<u>National Quality Assurance Institute</u> of <u>Standards and Technology</u>

NIST Update

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SWGDAM January 11, 2007

Standard 1. Scope

Scope of Our Work

 The NIST Human Identity Project Team is trying to lead the way in forensic DNA... through research that helps bring traceability and technology to the scales of justice.

Standard 2. Definitions

NIST and NIJ Disclaimer

<u>Funding</u>: Interagency Agreement 2003-IJ-R-029 between the National Institute of Justice and NIST Office of Law Enforcement Standards

Points of view are mine and do not necessarily represent the official position or policies of the US Department of Justice or the National Institute of Standards and Technology.

Certain commercial equipment, instruments and materials are identified in order to specify experimental procedures as completely as possible. In no case does such identification imply a recommendation or endorsement by the National Institute of Standards and Technology nor does it imply that any of the materials, instruments or equipment identified are necessarily the best available for the purpose.

Standard 3. Quality Assurance RESEARCH Program

Current Areas of NIST Effort with Forensic DNA

Standards

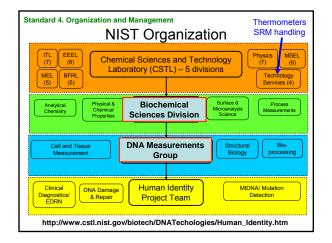
- Standard Reference Materials
- Standard Information Resources (STRBase website)
- Interlaboratory Studies

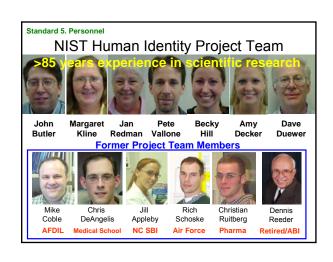
Technology

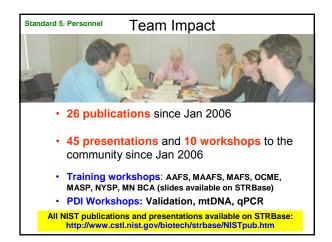
- Research programs in SNPs, miniSTRs, Y-STRs, mtDNA, qPCR
- Assay and software development, expert system review

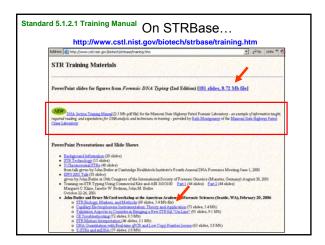
Training Materials

- Review articles and workshops on STRs, CE, validation
- PowerPoint and pdf files available for download
 - http://www.cstl.nist.gov/biotech/strbase/NIJprojects.htm

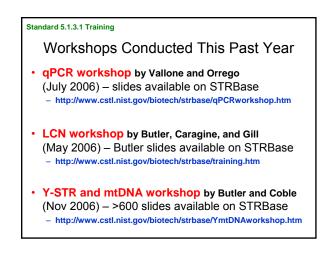


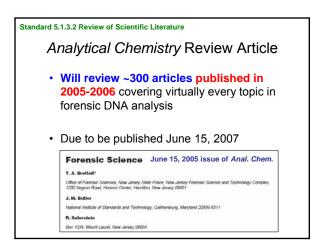


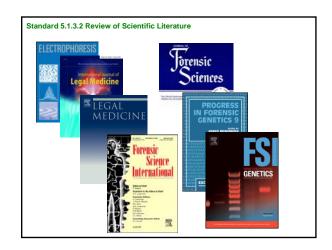


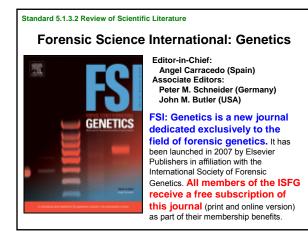


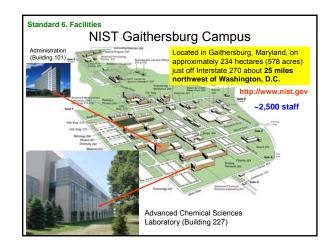


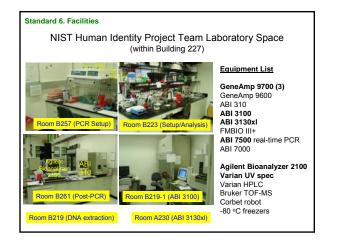


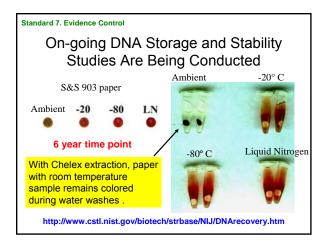












Standard 8. Validation Validation Information • President's DNA Initiative: Validation Workshop (Aug 2005) with Robyn Ragsdale – slides on STRBase; NFSTC working on DVD • ABI Roadshow/HID University: Validation Workshop (May 2006) – slides available on STRBase • We would love to have more internal validation information for STRBase Validation Section (e.g., Y-STRs) Profiles in DNA (Promega Corporation), vol. 9(2), pp. 3-6 Profiles in DNA (Promega Corporation), vol. 9(2), pp. 3-6 VALIDATION http://www.promega.com/profiles/902/ProfilesInDNA_902_03.pdf Debunking Some Urban Legends Surrounding Validation Within the Forensic DNA Community

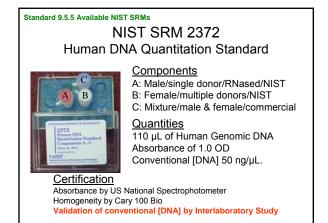
Validation Within the Forensic DNA Community By John Butler National Institute of Standards and Technology, Gaithersburg, Maryland, USA

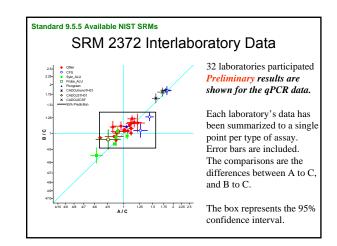
Standard 9.5.5 Available NIST SRMs

Standard Reference Materials

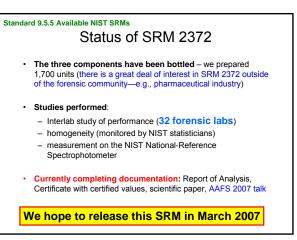
- Relevant Forensic DNA SRMs
 - SRM 2391b (DNA profiling STRs, D1S80, DQA1/PM)
 - SRM 2392-I (mtDNA)
 - SRM 2395 (Y-chromosome)
 - SRM 2372 (Human DNA quantitation); in development
- Provides national/international traceability and compatibility (aids in ISO 17025 compliance)

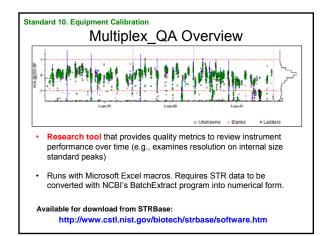
http://www.nist.gov/srm

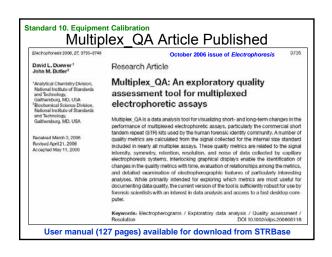




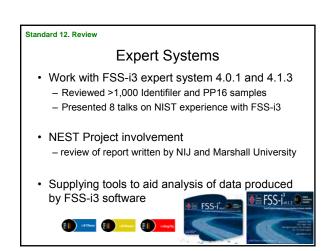












Standard 13. Proficiency Testing Interlaboratory Studies Conduct interlab studies to assess proficiency of the community with mixture interpretation and DNA quantitation Participate in EDNAP/ENFSI studies miniSTRs vs SNPs (Peter Gill) mtDNA SNP typing (Walther Parson) MiniFiler degraded DNA (Peter Gill)

 Passed QA test with Y-STRs to supply data to YHRD database



miniSTR Nomenclature Changes

- Nomenclature changes to miniSTR loci D1S1677, D4S2364, D10S1248, D14S1434, and D22S1045 compared to Coble and Butler (2005)
- JFS March 2007 Letter to the Editor regarding a D10S1248 nomenclature error
- These loci are being to be used in Europe and Asia as well as paternity testing here in the U.S.

Variant Allele Sequencing Service (Free)							
				Locus	Variant Allele	Sample Source	Comments
				трох	10,3	Maryland State Police	Deletion of a "G" that is 157 bp from the repeat region unde PowerPlex 1 I and Identifiler primers does not affect prime bunding or allele sizing. However, PowerPlex 2 I and PowerPlex 16 products are 1 bp smaller because they are further away from the repeat and encompass the deletion.
FGA	46.2	Denver Crime Laboratory	Checked with Identifiler allelic ladder				
D18551	null allele 18	FSS and Kuwait government lab	Base change was a C-to-T transition 172 bp downstream o the repeat region which impacts the ABI D18551 reverse primer but not the PowerFlex 16 D18551 reverse primer that is internal to this mutation				
D18S51	40	Nebraska State Crime Lab	DNA sequence analysis showed 40 GAAA repeats				
D18551	*5.3*	DNA Solutions	DNA requence analysis revealed a 9 bp deletion beyond the end of the 3th repeat unit to produce a *5.3* allele				
D Y \$392	*10.2*	AFDIL	DNA sequence analysis revealed a C-to-G transversion 180 by optream of the STR repeat region, the mutation causes an apparent mobility shift of approximately 0.75 by such that he allele fails outside of the +/-0.5 by senotyping bin				
D¥\$635	21.3	NIST U.S. population samples	DNA requesce analysis revealed a deletion of a "T" in the repeat region, full repeat was [TCTAL/TGTA), [TCTAL/TGTA], [TCTAL/TGT				
Penta D	18	DNA Solutions	DNA sequence analysis confirmed 18 repeats				
Penta D	*8.2*	University	DNA sequence analysis revealed a 13 bp deletion prior to a [AAAGA] ₁₁ repeat				
Penta D	6	Peter de Knajff's lab at Leiden University	DNA sequence analysis confirmed 6 repeats				

