Quarterly Reviews of Biophysics

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A quantitative model of a cooperative two-state equilibrium in DNA: experimental tests, insights, and predictions - CORRIGENDUM

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doi: https://doi.org/10.1017/S0033583521000032, published by Cambridge University Press, 16 March 2021.

Corrigendum

Cite this article: Schurr JM (2021). A quantitative model of a cooperative two-state equilibrium in DNA: experimental tests, insights, and predictions - CORRIGENDUM. *Quarterly Reviews of Biophysics* **54**, e7, 1–2. https://doi.org/10.1017/S0033583521000056

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In the aforementioned article, the author and Publisher would like to correct four errors. These are as follows:

(1) On the second line of page 6 the formula should read: $\kappa_{\beta af} = (P_f / h_a)\ k_B T$
(2) The third row of Table 3 should be f_{bcir} and not F_{bcir}. A revised table 3 is below:

Table 3. Calculated properties of circular DNAs with 205–4362 bp in ~40 mM univalent cations plus 10 mM Mg^{2+} at 310 K.

N (bps)	205	207	210	217	551	1182	2434	4362
$\alpha_{lin} \times 10^{19}$ (J)	6.63	6.63	6.63	6.63	6.63	6.63	6.63	6.63
$\alpha_{cir} \times 10^{19}$ (J)	9.23	9.20	9.15	9.05	7.14	6.74	6.65	6.64
f_{bcir}	0.811	0.809	0.805	0.796	0.591	0.533	0.520	0.517
h_{cir} (nm)	0.340	0.340	0.340	0. 340	0.329	0.327	0.326	0.326
$\kappa_{\beta cir} \times 10^{19}$ (J)	5.71	5.71	5.72	5.74	6.19	6.33	6.36	6.37
P_{cir} (nm)	45.3	45.4	45.4	45.5	47.6	48.3	48.4	48.5
E_T (theory)	3903	3889	3867	3818	2631	1654	1245	1140
E_T (expt)		(3910, 3980)			3230	1870	1220	1130
H (bp/turn)		(10.46, 10.54)			-	-	-	-

Beginning with α_{lin} for a long linear DNA reckoned from Eq. (11), values were computed as described above for the 181 bp DNA. E_T is reckoned from Eq. (16) and compared with experimental values obtained from topoisomer distributions (Horowitz and Wang, 1984) (HW). The dual values of the experimental E_T and helix repeat, *H*, were obtained by least-squares fitting of the experimental topoisomer ratios for 205, 207, and 217 bp DNAs to equations (6b) and (5), respectively, of HW.

(3) In Table 6, the final value should be 4.87 instead of 4.87s. A revised table 6 is below:

Table 6. Calculated properties of different DNA models in 0.1 M NaCl at 293 K.

Model	N_{spr}	n_1	n_2	n_3	f_b	$\alpha_{u1} \times 10^{+19}$ (J)	$\alpha_{u2} \times 10^{+19}$ (J)
Control	1088	251.6	711.5	125.5	0.347	5.70	Unknown
Insert	1096	911.6	185.4	0	0.169	4.98	Unknown
$Redcontrol_1$	22	5	14	3	0.364	5.79	6.14
$Redcontrol_2$	22	6	14	2	0.364	5.79	6.19
$Redinsert_1$	22	18	4	0	0.182	5.02	5.08
$Redinsert_2$	22	19	3	0	0.136	4.71	4.87

The *Nspr* are the numbers of springs between the subunits of each model. The n_1 are the mean number of bp in the central domain, which is state *b* in Control DNA, and is state *a* in Insert DNA. The *n*2 and *n*3 are the numbers of subunits in the second and third domains outward from the center (counting those on both sides). The α_{u1} and α_{u2} values are reckoned as described previously (Schurr, 2019*b*).

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(4) On page 10, lines 22–24 of the right-hand column should read: "This implies a non-Gaussian distribution of writhe in the unconstrained DNA, which arises from thermally accessible figure eight configurations in addition to slightly writhed circles."

The author and Publisher apologise for these errors.

Reference

Schurr JM (2021). A quantitative model of a cooperative two-state equilibrium in DNA: experimental tests, insights, and predictions. *Quarterly Reviews of Biophysics* **54**, e5, 1–25. https://doi.org/10.1017/S0033583521000032

https://doi.org/10.1017/S0033583521000056 Published online by Cambridge University Press