



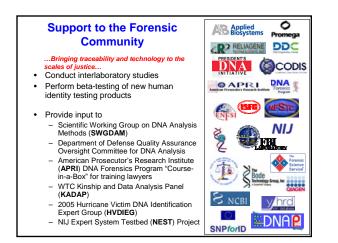
#### National Institute of Justice

#### **Current Areas of Effort with Forensic DNA**

the U.S. Department of Justice

- 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



Sept 29-30, 2004 Nov 1-2, 2006

October 11, 2006

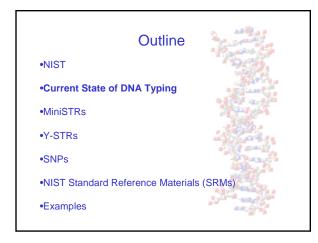


August 24-26, 200 March 13-15, 200

July 26-27, 2006

Apr 3-4, 2007





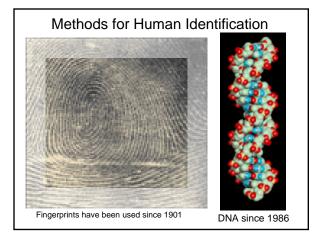
Chiapas

August 17,

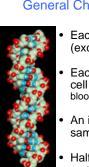
May 19, 2005 June 8, 2005 June 6, 2006 Aug 7, 2006 Dec 5-6, 2006

April 4, 2006









#### General Characteristics of Genomic DNA

 Each person has a unique DNA profile (except identical twins)

 Each person's DNA is the same in every cell (DNA from skin cells will match DNA from blood cells)

- An individual's DNA profile remains the same throughout life
- Half of your DNA comes from your mother and half from your father

### Forensic DNA Testing

Probe subsets of genetic variation in order to differentiate between individuals

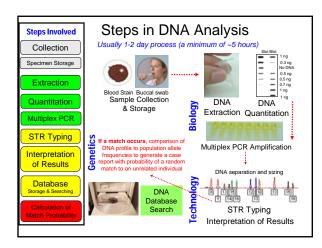
DNA typing must be done efficiently and reproducibly (information must hold up in court)

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

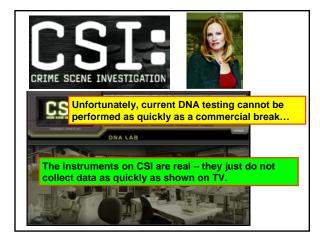
### Applications of Human Identity Testing

- Forensic cases -- matching suspect with evidence
- Paternity testing -- identifying father
- · Missing persons investigations
- · Military DNA "dog tag"
- Convicted felon DNA databases
- Mass disasters -- putting pieces back together
- · Historical investigations and genetic genealogy

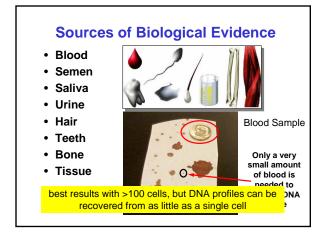
Involves generation of DNA profiles usually with the same genetic markers and then MATCHING TO REFERENCE SAMPLE



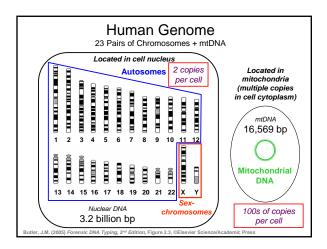










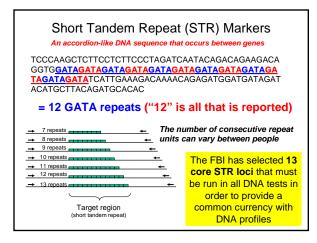




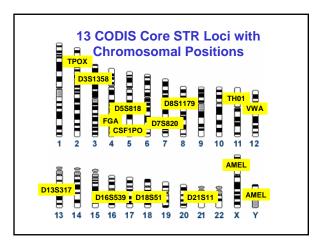
## What Type of Genetic Variation?

Length Variation
 short tandem repeats (STRs)
 <u>CTAGTCGT(GATA)(GATA)(GATA)GCGATCGT</u>

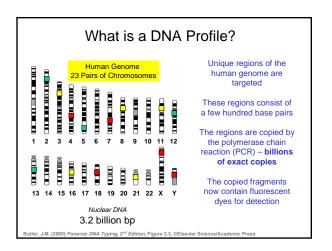
Sequence Variation
 single nucleotide polymorphisms (SNPs)
 insertions/deletions
 <u>GCTAGTCGATGCTC(G/A)GCGTATGCTGTAGC</u>



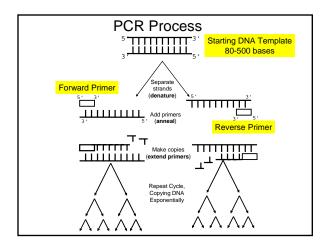




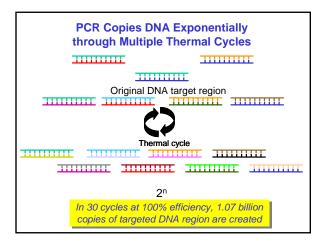


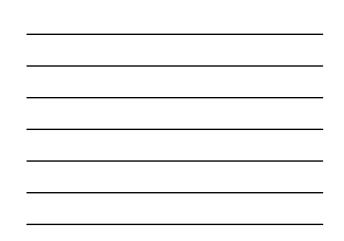


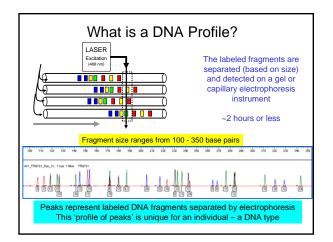




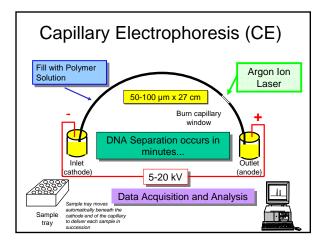


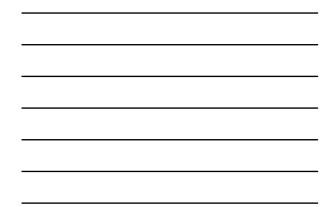


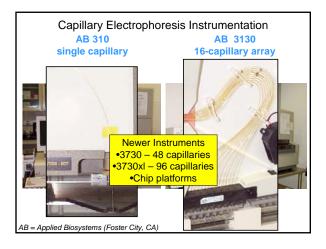




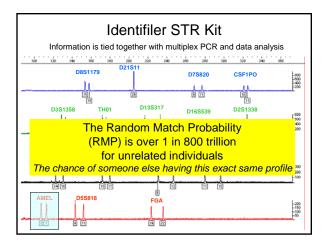




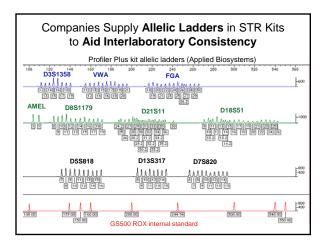




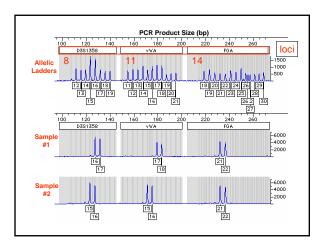




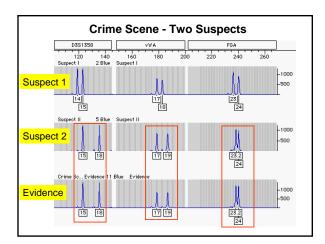




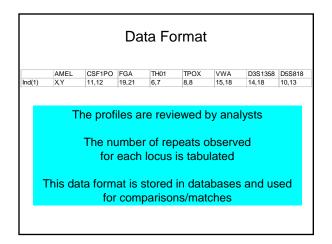


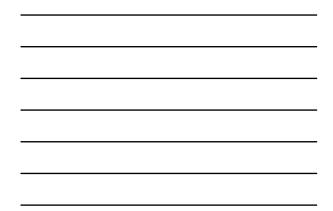


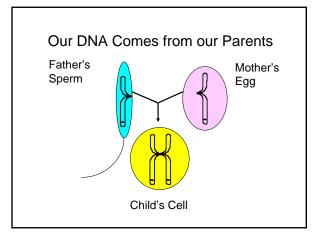




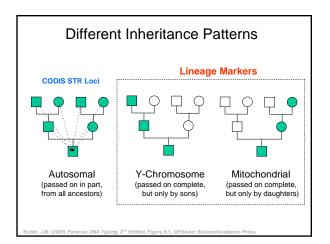




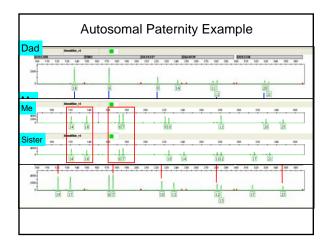




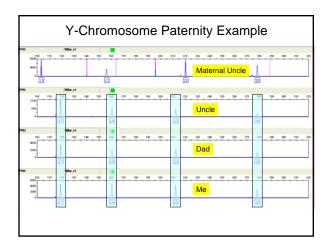




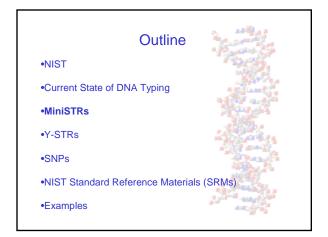












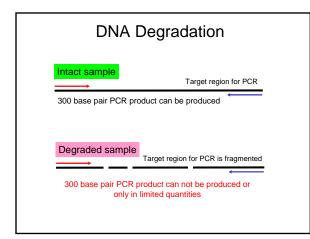


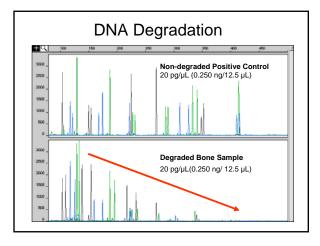
# miniSTRs

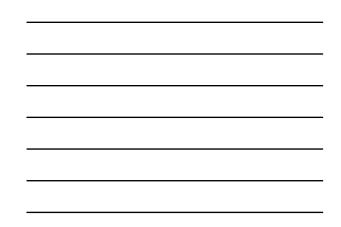
- Simply a smaller PCR product size
- Typically less than ~200 base pairs
- Contains the same information as a traditional STR (repeat length)
- Useful for typing degraded DNA samples
- New loci helpful for missing persons paternity testing/mass disasters

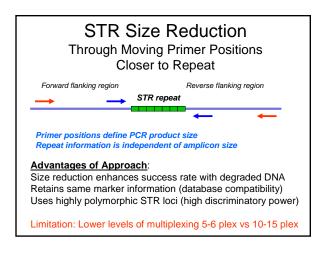
## **DNA** Degradation

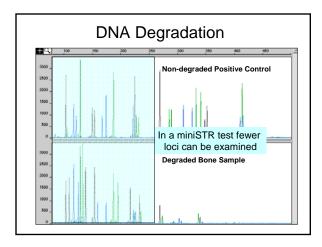
- What causes DNA degradation?
   Heat, humidity, long term exposure to the elements
  - DNA breaks down into small fragments; smaller than the targeted PCR product size
- Mass disasters (aviation, WTC)
- Aged samples (missing persons, remains of soldiers, ancient DNA)



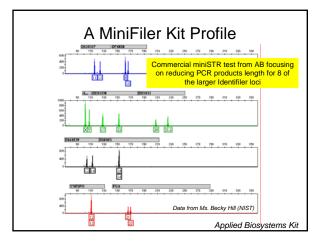


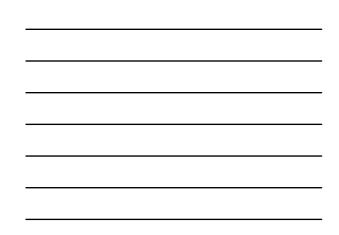


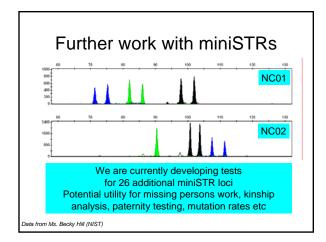




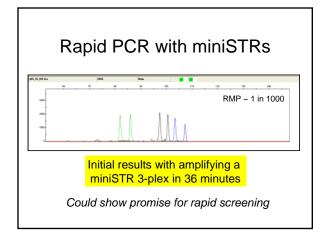






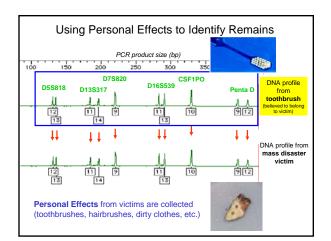


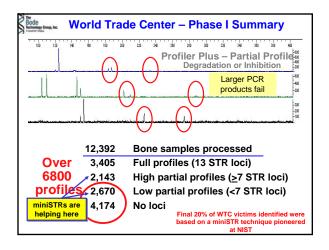




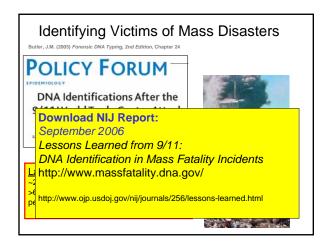


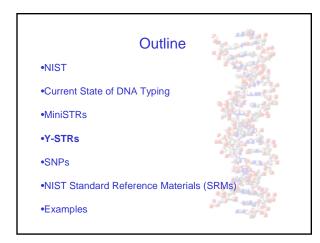






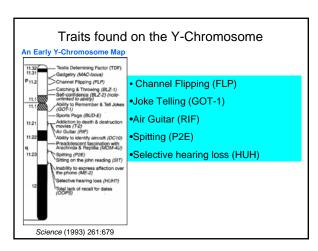


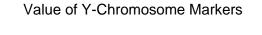




## Y-STRs

- Similar to autosomal STRs just located on the Y-Chromosome
- Since only males posses a Y-Chromosome these markers are useful in male-female mixtures (sexual assault cases)
- A limitation of the Y-STRs lies in that do not have the discrimination capacity of autosomal STRs (no recombination)



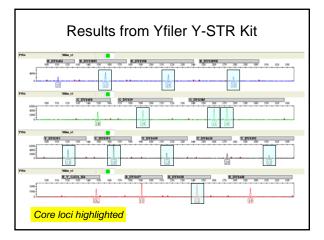


Application	<u>Advantage</u>	
Forensic casework on sexual assault evidence	Male-specific amplification (can avoid differential extraction to separate sperm and epithelial cells)	
Paternity testing	Male children can be tied to fathers in motherless paternity cases	
Missing persons investigations	Patrilineal male relatives may be used for reference samples	
Human migration and evolutionary studies	Lack of recombination enables comparison of male individuals separated by large periods of time	
Historical and genealogical research	Surnames usually retained by males; can make links where paper trail is limited	
I.M. Butler (2005) Forensic DNA Typing, 2 <sup>nd</sup> Edition; Table 9.1		

#### Disadvantages of the Y-Chromosome

- Loci are not independent of one another and therefore rare random match probabilities cannot be generated with the product rule; must use haplotypes (combination of alleles observed at all tested loci)
- Paternal lineages possess the same Y-STR haplotype (barring mutation) and thus fathers, sons, brothers, uncles, and paternal cousins cannot be distinguished from one another
- Not as informative as autosomal STR results

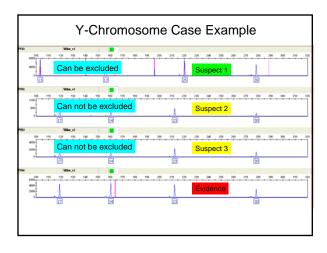
   More like addition (10 + 10 + 10 = 30) than multiplication (10 x 10 x 10 = 1,000)

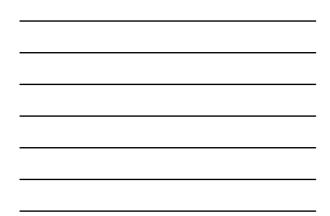


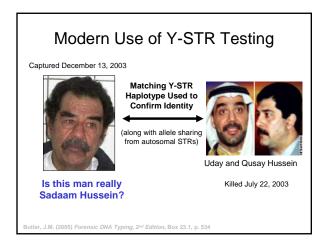


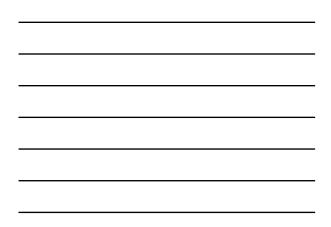
### The Meaning of a Y-Chromosome Match

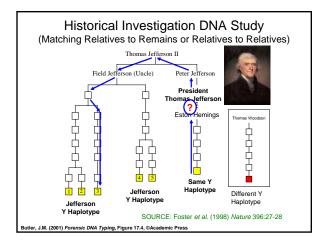
Conservative statement for a match report: The Y-STR profile of the crime sample matches the Y-STR profile of the suspect (at xxx number of loci examined). Therefore, we cannot exclude the suspect as being the donor of the crime sample. In addition, we cannot exclude all patrilineal related male relatives and an unknown number of unrelated males as being the donor of the crime sample.







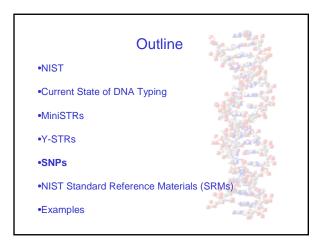






#### What has happened in the past few years...

- "Full" Y-chromosome sequence became available in June 2003; over 350 Y-STR loci identified (only ~20 in 2000)
- Selection of core Y-STR loci (SWGDAM Jan 2003)
- Commercial Y-STR kits released
   PowerPlex Y (9/03), Yfiler (12/04)
- Many population studies performed and databases generated with thousands of Y-STR haplotypes
- Forensic casework demonstration of value of Y-STR testing along with court acceptance





# What Type of Genetic Variation?

•Length Variation short tandem repeats (STRs) <u>CTAGTCGT(GATA)(GATA)(GATA)GCGATCGT</u>

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

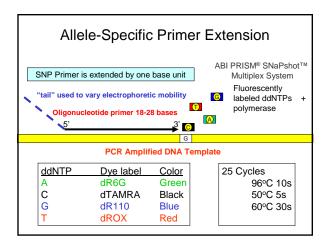
## SNPs

- More abundant than STRs (one very 1000 bases
- Typically bi-allelic versus multi-allelic STRs
- · Used for disease association studies
- Autosomal, Y-chromosome and mitochondrial SNPs
- Lower mutation rate than STRs

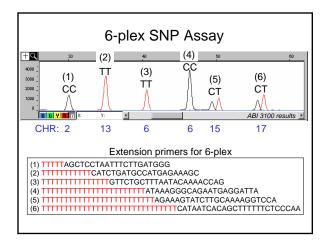
### P.M. Vallone – NIST Seminar - University of Rhode Island

## Utility of SNPs

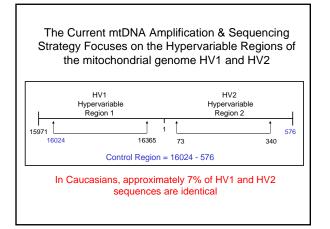
- Similar to STRs identification (but more are needed (50 versus 15)
- Work with degraded DNA (small PCR products < 100 bp)</li>
- In lineage markers Y-chromosome and mitochondrial DNA
- To estimate population of origin ancestry
- Possible phenotypic information hair and eye color



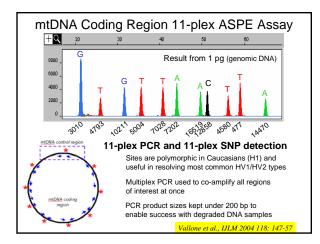




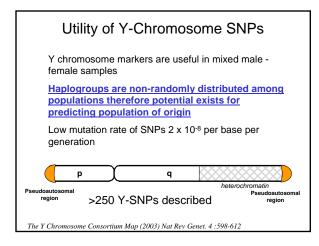




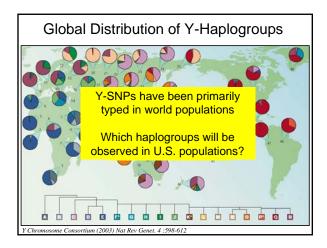




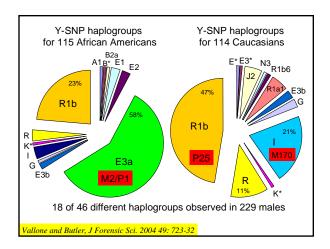








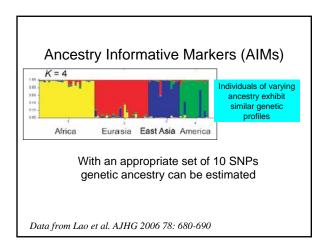






### Ancestry Informative Markers (AIMs)

- AIMs are polymorphisms that relate information about population structure
- Exhibit different frequencies in specific population groups
- Could be used to estimate the population of origin for an individual (Caucasian, Hispanic, African American, Asian etc)



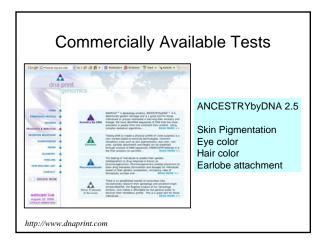


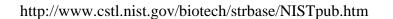
### Pigmentation Genetics & Golden Gene

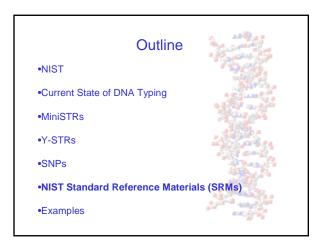
• Lighter variations of pigmentation in humans are associated with diminished humber, it and density of metaneous the hieranted. The evolutionarily conserved ancestral allele of a human coding polymorphism predominates in African and East Asian populations. In contrast, the variant allele is nearly fixed in European populations...and correlates with lighter skin pigmentation in admixed populations

heterozygosity, and correlates with lighter skin pigmentation in admixed populations, suggesting a key role for the *SLC24A5* GENE in human pigmentation.

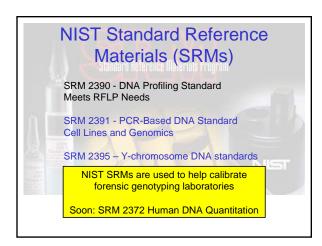
Science 16 December 2005: Vol. 310. no. 5755, pp. 1782 - 1786

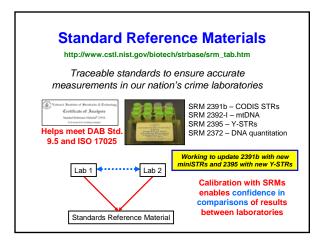




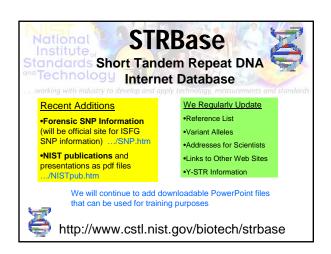




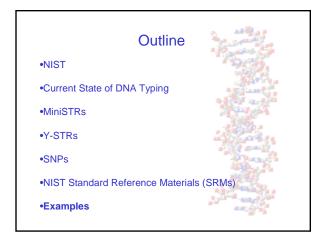










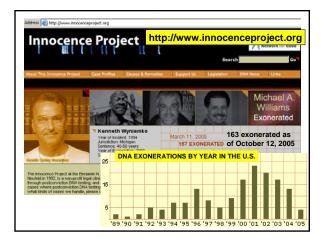




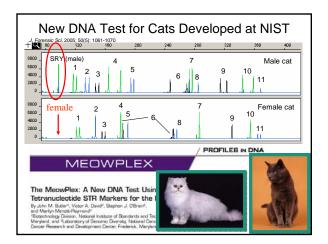
Larry Birkhead receives a handshake from DNA expert Dr. Michael Baird outside the court after a paternity hearing in Nassau, Tuesday, April 10, 2007.



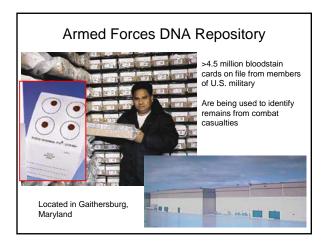






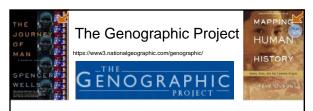






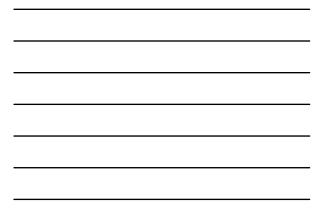


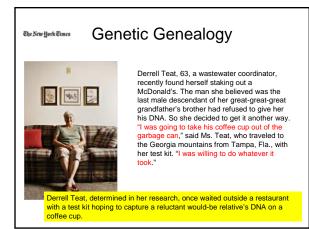




- Different populations carry distinct markers. Following them through the generations reveals a genetic tree on which today's many diverse branches may be followed ever backward to their common African root
- Our genes allow us to chart the ancient human migrations from Africa across the continents
- Funded \$50 million for 5 years by IBM and National Geographic
   Will gather and run DNA samples from ~100,000 people around the world with Y-SNPs and mtDNA







### Tsunami Survivor "Baby 81" Connected to His Parents with DNA

Wednesday, March 2, 2005 Posted: 9:27 AM EST (1427 GMT)

NEW YORK (AP) -- The parents of the infant tsunami survivor nicknamed "Baby 81" say they found it difficult to feel overjoyed about their reunion in the midst of so much tragedy. The 4-month-old Sri Lankan baby and

The 4-month-old Sri Lankan baby and his parents, who were reunited after court-ordered <u>DNA tests proved their</u> <u>relationship</u>, appeared on ABC's "Good Morning America" Wednesday, a day after their 20-hour-long flight landed in New York.



http://www.cnn.com/2005/US/03/02/baby.81.ap/index.html

