the more extended ring conformation should be associated with the more extended backbone chain. In Z-DNA, the extended C2′-*endo* form is adopted at cytosine, where a zigzag double chain reversal must be accommodated, while the more compact C3′-*endo* occurs at the straight backbone segment running past a guanine.

The cramped *syn* glycosyl conformation is strongly disfavoured, although not absolutely forbidden, at pyrimidines, most probably because of steric clash between the pyrimidine O2 and the *syn* ring (Haschmeyer & Rich, 1967; Davies, 1978; Ho & Mooers, 1996; Basham *et al.*, 1998). Hence, the Z-DNA helix is effectively limited to alternating pyrimidine/purine sequences, with a price that must be paid for intermittent substitution of A and T for G and C, and an even higher price paid for breaking the pyrimidine/purine alternation. This is reflected in the X-ray crystal structures listed in Table A23.3.1.3. Only one non-alternating sequence has been completely solved and published: *C-G-G-G-*C-G (Z40), where adoption of the Z form has been forced by 5-methylation of cytosines (*C). A second non-alternating sequence that includes AT base pairs, *C-G-A-T-*C-G (Z13), was solved in 1985, but its coordinates have never been made public. It, too, required methylation of cytosines to induce the Z form. A third sequence, C-C-G-C-G-G (Z42), opens its terminal base pairs to make intermolecular base pairs with crystal neighbours. The 52 remaining Z-DNA structures in Table A23.3.1.3 all have strict alternation of pyrimidines and purines.

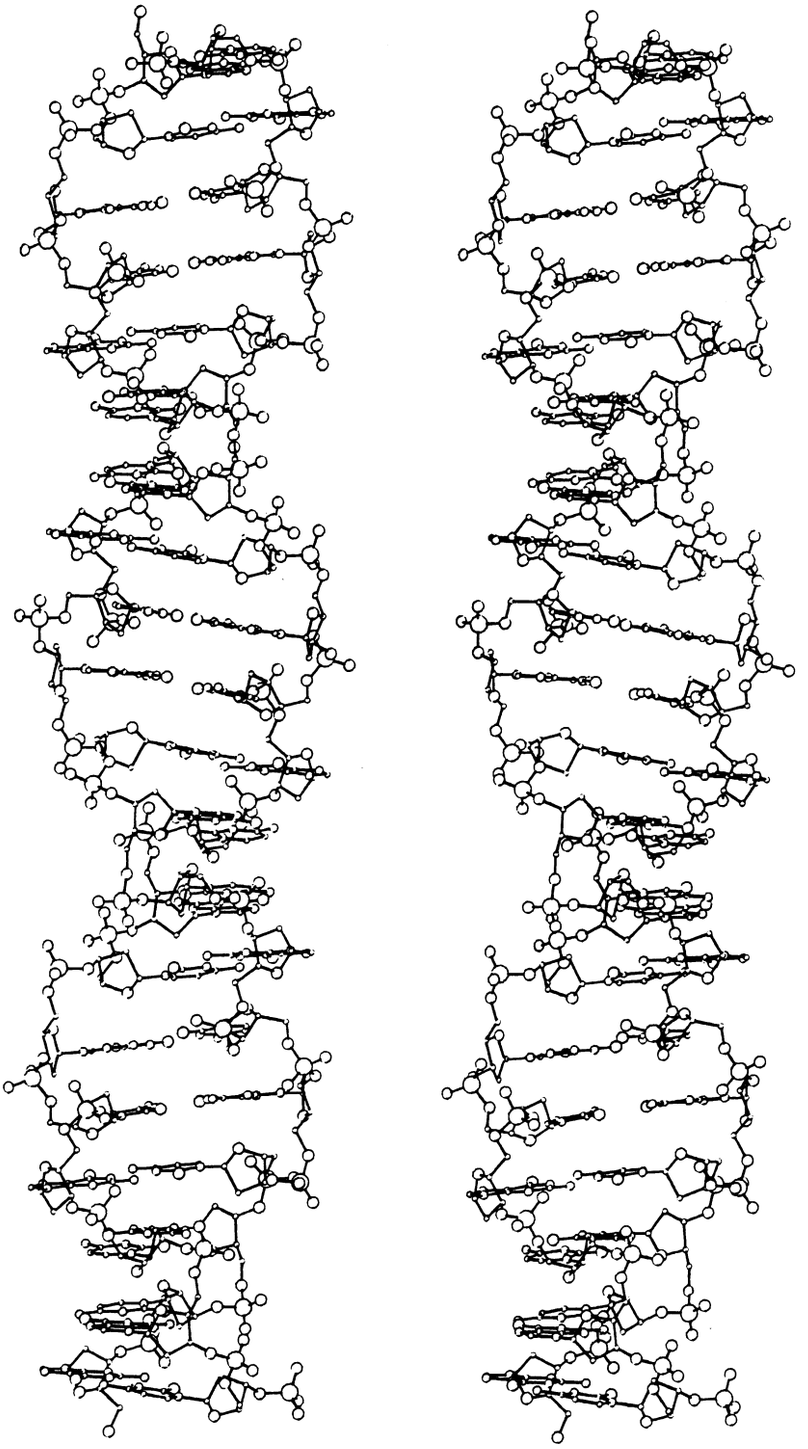

Fig. 23.3.3.3. The Z-DNA stereo pair drawing from which Fig. 23.3.1.4 was derived, with repeating sequence -(G-C-G-C)$_n$-. Note the left-handed zigzag path of the sugar–phosphate backbone, which led to its designation as the Z helix. (From Dickerson, 1983.)

23.3.3.4. *Helical twist and rise, and propeller twist*

The helical repeat unit in Z-DNA is therefore two successive base pairs, rather than the single base pair of A- and B-DNA. Ho & Mooers (1996) propose that the C-G or $^{5'}$pyrimidine-P-purine$^{3'}$ step be considered the fundamental unit of the Z-helical structure, because of the tight overlap between the two base pairs. As can be seen in Fig. 23.3.3.3, in a C-G step the pyrimidine rings from the two base pairs actually stack over one another, whereas the purine rings are packed against neighbouring sugar O4′ atoms. Helix-axis rotation at this step is only −8°, whereas the preceding and following G-C steps have a mammoth −52° twist. Hence, although Z-DNA has 12 base pairs per turn, it technically is not a dodecamer helix, but a hexamer with a two-base-pair repeating unit and a total rotation of −60° per unit.

This virtual restriction to purine/pyrimidine alternation means that Z-DNA cannot be involved in the coding of genetic information. A and B helices have no such restriction; their structures can accommodate a random sequence of bases. Average twist angles are as shown in Table 23.3.3.1, although extreme variation in twist is observed at individual steps in single-crystal structure analyses, from as little as 16° to as much as 55°. Base-sequence preferences for local helix parameters are discussed below.

In both B and Z helices, base pairs are very nearly perpendicular to the helix axis, whereas in the winding double ribbon of A-DNA, the long axis of each base pair is inclined by 10 to 20° away from perpendicularity to the axis. Hence, the rise per base pair for all B-helical steps and for G-C steps of Z-DNA is equal to the thickness of a base pair, 3.4 Å. The rise at a C-G step of

references