WHY DO DNA HELICAL MODELS EXHIBIT WEDGE ROLLS? A MATHEMATICAL RATIONALE*

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ABSTRACT

The base-pair parameters wedge-tilt and wedge-roll are extremely useful for describing curved DNA structures. The wedge effect has generally been assumed to be due to the differences between the base-pair tilts and rolls of two successive base-pairs in a DNA molecule. A mathematical formalism has been established here, which shows that, wedge-roll is a function of base-pair tilt and helical twist, similarly the wedge-tilt is a function of base-pair roll and helical twist. This provides a straightforward explanation for the reported wedge-roll in A-DNA helical model of 12° and gives a value of -3.8° for B-DNA fiber model. The wedge-rolls and wedge-tilts calculated for the oligonucleotide crystal structures, using these relations, are in excellent agreement with the values reported earlier, which were calculated directly from the coordinates, using a global helix axis.

INTRODUCTION

The uniform helical models proposed on the basis of X-ray fiber data assume that all the nucleotide units have an identical structure. Since there is no variation between the units, the base-pairs in them are simply characterized in terms of their orientation with respect to the helix axis (Z-axis). The base-pair orientation is described in terms of two angles: tilt (θ₁) and roll (θ₂) and the displacement (D Å) of the base-pair centre from the helix axis. However, the recently studied oligonucleotide crystal structures and the models for curved DNA indicate that the relative orientations of neighboring base-pairs may also be described in terms of two wedge parameters, wedge-roll (θ₃) and wedge-tilt (θ₄). The wedge-roll in a straight B-DNA model has been assumed to be zero while the large wedge-roll value for fiber A-DNA has been explained descriptively and pictorially as being due to the large displacement of the tilted base-pairs from the helix axis. However no rigorous mathematical or geometrical explanation is available. We show here, from simple mathematical relations between the orientation vectors of two neighbouring base-pairs in a regular helix that the wedge-roll can be simply expressed in terms of the base-pair tilts and helical twist, a relationship shown graphically in our earlier paper. Similarly the wedge-tilt is related to the intrinsic rolls of the base-pairs.

METHOD

The orientation vectors for each base-pair have been termed as the local base-pair axes. The average of the two base normals defines the base-pair normal (local Z-axis) while the line joining C₈ (purine)-C₆ (pyrimidine) defines the Y-axis. The X-axis is now defined by the direction normal to both this axis and the base-pair normal, such that a right-handed frame of reference is obtained (figure 1). These axes can be defined in an external cartesian frame of reference by their direction cosines (lₓ, mₓ, nₓ) and (lᵧ, mᵧ, nᵧ), and the unit vectors along the X and Y-axes of the first base-pair are given by

\[ X₁ = lₓ i + mₓ j + nₓ k \]  \hspace{1cm} (1)

\[ Y₁ = lᵧ i + mᵧ j + nᵧ k \]  \hspace{1cm} (2)

Since the Z-axis of the external frame can be chosen to coincide with the helix axis, the second base-pair is related to the first by a rotation (corresponding to helical twist Θ) and a translation (helical rise) about this axis. The unit vectors X₂ and Y₂ are therefore given by the following relations

\[ X₂ = (lₓ \cos \Theta - mₓ \sin \Theta)i + (lₓ \sin \Theta + mₓ \cos \Theta)j + nₓ k \] \hspace{1cm} (3)

\[ Y₂ = (lᵧ \cos \Theta - mᵧ \sin \Theta)i + (lᵧ \sin \Theta + mᵧ \cos \Theta)j + nᵧ k \] \hspace{1cm} (4)

where \( \Theta \) = helical twist angle; \( nₓ = \sin(\Thetaₓ) \) and \( nᵧ = \sin(\Thetaᵧ) \).