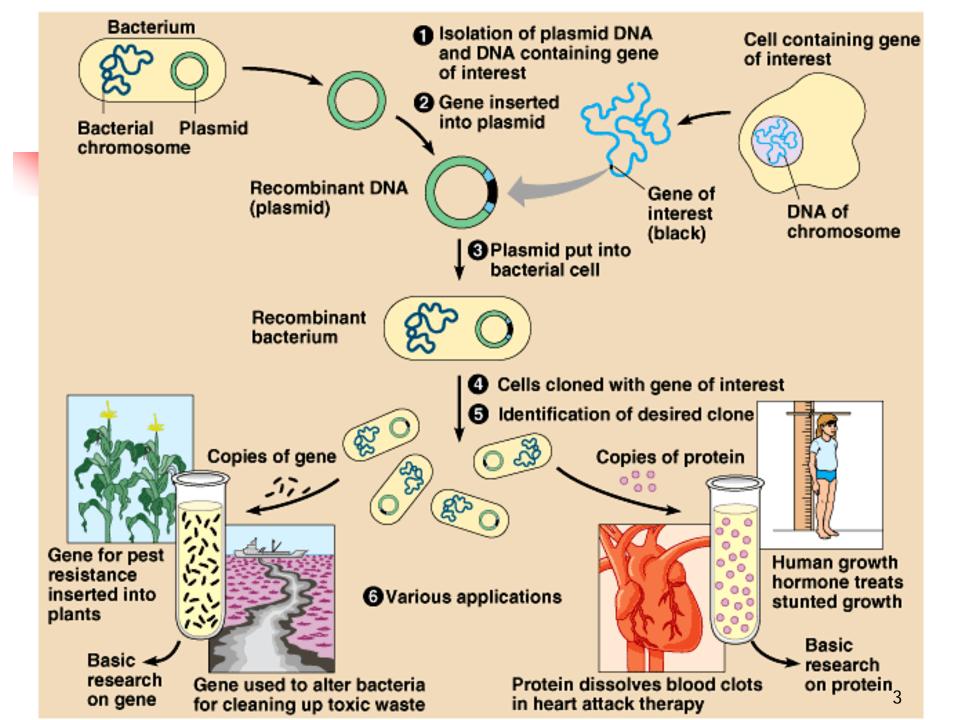
第七章 基因工程 Gene Engineering



General process of gene engineering



第一节 重组DNA分子的构建

Construction of recombinant DNA molecules

I. Fragmenting Complex Genomes into Bite-Size Pieces for Analysis

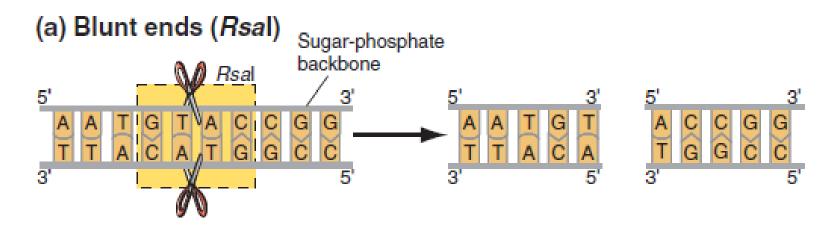
Restriction Enzymes Fragment the Genome at Specific Sites

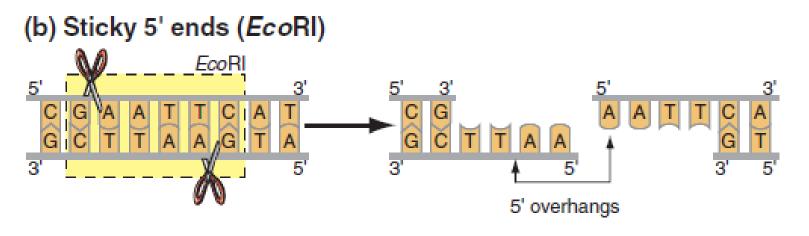
Restriction Enzymes

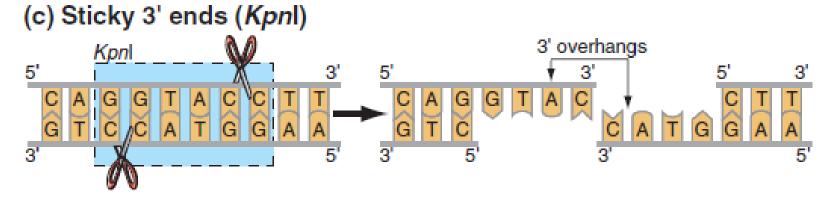
An endonuclease (核酸内切酶) that recognizes specific nucleotide sequences in DNA and breaks the DNA chain at that sites

Specific nucleotide sequences
Palindrome
回文结构

Enzyme	Sequence of Recognition Site	Microbial Origin		
Taql	5' TCGA 3' 3' AGCT 5'	Thermus aquaticus YTI		
Rsal	⁵ GTAC ³ 3 CATG 5	Rhodopseudomonas sphaeroides		
Sau3Al	⁵ GATC ³ 3 CTAG ₅	Staphylococcus aureus 3A		
<i>Eco</i> RI	^{5'} GAATTC ^{3'} 3' CTTAAG 5'	Escherichia coli		
<i>Bam</i> HI	^{5'} GGATCC ^{3'} 3 CCTAGG _{5'}	Bacillus amyloliquefaciens H.		
<i>Hin</i> dIII	^{5'} AAGCTT ^{3'} 3' TTCGAA _{5'}	Haemophilus influenzae		
Kpnl	^{5'} ggtacc ^{3'} _{3'} ccatgg 5'	Klebsiella pneumoniae OK8		
Clal	5' A T Ç G A T ^{3'} 3' T A G C T A 5'	Caryophanon latum		
BssHll	^{5'} GCGCGC ^{3'} 3' CGCGCG 5'	Bacillus stearothermophilus		
Notl	⁵ 6 6 6 6 6 6 6 5' 3 6 6 6 6 6 6 6 5'	Nocardia otitidiscaviarum 6		
		_		



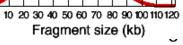




The Size of the Recognition Site Is the Primary **Determinant of Fragment Length**

(a) Calculating Average Restriction Fragment Size 1. Probability that a four-base recognition site will be found in a genome =(b) Intact Human DNA Distribution of fragment sizes after digestion $1/4 \times 1/4 \times 1/4 \times 1/4 = 1/256$ Four-base 0.256kb = 256 bp 2. Probability that a six-base recognition site will be found = $1/4 \times 1/4 \times 1/4 \times 1/4 \times 1/4 \times 1/4 = 1/4096$ Number of fragments of each size 1 kb Rsal sites 0.05 0.1 0.2 0.3 0.4 0.5 Fragment size (kb) Six-base 4.096 kb Number of fragments of each size EcoRI sites 1 2 3 4 5 6 7 8 9 10 11 12 Fragment size (kb) Eight-base 64 kb Number of fragments of each size Notl sites

Different Restriction Enzymes Produce Different Lengths of Fragments

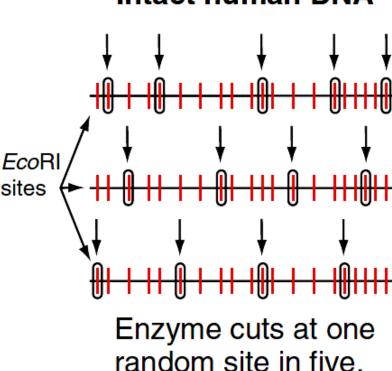


0.6

The Timing of Exposure to a Restriction **Enzyme Helps Determine Fragment Size**

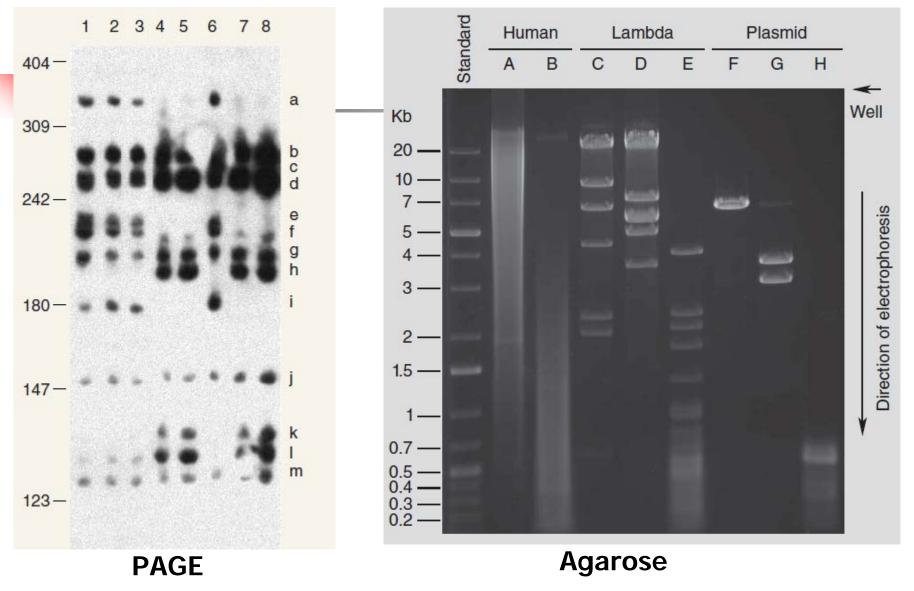
Intact human DNA **Eco**RI sites Enzyme cuts at one

Control the amount of enzyme or the amount of time the DNA is exposed to the restriction enzyme.



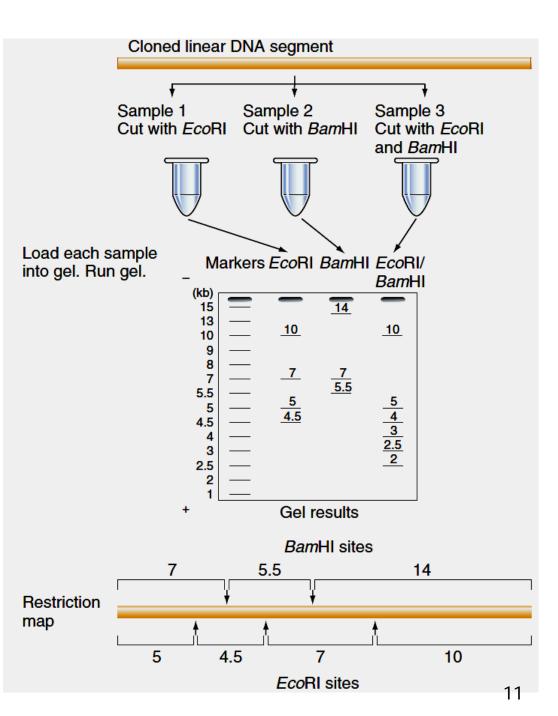


Gel Electrophoresis Distinguishes DNA Fragments According to Size



Different types of gels separate different-sized DNA molecules

Restriction Maps Provide a Rough Roadmap of DNA Fragment



II. Generating Recombinant DNA Molecules

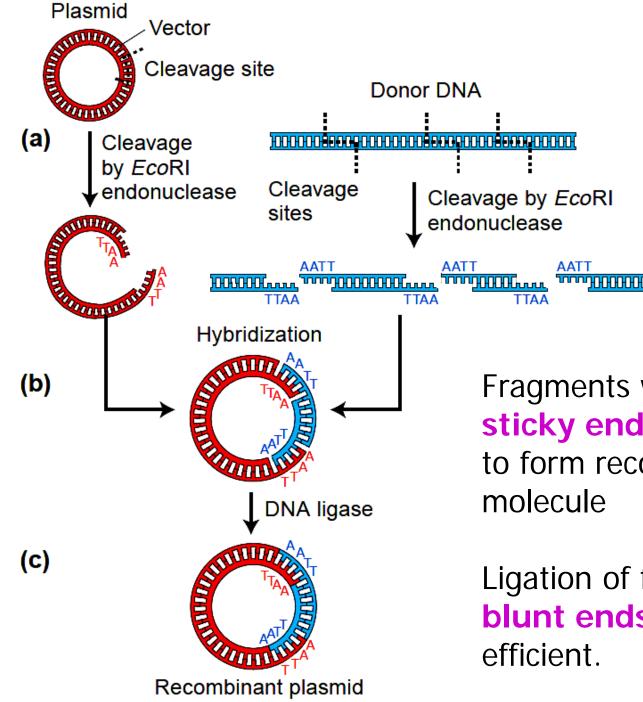
Cloning Step 1: Ligation of Fragments to Cloning Vectors Creates Recombinant DNA Molecules

Vectors: To serve as a vector, a DNA molecule must have several properties:

- Autonomously replicate(自主复制)
- Contain convenient restriction sites
- Carry a selector marker gene (选择标记基因)
- Easy to recover from the host cell

There Are Several Types of Vectors

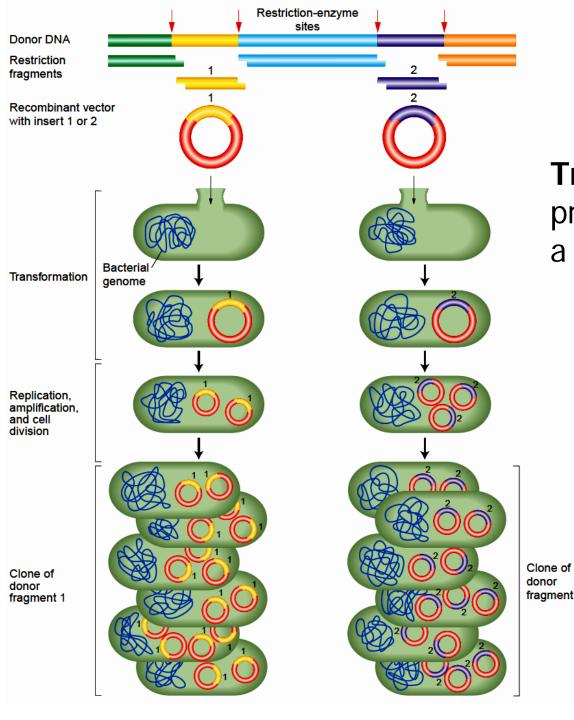
TABLE 9.2 Various Vectors and the Size of the Inserts They Carry								
Vector	Form of Vector	Host	Typical Carrying Capacity (Size of Insert Accepted)	Major Uses				
Plasmid	Double-stranded circular DNA	E.coli	Up to 15 kb	cDNA libraries; subcloning				
Bacteriophage Iambda	Virus (linear DNA)	E.coli	Up to 25 kb	Genomic and cDNA libraries				
Cosmid	Double-stranded circular DNA	E.coli	30–45 kb	Genomic libraries				
Bacteriophage P1	Virus (circular DNA)	E.coli	70–90 kb	Genomic libraries				
BAC	Bacterial artificial chromosome	E.coli	100–500 kb	Genomic libraries				
YAC	Yeast artificial chromosome	Yeast	250–2000 kb (2 megabases)	Genomic libraries				



Fragments with identical sticky ends can be joined to form recombinant DNA molecule

Ligation of fragments with blunt ends is much less efficient.

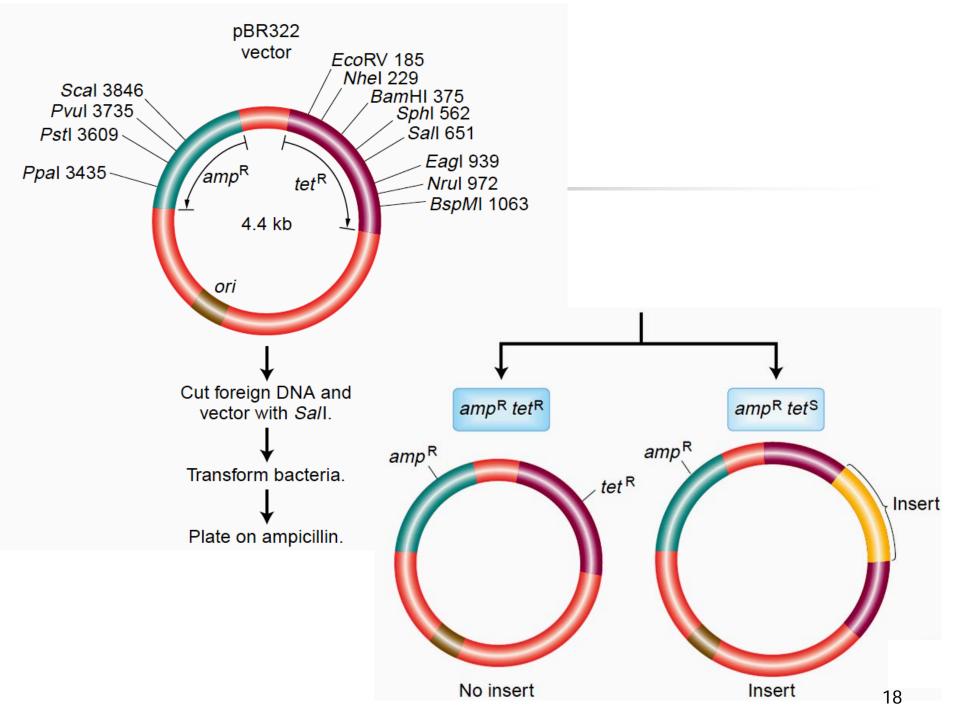
Cloning Step 2: Host Cells Take up and Amplify Vector-Insert Recombinants

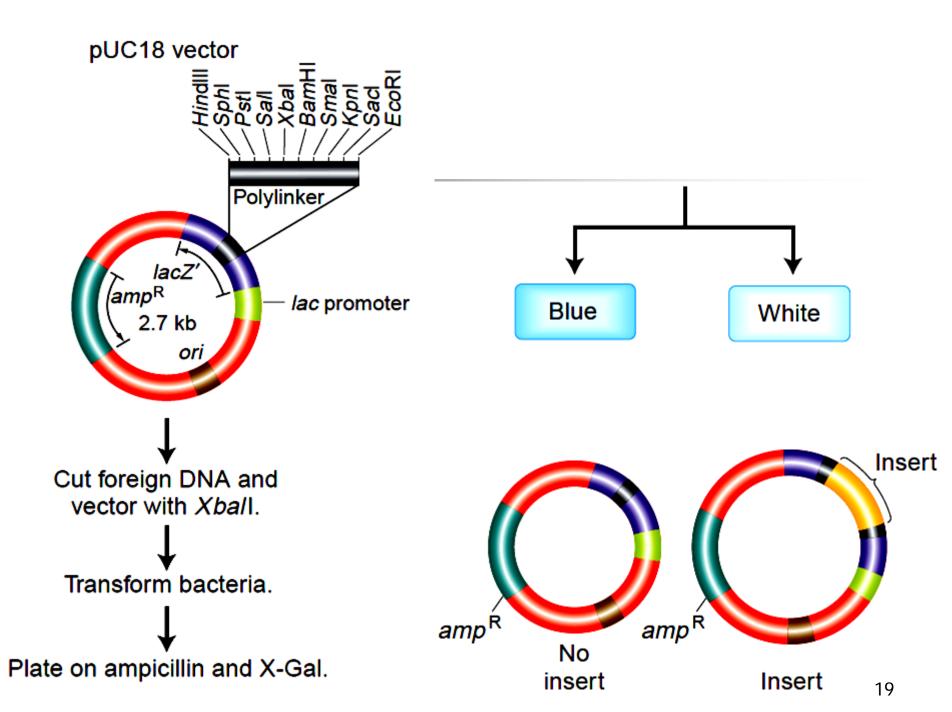


Transformation: a process of cell taking up a foreign DNA molecule

How Do You Know Which Cells Have Been Transformed?

How Do You Know Whether the Plasmids Inside Bacterial Cells Contain an Insert?





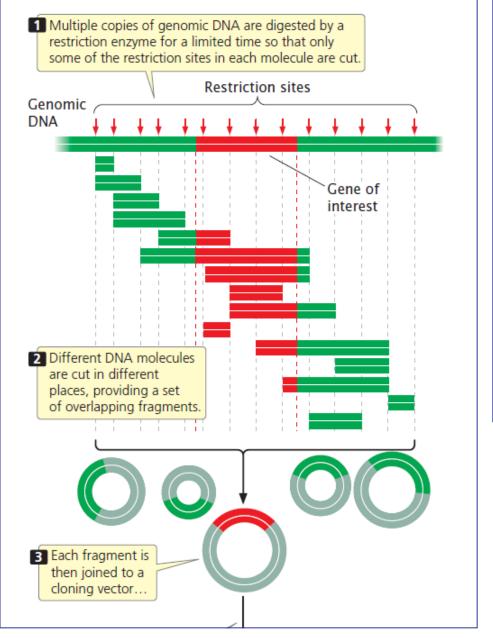


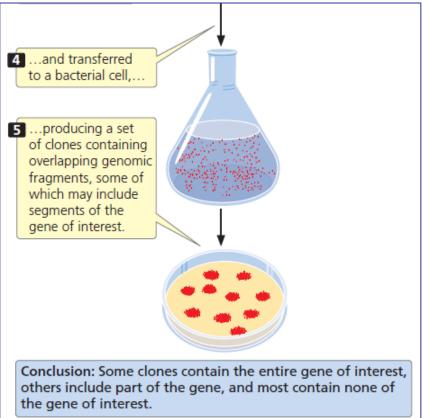
第二节 DNA文库 DNA libraries

Library: a collection of DNA clones that contains multiple copies of nearly every fragment in the whole genome inserted into a suitable vector and placed into storage.

1. Genomic library (基因组文库)

Making a genomic library





A genomic library contains all of the DNA sequences found in an organism's genome

Calculate the number of clones in a library

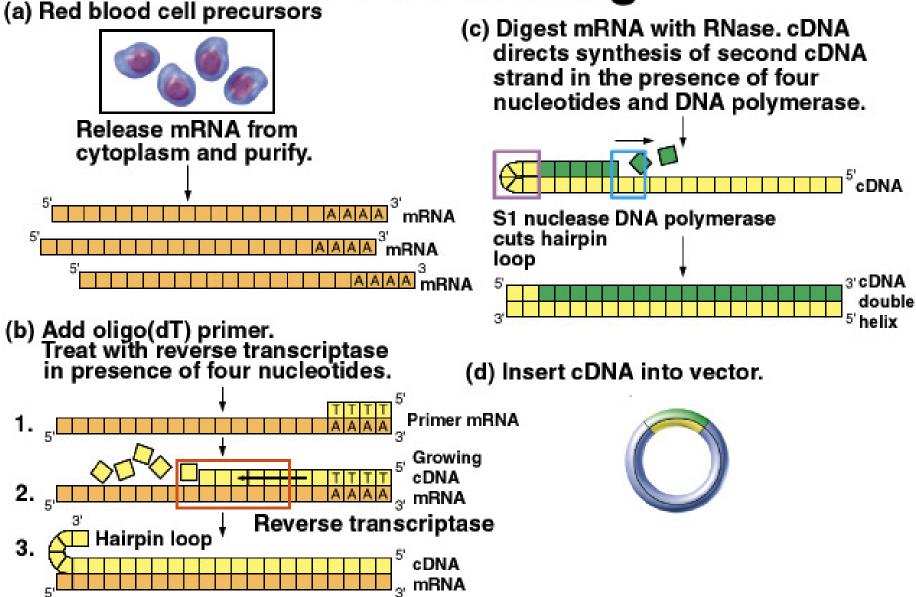
	Genome size (bp)					
Average size of	2×10^6 (bacteria)		2×10^7 (fungi)		3×10^9 (human)	
clone fragment	Theoretic		Theoretic		Theoretic	
(bp)	number		number		number	
5×10 ³	400		4000		600000	
10×10^{3}	200		2000		300000	
20×10^{3}	100		1000		150000	
40×10 ³	50		500		75000	

$$N = \frac{\ln(1-P)}{\ln(1-f)}$$

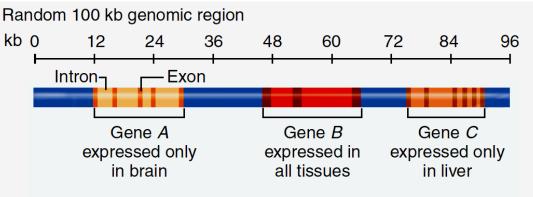
- N: number of required clones
- P: the probability of recovering
 - a given sequence
- f: the fraction of the genome in each clone

2. cDNA library (cDNA文库)

cDNA cloning



 cDNA libraries represent only the *expressed* genes in a given cell type, tissue, or stage of embryonic development. Genomics *vs*. cDNA libraries



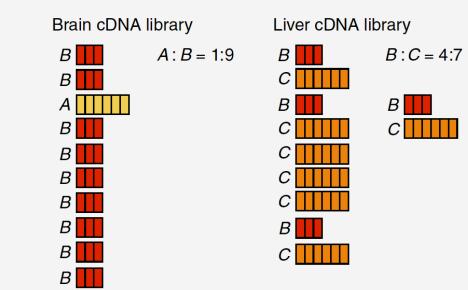
Clones from a genomic library with 20 kb inserts that are homologous to this region



Contains part of gene *A* Contains parts of genes *B* and *C* Contains all of gene *C*

Contains only last exon of gene A

Clones from cDNA libraries



第三节 目的DNA的分离 Screening DNA libraries for genes of interest

 Screening by functional complementation
 利用功能互补进行筛选



Isolate Gal gene of yeast

Making a library of wild type yeast DNA

Recovery of the wild type GAL gene

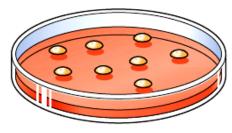
2. Screening with probe (探针)

DNA probes:

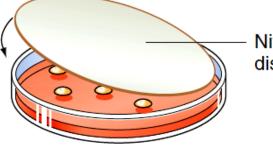
Short single-stranded DNA, from 10 to several thousand nucleotides in length, are usually labeled by radiation or fluorescent dye (荧光染料)

Hybridization is used to identify similar DNA sequences

Master plate containing genomic library of mouse clones.



Overlay a nitrocellulose disk to make a replica of the plate.



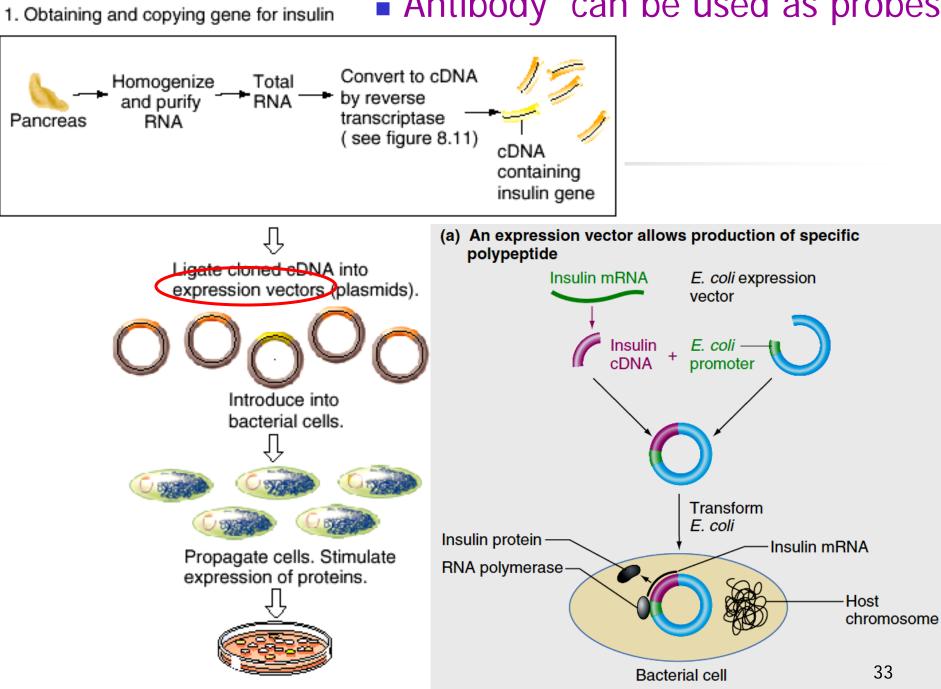
 Nitrocellulose disk

l abeled Disk replica human cystic fibrosis Add labeled probe. sequences Colonies with complementary DNA sequences hybridize to probe and restrain it. Human probe Mouse gene Original plate Wash disk, expose to X-ray film.

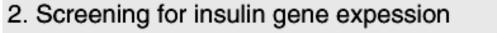
Remove disk from plate and lyse cells on it and denature DNA with NaOH. Bake and treat with UV light to bind DNA strands to disk.

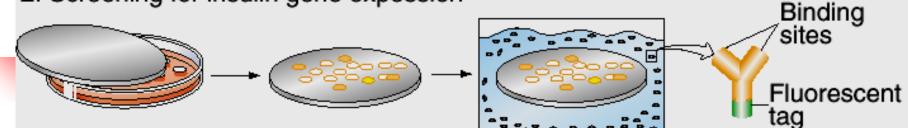
Compare with original plate to locate bacterial clone with desired genomic fragment.

Screening a library of clones by hybridization to a labeled probe. See movie



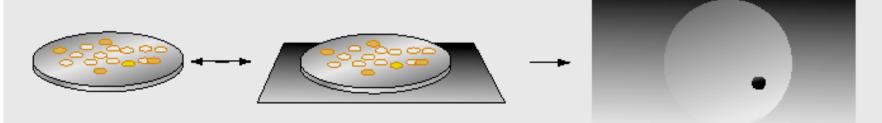
Antibody can be used as probes





Overlay plate with nitrocellulose paper. Lyse cells. Treat with NaOH. Proteins adhere to paper.

Incubate paper in solution of labeled insulin antibody. Antibodies will bind to insulin protein.

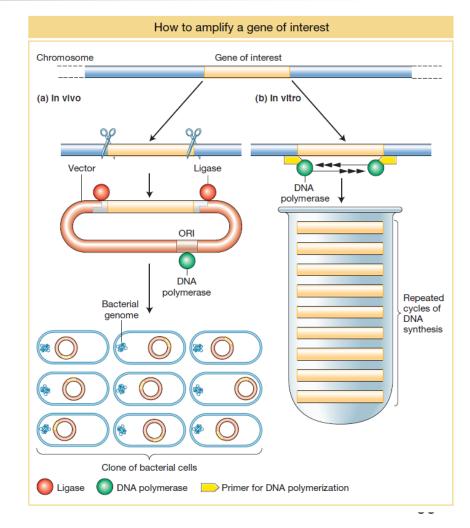


Wash filter. Make autoradiograph. Compare with original plate in order to find bacterial clone containing human insulin gene.

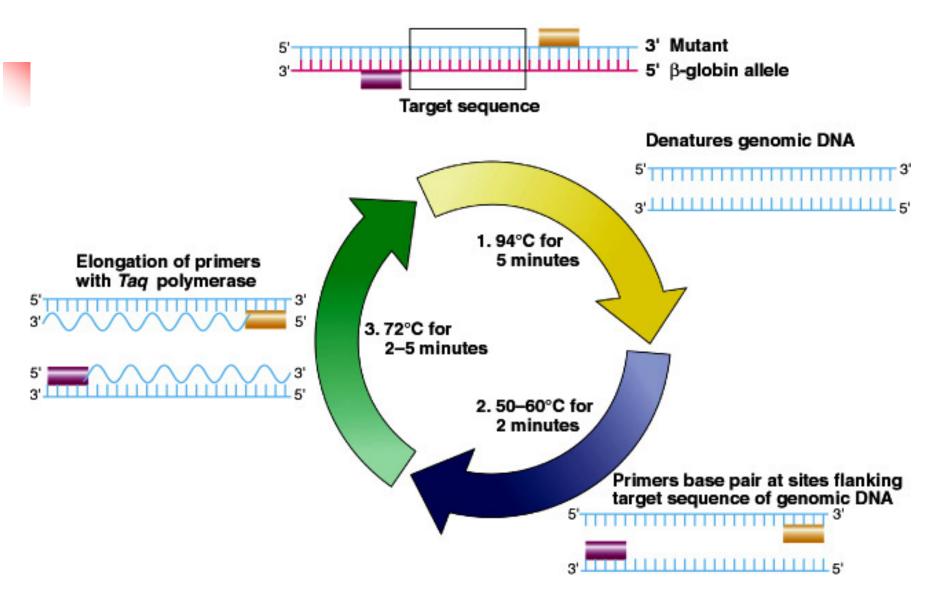
3. PCR Provides a Rapid Method for Isolating DNA Fragments

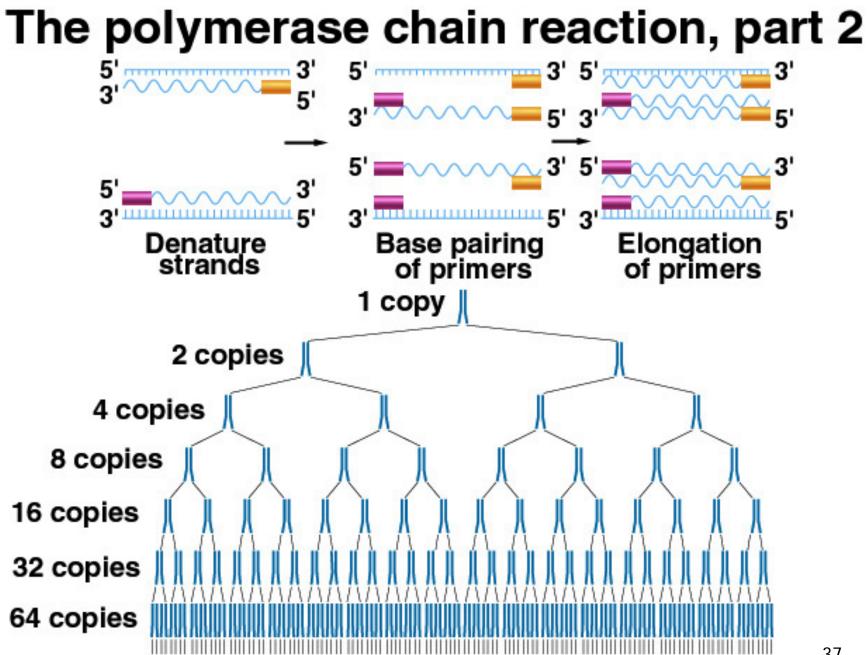
Polymerase chain reaction, PCR

A method for amplifying specific DNA segments that exploits certain features of DNA replication.



The polymerase chain reaction, part 1







Amplify a DNA fragment in a genome

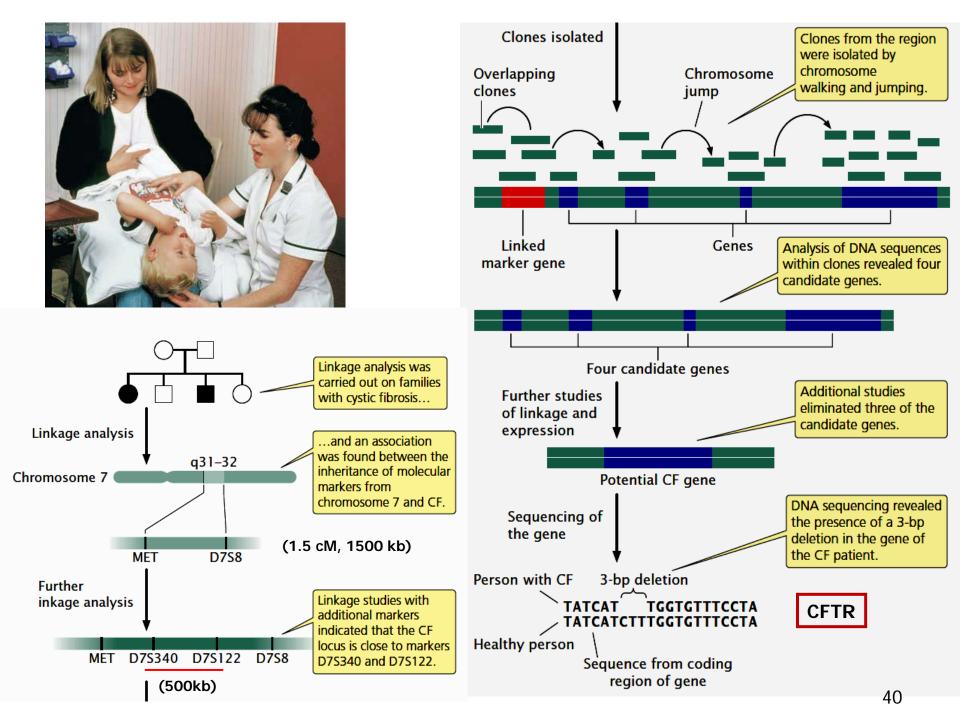
see movie

4. Finding Specific Clones On The Basis Of Genetic-map Location (Positional Cloning)

Cystic fibrosis (CF, 囊性纤维化) was the first genetic disease for which the causative gene was isolated entirely by positional cloning

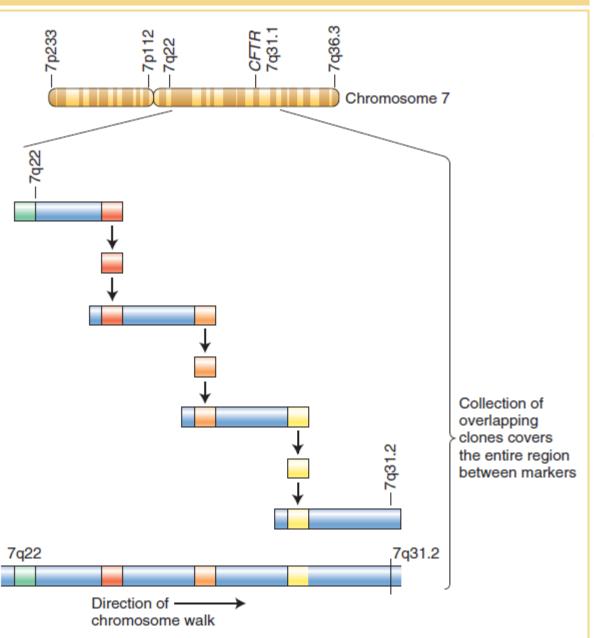
• An autosomal recessive disorder characterized by chronic lung infections, insufficient production of pancreatic enzymes that are necessary for digestion, and increased salt concentration in sweat.

 It is among the most common genetic diseases in Caucasians, occurring with a frequency of about 1 in 2000 live births. About 5% of all Caucasians are carriers of the CF mutation.



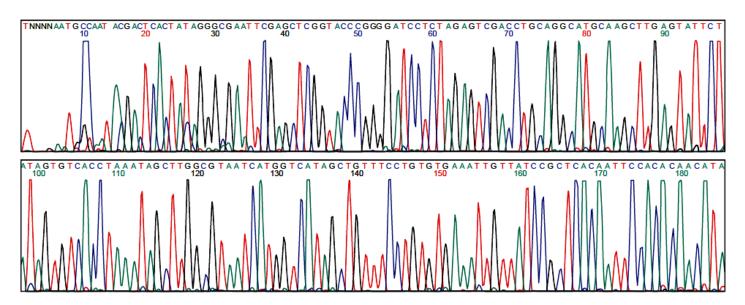






5. DNA Sequencing Is the Ultimate Way to Characterize DNA Structure at the Molecular Level

Dideonucleotide chain-termination sequencing (Sanger sequencing)



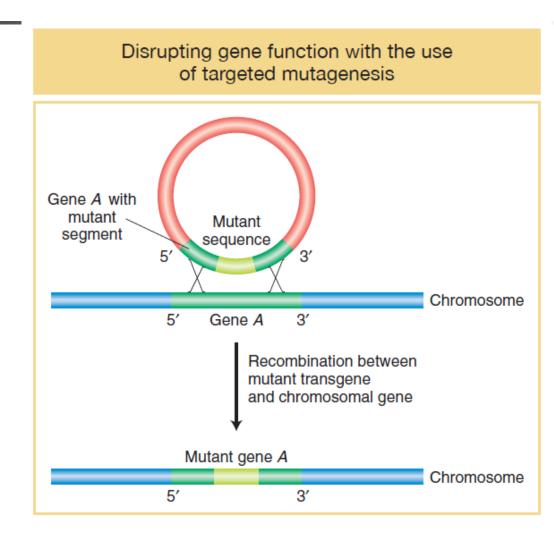
Next generation sequencing technology

第四节 基因功能研究

The gold standard for establishing the function of a gene or genetic element is to disrupt its function and to understand phenotypes in native conditions.

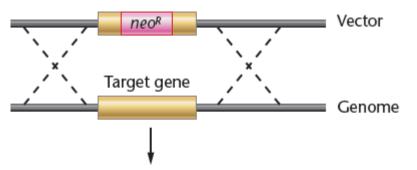
Reverse-genetic analysis starts with a known molecule—a DNA sequence, an mRNA, or a protein—and then attempts to disrupt this molecule to assess the role of the normal gene product in the biology of the organism.

Targeted gene knockout

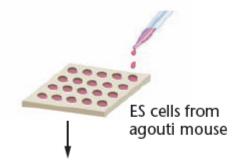


A basic strategy for producing a knockout mouse

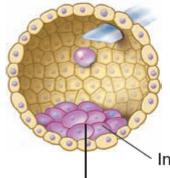
1. Designing the targeting vector



2. Transform ES cells with targeting vector and select cells for recombination

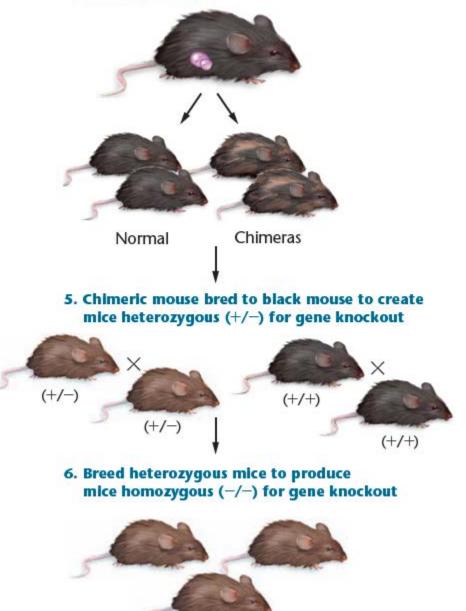


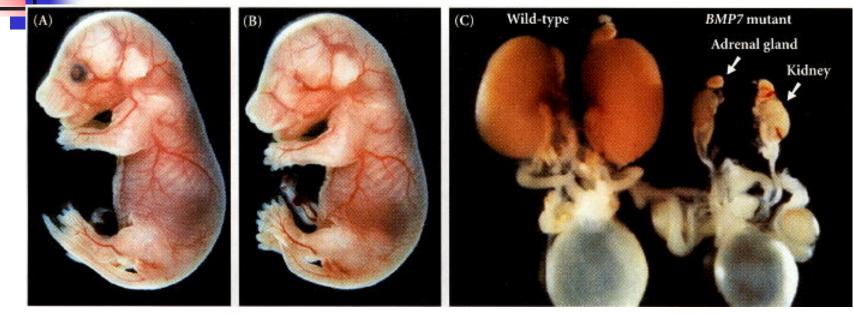
3. Microinject ES cells into blastocyst from black-colore mouse



Inner cell mass

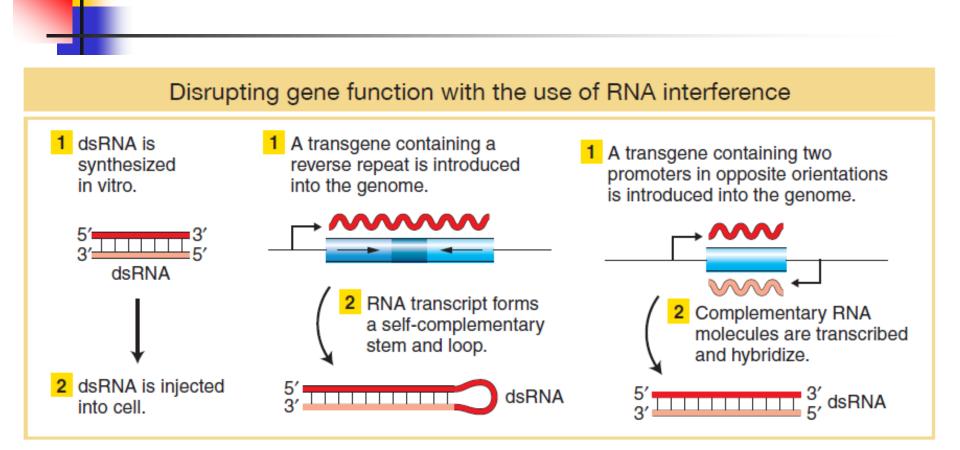
4. Transfer into pseudo-pregnant foster mother, birth of chimeras





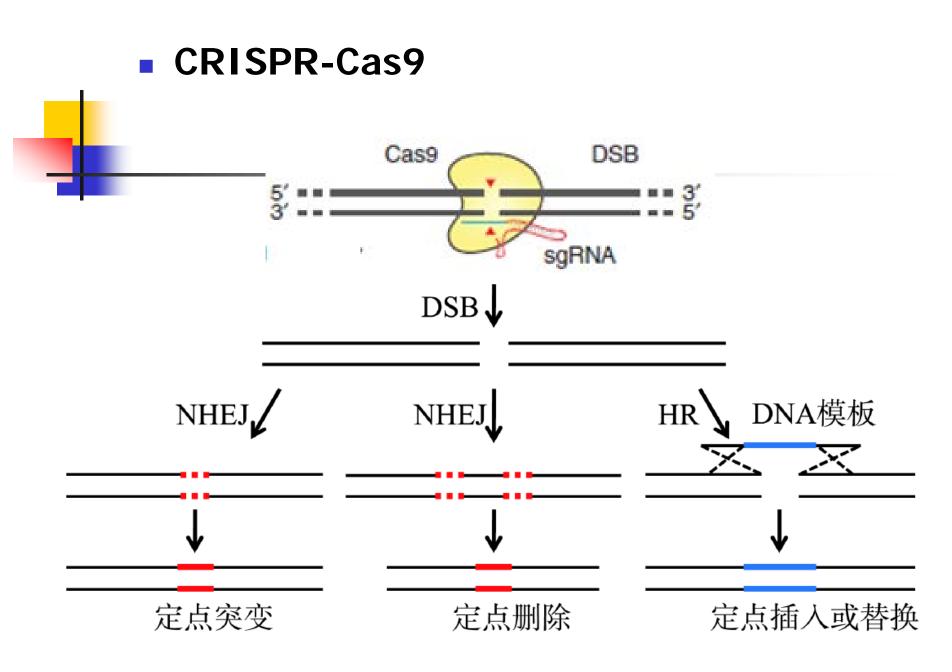
+/+ -/-

Morphological analysis of BMP7 knockout mice



RNA interference (RNAi)

47



Knock-in: making a transgenic organism

In a transgenic, the transgene is often overexpressed in order to study its effects on the appearance and functions

The figures and tables are cited from:

- Genetics (From genes to genomes), Leland Hartwell, Mcgraw-Hill Companies, Inc
- Concept of Genetics, William S.Klug, Prentice Hall, Inc
- Introduction to Genetics Analysis, Anthony J.F. Griffiths, W.H.Freeman, Inc
- Principle of Genetics, D.Peter Snustad, John Wiley & Sons, Inc
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 Pierce, W. H. Freeman