**National Institute of Standards and Technology** • U.S. Department of Commerce

**DNA Mixture Interpretation Webcast**
April 12, 2013

**http://www.nist.gov/oles/forensics/dna-analyst-training-on-mixture-interpretation.cfm**

http://www.cstl.nist.gov/strbase/mixture.htm

# Introduction

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# Introduction

- We are all seeing or being asked questions that show limited understanding of the science involved in reliable DNA interpretation

- Need to be prepared to go back and examine old cases with new SOPs to test reliability

- People are making decisions based on reports – there are scientific and ethical issues involved

- We have to be scientists first – then we can transition it into the legal realm of the court room

- Whatever our background, we need to seek help from others to do our job well

- The samples being tested now are not what have been validated in many labs (single-source or 2-person mixtures)

# Welcome to the NIST Campus

# Why are mixtures difficult?

- **The answer is:  We are working with evidence**

  A. We do not know the **number** or **ratio** of contributors before testing the sample

  – **and**

  B. We cannot control the PCR chemistry sufficiently to prevent variation in the amount of product produced for two alleles at the same locus even in a single source sample.

  – Therefore we have **peak height** and **peak height ratio variation**

# Variation is everywhere:

- Without understanding the basics of the PCR and the intrinsic variation produced, we cannot interpret the complicated profiles.

- We cannot interpret the complicated profiles using "analyst experience".

- For many mixtures our "experience" and our original kit validations can no longer account for all the variables.

# In the last 15 years:

- From 1998-2000 large STR multiplex kits were developed and put into use for forensic casework.

- Labs rapidly converted to STR analysis

- Accreditation became the norm

- CODIS (NDIS) database has grown from zero to 10,142,600 offender samples (as of Jan 2013)

- Case samples in the database are now 422,500

- Hits have grown from zero to a total of 200,300

- More hits ---- more successes ---- more samples ---- **more mixtures!**

# Analysis of backlog rape kits

- Massively supported by NIJ

- Begins about 2003 and still continues
  - Many cases done in private laboratories

- Many samples contain two person mixtures

- Subtraction of victim's known type allows deduction
  of unknown contributor and upload to CODIS
  - No need to set aside suspect's profile, there was no suspect

- More success ---- more samples ---- **more mixtures!**

# Following successes in Britain:

- DNA is extended to less serious crimes
  - Burglaries
  - Car thefts
  - Analysis of weapons
  - Clothes
- This produces
  - Low template DNA &
  - **More mixtures**

# Everyone makes The Leap

- If we can do two person mixtures we can also do "**more** person" mixtures!

- And…..it can still be simple!  All we need is-
  - a **S**tochastic **T**hreshold &
  - a **C**ombined **P**robability of **I**nclusion statistic

# What's wrong with this picture?

- There is nothing simple about the variation which is observed in mixtures from multiple contributors

- "The use of bounds **applied to data that show continuous variation** is common in forensic science and is often a pragmatic decision. However it should be borne in mind that applying such bounds has arbitrary elements to it and that **there will be cases where the data lie outside these bounds**."

Bright, J.A., et al. (2010). Examination of the variability in mixed DNA profile parameters for the Identifiler multiplex. *Forensic Science International: Genetics, 4,* 111-114.

# Why are we reluctant to embrace the complexities of our system?

- The courts do not appear to embrace complexity; lawyers and judges want us to make the complicated into the simple

- Many lab directors would prefer something simple --- complexity and production do not easily go hand in hand

- The NAS does not recognize that DNA mixture interpretation procedures used in the US are <u>not</u> generally keeping pace with the literature on the topic or practice in Europe, New Zealand and Australia.  NAS gives DNA a <u>pat on the back</u> for being *scientific*.

# And….

- The amount of learning required on our part is, in many cases, is extensive.

- The FBI QA Standards require 8 hours of continuing education/year which is not enough.

- Implementation of computer software approaches which model variation & remove the need for "line in the sand" thresholds will add information for our use in analysis and reporting. (This will also require training.)

- More extensive training in statistical approaches and the use of likelihood ratios will make better use of data and ultimately benefit the criminal justice system.

- Math phobia is out-get rid of it!

# Lastly…

- Collectively, in talking to people across the country, we see a continued need for improvement.

- Of course there will be cases that were reported using an older SOP after the lab has implemented a more "mixture savvy" SOP.

- There will be instances when old reports need to be updated with new interpretation.

- This is the only scientifically appropriate route.

- These changes and adjustments are manageable and within our collective capability.