Protein-induced transformation of unilamellar to multilamellar vesicles triggered by a polysaccharide

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Supplementary Material

Bayesian analysis results

An analysis on the Markov Chain Monte Carlo random walks (after the convergence of the simulated annealing process) in the parameter space of the fitting parameters was performed to estimate the mutual dependencies between the fitted parameters P_i and their uncertainties δP_i. The corner plots of Figure S1 show the pair distributions of the relative deviations of the fitted parameters P_i from their optimum values P_i^{opt} i.e. $\frac{P_i - P_i^{opt}}{P_i^{opt}}$ for samples 2 and 13 (selected as representative of all data sets). The distributions of the individual parameters are shown in the diagonal elements of corner plots. The distribution probabilities were normalized to unity in regard to their maximum value (color bar of Figure S1). The distributions appear fairly symmetric with no obvious mutual dependence between parameters.

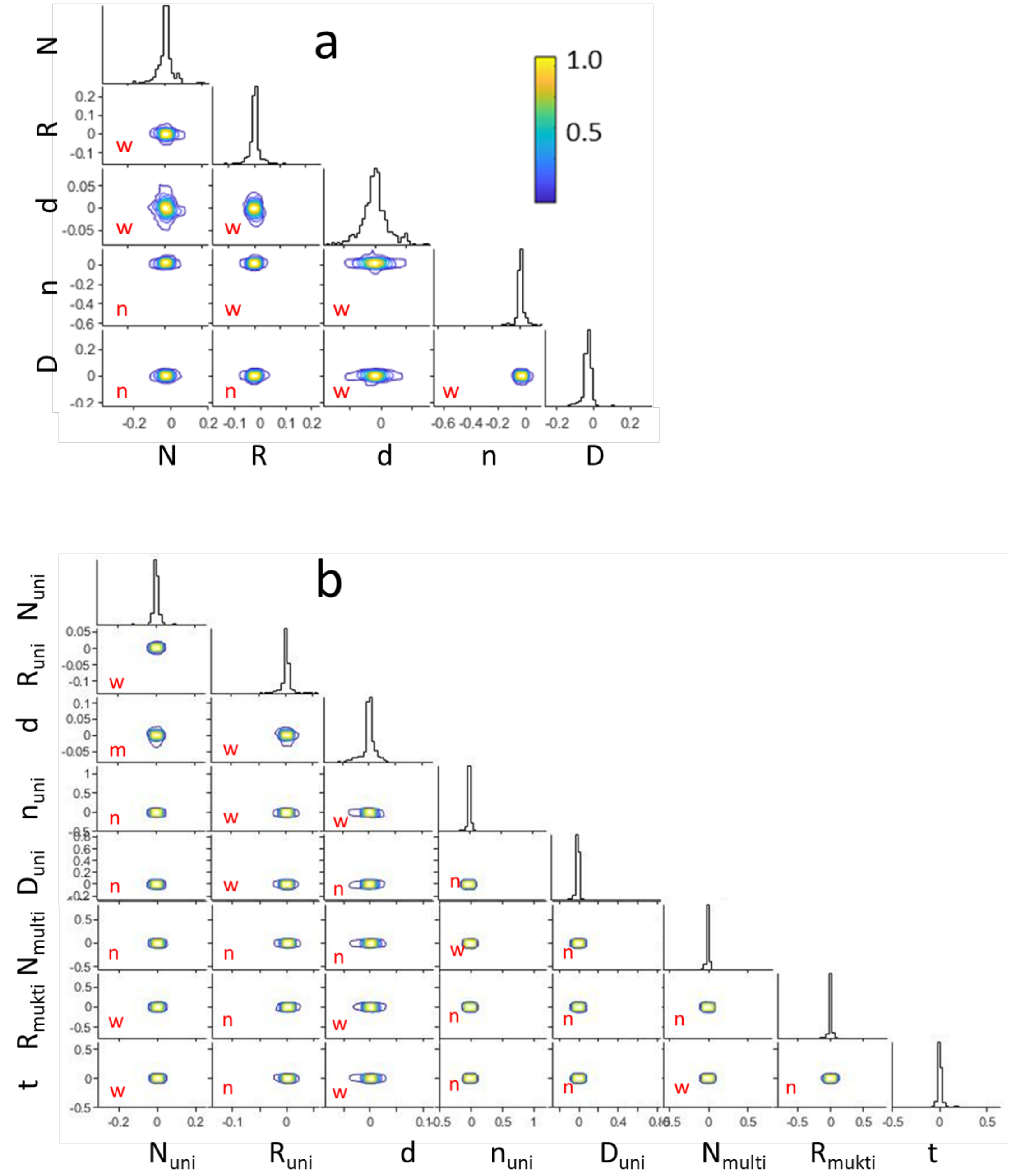

Figure S1: Corner plots of fitted parameters from sample 2 (a) and sample 3 (b). Interdependencies are shown as “n” for negligible, “w” for weak and “m” for moderate.

The correlation coefficients r for every parameter pair were calculated and their mutual dependence was categorized as “negligible” for $0 \leq |r| < 0.1$,” weak” for $0.1 \leq |r| < 0.4$, “moderate” for $0.4 \leq |r| < 0.7$, “strong” for $0.7 \leq |r| < 0.9$ and “very strong” for $0.9 \leq |r|$. The values of the correlation coefficients for samples 2 and 13 are shown in Tables S1 and S2. The data and analysis of these two examples illustrate the behavior of all data sets in regard to the

Bayesian analysis. In all cases correlations between parameters are negligible or weak except from a moderate interdependence (r=-0.57) between the prefactor N and the bilayer thickness d in sample 13. This justifies the use of the selected models from vesicles of different lamellarity.

Table S1. Correlation coefficients between the fitted parameters from Bayesian analysis on the data of sample 2.

Parameter	N	R	d	n	D
N	1.00	-0.11	-0.19	0.08	0.04
R	-0.11	1.00	-0.17	-0.34	0.08
d	-0.19	-0.17	1.00	-0.25	0.14
n	0.08	-0.34	-0.25	1.00	0.15
D	0.04	0.08	0.14	0.15	1.00

Table S2. Correlation coefficients between the fitted parameters from Bayesian analysis on the data of sample 13.

Parameter	N_{uni}	R_{uni}	d	n_{uni}	D_{uni}	N_{multi}	R_{multi}	t
N	1.00	-0.16	-0.57	-0.02	0.00	-0.02	0.15	0.21
R	-0.16	1.00	-0.22	0.16	0.18	-0.05	-0.08	-0.04
d	-0.57	-0.22	1.00	-0.14	0.04	-0.02	-0.28	-0.12
n	-0.02	0.16	-0.14	1.00	0.01	-0.11	-0.09	0.09
D	0.003	0.18	0.04	0.01	1.00	-0.03	-0.01	0.00
N_{multi}	-0.02	-0.05	-0.02	-0.11	-0.03	1.00	-0.05	-0.11
R_{multi}	0.15	-0.08	-0.28	-0.09	-0.01	-0.05	1.00	0.07
t	0.21	-0.04	-0.12	0.09	0.001	-0.11	0.07	1.00

Cryo-TEM results

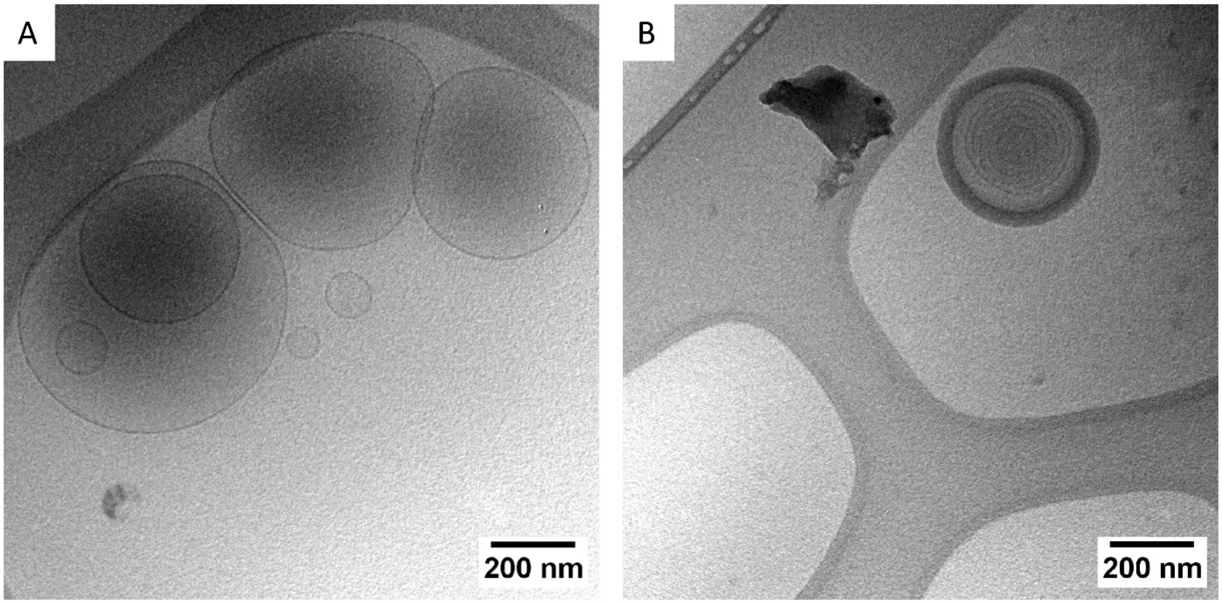

Figure S2: Cryo-TEM images from vesicles (a) with added BSA (sample 7) and (b) HA-decorated DDAB vesicles with added BSA (sample 14) in D_2O.