Magnetic control over the fractal dimension

of supramolecular rod networks

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1   **Abstract:** Controlling supramolecular polymerization is of fundamental importance to create advanced
2   materials and devices. Here we show that the thermodynamic equilibrium of Gd^{3+}-bearing supramolecular rod
3   networks is shifted reversibly at room temperature in a static magnetic field of up to 2 T. Our approach opens
4   opportunities to control the structure formation of other supramolecular or coordination polymers that contain
5   paramagnetic ions.

6   Supramolecular polymers consist of monomers held together by reversible non-covalent interactions.[1] Their
7   properties are commonly controlled by external stimuli,[2] such as temperature,[1] enzymes,[3–5] mechanical
8   forces,[6,7] light,[8–10] pH[11–13] or redox potential.[14,15] In addition, external aligning forces due to electric fields,
9   centrifugal gravity or flow have been shown to affect the growth and orientation of supramolecular polymers.[16]
10   When using magnetic fields, large values ~10 T are needed align diamagnetic molecules that contain no
11   paramagnetic atoms or magnetic nanoparticles).
12   By introducing ferrimagnetic or paramagnetic species, alignment can be obtained at lower fields (mT to T),
13   for example by using magnetite nanocrystals[17], clay particles[18], bicelles[19], or self-assembled dumbells[20]. From
14   an energetic point of view, it must be that many paramagnetic moments act together, when combined into a
15   self-assembled structure. As an indication, in a uniform 1 T field the magnetic energy $U_m = -\frac{1}{2}\,mB$ of a single
16   paramagnetic Gd^{3+} ion at room temperature, is $-3\cdot10^{-25}$ J,[21] four orders of magnitude smaller than the thermal
17   energy at room temperature $E_T = k_B T = 4\cdot10^{-21}$ J. The studies described so far have focused on magnetic fields
18   applied during irreversible assembly processes, such as crystallization[22], drying, pH-change[23], cross-diffusion[24]
19   in layered systems or orientation of pre-formed particles[25].
20   Here, we set out to understand how 1–2 T magnetic fields can perturb equilibrium supramolecular polymers
21   in solution, in a reversible manner. That is, by applying the magnetic field we perturb the thermodynamic
22   equilibrium, and reach a new magnetically-induced equilibrium. We will show that whereas single polymer rods
23   are not affected by the magnetic field, networks of rods are. Overall, the mass contained in the rod assemblies
24   increases in presence of the magnetic field. Removal of the field causes the system to relax back to its original
25   thermodynamic equilibrium.
26   Specifically, we use a previously studied C_3-symmetrical benzene-1,3,5-tricarboxamide BTA derivative,
27   extended by fluorinated L-phenylalanine and connected to 1,4,7,10-tetraazacyclododecane-N,N',N'',N'''-
28   tetraacetic acid (DOTA) groups[26] (see also the work on closely related derivatives[27–29]). The latter molecule will
29   be called Gd-BTA when chelated to gadolinium(III), or Y-BTA when chelated to yttrium(III) as a negative
30   diamagnetic control (Fig. 1a,b). Previously, it was shown that Gd-BTA assembles into supramolecular rods
31   using a cooperative (nucleation/elongation) polymerization mechanism, with dimensionless nucleation constant

32 $K_{nuc} = 10^{-4}$ and $K_e = 1.4 \times 10^{-6}$ M^{-1}.[26] At 100 µM Gd-BTA concentration in 100 mM citrate buffer, as in the current

33 work, there was no sign of macroscopic gelation or changes in viscosity, as compared to buffer alone.

a)
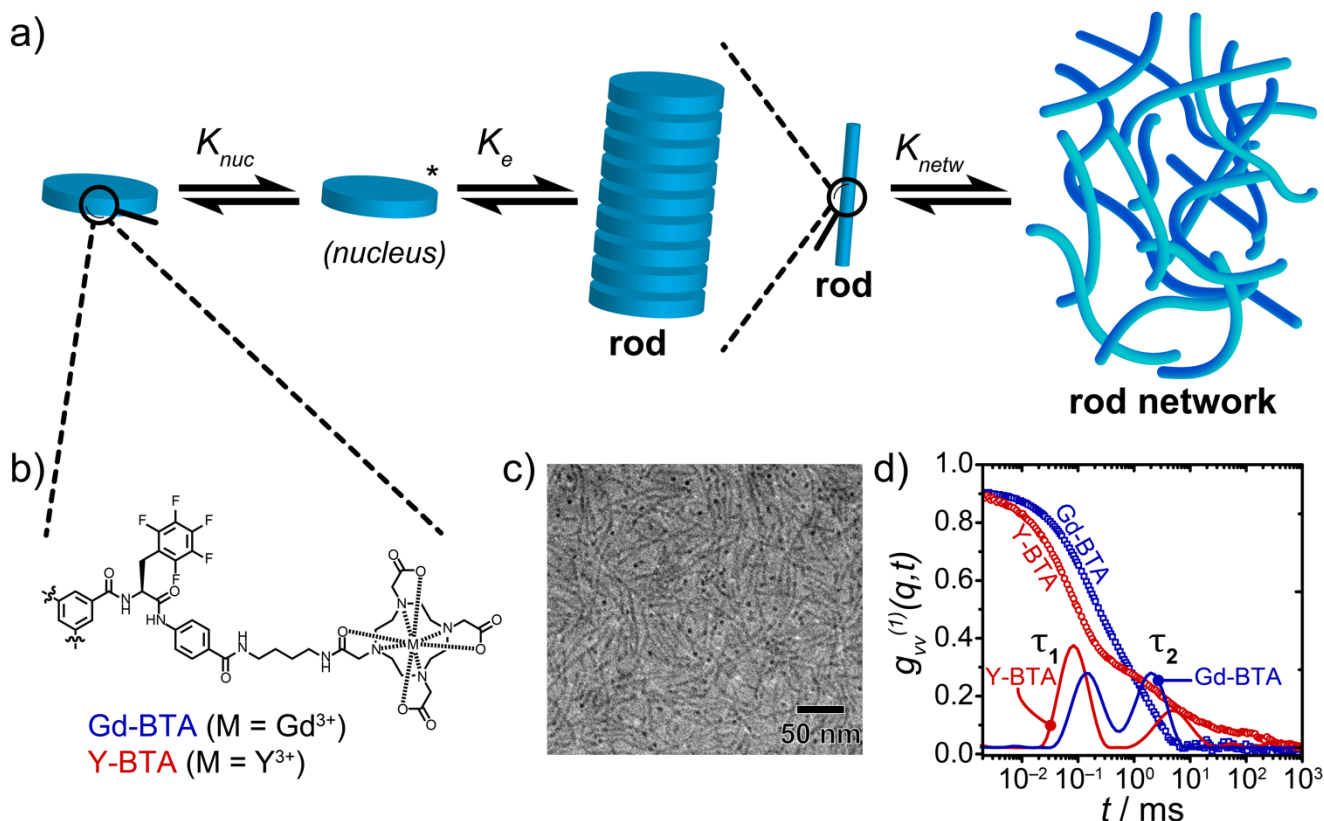
34 **Figure 1. The formation and analysis of rod networks, consisting of supramolecular rods**. a) Scheme depicting

35 nucleation K_{nuc} (10^{-4}), elongation K_e (1.4×10^6 M^{-1}) and solution network formation K_{netw}. b) Molecular structures of Gd-BTA

36 and Y-BTA. Only 1 out of three arms is shown for compactness. c) Polarized field correlation function $g_{VV}^{(1)}(q,t)$ at 100 µM

37 concentration in 100 mM citrate buffer at pH 6 measured at q = 0.0288 nm^{-1}, shown by the hollow symbols. The solid lines

38 show the corresponding bimodal distribution of relaxation times. d) Cryo-transmission electron microscopy image of the rods

39 and rod networks formed by Gd-BTA at 100 µM in 100 mM Citrate (pH = 6). The scale bar is 50 nm.

40 In the current work, we show that the rods assemble further into rod networks (simplistically represented by

41 K_{netw} in Fig. 1a), as can be seen from cryo-TEM in Figure 1c. The rods and rod networks can also be measured

42 in their native solution state, using dynamic light scattering. Figure 1d shows the vertical–vertical (vv) polarized

43 electric field autocorrelation function $g_{VV}^{(1)}(q,t)$ at a scattering wavevector q = 0.0288 nm^{-1}, which shows a decay

44 versus time shift t. The latter function can be used to extract a distribution of relaxation times τ (solid lines in

45 Figure 1d) by using the inverse Laplace transformation.[30] Starting with Gd-BTA (blue line), we can see that

46 there are two distinct relaxation processes with typical timescales $\tau_{1,Gd-BTA}$ and $\tau_{2,Gd-BTA}$, corresponding to rods

47 and rod networks, respectively, that differ by more than an order of magnitude. Both processes are q^2-dependent

48 and are thus diffusive, allowing us to fit their diffusion constants $D_H = \Gamma \cdot q^{-2}$ (where Γ is the decay constant),

49 and convert the latter into hydrodynamic radii using the Stokes–Einstein equation $R_H = k_B T / 6\pi \eta D_H$ (where η is

50 the dynamic viscosity). Table 1 shows the hydrodynamic radii for both Gd-BTA and Y-BTA samples. We can

51 convert the values of $R_{H,1}$ into rod lengths using the Tirado[31] model (with a fixed radius of 3.1 nm deduced from

52 cryo-TEM, Figure 1c). This results in rod lengths in solution of ~245 nm for Gd-BTA and ~120 nm for Y-BTA

53 (see Table 1, middle column). Though in a prior study[26] we had shown that Y(III) was a good control ion—that
54 is, having identical assembly behavior and sizes as compared to its Gd(III) analog—in this case, the Gd-BTA
55 rods are twice as long as those of Y-BTA (cf. Table 1). Yttrium is often 8-coordinated, whereas gadolinium can
56 be 8 or 9-coordinate, which could manifest itself as having one or two coordinated H_2O molecules at the Gd
57 atom in solution, respectively. Since we have other control experiments—i.e., Gd-BTA in absence of the
58 magnetic field—we disregard the rod size difference between Y-BTA and Gd-BTA for now.

59 **Table 1. Results from light scattering experiments.** Hydrodynamic radii R_H of rods and the rod network from dynamic
60 light scattering (Figure 1d) and the respective rod lengths fit to the Tirado model.[31]

| Species	Rods: $R_{H,1}$ (nm)	Rod length from $R_{H,1}$ (nm)	Rod network: $R_{H,2}$ (nm)
Gd-BTA	30.5 ± 4.5	245 (calc.)	348.2 ± 69
Y-BTA	17.9 ± 1.5	120 (calc.)	503.7 ± 169.6

61   The structure of the rod networks can be studied in more detail by static light scattering, where the Rayleigh
62 ratio has a power law dependency $R(q) \propto q^{-d_F}$ (Fig. 2a), with d_F the fractal dimension. In general, $d_F = 1$ (one-
63 dimensional) describes a line, and the upper limit $d_F = 3$ (three-dimensional) a sphere.[32] In the absence of a
64 magnetic field we find d_F of our rod network to be 1.7 ± 0.2, in agreement with literature[33,34]. The d_F value was
65 independently confirmed by box-counting cryo-TEM images of Gd-BTA, with values of 1.77–1.85 (see SI
66 Section 2). In the experiments that follow we use d_F to quantify the rod network *topology*, and the Rayleigh ratio
67 $R(q)$ to determine the approximate *mass* contained in the network.
68   Practically, a light scattering cuvette was placed between the pole pieces of an electromagnet for 1 h, then
69 analyzed by light scattering (~1 h) without field, and placed back in the magnetic field. This cycle was repeated
70 6–7 times (12–14 h in total). Within the first hour, the fractal dimension d_F changes from 1.7 ± 0.2 to 2.2 ± 0.2
71 (1 T) or 2.6 ± 0.2 (2 T) and then remains constant for the rest of the experiment (see Fig. S1 in the SI). This
72 implies that the increased magnetic field leads to an increasingly dense network structure, ending up at 2 T with
73 randomly branched clusters.[35–37] In contrast, the $R(q)$ for the Gd-BTA rod network keeps on increasing gradually
74 over time, and reaches a plateau only after 10–12 h. The final plateau values are 20% (1 T) or 35% (2 T) higher
75 than the original value, in no field. The latter shows that more rods are contained in the rod network, pointing at
76 an increase in K_{netw} upon applying the magnetic field, as we will discuss below. After removal of the magnetic
77 field, the samples returned to their original $R(q)$ values within one day.
78   Surprisingly, the individual rods (open symbols, Fig. 2b) are not detectably affected by the magnetic field,
79 since their $R(q)$ remains constant. If the sample is not exposed to the magnetic field, the value of $R(q)$ for the
80 network remains constant as well (see grey dashed box in Fig. 2b). Likewise, for weakly diamagnetic Y-BTA,
81 no changes were observed.
82   Our qualitative interpretation thus far is that the network topology changes fast (< 1 hour), and this slowly
83 drives additional rods to assemble into rod networks, taking ~12 hours as evidenced by the increase in Rayleigh
84 scattering $R(q)$ intensity. It is known that isodesmic supramolecular polymers elongate in aligning fields
85 (including electric fields, flow fields, or gravitational/centrifugal fields).[16] In the latter case, the field (partially)
86 aligns the polymer which entropically favors the polymer to elongate. The latter in turn increases the degree of

87 alignment of the polymer as it is now longer, and it provides positive feedback. Analogously, we believe that the
88 magnetic field entropically favors rods to assemble increasingly into rod networks.
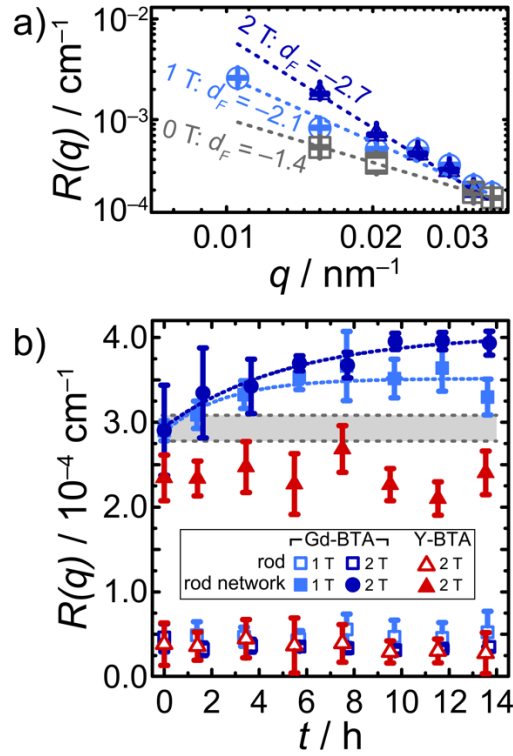
Figure 2. Quantification of rod network topologies upon exposure to magnetic fields. a) Rayleigh ratio $R(q)$ of Gd-
BTA rod networks as a function of wavevector q at 0, 1 or 2 T applied magnetic field. The slopes of the curves give the
fractal dimension d_F (values shown in the graph). Error bars are standard deviations calculated over 5 measurements. b)
Rayleigh ratio $R(q)$ at q = 0.0288 nm^{-1} over time for rods and rod networks, denoted by hollow and filled symbols,
respectively. The gray area represents the control for Gd-BTA in absence of a magnetic field (mean and standard deviation).
Error bars show standard deviations over 50 measurements.

95 To come to a more quantitative understanding we have compared the magnetic properties of Gd-BTA and
96 Y-BTA. We first checked for interactions between the Gd^{3+} ions by measuring the susceptibility χ versus
97 temperature in a SQUID (superconducting quantum interference device) magnetometer. The data in Fig. 3a)
98 show Curie–Weiss behavior $\chi = C(T - \theta)$ with a very small negative paramagnetic Curie temperature of $\theta = -$
99 0.7 K. Such weak antiferromagnetic coupling between the Gd^{3+} ions in the rods is negligible at room
100 temperature, and it cannot explain our observed field effect on the rod network (Fig. 2b). We also subjected
101 samples to a constant 5 T field for up to 12 h while monitoring the magnetic susceptibility. For Gd-BTA, the
102 susceptibility decreased by ~2% with respect to the original value χ_0 on a timescale commensurate with that
103 found in the light scattering experiments (Fig. 3b). The latter results indicate a minor alignment of the rods in
104 the network upon exposure to the magnetic field. By optical birefringence in our light scattering setup, however,
105 no changes could be observed at 1 or 2 T. As expected, changes were not observed in the case of Y-BTA or a
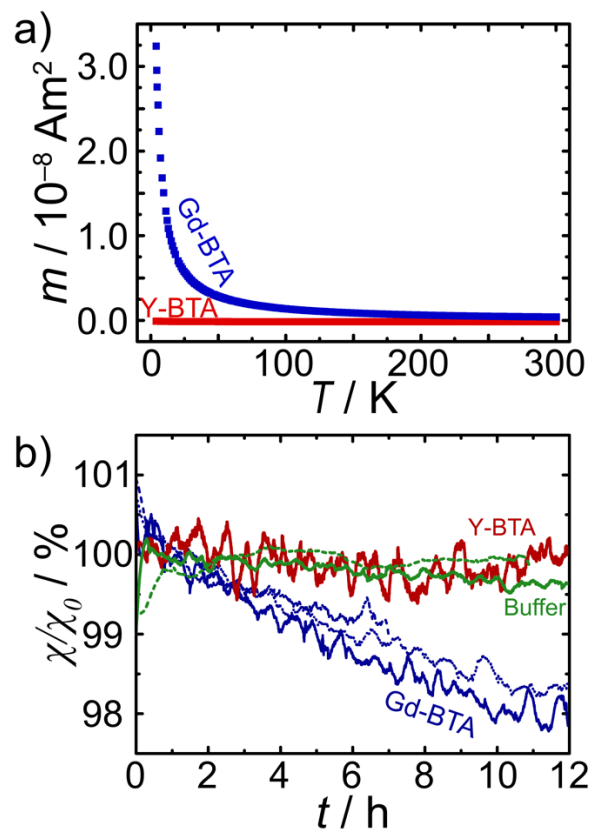106 buffer solution.

Figure 3. Magnetic characterization of supramolecular rods and rod networks. a) Temperature-dependent magnetization curve of Gd-BTA and Y-BTA in powder form, blue and red respectively. *m* represents the magnetization of the sample in A m^2. Gd-BTA shows a weak antiferromagnetic coupling of –0.7 K while the Y-BTA molecule showed no paramagnetism. b) Room-temperature time-dependent magnetization of Gd-BTA and Y-BTA (blue and red lines respectively) in solution, and as a negative control the buffer separately (in green). The samples were place in the SQUID under 5 T magnetic field and their magnetization was measured over the course of 12 h. The solid and dotted lines are separate experiments. The increase of the demagnetizing factor of the Gd-BTA with time is due to the evolution of the supramolecular structure.

Let us now consider how the magnetic field could affect the network structure. Under normal conditions the distribution of rods versus rod networks is governed by an equilibrium constant, K_{netw} as seen in Fig. 1a. This is a simplified representation, since a single equilibrium constant does not consider the length and distribution of the rods. Keeping that in mind, we can express K_{netw} as:

$$K_{netw} = e^{-\frac{\Delta G_0 + \Delta G_m}{RT}}$$

where ΔG_0 is the Gibbs free energy at 298 K and 0 T. The additional term, ΔG_m, is a magnetic Gibbs free energy induced by the magnetic field, which has two components: 1) an isotropic term $U_i = -\frac{1}{2} MB$ stemming from the isotropic sum of all individual Gd^{3+} ion contributions (see supporting information section 3), and 2) an anisotropic free energy is defined as:[21]

$$U_a = \frac{1}{4} \mu_0 M_s^2 (1 - 3N)$$

with N the effective demagnetizing factor ($N = 0$ for an axially magnetized long rod), M_s the induced magnetization and μ_0 the vacuum permeability. For our rods with $M_s = 600$ A m^{-1} (see section 3 of the SI), the

127 anisotropy energy is therefore 0.17 J m^{-3}. The volume V of a supramolecular network that can have its structure
128 modified by the applied field can be estimated by setting $U_aV = kT$, which gives $V = 24 \cdot 10^{-21}$ m^3, or a size of
129 about 300 nm.
130   In conclusion, we have shown pronounced changes in the network structure of supramolecular polymer rods
131 containing paramagnetic ions on applying magnetic fields of 1–2 T. The magnetic free energy contributions are
132 insignificant at the single rod level, but they become significant at the network scale. It is the magnetic dipole
133 anisotropy energy that drives the network changes. Our approach could guide structure formation of other
134 supramolecular and coordination polymers using rare earth or other paramagnetic ions.

135 **ASSOCIATED CONTENT**
136 Supporting Information

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160 **Notes**
161 The authors declare no competing financial interest.

162 **ACKNOWLEDGEMENTS**

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