Supporting Information

for

Two-Dimensional Packing of Short DNA with Non-Pairing Overhangs in Cationic Liposome–DNA Complexes: From Onsager Nematics to Columnar Nematics With Finite-Length Columns

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Table S1. Sequences of the sense and anti-sense strands of the short DNA molecules studied.

	sequence[a]	duplex name
s	CTTACGCTGAGTT	11bp DNA-2T
as	CTCAGCGTAAGTT	
s	CTTACGCTGAGTTTTT	11bp DNA-5T
as	CTCAGCGTAAGTTTTT	
s	CTTACGCTGAGTTTTTTTTTT	11bp DNA-10T
as	CTCAGCGTAAGTTTTTTTTTT	
s	ATCACTTACGCTGAGTACTTCGAATT	24bp DNA-2T
as	TTCGAAGTACTCAGCGTAAGTGATTT	
s	ATCACTTACGCTGAGTACTTCGAATTTTT	24bp DNA-5T
as	TTCGAAGTACTCAGCGTAAGTGATTTTTT	
s	ATCACTTACGCTGAGTACTTCGAATTTTTTTTTT	24bp DNA-10T
as	TTCGAAGTACTCAGCGTAAGTGATTTTTTTTTTT	
s	ACAGATGCACATATCGAGGTGGACATCACTTACGCTGAGTACTTCGAATT	48bp DNA-2T
as	TTCGAAGTACTCAGCGTAAGTGATGTCCACCTCGATATGTGCATCTGTTT	
s	ACAGATGCACATATCGAGGTGGACATCACTTACGCTGAGTACTTCGAATTTTT	48bp DNA-5T
as	TTCGAAGTACTCAGCGTAAGTGATGTCCACCTCGATATGTGCATCTGTTTTTT	
s	ACAGATGCACATATCGAGGTGGACATCACTTACGCTGAGTACTTCGAATTTTTTTTTT	48bp DNA-10T
as	TTCGAAGTACTCAGCGTAAGTGATGTCCACCTCGATATGTGCATCTGTTTTTTTTTTT	

[a] sense (s) and anti-sense (as) strands as indicated

Derivation of Equations S1 and S2

As outlined in the text,

$$\sigma_M = \sigma_{CL} \frac{N_{CL}}{N_{CL} + rN_{NL}} \text{ , where } \sigma_{CL} = \frac{eZ_{CL}}{a_{CL}}$$

For $r = 1 + \varepsilon$ with $|\varepsilon| << 1$

$$\frac{N_{CL}}{N_{CL} + rN_{NL}} = \frac{N_{CL}}{N_{CL} + N_{NL} + \varepsilon N_{NL}} = \Phi_{CL} \frac{1}{1 + \varepsilon \Phi_{NL}} \text{ ,}$$

$$\text{since } \Phi_{CL} = \frac{N_{CL}}{N_{CL} + N_{NL}} = 1 - \Phi_{NL} = 1 - \frac{N_{NL}}{N_{CL} + N_{NL}} \text{ .}$$

$\Phi_{NL} \leq 1$ by definition, and thus $|\varepsilon\Phi_{NL}| \leq |\varepsilon| << 1$.

Therefore, $\frac{1}{1 + \varepsilon \Phi_{NL}} \approx 1 - \varepsilon \Phi_{NL}$ (Taylor series expansion).

Substituting these results into the equation for σ_M, we obtain

$$\sigma_M = \sigma_{CL} \frac{N_{CL}}{N_{CL} + rN_{NL}} = \sigma_{CL} \Phi_{CL} \frac{1}{1 + \varepsilon \Phi_{NL}} \approx \sigma_{CL} \Phi_{CL} (1 - \varepsilon \Phi_{NL}) = \sigma_{CL} (1 - \Phi_{NL})(1 - \varepsilon \Phi_{NL}) \qquad \text{(S1)}$$

Equating this with the other expression for σ_M, we obtain

$$\sigma_M = \frac{e}{3.4\,\text{Å}\, d_{\text{DNA}}} \approx \sigma_{CL} (1 - \Phi_{NL})(1 - \varepsilon \Phi_{NL}) = \frac{eZ_{CL}}{a_{CL}} (1 - \Phi_{NL})(1 - \varepsilon \Phi_{NL})$$

$$\Leftrightarrow \quad d_{DNA} \approx \frac{a_{CL}}{3.4\,\text{Å}\, Z_{\text{CL}}} \frac{1}{(1 - \Phi_{NL})(1 - \varepsilon \Phi_{NL})} \qquad \text{(S2)}$$