

DNA Genetic Code of Life



Entire Genetic Code of a Bacteria



DNA Fingerprinting



Cloning: Ethical Issues and Future Consequences



Plants of Tomorrow

HC70AL Spring 2011 Gene Discovery Laboratory

How To Sequence DNA?

4/4/11







DNA Genetic Code of Life



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DNA Fingerprinting



Cloning: Ethical Issues and Future Consequences



Plants of Tomorrow

Announcements

- Read Chapters

 Arabidopsis Seed Development
 Plant Life Cycle
 What it Means to Be a Scientist
 Sanger & Hood Articles
- 2. Review Last Week's Lecture
- 3. Think About Research

Recall.....The Structure of DNA





- 2. Phosphate-Sugar Backbone
- 3. Bases H-Bonded in Interior
- 4. Complementary Base Pairing
- 5. Anti-Parallel Chains
- 6. 10 Bases/Turn Helix
- 7. 34A/Turn
- 8. 3.4A/Base Pair
- 9. No Sequence Constraint
- 10. Synthesis 5' to 3'



Recall.....Nucleotides Have Polarity Based on What is Bonded to the Five-Carbon Sugar Phosphate on 5'Carbon and OH on 3'Carbon



DNA Sequence Defined By Nucleotide Order

DNA Sequence = Functional Uniqueness = Biology

Figure 1-2a Molecular Biology of the Cell, Fifth Edition (© Garland Science 2008)

Recall...Structure and Polarity of the Deoxyribose Sugar



Recall....DNA Replication Occurs Semi-Conservatively



- 1. DNA Structure Allows DNA Sequence to Be Maintained by Complementary Base Pairing
- 2. Each Strand Serves as a Template for the Synthesis of a Complementary Strand
- 3. New DNA Molecules are Precise Copies of Parental DNA - Each Containing One Newly Synthesized Complementary Strand

Meselson & Stahl, PNAS, 1957

Requirements For DNA Synthesis

- Template
- All Four Nucleotides
- Origin of Replication (in vivo)
- Short Primer to Initiate Synthesis
- DNA Polymerase



DNA Synthesis Is Always in a 5' to 3' Direction-Part Two



DNA Sequence of One Strand is a Template for the New Strand



What Happens to DNA Synthesis if the 3' Carbon of the Deoxyribose Sugar Does Not Have an -OH Group?



Maxam-Gilbert Chemical Chain-Breakage DNA Sequencing

- 1. Chemicals Break Phosphodiester Bonds at Specific Bases Randomly
- 2. Base Sequence Determined By Chemical Used To Break DA Into Fragments
- 3. Base broken is at the End of a DNA Fragment
- 4. Fragments Sized By Gel Electrophoresis
- 5. Single-Stranded DNA Labeled at One End (e.g., 3' End) Providing Direction For Sequence



Using Gel Electrophoresis To Separate DNA Fragments By One Nucleotide Spacings and Read DNA Sequence After Autoradiography



G A+G C C+T Chemical Reaction

Recall.....Sizing DNA Fragments Using Gel Electrophoresis



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Determining DNA Sizes Relative to the Sizes of Known Standards



A DNA size standard and a DNA of unknown size were placed in the left and right lanes, respectively.

Using Sanger Chain-Terminating DNA Synthesis to Sequence DNA



Sanger Sequencing Requires Requires: 1. Template (specific DNA fragment) 2. All Four dXTPs and ddXTPs 3. Short Primer To Initiate Synthesis 4. DNA Polymerase

What Happens to DNA Synthesis if the Complemetary Nucleotide is a ddXTP?



Recall... The Sugar is the Hub and Sets the Polarity of the DNA Molecule

Sanger Chain-Terminating DNA Sequencing-The "Old Way"



DNA sequencing with chain-terminating inhibitors PNAS 74, 5463-5467, 1977

F. Sanger, S. Nicklen, and A. R. Coulson



Nobel Prize For Chemistry in 1958 - Protein Sequencing Nobel Prize For Chemistry in 1980 - DNA Sequencing Sanger Chain-Terminating DNA Sequencing Reactions



Sanger Chain-Terminating DNA Sequencing



<u>Note:</u> Random Chain Termination

Problems With Maxam-Gilbert and "Old Time" Sanger Sequencing for Genome Sequencing

- Manual Process That is Labor Intensive
 - Gels
 - Base Detection
 - Chemical Reactions & DNA Synthesis
- Low Throughput (i.e., thousands of base sequences)
- · Slow
- Use of Radioactivity & Autoradiography to Detect Gel Fragments
- Separate Reactions or Synthesis For Each Base
- Need Specific Cloned DNA Fragments
- Cannot Automate
- Expensive (\$5-\$10 per base or more!)

Using Fluorescent ddXTPs to Visualize DNA Sequence And Size of DNA Fragments on a Gel Continuously



What Was the "Game Changer" That Allowed Genomes To Be Sequenced For the First Time?



Automated Sanger Dideoxy DNA Sequencing

Fluorescence detection in automated DNA sequence analysis

Lloyd M. Smith, Jane Z. Sanders, Robert J. Kaiser, Peter Hughes, Chris Dodd, Charles R. Connell^{*}, Cheryl Heiner^{*}, Stephen B. H. Kent & Leroy E. Hood

> Division of Biology, California Institute of Technology, Pasadena, California 91125, USA * Applied Biosystems, Inc., Foster City, California 94404, USA



Nature 321, 674-679 (1986)

The Breakthroughs.....

- Fluorescent ddXTPs
- Computer Automation
 - Size DNA
 - Detect Specific Bases
- Bioinformatic Analyses
 - · BLAST
 - GenBank



<u>However</u>: Still Need Genome Libraries, Cloned DNA Fragments, Manual DNA Synthesis, & Lots of \$\$\$. DNA Sequencing Reads ~500 Bases.



Applied Biosystems DNA Sequencer

<u>A DNA Sequencing "Factory"</u> ·100 lanes/machine

- 500 bp/reaction/lane
- \cdot 3 hour run time
- ~ 50 kb/run
- ~ 400 kb/machine/day

Need Lots of Machines to Sequence a Genome!!



Using Fluorescent ddXTPs to Visualize DNA Sequence And Size of DNA Fragments on a Gel Continuously





Need Precise Base-Calling Software



Reading the DNA Sequence



Using Bioinformatics to Identify a Gene





DNA Sequencing Throughput Has Exploded!



Cost of Sequencing is Going Down Precipitously!

GOING DOWN An exponential decrease in the cost of sequencing DNA could soon result in a \$1,000 genome.













PRIZE[®]

NextGen Sequencing Has Lead To An Explosion of Whole Genome Sequencing



- No Cloning
- Random Shearing of DNA
- Attachment to Microbeads
- One DNA Sequence per Microbead
- PCR Amplification
- Sequencing By DNA Synthesis
- Fluorescent Nucleotides
- Sequence Millions of Unique DNA
- Fragments at Same Time
- (Massively Parallel DNA Sequencing)
- Sequence By DNA Synthesis One Nucleotide at a Time
- Uses Nanotechnology & Robotics
- One "Lane" Can Sequence 20 Gb or 160 Gb per Sequencing Run or ~50X the Human Genome (2 hours)

New Sequencing Technologies Have Lead To An Explosion of Whole Genome Sequencing

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TABLE 10.1	Number of Species with Fir National Center for Biotech	nished Whole-Genome Sequence of February Information as of February Informa	ences Deposited at the pruary 1, 2010 (2/9/11)
Organism	Whole Genome	In Progress	s Total
Prokaryotes	1058	2354	3412
Mammals	56	69	125
Birds	2	12	14
Fishes	15	17	32
Insects	36	7	43
Flatworms	3	2	5
Roundworms	12	14	26
Amphibians	1	0	1
Reptiles	1	0	1
Other animals	11	18	29
Plants	25	88	113
Fungi	129	91	220
Protists	54	58	112
Total	1403 158	2730	9640 11,221 4133

http://www.genomesonline.org/cgi-bin/GOLD/bin/gold.cgi