possible to those observed in the crystals. The only remaining conformational angle χ about the glycosidic bond has a value near 0° for the left-handed structure while $\chi \simeq 75°$ for the right-handed structure, as reported previously[7].

In Fig. 3, for the C3' *endo* case, except UpA and TpA, the other observed conformations are clustered in R_1 with $n = 8$ to 11 and $h = 2$ to 3 Å. Thus double helical structures can indeed be generated with the observed backbone conformational angles in the C3' *endo* region. In the case of both L_1 and L_{II} regions, the bases overlap, so double helical structures are possible.

Thus for the *gg* conformation about the C4'–C5' bond, the helical domains occur in the β–γ space at the g^-g^- and tg^- regions, which are precisely the observed regions of conformations for the fragments given. Small variations in dihedral angles bring about changes in the sense of the helix and both right- and left-handed double helical structures are possible. It is clear that conformations similar to the fragments in sets I, II and III can lead to right helical, left helical and bend (or fold) structures respectively. A structural model for B DNA can thus be constructed with right and left helical segments having backbone conformations similar to sets I and II respectively. Conformations similar to set III serve to link consecutive right and left segments of a chain. A structure thus arrived at is a type II structure proposed previously by us[7] as an alternative structure for DNA. The type II structure is not a double helix but consists of a pair of polynucleotide strands held together by Watson–Crick base pairing. Each of the two strands has alternating right- and left-handed segments approximately five base pairs long. As a consequence of mixing right-handed with left-handed helical segments and vice versa, each strand has bends or folds. These bends impart a significant amount of flexibility to the polynucleotide. This inherent flexibility of the type II structure can permit the initiation of the supercoiled structure of DNA following energetically allowed folds. This flexibility along the backbone could provide a possible solution to the compression of DNA within chromatin[19].

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Corrigendum

In the article 'Decision making in animals' by D. J. McFarland, *Nature* **269**, 15 (1977), the sentence starting in line 16 on page 18 should read: On this basis we can express the expected probability of fertilisation, given that the male is still involved in the courtship as

$$\varepsilon \int_0^T [u_1(t) + e^{\varphi S(t)t} u_3(t)] S(t)x(t)\, dt.$$

Also on page 18, the scheme based on Dempster's formulation (ref. 14) should read as shown below:

Objective: Maximise likelihood of successful fertilisation

$$\int_0^\infty \{\exp\left[-\varphi S(t)t\right] S(t)u_1(t)x(t) + S(t)u_3(t)x(t)\}\, dt$$

Plant equation: $\dot{x}(t) = -x(t)^{-\rho}u_2(t) + \theta$

Work during courtship: $\dfrac{u_1(t)}{\delta} + \dfrac{u_2(t)}{\gamma} + \dfrac{u_3(t)}{\tau} \leqslant 1$

Energy expended during courtship:

$$\int_0^\infty \left[\frac{u_1(t)}{\delta} + \frac{u_2(t)}{\gamma} + \frac{u_3(t)}{\tau}\right] dt \leqslant E$$

Hamiltonian:

$$H = e^{-\varphi S(t)t} S(t)u_1(t)x(t) + S(t)u_3(t)x(t)$$
$$- F(t)\left[-x(t)^{-\rho}u_2(t) + \theta\right]$$

(Costate) Hamiltonian equation:

$$\dot{F}(t) = \frac{\partial H}{\partial x} = e^{-\varphi S(t)t}S(t)u_2(t) - \rho\frac{F(t)}{x(t)^{1+\rho}}u_2(t) + S(t)u_3(t)$$

states: S = spermatophore count (0–3)
          x = oxygen 'debt'
controls: u_1 = rate of display behaviour (maximum rate δ)
          u_2 = rate of creep behaviour (maximum rate γ)
          u_3 = rate of spermatophore transfer (maximum rate τ)
parameters: φ = basic discount rate of display behaviour
          ρ = control parameter for rate of decrease of x through skin respiration during creep behaviour
          θ = rate of increase of oxygen debt with time (during display and transfer behaviour)
          E = maximal energy expended in courtship
          F = costate variable = marginal value of likelihood of success per unit of x

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