Supplementary Information

Dendrimer-induced DNA Bending

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1. Experimental section

Materials. The DNA used for preparing the dendriplexes for supramolecular structure characterizations was a linear DNA from calf thymus purchased from MP Biomedicals. PAMAM G4 dendrimer with a diaminobutane (DAB) core (polydispersity index < 1.01) in methanol solution was acquired from Dendritic Nanotechnologies (Mount Pleasant, MI, USA). After thoroughly drying, the solid was redissolved in distilled water to produce a 0.2% (w/v) stock solution. The solutions were stored at 4 °C till use.

Preparation of dendriplexes. All dendriplexes were prepared at room temperature (ca. 27 ^{o}C). Dendrimers with different average degrees of protonation (dp) were prepared by adding predetermined amounts of 0.01 N HCl into the aqueous solutions. The values of dp were determined from the pH (measured by an ISTEK Model 720P pH meter) of the protonated dendrimer solutions.[1] The dendriplexes were prepared by pouring the prescribed amount of 0.2 % (w/v) solution of calf thymus DNA into the 0.2% (w/v) protonated dendrimer solution. The complexation was usually manifested by precipitation. The dendriplexes were left at room temperature for 16 h for equilibration.

SAXS experiments. Aqueous suspensions of dendriplexes were directly introduced into the sample cell comprising two ultralene windows for SAXS measurements. The

SAXS experiments were performed at room temperature using Beamline BL17A1 at the National Synchrotron Radiation Research Center (NSRRC), Hsin-Chu, Taiwan. The wavelength (λ) of the X-ray was 1.333 Å and a two-dimensional MAR image plate with 100 x 100 μm^2 pixel resolution was used to collect the scattering intensity data. The sample-to-detector distance and flat-field correction were calibrated by the mixture of silver behenate and Si powders. The intensity profile was output as the plot of the scattering intensity (I) vs. the scattering vector, $q = 4\pi/\lambda \sin(\theta/2)$ (θ = scattering angle).

A grazing incidence SAXS (GISAXS) measurement was performed to obtain the 2-D SAXS pattern of an oriented thin film of dp/0.3 dendriplex for facilitating the structure determination. The dendirplex suspension in pure water was centrifuged to yield a clear separation between supernatant and precipitate. The precipitate was taken out and spread over cleaned silicon wafer surface (20 x 14 mm^2) manually by a blade to create an oriented thin film. A small amount of supernatant solution was added onto the surface to keep the dendriplex thin film wet. The sample was subsequently placed in a temperature-humidity controlled chamber that was equipped with Mylar windows for X-ray passage. The chamber also enclosed poly(ethylene glycol) solution for the humidity control.[2] The measurement was conducted at 30 ^oC and 94.5 % relative humidity using 12 keV beam at the incidence angle $\theta_{in} = 0.3^o$ and SD = 1906 mm at Beamline 23A of NSRRC.

2. Construction of a DNA superhelix for SAXS profile calculation

The DNA superhelix was approximated by a uniform helical cylinder with a prescribed pitch length *P* and pitch angle, as shown in Fig. S1. The radius of the superhelix (R_h) given by $R_h = P/(2\pi\tan\theta)$ is defined as the radial distance between the centerline and central trace of the helix ($R_h = 0$ for completely straightened DNA, see Figure S1). Therefore, the helical trace of the cylinder can be calculated from the

following equations[3]

$$x(z) = R_h \sin(\frac{2\pi z}{P} + \phi); y(z) = R_h \cos(\frac{2\pi z}{P} + \phi)$$

where ϕ is phase angle that prescribes the direction of the groove of the superhelix. The regular pitch of a helix can give rise to a scattering peak locating at $q_p = 2\pi/l_P = 2\pi/P\cos\theta$, where l_P is the projection of P onto the normal of the helical segment (see Fig. S1). It can be shown that $q_p \approx 2\pi/l_P$ as long as $2\pi R_h$ is significantly larger than P.

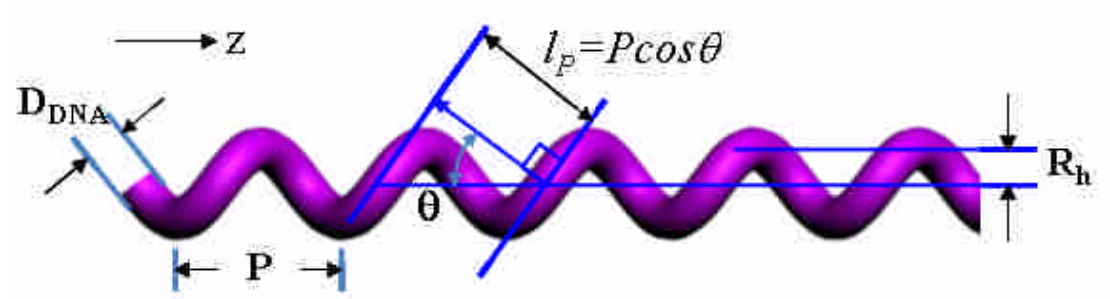

Fig. S1 Definitions of the geometric parameters of a DNA superhelix used for model calculation. P and θ represent the pitch length and pitch angle, respectively. R_h is the radius of the superhelix defined as the radial distance between the centerline and central trace of the helix. l_P is the projection of P onto the normal of the helical segment.

3. Calculation of SAXS profile of a chromatin-like fiber

After constructing the chromatin-like fiber with prescribed values of P and d, we divided the system into numerous volume elements (each with the size of 5 x 5 x 5 Å^3) and the partial structure factors associated with DNA-DNA correlation [$S_{DD}(q)$], dendrimer-dendrimer correlation [$S_{dd}(q)$] and DNA-dendrimer correlation [$S_{Dd}(q)$] of the randomly oriented chromatin-like fiber were calculated by the Debye equation[4]

$$S_{nm}(q) = \frac{1}{N^2}\sum_{i=1}^{N}\sum_{j=1}^{N}\frac{\sin\left(q\left|\mathbf{r_i} - \mathbf{r_j}\right|\right)}{q\left|\mathbf{r_i} - \mathbf{r_j}\right|} \qquad \text{(S1)}$$

where n and m stands for either DNA (D) or dendrimer (d) and $|\mathbf{r}_i - \mathbf{r}_j|$ is the distance

between *i* and *j* volume element. $S_{dd}(q)$ was further corrected by adding an additional component arising from internal monomer density fluctuations.[5] The SAXS intensity was finally calculated from the three partial structure factors by

$$I(q) = \Delta\rho_D{}^2 S_{DD}(q) + 2\Delta\rho_D \Delta\rho_d S_{Dd}(q) + \Delta\rho_d{}^2 S_{dd}(q) \qquad \text{(S2)}$$

where $\Delta\rho_D$ (= 5.7 x 10^{10} cm^2) and $\Delta\rho_d$ (= 2 x 10^{10} cm^2) is the scattering length density contrast of DNA and PAMAM dendrimer, respectively. It should be noted that, in contrast to the model fitting for quantitative analysis of scattering data, the present calculation was mainly for seeking the type of structure that can yield the scattering features consistent with the experimentally observed ones. No attempt was made to optimize the values of the structure parameters to yield the best fit to the experimental data, because the model adopted here was a simplification of the real structure without taking into account other complicated factors such as the possible distributions of *d* and *P* and the interaction between the chromatin-like fibers (which would affect the intensity in the low-q region).

4. Analysis of the 2-D GISAXS pattern (Fig. 4a) of dp/0.3 dendriplex

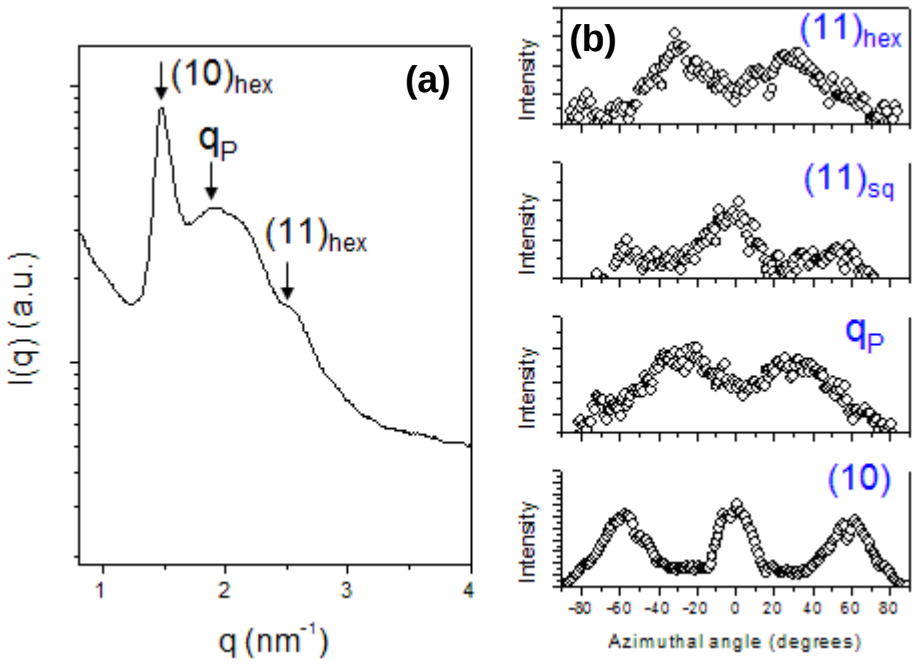

Fig. S2 (a)The 1-D SAXS profile obtained from the radial average of the 2-D pattern in Figure 4a. (b) The azimuthal scans of the four sets of arcs in GISAXS pattern. The fact that the 1-D profile was virtually identical to that in Figure 1 attested that these four sets of arcs corresponded to the four peaks observed for the bulk sample in excess water.

5. Calculation of SAXS profile for hexagonally-packed superhelix structure

Attempt has been made here to calculate the isotropic SAXS profile to check if the features of the observed pattern in Fig. 1 can be produced by the model of hexagonally-packed DNA superhelices. For the calculation, DNA superhelices with P = 6.6 nm and $\theta = 60^{o}$ were placed in a hexagonal lattice with the interplanar distance of (10) plane ($D_{(10)}$) of 4.3 nm. To reach maximum contact with dendrimer surface, the phase angle of the DNA superhelix was set to vary in the sequence of $+0^{o}$, $+120^{o}$, and $+240^{o}$ along *a*-axis and *b*-axis of the hexagonal lattice (Fig. S3). Dendrimer macrocations were subsequently placed into the groove regions of the channels (each formed by three DNA superhelices).

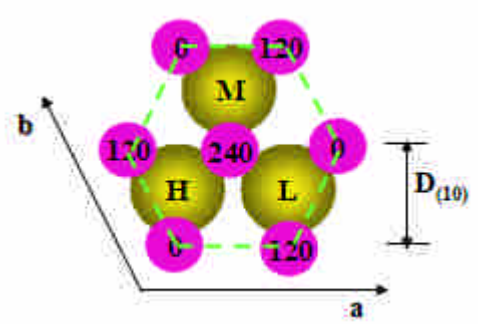

Fig. S3 Top view of the hexagonally-packed DNA superhelices. The purple balls represent the DNA cross section and the numbers shown within the balls are the phase angles of the superhelices. The dark yellow balls are dendrimers.

For the SAXS pattern calculation, the hexagonal lattice was set to consist of five unit cells with six dendrimer macrocations placing in a given channel. Again, system was divided into numerous volume elements (each with the size of 5 x 5 x 5 $Å^3$) and

the partial structure factors associated with DNA-DNA correlation [$S_{DD}(q)$], dendrimer-dendrimer correlation [$S_{dd}(q)$] and DNA-dendrimer correlation [$S_{Dd}(q)$] were calculated using Eq. (S1). The SAXS intensity was finally calculated from the three partial structure factors by Eq. (S2).

References

1. Niu, Y.; Sun, L.; Crooks, R. M. *Macromolecules,* 2003, **36**, 5725–5731.
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