Cytosine-Substituted Nitronylnitroxide Radical: A Key Component for Bio-Inspired Molecule-Based Magnetics

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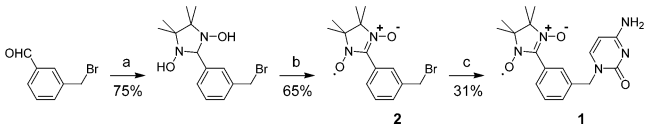
A cytosine-substituted nitronylnitroxide radical (**1**) was synthesized. The nucleobase moiety plays a primary role in molecular packing in the crystal. It has been found from X-ray structure analyses and magnetic susceptibility measurements that the intermolecular magnetic interactions in the crystal are propagated by orbital overlaps between the phenylnitronylnitroxide moieties of the adjacent molecules, whereas the relative arrangement of the molecules are governed by the hydrogen bonding of the nucleobase moiety, giving a doubled chain structure. The hydrogen-bonded aggregation of the cytosine-substituted radical molecules can be a useful element for molecular assembly of bio-inspired molecule-based magnets in terms of crystal engineering for nucleobase-substituted radicals.

Molecule-based magnetism has witnessed a rapid development in the past decades.[1] In the molecule-based magnetics, full control of molecular packing, or relative arrangement of open-shell molecules in a crystalline solid state, has been an unresolved, long-standing issue that has a crucial relationship to magnetic properties of molecular assemblages such as ferromagnetism. Biomolecule-based architecture such as a DNA duplex with nucleobase pairing is fascinating from the viewpoint of magnetic materials. Introduction of electron spins to the biomolecule-based nanostructure should bring about further developments in spin-mediated nanotechnology as well as in molecule-based magnetics. In this paper, we propose a control of the molecular packing of organic open-shell compounds by employing nucleobases as a structure-determining element in crystalline solids.

Hydrogen-donating and accepting molecules other than naturally found nucleobases, such as phenol, carboxylic acid, and pyridine derivatives, have been introduced to the stable radical family of nitroxide and imino- or nitronylnitroxide.[2] The magnetic properties of these compounds have been examined in view of hydrogen-bonded assemblage of the open-shell building blocks.[2] Tetrathiafulvalene cation radicals with nucleobase substituents[3] and paramagnetic transition metal complexes embedded in a DNA duplex[4] have been reported as well. To our knowledge, however, there have been only two examples of stable, neutral organic radicals with well-characterized crystal structure, to which a naturally found nucleobase moiety has been introduced;[5] one is 5-uradinyl and the other is 6-uradinyl substituted imino- or nitronylnitroxide. For the 5-uradinyl nitronylnitroxide, magneto-structural correlation has not been fully clarified.[5a] The 6-uradinyl iminonitroxide has been found to exhibit intermolecular antiferromagnetic interaction to give a molecular dimer in a singlet ($S = 0$) ground state.[5b] An extended doubled chain structure is reported in this paper for a new nitronylnitroxide radical **1** (Scheme 1), which has a cytosine group serving as the structure-determining element. The synthesis, X-ray crystallography, and magnetic susceptibility of **1** are described.

SCHEME 1: Synthesis of Cytosine-Substituted Radical 1[a]



[a] Steps: (a) 2,3-Bis(hydroxylamino)-2,3-dimethylbutane (1 equiv) in methanol; (b) PbO_2 (7 equiv) in dichloromethane; (c) cytosine (1 equiv), K_2CO_3 (1 equiv), and KI (1 equiv) in acetonitrile.

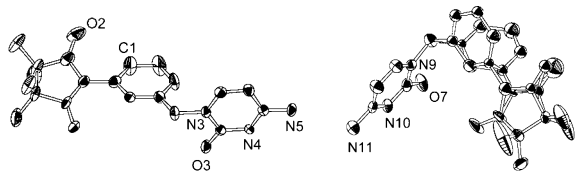


Figure 1. ORTEP drawings of **1** with the thermal ellipsoids of 50% probability. The hydrogen atoms are omitted for clarity.

The cytosine-substituted radical **1** was synthesized by a direct coupling of cytosine with the 3-(bromomethyl)phenyl derivative of nitronylnitroxide **2** (Scheme 1). The precursor **2** was prepared by following the reported method.[6] Single crystals of **1** were obtained by recrystallization from methanol. The crystalline solid of **1** was stable under aerated conditions at room temperature.

In Figure 1 is depicted the molecular structure of **1**.[7] The unit cell contains two crystallographically independent molecules, A and B. Molecule B has a positional disorder of atoms in the phenylnitronylnitroxide moiety.[8] The phenyl and the cytosine rings have large dihedral angles in both A and B (93.7° in A, 86.2° and 88.2° in B) around the methylene bridges. It is expected that the delocalization of unpaired electron spin in **1**

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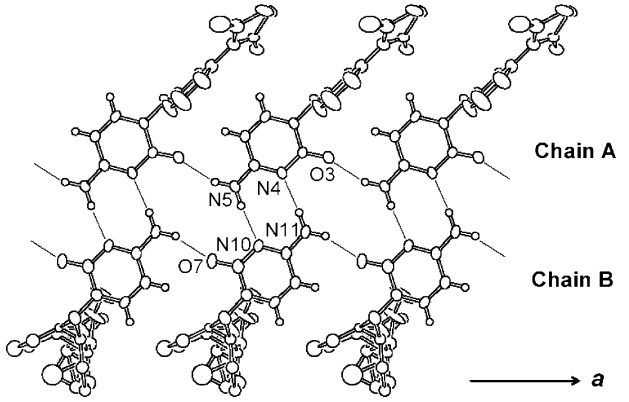

Figure 2. Doubled chain of **1** in the crystal. The thin solid lines represent the intermolecular hydrogen bonds between the cytosine moieties. The hydrogen bond lengths are 2.953(9) Å (N5H−O3), 2.963(9) Å (N11H−O7), 2.988(9) Å (N5H−N10), and 2.968(9) Å (N11H−N4). The methyl groups are omitted for clarity.

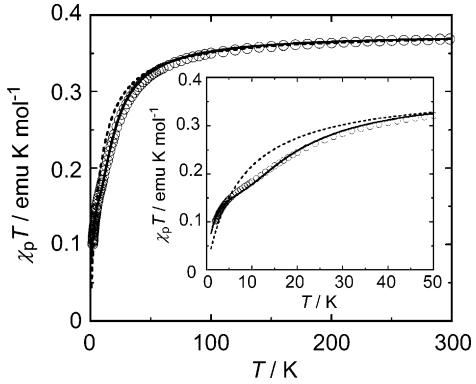

Figure 3. Paramagnetic susceptibility χ_p of **1** measured on a SQUID magnetometer with $B = 0.1$ T in the χ_pT vs T plot. In the inset are shown the χ_pT values at low temperatures. The solid line denote the calculated values from eq 1 ($J_A/k_B = -19.0$ K, $\theta_{AB} = -1.5$ K), and the dashed line represents the simple Curie−Weiss law with $\Theta = -7.5$ K.

is truncated at the methylene bridge. It was found from DFT calculations that the cytosine moiety has little spin density,[9] supporting the truncation of π-conjugation. Thus, the cytosine group in **1** plays a role primarily in determining the molecular packing instead of propagating intermolecular magnetic interactions.

As shown in Figure 2, the molecular packing of **1** features in intermolecular hydrogen bonds between the nucleobase substituents. The lengths of the intermolecular hydrogen bonding are very close to those of pristine cytosine.[10] The relative arrangement of the molecules is governed by the hydrogen bonding of the cytosine moiety. Molecules A and B are assembled to form chains A and B, respectively. The two parallel chains are related by inversion symmetry in the motif of ···-A−B−B-A−A-B-··· in the crystal.[11]

Intermolecular short distances close to the van der Waals contact[12] were found between inversion-related molecules A in the adjacent chains; 3.28 Å between O2 and O2′, and 2.74 Å between O2 and H1′ attached to C1′.[11] No other intermolecular short contacts were found around the N−O groups within or between the chains.

Temperature dependence of paramagnetic susceptibility χ_p is shown in Figure 3 in the χ_pT vs T plots. The χ_pT value at 300 K is 0.37 emu K mol^{-1}, as expected for 1 mol of $S = {}^1/_2$ spin. The χ_pT value decreases as the temperature is lowered, indicating that antiferromagnetic interactions dominate between the molecules in the crystalline solid state. The intermolecular short contacts around O2 should be responsible for the antiferromagnetic interaction. The decrease in χ_pT gets less steep around 10 K, and the χ_pT value goes down again below 5 K. The stationary behavior of χ_pT indicates the occurrence of additional weak antiferromagnetic interactions. The temperature dependence of χ_pT was analyzed with

$$\chi_p = \frac{N_A g^2 \mu_B{}^2}{3k_B(T - \theta_{AB})} \frac{1}{2}\left[\frac{3}{3 + \exp(-2J_A/k_BT)} + \frac{3}{4}\right] \quad (1)$$

where the first term in the bracket represents the ground-state singlet dimer of molecule A with the antiferromagnetic interaction J_A attributed to the short contacts around O2. The second term corresponds to molecule B. Weak intermolecular interactions other than J_A are approximated by the mean field θ_{AB} in eq 1. The observed χ_pT was reproduced by eq 1 with the parameters $J_A/k_B = -19.0 \pm 0.3$ K, $\theta_{AB} = -1.5 \pm 0.1$ K. The g-factor g is fixed as $g = 2.006$, which was observed in an ESR spectrum of a dichloromethane solution. A simple Curie−Weiss model with the single parameter $\Theta = -7.5$ K fails to reproduce the low-temperature χ_pT values as shown in Figure 3. The stationary behavior of χ_pT around 10 K corresponding to half moles of $S = {}^1/_2$ spin is ascribed to the formation of the ground-state singlet dimer of molecule A.

Cytosine has been found to be an efficient building block for organization of open-shell molecules in a crystalline solid state, exemplifying that the hydrogen-bonded aggregation of the cytosine-substituted radical molecules can be a useful element for molecular assembly of bio-inspired molecule-based magnets in terms of crystal engineering for nucleobase-substituted radicals. Syntheses of guanine-substituted nitronylnitroxide radicals and their molecular complexes with **1** are in progress. Heteromolecular complexation based on complementary nucleobase pairing will lead to molecule-based heterospin magnetics such as organic molecule-based ferrimagnetics.[13]

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Supporting Information Available: Crystallographic data (CIF file), ORTEP drawings, and table of atomic spin densities calculated by the DFT methods. This material is available free of charge via the Internet at http://pubs.acs.org.

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(7) The crystal structure was solved by direct methods using a program package *CrystalStructure* (ver.3.60) by Rigaku/Molecular Structure Corporation. Crystallographic data: $C_{36}H_{44}N_{10}O_6$, $M = 712.81$, $0.05 \times 0.1 \times 0.4$ mm^3, Mo Kα, 193 K, triclinic, space group $P\bar{1}$, $a = 6.9780(1)$ Å, $b = 14.529(1)$ Å, $c = 20.034(1)$ Å, $\alpha = 78.023(8)°$, $\beta = 75.20(2)°$, $\gamma = 78.00(2)°$, $V = 1895.0(2)$ Å^3, $Z = 2$, $D_{calc} = 1.249$ g cm^{-3}. $R = 0.127$, $R_w = 0.214$ (GOF = 1.00) for 4180 reflections ($I > 2\sigma(I)$) and 515 parameters. The R value being larger than 0.1 results from the disorder as described in the text.

(8) A lowered symmetry with the doubled number of independent molecules, i.e., space group $P1$ or a doubled cell parameter along the a axis, has not improved the refinement, retaining the disorder. On the final difference Fourier map, density peaks were found around the disordered rings of molecule B with the maximum and minimum of +0.93 and −0.48 e/Å^3, respectively. The refinement including the residual peaks was unsuccessful, resulting in divergence of the least-squares calculation.

(9) The spin density distribution of molecule A was calculated with the unrestricted density functional theory at the UB3LYP/6-31+G(d,p) level using a program package Gaussian98 (Revision A.9, Gaussian, Inc., Pittsburgh, PA, 1998). The molecular geometry was taken from the X-ray crystal structure.

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