

A DNA Discovery Kit® Resource

**Teacher Notes,
Background Information &
Supplementary Material
for
Teaching DNA**

By Michael H. Patrick, Ph.D.

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I. DNA Background Information

The purpose of these questions is to put DNA into a framework in which its structure explains a fundamental question: how heredity works at the molecular level. This is not intended to be a comprehensive reference text. Additional background and references, both print and electronic, can be found in: “Understanding the BioMolecular World: A Teaching Guide 2004”, which is available in pdf format from www.rpc.msoe.edu/cbm. (Hereafter, this will be referred to as “The Teaching Guide”)

1. WHAT IS DNA AND WHAT DOES IT DO?

a. Genetics As An Underlying Conceptual Framework

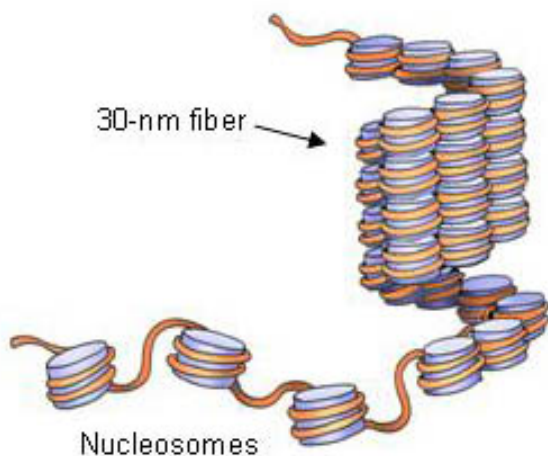
Three points to review and emphasize:

- A gene is an unseen unit of genetic information that helps us understand the continuity and diversity of observable, heritable, physical traits. The science of genetics discovered the rules by which we can account for the heredity patterns of observable traits.
- The science of cell biology developed the chromosomal theory of inheritance, showing that chromosomes are the physical basis of inheritance and thus contain the genes.
- The sciences of biochemistry and molecular biology showed that chromosomes are complex structures containing proteins and nucleic acids, but the molecule responsible for storing genetic information, having it expressed and duplicated, is DNA.

b. Cell Structure and the Physical Basis of Inheritance

Background information:

DNA is a very, very long molecule; for example, if human DNA from a single cell were one molecule, it would be about 2 m long. In order to fit into a nucleus with a diameter of only 10 μm , it is packed into chromatin, the basic repeat element of which is the nucleosome. A nucleosome consists of 147 base pairs of DNA wrapped 1.7 times around an octamer of histone proteins. Individual nucleosomes are connected by 20 to 60 bp of linker DNA to form a 10 nm “beads-on-a-string” array, which can be compacted into a 30 nm chromatin fiber, the structure of which is still poorly understood.



The folding hierarchy continues with increasing DNA-packing density until the metaphase chromosome is attained.

Fig.1 Illustration by Mark Hoelzer, 3D Molecular Designs, LLC

c. Discussion and activities:

- Textbook pictures or drawings of chromosomes stained to show transverse bands in human karyotypes, or pictures of *Drosophila* polytene chromosomes can confuse students; they often wrongly conclude that these bands represent genes. Showing these pictures or carrying out karyotype analysis exercises are useful ways to talk about chromosomes. What these banding patterns represent is still not completely understood, but they appear to represent regions of higher or lower degrees of condensation. The primary use of banding patterns is to identify different chromosomes, which is important for the clinical geneticist in diagnosing some genetic disorders arising from chromosomal abnormalities.

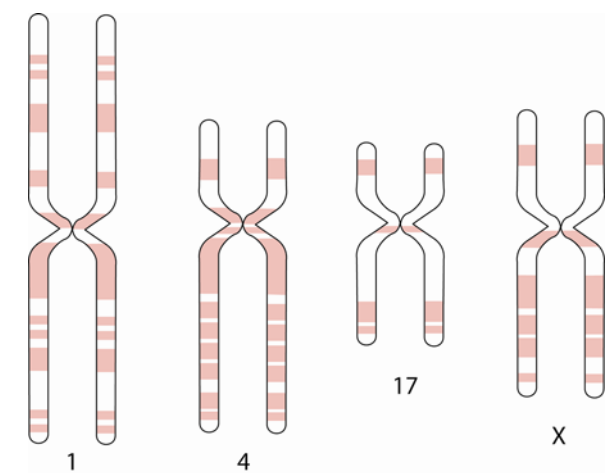


Fig.2 Illustration by Mark Hoelzer, 3D Molecular Designs, LLC

- Compacting DNA into chromosomes results in different numbers of chromosomes for different species. Shown on the right is the diploid number of chromosomes for a few organisms. The number of chromosomes, however, is not correlated with the total amount of DNA in the different species' genomes.

Bacteria	1	Honeybee (female)	32
Fruit fly	8	Fox	34
Red clover	14	Cat	38
Garden pea	14	Mouse	40
Yeast	16 (haploid)	Rat	42
Maize (corn)	20	Rabbit	44
Frog	26	Human	46
Hydra	30	Chicken	78

2. HOW DOES A DNA MOLECULE STORE INFORMATION

a. Information: General Considerations

Information starts with a message: a linear array of symbols which, in a normal language, may be a set of words, letters, syllables. To illustrate this, contrast:

- a random assortment of letters with the same number and kind of letters in a meaningful sentence
- a single letter repeated several times vs a sentence in which different letters form meaningful words; or a chain of pop-it beads of one color vs a chain of the same length in which four different colored pop-it beads are used

But information needs to be

- stored (*what criteria must be applied? stability, transportability, fidelity of replication....examples: stone tablets vs. writing in sand vs writing on paper vs computers vs CDs*)
- accessed and used, which can be done in one of two ways:
 - digital: this means having to do with numbers; so storing information “digitally” means storing it as numbers, the simplest being 0 or 1 (Boolean or binary mathematics). So, a digital computer performs tasks by changing one set of numbers into another set; the numbers represent a quantity.
 - analogue: an analogue computer solves by measuring quantities (e.g. weight, speed, voltage); it replaces a calculator with a system that performs the calculation (*e.g. rise and fall of mercury in a thermometer imitates the movement of the temperature.*)

Example:

Producing 137 W electrical light through: (A) use of a single 250 W bulb supplied by electricity through a rheostat, or dimmer; the desired voltage is obtained by analogue computation (the power is determined by a continuous range of voltage settings) (B) a series of bulbs, each having a wattage double the preceding bulb (1,2,4,8,16,32,64,128,...); . Turning on only the 1,8, and 128 W bulbs would give the desired total wattage. Since a bulb is either on (1) or off (0), the message for 137 W would be: 10010001. Thus, this is a digital computational device to generate the desired power. The digital mode is precise and easily replicated; the analogue procedure is less precise and not easily as replicable.

b. What About Genetic Information?

- It is digital

This we know already from the work of Mendel: genes do not blend, they are either there or they are not. We can even imagine them as “beads on a string”. What Crick and Watson did was to show that even within a gene it is digital. Even down to the finest minute structure of a gene, everything is digital code...just like computer except that genetic information is written in a quaternary code whilst computer information is binary.

See: “Modeling DNA as Information” in the The Teaching Guide. These activities build on the material in the student manual, pp. 2 & 3: symbolic representation on paper to the use of physical objects (e.g. pop-it beads). From this, it is not a big leap to see that a linear chain of chemical units can be informational, as shown in one of the simulations in the The Teaching Guide. The example of the number of possible combination of 4 letters (nucleotides) in a 10 nucleotide chain can be calculated as follows:

--how many possible letters (nucleotide) are there for the first place in the chain? (4)

--how many for the second? (4)

--and for the third? (4)

--and for the tenth? (4)

--so, to join together 10 in a row, there must be:

$$4 \times 4 \times 4 \times 4 \times 4 \times 4 \times 4 \times 4 \times 4 \times 4 = 4^{10} = 1,048,576 \text{ or, about a million}$$

- It must be stable, it must be easily read, it must be able to be duplicated faithfully.

Possible discussion for an advanced class:

*About four years before Watson & Crick’s work on DNA, John von Neuman...father of cybernetics...gave a lecture explaining how a machine could reproduce itself. All it needs, he said, is a description of itself. No machine, he further explained, could reproduce itself or its parts without a making a mold. But to make the mold, it would need a description of itself. For example: “Build magnetic core by tightly winding grade ## electrical wire around a cylindrical (h = 20 cm, d = 2 cm) 500 times.....etc. etc.....”. And, of course, it would need all the raw materials. The machine’s offspring could reproduce as well, if the machine made a copy of the description of itself and inserted that copy into every new machine, and the new machine carried out the process without error. What is the analogy between von Neuman’s machine and DNA? Like the description of the machine, DNA is a coded description of the organism and is responsible for its capacity to reproduce. Unlike von Neuman’s machine, living things don’t usually make **exact** copies of themselves.*

Just how error-free is the process of genetic duplication; what is the consequence of a completely error-free process? Experimentally, the error rate in a growing culture of bacteria has been found to be around 1 per 10^9 nucleotides per replication, arising through some combination of errors in DNA synthesis and faulty DNA repair. If the bacterium has a genome size around 10^7 nucleotide pairs (np), then the error frequency is 10^7 np/ genome $\times 10^{-9}$ errors/np = 10^{-2} errors/genome. So, there will be one spontaneous, random mutation in every 100 cells. It is easy to see that as the size of the genome increases, and/or the number of cells in the organism

3. WHAT DOES DNA LOOK LIKE?

a. **Extraction And Examination Of DNA:** *For DNA extraction protocols, see [The Teaching Guide](#); included here are also classroom protocols for an advanced class to answer the question “How Do You Know It’s DNA?”*

AN INTRODUCTORY CLASS DNA EXTRACTION ACTIVITY (*Questions in bold italics; Answers in italics*)

- **describe the extracted material; how would you go about proving this is DNA?**
- **what do you think this would look like under a microscope?**
- **take a small amount of the extracted DNA and place it on a slide and smear it around a bit; let it dry and examine it under the microscope using both low and high power, before and after adding a few drops of water. Describe what you see** (it will, of course, be amorphous-looking material, since the individual molecules are too small to be observed by visible light)
- **how do you think DNA can be seen** (by magnifying it using electromagnetic radiation of much smaller wavelength)
- **describe what you think DNA would look like if we magnified it 10,000 times with an electron microscope** (see picture on left of p.4 in the student manual; it looks like tiny spaghetti noodles all bunched together). **What about 40,000 times** (picture on right: it looks like a very small, granular rope. The point is that you can see that it is a very long, thin molecule, but you can't see the details. The technique involves letting DNA carefully diffuse onto a surface coated with a monolayer of a basic protein like cytochrome c. Contrast shadowing is accomplished by evaporating a heavy metal, like platinum, at an angle. The grainy background is simply the metallic outline of the background matrix material)

b. **Scaling Activity**

The E.coli genome

known: 4,639,221 nucleotide pairs

if the double-stranded circular DNA is made linear, it would stretch to a length around 1600 μm (the average distance between two nucleotide pairs in DNA is 0.34 – 0.36 nm; the diameter of the cylindrical molecule is 2 nm)

representation: *Using a scaling factor of 10,000, you will need something 16 m long and 2 μm thick. Since it is unlikely you will be able to locate material with these dimensions, the next best thing is to use fine thread. An E.coli cell is roughly a cylinder 2 μm in length; scaling this up by 10,000 gives a “cell” 2 cm long, which can be modeled by a gel cap.*

activity: a. *Stretch out the thread and compare to length of cell; try to stuff the thread into the cell (the best way is to severely knot the string).*

b. *For the next activity, substitute thick (colored) yarn for easier visibility. Ask the question: how big is a gene, compared to the whole genome. This is a calculation for an advanced class: assume the average size of a protein is 4×10^4 daltons. If an average amino acid has a molecular weight about 100 daltons, then there are roughly 400 amino acids in an average protein. Each amino acid is coded for by a nucleotide triplet, so the protein-coding part of an average gene is about 1200 nucleotides. If each nucleotide is separated by about 0.35 nm, then this DNA is 420 nm long. Scaling this up by a factor of 10,000 gives a length of yarn about 4mm in length. Color this black. Using this model, how many genes would be in the E.coli genome?*

(16 m DNA \div 0.004 m/gene \approx 4000 genes)

c. *You can then compare this with an average gene represented as information. The sequence of any of the E.coli genes can be downloaded from GenBank, printed out and, by cutting and pasting, assemble a linear, paper model of the gene in terms of the nucleotide*

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sequence. GenBank can be located by a Google search or as a link from the Center for BioMolecular Modeling (www.rpc.msoe.edu/cbm)

c. Molecular Structure Of DNA

- **X-ray Diffraction:** *Two classroom activities to demonstrate fiber diffraction are (i) **The Diffraction Contraption**, described in The Teaching Guide; (ii) **The DNA Optical Transform Kit**, which can be ordered from the Institute for Chemical Education (www.ice.chem.wisc.edu/ice)*
- **Student Manual:** *From the three pictures on p.4 , several different features could be mentioned, but the one that is most unique that there are two helical backbone chains that appear to be wrapped around each other. For many students, this is not necessarily obvious, since it requires “seeing” the two dimensional representation in three dimensions. This provides an opportunity to discuss the nature of modeling the unseen and why no one model is sufficient and the difficulty of trying to infer something in 3 dimensions from a 2 dimensional representation, as in the representation on p. 5.*

II. Building a DNA Molecule

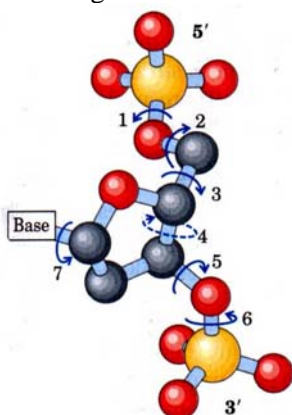
(Additional background and resource material on DNA structure and function can be found in *The Teaching Guide*.)

A. NUCLEOTIDES AND POLYNUCLEOTIDES

- A nucleotide is made up of three different, covalently-bonded, molecular subunits: a 5 member sugar ring (a pentose), a phosphate, and a “base”...a single (pyrimidine) or double (purine) ring structure made up of carbon and nitrogen to which other chemical groups can be attached (carbonyl, amino).
- The sugar-phosphate component is the same for all nucleotides; the base component can be any one of four different ones
- Carbon atoms in sugars generally are bonded to H and OH: $\begin{matrix} \text{H} \\ | \\ \text{— C —} \\ | \\ \text{OH} \end{matrix}$;

the pentose in DNA has an exception; one of the carbons is bonded to 2 H's; thus, it is called “deoxyribose”. **For advanced classes**, call attention to the fact that in RNA, the nucleotide has all of its carbons bonded to both H and OH; so, the sugar is called simply “ribose”

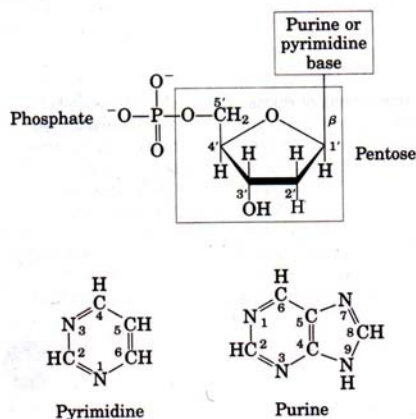
- The different components of the nucleotide do not lie in the same plane but are joined at different angles.



For advanced classes: compare the nucleotide in the DNA Discovery Kit[®] with one that can be built from a molecular modeling kit. The point is that, with the exception of the pentose ring, there is free rotation about each of the single bonds; (even the pentose ring has one bond..between C2' and C3' ...that has partial rotation, allowing the ring to slightly buckle). Although any torsional angles are possible in the free nucleotide, as part of a polynucleotide these angles adopt values that provide a minimum energy structure. The DNA Discovery Kit[®] was designed based on atomic coordinates, defined by bond length and bond angle, for the classical “B-form” DNA. (Figure reproduced from “Lehninger Principles of Biochemistry” by D. Nelson and M. Cox 4th Edition, W.H. Freeman, with permission of the publisher.)

Fig.5

- **For advanced classes**, students can be introduced to the numbering convention used for nucleotides, as shown below.



The use of primes for numbering the sugar is an arbitrary convention to distinguish between numbering of atoms in the bases. By convention, nucleotides are represented as 5' monophosphates rather than 3' monophosphates. Thus, the nucleotides in the DNA Discovery Kit[®] are 5' monophosphates.

Fig.6

- As part of a polynucleotide chain, the most stable arrangement of the atoms in a nucleotide is one in which the backbone adopts a right-handed helical path in space. The consequence of this is that the bases will attempt to stack over each other to stabilize the molecule through van der Waals interactions (also called “stacking forces” for polynucleotides). To do this, one nucleotide must rotate with respect to the preceding one in order to maximize this overlap. The result is the formation of a helical molecule, the beginnings of which can be seen even for a dinucleotide. [For advanced classes](#), additional points about polynucleotides:

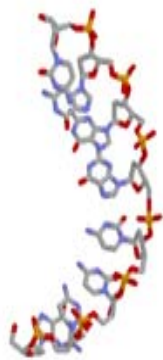


Fig.7

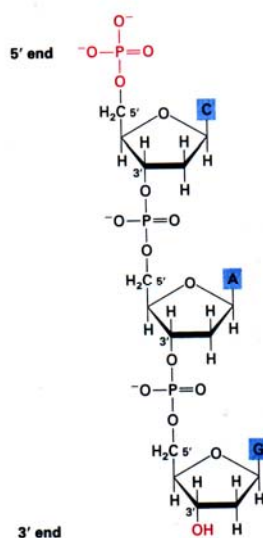


Fig.8

Students often have difficulty understanding “**helix**” and “**handedness**”. A helix is a spiral of constant diameter. A spiral staircase, for example, is really a helical staircase, most often with a single banister on the outside. If you are going up the staircase and your right hand is on the banister, then this staircase is an example of a right-handed helix.

-----The covalent bond joining two nucleotides is a **phosphodiester bond** linking a 5’ phosphate of one nucleotide to a 3’ OH of the next one. Thus, a polynucleotide is **asymmetric**: one end will have a 5’ phosphate, the other will have a 3’ OH.

----- The negative charge is the reason why DNA is “A”...an acid. There are three titratable protons on a phosphate group; two are used to form ester linkages with the sugars, leaving one which has a pK_a around 6. This means that at neutral pH, the phosphate (and therefore a polynucleotide) will be negatively charged and, consequently, need to be neutralized by positive ions.

B. BUILDING A DOUBLE-STRANDED DNA

1. Hydrogen Bonding, Tautomers, and Base Pairs

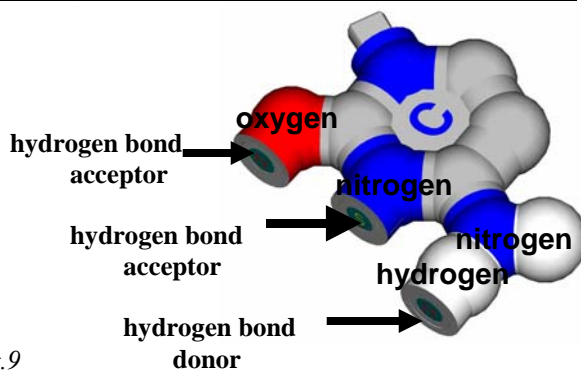


Fig.9

Hydrogen atoms can be shared between two electronegative atoms, such as N and O. It is not an intuitive concept; quantum theory posits the hydrogen electron cloud as spread out between neighboring donor (e.g. $-NH$) and acceptor (e.g. $=O$) atoms. It is about 1/20 as strong as a covalent bond. Students often get the impression that the only hydrogen bonds between DNA bases are the type associated with Watson-Crick base pairing. This is not so, which this exercise shows. **All purine-purine, pyrimidine-pyrimidine, and purine-pyrimidine can and do form...some even in DNA. But the ONLY pairings possible in the Watson Crick DNA structure are A:T & G:C.** This follows from other structural considerations, as discussed below.

The strength of the base pairs formed by hydrogen bonds is directly related to the number of H bonds that form between the bases; so G:C, with three hydrogen bonds, is 30% stronger than A:T, which form only two.

- For advanced classes**, it should be pointed out that the amino and carboxyl groups actually exist in two forms: the nitrogen as either amino ($-\text{NH}_2$) or imino ($=\text{NH}$), and the carboxyl as keto ($=\text{O}$) or enol ($-\text{OH}$). These groups are in equilibrium with each other, but the equilibrium lies far to the side of amino/keto. The diagram at the right shows the tautomeric forms of the nitrogens and oxygens in cytosine and guanine. The important point is that the hydrogen bonding properties of the tautomers differ. The keto tautomer is an H bond acceptor whereas the enol tautomer is an H bond donor. Similarly, the amino tautomer is an H bond donor while the imino tautomer is an H bond acceptor. The only tautomers that can be accommodated in the Watson-Crick base-paired DNA are keto/amino; the capacity to form the alternative tautomer, however, is a frequent source of errors during DNA synthesis.

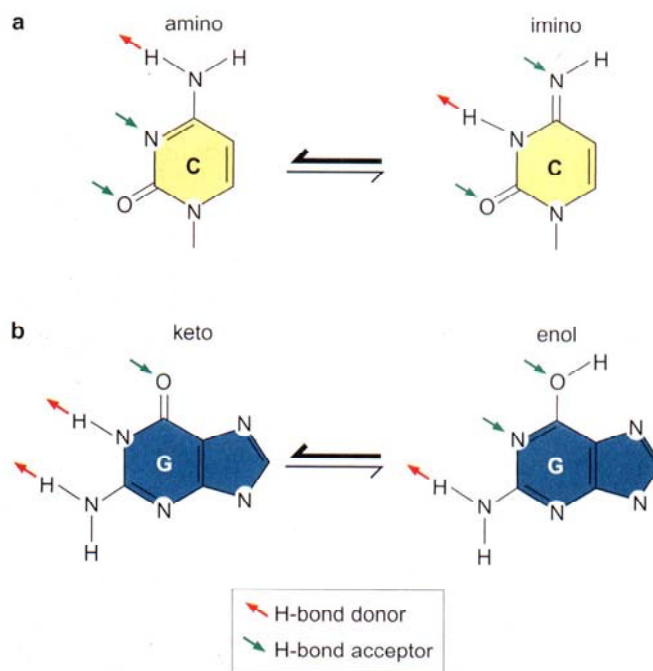


Fig.10

- Watson-Crick base pairing is often said to be “complementary”. This term refers to the geometry of the two bases...i.e. it is a “size complementarity”: hydrogen bonds between the purines and the pyrimidines ensure that the correct large bases pair with the correct small bases. Thus, the molecular biology mantra: A pairs with T, G pairs with C. ***An additional exercise to make this point is to make measurements on the different kinds of base pairs. For example, measure the width of a base pair from both glycosidic bond atoms (N_1-C_1' of the pyrimidine and N_9-C_1' of the purine); make a table of the measurements for each base pair. The point is that only A:T, T:A, G:C, and C:G allow construction of a hydrogen bonded double helix*** (The repeating negative charge of the DNA backbone is tightly tied to the rule-based molecular recognition needed for transmission of genetic information. The repeating negative charge keeps contacts between two complementary DNA strands as far away from the backbone as possible, enforcing Watson-Crick pairing. Without the repeating charge, DNA would bend, fold, and aggregate. A corollary to this is that the repeating charged phosphates of the DNA (and RNA) backbone may be key to evolution: i.e. a repeating charge may be a universal structural feature of all molecules carrying genetic information in an aqueous environment.)
- Watson and Crick deduced that only way to construct a double helix that agrees with the x-ray fiber diffraction data obtained by Rosalind Franklin was to have antiparallel strands with As pairing with Ts and Gs with Cs. This is the conclusion students will reach after doing these exercises. Both strands have helical geometry but base pairing holds them together. The antiparallel orientation is a stereochemical consequence of the way that A and T, and G and C, pair with each other. Another consequence is that the overall geometry of the double helix maximizes the overlap between base pairs; even though a given base pair is rotated about 36°

with respect to the one above and below, there is considerable overlap of the surface areas....i.e. they are stacked pretty tightly. This stacking overlap contributes significantly to the stability.

2. Other Properties And Features Of Double Stranded DNA

- The two strands are wrapped about one another; i.e. they are “plectonemically” coiled (if they were side-by-side, they would be “anonemically” coiled. *A variation of the Mibni-Toober exercise on the student sheet is to make a Mini-Toober double helix, then carefully untwist the two helical Mini-Toobers. Ask a student volunteer to “put them together” to make a double-stranded DNA that looks like the model they built with the DNA Discovery Kit[®]. Most will try to put the two side by side in a variety of ways, and, of course, the strands don’t stay together. And, they can’t pull apart the two polynucleotides in the model they constructed. Eventually, one or more will deduce that the two Mini-Toober helices have to be “twisted” into each other. (The consequences for DNA replication are, of course, profound....especially when the genome is circular, as it is in many organisms. The amazing ways cells have evolved to solve this and prevent replication from getting “tied in knots” is treated briefly in The Teaching Guide.)*
- **Why is DNA double-stranded?** The short answer is that a single strand of DNA has all the information necessary to serve as a genetic storehouse and template for expressing and replicating these genes. Indeed, the genome of the bacterial virus, ϕ x174, is a single-stranded DNA molecule. (Moreover, there is a class of viruses...such as HIV.... for which the genome is a single-stranded RNA molecule.) Nonetheless, the genome of most organisms is double-stranded DNA. This redundancy has a profound purpose since DNA is susceptible to both chemical and physical (e.g. radiation) damage; a damaged base is potentially lost information. But, since the information is duplicated in a complementary sequence, then the information to replace or fix the damage is always there, no matter in which strand the damage occurs.
- **For advanced classes: major and minor grooves**

The DNA double helix is also characterized by two grooves that are not equal in size to each other. The reason is a consequence of the geometry of the base pairs. The base pairing and stacking determines the manner in which the sugar protrudes from the helix center. This creates an asymmetry which can be seen looking down the helical axis. The consequence is that as the two strands wrap around each other, grooves of different sizes are created. This also means that the double helix is rich in information in these grooves.

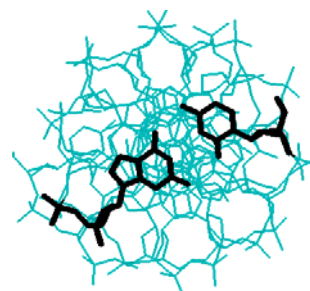


Fig.11

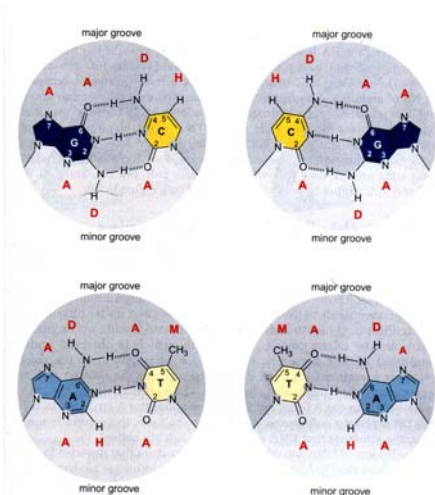


Fig.12

The edges of each base pair are exposed in the major and minor grooves, creating a pattern of hydrogen bond donors and acceptors and of van der Waals surfaces (e.g. hydrogens, methyl groups) that identifies the base pairs. For example, in the major groove an A-T base pair carries a signature of: acceptor – donor – acceptor – methyl (which is just the reverse for a T-A pair). And for a G-C pair, this signature would be: acceptor – acceptor – donor – hydrogen. These patterns are important since they allow proteins to unambiguously recognize DNA sequences; they do this through amino acids that can fit within the groove and establish non-covalent bonds with the bases *without* having to open and thereby disrupt the double helix.

Exercise: a class can construct several 4 – 8 nucleotide pair double helix, each with a different sequence. Locate the major and minor groove; determine the “code” a regulatory protein could “see” in the major groove for each sequence. Discuss models for how a protein could use this information to regulate the expression of information in DNA. (A RasMol-based computer visualization exercise, as well as further discussion of DNA-protein binding and gene regulation can be found in *The Teaching Guide*.)

- **For advanced classes: finding out how DNA structure was determined**

1. Chargaff’s rules: The question the biochemist, Erwin Chargaff sought to answer in the 1940s was whether Levine’s tetranucleotide hypothesis was correct (*i.e. that DNA was an endless repetition of the four bases: (ATGC)_n*, as discussed in *The Teaching Guide*) By determining the molar concentrations of bases from acid hydrolysates of DNA from several species, Chargaff was able to show that the simple [A]=[T]=[C]=[G] predicted by this hypothesis was wrong. More importantly, he was able to deduce, from his now-famous “Chargaff’s Rules”, the basis for Watson-Crick base pairing....and also showed that the potential for information in DNA was enormous. Students can do this exercise with chromatographic simulation using paper base cutouts, or the bases from the DNA Discovery Kit[®] (mix them up and have students separate each and determine the amounts of each). Ask students to use the data to predict something about the structure of DNA; or just to test out the tetranucleotide hypothesis.

2. Relating the model to measured parameters of DNA structure: diameter, pitch, and rise.

Measure these parameters on a 12 nucleotide pair DNA Discovery Kit[®] model, and compare these with data determined from Rosalind Franklin’s photographs (helix diameter: 2 nm, rise = 0.34 nm, pitch \cong 10 base pairs per turn, which means that each base pair is displaced about 36° with respect to the previous one). From this, calculate the scaling factor for the model (e.g. if the actual rise is 0.34 nm and the measured rise in the model is 1.5 cm, then the scaling factor is $(1.5 \text{ cm})(10^7 \text{ nm/cm}) / 0.34 \text{ nm} = 4.4 \times 10^7$, or roughly 40 million.)

3. **Other questions (see [The Teaching Guide](#))**

- Why does the pentose have a 2'H instead of an OH?
- Why thymine and not uracil?
- Can information be added or modified (without mutation)?
- How did we learn that the Watson-Crick model was right? What did it predict?
- How does RNA differ from DNA?

4. **Computer-Based Visualization Resources On DNA Structure**

- www.molviz.org (DNA tutorial)
- www.molvis.sdsc.edu/atlas/atlas.htm (Atlas of Macromolecules for Protein Explorer)
- www.moleculesinmotion.com/ (Molecules in Motion: “Exploring DNA”, “DNA as the Double Helix”)

These molecular visualization programs use the RasMol/Chime derivation, “Protein Explorer”. There is a self-paced tutorial for the use of this user-friendly, powerful visualization program. For all of these, your computer will have to have installed MDL Chime; in addition, they work best with Netscape 4.5 – 4.8. Both of these can be downloaded free from these sites. These web-based resources requires that your computer has MDL Chime installed. This is a free download.

ACKNOWLEDGEMENTS

Figs 5 & 6: From: Figs. 8-1 p. 274 and 8-8 p. 284, respectively, from “Lehninger Principles of Biochemistry” 4/e, by Dave Nelson and Michael Cox, © 2004 by W.H. Freeman and Company. Used with permission.

Figs. 7 & 11: pdb 1BNA/RasMol

Fig.8: From: Fig. 4-2 p. 103 from “Molecular Biology of the Cell” 5/e, by Harvey Lodish et al © 2004 by W.H. Freeman and Company. Used with permission.

Fig.10 & 12: From: Figs.6.5, p.101 and 6.10, p.105 from “Molecular Biology of the Gene”, 5/e by James D. Watson et al © 2004 by Pearson Education, Inc. Reprinted by permission.