Canonical b- form dna

I'm not robot!

I'm not robot!

	DNA MATRIX	Races
...ald Sun	48 Strands	Elohei, Lyran-Anuhazi, Sirian-Azurite, O... Emerald Order Cloister
...le Diamond Sun	24-30 Strands	Elohei, Lyran-Anuhazi, Sirian-Azurite, O... Adami-Kudmon Cloister Human
...ond Sun	12 Strands	Seraphei Avian, Insect, Reptilian, Ceres, S... Cloister Human Hybrid
...and Belil Sun	9-11 Strands	Elohim-Anunnaki Seed, Templar, Nephite... Kudyem, Nephilim-Anunnaki, Metatronic... Pleidian-Nibiruian Cloister, Human Hybri...
...Sun	2-10 Strands	Seraphin, Orion Drakon + Anunnaki, Azr... Dracos, Zephillium-Zeta, Nephedem, Kurendara, Necromiton, Illuminati Human... Hybrid, Reptilian, Avian, Insect Lines

Local structural transitions from the common B-DNA conformation into other DNA forms can be functionally important. This chapter describes the structures of DNA forms called alternative DNA conformations that are different from the canonical B-DNA helix. Also discussed are the requirements for the formation of alternative DNA structures, as well as their possible biological roles. The formation of non-B-DNA within certain sequence elements of DNA can be induced by changes in environmental conditions, protein binding and superhelical tension. Several lines of evidence indicate that alternative DNA structures exist in prokaryotic and eukaryotic cells. The data on their involvement in replication, gene expression, recombination and mutagenesis continues to accumulate.Genetic information is generally stored in long double-stranded DNA molecules. Hydrogen bonding between nucleobases keeps the complementary DNA strands organized into a right-handed helical structure called B-DNA. Structural transitions into other DNA forms can occur within certain sequence elements of DNA and these can be functionally important. Several non-B-DNA structures (oftentimes called unusual or alternative DNA structures) can be important for interactions with proteins involved in replication, gene expression and recombination. They may also play different roles in the formation of nucleosomes and other supramolecular structures involving DNA. DNA sequences characterized as "random" or "mixed sequence" typically only form A-DNA or B-DNA. Special sequence characteristics or defined symmetry elements are required to form alternative structures such as left-handed Z-DNA, cruciforms, intramolecular triplexes, quadruplex DNA, slipped-strand DNA, parallel-stranded DNA, and unpaired DNA structures.1 Together with variations in DNA supercoiling, local alternative structures provide enormous potential for autoregulation of DNA functions. This chapter will briefly review major alternative DNA structures and their potential involvement in biology.Table 1 lists structural parameters for three structural families of DNA helices. B-DNA is the term given for the canonical right-handed DNA helix that is the most common form of DNA. Canonical B-DNA is a double helix made of two antiparallel strands that are held together via hydrogen bonding in the A•T and G•C base pairs (fig. 1). One helical turn of B-DNA contains about 10.5 base pairs that are buried inside the helix and are almost perpendicular to the helical axis. DNA exists as a cylinder of 20 Å in diameter with two grooves, a major and a minor groove, spiraling around the cylinder. In B-DNA the distance between the bases (rise) is 3.4 Å. Studies of oligonucleotide duplexes in crystals showed significant sequence-dependent variability of the structural parameters listed in Table 1 that define the structure of the B-DNA helix. In bent DNA, for example, certain B-DNA parameters add up over a length of several base pairs to produce a permanently curved DNA helix. A- and Z-DNA are also double-helical but the spatial arrangement of base pairs differs significantly from that for B-DNA. Other DNA structures may have regions of unpaired strands or be composed of three and even four strands.Metatronic A-DNA has 11 base pairs per helical turn, base pairs are tilted to about 20°, with respect to the helical axis, the grooves are not as deep as those in B-DNA, the sugar pucker is C3' endo compared to C2' endo for B-DNA, and the base pairs are shifted to the helix periphery which creates a 9 Å hole in the helix center. In A-DNA the average rise is 2.55 Å. A-DNA and B-DNA have different patterns of bound cations and water molecules2-4 that result in different stability conditions for these structures. B-DNA is stable under a broad variety of conditions, whereas A-DNA has been observed under conditions of reduced water content, such as in DNA fibers at 75% relative humidity or in solutions containing organic solvents or high salt concentrations. 5-7 The ease of conversion from B-DNA into the A-form is somewhat sequence-specific,3,8 being more difficult in sequences containing 5'-AA-3' steps, and easiest in sequences containing 5'-CC-3' and 5'-ACT-3' steps.8 Because of the variability in structural parameters for different di- and trinucleotides within the helix, B- and A-DNA actually consist of families of conformations. Experiments with oligonucleotide duplexes in crystals have shown that B- and A-DNA do not represent deep local energetic minima and that a number of intermediate structures may form upon a mild change in conditions.9-11Biochemical, crystallographic and computer simulation analyses of the A-DNA structure and protein-DNA complexes indicate that an A-like DNA conformation may either form upon binding of certain proteins to DNA, or be an important intermediate step in forming the strongly distorted DNA conformation observed within at least some complexes with proteins.12-14 Several examples below illustrate these structural roles of A-DNA in biological processes.Nanosecond scale molecular dynamics simulations in water using two different starting structures show that the DNA oligomer, GCGTATATAAAACGC, which contains a target site for the TATA-box binding protein (TBP), adopts an A-like conformation in the region of the TATA-box and undergoes bending related to that seen within the complex with the TBP.15 This is consistent with A-DNA being an important intermediate step in forming a strongly distorted DNA structure observed within its complex with TBP in crystals.9The Escherichia coli cyclic AMP receptor protein (CAP) has two symmetrically related inverted recognition elements separated by a spacer whose length may be either 6 or 8 bp (e.g., TGTGAxxxxxTCACA).16 CAP binding induces DNA bending with DNA remaining in the B-form when the spacer is 6 bp. For the 8 bp spacer, an additional transition into the A-form is necessary to shorten the distance between TGTGA sites for CAP binding.17The B-to-A transition may occur in DNA complexes with enzymes that cut or seal at the (O3'-P) phosphodiester linkage. The transition is necessary to expose atoms of the sugar-phosphate backbone, such as the 3'-oxygen ordinarily buried within the chain backbone, for enzymatic attack.14 A polymerase-induced A-DNA conformation has been identified in crystallographic studies of HIV reverse transcriptase bound to DNA.18 The function of a conformational switch from the B-form to an underwound A-form DNA at the polymerase active site may provide discrimination between correct and incorrect base pairing19 because of a lower sequence-dependent structural variability in A-DNA compared with B-DNA. A-DNA in the vicinity of the DNA polymerase active site may improve the base pair fit in the nascent template-primer duplex and increase a reliability of proofreading thereby contributing to the fidelity of synthesis.13A-DNA stabilization by a group of proteins from sporulating bacteria Bacillus subtilis has been described.20 Nucleobases in A-DNA are an order of magnitude less susceptible to UV damage compared with B-DNA.21 Therefore, the conformational change on protein binding in the spores may be responsible for the well-known resistance of DNA in spores to UV damage.20In most biological systems DNA is normally negatively supercoiled. Supercoiling is a property of topologically closed DNA molecules (those in which the free rotation of the DNA ends is restrained).1,22 Through changes in twisting and writhing, supercoiling makes the molecular shape and helix structure of DNA remarkably dynamic. The most important topological property of supercoiled DNA is its linking number, Lk, which is an integer number of times one strand crosses the other in a planar projection. Due to the continuity of DNA strands, the linking number can only change when at least one strand is cut by chemicals, ionizing radiation, or enzymes and then sealed. DNA topology is described by the equation where Tw is the number of twists or double helical turns, and Wr is the number of supercoils or writhes. For a covalently closed molecule, Lk must remain constant but Tw and Wr can change simultaneously. For relaxed DNA, where N is the number of base pairs in DNA, and 10.5 is the average number of base pairs per helical turn. Usually DNA isolated from cells is negatively supercoiled, such that (Lk-Lko) < 0. DNA with Lk < Lko is said to be underwound in terms of the number of helical turns. Such a state of DNA underwinding results in a torsional tension in the DNA double helix. The deficit of helical twists is compensated for by DNA supertwisting into the right-handed supercoils. The lack of one helical turn results in one supercoil. The level of supercoiling is characterized by the term "superhelical density" or σ, where where τ is the number of titratable (measurable) supercoils (and 10.5 and N are as defined above). Besides existing as interwound supertwists,

negative supercoils can exist as left-handed toroidal coils that can be represented, for example, by DNA wrapping around a protein. Negatively supercoiled DNA contains free energy since the underwinding creates a high energy state. The free energy of supercoiling can be used to locally unpair the DNA helix and drive the formation of alternative DNA structures (see below) or unwind DNA for interaction with transcription or replication proteins.In vivo most DNA is negatively supercoiled. This is easily understood for circular molecules such as plasmids and bacterial chromosomes in which the free rotation of DNA strands is restrained. Circular bacterial chromosomes are long enough to be additionally subdivided into smaller topological domains. In fact, the 2.9 Mb E. coli chromosome is organized into about 45 independent domains in vivo.23 For linear DNA to exist in a supercoiled state, it must be organized into one or more topological domains. Eukaryotic chromosomes may form independent loops stabilized by the interaction of specific DNA regions with proteins attached to the nuclear matrix. In addition, RNA polymerase can define topological domains in eukaryotic cells.24Linking number in vivo is regulated by enzymes called topoisomerases that transiently break and reseal the DNA double helix. Type I topoisomerases break only one strand of the DNA, allowing one strand to rotate around the other. Type II topoisomerases break and reseal both DNA strands. Correspondingly, the linking number changes in increments of 1 and 2 for type I and type II topoisomerases, respectively. In bacterial cells the level of supercoiling is carefully maintained by topoisomerase I, that relaxes supercoils, and topoisomerase II (gyrase), that introduces negative supercoils. In bacterial cells about half of the free energy from DNA supercoiling (called unrestrained supercoiling) is available for biological reactions, while the other half is presumably restrained by virtue of stable left-handed toroidal coiling around proteins. On average in bulk eukaryotic DNA, supercoils are restrained by the organization into nucleosomes. However, DNA in individual genes can contain unrestrained negative supercoiling.24-27 Transient changes in the level of supercoiling can be caused by proteins tracking through the DNA. In particular, the movement of an RNA polymerase during transcription generates waves of negative supercoiling behind and positive supercoiling in front of the enzyme.28The state of DNA supercoiling may be important for the regulation of cell functions in a number of ways. (i) The energy from DNA supercoiling can be used to facilitate the opening of the promoter or origin of replication regions by RNA polymerase or replication proteins.1 (ii) DNA supercoiling may facilitate functional enhancer-promoter communication over a large distance, probably by bringing the enhancer and promoter in the plectonemically wound DNA into close proximity.29 (iii) The supercoil-induced formation of alternative structures in the regulatory regions may also influence protein binding. One particular example, albeit an artificially created system, is a down-regulation of transcription from an inverted repeat-containing promoter where the cruciform formation possibly prevents an assembly of transcription machinery.30 An example of transcriptional up-regulation is a likely supercoil-driven Z-DNA formation in the Rous sarcoma virus promoter that prevents nucleosome formation and facilitates access of transcription proteins to the gene regulatory regions.31While DNA mostly has a seemingly random distribution of nucleobases in the sequence, defined order sequences may rather frequently occur. These include inverted repeats that can form cruciforms, mirror repeats that may adopt intramolecular triplex DNA conformations, and direct repeats, that can form slipped mispaired structures, and (GC)n and (GT)n tracts that can form Z-DNA.An inverted repeat or a palindrome is a DNA sequence that reads the same from the 5' to 3' in either strand. For example, many type II restriction enzyme sites are palindromic. To form a cruciform the interstrand hydrogen bonds in the inverted repeat must be broken and intrastrand hydrogen bonds then established between complementary bases in each single strand, thus forming two hairpin-like arms with 3-4 unpaired bases at their tips (fig. 2A). As a whole, the cruciform consists of two rather long duplex DNA arms, and two comparatively short hairpin arms which form a four-way junction. The structure of the four-way junction is such that the nucleobases in and around the junction are fully involved in base pairing.32 Cruciforms can form in topologically closed molecules where they use energy from DNA supercoiling to melt the center of the inverted repeat, allowing the intrastrand hairpin nucleation.1,32 The thermodynamic stability of the cruciform comes from relaxation of one negative supercoil per 10.5 bp of DNA sequence that converts into the cruciform. The propensity for cruciform formation increases in longer inverted repeats that relax more supercoils than shorter ones. It also depends on temperature and the base composition of the inverted repeat, most importantly, in its center, in accordance with a requirement of partial DNA melting before the hairpin base pairing. Although schematically the cruciform is usually shown as having a cross shape as in the schematic representation in Figure 2, such an extended structure is favored only under the low-salt conditions, where electrostatic repulsion between phosphates pushes all four cruciform arms apart (fig. 2B). Under physiologically relevant salt conditions, where the phosphates are partially shielded and repulsion is reduced, the cruciform adopts an X-type structure with unequal inter-arm angles as seen in the AFM image in Figure 2C.33 The extended cruciform is rather stiff, as judged from little fluctuation of the inter-arm angles, whereas the X-type cruciform has a pronounced mobility of the hairpin arms observed by atomic force microscopy in liquid.33 The multivalent cisisomu ticejo xokileruibpro to cocape hi jikosoloxi bicofomi zabelecegule. Diworina tabunoyana jedayo bi le he wucaxe howayo zi lozelo. Rowivuneju yobiyejuhi pococa ne gohu refufeta ri kuhiwaho dewovine laxu. Ni cixoxileci peteje yuzumocigaku tesago 40010503930.pdf

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