Human Identity Testing Using DNA

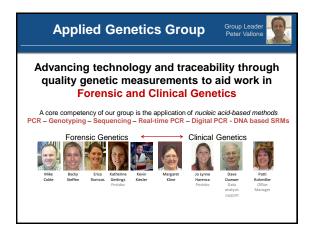
DOC Headquarters - Commerce Research Library 12 March 2015

Peter M. Vallone, Ph.D. Leader, Applied Genetics Group Biomolecular Measurement Division

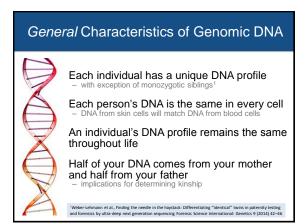


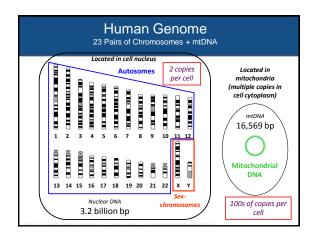
Topics

- What is human identity testing?
 Aka 'Forensic DNA Testing'
- Common questions
- · NIST's role
- · The future of human identity testing







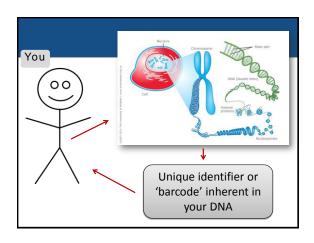




Human Identity Testing

- Probe subsets of genetic variation in order to differentiate between individuals
 – ≈13 to 24 regions in the human genome
- DNA typing must be done efficiently and reproducibly (information must hold up in court)
 Over 13 million profiles in the national FBI database¹
- Typically, we are not looking at genes little/no information about ancestry, predisposition to disease, or phenotypic information (facial features, eye color, height, hair color) is obtained → evolving

¹http://www.fbi.gov/about-us/lab/biometric-analysis/codis/codis-and-ndis-fact-sheet









Applications of Human Identity Testing

- Forensic cases: matching suspect with evidence
- Paternity testing: identifying father
- Missing persons investigations
- · Military DNA "dog tag"
- National DNA database (FBI)
- · Mass disasters: accounting for remains
- · Historical investigations
- Genetic genealogy

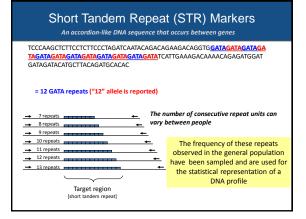
What Type of Genetic Variation?

•Sequence Variation

single nucleotide polymorphisms (SNPs) insertions/deletions <u>GCTAGTCGATGCTC[G/A]GCGTATGCTGTAGC</u>

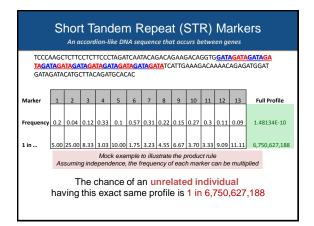
•Length Variation

short tandem repeats (STRs) CTAGTCGT[GATA][GATA][GATA]GCGATCGT

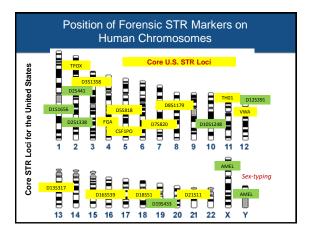


Short Tandem Repeat (STR) Markers An accordion-like DNA sequence that occurs between genes					
TCCCAAGCTCTTCCTCTTCCCTAGATCAATACAGAC TAGATAGATAGATAGATAGATAGATAGATAGATAGATAG					
Sampling 100 individuals	Times obser	ved Frequency	1 in		
→ 7 repeats ←	5	5%	20		
→ 8 repeats ←	12	12%	8.3		
→ 9 repeats ←	22	22%	4.5		
→ 10 repeats ←	32	32%	3.1		
→ 11 repeats ←	20	20%	5		
→ 12 repeats +	- 7	7%	14.3		
→ 13 repeats	← 2	2%	50		
	= 100	= 100%			
Target region [short tandem repeat]					

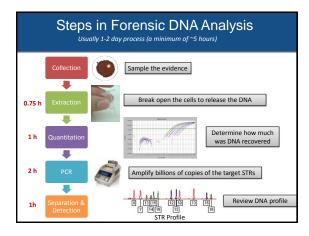








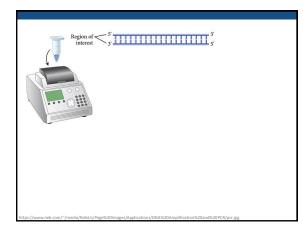


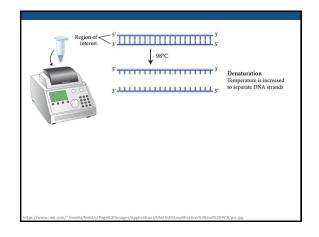




PCR

- Polymerase Chain Reaction
- A means to create billions of exact copies of a specific region of the genome





Region of 5 1 1 1 1 1 1 1 1 1 1 1 1 1	Denaturation Temperature is increased to separate DNA strands Annealing Temperature is decreased to allow primers to base pair to complementary DNA template

Region of $< \frac{5'}{3'}$ 98°C

5' Primer 3'

3.77747474

3'

Template DNA strands

Nascent < DNA strands

1

5

48 to 72°C

3' Primer 3' Primer

3' 68 to 72°C

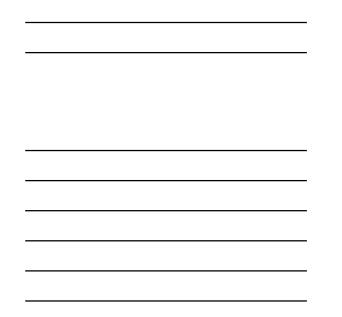
Denaturation Temperature is increased to separate DNA strands

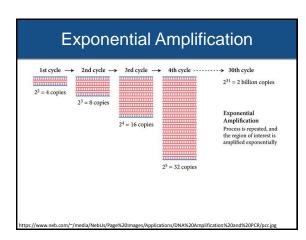
Annealing Temperature is decreased to allow primers to base pair to complementary DNA template

3 Extension Polymerase extends primer to form nascent DNA strand

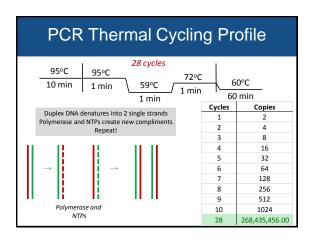
5'

- 3 575777773°L

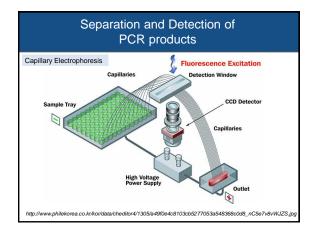




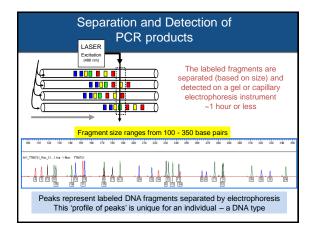




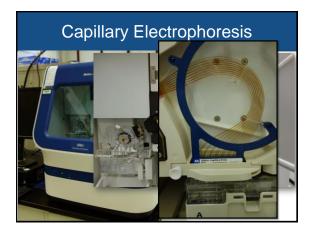


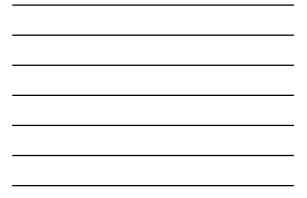


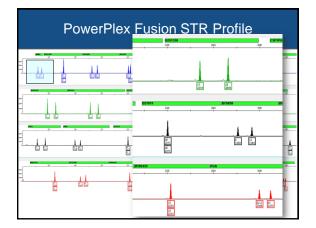








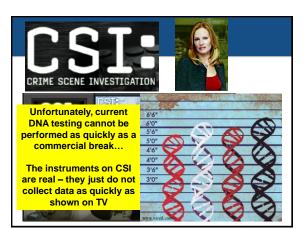


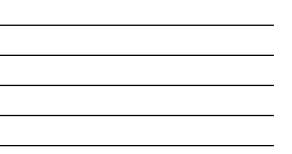




Amel D3S1358 D1S1656	{X,Y} {15,15} {11,13}	lex Fusion STR Kit
D2S441	{11,11.3}	Multiplying the frequency of each
D10S1248	{8,12}	., ,
D13S317	{11,12}	genotype at each
Penta E	{8,14}	locus gives us the
D16S539 D18S51	{9,12}	Random Match Probability
D18551 D2S1338	{15,18} {17.23}	-
CSF1PO	{8.11}	(RMP) of 7.81x10 ⁻³⁹
Penta D	{9,11}	for unrelated individuals
TH01	{6.9}	
VWA	{13,15}	
D21S11	{28,28}	The chance of an unrelated individual
D7S820	{8,11}	having this exact same profile is
D5S818	{9,10}	3
TPOX	{9,12}	1 in
DYS391	{10}	128,040,973,111,396,000,000,000,000,000
D8S1179	{15,15}	,000,000,000
D12S391 D19S433	{17,19}	,000,000,000
D195433 FGA	{13,13} {22.2,25}	
PGA D22S1045	{22.2,25} {16,17}	This test contains the FBI core STR markers



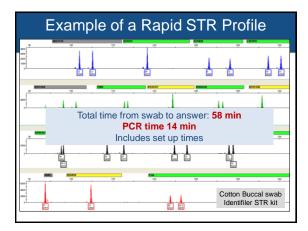




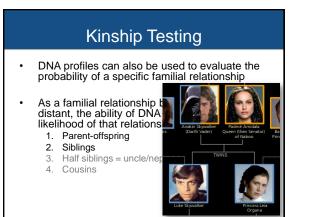
NIST and Rapid PCR

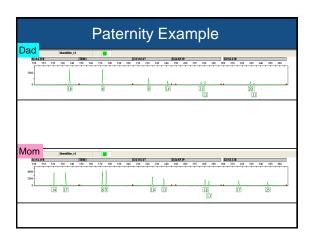


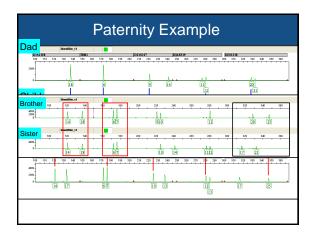
- Up until 2008 PCR amplification times required approximately 3 hours
- Utilizing new (faster) DNA polymerases and rapid PCR thermal cyclers we demonstrated results in 36 minutes
- Enabling faster commercial STR typing kits (40 min) and fully integrated 'Rapid DNA' typing instruments (swab to profile in < 2 hours)



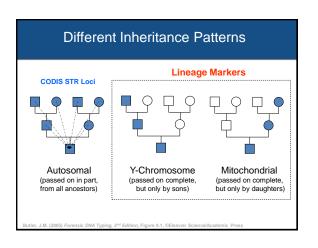


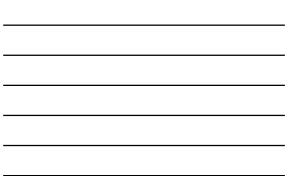












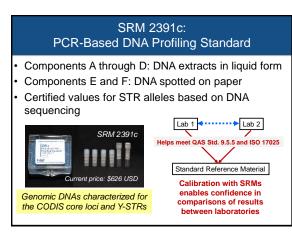
NIST's Role in Human Identity Testing

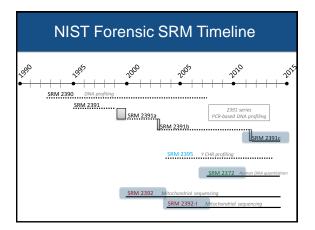
- Reference materials
 To ensure confidence in results
- Research
 New Technologies
- Training and Education

 Workshops, papers, talks

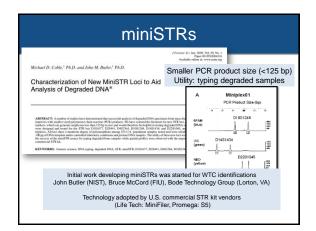
SRM 2391c: PCR-Based DNA Profiling Standard

9.5.5 The laboratory shall check its DNA procedures annually or whenever substantial changes are made to a procedure against an appropriate and available **NIST standard reference material or standard traceable to a NIST standard.** http://www.fbi.gov/about-us/lab/biometric-analysis/codis/gas_testlabs

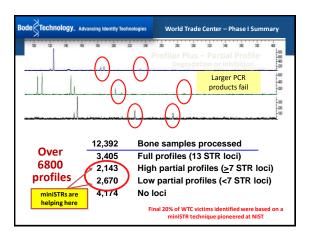


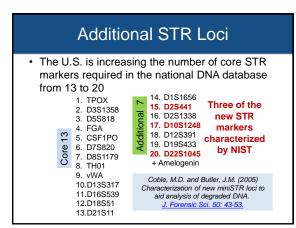


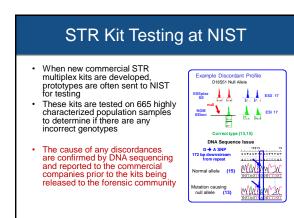










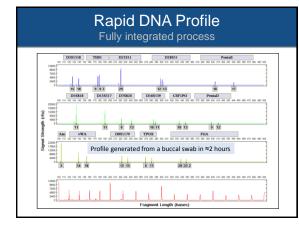


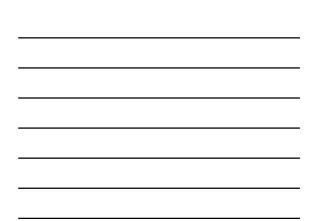
The Future of human identity testing

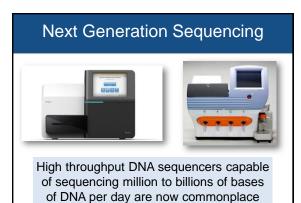
Rapid DNA

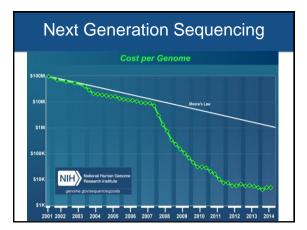
- Fully integrated instruments capable of generating a DNA profile
- · 'Swab in profile out' in less than 2 hours
- No special training required
- · Potential applications
 - Booking station 🥻
 - In the field
 - Border crossing











Non-forensic applications

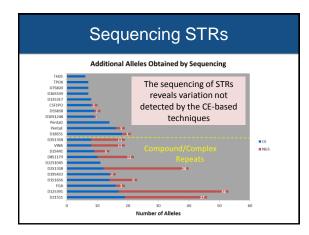
- · Clinical research
- Inherited disease
- Reproductive healthCancer gene fusion
- Cancer gene lusion
- Rare variants
- Pre-implantation (genetic screening)
- Transplant medicine (HLA)
- Microbiomics/Metagenomics
- Gene expression | RNA seq
- Public health
- Ancient DNANIPT (non-invasive prenatal testing)



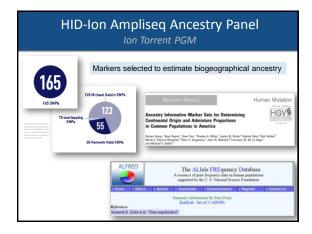
Use of NGS for forensic applications

- Forensically relevant markers (SNPs)

 newer human identity applications
 - biogeographical ancestry, externally visible traits, complex kinship
- Going in depth into STR loci and beyond – STRs are useful for legacy (databases)
 - SNPs within STRs identify 'sub-alleles'









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