Formation of complementary and cooperative hydrogen-bonding networks of sugar-based bolaamphiphiles in water

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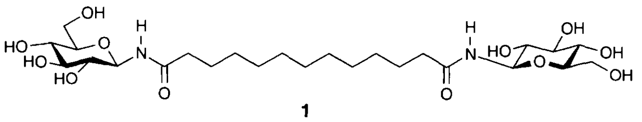
Synthetic glucopyranose-based bolaamphiphiles self-assemble to form a molecular layered structure in water by complementary and cooperative hydrogen-bonding networks of sugar hydroxy and amide groups.

Hydrogen-bonding of molecular self-assemblies plays an important role in biological systems and has attracted our attention as a key methodology to form spontaneously stable and structurally well-defined nanostructures.[1] In spite of much excellent work on the formation of molecular aggregates *via* hydrogen bonding, most have been performed in non-polar or aprotic solvents.[2] This is because hydrogen-bond formation competes with solvation in polar media. In the present study, a sugar-based bolaamphiphile[3] was designed and synthesized† to generate nanostructures by effective and strong hydrogen bonds in water. Molecule **1** has two hydrophilic D-glucopyranose rings connected by a hydrophobic alkylene chain through two amide bonds, Scheme 1. The reasons why these building elements were selected for the bolaamphiphile, are as follows: (i) aldopyranose rings have multiple and more directional hydroxy groups than acyclic sugars.[3] Consequently, the formation of strong and cooperative hydrogen-bonding networks[4] between the bolaamphiphiles can be expected; (ii) a variety of hydrogen-bonding modes involving the NH donor and carbonyl-O acceptor could be utilized to form a molecular self-assembly.[5] By the combination of these structural characteristics, spontaneous association of the bolaamphiphiles is anticipated in water as a result of three cooperating noncovalent forces; hydrogen bonds among sugar moieties and amide groups, and hydrophobic association between the long hydrocarbon bridge. Here effective hydrogen-bond formation is reported for the bolaamphiphile **1** in which two D-glucopyranose rings are linked by a β-*N*-glycosidic bond to 1,11-undecane dicarboxylic acid. So far only one X-ray analysis has been reported for a β-*N*-glycoside derivative.[6] Several β-anomer structures with long chains are already known,[7] the present structure further contributes to this list.

The bolaamphiphile **1**, $C_{25}H_{46}N_2O_{12}$, crystallized as thin platelets from boiled water. The crystals were stable at temperatures lower than 222 °C at atmospheric pressure. The high crystallinity of the bolaamphiphile **1** presents a striking contrast to the thermotropic liquid crystalline behaviour of bolaamphiphic polyols.[8] Successful X-ray diffraction analysis of a single crystal of **1**‡ showed that this molecule crystallizes in monoclinic space group $P2_1$. There are two molecules in the unit cell. The crystal packing pattern shows a layered structure in which the alkylene chains are arranged in an antiparallel pleated sheet, as shown in Figs. 1(*a*) and (*b*). The absolute configuration of the molecule is uniquely determined by the known chirality of the D-glucopyranose ring.[9] The atom numbering and the crystal structure of **1** are also given in Fig. 2. It should be noted here that these arrangements are stabilized by precise intra- and inter-layer hydrogen-bonding networks. Two glucopyranose rings adopt a $^4C_1$ chair conformation.



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Scheme 1

The distances between two adjacent alkylene chains are 4.92 Å [Fig. 1(*b*)] and 6.22 Å [Fig. 1(*a*)]. The former can be seen typically for the alkylene-chain packings with hydrogen-bonded amide groups.[5] The latter distance is strongly affected by the packing mode of pyranose rings. As a result, the alkylene chains should have an inclination of 48.7° with respect to the normal to the layer plane.[10] The hydrogen-bonding patterns of sugar hydroxy groups are similar for both sides of the molecule, except for O(2)–H and O(12)–H. Intra- and inter-layer hydrogen-bonding networks of sugar hydroxy groups are formed in the equatorial direction of the pyranose rings [Fig. 1(*a*) and (*b*)]. Intralayer hydrogen bonds are formed between the hydroxy groups and oxygen atoms, O(3)–H···O(5), O(3)–H···O(6) and

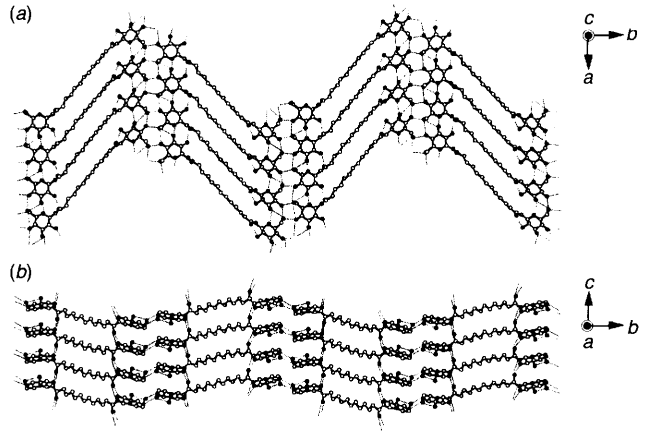

Fig. 1 Molecular packing of **1**, viewed along (*a*) the *c* axis and (*b*) the *a* axis, representing the inter- and intra-layer hydrogen-bonding networks. Hydrogen atoms have been removed for clarity.

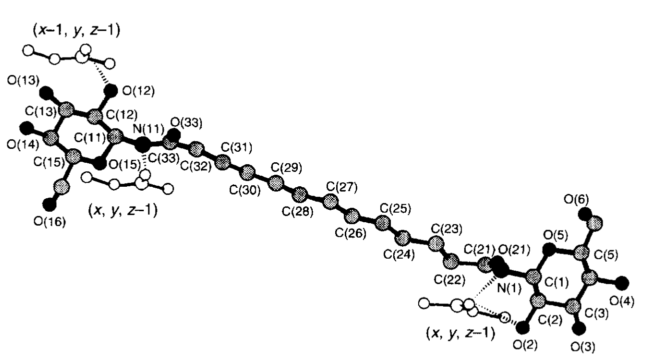

Fig. 2 Crystal structure of **1** showing components of molecules at (x – 1, y, z – 1) and (x, y, z – 1)

O(4)–H···O(6), and there are interlayer hydrogen bonds between the hydroxy groups, O(4)–H···O(6). These intralayer hydrogen-bonding patterns are very similar to those found in the crystal structure of merosingrin.[11] The hydrogen-bonding patterns of the amide groups were arranged in a pseudo-translation motif.[5] It is of particular interest that the hydroxy group O(2)–H bonds to O(21) of (x, y, $z - 1$) **1**, while the O(12)–H bonds to O(33) of ($x - 1$, y, $z - 1$) **1**, as shown in Fig. 2.

In Fig. 2, the least-square plane through the N(1), C(21) and O(21) atoms of the amide group (plane A) forms an angle of 66.1° to that through the C(2), C(3), C(5) and O(5) atoms of the glycopyranose ring. On the other side of **1**, the least-square plane through the N(11), C(33) and O(33) atoms of the amide group (plane B) forms an angle of 72.9° to that through the C(12), C(13), C(15) and O(15) atoms of the glucopyranose ring. These deviations of the angles from 90° are affected by the formation of the intralayer hydrogen-bondings of O(2)–H of (x, y, z)···O(21) of (x, y, $z - 1$) and O(12)–H of (x, y, z)···O(33) of ($x - 1$, y, $z - 1$). The lest-square planes of the amide groups (planes A and B) are also inclined (*ca.* 13.4 and 16.8°, respectively) to that through 11 carbon atoms of the spanned alkylene chain. The alkylene chain may be considered to be a flexible spacer with two terminal hinges at the amide link. As a result of the formation of inter- and intra-layer hydrogen bonds, the least-squares plane through the C(22), C(23) and C(24) atoms of the alkylene chain forms an angle of 30.9° to that through the C(30), C(31) and C(32) atoms. In other words, the alkylene chain is constrained to be slightly left-handed twisted with an all-*trans* type conformation and is also bowed with subtending angles of 5.9°, when viewed from the perpendicular axis to the plane A. Both amide planes A and B were found to be almost parallel (8.5°). These phenomena might be anomalous for the conformation of alkylene chains that are not restricted by a covalent cyclic structure.

Footnotes

† Compound **1** gave satisfactory spectra and C, H and N analytical data.

‡ *Crystal data* for $C_{25}H_{46}N_2O_{12}$: monoclinic $P2_1$; a = 6.220(1), b = 48.25(1), c = 4.922(2) Å, β = 105.67(2)°, V = 1422.3(6) Å^3, Z = 2, D_c = 1.32 g cm^{-3}, T = 297 K. A Mac Science MXC18 diffractometer was used to collect 3308 data points of which 2256 data with $[F > 3\sigma(F)]$ were used in the solution and refinement. X-Ray data were corrected for absorption [λ(Mo-Kα) = 0.71073 Å]. All measurements were performed using the ω scan method in $3 < 2\theta < 55°$. Each peak was observed without overlapping. The structure was solved by the direct method (SIR92 in CRYSTAN-GM) and refined by CRYSTAN-GM.[12] H atoms of hydroxy groups and amides were solved by differential-Fourier, and remaining H atoms were then placed at calculated positions. Structure refined to R_F = 0.0503 and R_{WF} = 0.0782; GOF = 0.75463, highest final difference peak, 0.21 e Å^{-3}.

Atomic coordinates, bond lengths and angles, and thermal parameters have been deposited at the Cambridge Crystallographic Data Centre (CCDC). See Information for Authors, Issue No 1. Any request to the CCDC for this material should quote the full literature citation and the reference number 182/39.

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