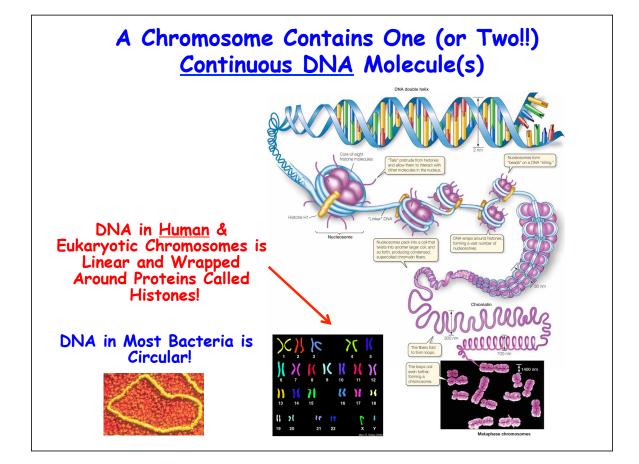


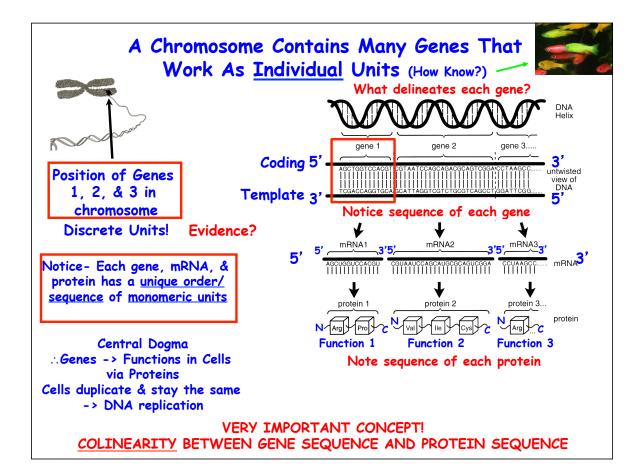
Plants of Tomor

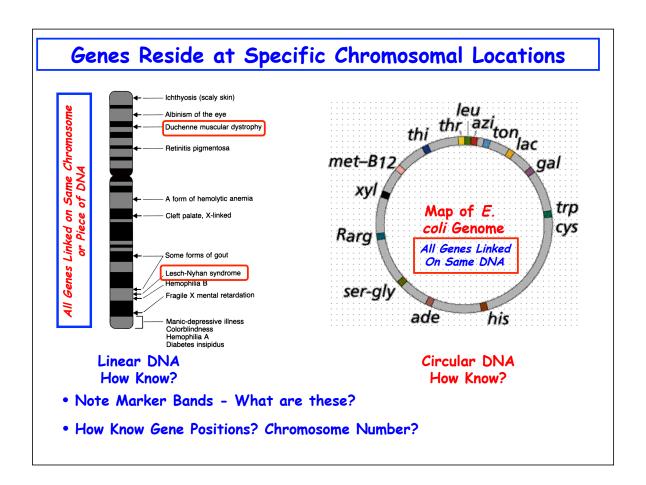


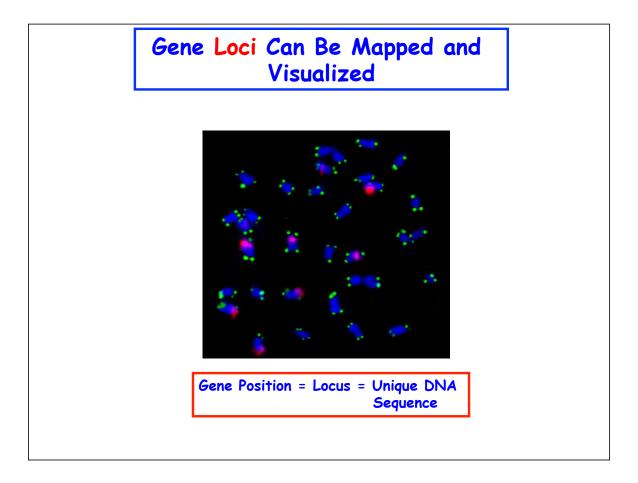
## THEMES

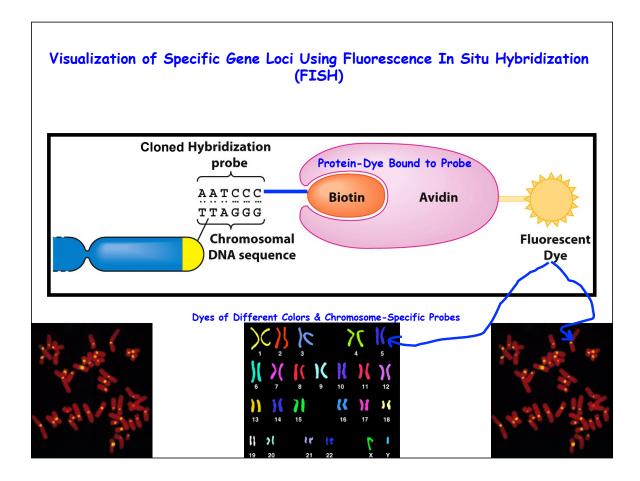
- 1. What is the Anatomy of a Gene?
- 2. How Are Genes Regulated Switched On & Off?
- 3. How Does DNA Replication Occur?
- 4. What is the Polymerase Chain Reaction (PCR) and How is PCR used?
- 5. How Do Mutations Occur?
- 6. How Can Pedigrees Be Used To Follow the Inheritance of Mutant Genes?
- 7. How Do Mutations Change Phenotypes?
- 8. What is the Colinearity Between Genes & Proteins (how does DNA→protein)?
- 9. What Is the Genetic Code?
- 10. How Do Gene Expression Processes Differ in Eukaryotes & Prokaryotes?
- 11. How Can Splicing Cause One Gene To Specify Several Different Proteins?
- 12. Yo!-It's in the DNA Sequences- What Are the Implications For Genetic Engineering?

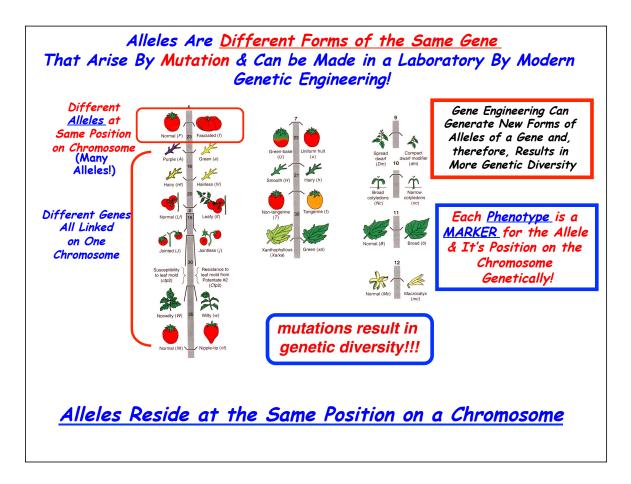


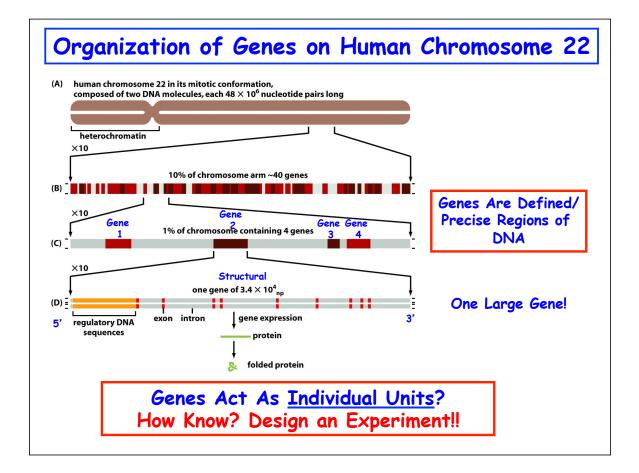


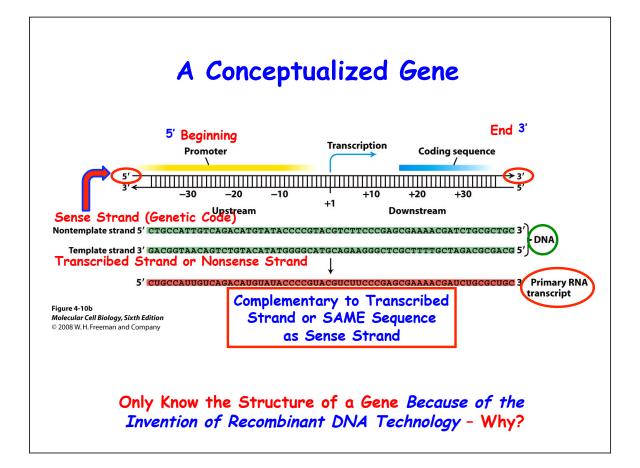


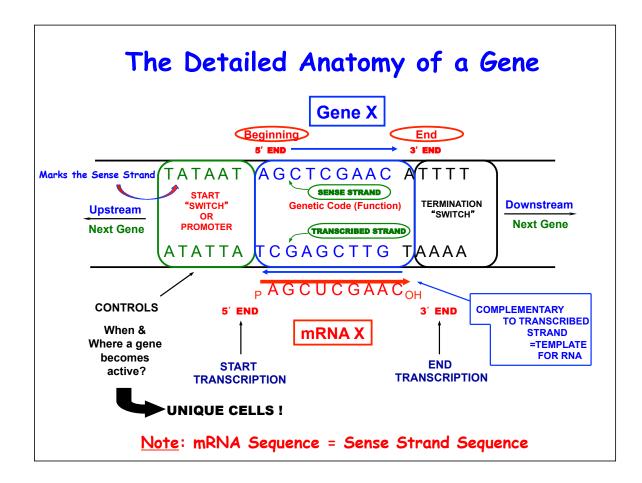


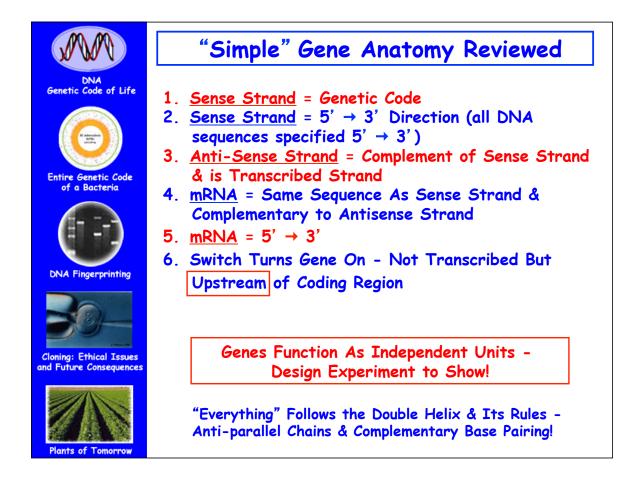


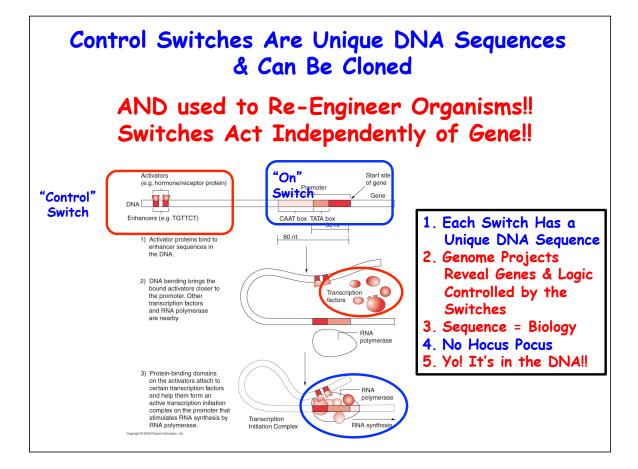


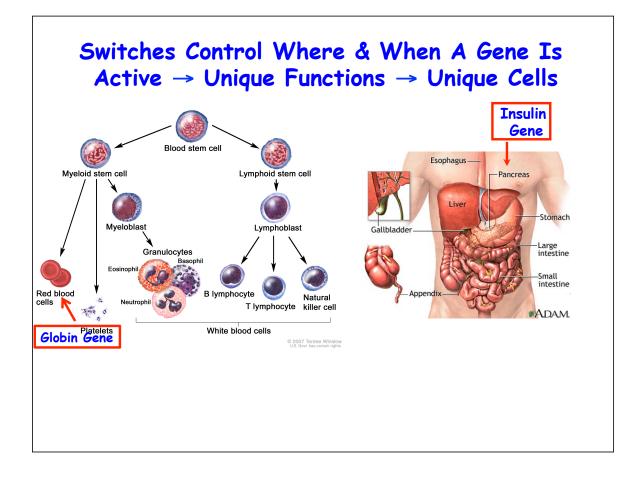


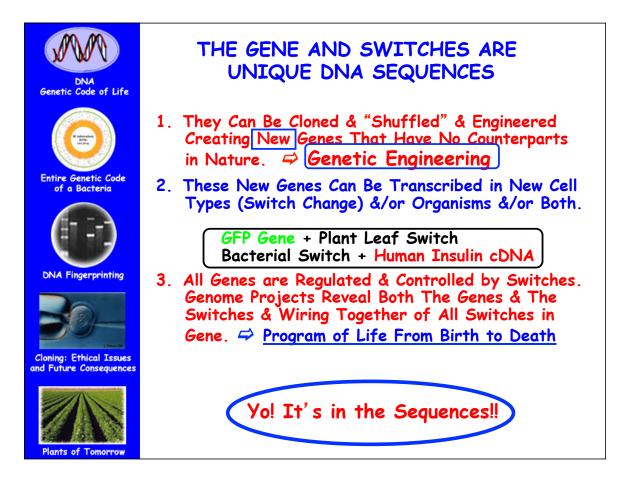


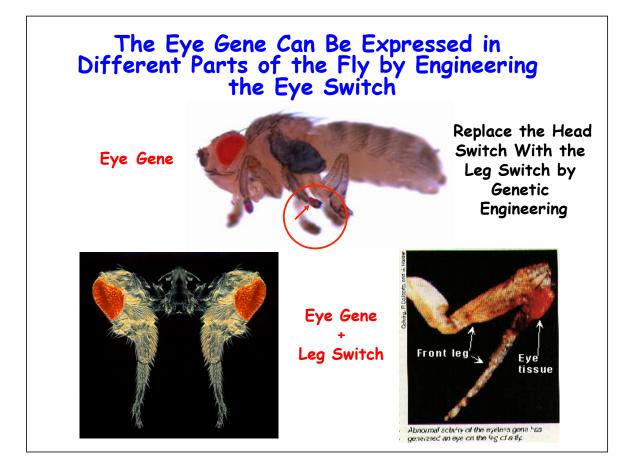


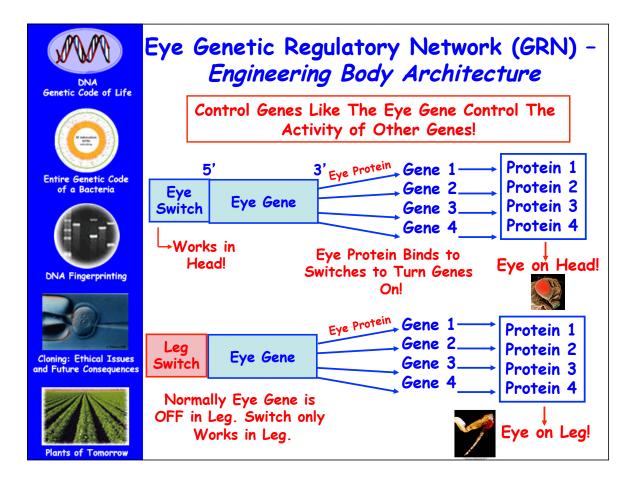


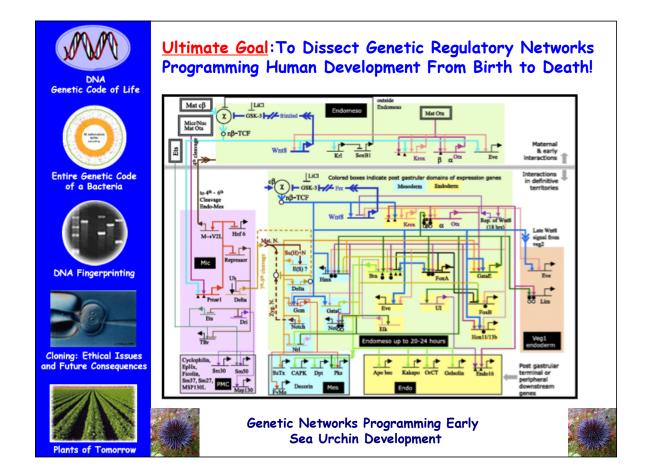


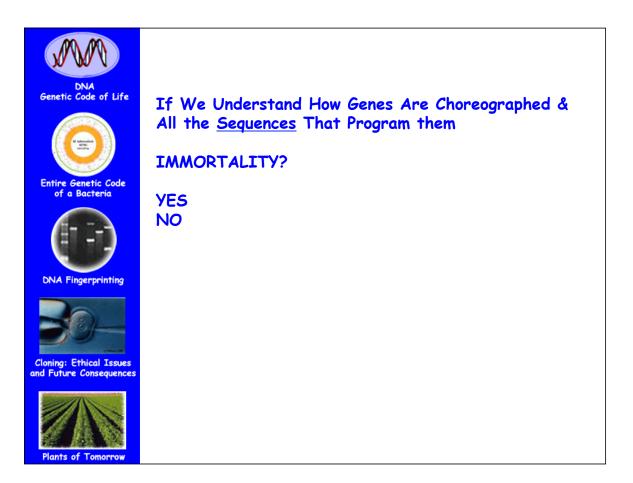




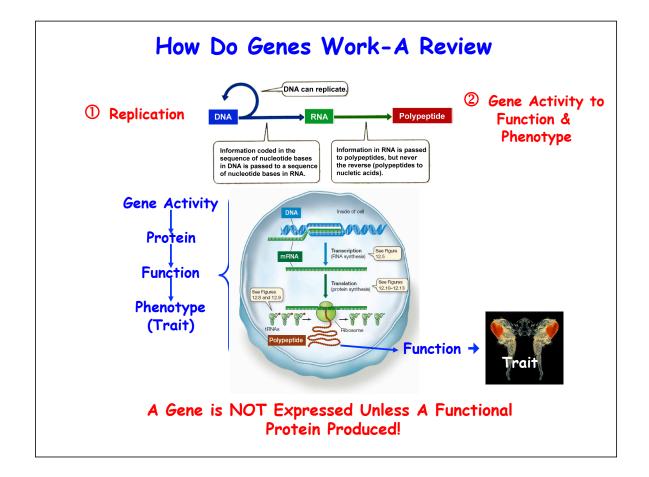


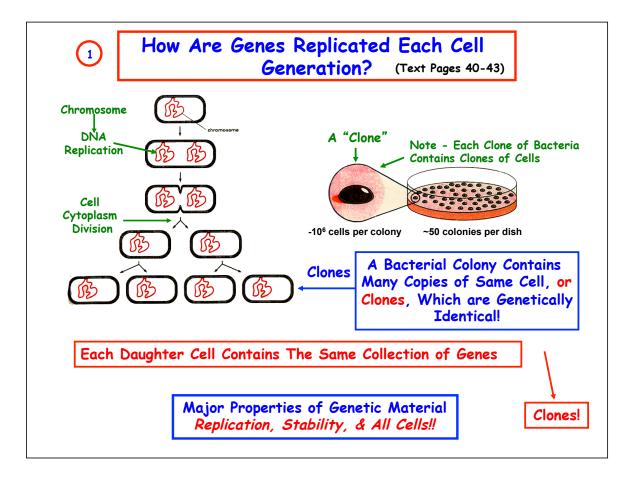


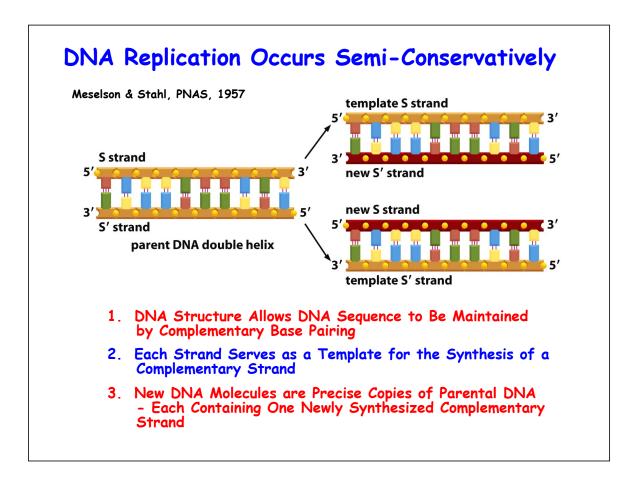


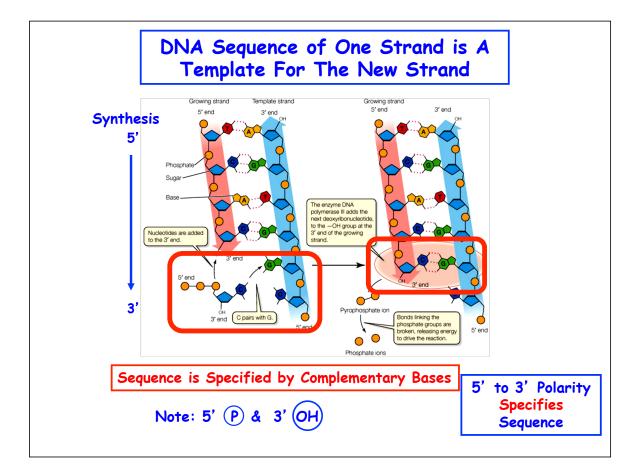


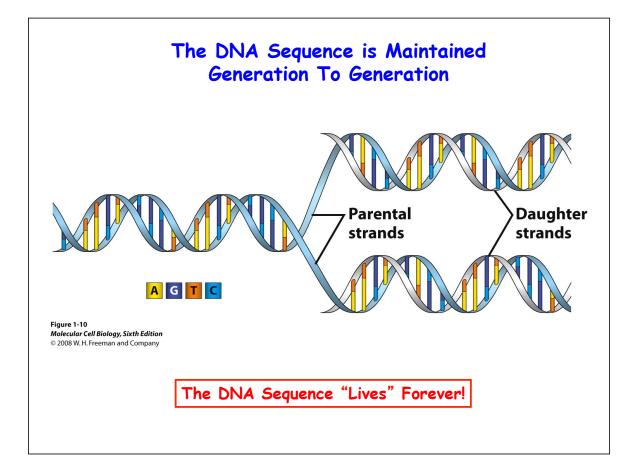


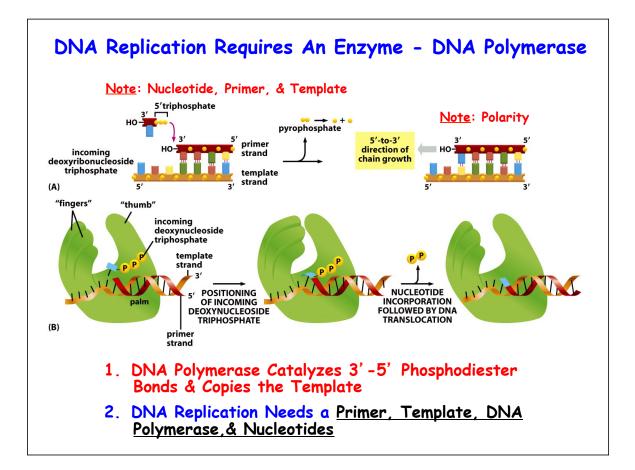


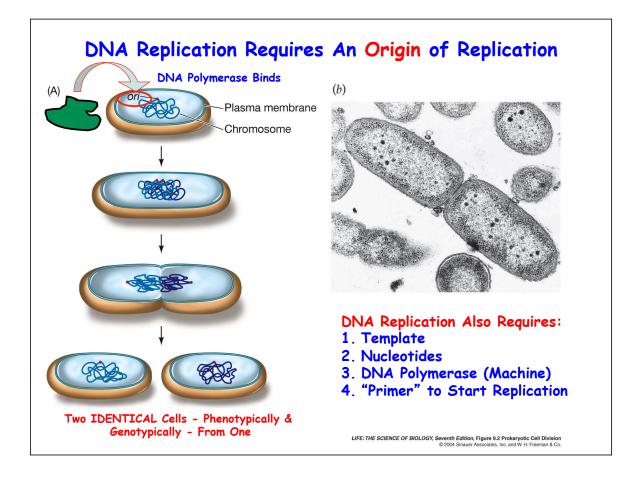


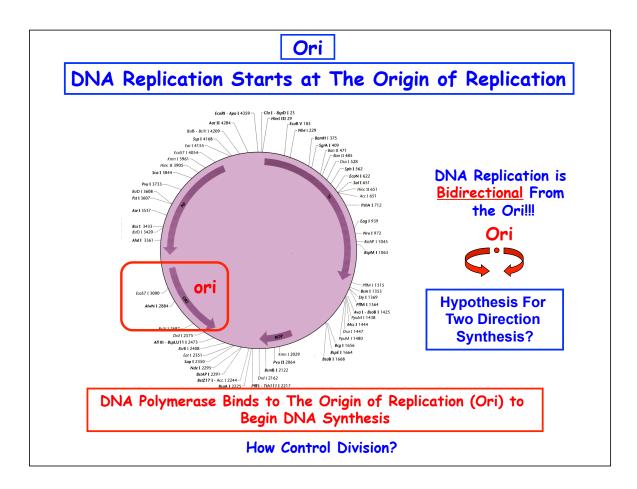


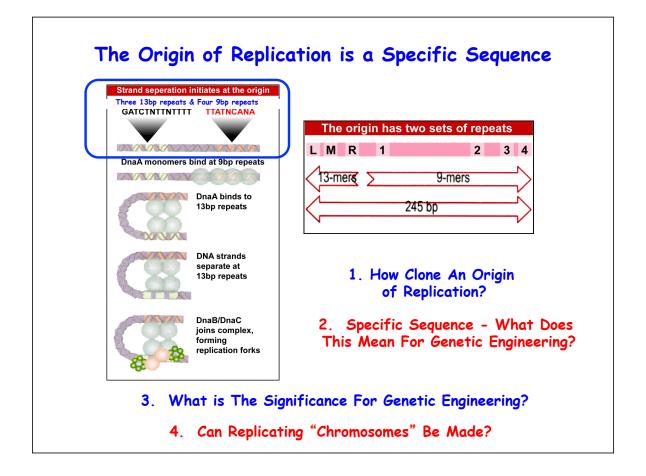


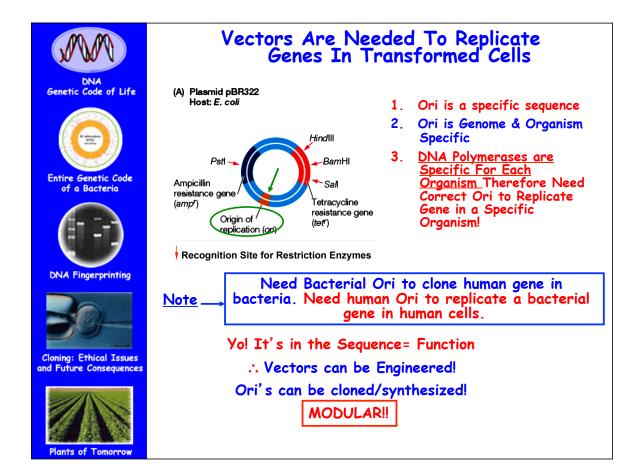


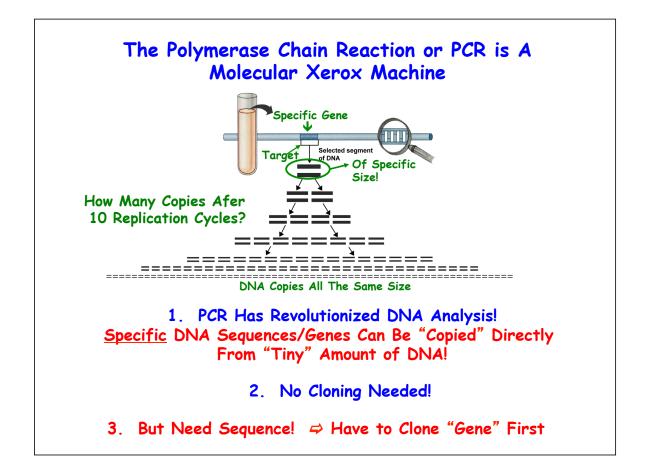


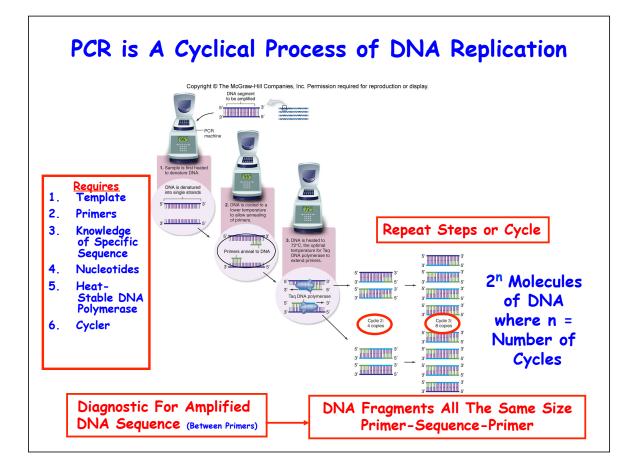


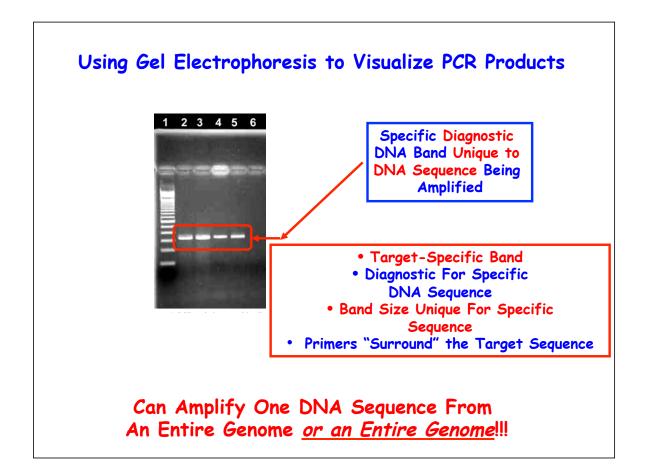


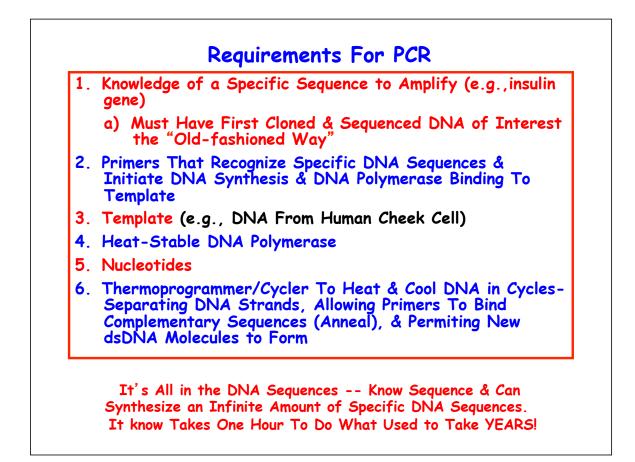


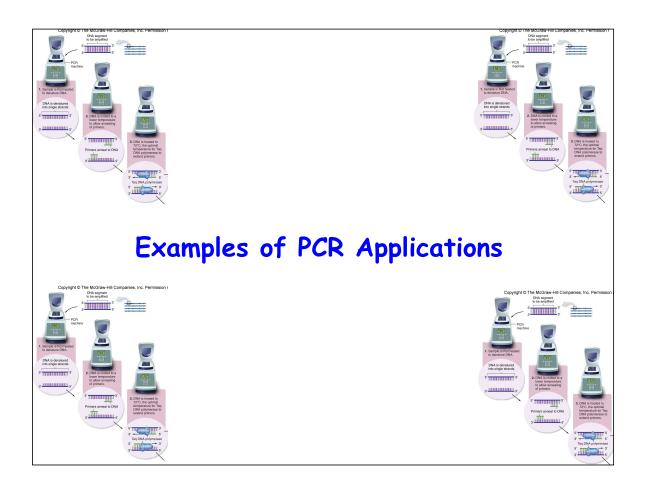


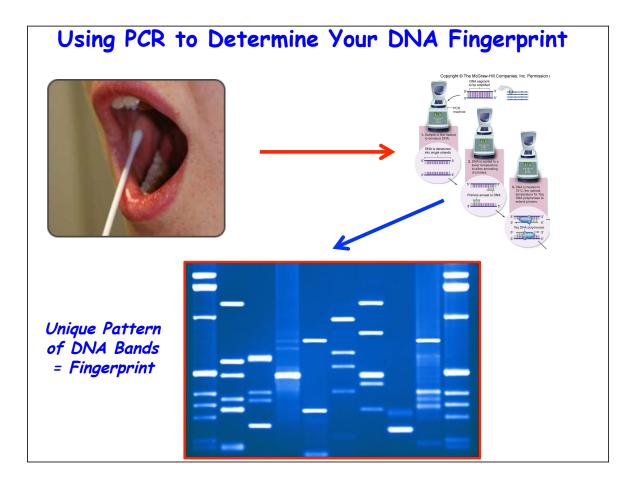


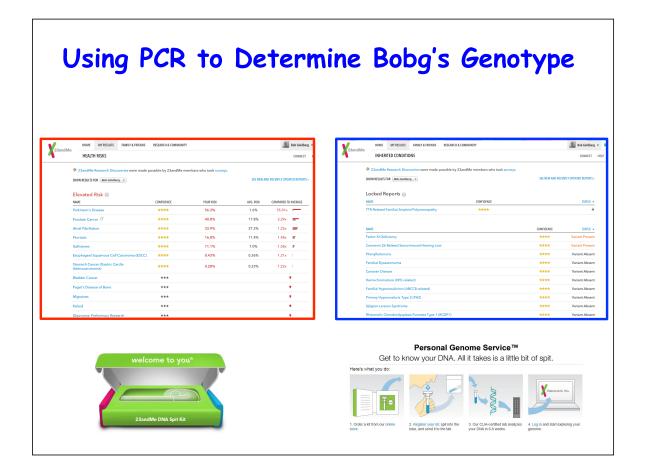




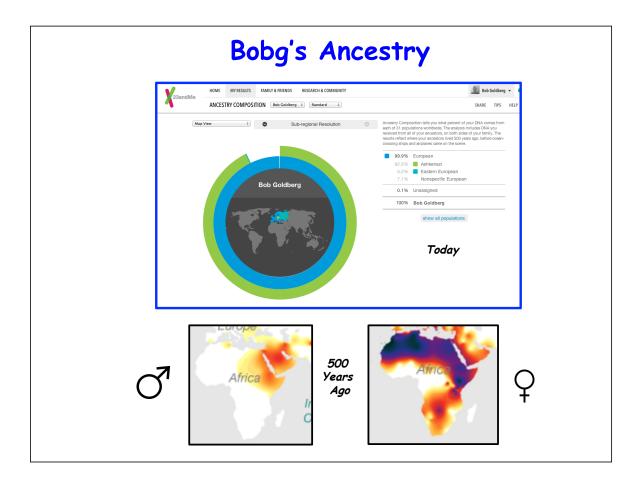












# Using PCR to Amplify Neanderthal Bone DNA & Sequence The <u>Entire</u> Genome!

## Analysis of one million base pairs of Neanderthal DNA From a 45,000 Year-Old Bone

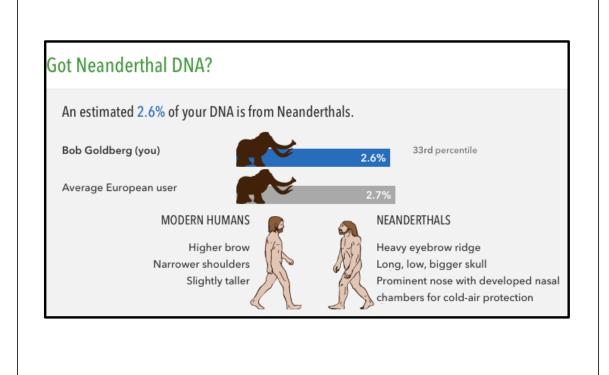
Richard E. Green<sup>1</sup>, Johannes Krause<sup>1</sup>, Susan E. Ptak<sup>1</sup>, Adrian W. Briggs<sup>1</sup>, Michael T. Ronan<sup>2</sup>, Jan F. Simons<sup>2</sup>, Lei Du<sup>2</sup>, Michael Egholm<sup>2</sup>, Jonathan M. Rothberg<sup>2</sup>, Maja Paunovic<sup>3</sup>‡ & Svante Pääbo<sup>1</sup>

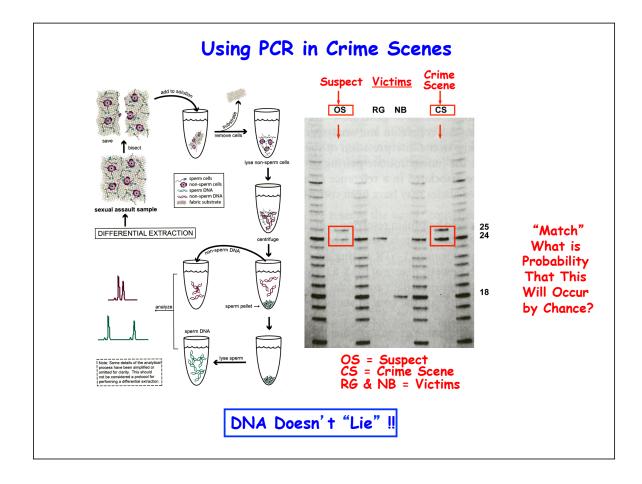


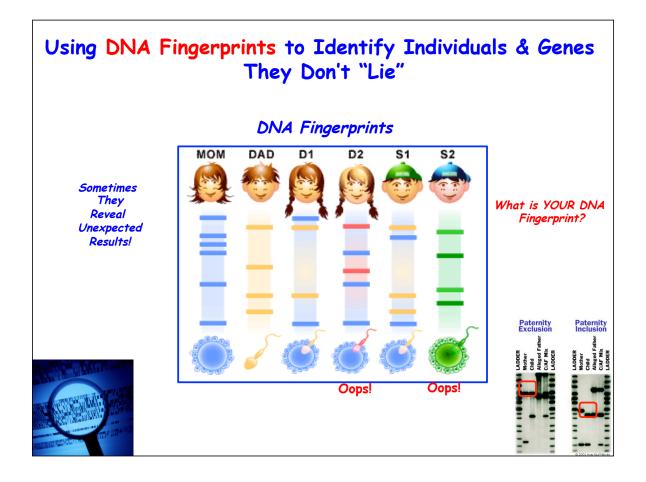
Nature, November, 2006

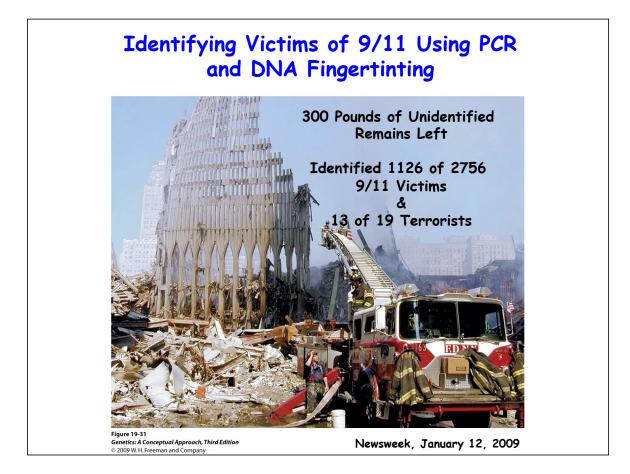


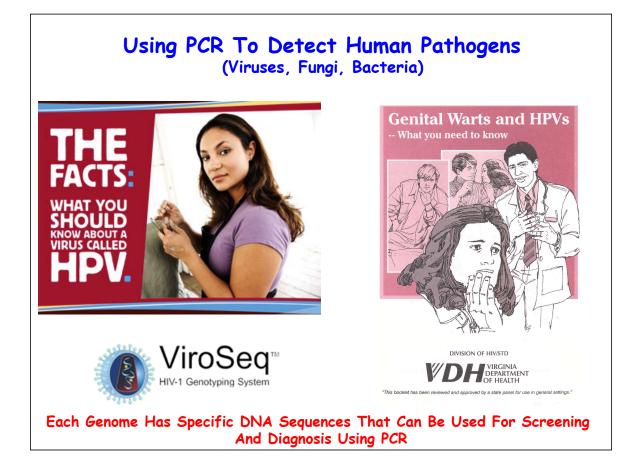
# Bobg's Neanderthal DNA Content

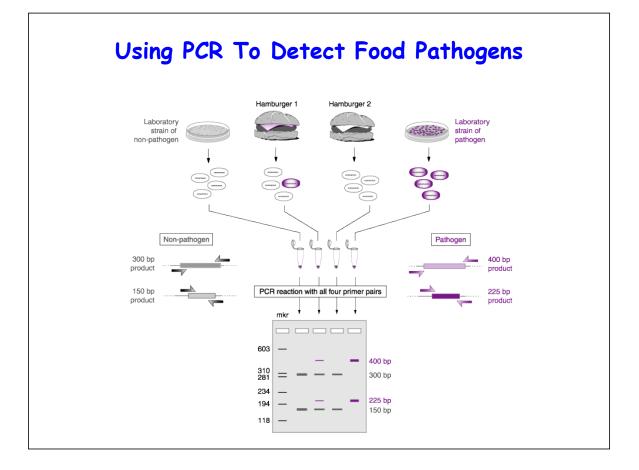


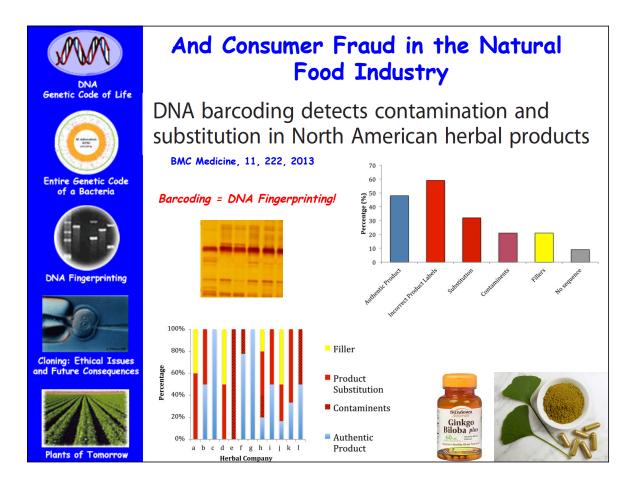




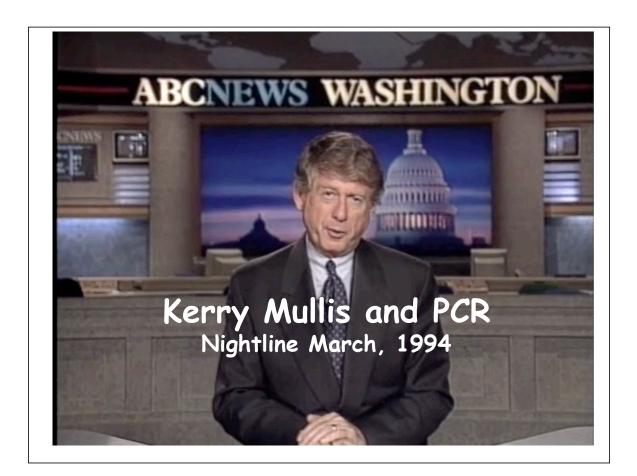


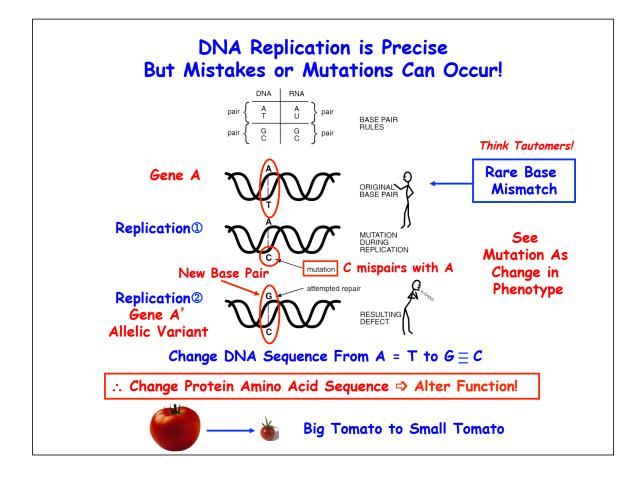


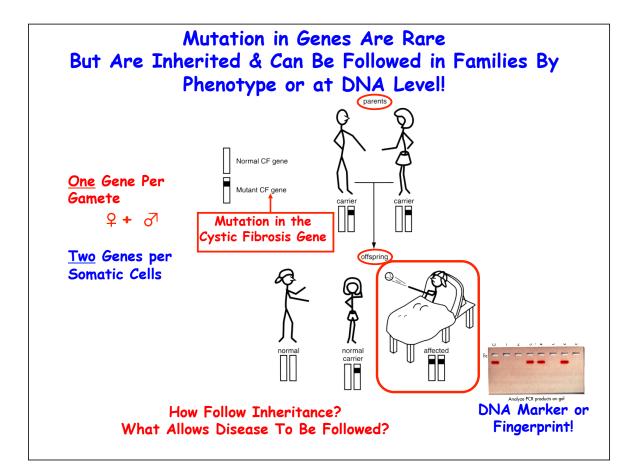


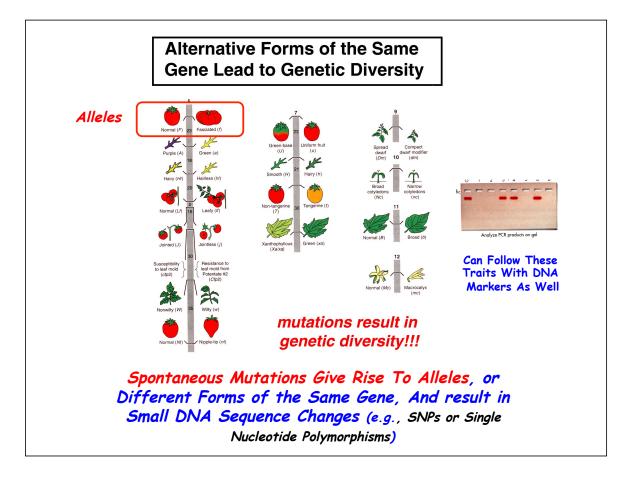


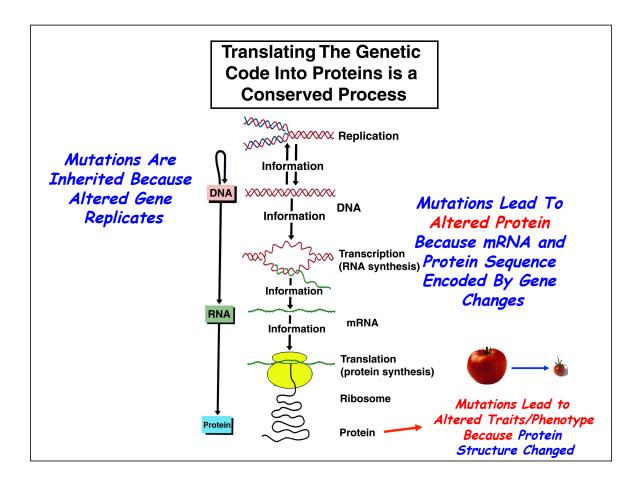


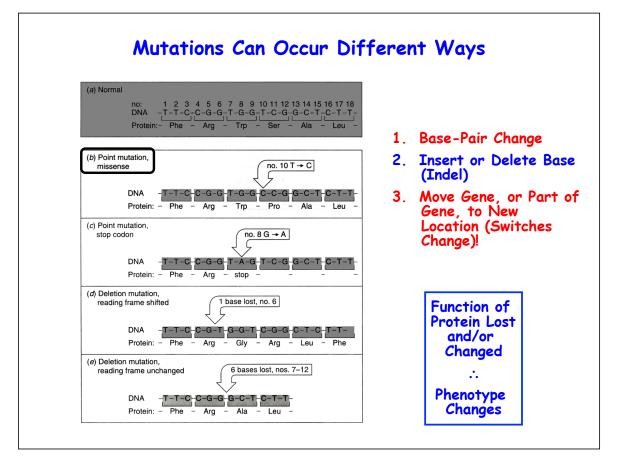




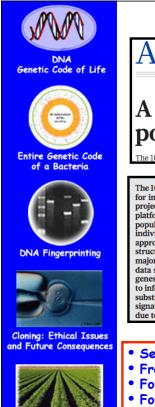








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TABLE 13.2	Some Important Genetic Disorders			
Disorder	Symptom	Defect	Dominant/ Recessive	Frequency Among Human Births
Hemophilia	Blood fails to clot	Defective blood-clotting factor VIII	X-linked recessive	1/10,000 (Caucasian males)
Huntington disease	Brain tissue gradually deteriorates in middle age	Production of an inhibitor of brain cell metabolism	Dominant	1/24,000
Muscular dystrophy (Duchenne)	Muscles waste away	Degradation of myelin coating of nerves stimulating muscles	X-linked recessive	1/3700 (males)
Hypercholesterolemia	Excessive cholesterol levels in blood lead to heart disease	Abnormal form of cholesterol cell surface receptor	Dominant	1/500
DIPLOID GENOTYPE DIPLOID PHENOTYPE		Dominant minant = Dominant = Dominant = Utant Mutant	R Recessive Wild type	Recessive Recessive Recessive Mutant



**Plants of Tomorrow** 

ARTICLE

Nature, October 10, 2010

doi:10.1038/nature0953

# A map of human genome variation from population-scale sequencing

The 1000 Genomes Project Consortium\*

The 1000 Genomes Project aims to provide a deep characterization of human genome sequence variation as a foundation for investigating the relationship between genotype and phenotype. Here we present results of the pilot phase of the project, designed to develop and compare different strategies for genome-wide sequencing with high-throughput platforms. We undertook three projects: low-coverage whole-genome sequencing of 179 individuals from four populations; high-coverage sequencing of two mother-father-child trios; and exon-targeted sequencing of 697 individuals from seven populations. We describe the location, allele frequency and local haplotype structure of approximately 15 million single nucleotide polymorphisms, 1 million short insertions and deletions, and 20,000 structural variants, most of which were previously undescribed. We show that, because we have catalogued the vast majority of common variation, over 95% of the currently accessible variants found in any individual are present in this data set. On average, each person is found to carry approximately 250 to 300 loss-of-function variants in annotated genes and 50 to 100 variants previously implicated in inherited disorders. We demonstrate how these results can be used to inform association and functional studies. From the two trios, we directly estimate the rate of *de novo* germline base substitution mutations to be approximately 10<sup>-8</sup> per base pair per generation. We explore the data with regard to signatures of natural selection, and identify a marked reduction of genetic variation in the neighbourhood of genes, due to selection at linked sites. These methods and public data will support the next phase of human genetic research.

- Sequenced Genomes of ~900 individuals
- From Seven Different Global Populations
- Found 250-300 Loss-Of-Function Mutations (KOs) Per Person
- Found 50-100 Mutations Implicated in Genetic Disorders Per Person
- 10<sup>-8</sup> bp Mutations Per Generation (30 per Genome)

## ARTICLE

doi:10.1038/nature11396

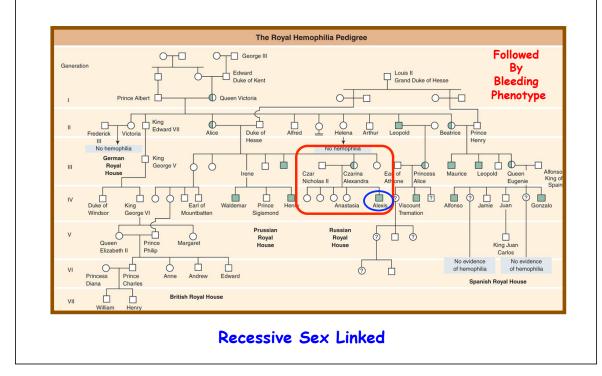
# Rate of *de novo* mutations and the importance of father's age to disease risk

Augustine Kong<sup>1</sup>, Michael L. Frigge<sup>1</sup>, Gisli Masson<sup>1</sup>, Soren Besenbacher<sup>1,2</sup>, Patrick Sulem<sup>1</sup>, Gisli Magnusson<sup>1</sup>, Sigurjon A. Gudjonsson<sup>1</sup>, Asgeir Sigurdsson<sup>1</sup>, Aslaug Jonasdottir<sup>1</sup>, Adalbjorg Jonasdottir<sup>1</sup>, Wendy S. W. Wong<sup>3</sup>, Gunnar Sigurdsson<sup>1</sup>, G. Bragi Walters<sup>1</sup>, Stacy Steinberg<sup>1</sup>, Hannes Helgason<sup>1</sup>, Gudmar Thorleifsson<sup>1</sup>, Daniel F. Gudbjartsson<sup>1</sup>, Agnar Helgason<sup>1,4</sup>, Olafur Th. Magnusson<sup>1</sup>, Unnur Thorsteinsdottir<sup>1,5</sup> & Kari Stefansson<sup>1,5</sup>

Mutations generate sequence diversity and provide a substrate for selection. The rate of *de novo* mutations is therefore of major importance to evolution. Here we conduct a study of genome-wide mutation rates by sequencing the entire genomes of 78 Icelandic parent-offspring trios at high coverage. We show that in our samples, with an average father's age of 29.7, the average *de novo* mutation rate is  $1.20 \times 10^{-8}$  per nucleotide per generation. Most notably, the diversity in mutation rate of single nucleotide polymorphisms is dominated by the age of the father at conception of the child. The effect is an increase of about two mutations per year. An exponential model estimates paternal mutations doubling every 16.5 years. After accounting for random Poisson variation, father's age is estimated to explain nearly all of the remaining variation in the *de novo* mutation counts. These observations shed light on the importance of the father's age on the risk of diseases such as schizophrenia and autism.

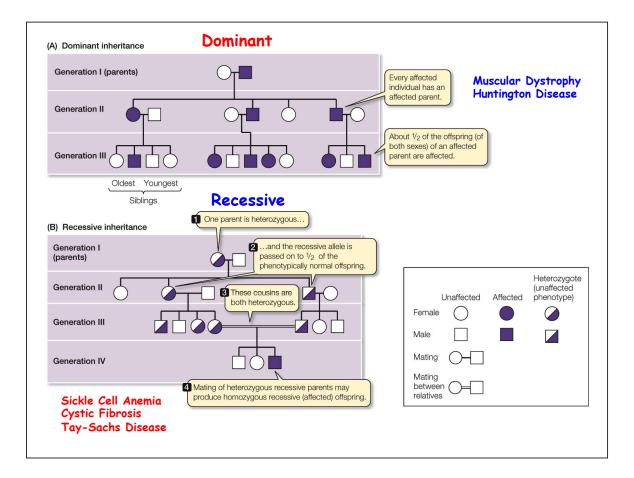
#### August 22, 2012

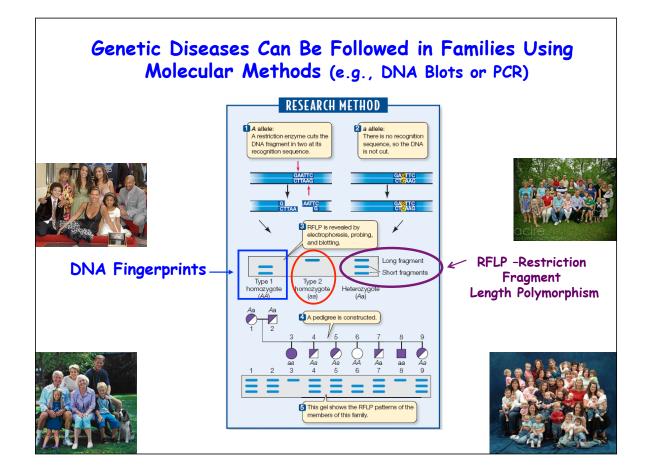
Father's Age Is Linked to Risk of Autism and Schizophrenia

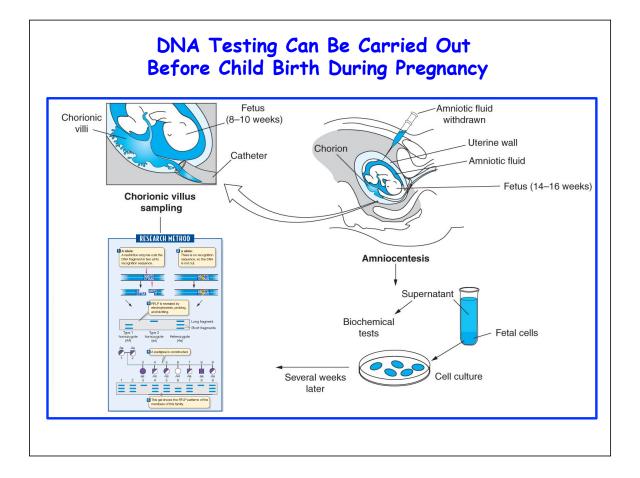


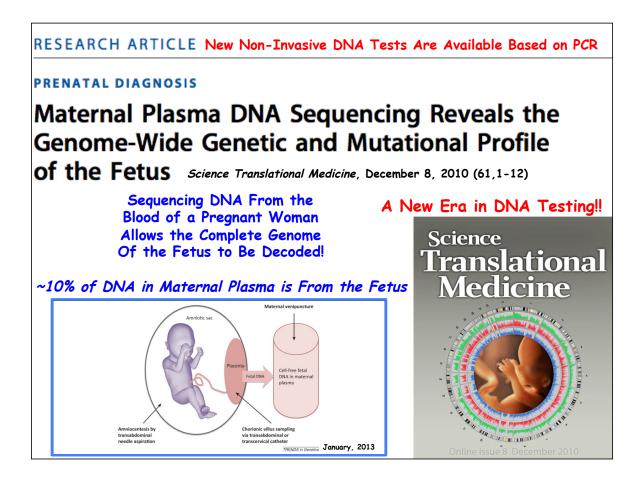
#### Pedigrees Can Be Used To Follow Disease Genes in Human Families

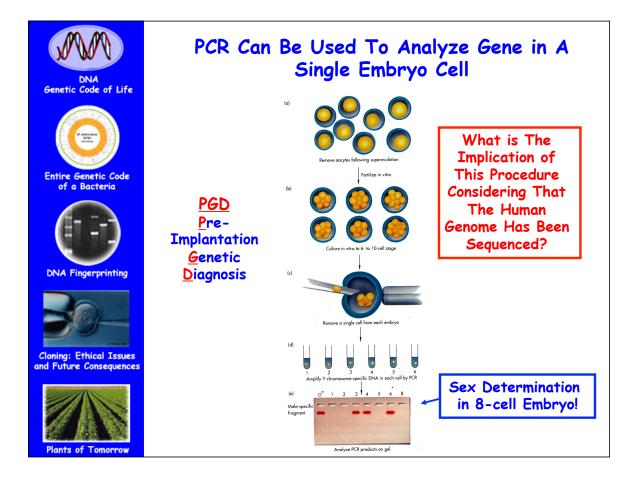












### Determining the Genetic Identity of a Human Embryo Before Implantation!

