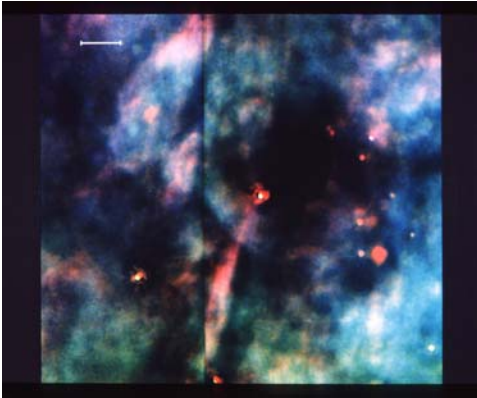


TAO of Mayan Healing 9

Sound and Vibration Accelerates changes in the DNA



In 1998 it was reported that scientists can point to a region in space that generates the kind of light that could help create the early building blocks of life, namely, the amino acids that are your DNA.

The region is one of the brightest star nurseries in the night sky, a nebula of dust and gas that lies 1,600 light years away in the sword of the constellation Orion. In the midst of the Great Nebula of Orion, an international team of astronomers has detected a phenomenon called “Circular Polarized Light”. It is this kind of light, created in laboratories but never before seen in space, that scientists state can selectively facilitate the formation of amino acids and other specific building blocks of life.

Therefore, James Hough of Britain’s University of Hertfordshire, who was involved in the discovery, confirms the fact that life evolved on Earth due as much to the environment of space as to the environment of Earth itself.

A research team, which includes astronomers from Australia, Britain, France and Japan, say circular polarized light (CPL), can explain why the proteins in nearly every organism on Earth are so-called left-handed.

On Earth, every amino acid comes in two forms. They are identical, except one is the mirror image of the other much like our hands. To distinguish them, scientists call the forms right-handed and left-handed.

Every organism on Earth essentially uses only one form of amino acid, the left-handed one to make proteins. This curiosity has puzzled scientists for the past 150 years. The detection of circular polarized light in space is a way to unlock the mystery of mirror images that are found in DNA pairings.

The conclusions point to asymmetry being necessary for life to be possible at all. At the cellular level, everything has a mirror image, utilizing the right and left amino acids.

Earlier proof of this theory came last year with the discovery of the left-handed amino acids that were found in a meteorite that fell on Australia. This discovery suggested the selection took place in space, not Earth, long before life began. Therefore, the current ability to see the circular polarized light as it creates these amino acids also supports this finding.

Every discovery that is made in the Universe, points to the basic idea, that we are all created of the same basic amino acids that are the protein building blocks of life. The

stars are formed from these nebulas as are we.

DNA - your cellular blueprint.

The purpose of this section is to establish a working paradigm of understanding of the workings of DNA that will allow you to have a new perspective of your own cellular biology.

The fundamental power of the DNA is contained in the output of a simple coding system that becomes the diversity of our life expression. Knowing how DNA works is an introduction to the most intimate aspects of your cellular biology. This code gives the instructions for form, cell by cell, to every living organism from the microscopic one cell form to the largest whales. The DNA structure contains the history of everything the cell has been is now and will become. The timeline encoded in your DNA defines your cycles of growth, repair, replications and dissolution. It operates your biological clock while carrying your ancestral imprints.

DNA stands for deoxyribonucleic acid. This has the properties of a weak acid. The “deoxyribo” refers to the name of a simple sugar molecule called deoxyribose and is part of the backbone of the DNA. You have one molecule of the deoxyribose on every step of the ladder that connects both sides of the structure. So the saying “sugar and spice and everything nice” takes on a new meaning in your structure.

Nucleic, refers to the fact that DNA resides in the cell’s nucleus within a specialized nuclear membrane. The basic structure follows a pattern of two long strands, spiraling around each other, one going east, and one going west. These strands are the backbone of all structure with rungs between them carrying the specific information.

A single phosphate molecule (salt) resides in the ladder connecting the dioxyribose units to complete the DNA spiral as support. Histone 1 from the nucleus makes the connection. Histones 2,3,4,5 make the repairs.

The rungs between the spiral supports that hold the actual information are made up of only four different molecules called bases. I will list each here:

Adenine-A- Crystalline purine base

Cytosine -C- Nitrogenous base

Guanine - G- Organic base.(found in high quantities in the manure(guano) of sea birds off the coast of Peru)

Thymine - T- Crystalline pyrimidine base. (Greek-der. spirit)

These bases are always in pairs. Each side support unit of the spiral projects one base into the center of the spiral, and they pair up in a very specific way.

Adenine always pairs with Thymine. (both crystalline)

Base for your spiritual and emotional aspects
Cytosine always pairs with Guanine. (nitrogen and organic)
Base for your intellect and physical aspects

The precise complementing of the DNA base pairs sustains the integrity of the code from generation to generation. When a DNA molecule replicates itself into two copies of itself, it follows a simple process.

The two chains split apart in the middle.
The pattern on both halves attracts its complementary pattern to itself.
This forms two new complete spirals.

In the individual organism, duplication of DNA is required for cells to divide and provide each new cell with its own copy of the full DNA blueprint. The DNA code on each side of the spiral is read in a specific direction, always opposite to the other. Sequence patterns in the chains instruct the cell chemistry as to which parts of the DNA should be read in which direction to get the code.

The Codons, each sequence of three bases, delivers a specific instruction to the cell chemistry. Since there are 4 bases, the number of combinations of 3 bases in sequence is $4 \times 4 \times 4$, or 64.

There are exactly 64 different codons that regulate cell chemistry and function. The most central operation of the codons is to direct the manufacture of proteins. A protein is a complex molecule made of a string of simpler building blocks called amino acids. A protein can be structural like collagen or elastin that supports. Proteins can be functional such as muscles that contract, or enzymes that catalyze the many chemical reactions that preserve the life of a cell.

How does the DNA make these proteins?

1. The particular sequence of information to be read is copied onto a molecule called RNA, or ribonucleic acid. RNA is essential to the synthesis (putting together elements to create the whole) of proteins in a cell. This is called transcription.
2. This RNA departs the nucleus (center of the cell) and moves to the liquid outside part of the cell called the cytoplasm. Because this form of RNA delivers information from the nucleus to the rest of the cell, it is called the messenger RNA, or mRNA.
3. RNA then directs the process of translation of the DNA sequence into the protein encoded in the pattern.
4. A start codon initiates the process with the amino acid methionine which is a sulphur base. This is the first of the amino acids.
5. The subsequent codons tell the cell machinery which of the 20 amino acids to add next

to the growing protein chain. This is the elongation's phase of protein synthesis.

6. The termination codon tells the cell when the chain is finished. This is the blueprint for the structural and functional proteins that condition and regulate life processes. The DNA sequence that encodes for a protein is known as a gene. The information content of a human DNA double helix is so enormous that it contains approximately 100,000 genes.

Each basic double helix of DNA makes one complete turn of the spiral every 10 base pairs. The average strand length has about 7 million full turns, which forms a coil within a coil containing 80 base pairs per loop. This structure then coils again up to 5-7 levels of supercoiling overall. All of it is packed into the tiny nucleus of a cell that resembles the double torus.

Genome- This term refers to the entire genetic code for an organism. The nucleus of each cell of the body contains the full genome, the complete genetic code for the whole body. Thus, each cell contains the full blueprint and memory needed to recreate the entire organism.

When the DNA is divided into multiple chains in a cell, as in human cells, each chain of DNA is called a chromosome. The full complement of human DNA is divided into 46 chromosomes, each one containing genes that distinguish one chromosome from another. When scientists were staining cells under a microscope with dyes, the chromosomes were seen to take up color intensely. Therefore the name chromosome was derived from the Greek words of "chromo" for color, and "soma" for body.

Understanding the biology of the cell will help you to understand your complex patterning and cellular nutritional needs. This knowledge will allow you to experience the many changes that are possible as you learn to work with energy. This "cell memory" is an important part of the foundation for all the teachings. Your patterning and behavior are affected each time you receive the energy for clearing, healing and balancing.

When working with the energy body, you do not need a language, you need only to portal the energy through the spin points and the cells respond to the intent of the energy they are receiving. Each cell responds as the energy activates the memory held in the DNA sequencing and releases the old patterning for dis-ease or pain as the person receiving the energy sets the intent for the clearing.

The energy that comes to us from the universe already contains the amino acids that are in the cells. When you look at the concept as a whole, you can understand why this new discovery of the creation of the amino acids in space is so important to the entire species. If each cell contains the whole, and each cell is composed of these amino acids, the possibilities for our future are limitless.

Sound and Vibrations of Chime affects the DNA



Working with a chime in the tone of E in the emotional field of the aura at 3-6 inches around the physical body allows the tone of energy to connect to the cellular level for release of emotional issues that create discomfort, pain, stress and disease. Accessing the energy meridians through the spin points on the body and applying a light pressure with the finger tips

stimulates the release of stored issues facilitating the client to experience a state of wellness after the session. During the practice of "Mayan Tonal Acupressure" many states of disease release as the cells respond.

Recent guidance to study the Histones in the DNA brought new confirmation that the DNA strands form a double torus, matching the energy movement found in space to the cells. Also the Histones in the chromatin are responsible for repair, regeneration, transcription and connecting the ladders between the DNA strands.

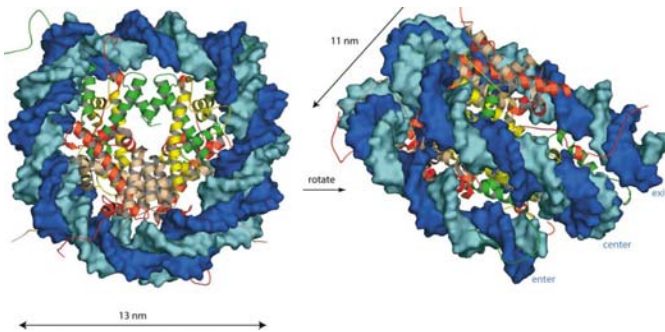


Figure 1. The Atomic Structure of the Nucleosome Core Particle
Each strand of DNA is shown in different shade of blue. The DNA makes 1.7 turns around the histone octamer to form an overall particle with a disk-like structure. Histones are colored as in (A) and (B) of Figure 2.

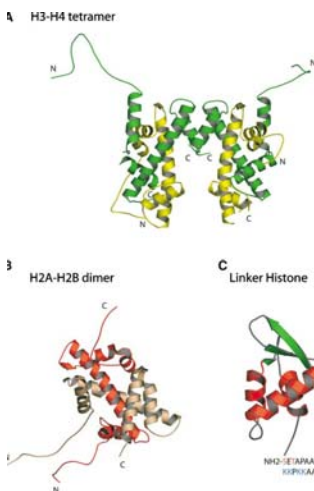
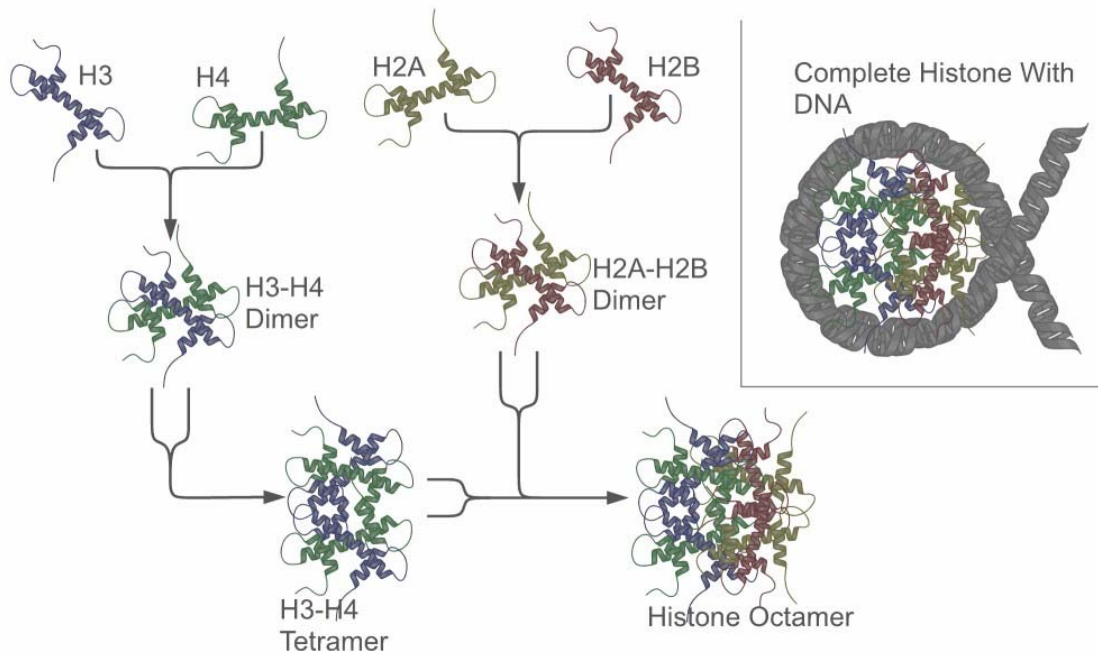


Figure 2. The Atomic Structure of the Core (A and B) and Linker (C) Histones (A) A tetramer of H3 (green) and H4 (yellow). (B) A dimer of H2A (red) and H2B (pink). (C) The linker histone has a conserved wing helix fold; the variant H5 is shown, (Ramakrishnan et al., 1993). The N- and C-terminal tails of linker histones are disordered and consist of numerous lysines and serines; the amino acid sequence corresponding to a human H1 is shown.

Within the core particle, the DNA is wrapped so that near identical structure to the structure obtained from recombinant histones that are free of such modification it forms 1.7 turns of a left-handed superhelix within the nucleosome core particle (Figure 1). Where the DNA enter and leaves the nucleosome, there are contacts with the N-terminal tail of the histone H3. The helical shaping the nucleosome structure, is 10.2 base pair as compared to 10.6 base pair for the helical periodicity of a free B-DNA.

This small adjustment between free and nucleosomal DNA is largely a result of the torsion during wrapping into a superhelix, which also allows of the entering and exiting linker DNA segments. In contrast to the solenoid model, the zigzag model uses the the minor grooves to bind to histones.

Therefore, the linker histone has an important function in the higher structure organization and its stability. We now know that arrays of nucleosomes fold into a 30 nm chromatin fiber to further combine. We have also learned much more about the linker histone H1, without having seen its structure in the context of the nucleosome core particle. There are multiple isoforms of linker histone H1 that are important for cell organization of nucleosomes. Mouse embryos with substantially reduced H1 die by midgestation, thus a threshold of H1 concentration is crucial for proper embryonic development. Biochemical and EM studies favor a zigzag model over the solenoid model for the arrangement of nucleosomes of about 90 amino acids with a long unstructured C-terminal tail and a shorter N-terminal tail.¹



■ Diagram of the center (still point) of the Nucleosome in the atom

You will notice that histone 1 is not pictured. It's structure has not been seen yet, but it is crucial for proper embryonic development and is thought to be a linker for changes in the DNA based on frequency and vibration stimulation.

God has a sense of humor

After I finished this section on the histones and considered this lesson to be finished a surprise was waiting in the New York Times. Reading scientific papers for the past year as guided to look for the activity of the histones in the still point of the nucleosome had been a time-consuming task. Due to the article that was published this morning, July 25, 2006, we now have the latest research that confirms the guidance, right down to the deadline.

Researchers believe they have found a second code in DNA in addition to the genetic code.

¹ The Nucleosome: From Genomic Organization to Genomic Regulation: Sepideh Khorasanizadeh

The genetic code specifies all the proteins that a cell makes. The second code, superimposed on the first, sets the placement of the nucleosomes, miniature protein spools around which the DNA is looped. The spools both protect and control access to the DNA itself.

The discovery, if confirmed, could open new insights into the higher order control of the genes, like the critical but still mysterious process by which each type of human cell is allowed to activate the genes it needs but cannot access the genes used by other types of cell.

The new code is described in the current issue of Nature by Eran Segal of the Weizmann Institute in Israel and Jonathan Widom of Northwestern University in Illinois and their colleagues.

There are about 30 million nucleosomes in each human cell. So many are needed because the DNA strand wraps around each one only 1.65 times, in a twist containing 147 of its units, and the DNA molecule in a single chromosome can be up to 225 million units in length.

Biologists have suspected for years that some positions on the DNA, notably those where it bends most easily, might be more favorable for nucleosomes than others, but no overall pattern was apparent. Drs. Segal and Widom analyzed the sequence at some 200 sites in the yeast genome where nucleosomes are known to bind, and discovered that there is indeed a hidden pattern.

Knowing the pattern, they were able to predict the placement of about 50 percent of the nucleosomes in other organisms.

The pattern is a combination of sequences that makes it easier for the DNA to bend itself and wrap tightly around a nucleosome. But the pattern requires only some of the sequences to be present in each nucleosome binding site, so it is not obvious. The looseness of its requirements is presumably the reason it does not conflict with the genetic code, which also has a little bit of redundancy or wiggle room built into it.

Having the sequence of units in DNA determine the placement of nucleosomes would explain a puzzling feature of transcription factors, the proteins that activate genes. The transcription factors recognize short sequences of DNA, about six to eight units in length, which lie just in front of the gene to be transcribed.

But these short sequences occur so often in the DNA that the transcription factors, it seemed, must often bind to the wrong ones. Dr. Segal, a computational biologist, believes that the wrong sites are in fact inaccessible because they lie in the part of the DNA wrapped around a nucleosome. The transcription factors can only see sites in the naked DNA that lies between two nucleosomes.

The nucleosomes frequently move around, letting the DNA float free when a gene has to be transcribed. Given this constant flux, Dr. Segal said he was surprised they could predict as many as half of the preferred nucleosome positions. But having broken the code, “We think that for the first time we have a real quantitative handle” on exploring how the nucleosomes and other proteins interact to control the DNA, he said.

The other 50 percent of the positions may be determined by competition between the nucleosomes and other proteins, Dr. Segal suggested.

Several experts said the new result was plausible because it generalized the longstanding idea that DNA is more bendable at certain sequences, which should therefore favor nucleosome positioning.

“I think it’s really interesting,” said Bradley Bernstein, a biologist at Massachusetts General Hospital.

Jerry Workman of the Stowers Institute in Kansas City said the detection of the nucleosome code was “a profound insight if true,” because it would explain many aspects of how the DNA is controlled.

The nucleosome is made up of proteins known as histones, which are among the most highly conserved in evolution, meaning that they change very little from one species to another. A histone of peas and cows differs in just 2 of its 102 amino acid units. The conservation is usually attributed to the precise fit required between the histones and the DNA wound around them. But another reason, Dr. Segal suggested, could be that any change would interfere with the nucleosomes’ ability to find their assigned positions on the DNA.

In the genetic code, sets of three DNA units specify various kinds of amino acid, the units of proteins. A curious feature of the code is that it is redundant, meaning that a given amino acid can be defined by any of several different triplets. Biologists have long speculated that the redundancy may have been designed so as to coexist with some other kind of code, and this, Dr. Segal said, could be the nucleosome code.

Circadian Cycle of Regeneration

Almost all the repair, regeneration and changes in your DNA take place each night between 10 pm and 2 am. Your organs, skin cells and glands are also in a state of regeneration and repair during these hours that can only be accomplished in the sleep state. If you miss these hours of sleep your body will not be in the highest state of vibrancy and wellness.

Commentary from Molecular Biologist, Georgia Tech Ph.D. researcher..

In addition to the molecular necessity of intervening sequences for genetic function, there is also a less immediately tangible requirement for non-coding DNA stretches for biological health. It has been hypothesized that DNA serves as an antennae for electromagnetic capacitance. If the genome has been fragmented to such a degree that it can no longer vibrate with the long wave within which other waveforms nest, those waveforms (memories) will be lost. The tingle of life transmitted through healthy, coherent DNA becomes absent. Humans feeding upon chickens and grains adulterated through genetic engineering may soon find themselves feeling devoid of the charge gleaned from organisms whose DNA was able to infuse their tissues with the electromagnetic charge known as life force. With rampant cases of chronic fatigue syndrome in adults, and attention deficit disorder in children, one may infer that our cellular batteries are being insufficiently charged.

Adonia McKinzi, Ph.D.
Molecular Biologist, Georgia Tech

DNA sequences show fractal correlations that are affected by sound

Commuter traffic, earthquakes and the selection of presidential candidates usually seem to take place in random ways. But investigators of chaos theory who turn to patterns called fractals manage to find order in the midst of such unpredictable events. Now add DNA to the catalogue of things fractal-like. 'There is some magical phenomenon going on that we just do not understand,' says H. Eugene Stanley, a physicist at Boston University. The orderly patterns of fractals emerge because an incident in the apparently chaotic system is actually correlated with a previous occurrence, much as a long-lasting pocket of slowly moving vehicles can result from one rubber-necking motorist briefly hitting the brake.

Calculations by Stanley's research group and by Wentian Li of the Rockefeller University and Richard F. Voss of the EBM Thomas J. Watson Research Center have shown that the position of nucleotides-adenine, guanine, cytosine and thymine- in a DNA sequence depends to some extent on the nucleotides that preceded it. The patterns in nucleotide sequences are similar to flicker, or 1/f, noise (pronounced "one over eff"). These fluctuations are time-scale analogues to the shapes of fractals, such as snowflakes and coastlines, which have the property of self-similarity: the component parts resemble the structure as a whole. The patterns of 1/f noise are just as prevalent in nature as their geometric counterparts; they can be found in such diverse phenomena as electric circuits and flood records. 'It is a special form of correlations found in natural phenomena and in human behavior,' says Voss, who found its presence in music.

If signals are completely random, as are the outcomes of flipping a coin, the results would show a "white noise" signature. Unless the coin is weighted, the probability of heads will be one half regardless of what came before. The outcome would be a collection of random signals similar to those that produce the nishing sounds between FM stations. In fact, 'if you want to store as much information as possible over some length,

the best storage method will be like white noise," notes Chung-Kang Peng, a member of Stanley's group. It is because every signal would be completely independent and carry its own message. If genetic data were stored as white noise, the probability of finding the same information along a strand of DNA the decay is much slower than exponential decrease. 'If the second nucleotide knows 50 percent of what the first knows, then the third knows only 25 percent,' Peng says.

But base pairs in DNA do not seem to occur in a completely random fashion. The researchers applied different statistical techniques to DNA sequences catalogued in GenBank a storehouse of genetic codes at Los Alamos National Laboratory. They found that the decay is much slower than exponential decrease. , The sequences show approximate $1/f$ Patterns. Roughly speaking, the f here represents the number of bases over which a particular nucleotide repeats. Along with Stanley's group, Li, a physicist, found that correlations exist in the intron sequences of DNA. Molecular biologists have sometimes referred to introns as 'junk DNA' because they do not encode structural information. The real information-carrying regions are located in sequences called exons. Yet unlike introns, exons lack long-range correlation and resemble white noise. Exactly why intron but not exon sequences show the correlations is not entirely known. The researchers think the long-range correlations which extend over thousands of base-pair positions represent a trade-off between efficient information storage and protection against error in the genetic code. Because changing part forces a change in other parts, there is some redundancy in the code. Thus, the correlations 'would give some immunity to error during transcription' Voss says. Exons, which hold the crucial data, would not exhibit long-range correlations because they need to carry as much information as possible.

Indeed, Voss has turned up some intriguing results based on evolutionary classification. He found that the sequences for organisms lowest on the evolutionary scale (bacteria and bacteriophages) were the least conelated. The correlations increased for higher organisms reaching perfect $1/f$ patterns in invertebrates. Then the scaling correlations decreased for vertebrates, mammals, rodents and finally primates. Stanley and his colleagues will soon publish a slightly different result showing the correlations increased as they moved up the entire evolutionary ladder. The group discovered that 'as you evolve, the long-range correlations become stronger and stronger Stanley says.

The results indicate that simpler organisms (those with short sequences) would not need the error protection required to maintain the more complex DNA sequences. "There seems to be a general principle involved" Voss observes. Nature has these fractal and $1/f$ type fluctuations" he remarks.

That may explain in part why music is pleasing. "One speculation is that music is trying to imitate nature and builds in $1/f$ noise," Voss explains. But a cohesive model to account for the ubiquity of $1/f$ and fractal phenomena eludes researchers. Like many a scientist and harried office worker before him, Li laments: "There is still a lot of work to be done." -Philip Yam



Use of selected words as sound and vibration in yeast DNA changes in a regular way in non-coding regions top but not in coding regions bottom.