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Supramolecular Structures by Recognition and Self-Assembly of Complementary Partners: An Unprecedented Ionic Hydrogen-Bonded Triple-Stranded Helicate

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The search for new building blocks and structural motifs for crystal engineering has been an intensive research area in recent years.[1] The design of organic solids has largely capitalized on the recognition-controlled self-assembly of complementary molecules,[2] and hydrogen bonding has been widely exploited for this purpose.[3] Hydrogen-bonded supramolecular structures have, for example, attracted increasing interest in the field of nonlinear optical (NLO) materials,[3e,4] where organic crystalline salts have played a central role.[3e,4a] In the controlled assembly of solid-state structures, the availability of building blocks that reliably give predictable architectures is of paramount importance. Not surprisingly, since the helical motif is a structural feature predominant in Nature, helical architectures have been actively sought.[5] Although H-bonded synthetic helices based on a single chemical component are relatively common,[6] supramolecular structures based on molecular recognition between complementary partners and self-assembly into purely H-bonded helical architectures without the assistance of coordinating metal ions are rare,[7] particularly in the case of double-[7a] and triple-[7d,f] stranded helices, and even more rare are in the case of synthetic organic salts in which, in contrast to biological molecules, helices appear to be exceptional and essentially serendipitous.[8] In the vast realm of useful building blocks, *trans*-1,2-diaminocyclohexane (DAC) has been shown to be a valuable assembler of H-bonded supramolecular structures with diols,[9] featuring the helical motif as the dominant element of its architectural design. Molecular recognition and self-assembly has also been observed with carboxylic acids, giving rise to salt-type H-bonding networks, which, however, lead to layered structures,[9c] a far more common pattern for synthetic crystalline salts.[3e,4a,10] On the basis of the marked structure-directing ability of DAC,[9a] we thought that salts possessing H-bonded supramolecular helical architectures may also be assembled by selecting the correct partners. We report here that this has indeed been achieved by choosing a dicarboxylic acid that correctly matches the complementarity prerequisites of DAC; molecular recognition of partners resulted in the self-assembly of a strongly H-bonded ionic triple-stranded helicate of controlled helical sense, unprecedented in the family of synthetic organic salts.

Results and Discussion

Molecular recognition criteria derived from a thorough analysis of the DAC-based diamine-diol assemblies re-

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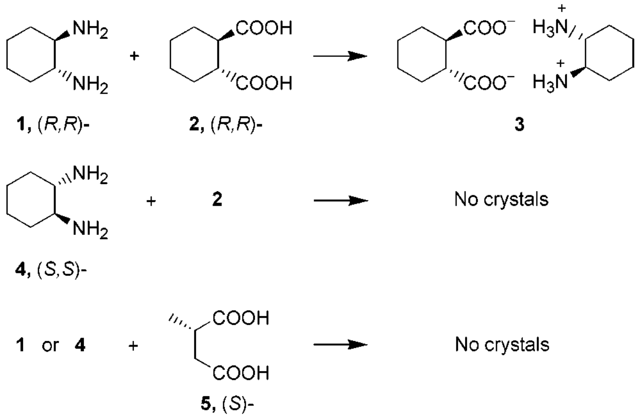
Scheme 1



ported to date[9a] indicated that 1,2-*trans*-disubstitution would be required for a well-matched partner for DAC by symmetry considerations, and that the cyclohexano substituent would be the best suited residue by steric and geometric considerations. A *trans*-1,2-cyclohexanedicarboxylic acid appeared therefore the partner of choice for building a ionic assembly, provided that proton transfer would occur.[11]

When equimolar amounts of enantiomerically pure (1*R*,2*R*)-*trans*-1,2-diaminocyclohexane (**1**) and (1*R*,2*R*)-*trans*-cyclohexane-1,2-dicarboxylic acid (**2**) were dissolved in a small amount of D_2O ($c \cong 0.6$ M), initial complete solution was immediately followed by precipitation of a white solid (**3**), which required a 3-fold amount of D_2O to obtain complete dissolution (Scheme 1). Slow evaporation of the solvent gave large colorless crystals of X-ray quality. In contrast, no solid separated from a solution of the same initial concentration of **2** and (1*S*,2*S*)-*trans*-1,2-diaminocyclohexane (**4**), which left a glassy material by evaporation of the solvent. This evidence suggested that recognition and self-assembly had occurred between **1** and **2**, inducing precipitation of a less soluble aggregate, and that the former was the only well-matched enantiomeric combination. As methyl substituents may replace the cyclohexane ring in the self-assembly of conformationally restrained adducts,[9a] the assembling of DAC with methylsuccinic acid was attempted; however, no crystalline material could be obtained by treating both enantiomers of DAC (**1** and **4**) with enantiopure (*S*)-methylsuccinic acid (**5**), showing that the complementarity requirements for recognition and self-assembly which have been met in **3** are remarkably strict. The molecular structure obtained from the X-ray analysis of crystals of **3** revealed that both acidic protons of **2** had been transferred to the amine nitrogen atoms of **1** and that the resulting diammonium dicarboxylate formed a doubly H-bonded ionic 1:1 adduct (Figure 1A). The crystal structure revealed that an infinite number of adduct units self-assembled along the crystallographic *a* axis into a monodirectional supramolecular structure of roughly 14 Å diameter, held together by a heavy network of hydrogen bonds (Figure 1). From the top view down the axis of the assembly (Figure 1B), four columns of perfectly stacked cyclohexane residues can be seen, which surround a polar core consisting of two concentric tubular arrays of tightly H-bonded oxygen and nitrogen atoms,

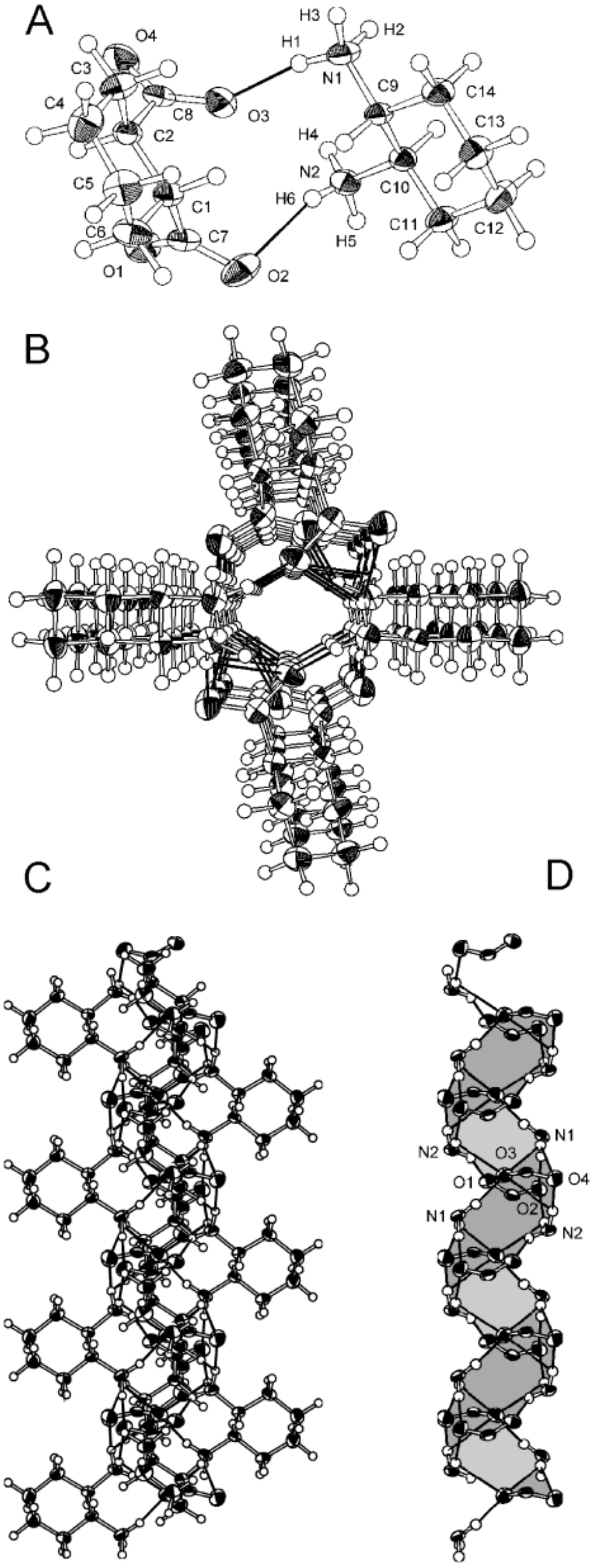


Figure 1. A: molecular structure of **3** with atom numbering scheme; H-bonds are represented as solid lines and thermal ellipsoids at the 50% probability level. B: top view of the H-bonded assembly of **3** down the *a* axis; H-bonds within 2.7 Å are represented as solid lines. C: side view of the H-bonded assembly of **3** along the *a* axis; H-bonds within 2.7 Å are represented as solid lines. D: simplified representation of C with heteroatom numbering, showing only the ammonium and the carboxylate groups involved in the H-bonding network. The right-hand helically folded shape of the network is highlighted in shades of gray.

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[11] Full proton transfer has not always been observed, giving rise to neutral H-bonded assemblies; see for example ref 7g.

Table 1. Hydrogen-bond Distances (Å) and Angles (deg) in the Assembly of 3[a]

donor-H···acceptor (equiv positions)[b]	donor···acceptor distance	H···acceptor distance	donor-H···acceptor angle
N1−H1···O3(0)	2.728(3)	1.80(3)	166(3)
N2−H6···O2(0)	3.035(3)	2.18(3)	160(3)
N2−H6···O3(0)	3.022(3)	2.65(3)	106(2)
N1−H3···O2(1)	2.682(3)	1.64(4)	178(3)
N1−H2···O4(2)	3.201(3)	2.31(3)	157(3)
N2−H4···O1(2)	2.776(3)	1.91(4)	145(3)
N1−H2···O3(2)	3.077(3)	2.32(3)	137(3)
N2−H5···O3(3)	3.178(3)	2.59(3)	117(2)
N2−H5···O4(3)	2.735(3)	1.74(3)	173(3)
O6−H4···O2(0)	2.797(3)	1.82(5)	164(4)
O7−H6···O1(0)	3.011(3)	2.19(5)	159(4)
O5−H2···O4(2)	2.758(3)	1.67(7)	177(6)

[a] Hydrogen-bonds found within a 2.7 Å distance are reported. [b] Equivalent positions: (0) x,y,z; (1) $x - 1, +y, +z$; (2) $x - 1/2, -y - 1/2, -z - 1$; (3) $x + 1/2, -y - 1/2, -z - 1$.

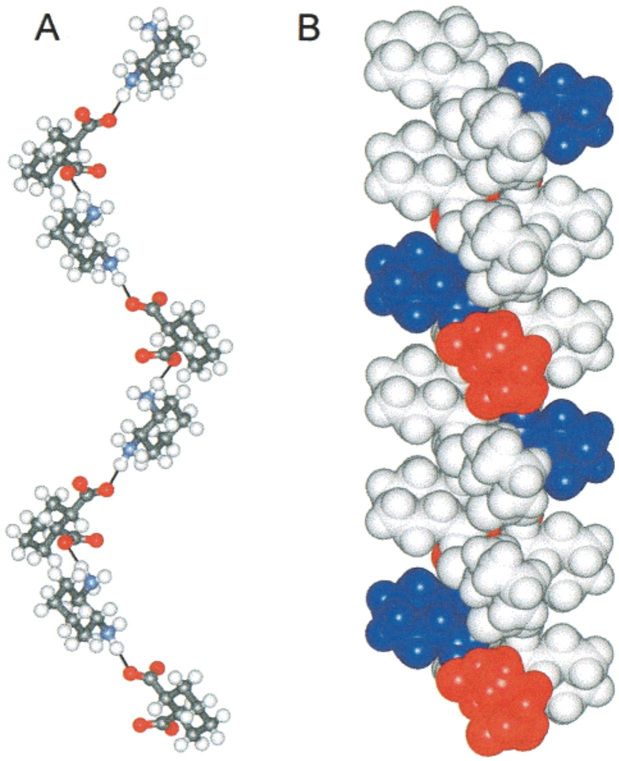

Figure 2. A: Single strand of the diammonium/dicarboxylate molecules related by the crystallographic 2_1 skew axis *and* linked by a row of H-bonds, extracted from the structure of the assembly of **3**. Oxygen atoms are represented in red, nitrogen atoms in blue, and H-bonds as solid lines. B: Space-filling (CPK) representation of the triple-stranded helical structure of the assembly of **3** (side view along the *a* axis). One of the three strands of diammonium/dicarboxylate molecules linked by the same row of H-bonds is represented in blue and red colors, respectively, and shows the left-handed helical sense of the helicate.

the inner channel showing an average diameter of 4.4 Å. Up to nine independent H-bonds were found in the central core within 2.7 Å (Table 1), including four very short contacts (<1.92 Å).

The marked tendency of partners for recognition and self-assembly is further confirmed by the exclusion from the aggregate of water molecules, secluded into interstitial voids between individual columns,[12] that shows that stronger H-bonding interactions are established between partners than with water molecules. The side view of the assembly (Figure 1C) displays the helical motif of the H-bonded core; this is better appreciated from a simplified ORTEP projection, in which only the ammonium and the carboxylate groups involved are shown (Figure 1D): [12] the H-bonding network develops in the shape of a ribbon, which coils around the axis of the assembly in a right-handed helix. In addition to the helical H-bonding network, the system also possesses a helical tertiary structure, which can be visualized by selecting the contiguous diammonium−dicarboxylate molecules related by the crystallographic 2_1 skew axis *and* linked by the same row of H-bonds, and noting that cyclohexane residues envisage a strand coiling about the axis (Figure 2A).[12] Three strands run parallel in the assembly, giving rise to a triple-stranded helicate, whose pitch is 20.31 Å and whose helical sense is left-handed; this feature is better perceived from a space-filling representation of the assembly, in which one of the three strands is shown in blue (**1**) and red (**2**) colors (Figure 2B).[12] It is noteworthy not only that the present structure shows the expected triple-stranded helical architecture, but also that its helical sense is fully in agreement with predictions based on rules inferred for the diamine-diol systems;[9a] these would indeed predict that when the H-bonding network and the supramolecular structure of the assembly are both helical, they would show opposite chirality: the helical sense of the former would take priority over that of the latter, while the chirality would be determined by the absolute configuration of DAC, the (*R*,*R*) diamine giving a right-handed helix.

Conclusion

The ionic H-bonded trihelicate presented here is a clear example of a supramolecular architecture assembled by design, based on the understanding of the structure-directing features encoded in the constitution of DAC, which allowed us to anticipate that a dicarboxylic acid of C_2 symmetry and of matching configuration would be recognized as a complementary partner to form a salt capable of self-assembling into a helical architecture purely by hydrogen bonding, provided that it would possess a conformationally rigid structure of low steric demand. In crystal engineering of organic salts, anions are usually the pattern generators organizing cations into H-bonded networks;[3e,4a,b,8b] the described structure represents, to our knowledge, an unprecedented case of cation-directed assembly of organic helicates, which makes of DAC a unique, reliable, and predictable building block for the construction of organized supramolecular architectures.

Experimental Section

Materials. (1*R*,2*R*)-(−)-*trans*-1,2-diaminocyclohexane (**1**, Fluka, mp 43−45 °C, $[\alpha]^{20}_{D}$ −25.5°, c = 5 in 1 N HCl), (1*R*,2*R*)-(−)-*trans*-cyclohexane-1,2-dicarboxylic acid (**2**, Fluka, mp 177−182 °C, $[\alpha]^{20}_{D}$ −20°, c = 1 in acetone), (1*S*,2*S*)-(+)-*trans*-1,2-diaminocyclohexane (**4**, Fluka, mp 40−43 °C, $[\alpha]^{20}_{D}$ +25.5°, c = 5 in 1 N HCl), (*S*)-(−)-methylsuccinic acid (**5**, Aldrich, mp 116−119 °C, $[\alpha]^{20}_{D}$ −8.3°, c = 5.1 in H_2O), deuterium oxide (CIL, D 99.9%) were used as received without further purification.

Physical and spectroscopic data for 3: colorless crystals (D_2O); mp 199−200 °C; $[\alpha]^{25}_{D}$ = −20.3° (c = 5.6 in D_2O); ^{1}H NMR (200 MHz, 0.2 M in D_2O, 23 °C): δ = 4.67 (s; NH_3^+ + H_2O), 3.21−3.06 (m, 2H; C*H*NH_3^+), 2.15−2.10 (m, 2H; C*H*CO_2^-),

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[12] See Supporting Information.

2.00−1.94 (m, 2H), 1.76−1.57 (m, 6H), 1.43−1.08 (m, 8H); ^{13}C NMR (50 MHz, 0.2 M in D_2O, 23 °C): $\delta = 185.65$ (CO), 53.00 (CHNH$_3^+$), 50.04 (CHCO$_2^-$), 30.50, 30.21 (CH$_2$CHNH$_3^+$, CH$_2$CHCO$_2^-$), 26.18 (CH$_2$CH$_2$CHCO$_2^-$), 23.55 (CH$_2$CH$_2$CHNH$_3^+$).

Crystal Structure Analysis of 3. cell parameters and intensity data were obtained on a Siemens P4 diffractometer, using graphite monochromated Cu Kα radiation ($\lambda = 1.5418$ Å). Cell parameters were determined by least-squares fitting of 25 centered reflections. The intensities of two standard reflections were measured every 60 min to check the stability of the diffractometer and the decay of the crystal. Intensity data were corrected for Lorentz and polarization effects, and an absorption correction was applied using the analytical method based on the measure of the indexed faces of the crystal used and on direction cosines of the reflections ($T_{\max} = 0.884$, $T_{\min} = 0.585$). The structure was solved by direct methods (SIR-97, A. Altomare, G. Cascarano, C. Giacovazzo, A. Guagliardi, M. C. Burla, G. Polidori, M. Camalli. *J. Appl. Crystallogr.* **1994**, *27*, 435) and refined by the full-matrix least squares program SHELX-97 (G. M. Sheldrick, Göttingen, 1997). The hydrogen atoms bound to the carbon atoms were introduced in calculated positions and their coordinates refined in agreement with those of the linked atoms with an overall isotropic temperature factor converging to $U = 0.049(2)$ Å^2. The hydrogen atoms of the ammonium groupings as well as those of the water molecules were found in a ΔF Fourier synthesis and fully refined. All the non-hydrogen atoms were refined anisotropically. Crystallographic data (excluding structure factors) for the structure reported in this paper have been deposited with the Cambridge Crystallographic Data Centre as supplementary publication no. CCDC-147076. Copies of the data can be obtained free of charge on application to CCDC, 12 Union Road, Cambridge CB2 1EZ, UK (fax: int. code + (44) 1223−336033; e-mail: deposit@ccdc.cam.ac.uk).

Crystal data for 3: $C_{14}H_{26}O_4N_2{\cdot}3H_2O$, crystal dimension 0.8 × 0.4 × 0.1 mm, orthorhombic, space group $P2_12_12_1$, $a = 6.771(1)$, $b = 15.680(2)$, $c = 17.314(4)$ Å, $V = 1838.2(6)$ Å^3, $Z = 4$, $\rho_{\text{calcd}} = 1.230$ g cm^{-3}, $2\theta_{\max} = 128°$; $\theta{-}2\theta$ scan mode, room temperature, 2083 unique reflections having $[I > 2\sigma(I)]$, 258 parameters, $R[I > 2\sigma(I)] = 0.0369$, $wR[I > 2\sigma(I)] = 0.1049$ refined against F^2, residual electron density: max = 0.265 and min = −0.155 e/Å^3.

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Supporting Information Available: Crystal cell, ORTEP, and spacefilling stereoviews, and a stereoview of a single strand of the assembly of **3**. Tables of crystal data, atomic coordinates, H-bond lengths and angles, and anisotropic thermal parameters for **3**. This material is available free of charge via the Internet at http://pubs.acs.org.

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