

HC70A & SAS70A Spring 2017 Genetic Engineering in Medicine, Agriculture, and Law

Professors Bob Goldberg & John Harada Lecture 5

The Nuts & Bolts of Genetic Engineering: From Mutations to Drug - The Factor XIII Story







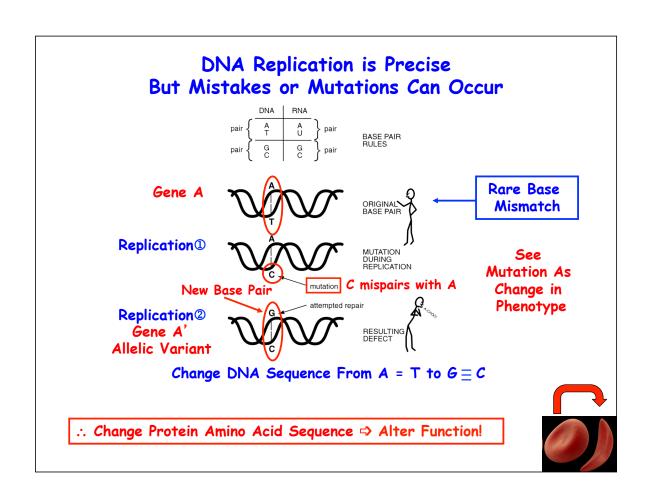
THEMES

- 1. What Causes Gene Mutations?
- 2. How Do Gene Mutations Lead to Genetic Variability?
- 3. How Can We Test For Gene Mutations at the DNA Level?
- 4. What is Hemophilia and How is it Inherited?
- 5. How Can a Disease Gene Be Found When It is Not Known Where the Gene is Expressed?
- 6. What Vectors Can Be Used For Cloning DNA?
- 7. What is the Advantage of Using a Virus Vector For Constructing Genome Libraries?
- 8. How To Make a Library of the Human Genome?
- 9. How Find a Gene With Only a Knowledge of the Protein Sequence?
- 10. How Use DNA Testing to Detect Factor VIII Disease Alleles?
- 11. How Isolate a Factor VIII cDNA Clone?
- 12. How Produce Factor VIII Protein For Use as a Drug?

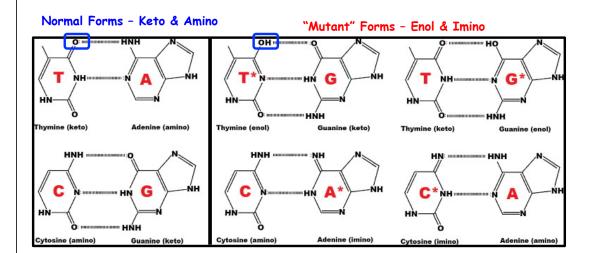


WHAT ARE THE PROPERTIES OF A GENE?

- 1. Replication
- 2. Stability (Mutations)
- 3. Universalitya) All Cellsb) All Organisms
- 4. Direct Cell Function/ Phenotype



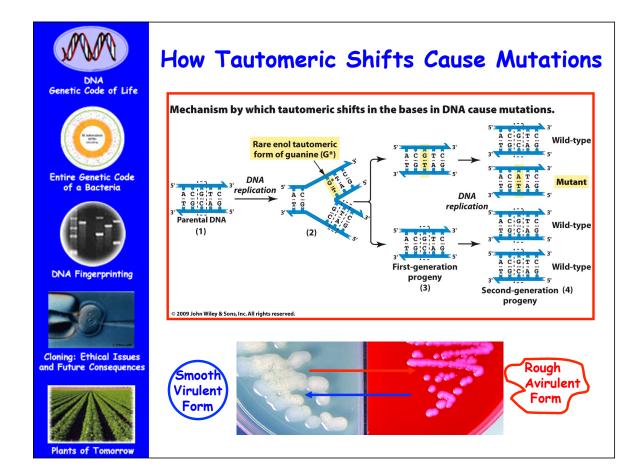
TAUTOMERS CHANGE BASE PAIRING RULES

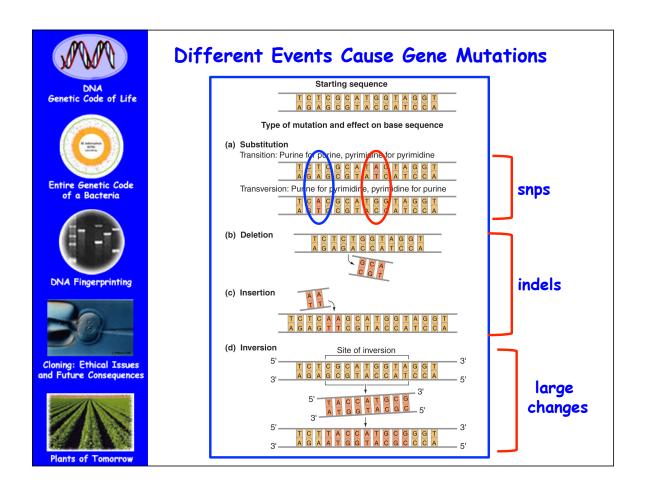


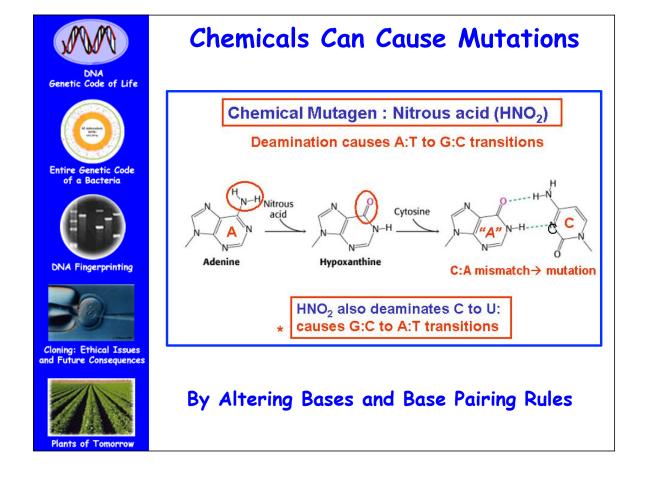


And Lead To Mistakes in DNA
Replication & Mutations > Genetic
Diversity
Chemistry Leads to Biology!!















doi:10.1038/nature09534

A map of human genome variation from population-scale sequencing

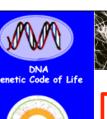
The 1000 Genomes Project Consortium*

Nature, October 10, 2010

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
- 10⁻⁸ bp Mutations Per Generation (30 per Genome)









DNA Fingerprinting





Plants of Tomorrow



From Gene To Drug



Due to Mutations in a Different Class of Blood Proteins

The Molecular Genetics of Hemophilia

(Potentially Lethal Disease)

Hemophiliacs bleed because a defective gene deprives them of a key blood-clotting protein. The protein has now been made artificially by isolating the normal gene and then inserting it into cultured cells

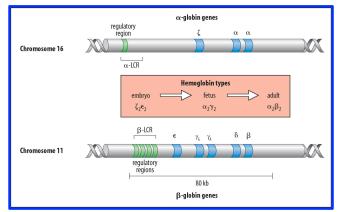
by Richard M. Lawn and Gordon A. Vehar

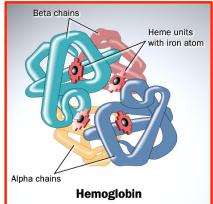
A Case Study of Cloning Genes and mRNAs

Reference: Scientific American, March 1, 1986 (Pick Up After Class)

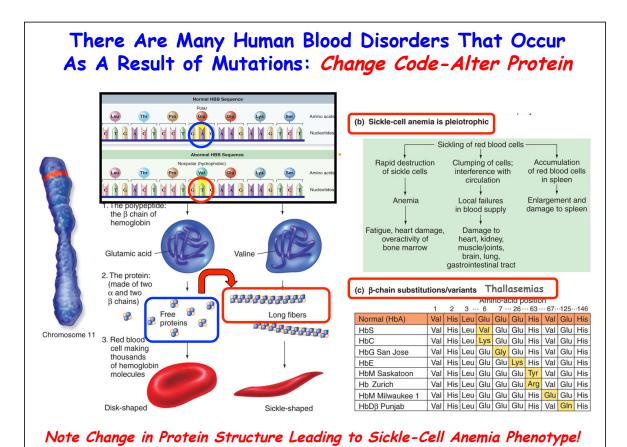


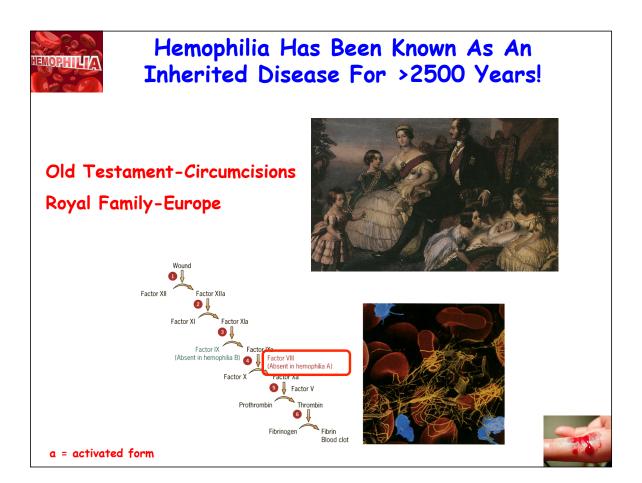
There Are Two Globin Gene Clusters in Human Chromosomes That Encode the Oxygen Carrier of Blood Cells - Hemoglobin

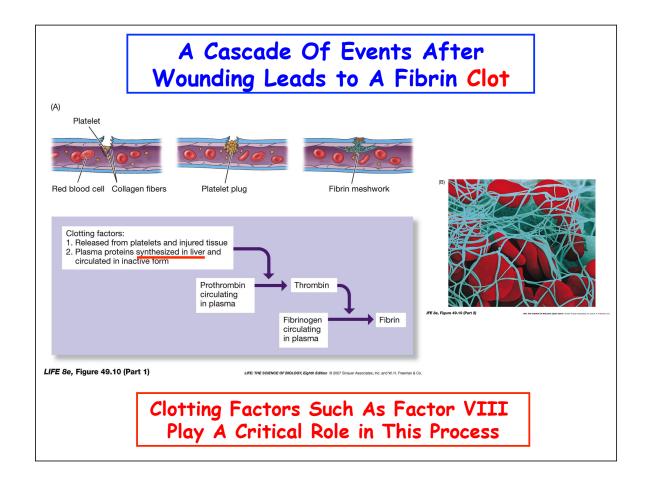




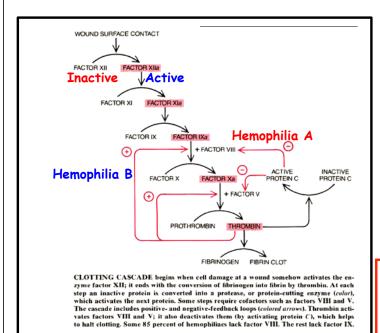
Max Perutz and John Kendrew - Nobel Prize in 1962 For Using X-Ray Diffraction to Determine the Structure of Hemoglobin







How Does Blood Clot After Wounding?



Eight Proteins/Genes Required:

- 1. Factor VII
- 2. Factor XI
- 3. Factor IX
- 4. Factor VIII
- 5. Factor X
- 6. Protein C
- 7. Prothrombin
- 8. Fibrinogen

What Happens If Any of These Proteins, or Genes, are Mutated?



No Blood Clot!



Blood Clotting Factors

Disorder	Pathophysiology/ deficiency	Inheritance
Haemophilia A	VIII	X linked recessive
Haemophilia B	IX	X linked recessive
Haemophilia C	XI	Autosomal dominant or recessive
VW disease	VW factor	Autosomal dominant or recessive
Factor X deficiency	Factor X	Autosomal recessive
Factor V deficiency	V	Autosomal recessive
Factor VII deficiency	VII	Autosomal recessive
Prothombin deficiency	II	Autosomal recessive
Afibrinogenemia/	1	Autosomal dominant
dysfibrinogenemia		
VW factor - Von Willebrand	I factor	

Factor	Other name	Incidence	Bleeding severity
Factor I	Fibrinogen	1 in 1,000,000	Usually mild, except with complete absence of fibrinoger
Factor II	Prothrombin	1 in 1,000,000	Usually mild
Factor V	Parahemophilia	1 in 1,000,000	Usually mild
Combined factor V and factor VIII		1 in 1,000,000	Usually mild
Factor VII	Alexander's	1 in 1,000,000	Severe when factor VII levels are low
Factor X	Stuart Prower	1 in 500,000	Moderate to severe when factor X levels are below 10 %
Factor XI	Hemophilia C	1 in 100,000	Mild to moderate when factor XI levels are below 15%
Factor XIII		1 in 3,000,000	Severe

Hemophiliacs Have Mutations in Factor VIII, Factor IX, or Factor XI Genes

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TABLE 13.2 Some Important Genetic Disorders									
Disorder		Symptom	Defect	Dominant/ Recessive	Frequency Among Human Births				
Cystic fibrosis		Mucus clogs lungs, liver, and pancreas	Failure of chloride ion transport mechanism	Recessive	1/2500 (Caucasians)				
Sickle cell anemia		Blood circulation is poor	Abnormal hemoglobin molecules	Recessive	1/600 (African Americans)				
Tay-Sachs disease		Central nervous system deteriorates in infancy	Defective enzyme (hexosaminidase A)	Recessive	1/3500 (Ashkenazi Jews)				
Phenylketonuria		Brain fails to develop in infancy	Defective enzyme (phenylalanine hydroxylase)	Recessive	1/12,000				
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				

18,000 People in US Have Hemophilia & 400 Babies/Year Are Born With Disorder Prior to 1960s – Average Life Span Was 11 Years

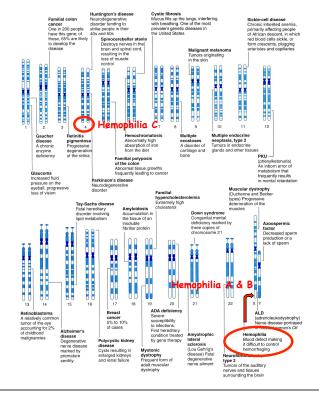
Hemophilia ADefective Factor VIII Gene1/10,000 males80%Hemophilia BDefective Factor IX Gene1/30,000 males20%Hemophilia CDefective Factor XI GeneAutosomal<1%</td>

Hypothesis For High Frequency in Males?

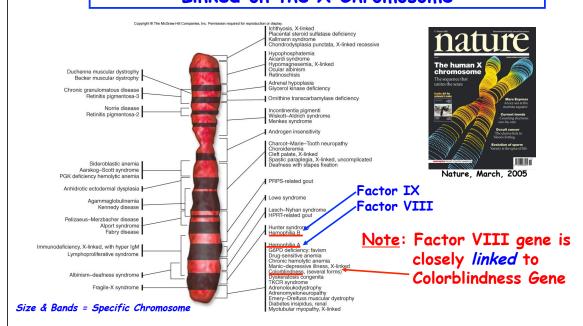
Both Factor VIII & IX Genes on X-Chromosome $(9 \rightarrow 3)$ s)



Human Disease Genes Have Been Mapped To Specific Chromosomal Locations



Factor VIII and Factor IX Genes are Closely Linked on the X Chromosome



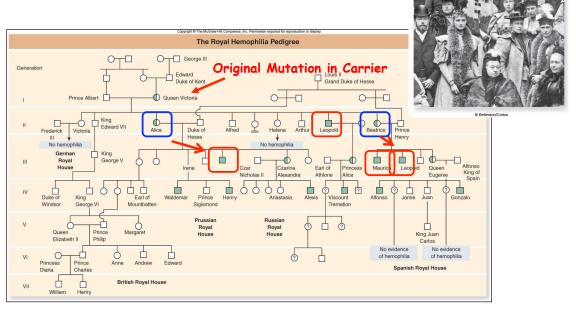
The X chromosome has ~1098 Genes and 150,000,000 bp (150 Mb). 168 Mendelian Diseases Explained by 113 X-Linked Genes



Pedigrees Can Be Used To Determine If a Trait is Dominant or Recessive

Each Type of Inheritance Predicts Specific Results in Each Generation

Hemophilia A and B Genes Are Sex Linked & Recessive Traits When Mutated



- Note: 1. Males Obtain Detective Gene From Mothers
 - 2. 50% of Sons Of A Maternal Carrier Have The Defective Gene

Hemophilia A and B Sex-Linked Inheritance

Carrier Female

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2
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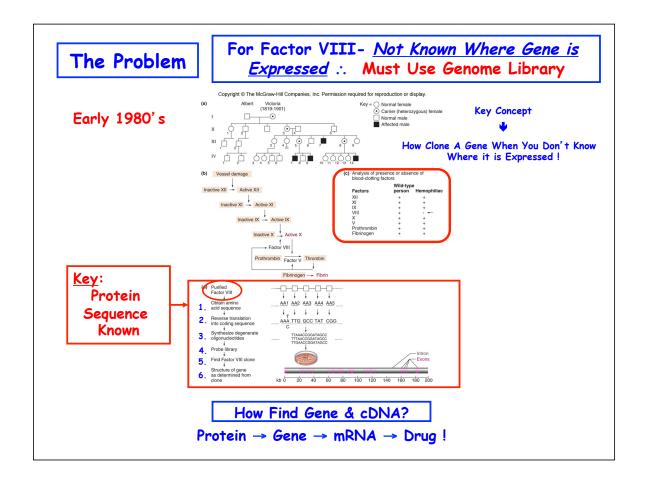
Egg	X	X
Sperm		
X	XX	XX
	♀ <i>Carrier</i>	♀ Healthy
Υ	XY	XY
		♂ Healthy

Sex-Linked Inheritance

 \circ Carriers \rightarrow 1/2 Sons Afflicted + No Daughters! Only One X-Chromosome is in σ

What Was Known About Factor VIII Before Gene Cloned?

- 1. Blood Protein (But Perhaps Synthesized Elsewhere!)
- 2. Could be purified in small amounts from >20 Liters of human blood + cow blood + pig blood
- 3. Short Stretch of <u>Protein</u> Sequenced = Known Protein Sequence!
- 4. Hemophilia A could be treated by <u>blood transfusions</u> from normal individuals, ∴ clotting factor <u>in blood</u>
- 5. 1980s AIDS Epidemic Caused Many Hemophiliacs to Get HIV/AIDS (~50% of hemophiliacs got AIDS in 1985)



Knowledge of the Protein Sequence and the Genetic Code Makes it Possible to Identify a Gene **Cloned gene** DNA sequencing Database search to identify protein-coding sequence **Expression in cultured** PCR isolation of corresponding cells Protein Localization **Biochemical studies** Determination of structure Figure 5-1 Molecular Cell Biology, Sixth Edition © 2008 W. H. Freeman and Company Factor VIII Strategy (1985) 1. Protein \rightarrow Gene \rightarrow Drug 2. |Gene → Protein Using Sequencing GenBank

Steps Required to Clone Factor VIII Gene and cDNA

Just Sequence Everything + Identify Protein-

GenBank Huge

and Genetic Code

Gene

Genomics

2016

- 1. Make Genome Library Because Factor VIII Gene in Genome!
- 2.Purify Protein from Blood- that's where it works (wasn't known where made)
- Reverse Translate using the genetic code a portion of the protein sequence
- 4. Synthesize a DNA probe complementary to Factor VIII gene corresponding to protein sequence
- 5. Screen Genome Library Entire Gene on The Clone?

GENOMIC CLONING

TOTAL

TOTAL

THINAS

TOTAL

THINAS

THANSERIA

T

cDNA

- 1.Use Gene probe to screen cDNA library for Factor VIII cDNA clone
- 2. How know what mRNA to use to make cDNA library?
- 3.Use gene probe to probe RNA blots containing mRNA from all major organs (liver, kidney, blood, etc.)
- 4.Find Factor VIII
 mRNA in livermale, liver- secrete
 into blood
 Why Need cDNA?
 Story continued

Want cDNA to Manufacture Factor VIII as a Drug to Treat Hemophilia A!

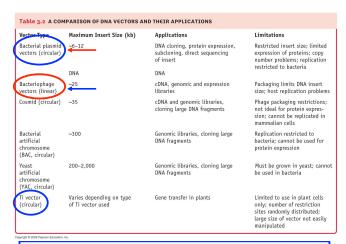
Step One

How to Construct a Human Genome Library to Find the Factor VIII Gene?

If It is Not Known Where Gene is Active Can "Look" to Genome Instead of mRNA to Find + Clone Gene!

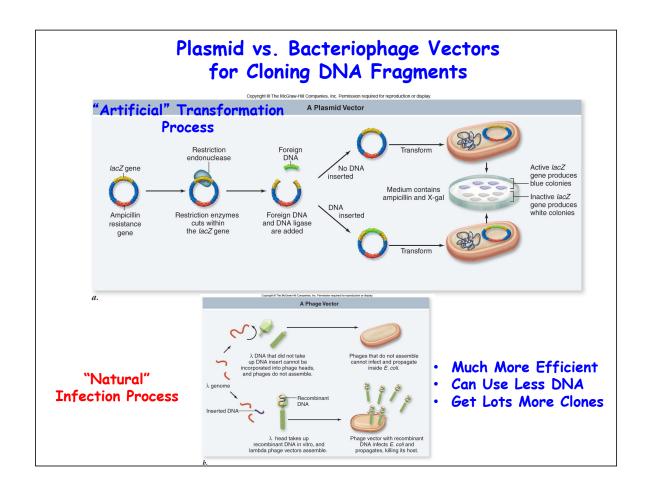


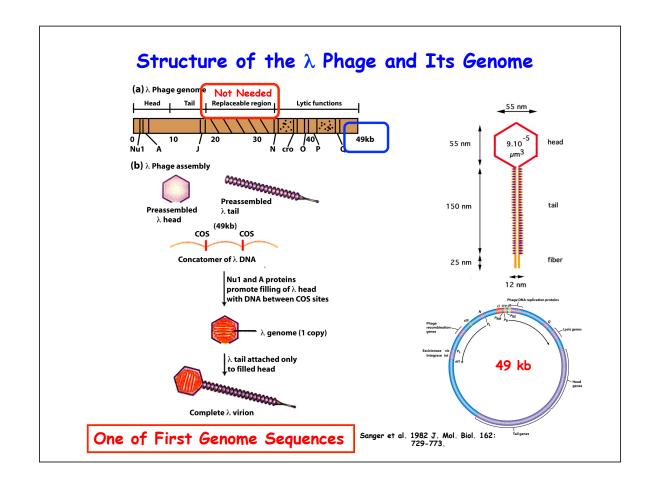
Vectors Used in Genetic Engineering Have Similar Conceptual Properties But are Used in Different Situations

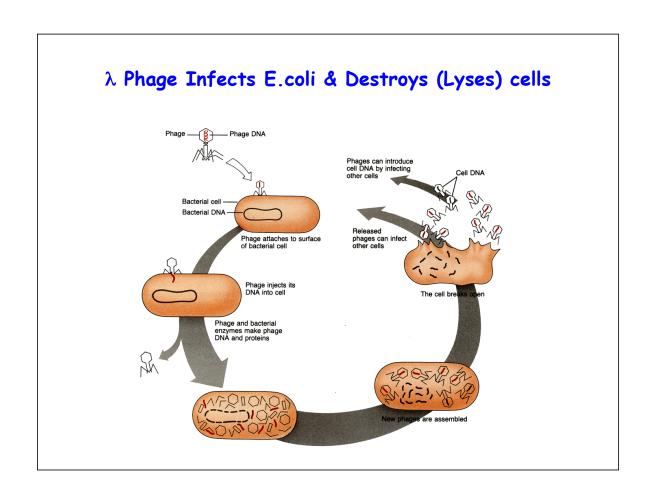


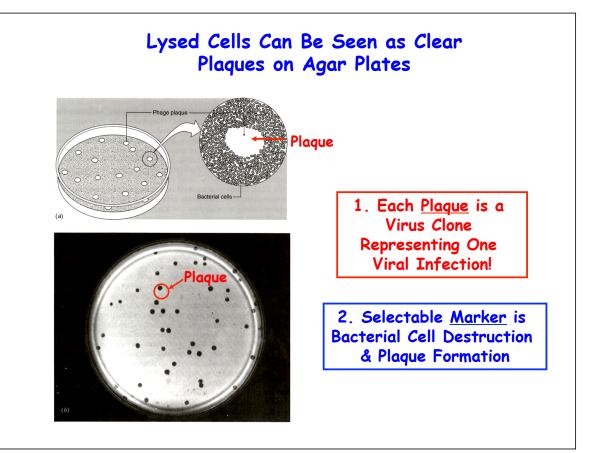
Plasmids vs. Bacteriophage Vectors

- 2. Selectable
- 3. Can be used to insert foreign genes/restriction sites
- 4. Easily isolated + transferred back to cells

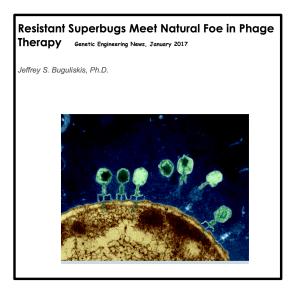


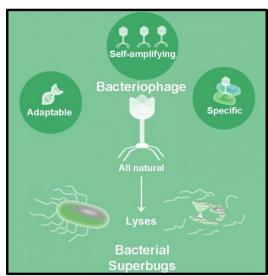






Using Phage as "Drugs" to Treat Antibiotic Resistant Bacteria That Cause Sepsis





Each year in the United States, at least 2 million people become infected with bacteria that are resistant to antibiotics and at least 23,000 people die each year as a direct result of these infections. Many more people die from other conditions that were complicated by an antibiotic-resistant infection.

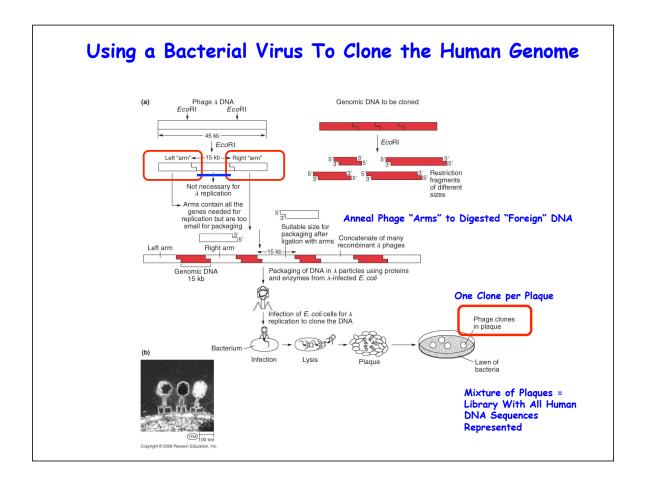
Advantages of λ Virus as a Vector for Cloning DNA

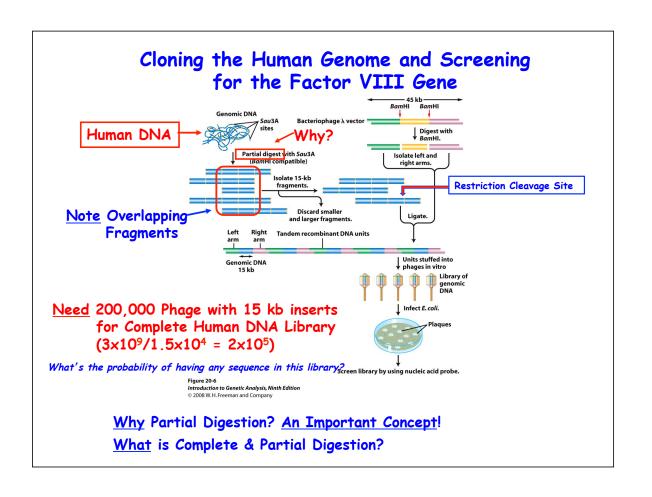
- 1. Long DNA Segments can be Cloned (~20kb) Need fewer clones for whole Genome!
- 2. Can clone DNA Segments in Viral Genome & Self-Assemble with viral proteins into virus in a test tube!
- .. Make Recombinant Viruses in the Lab!
- 3. <u>Use "Natural" Infection</u> process to Generate Large Number of Clones for a Eukaryotic Genome Library.

Much higher efficiency for getting recombinant DNA

→bacterial cells compared with DNA transformation.

.. set more clones per amount of recombinant DNA!



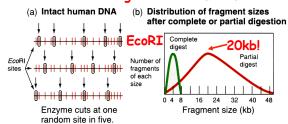


What is the Purpose of Partial Digestion of Human DNA?

Sau 3A= 4bp= ${}^{5'}GATC^{3'}$.: 1 site every 280bp if digest to completion = 1×10^7 DNA fragments

Eco RI= 6bp= ${}^{5'}GAATTC^{3'}$.: 1 site every 3100 bp if digest to completion (cleaves every site) = $\underline{972,000}$ DNA fragments

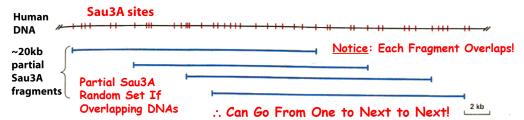
- 1. Complete Digestion Produces fragments that are too small to clone in λ virus (need 20Kb)
- 2. Complete Digestion would create huge genome libraries with large # clones to screen
- 3. Complete Digestion would break up genes of different DNA fragments-particularly if <u>human genes big</u>- ∴ would have one gene on many different clones- parts separated!
- 4. Complete Digestion provides no way to find <u>neighbors</u> of clones in genome- what's next to gene in chromosome!



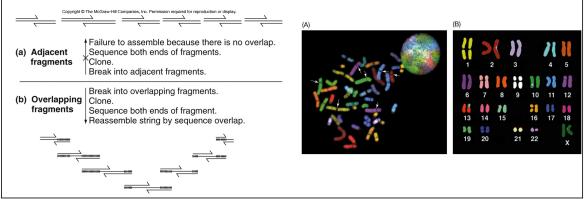
Principle of Genome Sequencing Too!!

Partial Digestion Produces A series of Large, Overlapping DNA Fragments/ Clones Can connect one clone with another!! Build up clones of each chromosome!!

Constructing a Human Genome Library by Partial Digestion Creates a Set of Overlapping DNA Fragments/ Clones



.. An overlapping set for each of the 24 chromosomes would allow clones to be ordered from beginning to end by restriction mapping because each chromosome contains one DNA molecule!



Step Two

How Find the Factor VIII Gene in a Human Genome Library?

The Genetic Code

Second Letter

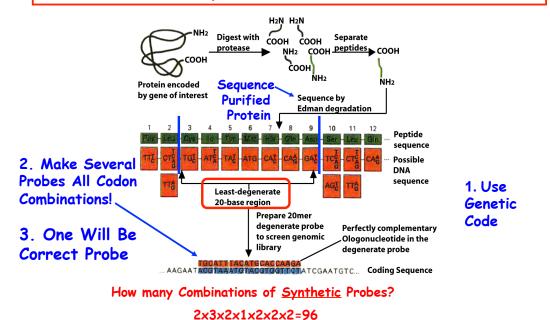
		ι	J	(3		A	9	•		_
	0	UUU UUC UUA UUG	Phe Leu	UCU UCC UCA UCG	Ser	UAU UAC UAA UAG	Stop Stop	UGU UGC UGA UGG	Cys Stop Trp	⊃∪∢G	
1st	O	CUU CUC CUA CUG	Leu	CCU CCC CCA CCG	Pro	CAU CAC CAA CAG	His Gln	CGU CGC CGA CGG	Arg	∪ C ⊄ G	3rd
letter	A	AUU AUC AUA AUG	lle Start Met	ACU ACC ACA ACG	Thr	AAU AAC AAA AAG	Asn Lys	AGU AGC AGA AGG	Ser Arg	UCAG	letter
	G	GUU GUC GUA GUG	Val	GCU GCC GCA GCG	Ala	GAU GAC GAA GAG	Asp Glu	GGU GGC GGA GGG	Gly	UCAG	

Properties

- Universal
- Three Nucleotides
 - Punctuation
 - Degenerate

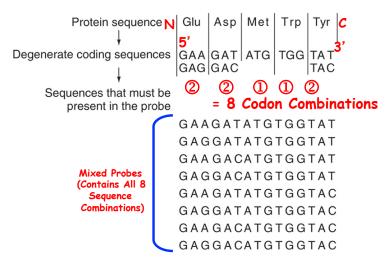
Factor VIII Protein → Gene

Using the Factor VIII Protein Sequence and Genetic Code as a Guide to Synthesize a Factor VIII Probe

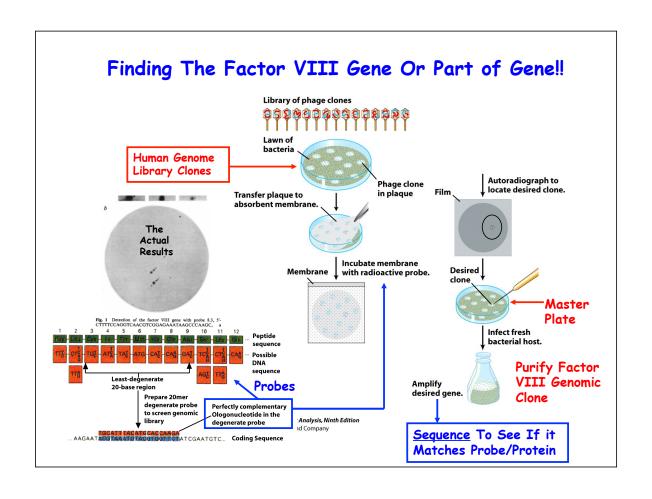


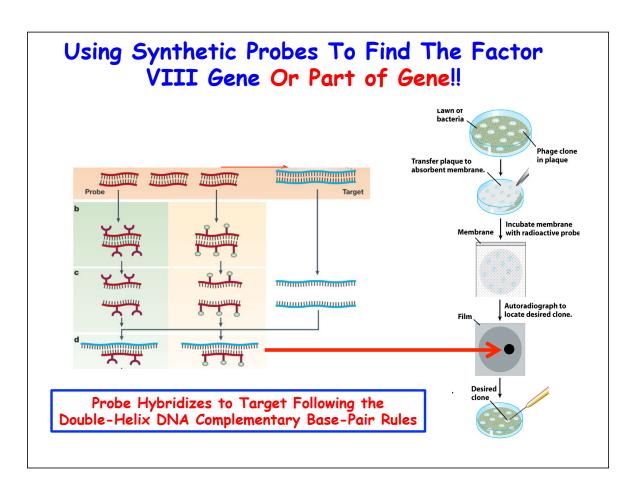
Using the Genetic Code to go From Protein Sequence to Gene Sequence

(b) Synthesizing DNA probes based on reverse translation

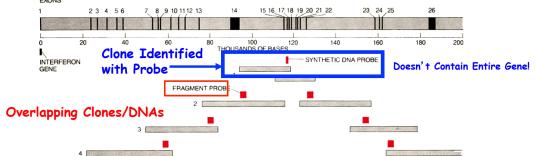


- 1. Need Amino Acid Sequence of Part of the Protein
- 2. Need DNA Sequences Representing all Codon Combinations
- 3. <u>Synthesize</u> DNA Sequence Probes!





The Result-The Factor VIII Gene is Huge- 186,000 bp- The Probe Identified a Clone Containing Only One Part of Gene !!! Why?

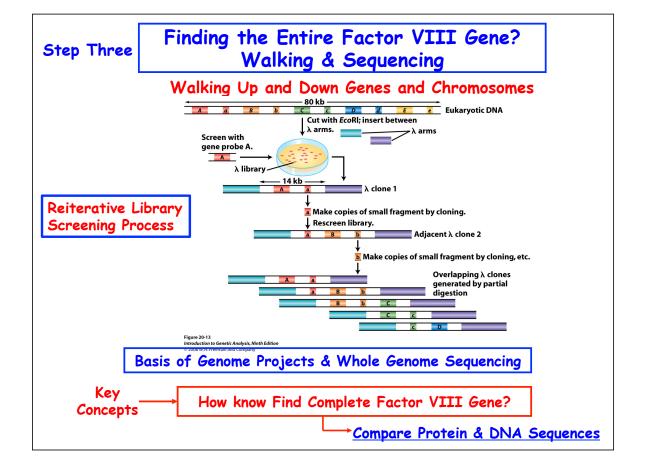


How Find Clones with Rest of Gene?

Key Question!

Remember - the library contains overlapping DNA clones ... can use one part of first clone to re-screen library & "walk" to other gene regions - using restriction maps & sequencing (compare with protein sequence) as guides!

Sequence ----> GenBank



The Factor VIII Gene Was Found To Be Very Large

- 186,000 Nucleotides in Length (Won't Fit in One Phage Clone)
- 25 Introns
- 9,000 Nucleotide Coding Sequence (cDNA)
- · 2,351 Amino Acids in Protein

X Chromosome Factor VIII Gene

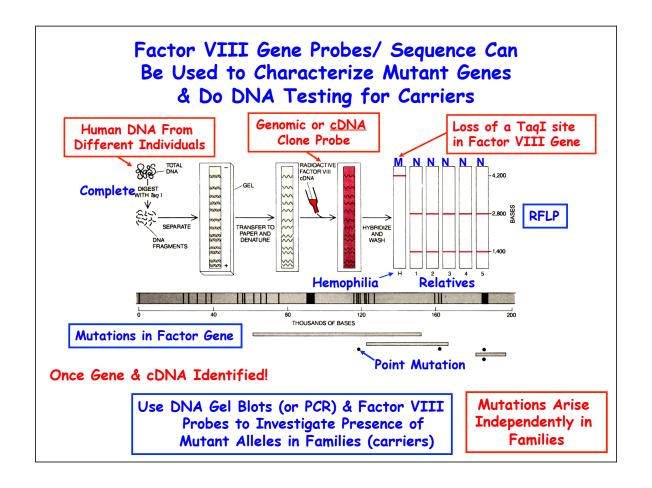
Using NCBI to Search For Gene Information S NCBI Entrez, The Life Sciences Search Engine PubMed Entrez Human Genome GenBank Map Viewer BLAST Search across databases eat-4 elegans GO CLEAR Help 10 PubMed: biomedical literature ? none Books: online books 2 citations and abstracts PubMed Central: free, full text OMIM: online Mendelian ? iournal articles Inheritance in Man Site Search: NCBI web and FTP ? none W Nucleotide: sequence UniGene: gene-oriented clusters ? ? database (GenBank) of transcript sequences CDD: conserved protein domain 3 Protein: sequence database ? datahase Genome: whole genome 3D Domains: domains from ? ? none sequences Entrez Structure Structure: three-dimensional UniSTS: markers and mapping ? 2085 ? none (macromolecular structures PopSet: population study data Taxonomy: organisms in ? ? none none GenBank

Factor VIII Mutations Occur Throughout the Gene

[Haemophilia 11, 481-491 (2005)]

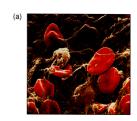
VIII:C (%)	Family history	Consanguinity*	Inversion	Codon†	Mutation	Amino acid change	Exon	Conservation‡
	Sporadic	NC	Normal	51	TTT → TCT§	Phe → Ser	2	FFFF, identical
.20	Sporadic	NC	Normal	80	$GTT \rightarrow GAT$	Val → Asp	3	VVVV, identical
1	Sporadic	NC	Normal	102	GGT → GTT§	Gly → Val	3	GGGG, identical
2	Sporadic	NC	Normal	104	TCC → CCC§	Ser → Pro	3	SSSS, identical
5	Sporadic	NC	Normal	143	GAG → AAG§	Glu → Lys	4	EEEE, identical
1	Sporadic	NC	Normal	233	delCA§	Thr \rightarrow fs (TGA-264)	6	
2.70	Inherited	NC	Normal	321	$GAA \rightarrow AAA$	Glu → Lys	8	EEEE, identical
)	Sporadic	NC	Normal	372	$CGC \rightarrow CAC$	Arg → His	8	RRRR, identical
Į.	Inherited	NC	Normal	527	$CGG \rightarrow TGG$	Arg → Trp	11	RRRR, identical
1	Sporadic	NC	Normal	528	TGC → TAC§	Cys → Tyr	11	CCCC, identical
1	Inherited	NC	Normal	592	$CAA \rightarrow TAA$	Gln → Stop	12	QQQQ, identical
1	Inherited	NC	Normal	864	delGACA	Gly → fs [TAA-867]	14	
					insCAATTAAATGAGAA§			
l.	Sporadic	NC	Normal	948	insA§	Lys → fs (TGA-984)	14	
l	Sporadic	NC	Intron 1	1107	AGG → TGG§	Arg → Trp	14	RGKK, dissimilar
	Sporadic	NC	Normal	1107	AGG → TGG§	Arg → Trp	14	RGKK, dissimilar
l.	Inherited	NC	Normal	1191-1194	delA	Ile → fs (TAG-1198)	14	
.40	Sporadic	NC	Normal	1191-1194	insA	lle → fs (TAA-1220)	14	
1	Sporadic	C	Normal	1227	delC§	Leu → fs (TGA-1231)	14	
2.10	Sporadic	NC	Normal	1241	$GAC \rightarrow GAG$	Asp → Glu	14	DGGE, similar
1	Sporadic	NC	Normal	1392	1392del1418§	Pro → fs (TAG-1446)	14	
1	Incrited	C	Normal	1392	1392del1418§	Pro → fs (TAG-1446)	14	
	Sporadic	NC	Normal	1441	insA§		14	
1	Incrited	C	Normal	1441	insAS			
1	Inherited	NC	Normal	1502	CAG → TAG§	Gln → Stop	14	QREQ, dissimilar
1	Inherited	NC	Normal	1504	delGT§	Val → fs (TGA-1517)	14	
1	Sporadic	NC	Normal	1535	$TGG \rightarrow TGA$	Trp → Stop	14	WLWM, dissimilar
hibitor 96 BU								
1	Sporadic	NC	Normal	1571	TAT → TAAS	Tyr → Stop	14	Y-YY, dissimilar
1	Sporadic	NC	Normal	1.581	AAA → TAAS	Lys → Stop	14	KEKK, dissimilar
1.20	Sporadic	NC	Normal	1696	$CGA \rightarrow GGA$	Arg → Gly	14	RRRR, identical
1.80	Sporadic	NC	Normal	1729	delAS	Gln → fs (TAA-1752)	1.5	
L	Inherited	NC	Normal	1751	GAA → AAAS	Glu → Lvs	15	EEEE, identical
1	Sporadic	NC	Normal	1775	TTC → TCC§	Phe → Pro	16	FFFF, identical
1	Sporadic	NC	Normal	1835	TGG → TGAS	Trp → Stop	16	WWWW, identical
7.60	Sporadic	C	Normal	1882	ATC → ATAS	lle → Ile	17	IIII, identical
3	Inherited	C	Normal	1966	CGA → CAA	Arg → Glu	18	RRRR, identical
1	Sporadic	NC	Normal	1966	CGA → TGA	Arg → Stop	18	RRRR, identical

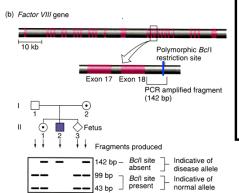
Need To Screen Across the Gene for Markers -- Family Specific



Using PCR and RFLPs (Markers) to Detect the Hemophilia A Disease Allele/Gene

- 1. Use PCR to amplify a specific Factor VIII gene region
- 2. Use restriction enzyme
 (BcL I) to distinguish
 between normal allele
 (1 site) & disease allele
 (no site)
 - = = Normal allele
 - = Disease allele

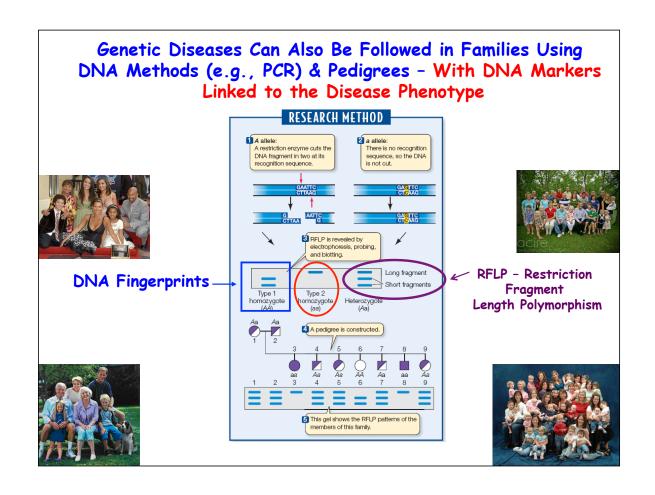


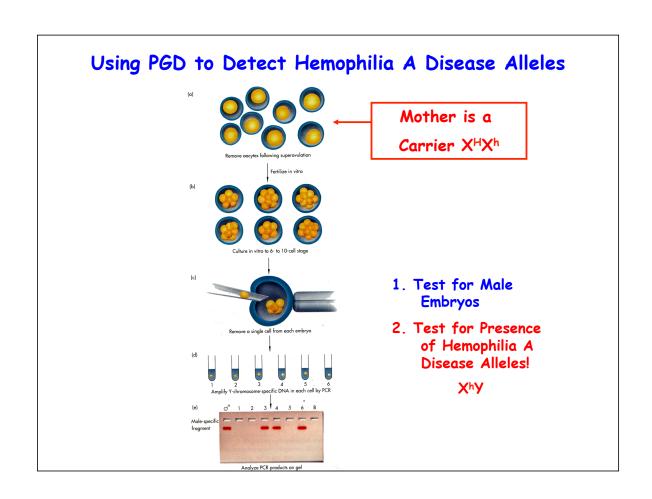


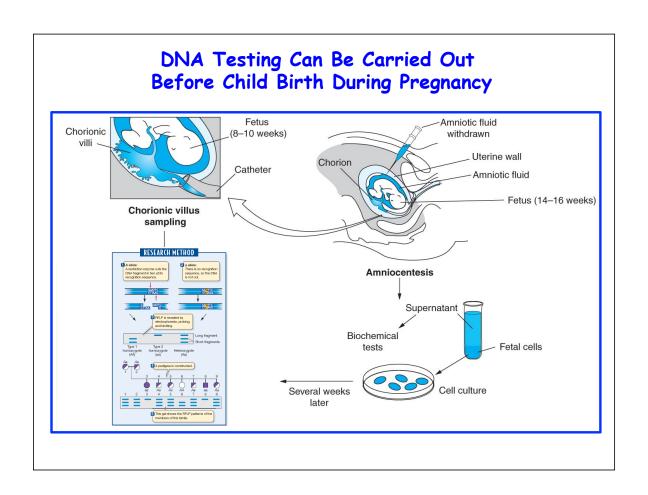
The 21st
Century
Approach!

- 1. Sequence the Entire Gene & Find Mutation
 - 2. Then
 Synthesize
 Primers to
 Test Family
 Members
 Using PCR

Only Can Do This With a Knowledge of DNA Sequence of Wild-type (Normal) and Disease Genes (Can Vary family to Family)







PRENATAL DIAGNOSIS

Maternal Plasma DNA Sequencing Reveals the Genome-Wide Genetic and Mutational Profile

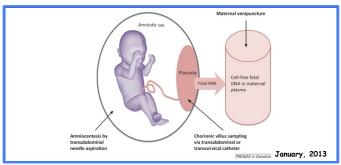
of the Fetus Science Translational Medicine, December 8, 2010 (61,1-12)

Sequencing DNA From the Blood of a Pregnant Woman Allows the Complete Genome Of the Fetus to Be Decoded!

A New Era in DNA Testing!!



~10% of DNA in Maternal Plasma is From the Fetus



DNA Tests Can Now Be Used To Detects Hundreds of Genetic Disease Alleles

TABLE 11.1 GENETIC DISEASE TESTING	
Genetic Disease Condition	Genetic Basis for Disease and Symptoms
Cancers (brain tumors; urinary bladder, prostate, ovarian, breast, brain, lung, and colorectal cancers)	A variety of different mutant genes can serve as markers for genetic testing. $% \begin{center} \end{center} \begin{center} \$
Cystic fibrosis	Large number of mutations in the cystic fibrosis transmembrane conductance regulator (CFTR) gene on chromosome 7. Causes lung infections and problems with pancreatic, digestive, and pulmonary functions.
Duchenne muscular dystrophy	Defective gene (dystrophin) on the \boldsymbol{X} chromosome causes muscle weakness and muscle degeneration.
Familial hypercholesterolemia	Mutant gene on chromosome 19 causes extremely high levels of blood cholesterol.
Hemophilia	Defective gene on the X chromosome makes it difficult for blood to clot when there is bleeding.
Huntington disease	$\label{lem:mutation} \mbox{Mutation in gene on chromosome 4 causes neurodegenerative disease in adults.}$
Phenylketonuria (PKU)	Mutation in gene required for converting the amino acid phenylalanine into the amino acid tyrosine. Causes severe neurological damage, including mental retardation.
Severe combined immunodeficiency (SCID)	Immune system disorder caused by mutation of the adenosine deaminase gene. $% \label{eq:controller}$
Sickle cell disease	Mutation in ß-globin gene on chromosome 11 affects hemoglobin structure and shape of red blood cells, which disrupts oxygen transport in blood and causes joint pain.
Tay-Sachs disease	Rare mutation of a gene on chromosome 5 causes certain types of lipids to accumulate in the brain. Causes paralysis, blindness, retardation, and respiratory infections.



Genetic Screening Issues

·Why Screen For Genes?

·When is a Test Accurate Enough?

·Mandatory or Voluntary Screening?

·Who Should Be Tested?

·Employer & Insurance Company Testing?

•Protection From Genotype Discrimination?

·Testing for Genetic Diseases With No Cures?

·How Ensure Privacy & Confidentiality?

Obligations to Inform Others (Spouse/Sibling) of Genetic Disorder Knowledge?

·Genetic Databases??

·Patents on Tests?

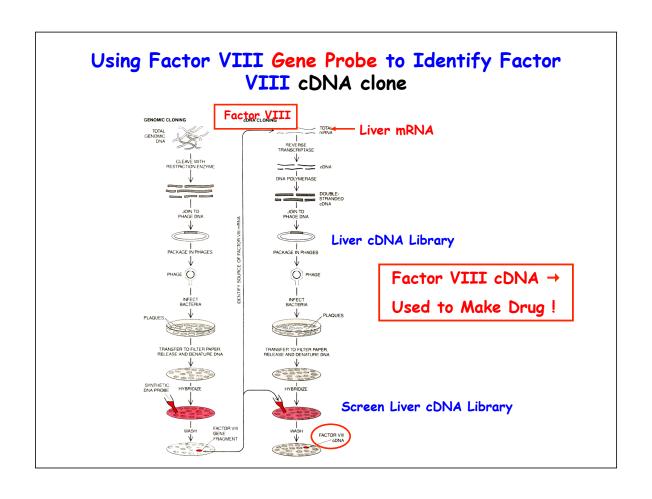


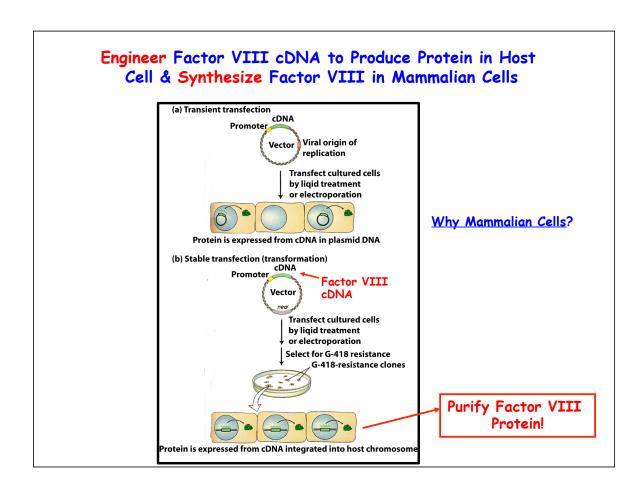
Step Four

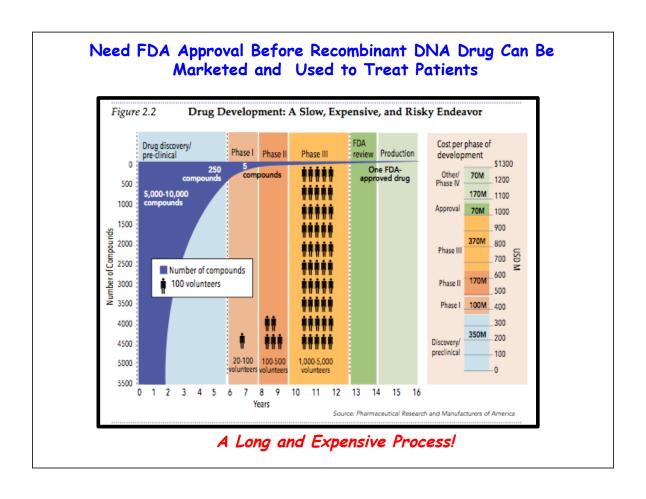
How Find Factor VIII mRNA to Generate a cDNA for Protein Production in Host Cells?

Recall: Eukaryotic Genes Provide
Obstacles for Efficient Protein
Production in Genetically
Engineered Cells! Reasons???

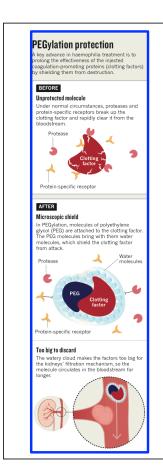
Making the Drug Need cDNA Not Gene Factor VIII Gene Can Be Used to Find Out Where It is Active Using RNA Blots Copyright © The McGraw-Hill Companies, Inc. Permission required for reproduction or display. ssue 1 Tissue 2 Tissue 3 Tissue 4 4. Wash away unhybridized probe. Make a Tissue 4 (blood) Tissue 2 (testes) Onet defit The Figure Purify RNA RNA Blot Is Like a DNA kb Blot Except That RNA is on Gel & Blotted Testes RNA Lung RNA Load RNA samples in wells of a gel. Separate RNA samples by gel electrophoresis. Blot onto filter. Expose filter to labeled hybridization probe Factor VIII Gene Is Highly Active in Liver! Could Also Use PCR (RT-PCR) (4): Reprinted with permission from Nature 1990 Jul 19; 346(6281):216-7, Sinclair et al. © 1990 Macmillian Magazines Limited











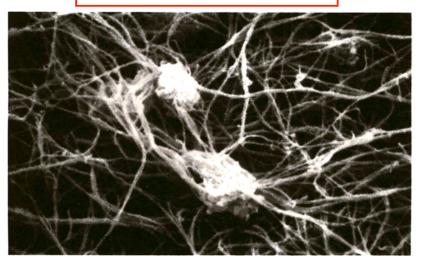
New Longer Lasting Factor VIII and Factor IX Drugs

Ten years from gene → drug! (Off Patent in 2011)

DRUGS TO HELP THE BLOOD A number of treatments to aid blood clotting are in clinical trials or have been approved this year.									
	Product	Approach	Company	Half-life (hours)	Status				
Factor VIII infusions (for	Eloctate	Fc fusion protein	Biogen Idec	20	FDA approved in June 2014				
haemophilia A) Conventional	BAX 855	PEGylation	Baxter International	19	Submission for approval planned for late 2014				
infusion half- life: 8-12 hours	BAY94- 9027	PEGylation	Bayer	19	Submission for approval planned for mid-2015				
	N8-GP	PEGylation	Novo Nordisk	19	Submission for approval planned for 2018				
Factor IX infusions (for	rIX-FP	Albumin fusion	CSL Behring	92	In clinical trials				
haemophilia B) Conventional	N9-GP	PEGylation	Novo Nordisk	110	Submission for approval planned for 2015				
infusion half- life: 18–24 hours	Alprolix	Fc fusion protein	Biogen Idec	87	FDA approved in March 2014				
FDA, US Food and D	rug Administ	ration.							

Using Factor VIII to Treat Hemophilia

Formation of a Blood Clot



ribbles 3 from 3 from 3 from the bulk of the clot. The electron zymatic reactions culminating in the conversion of fibrinogen, a solmic reaction, which was made by Jon C. Lewis of Wake Forest University, shows a clot formed in a suspension of platelets and fibrin. protein in the blood-clotting cascade is either missing or defective.

A Triumph of Genetic Engineering

The Future: Gene Therapy - A Permanent "Cure"

December 10, 2011

Treatment for Blood Disease Is Gene Therapy Landmark

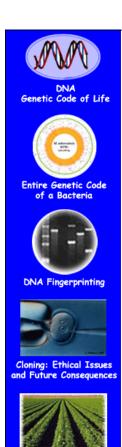
By NICHOLAS WADE



Gene Therapy Shows Promise for Treating Hemophilia

The First Ever In-Human Gene **Editing Will Try and Combat** Factor IX - Hemoglobin B Hemophilia

FDA-Approved Clinical Trial



Plants of Tomorrow

The Factor VIII Story -- A Summary

- 1. Purify Small Amounts of Factor VIII
- 2. Obtain Partial or Complete Amino Acid Sequence
- 3. Use the Genetic Code to Synthesize Degenerate DNA Probes
- 4. Isolate Factor VIII DNA Clones Complementary to Probe in Genome Library
- Determine if Factor VIII Clones Contain the Complete Gene By Sequencing and Comparing With Protein Sequence
- 6. If Not, "Walk" to Obtain Overlapping DNA Clones That Collectively Contain the Factor VIII Gene
- 7. Sequence Clones To Determine Where the Factor VIII Gene Starts and Stops
- 8. Use Factor VIII Genome Probe to Find Out What Body Organ/Tissue Expresses the Factor VIII Gene
- 9. Make a cDNA Library From the Target Organ/Tissue and Isolate a Factor VIII cDNA Clone
- Sequence the Factor VIII cDNA Clone and Compare With Factor VIII Gene Sequence to Map its Anatomy (I.e., introns, exons, swtiches) and Ensure That it Contains the Complete Protein Coding Sequence
- 11. Use Factor VIII cDNA and/or Genome Fragments as a Probe to Find RFLP Markers For Disease Alleles -- Or Sequence Disease Alleles to Find Relevant RFLP Markers By Comparison With Wild-Type Sequence
- 12. Insert Factor VIII cDNA Into an Expression Vector and Synthesize Factor VIII Protein in Host Cells (e.g., Mammalian Cells)