# AN ALTERNATIVE STRUCTURE FOR DNA AND ITS RELEVANCE TO DNA SUPERCOILING

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ABSTRACT

A space-filling (CPK) model of an alternative structure for DNA is given. The structure consists of two strands of opposite polarity each having alternating right and left-handed helical segments. Each segment is approximately five base-pairs long. The strands are held together by Watson-Crick base pairing. Such a structure avoids intertwining and thus offers a natural solution to the problem of a strand separation during replication. In addition, the axes of consecutive helical segments could trace a curve, facilitating supercoiling. The overall energetics of this structure favour it over existing models.

TWO possible alternatives (Type I and Type II) to the classical structure of DNA (B form) were recently proposed by us[1]. These structures maintain Watson–Crick base pairing[2] but avoid intertwining of the two anti-parallel strands. Investigators from New Zealand[3] simultaneously proposed a possible structure for DNA which is very similar to our Type I structure. Both the Type I and Type II structures contain alternating right- and left-handed helical segments, each approximately five base pairs long. In the Type I structure all the sugars in a strand point in the same direction whereas in Type II sugars in alternate segments point in opposite directions. One important property of both these types of structures is that there is no intertwining of the two strands as in the double helix.

We have now made further investigations on structural features of both the Type I and Type II models. On attempting to build space-filling (CPK) models of these two structures, we found that this could be done only with Type II and not with Type I. A CPK model of the type II structure is shown in Fig. 1. A more detailed analysis of both the Type I and Type II conformations has shown that the Type II structure is energetically more favourable. In our opinion these results rule out the possibility of our Type I structure and as well as that proposed by Rodley *et al.*[3]. We discuss here some properties and implications of the Type II structure.

FIG. 1. A space-filling (CPK) model of the Type II structure.

As mentioned earlier, in the Type II structure, sugar residues in alternating segments along a strand point in opposite directions, each of the two strands having alternating right- and left-handed helical segments approximately five base pairs in length. As a consequence, each strand has bends or folds at places where helical segments of opposite sense are linked. These bends impart a significant amount of flexibility to the polynucleotide, because one has three degrees of freedom to define the relative orientations of two successive segments in terms of their axes. The three degrees of freedom as shown in Fig. 2 are : (*i*) a finite twist, $\theta$, in the coiling of successive helical segments, but maintaining the same helical axis. (*ii*) a lateral displacement, *d*, of the axes of two consecutive segments, and (*iii*) a relative tilt, $\alpha$, of the axes of successive segments. We have found that $\theta$ for 10 base pairs is given by $0 \leqslant \theta \leqslant 30°$ to $40°$. Such a twist will result in a major coiling of the duplex with a minimum number of 90 to 120 base pairs in a repeat of the major coil. The lateral shift, *d*, always maintains the vertical separation of base pairs at 3·4 Å. The relative tilt, $\alpha$, allows the base pair separation at the bend to vary from 3·4 to 4·0 Å.

We have made use of one or all of the above three degrees of freedom to generate supercoiled structures of DNA without breaking any hydrogen-bonded base pair in this process. The resulting duplex requires no additional backbone strain or unfavourable base stacking. Thus, by keeping the axes of the segments parallel (*i.e.*, $\chi = 0$) but displaced by distance $d$ (< 1 Å) between alternate segments and with a finite twist $\theta$ (< 30°), one can generate supercoiled and looped DNA duplexes of SV40 DNA, with dimensions similar to those observed for SV40 DNA[4]. In other words, supercoiling of DNA can occur in this model without an increase in the free energy of the structure.

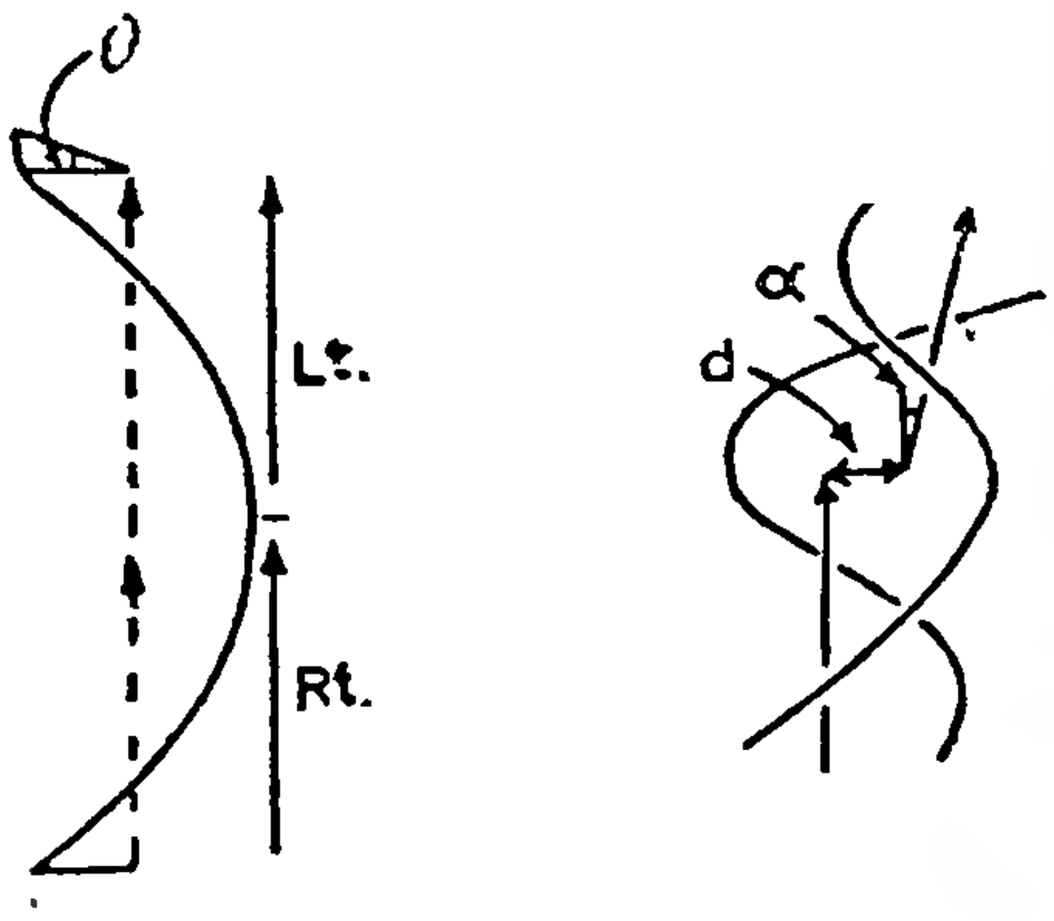


FIG. 2. The three degrees of freedom to define the relative orientation of two consecutive segments of opposite sense. $\theta$, the angle of twist for 10 base pairs about a common helix axis; $d$, lateral displacement of the axis; $\alpha$, angle of tilt between axes of two successive segments (*see* text for details).

Let us consider whether this flexibility of the Type II structure could provide a possible solution to the compression of DNA within chromatin[5]. It has been known that the classical double helix is unable to withstand such compression without introducing abrupt discontinuities in the helix[6]. On the other hand, our Type II structure permits the construction of a model of chromatin in which a DNA duplex of diameter 20 Å is wrapped around a core of radius 30 Å, with a pitch of 100 Å for 100 base pairs (*see* Fig. 3). This does not demand any destabilization due to destacking, breaking of hydrogen bonds or steric strain. The octamer[7] histone core of radius 30 Å can readily be accommodated in the inner core of such a supercoil. It, therefore, appears that the inherent flexibility of the Type II structure could result in the initiation of supercoiled structures of DNA following energetically allowed folds. The details will be published elsewhere.

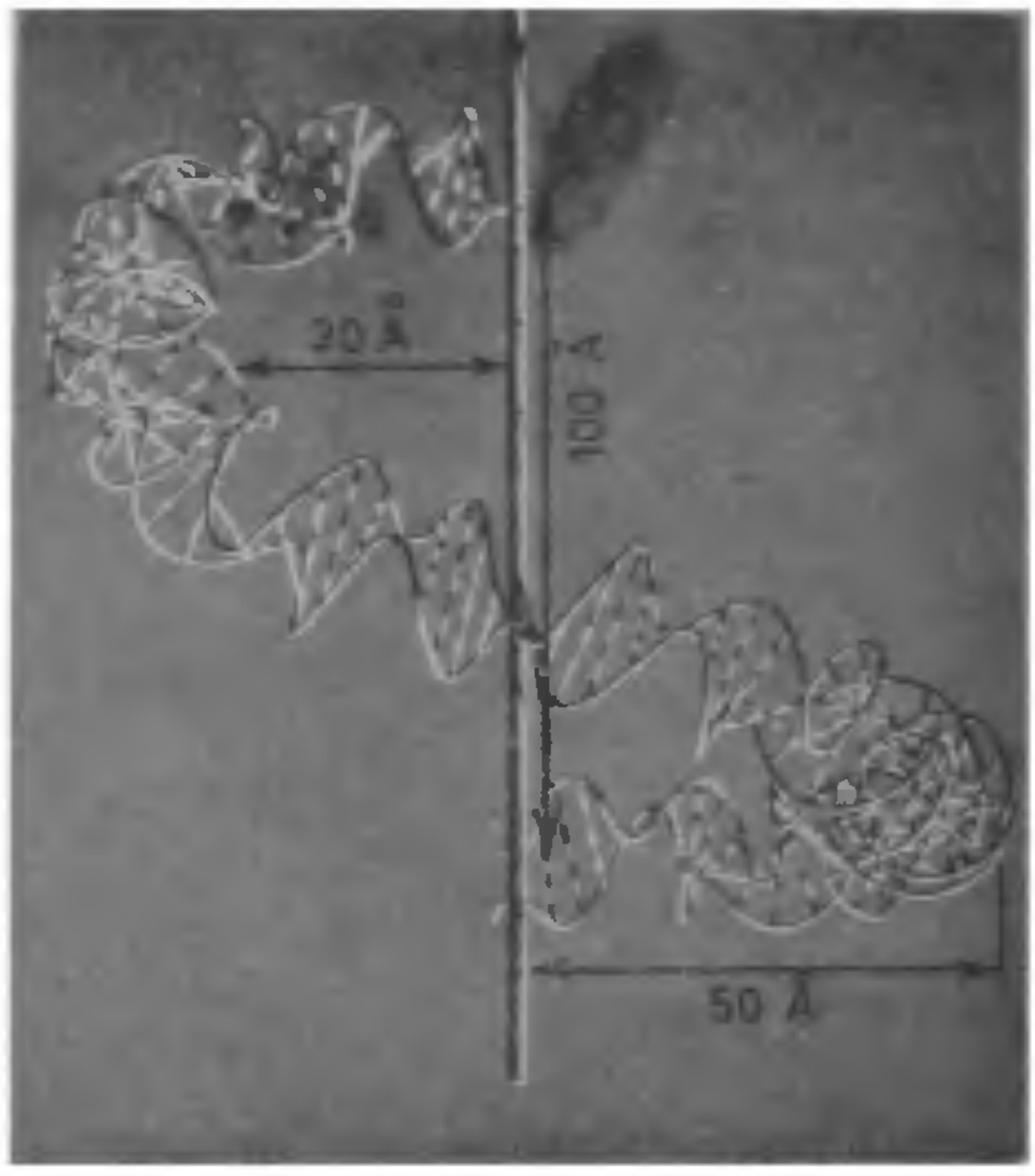


FIG. 3. A wire model of supercoiling of DNA in chromatin. A duplex of DNA of diameter 20 Å is bent to give a radius of curvature of 30–50 Å to wrap around a nucleosome core of diameter 60 Å. Figure shows one turn of the left-handed supercoil with a pitch of 100 Å for 100 base pairs. Neither unfavourable base stacking nor breakage of hydrogen bonds is involved is building the supercoil.

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