Table 2 Elastic properties of defined length DNA helices

Sample	C (erg)	τ (μs)	P (bp)	E (dyn cm^{-2})	Length (bp)
poly(dG)·poly(dC)	4.0×10^{-11}	60.0	400	2.3×10^{9}	400
poly(dA-dC)·poly(dT-dG)	9.0×10^{-13}	16.0	250	1.4×10^{9}	400
Chicken DNA	1.0×10^{-12}	15.0	250	1.4×10^{9}	400
poly(dA)·poly(dT)	2.0×10^{-12}	3.5	150	8.2×10^{8}	400
poly(dG)·poly(dC)	4.0×10^{-11}	40.0	260	1.5×10^{9}	260
poly(dA-dC)·poly(dT-dG)	1.0×10^{-12}	6.0	175	1.0×10^{9}	260
Chicken DNA	1.0×10^{-12}	6.0	175	1.0×10^{9}	260
poly(dA)·poly(dT)	2.0×10^{-12}	3.0	125	7.3×10^{8}	260
poly(dG)·poly(dC)	4.0×10^{-11}	100	500	2.9×10^{9}	900

Parameters are derived from a best fit of equations (1) and (2) to anisotropy decay data. 400±60, 260±40 and 800±200 bp long DNA fragments were prepared as described in the legend to Fig. 1. C, Torsional spring constant calculated from equations (1) and (2); τ, exponential time constant for motion of the long helix axis estimated from a fit of the slowest part of the anisotropy decay data to a single exponential; P, the apparent persistence length of the fragments; E, Young's modulus, calculated from fits of data to equations (1) and (2). In these measurements, the laser pulse has a finite width and therefore must be convoluted into the initial 20 ns of anisotropy decay simulation. When fitting our data to equations (1) and (2), we have included such a convolution (the pulse has been included as a 20-ns gaussian excitation profile, using 100 points at 0.2-ns intervals).

limit that the contour length of a helix is much longer than its persistence length[9]. That criterion is not met for 400-bp long poly(dG)·poly(dC). As seen in Table 2 the persistence length of 400-bp dG·dC helices is equal to the contour length, implying that the long helix axis is sufficiently stiff that its tumbling motion is nearly that of rigid rod. Measurements with a longer DNA fragment (Table 2) show that the persistence length of poly(dG)·poly(dC) is actually near to 500 bp. Work is now in progress to characterize the length dependence of these bending parameters in more detail.

As seen in Table 2, the torsional modulus of these helix fragments is also dependent on base composition. Best fits of the data to equations (1) and (2) show that, independent of length, the torsional modulus C for poly(dG)·poly(dC) is at least 20 times that of poly(dA)·poly(dT), and 40 times that of poly(dA-dC)·poly(dT-dG) or chicken DNA. There are no measurements of fractionated synthetic DNA fragments in the literature to compare with our results. However, for comparison, the value of the torsional modulus that we obtain for random sequence chicken DNA is in good agreement with that calculated from fluorescence measurements[13] and from studies of closed circular DNA supertwisting[14], an equilibrium technique which requires no extrinsic dye probe.

Clearly, additional work is required to understand the origins of DNA flexibility at the molecular level. We have, however, shown in a direct way that DNA sequences with altered stiffness do exist. We suggest that such stiffness variation may be important when considering DNA packaging. For instance, DNA in chromatin is bent to a radius of curvature of 45 Å in the nucleosome core particle[15]. If DNA is modelled as an elastic coil, the energy U required to bend the helix is simply related to the persistence length P: $U = PLkT/R^2$, where L is the length of helix to be bent to a radius of curvature R (ref. 10).

On the basis of our measured values for the persistence length, we calculate that, in a nucleosome, the energy required to bend 146 bp of poly(dG)·poly(dC) will be nearly twice that to bend random sequence DNA (or poly(dA-dC)·poly(dT-dG)) and nearly three times that for poly(dA)·poly(dT). Such variation in bending energy provides a mechanism by which the stability of a nucleosome complex may vary with DNA sequence. Ignoring variations in the strength of histone–DNA interactions, the work presented here suggests that G+C-rich DNA sequences could be sites of weakened nucleosome structure while A+T-rich regions may be sites where nucleosome formation is favoured energetically.

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Errata

IN the letter 'Z-DNA immunoreactivity in rat tissues' by G. Morgenegg *et al.*, *Nature* **303,** 540–543 (1983), line 8 in paragraph 3 should refer to "modified DNAs in either the A or B-forms", not the Z or B-forms as published.

IN the matters arising reply to 'Overlapping spreading centres on East Pacific Rise' by H. Schouten and K. D. Klitgord, *Nature* **303,** 549–550 (1983), the authors should be shown as K. C. Macdonald and P. J. Fox, and P. J. F.'s address is the Graduate School of Oceanography, University of Rhode Island, Narragausett, Rhode Island 02881, USA.

IN the letter 'On neutron star structure and the millisecond pulsar' by A. K. Harding, *Nature* **303,** 683–685 (1983), the relation 4 lines above equation (3) should read $P_{eq} = 1\times10^{-3}\,(M/M_\odot)^{-1/2}R_6^{3/2}$ s and equation (3) should read:

$$B_8 < 1.8\,R_6^{-5/4}\,(M/M_\odot)^{1/4}M_{17}^{1/2}$$

IN the letter 'Single amino acid substitutions in influenza haemagglutinin change receptor binding specificity' by G. N. Rogers *et al.*, *Nature* **304,** 76-78 (1983), in the list of conserved amino acid residues in the second paragraph of page 78, Gln should read Glu.

Corrigendum

IN the letter 'Three mutant insulins in man' by S. Shoelson *et al.*, *Nature* **302,** 540–543 (1983), the fourth author's name was shown incorrectly and should read K. Nanjo.

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