy: DNA is not proof of blood; transfer possible*

Overstating Scientific Conclusions

EXAMPLE 3: *Herskovic Case*

- Victim testified that ringleader of a gang assault pulled off his sneaker and threw it. A few cells of touch DNA found on heel of victim's sneaker. LCN testing resulted in "non-deductible mixture." FST analysis resulted in "133 times more likely that mixture was Herskovic's DNA mixed with victim than unknown person's DNA mixed with victim." Based on this evidence alone, prosecution concluded that Herskovic was the man who threw the sneaker during the assault.
  - LCN and FST both unreliable, and used in combination
  - No match here – and "133 times" should not be proof beyond a reasonable doubt
  - Assumption of two-person mixture not valid
  - Hasidic shared ancestry not accounted for by analyst defined parameters
  - **BUT – EVEN ASSUMING A DNA MATCH:**
    - Source of DNA unknown: Could be skin, saliva, etc.
    - Method of deposit unknown: could have stepped in spit on sidewalk
    - Secondary and tertiary transfer possible
      - Secondary: Herskovic shook hands with assailant, who touched sneaker. Herskovic's DNA on sneaker.
      - Tertiary: Herskovic opened a door. Assailant then touched the doorknob, and later the sneaker. Herskovic's DNA on sneaker.
    - ***Analyst admitted all of this on stand, and Herskovic was still convicted***

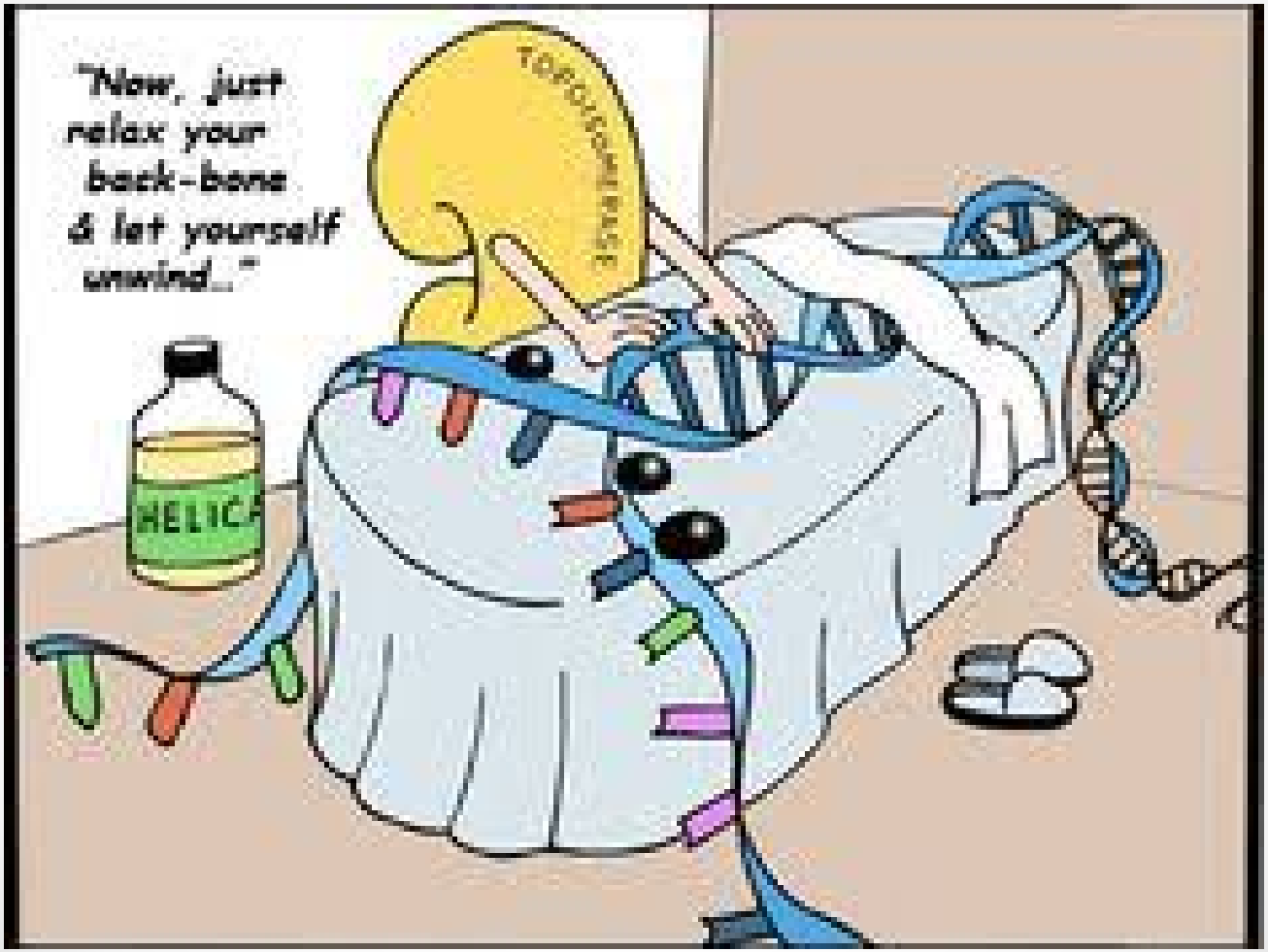
Other Examples

- *People v. Wright*, 25 N.Y.3d 769 (2015)
  - DNA analysis of ligature found around victim's hands showed that defendant "could not be excluded" as a donor.
  - Prosecutor interspersed references to ligature with comments about defendant's DNA profile, mischaracterizing probativeness of DNA evidence.
  - Court reversed, holding that prosecutor presented DNA results "in a manner that was contrary to the evidence and the science" and that defense counsel was ineffective for failing to object.
- *People v. Rozier*, 143 A.D.3d 1258 (4th Dept. 2016)
  - Expert testified that defendant was among "1 in 15 Americans who could not be excluded as a contributor" to DNA recovered from gun.
  - DA argued that DNA evidence was "overwhelming" and posited, "if the defendant had not possessed the gun, wouldn't science have excluded him?"
  - Reversed based on prosecutor's uncorrected exaggeration of the significance of DNA evidence during summation.

Trial Strategies

- **Don't delay**
  - Get the discovery *early*, and consult with an expert immediately to ensure it is complete and to highlight and understand problems
- **Use all available legal challenges**
  - Move for *Frye* hearing if problematic methodologies were used or deviation from protocol is observed
- **Cross effectively**
  - Use cross examination of expert not only to challenge procedures used, but also to highlight to jury how much analyst input is involved, and the limitations on the conclusions that can be drawn from the results
- **Have expert ready**
  - Consultation throughout testimony of prosecution's witness is important, and it may be necessary to call defense expert if cross is not sufficient to highlight weaknesses.
- **Be vigilant during prosecutor's summation**
  - Do not allow prosecutor to overstate conclusions. Object promptly **and** then move for mistrial at the conclusion of summation. Otherwise, errors may be deemed unpreserved.

GOOD LUCK!


"Now, just relax your back-bone & let yourself unwind..."
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