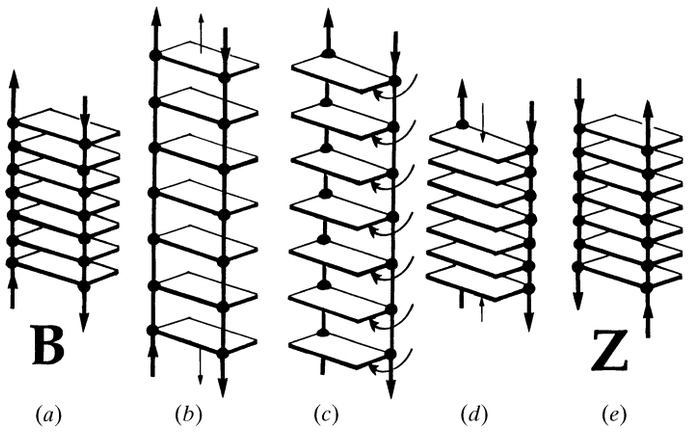

Fig. 23.3.3.6. Interconversion of a B to a Z helix. Because the strands have opposite directions in B (*a*) and Z (*e*), interconversion must involve opening up the helix (*b*), flipping each base pair to the other side (*c*), and re-stacking base pairs (*d*). (*d*) and (*e*) are identical upon rotation about a vertical axis.

pulled apart, as in part (*b*), and each base pair swung around to the opposite side of the backbone 'ladder' [part (*c*)]. This would automatically lead to *syn* conformations at both ends of the base pair, as drawn in Fig. 23.3.3.4(*b*). Returning pyrimidines to an *anti* conformation would create the zigzag backbone chain (Fig. 23.3.3.4*c*). Base pairs can then be re-stacked, as in parts (*d*) and (*e*) in Fig. 23.3.3.6 (which differ only by rotation of the entire helix about the vertical), to yield the backbone geometry of a Z helix. This is the simplest interconversion and one which was recognized and proposed in the very first Z-DNA structure paper (Z1). Other alternatives have been suggested, involving breaking individual base pairs, swinging the bases independently around their backbone chains, and re-forming the pairs. But one kind of special mechanism or another must be invoked if a B-to-Z interconversion is to be achieved.

23.3.3.7. *'Watson–Crick' Z-DNA*

Ansevin & Wang (1990) have proposed an alternative left-handed double helix, with many of the properties of Z-DNA, but possessing the same backbone chain orientations as A- and B-DNA. With such a helix, a B-to-Z conversion would require only a twisting of the duplex about its axis – no separation of bases or unpairing, and no pulling apart of the stack. Ansevin & Wang did not challenge the X-ray crystal structure analyses of short Z-DNA oligomers. Instead, they suggested that Z-DNA was globally the most stable form, adopted in short oligomers where chain unravelling and rearrangement is easy, but that their 'Watson–Crick' Z-DNA or Z(WC)-DNA was the structure that was actually produced by *in vitro* or *in vivo* manipulations of long DNA duplexes. They noted that most solution measurements focus on only two characteristics of the DNA: left-handedness and a dinucleotide repeat, both shared by Z-DNA and Z(WC)-DNA.

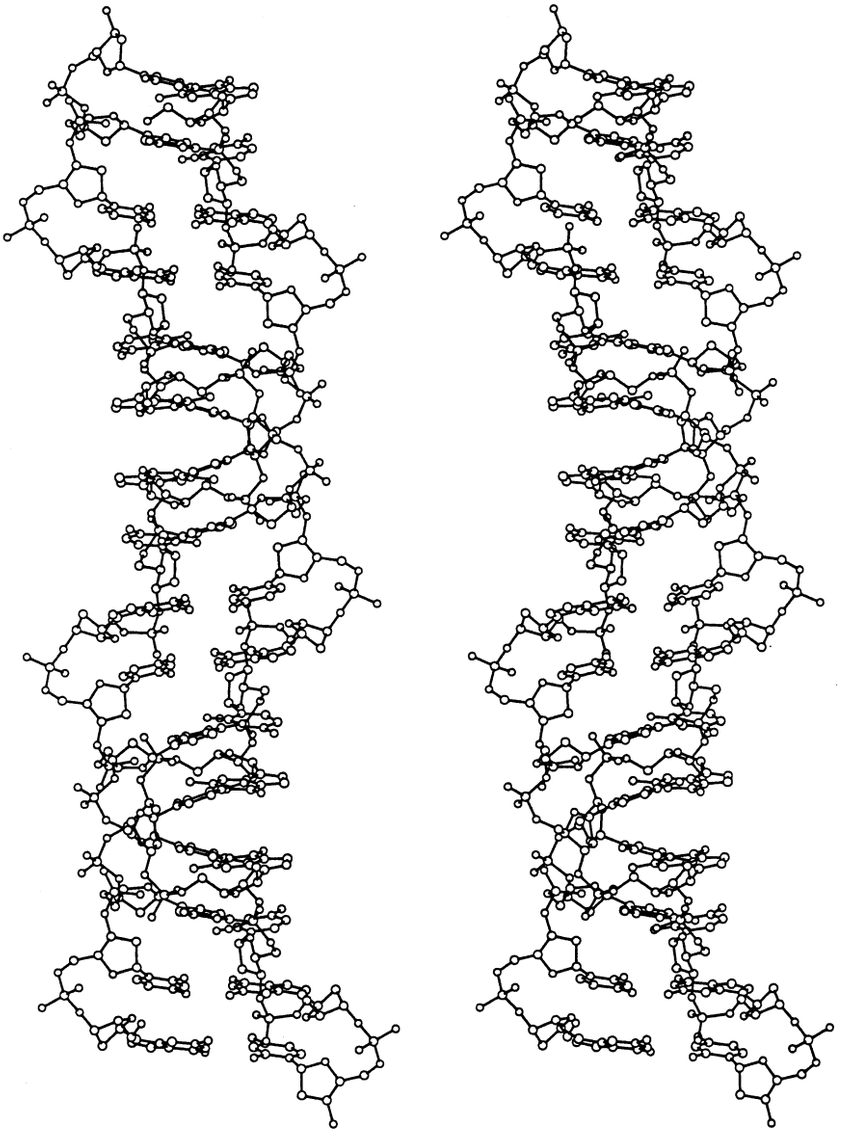

Fig. 23.3.3.7. Z(WC)-DNA, or 'Watson–Crick Z-DNA', a proposed left-handed, zigzag, alternating purine/pyrimidine helix with many of the properties of Z-DNA, but with the backbone chain sense found in A- and B-DNA (Ansevin & Wang, 1990). Coordinates courtesy of Allen T. Ansevin.

The Z(WC) helix is shown in Fig. 23.3.3.7, and a different stereo view appears as Fig. 7 of Dickerson (1992). Like Z-DNA, it is left-handed, with a deep minor groove and shallow major groove. Cytosines with *anti* glycosyl bonds and guanines with *syn* bonds alternate along each backbone strand. However, sugar puckering is reversed: cytosines are C3′-*endo*, while guanines are C2′-*endo*. In Z-DNA, the backbone chain runs parallel to the helix axis past G, and at right angles to the axis past C. In Z(WC)-DNA, this is reversed: parallel to the helix past C, and at right angles past G. Because of efficient stacking of base pairs, the logical two-base-pair structural unit in Z-DNA is $^{5'}$C–G$^{3'}$; in Z(WC)-DNA it is $^{5'}$G–C$^{3'}$. One such unit is clearly visible in the centre of Fig. 23.3.3.7. This behaviour is reflected in local twist angles:

Helix	C–G	G–C	Sum
Z-DNA	−8°	−52°	−60°
Z(WC)-DNA	−70°	+10°	−60°

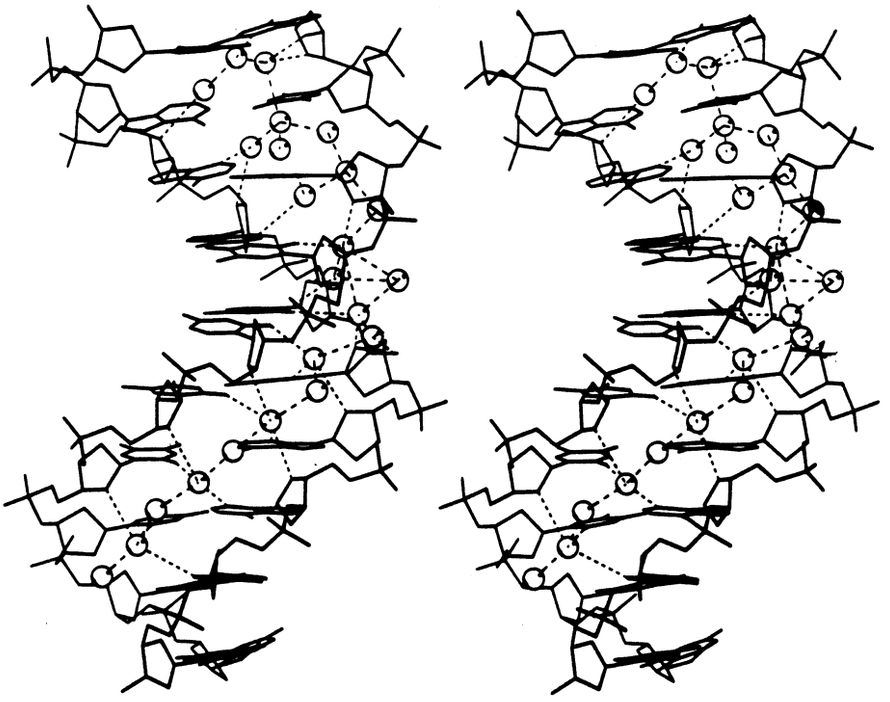

Fig. 23.3.4.1. Structure of C-A-A-A-G-A-A-A-A-G (B107). The lower half of the helix, with -A-A-A-A-G, exhibits the narrow minor groove commonly associated with the AT region of the helix and a single zigzag spine of hydration, as was first seen in C-G-C-G-A-A-T-T-C-G-C-G (B1–B6). The upper half, with C-A-A-A-G-, has the wider minor groove of general-sequence B-DNA and two separate rows of hydrating water molecules along the two walls of the wider groove.

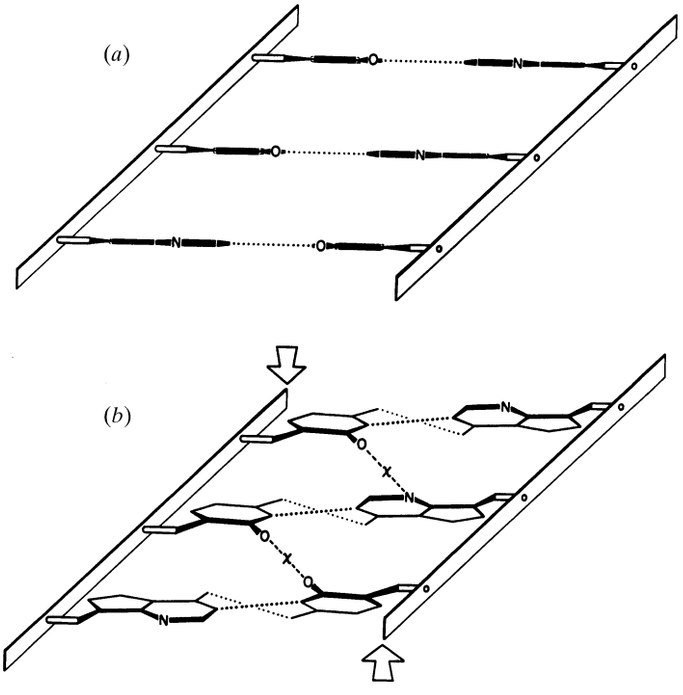

Fig. 23.3.4.2. Relationship between minor groove width and propeller twist. (*a*) View into the minor groove of B-DNA, with base pairs seen on edge and with the sugar–phosphate backbones shown schematically as inclined ladder uprights. (*b*) Consequences of propeller twisting the base pairs. Glycosyl bonds connected to sugar C1′ atoms are all displaced upward in the right strand and downward in the left strand. This shifts the backbone chains as indicated by the arrows. Hence, the gap between the chains is decreased, and the minor groove is narrowed.

The Ansevin–Wang helix has been sedulously ignored since its publication in 1990, especially by crystallographers. The Science Citation Index lists an average of *one* citation of their paper per year since publication, most commonly by spectroscopists. Ho & Mooers (1996) are almost alone among crystallographers in coupling the B-to-Z interconversion dilemma to the possible existence of a different kind of left-handed structure in long polynucleotides. Of course the Z(WC)-DNA structure, as presented here, is only a model; it could be far from the true structure in many respects. But its interest lies in the fact that a left-handed alternating helix with 'standard' backbone dirctions *can* be built with reasonable bond geometries and with properties that fit the various physical measurements as well as Z-DNA. It calls into question not the correctness of the Z-DNA structure obtained from short oligomers with free helix ends, but the relevance of that structure to the production of left-handed regions in longer duplexes with constrained ends.

23.3.4. Sequence–structure relationships in B-DNA

Two channels of information exist in B-DNA by which base sequence is expressed to the outside world. One of these is the Watson–Crick base pairing of A with T and G with C that is used in the storage of genetic information and in replication and transcription. The other channel, used in control and regulation of the expression of this genetic information, involves the hydrogen-bonding patterns of base-pair edges along the floors of the grooves and any systematic deformations of local helix structure that result explicitly from the base sequence.

The simplest and most direct expression of this second channel is the passive reading of hydrogen-bonding patterns along the floor of the major and minor grooves. This readout mechanism was first

references