













Sources of Biological Evidence

- Blood
- Semen
- Saliva
- Urine
- Hair
- Teeth
- Bone
- Tissue



Only a very small amount of blood is needed to

best results with >100 cells, but DNA profiles can be ONA recovered from fewer cells















Short Tandem Repeat (STR) Markers

An accordion-like DNA sequence that occurs between genes

= 12 GATA repeats ("12" is all that is reported)



The number of consecutive repeat units can vary between people

> The FBI has selected **13 core STR loci** that must be run in all DNA tests in order to provide a common currency with DNA profiles







Forensic DNA Testing

Probe subsets of genetic variation in order to differentiate between individuals (14 to 16 regions)

DNA typing must be done efficiently and reproducibly (information must hold up in court) Over 8 million profiles in the national FBI database

Typically, we are *not* looking at genes – little/no information about race, predisposition to disease, or phenotypic information (eye color, height, hair color) is obtained

NSF Workshop on Fundamental Research Challenges for Trustworthy Biometrics 2010



Applications

- Forensic cases: matching suspect with evidence
- Paternity testing: identifying father
- Missing persons investigations
- Military DNA "dog tag"
- Convicted offender DNA databases
- Mass fatalities
- Historical investigations
- Genetic genealogy
- DNA as a biometric tool



DNA Testing Requires a Reference Sample

A DNA profile by itself is fairly useless because it has no context...

DNA analysis for identity only works by comparison – you need a reference sample



Crime Scene Evidence compared to Suspect(s) (Forensic Case) Child compared to Alleged Father (Paternity Case) Victim's Remains compared to Biological Relative (Mass Disaster ID) Soldier's Remains compared to Direct Reference Sample (Armed Forces ID)















Large Random Match Probabilities?



- Let's assume each marker could be one of 10 states (or alleles)
- All loci are independent so we can multiply the
- 2 x 5 x 8 x 2 x 6 x 7 x 7 x 10 x 1 x 3
- 0.1 x 0.1 x
 0.1 x 0.1 x 0.1



Product Rule For heterozygous loci P = 2pqP = probability; p and q are frequencies of allelein a given population Example: For the locus D3S1358 an individual is 15,18 with frequencies of 0.2825 and 0.1450 respectively P = 2(0.2825)(0.1450) = 0.0819 or 1 in 12 For 5 loci the Profile Probability = $(P_1)(P_2)...(P_n)$ = (0.0819)(0.0875)(0.0687)(0.0245)(0.0984)0.000001187 or 1 in 842,539



Kinship Testing

- DNA profiles can also be used to evaluate the probability of a specific familial relationship
- As a familial relationship becomes more distant, the ability of DNA to confirm the likelihood of that relationship decreases
 - 1. Parent-offspring
 - 2. Siblings
 - 3. Half siblings = uncle/nephew = grandchild
 - 4. Cousins



Dad

Autosomal Paternity Example Identifiler_vl D351358 TH01 D135317 D165539 D251338





Complex Kinship Testing



The statistical power for complex kinship testing significantly decreases compared to one-to-one matching **Requirements:**

- Genotypes of individuals being tested
- Allele frequencies for the loci involved in the testing
- A Hypothesis!
- Basic statistical equations are known
- Difficult to identify distant relationships
- Discriminatory power comes from multiple family members and the use of informative markers



DNA as a Biometric



Current Biometrics

Some commonly measured features

- Physical
 - Fingerprints (Palm/hand geometry)
 - Iris, retinal
 - Face
 - Odor/scent
 - DNA?
- Behavioral
 - Gait
 - Voice
 - Vein (IR thermogram)
 - Hand geometry
 - Handwriting











Characteristics of a Biometric

- Universality
 - each person should have the characteristic
- Uniqueness
 - is how well the biometric separates individuals from another
- Permanence
 - measures how well a biometric resists aging and variance over time
- Collectability
 - ease of acquisition for measurement

Jain, A. K.; Ross, Arun; Prabhakar, Salil (January 2004), "An introduction to biometric recognition", IEEE Transactions on Circuits and Systems for Video Technology 14th (1): 4–20







DNA Typing as a Biometric

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Advantages

- High level of accuracy (Gold Standard)
- Solid foundation of Forensic DNA Testing (pop stats, molecular biology, court acceptance, protocols, training, education)
- Kinship determination (unique to DNA)
- Potential use for:
 - Phenotype (traits; eye/hair color)
 - Biogeographical Ancestry

- Expensive
- Time consuming
- Sample collection (invasive, stability issues)

Challenges

- Technical expertise required for analysis
- Low level template, mixtures, PCR inhibition
- Policy/Privacy/Ethical issues



Interest in Rapid DNA Typing

- DoD (field testing, rapid intelligence, mass fatalities)
- DHS (kinship determination, border security, immigration)
- DoJ (law enforcement, initial information)
- Industry (security, authentication)
- Each customer will have specific requirements
 - sample input
 information output
 degrees of 'accuracy'

 The time required for generating a STR profile will have to be significantly reduced





Goals for Rapid DNA Typing Systems

- Develop an integrated system capable of performing DNA testing in less than 1 hour
- Little user interaction (or experience)
- Rugged

Swab in...answer out

- Robust
- Simple data interpretation
- 4-16 samples per run
- Disposable chips (with reagents on board)



Rapid DNA Typing Systems Under Development

- Systems are currently under development and are not yet commercially available
- Network Biosystems (Woburn, MA) <u>http://www.netbio.com</u>
- ZyGEM and Lockheed Martin (Charlottesville,VA) http://www.zygem.com
- IntegenX (Pleasanton, CA) <u>http://www.integenx.com</u>
- Forensic Science Service (UK) <u>http://www.forensic.gov.uk/</u>

<u>Use of DNA as a Biometric Tool</u> American Academy of Forensic Science, Feb 22, 2010, Seattle, WA *http://www.cstl.nist.gov/biotech/strbase/NISTpub.htm* <u>Biometrics Consortium Conference</u> September, 2010 Tampa, FL http://www.biometrics.org/bc2010/program.pdf



DNA Analysis Approach (integrated) Challenges Steps Involved Collection Target Times Buccal swab, blood, other? Rapid extraction (solid or liquid phase?) Extraction ~15 min Reagents stable and compatible with device Can be skipped for a reference sample BUT Quantitation Does the extraction method allow for a target amount of DNA to be released? ~1 ng Rapid PCR amplification of a commercial STR kit Amplification ~20-30 min Locus balance, stutter, adenylation, heterozygote balance, reproducibility Separation/ ~20 min Resolution, reproducibility, sensitivity, post-run signal processing Detection Data Expert system software? How much user intervention is needed? Interpretation Can rapid typing be done reproducibly and accurately? Total Time ~1 hour Cost efficient? (instrumentation, reagents, consumables) General challenge of going from macro scale to micro scale!



NIST Efforts with DNA Biometrics

- Developing rapid PCR protocols
- Evaluating kinship analysis software
- Support for external rapid DNA efforts
- Designing standards materials for device testing
- Testing prototype rapid DNA devices



Thank you for your attention!

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http://biometrics.org/bc2009/presentations/wednesday/McCurdy%20BrA%20Wed%201040-1055.pdf



Recent Work with Rapid PCR

At NIST we are working on new PCR methods to reduce the time for PCR down to 20 minutes

Polymerase Chain Reaction (PCR)

is a means to create billions of exact copies of the human genome – necessary/essential for DNA typing

$$\begin{array}{r} \sim 3.5 \text{ h} \rightarrow 20 \text{ min}? \\ \hline \end{array}$$
Multiplex PCR Amplification



20 Minute PCR Amplification on Cepheid Cycler





Rapid PCR Article		
G Model FSIGEN-394; No of I	Pages 4 ARTICLE IN PRESS	
	Forensic Science International: Genetics xxx (2008) xxx-xxx	
ELSEVIER	Contents lists available at ScienceDirect Forensic Science International: Genetics journal homepage: www.elsevier.com/locate/fsig	
Short communication Demonstration of rapid multiplex PCR amplification involving 16 genetic loci☆ Peter M. Vallone*, Carolyn R. Hill, John M. Butler National Institute of Standards and Technology, Biochemical Science Division, 100 Bureau Drive, Mail Stop 8311, Gaithersburg, MD 20899-8311, United States		
Vallone, P.M., Hill, C.R., Butler, J.M. (2008) Demonstration of rapid multiplex PCR amplification involving 16 genetic loci. <i>FSI Genetics</i> 3(1): 42-45.		
Rapid PCR Amplification of STR Typing Kits 20th Annual International Symposium on Human Identification (Promega Meeting) October 14, 2009, Las Vegas, NV		
Rapid Amplification of Commercial STR Typing Kits, International Society of Forensic Genetics (ISFG), September 16, 2009, Buenos Aires, Argentina		
Use of DNA as a Biometric Tool American Academy of Forensic Science, Feb 22, 2010, Seattle, WA		
http://www.cstl.nist.gov/biotech/strbase/NISTpub.htm		



Future Directions

- Functional prototypes should be available for testing in the next 12-18 months
- 3-4 year horizon until concordance testing and validation
- Further education on the strengths and limitations of DNA



Possible Solutions: Supplemental genetic markers (Y-chromosome, X-chromosome, mitochondrial, additional autosomal STRs, SNPs)

Challenging applications of genetic information

Standard STR Typing (DNA Profile) Single source contributor High amounts of DNA	Complex Kinship Testing (Searching for brothers or other relatives) Distant relatives (half siblings, uncle/nephew, cousins) Family reference samples are needed
High quality data obtained Statistics are high (versus a reference/database) Direct Matching or Simple Parentage Testing	Statistics are lower for distant relatives 15 STR loci may not be sufficient -false positives/negatives Ancestry-matched allele frequencies required
'Touch' DNA Typing Multiple contributors possible Lower amounts of DNA, PCR inhibition Degraded DNA	CAUTION The <u>combination</u> of poor sample quality and complex kinship testing decreases the power of DNA testing
Lower quality data obtained (incomplete profile) Results are not always reproducible Matching and kinship statistics decrease Initial information, intelligence, missing persons	











Mixture Interpretation – A Major Challenge...

