ORIGINAL ARTICLE

Formation of host-guest and sandwich complexes by a β -cyclodextrin derivative

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Abstract A unimer with two host binding sites of β -cyclodextrin and two guest binding sites (two *p*-tertbutylphenyl moities) has been synthesized. The host and guest residues are linked through an EDTA bridge. Static and dynamic light scattering measurements evidence the formation of supramolecular entities in aqueous solution with a low degree of polymerization (<10). The formation of dendrimer-like structures is demonstrated by TEM measurements. From NMR experiments it is concluded that the *p-tert*-butylphenyl group is located at three different environments. Two of these sites correspond to the typical locations of a guest in equilibrium with a host, i.e., inside the host cavity and in the bulk solution. The third location corresponds to a *p-tert*-butylphenyl group sandwiched between the outer surface of at least two cyclodextrin residues and the bridge of the unimer, forming an external complex.

Keywords Inclusion complexes \cdot Sandwich complexes $\cdot \beta$ -cyclodextrin \cdot Supramolecular polymers

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Introduction

Supramolecular polymers [1], and particularly host/guest supramolecular polymers, is a research area of a growing importance. During the past few years, descriptions of different supramolecular polymers involving cyclodextrin derivatives (as host entities) have been published. These polymers can be classified as four main types [2] depending on whether the host and guest sites belong to the same (in this case the polymer is formed by interlocked unimers) [3-8] or to different species [2, 9-12] and on the number of topic sites in each species [2, 13–15]. Polytopic species can originate dendrimer-like structures [13]. Molecular necklaces or polyrotaxanes are also well documented [16–19]. Less attention has been paid to the formation of dendrimerlike structures from cyclodextrin derivatives in which the interlocking polytopic unimers simultaneously carry the two complementary units (i.e., hosts and guests sites).

Different cyclodextrin dimers have been published and used for several purposes [20]. Recently, the great capacity for solubizing cholesterol of the β -cyclodextrin (β CD) dimer 1 (Fig. 1) was studied [21]. This dianionic dimer, obtained from the reaction between EDTA dianhydride and the monoamine derivative of β CD, 6-NH₂- β CD, has two free carboxylic groups which can further react with hydrophobic groups which are appropriate guests for entering into the cavity of the cyclodextrin [22]. On the other hand, NMR spectroscopy is probably the most powerful technique to study the structure of inclusion complexes in aqueous solution [23-27]. Since NMR signals from aromatic protons of a phenyl ring are very distinctive and far from those of aliphatic protons, an aromatic residue seems to be a nice option as guest residue for 1. This will help in the elucidation of the structure of the complex. Furthermore, it is well known that *p-tert*-butylphenyl group **Fig. 1** Polytopic host/guest unimers with two host residues (β CD) and two *p-tert*butylphenyl guest moities



effectively enters into the cyclodextrin cavity [28–33], the association equilibrium constant being of the order 10^4 M⁻¹ [31].

With these precedents in mind we have synthesized the compound *t*BuPh2-CD2 (Fig. 1) carrying two bulky *p-tert*-butyl-phenyl groups and two β CD residues. The compound is highly soluble in water allowing to study its behaviour in aqueous solution by light scattering and NMR techniques.

Experimental

Synthesis

The synthesis of *t*BuPh2-CD2 was carried out according to Scheme 1.

Synthesis of <u>2</u>: Ethylenediaminetetraacetic dianhydride (2.40 g, 10.0 mmol), obtained from ethylenediaminetetraacetic acid (EDTA), and *p-tert*-butylanyline (3.08 g, 20.0 mmol) were dissolved in 20 and 30 mL of dried DMF, respectively. Triethylamine (10 mL) was added. The reaction mixture was stirred for 10 min at 0 °C and then 12 h at r.t., and finally concentrated in vacuo. The solid was obtained by addition of an acid solution (pH = 2) and was washed twice with acidic water. The final products were purified by recrystallization from methanol.

Synthesis of tBuPh2-CD2: In a dry 100 mL flask, <u>2</u> (0.6 mmol), 1-Hydroxybenzotriazole (HOBT (Aldrich); 0.27 g, 2.0 mmol) and 0.25 ml of diisopropylcarbodiimide (DIC, Avocado)) were mixed in 10 mL of dried DMF and a solution of β -CD-6NH₂ (2 g, 2.0 mmol) in 10 mL of dried DMF. The reaction mixture was stirred at r.t. for 24 h and then 0.25 g of HOBT, 0.25 ml of DIC and 1.2 g of β -CD-6NH₂ were added. The final product was purified by a

Sephadex C-25 column with water as eluent. Overall yield 81%. Solvents were from Panreac.

*t*BuPh2-CD2: ¹H RMN (D₂O; 300 MHz, δ/ppm): 7.25–6.66 (2Ha, 2Hb); 4.93 (bs, 14H₁-CD); 4.04–2.50 (m, 96 (H-CD + H_{EDTA}));1.28 (s, 18Hf). MALDI-TOF: [M + Na] m/z 2824.02 calculated for $C_{114}H_{179}KN_6O_{72}$. Found: 2824.08.

SLS and DLS measurements

The basic theories of static and dynamic light scattering techniques are very well-known and can be found elsewhere [34, 35]. Light scattering measurements were carried out in a Malvern 4700 apparatus and in a Brookhaven instrument constituted by a BI2030AT digital correlator with 136 channels and a BI200SM goniometer. The light sources were a Melles-Griot He-Ne laser operating at 632 nm (Malvern) and a Uniphase solid-state laser system model 4601 operating at 532 nm (Brookhaven). Dust was eliminated by filtering the samples with Nuclepore filters with a pore size of 0.1 μ m. The samples were placed in the cell for at least 30 min prior the measurement to allow for thermal equilibration. Their temperature was kept constant at 25 ± 0.5 °C by a circulating water bath. To prevent mold growing, these experiments were carried out in the presence of sodium azide (10 mg mL⁻¹). The refractive index measurements were performed in an ATAGO differential refractometer model DD7.

In the DLS experiments the intensity-intensity autocorrelation function was measured, at a particular value of the scattering vector q, and related to the normalized electric field autocorrelation function $g_1(q,\tau)$ by the Siegert relation. Therefore, $g_1(q,\tau)$ was analyzed through the cumulant expansion, and the so-called apparent diffusion coefficient





0

0

10

where c and M_{app} are the solute concentration (g mL⁻¹) and the apparent molecular weight, respectively, and K is a constant that depends on the solvent refractive index, the solution refractive index increment (dn/dc = 0.1506 mL g^{-1}), and the laser wavelength.

NMR measurements

multimodal distributions.

by the equation

 $\frac{cK}{\Delta R_{90}} = \frac{1}{M_{\rm app}}$

For NMR experiments D₂O (99.90%) was supplied by SDS (France). The solution pH was adjusted with KOD (Aldrich, 40% in D₂O). Samples were prepared directly in the NMR tubes. Spectra were recorded using an NMR spectrometer operating at 500 MHz for ¹H at 293.1 K.

Results and discussion

Light scattering results are reported in Fig. 2. They clearly indicate that the apparent molecular weight, $M_{\rm app}$, grows by increasing the concentration of tBuPh2-CD2, although the observed degree of polymerization (or aggregation number) is low (<10). This may be due to steric hindrance between the bulky constituents (cyclodextrin and p-tertbutylphenyl residues) of the unimer. Simple molecular models suggest that it is not possible to reach a configuration in which all guest residues fill all host cavities. Furthermore, growing oligomers can adopt a shrunk conformation in aqueous solution, avoiding the polymer growth, because of the polymer could be close to the theta condition, i.e., the aqueous medium does not represent a good solvent for the polymer which will hardly assume the

Fig. 2 Hydrodynamic radius and apparent molecular weight of tBuPh2-CD2 in aqueous solution

20

c/10⁻³M

30

3

0

40

most extended conformations, preventing further growth. This has been recently demonstrated for adamantyl-cyclodextrin supramolecular polymers [12]. Figure 2 also shows a good correlation between hydrodynamic radius and molecular weight.

Figure 3 shows TEM images of dendritic structures formed by tButPh2-CD2, reminding those observed for other systems [2]. The average width of the branches is 52 ± 12 nm, i.e., what we have been able to measure is too far from observing the branched structure at a molecular level. However, it is necessary to consider that structures with recognizable branches are only expected at large aggregation numbers [36], as we have recently demonstrated for the supramolecular polymer derived from an adamantyl dimer and a β -cylodextrin trimer. In the present case, some *p-tert*-butylphenyl groups are squeezed between external cyclodextrin walls (see below) reducing their chances of participating in the formation of branched structures. This is in agreement with the low degree of polymerization observed in aqueous solution determined from light scattering measurements. Anyway, we must remind that the experimental conditions for SLS and DLS experiments (results reported in Fig. 2) are very different



Fig. 3 TEM images obtained from solutions of tBuPh-2CD2 at an initial concentration of 2 mM in D_2O

from those required for obtaining TEM images (Fig. 3) and consequently the results are not directly comparable.

Further insights on the polymer structure were obtained from NMR experiments. Figure 4 shows the ¹H NMR spectrum of *t*BuPh2-CD2. Signals corresponding to the aromatic and *tert*-butyl groups are given at the insets. Under fast exchange-NMR time scale only one peak for *tert*-butyl protons and characteristic two doublets due to protons of a 1,4-disubstituted aromatic ring should be observed. The chemical shift of a given nucleus would depend on the chemical shifts of free and complexed (inside the cyclodextrin cavity) guest, statistically weighted by their molar fractions. Under a slow exchange regime, the chemical shifts of free and complexed guest protons would be detected. Under these conditions two peaks for the *tert*-butyl group and four doublets for the protons of the aromatic ring should be observed. However, the ¹H NMR spectrum evidences three peaks for protons of the *p-tert*butyl group ($\delta = 1.135-1.173$ ppm) and four doublets and a multiplet for the aromatic protons ($\delta = 6.70-7.20$ ppm). They integrate for eight and eighteen protons, respectively (see insets in Fig. 4), in perfect agreement with theoretical values. This suggests that the *p-tert*-butylphenyl group is located in three different environments. For reasons given below, they are named with subscripts 'f', 'i' and 's'.

Complete assignment of these resonances was achieved by the combination of ${}^{1}H{-}^{1}H$ COSY and ROESY techniques. The later one also gives information on the interactions between protons of the guest and protons of the host, allowing to differentiate between peaks corresponding to complexed and free guest groups. Figure 5 shows the ${}^{1}H{-}^{1}H$ COSY of the aromatic region where the arrows connect signals of protons belonging to the same phenyl residue in a given environment.

ROESY signals help in the assignment of the environment of the *t*-butyl protons as well as to differentiate between *ortho* and *meta* aromatic protons since only crosspeaks involving signals assigned to *meta* protons will interact with protons of the *t*-butyl group. There are five signals in Fig. 6. Three of them correspond to "expected" interactions implying tert-butyl and aromatic protons of species in the same environment (m_{f} - t_{f} , m_{i} - t_{i} and m_{s} - t_{s}). The other two signals correspond to "unexpected" interactions m_{f} - t_{i} and m_{i} - t_{f} (very week signal), suggesting interactions



Fig. 4 ¹H NMR spectrum of tBuPh2-CD2 in D₂O at a concentration of 10 mM

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between two tert-butylphenyl groups, one being included inside the cyclodextrin cavity and the other one being free. This requires that the free tert-butylphenyl group (as the one named B in Fig. 8) approaches to a cyclodextrin cavity, with another tert-butylphenyl inside (named C in

Fig. 8) by its primary rim. Although the distances between B and C protons (as drawn in Fig. 8) are around 7.5-8.5 Å (far from a ROESY distance), the approach between the two groups is possible because of the flexibility of the methylene groups of the bridge chain. Molecular models

Fig. 7 Region of the ROESY spectrum showing the cross-peaks observed for the interactions between cyclodextrin (host) protons and *p-tert*-butylphenyl residue (guest) protons



indicate that this is an easy movement. Figure 6 shows the final assignments. It can be noticed that *ortho* protons do not show any cross-peak with *t*-butyl peaks and that, with the mentioned exceptions, there is a one-to-one correspondence between aromatic protons and *t*-butyl protons within a given environment. It is time to justify the subscript names given to the signals, i.e., the environment in which the protons are located.

Before discussing further ROESY results, we must remind the structure of β -cyclodextrin. It is characterized as a wreath-shaped truncated cone. The H3 and H5 hydrogen atoms of each glucose residue protrude towards inside, forming constrictions to the entrance of guest molecules, while the H2 and H4 hydrogen atoms are outside the cavity [37]. ROESY experiments have widely been used to elucidate the structure of inclusion complexes



formed by a given guest and cyclodextrins. Under slow rate regime [25] complexed and free species are clearly differentiated [27], as well as the side of entrance of the guest into the cyclodextrin cavity [9]. Although proton spectra of 6-substituted β -cyclodextrins are rather complex, they have been solved in literature [27]. Figure 7 shows the crosspeaks interactions of the aromatic region with cyclodextrin protons. The most important cross-peaks involving H2, H3 and H4 protons of the cyclodextrin residue with the aromatic and *t*-butyl protons of the guest residue are highlighted. There is also an apparent signal at the ROESY spectrum, which would correspond to a $t_{\rm f}$ -H3 interaction, but it is a valley, not a peak.

Some facts can readily be noticed from the characteristic aromatic region of the ROESY spectrum: (1) Peaks corresponding to *ortho* protons (o_f , o_i and o_s) do not show any cross-peak with H2, H3 or H4 cyclodextrin protons. Grey strips in Fig. 7 help to visualize this fact. (2) This is also the case for the m_f peak (see the grey strip in the Figure). (3) Cross-peaks implying signals from m_s and m_i with H3 are observed; m_i also shows a weaker signal with H4. (4) Finally, there are cross-peaks implying t_i with H3 and H5, and t_s with H2.

Therefore, ROESY experiments confirm that the *p-tert*butylphenyl group can be located at three different environments.

The cross-peaks between the cyclodextrin protons and those of the *p-tert*-butylphenyl group allow identification of these sites. Proton signals with subscript "f" (which belong to the same *p-tert*-butylphenyl group as demonstrated above) do not interact with any cyclodextrin proton suggesting that the guest is located in the bulk solvent, i.e., the residue is uncomplexed. On the other hand, cross-peaks involving H3 protons of the cyclodextrin strongly suggest that the guest is located inside the cyclodextrin cavity [38]. Correspondingly, the guest peaks have been subscripted as "i" to indicate the formation of a guest/host inclusion complex. The absence of the o_i -H3 cross-peak suggests that the aromatic ring is not fully included inside the cavity but only the *t*-butyl group and the *meta*-protons are included. Finally, the interaction t_s -H2 (strong), together with m_s -H3, suggests that the *p-tert*-butylphenyl group lies nearby the outer surface of the cyclodextrin and far from the bulky solvent. The tBuPh2-CD2 unimer can provide a hydrophobic site outside the cyclodextrin cavity to hold the hydrophobic *p-tert*-butylphenyl group, in order to obtain a thermodynamic favourable interaction.

However, some unexpected signals of the included groups inside the β -cyclodextrin cavity with its external protons H2 and H4 can be noticed in the ROESY of Fig. 7 implying interactions as m_i -H4 and t_i -H2. These observations (guest-outside protons of the cyclodextrin) are not unusual and many examples for different guests (phthalhydrazide, [39] aspartame, [40] hydroxy-substituted naphthalenes, [41] bipyridine molecules, [42] ionic liquid surfactants, [43], etc.) can be cited. In fact this should not be surprising as distances between guest protons and the outside protons of the cyclodextrin are at a ROESY distances of 4Å. This can be checked in resolved crystal structures of guests inside the β -cyclodextrin cavity (see for instance ref. [7]). A discussion of this subject is far from the scope of the present manuscript.

To explore the hydrophobic site outside the cyclodextrin cavity to hold the hydrophobic *p-tert*-butylphenyl group, a molecular mechanics calculation was perfomed with two unimers. Although the final structure corresponding to the minimum energy depends on the initial configuration, the structure shown in Fig. 8 is frequently found. It can be noticed that there are three different locations for the ptert-butylphenyl group. The one included inside the cyclodextrin cavity is visible because of the cyclodextrin has been partially drawn in a "capped stiks" style. These tert-butyl residues have been highlighted in orange (Fig. 8). It can be noticed that the *p*-tert-butyphenyl group nearby the outer surface of the cyclodextrin is surrounded by a hydrophobic environment provided by the H2 and H4 hydrogen atoms of the cyclodextrin and methylene groups of the bridge. Thus the *p-tert*-butylphenyl group is sandwiched between the outer surface of at least two cyclodextrin residues and the bridge of the unimer. A similar complex has been proposed by Wagner et al. [44] for the interaction between 1-anilinonaphthalene-8-sulfonic acid and cucurbit[7]uril.

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