



**DNA** Fingerprinting



Cloning: Ethical Issues and Future Consequences



HC70A & SAS70A Winter 2018 Genetic Engineering in Medicine, Agriculture, and Law

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Lecture 4 What Are Genes & How Do They Work: Part Two

UCLA





THEMES

- 1. What Are Genes & Their Properties
- 2. How Do Switches Regulate Genes in Space & Time?
- 3. How Does DNA Replication Occur?
- 4. What is the Polymerase Chain Reaction (PCR) and How is PCR Used in Society?
- 5. How Do Mutations Occur?
- 6. How Can Pedigrees Be Used To Follow the Inheritance of Mutant Genes With Phenotypes and RFLPs?
- 7. How Do Mutations Change Phenotypes?
- 8. What is the Colinearity Between Genes & Proteins (i.e. how does the DNA sequence specify a protein sequence)?
- 9. What is the Genetic Code?
- 10. Yo!-It's in the DNA Sequences- What Are the Implications For Genetic Engineering?



























# Using Genetic Engineering to Change Body Architecture-Engineering Eyes on a Fly's Leg With a Single Gene!

Human

Mouse

Drosophila









#### GENES AND SWITCHES ARE UNIQUE DNA SEQUENCES

DNA Genetic Code of Life

Entire Genetic Code

of a Bacteria

**DNA** Fingerprinting

Cloning: Ethical Issues and Future Consequences

Plants of Tomorrow

- 1. They Can Be Cloned & "Shuffled" & Engineered Creating New Genes That Have No Counterparts in Nature
- These New Genes Can Be Transcribed in New Cell Types (Switch Change) &/or Organisms &/or Both (e.g., <u>Human Genes in Bacteria</u>)

Yo! It's in the Sequences!!



























1.	Knowledge of a <u>Specific Sequence</u> to Amplify (e.g., insulin gene)
	a) Must Have First Cloned & Sequenced DNA of Interest the "Old-fashioned Way"
<ul> <li>Requirements For PCR</li> <li>1. Knowledge of a <u>Specific Sequence</u> to Amplify (e.g., insugene) <ul> <li>a) Must Have First Cloned &amp; Sequenced DNA of Interthe "Old-fashioned Way"</li> </ul> </li> <li>2. Primers That Recognize Specific DNA Sequences &amp; Initiate DNA Synthesis &amp; DNA Polymerase Binding To Template <ul> <li>3. Template (e.g., DNA From Human Cheek Cell)</li> <li>4. Heat-Stable <u>DNA Polymerase</u></li> <li>5. Nucleotides</li> <li>6. <u>Thermoprogrammer/Cycler</u> To Heat &amp; Cool DNA in Cycle Separating DNA Strands, Allowing Primers To Bind Complementary Sequences (Anneal), &amp; Permiting New dsDNA Molecules to Form</li> </ul> </li> </ul>	
3.	<u>Template</u> (e.g., DNA From Human Cheek Cell)
4.	Heat-Stable <u>DNA Polymerase</u>
5.	Nucleotides
6.	<u>Thermoprogrammer/Cycler</u> To Heat & Cool DNA in Cycles- Separating DNA Strands, Allowing Primers To Bind Complementary Sequences (Anneal), & Permiting New dsDNA Molecules to Form

Synthesize an Infinite Amount of Specific DNA Sequences. It now Takes One Hour to Do What Used to Take YEARS!







## Using PCR to Determine Bobg's Genotype

23andMe	HOME	MY RESULTS	FAMILY & FRIENDS	RESEARCH & COMMUNITY	r		Rob Goldberg	
	HEALTH	RISKS					CONNECT	
	🔆 23andMe F	Research Disc	weries were made p	ossible by 23andMe m	embers who took surveys.			
	SHOW RESULTS FOR Bob Goldberg 2 SEE						NEW AND RECENTLY UPDATED REPORTS >	
	Elevated F	Risk 🕜						
	NAME			CONFIDENCE	YOUR RISK	AVG. RISK	COMPARED TO AVERAGE	
	Parkinson's Di	sease		****	56.3%	1.6%	35.01×	
	Prostate Cano	er O'		****	40.8%	17.8%	2.29x	
	Atrial Fibrillati	on		****	33.9%	27.2%	1.25x 💳	
	Psoriasis			****	16.8%	11.4%	1.48x 🕿	
	Gallstones			****	11.1%	7.0%	1.58x 🖛	
	Esophageal St	quamous Cell	Carcinoma (ESCC)	****	0.43%	0.36%	1.21x I	
	Stomach Cano Adenocarcino	er (Gastric Ca ma)	rdia	****	0.28%	0.23%	1.22x (	
	Bladder Cance	ar .		***			+	
	Paget's Diseas	e of Bone		***			+	
	Migraines			***			+	
	Keloid			***			+	
	Glaucoma: Pre	diminary Rese	arch	***			+	

23andMe	HOME	HOME MYRESULTS FAMILY & FRIENDS RESEARCH & COMMUNITY				👤 Bob Goldberg 👻	
	INHER	ITED CONDITIO	DNS			CONNECT	HELP
	× 23andMe	Research Disc	overies were made	possible by 23andMe members who took surveys.			
	SHOW RESULTS I	FOR Bob Goldbe	rg t	SEE NEW AND RECENTLY UPDATED REPORTS »			
1	Locked R	eports 🕜					
1	NAME			CONFIDENCE		STATUS 👻	
	TTR-Related I	Familial Amylo	id Polyneuropathy	****		8	
	NAME				CONFIDENCE	STATUS 👻	
i i i	Factor XI Def	iciency			****	Variant Present	
	Connexin 26-	Related Senso	rineural Hearing Los	55	****	Variant Present	
	Phenylketon	aria			****	Variant Absent	
	Familial Dysa	utonomia			****	Variant Absent	
	Canavan Dise	nase			****	Variant Absent	
	Hemochroma	atosis (HFE-rela	ited)		****	Variant Absent	
	Familial Hype	arinsulinism (Al	3CC8-related)		****	Variant Absent	
	Primary Hype	eroxaluria Type	2 (PH2)		****	Variant Absent	
	Sjögren-Larss	son Syndrome			****	Variant Absent	
				PCDP1)		March and All sound	



Personal Genome Service™ Get to know your DNA. All it takes is a little bit of spit.



#### Using PCR To Determine an Individual's Ancestry ----Q.C DNA Tribes Genetic Ancestry Analysis **Discover Your Past!** Determine if two people are relate Determine if two people descend Find out if you are related to othe • Test your autosomal DNA inherited from maternal and paternal, lineal and non-lineal ancestors. Most comprehensive test available: 896 world populations and 36 unique Genetic World Regions. Prove or disprove your family tre Provide clues about your ethnic Personalize and customize your analysis with Add-Ons any time. Our Premium Kit test now includes 21 powerful STR marker systems. PCR Started a New Industry Maternal & Paternal Testing Adopted? Find out about your ancestry... DNA can reveal ancestors' lies and secrets LA Times, January 18, 2009



# 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><sup>‡</sup> & Svante Pääbo<sup>1</sup>



Nature, November, 2006





Each Genome Has Specific DNA Sequences That Can Be Used For Screening And Diagnosis Using PCR



#### PCR Has Many Uses, Has Changed Many Fields, and Lead To New Ones That Have Had a Big Impact On Our Lives

- 1. <u>Amplify Any DNA Sequence</u>, or Gene, From "Tiny" Amounts of DNA or Biological Materials IF ORIGINAL SEQUENCE KNOWN
- 2. <u>Study DNA From Limited and/or Degraded Sources Such As:</u>
  - 1. A Single Human Hair or Cheek Cell
  - 2. An Ancient Fossil (e.g., Neanderthal Bone or Mammoth Hair)
  - 3. An Ancient Insect Trapped in Amber
  - 4. Human Remains (e.g., 9/11 Victims)
  - 5. A Single Human Embryo Cell
  - 6. Contaminated Meat To Determine the Causal Organism
- 3. Used In:
  - 1. DNA Fingerprinting-Individual Identification-Genetic Disease Screening
  - 2. Forensics (Crime Scenes, Mass Graves, Criminal Suspects, Wrongfully Convicted)
  - 3. Paternity & Family Relationships (e.g., Immigration, Tracing Lost Children)
  - 4. Disease Diagnosis & Pathogen Identification (Humans, Animals, & Plants)
  - 5. Human Origins & Migrations
  - 6. Ancient Genome Sequences & Evolutionary Studies
  - 7. Specific mRNA Detection
  - 8. "Cloning" Specific DNA Sequences
  - 9. Tracing Plant & Animal Sources (e.g., Poaching Stolen Cattle, Cactus)
- 4. <u>Need as Little as One Molecule of DNA</u> & Can Replicate an ∞ Amount of Specific Sequences

**Revolutionized** How To Study & Manipulate DNA















Genetic Code of Life



Entire Genetic Code



**DNA** Fingerprinting



Cloning: Ethical Issues and Future Consequences





The 1000 Genomes Project Consortium\*

Nature, October 10, 2010

doi:10.1038/nature09534

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  $10^{-8}$  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 2500 individuals & From 26 Different Global Populations

- Found 84 Million Variants (SNPs) & <0.5% Unique to a Population!
- Evidence For Common Ancestry of All Humans
- 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)

















### DNA Testing Can Be Carried Out Before Child Birth During Pregnancy



#### RESEARCH ARTICLE New Non-Invasive DNA Tests Are Available Based on PCR

#### PRENATAL DIAGNOSIS





















Cloning: Ethical Issues and Future Consequences



#### Expression of Jellyfish Green Fluorescence Protein (GFP) in Pigs Shows That Genetic Code is Universal!!

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#### Implications For Genetic Engineering -"Yo - Its in The DNA!!"

Modular Organization of Sequences

- 1. <u>DNA Replication</u> Ori
- 2. <u>Transcription</u> Switch/Regulator Terminator
- 3. <u>Processing of RNA</u> (Eukaryotes) Splicing Sites
- 4. <u>Translation</u> Start
  - Start
  - Stop
  - Genetic Code/Codons
- 5. <u>Coding Sequence</u> Genetic Code

Modules → Anything You Want To Do Using Genetic Engineering!



