

# Can the Validation Process in Forensic DNA Typing Be Standardized?

John M. Butler<sup>1</sup>, Christine S. Tomsey<sup>2</sup>, Margaret C. Kline<sup>1</sup>

<sup>1</sup>National Institute of Standards and Technology <sup>2</sup>Pennsylvania State Police DNA Laboratory

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|----|-------|------------------------|-------------|------------------------|---------------|-------|
| #  | Year  | Validation in<br>Title | Total Talks | Validation in<br>Title | Total Posters | %     |
| 1  | 1989  | 1                      | 10          |                        |               | 10.0  |
| 2  | 1991  | 0                      | 21          | 0                      | 14            | 0     |
| 3  | ~ `   | 100/ 0                 | ut of 1     | 220 pr                 | esentatio     | ne    |
| 4  | ~     |                        | ut of 1,    | zzo pre                | sentatio      | 115   |
| 5  |       | have                   | "valida     | tion" in               | the title     |       |
| 6  |       | nave                   | vanua       |                        |               |       |
| 7  | 1996  | 2                      | 30          | 1                      | 77            | 2.8   |
| 8  | 1997  | 3                      | 34          | 11                     | 81            | 12.1  |
| 9  | 1998  | 3                      | 25          | 14                     | 80            | 16.2  |
| 10 | 1999  | 0                      | 44          | 7                      | 70            | 6.1   |
| 11 | 2000  | 8                      | 33          | 11                     | 107           | 13.6  |
| 12 | 2001  | 4                      | 30          | 7                      | 76            | 10.4  |
| 13 | 2002  | 2                      | 27          | 8                      | 78            | 9.5   |
| 14 | 2003  | 4                      | 26          | 17                     | 86            | 18.8  |
| 15 | 2004  |                        |             |                        |               |       |
|    |       |                        |             |                        |               |       |
|    | TOTAL | 34                     | 384         | 91                     | 836           | 10.2  |

International Symposiums on Human Identification

# Statement of Project Purpose

- Review validation practices currently in use and available standards and guidelines
- Refine general philosophy of validation and steps involved with goal to see if these steps can be standardized
- Attempt to define a minimum number of samples that could be recommended for various validation scenarios

   Is there a consensus in the community (or can there ever be)?

Conventional forensic DNA typing methods are now widely used and accepted in courts of law. However, new technologies, software, or instrumentation will continue to be developed and therefore need to be validated in laboratories prior to use in casework.

Can we learn from the past as we move into the future?

# Validation Definitions

### ISO 17025

5.4.5.1 Validation is the confirmation by examination and the provision of objective evidence that the particular requirements for a specific intended use are fulfilled

### DAB Quality Assurance Standards for Forensic DNA Testing Laboratories

2 (ff) Validation is a process by which a procedure is evaluated to determine its efficacy and reliability for forensic casework analysis and includes:

To demonstrate that a method is suitable for its intended purpose...

# DAB Quality Assurance Standards for Forensic DNA Testing Laboratories

# Manufacturer

- (1) Developmental validation is the acquisition of test data and determination of conditions and limitations of a new or novel DNA methodology for use on forensic samples.
- (2) Internal validation is an accumulation of test data within the laboratory to demonstrate that established methods and procedures perform as expected in the laboratory.
  Forensic Lab

# SWGDAM Revised Validation Guidelines

Section 1.1 Validation is the process by which the scientific community acquires the necessary information to

(a) Assess the ability of a procedure to obtain reliable results.

(b) Determine the conditions under which such results can be obtained.

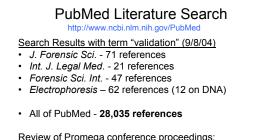
(c) Define the limitations of the procedure.

The validation process identifies aspects of a procedure that are critical and must be carefully controlled and monitored.

Reliability, Reproducibility, Robustness, Range

# Presentation Outline

- Summary of Findings (Community Consensus?)
   Literature review
  - Interviews with labs
  - Validation questionnaire
- · Steps Involved in Going "On-Line"
- Resources Under Development to Aid Future Validation Efforts

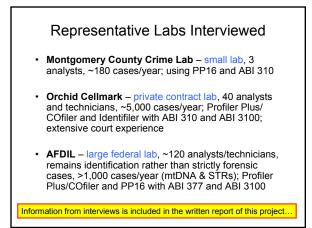


Review of Promega conference proceedings: 125 with "validation" in title of talk or poster

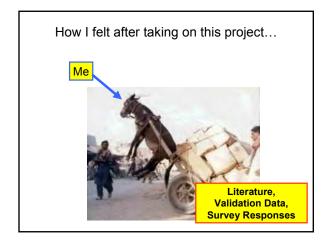
Total number of papers examined: 64

# Contacting the Community

- Validation Standardization Questionnaire handed out at NIJ DNA Grantees meeting (June 28-30, 2004)
- Emails sent to >200 scientists (July-Aug 2004)
  - Attendees from the NIJ DNA Grantees meeting
  - Participants in NIST interlaboratory studies
  - Contacts through STRBase website
- Responses from <u>52 scientists</u> were compiled
   Covering 27 states + Puerto Rico, 4 companies, 2 outside US
- Specific interviews were conducted to gain perspectives from a small lab, a large lab, a private lab, and court testimony experience



#### Validation Standardization Questionnaire (conducted June-August 2004) **Review of Survey Questions** What is validation? How do you know when you are finished validating a kit, instrument, software, or procedure? What steps are needed in internal validation and how many samples should be run at a minimum? How many total samples do you think it takes to internally "validate" a new forensic kit? How many different sets of samples are needed? Over what time period? Where do you look for guidance currently in terms of validation? What are some kits, software, instruments that you are considering for validation in the next year? How are validation, training, and proficiency testing related to one another? Do you think that the process of validation can be standardized? If a standard protocol or set of guidelines existed for validation, would you use it? If a standard set of samples existed for performing validation testing, would you use them? Used to help define specific examples .



#### Validation Standardization Questionnaire (conducted June-August 2004)

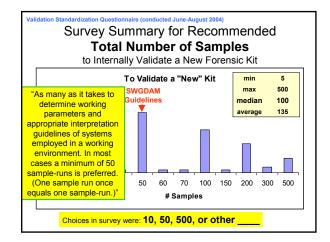
#### How do you know when you are finished with a validation study? (1)

- "When you have demonstrated that it works as expected over a range of samples that is representative of what is seen in casework"
- "When repeat performance gave the same result"
- "When you pull the toothpick out and it is dry?... Meet at least minimum expectations and DAB guidelines"
- "You are very comfortable that you know how it works and your documentation will convince a reviewer you have put the kit thru a rigorous review/test."

#### Validation Standardization Questionnaire (conducted June-August 2004)

#### How do you know when you are finished with a validation study? (2)

- "Once a reasonable body of data has been assembled and analyzed, quirks have been revealed, and the upper and lower limits of the system have been challenged using a range of samples that one could expect to encounter in the everyday operation of the system"
- "When you achieve accuracy and precision to the desired statistical level of certainty"
- "You can never know...but it is always nice to have more samples!"
- "Validation is never complete"

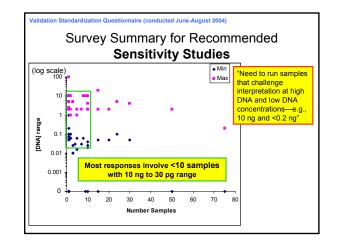


#### Validation Standardization Questionnaire (conducted June-August 2004)

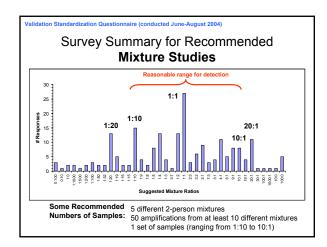
# Survey Summary for Recommended Precision Studies

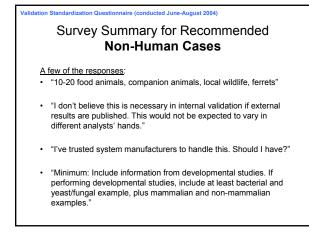
#### A few of the responses:

- "100 allelic ladder injections"
- "1 allelic ladder with 10 injections"
- "Depends upon the system being tested. For a databanking system, 50-100 runs of 50-100 specimens. Again, stats tell you when you've processed enough specimens to understand the system."
- "<u>Minimum</u>: Run one sample at least 8 times. <u>Recommended</u>: Run at least two samples plus allelic ladder at least 8 times." (24 sample-runs)



# http;//www.cstl.nist.gov/biotech/strbase/NISTpub.htm



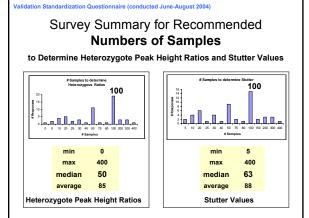


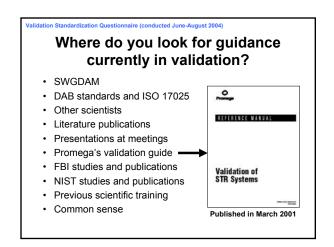
#### Validation Standardization Questionnaire (conducted June-August 2004)

# Survey Summary for Recommended Non-Probative Cases

#### A few of the responses:

- Most responses were between 5-10 cases (range 3-25)
- "More important that the number of cases is the range of forensic samples that are typed during validation."
- "Complete cases are not required to test a system. <u>Recommended</u>: Run at least 8 mock non-probative samples. <u>Note</u>: Non-probative samples are not guaranteed to provide complete profiles. They are needed only to show that false results are not generated. Lack of results or incomplete results do not affect the validity of a validation."

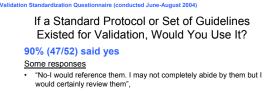






to a certain extent it can...but everyone will always have a different comfort level...and inflexible, absolute numbers for defined studies will not likely be widely accepted

# http;//www.cstl.nist.gov/biotech/strbase/NISTpub.htm

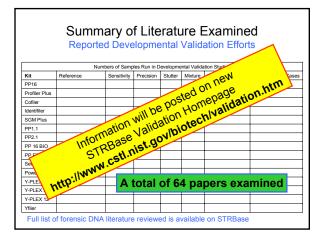


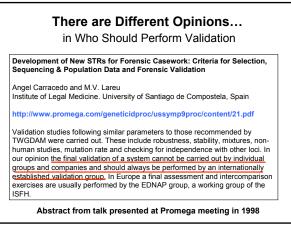
- "No-but it would be taken into consideration",
- · "Yes-we would have to or there would be problems in court",
- "Yes-as long as they remain updated, relevant and feasible guidelines and do not become dogma",
- · "Yes-if it would pass an audit for validation", and
- · "Yes-unless they were far less stringent than current practice."

Validation Standardization Questionnaire (conducted June-August 2004)
If a Standard Set of Samples Existed for Performing Validation Testing, Would You Use Them?
90% (47/52) said yes
Some responses
"Yes-would love to have something like that available; we are always eager to have benchmarks for assessment",
"Yes-these types of samples would cut down on time for validation. It would be efficient if they were ready for the particular type of validation...",
"Yes-as long as they are readily available at a reasonable price",
"No-this approach is not recommended. It is most important that systems work with the materials available in individual laboratories. Laboratories should be allowed, even encouraged, to select their own preferred materials. Choices for such selection of standard materials for assessment as the set of the set of the set of the set of the materials available is set of set of their own preferred materials. Choices for such selection of standard materials for assessment materials for assessment materials for assessment.

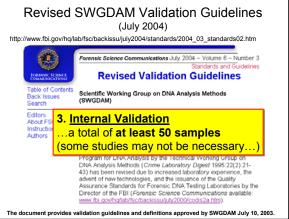
within laboratory analyses and cross-laboratory comparison already

exist from a variety of government and commercial entities."



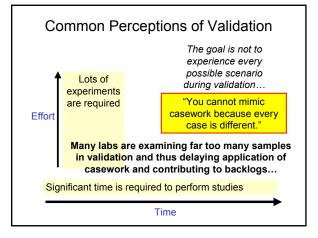


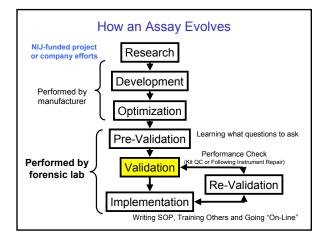
 Validation Section of the DNA Advisory Board Standards Issued July 1998 (and April 1999); published in Forensic Sci. Comm. July 2000
 STANDARD 8.1 The laboratory shall use validated methods and procedures for forensic casework analyses (DNA analyses).
 8.1.1 Developmental validation that is conducted shall be appropriately documented.
 8.1.3 Internal validation shall be performed and documented by the laboratory.

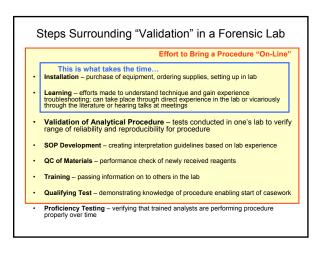


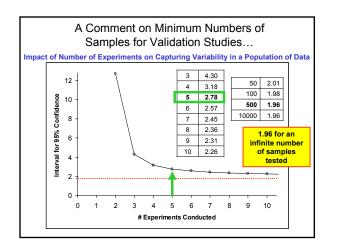
# A Thoughtful Comment from One Interviewee Before a set of validation experiments is performed... The question should be asked "Do we already know the answer to this question from the literature or a previous study performed in-house?" If the answer is "yes" and we document how we know this answer, then there is no need to perform that set of validation experiments.

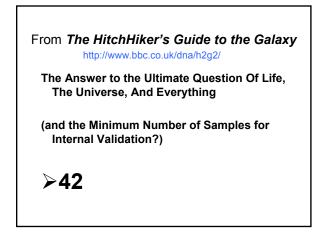
A good example of this scenario is non-human DNA studies.

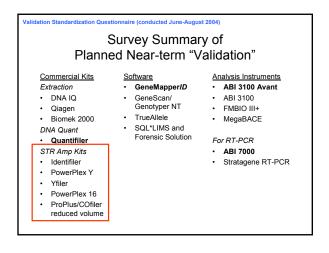














# Example: PowerPlex 16

Switch from ProfilerPlus/COfiler kits to PowerPlex 16
 Retaining same instrument platform of ABI 310

#### Recommendations:

- Concordance study (somewhat, but better to review literature to see impact across a larger number of samples and which loci would be expected to exhibit allele dropout-e.g., D5S818)
- · Stutter quantities, heterozygote peak height ratio
- · Some sensitivity studies and mixture ratios
- Do not need precision studies to evaluate instrument reproducibility

# Internal Validation

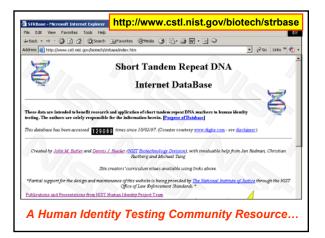
# Example: ABI 3100Avant

- Evaluation of a new ABI 3100Avant when a laboratory already has experience with ABI 310
- · STR kits used in lab will remain the same

#### Recommendations:

- · Precision studies to evaluate instrument reproducibility
- · Sensitivity studies
- Do not need new stutter, mixture ratio, peak height ratio, etc. (these relate to dynamics of the the kit used)

# Resources to Aid Future Validation Studies STRBase Validation Website http://www.cstl.nist.gov/biotech/strbase/validation.htm Examples with recommended minimum numbers Validation summary sheets NIST Calibration Data Set set of ~200 sample data files that can be used to evaluate common STR typing "artifacts" such as stutter, non-template addition, spikes, peak imbalance, tri-allelic patterns, variant alleles, single base resolution will help meet NDIS Appendix B requirements for Expert Systems evaluation Quality Control Program (Dave Duewer, NIST) Software to monitor STR electropherogram performance (resolution, sensitivity) over time



| atess http://ww   |                                |   | mepage on STRBase<br><mark>biotech/strbase/validation.</mark>  | _                                  |
|---|--------------------------------|---|--|------------------------------------|
| Validation In   | forma                          | tion to Aid   | Forensic DNA Laboratorie   | s                                  |
| Validation Summa  | ry Shee                        | ls  | ure  | used]                              |
| We are initiating an effort   | to catalog                     | Address 1 http://www.coll.root.go   | -Skitech/itcheen/-addater/VSS_PressPect Jpn  | . 00                               |
| Below is listed a compila<br>house assays, instrument<br><u>bibliography</u> is listed at th<br>Summary Sheet (nore the | ation, and s<br>e bottom of    | Mature Ratio (male female)  | Description of Samplers Total Juritation of Is 7 John and Promogal         Samplers 4 John           6 John 2 John Finders servers 11 relation (0.0.113.10.100.100.1100.01.00.00 | 40<br>40<br>132<br>132<br>54<br>24 |
| Kit, Assay, or Instrument   | Referen                        |   | 6 components of SRM 2305   | 6                                  |
| PowerPlax Y   | Scenke.                        | 377)  | 10 ladder replicates + 10 sample replicated + (0 ladders + 6 samples for 377)  | 36                                 |
| Profiler Plus   | Frank of<br>al (200)<br>Pawtow | Non-Probative Cases<br>Stutter<br>Peak Height Ratio<br>Cycling Parameters | 65 cates with 102 samples<br>412 males used<br>NA (accept for DVS306 but no studies were noted)<br>5 cates (2002/26/26/24) + 8 parch sizes x 2 samples   | 902<br>412<br>00                   |
| Cofiler   | LaFound<br>et al. (20          | Annealing Temperature   | S labo x S temperatures (54/50/60/62/64) x 1 sample  | 26                                 |
| SOM Pilus   | Cotton 4                       | Reaction volume<br>Thermal cycler test                                    | 5 volumes (50/25/15/12.56/25) x (5 amounts + 5 concentrations)<br>4 models (400/2400/9000/9700) x 1 sample + (3 models x 3 sets x 12 samples)  | 50<br>76                           |
| AmpFISTR Blue   | Wallin e                       | Male-specificity  | 2 females # 1 titration series (0.500 ng female ONA) x 5 amounts   | 10                                 |
| AmpFISTR Oreen I  | Hot et a                       | TagGold polymerase teration   | 5 amounts (1.38/2.06/2.75/3.44/4.13 U) = 4 guantities (1/0.5/0.25/0.13 ng D/4A)  | 20                                 |
| Profiler  | Holt et a                      | Primer par totation   | 5 amounts (0.5x/0.75x/1x/1.5x/2x) x 4 quantities (1.0.50.256 13 ng 0NA)  | 20                                 |
| Profilec Plus /D  | Leibelt                        | Magnesium titration:  | 5 amounts (1/1 25/1.5/1.75/2 mM Mg) x 4 quantities (1/0 5/0 25/0 13 ng DNA)  | 20                                 |
| Profiler Plus /D  |                                |   | TOTAL SAMPLES EXAMPL   |                                    |

| Validation                        | Summary Sheet for PowerPlex Y   |      |
|-----------------------------------|---|------|
| Study Completed (17 studies done) | Description of Samples Tested (performed in 7 labs and Promega)   | #Run |
| Single Source (Concordance)       | 5 samples x 8 labs  | 40   |
| Mixture Ratio (male:female)       | 6 labs x 2 M/F mixture series x 11 ratios<br>(1:0,1:1,1:10,1:100,1:300,1:1000,0.5:300, 0.25:300,0.125:300,<br>0.0625:300, 0.03:300 ng M:F ) | 132  |
| Mixture Ratio (male:male)         | 6 labs x 2 M/M mixtures series x 11 ratios  | 132  |
| Sensitivity                       | 7 labs x 2 series x 6 amounts (1/0.5/0.25/0.125/0.06/0.03)  | 84   |
| Non-Human                         | 24 animals  | 24   |
| NIST SRM                          | 6 components of SRM 2395  | 6    |
| Precision (ABI 3100 and ABI 377)  | 10 ladder replicates + 10 sample replicated + [8 ladders + 8 samples<br>for 377]  | 36   |
| Non-Probative Cases               | 65 cases with 102 samples   | 102  |
| Stutter                           | 412 males used  | 412  |
| Peak Height Ratio                 | N/A (except for DYS385 but no studies were noted)   |      |
| Cycling Parameters                | 5 cycles (28/27/26/25/24) x 8 punch sizes x 2 samples   | 80   |
| Annealing Temperature             | 5 labs x 5 temperatures (54/58/60/62/64) x 1 sample   | 25   |
| Reaction volume                   | 5 volumes (50/25/15/12.5/6.25) x [5 amounts + 5 concentrations]   | 50   |
| Thermal cycler test               | 4 models (480/2400/9600/9700) x 1 sample<br>+ [3 models x 3 sets x 12 samples]  | 76   |
| Male-specificity                  | 2 females x 1 titration series (0-500 ng female DNA) x 5 amounts each   | 10   |
| TaqGold polymerase titration      | 5 amounts (1.38/2.06/2.75/3.44/4.13 U) x 4 quantities (1/0.5/0.25/0.13 ng DNA)  | 20   |
| Primer pair titration             | 5 amounts (0.5x/0.75x/1x/1.5x/2x) x 4 quantities (1/0.5/0.25/0.13 ng DNA)   | 20   |
| Magnesium titration               | 5 amounts (1/1.25/1.5/1.75/2 mM Mg) x 4 quantities (1/0.5/0.25/0.13 ng DNA)   | 20   |
| Krenke et al. (2004) Forensi      | C Sci. Int., in press TOTAL SAMPLES EXAMINED  | 1269 |

# Laboratory Internal Validation Summaries

| laboratory's validation st<br>standard format romma<br>downloadable Excel file  | niders with a particular forenne DNA<br>rinng the studies conducted, a descrip<br>[ <u>click here]</u> .  | in buffer@mit.cov> if you would like to add a run<br>test, mitrument, or software program. Please submit<br>tion of samples run, and the number of samples exar   | t mforma<br>naned usi                              | don in a<br>ing this  |
|---|---|---|--|---|
| Kit, Assay or Instrum   |   | Individual Laboratories (not published in<br>Submitter<br>Christine Tomiey  | the life   | crature)  |
| Soliciting Int  | formation on Stud   | ies Performed by the Cor  | nmu  | unity   |
| Stury consuctors  |   | B RAD WID FOWEIFIEX ID VANDASION  | 1.590  | 0.10245108  |
|   |   |   |  |   |
| Single Source (Concordance)   | a samples provides concordances   | <ul> <li>200 samples (pert of population concordance study)</li> </ul>  | 208  | 100   |
| Mixtures  |   | 45  | 45   | 10  |
| Mixtures<br>Mixture Ratio   | 1 sample x 11 ratios (1.0, 191, 91, 41, 3   | 45<br>11,11,12,14,13,113,01) = 2 ejections (510 beconds)  | 45<br>22   | 10  |
| Mixtures<br>Mixture Ratio<br>Sensitivity  | 1 sample x 11 ratios (1.0, 191, 91, 41, 3   | 45<br>(1, 1.1, 1.2, 1.4, 1.9, 1.19, 0.1) x 2 synctrons (5/10 seconds)<br>0.06/0.03 ng) + (5 samples × 3 poets (white-velosite= drapout))  | 45<br>22<br>55                                     | 10<br>33<br>33  |
| Mixtures<br>Mixture Ratio<br>Sensitivity<br>Non-Human   | 1 sample x 11 ratios (1.0, 191, 91, 41, 3   | 45<br>11, 11, 12, 114, 119, 119, 011) = 2 impetions (510 seconds)<br>0.060(01ng) + (5 semples × 3 poets (white-visiteitow dropout))<br>11 extense   | 45<br>22<br>55<br>11                               | 10<br>33<br>33<br>0   |
| Mixtures<br>Mixture Ratio<br>Sensitivity<br>Non-Human<br>NIST SRM 2391b   | 1 sample x 11 robos (10, 121, 21, 41,<br>5 samples x 8 anouzts (501.6.50.250.125  | 45<br>11, 11, 11, 11, 11, 11, 11, 0, 11) = 2 Parctions (5/10 accords)<br>0.050, 021 rg) = (5 samples × 3 ports (white-vertextex-stropout))<br>11 ensures<br>12 components   | 46<br>22<br>55<br>11<br>12                         | 10<br>33<br>33<br>0<br>12                                       |
| Mixtures<br>Mixture Ratio<br>Sensitivity<br>Non-Human   | 1 sample x 11 rolos (10, 181, 81, 41, 3<br>5 samples x 8 anounts (501.0:50.256.125<br>(5 samples x 10 roject)   | 45<br>11, 11, 12, 12, 14, 13, 113, 0, 13 ± 2 #jections (5/10 seconds)<br>006.00 rg = (5 seques x 3 points (atheto-wheto-wheto-wheto-x)<br>11 ensues<br>12 components<br>no exity + 10 mjections of alekic leaders   | 45<br>22<br>55<br>11                               | 10<br>33<br>33<br>0<br>12<br>60                                 |
| Mutures<br>Muture Ratio<br>Senstivity<br>Non-Human<br>Non-Human<br>NST SRM 2391b<br>Precision (ABI 310)   | 1 semple x 11 ratios (1-0, 191, 91, 41, 3<br>5 semples x 0 enours: (501.0.50 250 125<br>(5 semples x 10 racid<br>5 ceses x 4 semples  | 45<br>11, 11, 11, 11, 11, 11, 11, 0, 11) = 2 Parctions (5/10 accords)<br>0.050, 021 rg) = (5 samples × 3 ports (white-vertextex-stropout))<br>11 ensures<br>12 components   | 45<br>22<br>55<br>11<br>12<br>60                   | 10<br>33<br>33<br>0<br>12                                       |
| Mixtures<br>Mixture Ratio<br>Sensibility<br>WST SRM 2391b<br>Precision (ABI 310)<br>Non-Probative Cases<br>Stutter  | 1 sample x 11 mbos (10, 191, 81, 81, 41, 3<br>5 samples x 8 anounts (5016.50.256.15<br>(5 samples x 10 micro)<br>5 cases x 4 samples<br>200 cargins (2  | 46<br>10. (S. 11, 11, 21, 11, 11, 11, 0, 1) = 2 Percetano (S.10 beconda)<br>0.050 03 ngi + (5 samples x 3 ports: (shifes-relative dropout))<br>11 annes<br>12 component<br>12 compared<br>12 compared<br>each (widence (BF/SE7 ActionUngect))   | 45<br>22<br>55<br>11<br>12<br>60                   | 10<br>33<br>33<br>0<br>12<br>60                                 |
| Matures<br>Mixture Ratio<br>Sensibility<br>Von-Human<br>Non-Procision (ABI 310)<br>Non-Probative Cases<br>Stuttie<br>Peak Height Ratio<br>Cycling Parameters  | 1 semple x 11 rebos (10, 191, 91, 91, 41,<br>5 semples x 8 enouve; (5016,50,250,125<br>(5 semples x 10 inject)<br>5 cates x 4 sempler<br>200 semples (<br>200 semples (   | 46<br>11, 11, 12, 13, 13, 13, 13, 03 x 2 spections (3/10 seconds)<br>000,03 (20 yr) +5 sempler x 3 ports (white-white-white-white-<br>11 annum<br>12 components<br>ons each - 10 spectrum of adole ladders<br>each (white-DFSGT/Actimulayet)<br>this under to no poculation sempler)  | 45<br>22<br>55<br>11<br>12<br>00<br>20<br>· · · 55 | 10<br>33<br>33<br>0<br>12<br>60<br>20                           |
| Mutures<br>Muture Ratio<br>Sensthing<br>Non-Human<br>NST SSM 2991b<br>Precision (ABI 310)<br>Sen-Probative Cases<br>Stuttie<br>Peak Height Ratio<br>Cycling Parameters<br>Avaialing Temperature                   | 1 senge x 11 mbo (10, 151, 51, 41, 5<br>5 senges x 0 movint (15/n 5.0.250.15<br>(5 senges x 0 movint (15/n 5.0.250.15<br>5 cess t x 4 senges<br>200 senges (1<br>200 senges (1<br>14 senges x 2 attement cyce                           | 46<br>1, 1, 1, 1, 2, 1, 4, 1, 8, 1, 13, 0, 13, 2 Peedtans (3/10 Inconst);<br>0.06/0.07(a); 5 samples x 3 ports (white-whetew dropox);<br>11 annuar;<br>12 composed is<br>23 composed is<br>24 composed is<br>24 composed is<br>25 composed is<br>26 composed is | 45<br>22<br>55<br>11<br>20<br>20<br>· · · 55<br>60 | 10<br>33<br>33<br>0<br>12<br>60<br>20                           |
| Mingres<br>Minture Ratio<br>Sensibility<br>Von-Human<br>UST SSM 2991b<br>Precision (ABI 310)<br>Von-Probative Cases<br>Stutte<br>Peak Height Ratio<br>Sycoling Parameters<br>Annealing Temperature<br>Proficiency | 1 serger x 11 rebox (15), 181, 81, 41,<br>5 sergers x 8 encurs (5016.50.250.125<br>5 ceses x 6 encurs (5016.50.250.125<br>5 ceses x 6 sergers<br>200 sergers (<br>14 sergers x 6 central sergers)<br>3 sergers 4 6 central sergers      | 46<br>1, 11, 12, 12, 13, 13, 13, 13, 23 pections (SHD seconds)<br>0.060 CT 021 + 55 seques x 3 pects (older-whetew dropoug<br>13 orange<br>12 comparets<br>no sec/h + 10 seques in allels leaders<br>4600 (windows IP SECF Actionagest)<br>dis used from operations insele(1)<br>dis used from operations   | 45 22 55 11 12 60 20 55 60 36                      | 10<br>33<br>33<br>0<br>12<br>60<br>20<br>-<br>-<br>-<br>0<br>12 |
| Mutures<br>Muture Ratio<br>Sensthing<br>Non-Human<br>NST SSM 2991b<br>Precision (ABI 310)<br>Sen-Probative Cases<br>Stuttie<br>Peak Height Ratio<br>Cycling Parameters<br>Avaialing Temperature                   | 1 sense x 11 ndos (10, 181, 81, 41,<br>5 senses x 8 encurs (501.650.250.15<br>6 senses x 8 encurs (501.650.250.15<br>6 case x 4 encurs<br>200 encurse)<br>200 encurse)<br>14 encurs x 2 dimension<br>3 senses x 4 concentrations<br>8 e | 4 4 5 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7   | 45<br>22<br>55<br>11<br>20<br>20<br>· · · 55<br>60 | 10<br>33<br>33<br>0<br>12<br>60<br>20                           |

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# **Further Information**

- Final version of this talk will be available:
   http://www.cstl.nist.gov/biotech/strbase/NISTpub.htm
- See also new STRBase Validation Homepage

   http://www.cstl.nist.gov/biotech/strbase/validation.htm
- My email address: john.butler@nist.gov

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