

POLYMORPHISM OF NUCLEIC ACID DUPLEXES AS REVEALED BY X-RAY DIFFRACTION ANALYSIS OF ORIENTED FIBERS

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Complementary base-paired polynucleotide duplexes are quite polymorphic. This is not surprising when one considers that the shape of their usual unit of structure, the nucleotide, has six endocyclic bonds and a fairly flexible furanose ring with which to contrive changes in shape. These different residue shapes confer very distinctive morphologies on the polymer helices which incorporate them (1, 2). These differences are indicated by the axial translation (h) and rotation (t) per nucleotide residue in each helix.

By these indices DNA-DNA duplexes are the most variable: in their right-handed helical forms $0.26 \text{ nm} \leq h \leq 0.34 \text{ nm}$ and $30^\circ \leq t \leq 48^\circ$; in the three left-handed helices (3, footnote 1) discovered so far the unit of structure is a dinucleotide and $0.72 \text{ nm} \leq h \leq 0.76 \text{ nm}$ and $-60^\circ \leq t \leq -25^\circ$.

The right-handed helices can be divided into two families named *A* and *B* after their eponymous members. In the *B* family the nucleotides have *C2'-endo* furanose rings, $0.30 \text{ nm} \leq h \leq 0.34 \text{ nm}$ and $36^\circ \leq t \leq 48^\circ$. There is an inverse relationship between h and t and it is noteworthy that the commonest form, *B*-DNA, has the extreme values ($h = 0.34 \text{ nm}$, $t = 36^\circ$). *B*-DNA is the form assumed by DNAs of any sequence when conditions are relatively hydrophilic. In the *A* family h is much more variable ($0.26\text{--}0.33 \text{ nm}$) than t ($30\text{--}32.7^\circ$). Once again, the commonest form, *A*-DNA, has the extreme values ($h = 0.26 \text{ nm}$, $t = 32.7^\circ$). The *A*-DNA conformation is remarkable in being observed not only with DNA-DNA duplexes (under relatively more hydrophilic conditions), but also in the short quasihelical stems of *t*-RNA and even in poly (X)·poly (X)² and poly (s²U)·poly (s²U)³ duplexes which have nonclassical purine-purine and pyrimidine-pyrimidine base-pairs, respectively.

The more unusual right-handed DNA-DNA helices are observed usually with DNAs containing special sequences and in circumstances in which *B*-DNA is less stable, e.g., *E*-DNA (4) with $h = 0.32 \text{ nm}$, $t = 48^\circ$ was observed in poly d(IIT)·poly d(ACC); *D*-DNA with $h = 0.30 \text{ nm}$, $t = 45^\circ$ was observed with poly d(IC)·poly d(IC) (5) and poly d(AT)·poly d(AT) (6). However, other sequences would not be excluded on steric grounds from being incorporated into these structures.

The left-hand helices (3) observed with poly d(GC)·poly d(GC) and poly d(AC)·poly d(GT) both have $h = 0.72 \text{ nm}$ and $t = -60^\circ$, and a minor variant observed with poly d(As⁴T)·poly d(As⁴T) has $h = 0.76 \text{ nm}$ and $t = -51.5^\circ$. In these two helical forms only alternating purine-pyrimidine sequences are permitted: the purine nucleoside has to be *syn* with a *C3'-endo* sugar, and the pyrimidine nucleoside *anti* with a *C2'-endo* sugar. A left-handed double helix which would accommodate any sequence has $h = 0.76 \text{ nm}$ and $t = -25^\circ$.

¹Arnott, S., and R. Chandrasekaran. Manuscript submitted for publication.

²Arnott, S., R. Chandrasekaran, W. A. Day, L. Puigjaner, and L. Watts. Manuscript submitted for publication.

³Arnott, S., R. Chandrasekaran, A. G. W. Leslie, L. Puigjaner, and W. Saenger. Manuscript submitted for publication.

The RNA-RNA duplex helices so far observed are all *A*-type and right-handed. Steric compression of the 2'-OH precludes *B*-type conformations. If one excludes the quasihelical fragments of *t*-RNA which have an *A*-DNA-like conformation, then for RNA-RNA double helices $0.27 \text{ nm} \leq h \leq 0.30 \text{ nm}$ and $30^\circ \leq t \leq 32.7^\circ$.

DNA-RNA hybrid duplexes are also *A*-type. In less hydrophilic environments they are like *A*-DNA ($h = 0.26 \text{ nm}$, $t = 32.7^\circ$). Otherwise they are usually like RNA duplexes ($h \sim 0.3 \text{ nm}$, $t \sim 30^\circ$).⁴ In one instance, with poly dI·poly rC, an unusual form has been observed, with $h = 0.32$ and $t = 36^\circ$. This member of the *A* family has a structure very like the original Crick and Watson model for *B*-DNA (7).

None of the RNA-RNA or RNA-DNA double helices exclude particular sequences through steric compression.

DNA must also have unwound conformations, albeit fleetingly, at some stages of its life cycle. One such conformation has already been trapped in oriented fibers and analysed.⁵

The partial dependence of the various nucleic acid conformations on intrinsic factors (such as base composition and nucleotide sequence) and on extrinsic factors (such as the dielectric constant of the environment, counteraction type, etc.) prompts speculation about the dynamics of interactions involving DNA. At the same time, the details of the structures observed disciplines these speculations.

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CORRELATED MOTIONS IN DNA

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The furanose ring of nucleic acids plays a key role in determining the conformations of nucleic acids because it shares a common bond C3'-C4'(ψ) with the sugar-phosphate backbone. This

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⁵Arnott, S., P. J. Bond, and R. Chandrasekaran. Manuscript submitted for publication.