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 nm $\leq h \leq$ 0.30 nm and 30° $\leq t \leq$ 32.7°.

DNA-RNA hybrid duplexes are also *A*-type. In less hydrophilic environments they are like *A*-DNA (h = 0.26 nm, t = 32.7°). Otherwise they are usually like RNA duplexes (h ~0.3 nm, t ~30°).[4] In one instance, with poly dI·poly rC, an unusual form has been observed, with h = 0.32 and t = 36°. 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, countercation 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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REFERENCES

1. Arnott, S. 1976. DNA secondary structures. *In* Organisation and Expression of Chromosomes. Dahlem Conferenzen, Berlin. V. G. Allfrey, E. K. F. Bautz, B. J. McCarthy, R. T. Schinke and A. Tissieres, editors. 209–222.
2. Arnott, S. 1977. Secondary structures of polynucleotides. *In* First Cleveland Symposium on Macromolecules. A. G. Walton, editor. Elsevier-North Holland, Amsterdam. 87–104
3. Arnott, S., R. Chandrasekaran, D. L. Birdsall, A. G. W. Leslie, and R. L. Ratliffe. 1980. Left-handed DNA helices. *Nature (Lond.).* **283**:743–745.
4. Leslie, A. G. W., S. Arnott, R. Chandrasekaran, and R. L. Ratliff. 1979. Polymorphism of DNA. *J. Mol. Biol.* In press.
5. Mitsui, Y., R. Langride, B. E. Shortle, C. R. Cantor, R. C. Grant, M. Kodama, and R. D. Wells. 1970. Physical and enzymatic studies on poly d(I-C)·poly d(I-C), an unusual double-helical DNA. *Nature (Lond.).* **228**:1166–1169.
6. Arnott, S., R. Chandrasekaran, D. W. L. Hukins, P. J. C. Smith, and L. Watts. 1974. Structural details of a double-helix observed for DNAs containing alternating purine and pyrimidine sequences. *J. Mol. Biol.* **88**:523–533.
7. Crick, F. H. C., and J. D. Watson. 1954. The complementary structure of deoxyribonucleic acid (DNA). *Proc. R. Soc. A.* **223**:80–96.

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

[4]Arnott, S., A. Banerjee, D. L. Budsoll, R. Chandrasekaran, P. Keller, A. G. W. Leslie, E. C. Selsing. Manuscript submitted for publication.

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

structural feature enables the transmission of conformational changes between the side-chain base and the backbone through conformational correlations between the base and sugar (χ, ψ'; χ, ψ) (1). Fig. 1 shows the dependence of the sugar-backbone torsion angle ψ' with the pseudorotation parameters $\underset{\sim}{P}$ (phase angle) and τ_m (amplitude of puckering) (2). For instance for the average puckering amplitude ($\tau_m = 39°$), the fluctuation range available to ψ' is ~6° for the preferred C3′-*endo* domain ($0 \leq \underset{\sim}{P} \leq 36°$). But, in the preferred C2′-*endo* domain ($144 \leq \underset{\sim}{P} \leq 198°$), the fluctuation range for ψ' increases to 26°. Consequently, thermally-induced local fluctuations of $\underset{\sim}{P}$ can be transmitted along the backbone through ψ', particularly when the sugar is in the C2′-*endo* domain. The sugar pucker-dependent flexibility of DNA is further exemplified by studies that have shown that due to steric interactions, the absence of the 2′–OH group in deoxyribose tends to increase the conformational flexibility about the internucleotide phosphodiester (ω, ω') especially when the sugar assumes the C2′-*endo* pucker (3).

Studies of(n,h) plots (4) have shown that the phosphodiester torsions (ω', ω) are correlated with the sugar pucker (ψ') and the C4′–C5′ torsion (ψ). Because the P–03′ (ω') bond is roughly parallel to the helix axis in B-DNA (Fig. 2), rotations about ω' will lead to unstacking of the bases. Correlated motions about the (ω', ψ') pair of bonds will determine the winding angle or the number of residues per helical turn. On the other hand, the P–05′ (ω) bond is roughly parallel to the base pairs in B-DNA type helices and rotations about ω and its correlated effects on ψ with ψ' will lead to a tilt of the bases and generate bending of helix. Thus, in DNA, the twisting (winding) is determined by the (ω', ψ') torsional coupling and the bending (superhelix formation) by the (ω, ψ) and (ω, ψ') couplings. In a closed circular DNA, the invariance of the linking number will lead to a further coupling between twisting and bending. Therefore, the correlated motions between the base-sugar (χ, ψ'; χ, ψ) and the sugar-phosphate backbone pairs of torsions (ω', ψ'), (ω, ψ), and (ω, ψ') will generate a range of conformationally related (polymorphic) structures of DNA.

The conformational fluctuations generated by these torsion angle variations can lead to local variations in the winding angle and bending with local loosening and eventually opening of the double helical structure. The latter phenomena would be intimately related to the local

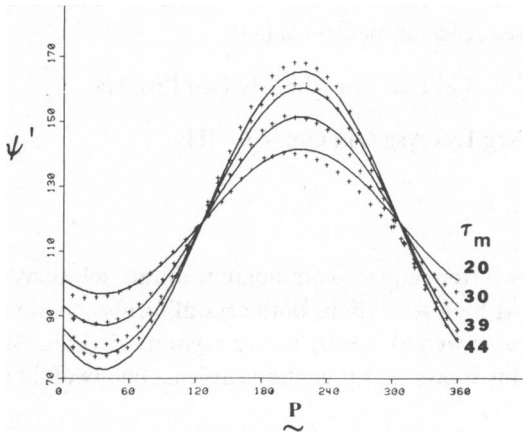

Figure 1

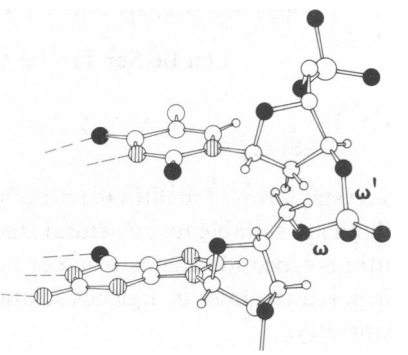

Figure 2

Figure 1 Dependence of ψ' with P and τ_m.
Figure 2 A DNA segment showing the ω and ω' bonds.

base sequence. These base-sequence-dependent fluctuations may be specific for protein recognition or drug binding.

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REFERENCES

1. Sundaralingam, M. 1975. Principles governing nucleic acid and polynucleotide conformations. *In* Structure and Conformation of Nucleic Acids and Protein-Nucleic Acid Interactions. M. Sundaralingam and S. T. Rao, editors. University Park Press, Baltimore. 487–524.
2. Altona, C., and M. Sundaralingam. 1972. Conformational analysis of the sugar ring in nucleosides and nucleotides. A new description using the concept of pseudorotation. *J. Am. Chem. Soc.* **94**:8205–8212.
3. Yathindra, N., and M. Sundaralingam. 1975. Backbone conformations in deoxyribonucleic acids. Conformational role of the 2'-hydroxyl group on the internucleotide phosphodiester conformations. *Biopolymers* **14**:2387–2399.
4. Yathindra, N., and M. Sundaralingam. 1976. Analysis of the possible helical structures of nucleic acids and polynucleotides. Application of (*n,h*) plots. *Nucleic Acids Res.* **3**:729–747.

STRUCTURAL STUDIES OF BEE MELITTIN

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INTRODUCTION

The question of how proteins refold in passing from an aqueous phase to an amphipathic environment such as a membrane is being addressed by a structural study of bee melittin. Melittin is the toxic, main protein of bee venom, and has been shown by others to integrate into natural and synthetic membranes and to lyse a variety of cells. This function is presumably related to its unusual sequence. Except for charges at the N-terminus and at lysine 7, the first 20 residues are largely apolar. In contrast, the last six residues contain four charges and two polar residues. The entire sequence of melittin is (1):

NH_2–Gly Ile Gly Ala Val Leu Lys Val Leu Thr Thr Gly Leu Pro Ala

Leu Ile Ser Trp Ile Lys Arg Lys Arg Gln Gln–$CONH_2$.

RESULTS

Two crystal forms of melittin have been grown from aqueous ammonium sulfate solutions (2), and both are suitable for structural studies at high resolution. Both crystal forms contain two melittin polypeptide chains (each of molecular weight 2,840) in the asymmetric unit. Since melittin is a tetramer in aqueous solution, this shows that it contains at least one twofold axis of symmetry.

The unit cell dimensions of the orthorhombic form II are convenient for diffractometry measurements, and data have been collected for the native protein to 2.0 Å resolution and for five heavy atom derivatives, four of them to 2.8 Å resolution and the other to 3 Å resolution.