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Key indicators

Single-crystal X-ray study T = 295 K Mean σ (C–C) = 0.002 Å R factor = 0.027 wR factor = 0.075 Data-to-parameter ratio = 15.3

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

Poly[[bis(1*H*-benzimidazole- κN^3)manganese(II)]- μ -aqua- μ -succinato- $\kappa^2 O:O'$]

In the title polymeric compound, $[Mn(C_4H_4O_4)(C_7H_6N_2)_2(H_2O)]_n$, the Mn^{II} atom is located on an inversion center and is coordinated by succinate dianions and benzimidazole and water molecules with an elongated octahedral coordination geometry. The long Mn-O(water) bond distance of 2.4982 (3) Å shows the rather weak nature of this bond. The succinate dianion and water molecule are located on an inversion center and a twofold axis, respectively; they bridge the Mn^{II} atoms to form a polymeric structure.

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Comment

As coordination of water to Mn is an important step in the photosynthesis process (Vincent & Christou, 1989), we have been interested in the coordination properties of manganese for several years (Nie *et al.*, 2001). The large Mn-O(water)-Mn bond angle and long Mn-O(water) bond distance observed in the title compound, (I), show the rather weak nature of the bond from water to the Mn^{II} atom.



A segment of the polymeric structure of (I) is illustrated in Fig. 1. The repeat unit of the polymeric complex consists of one Mn^{II} atom, one succinate dianion, two benzimidazole ligands and one coordinated water molecule. The Mn^{II} atom lies at an inversion center and is coordinated by succinate dianions, benzimidazole and water molecules with an elongated octahedral geometry (Table 1), similar to the situation in the Cd^{II} analog (Liu & Xu, 2004).

The water molecule (O3) is located on a twofold axis and links neighboring Mn^{II} atoms to form the 'water-bridged' polymeric chain (Fig. 2). The Mn-O3 bond distance is longer than the Mn-O1 bond distance in the equatorial plane by 0.377 (9) Å. The Mn-O3-Mn^{iv} bond angle of 152.31 (6)° [symmetry code: (iv) 1 - x, y, $-z + \frac{1}{2}$] is much larger than the value of 109° expected for a normal sp^3 -hybridized O atom, corresponding to the longer Mn-O3 bond. These observa-

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A segment of the polymeric structure of (I) with 40% probability displacement ellipsoids (arbitrary spheres for the H atoms) [symmetry codes: (ii) $-x + \frac{1}{2}$, $-y + \frac{1}{2}$, 1 - z; (iii) 1 - x, -y, 1 - z; (iv) 1 - x, y, $-z + \frac{1}{2}$].



Figure 2 The crystal packing. H atoms have been omitted.

tions indicate the weaker coordination interaction between the Mn^{II} atom and water molecule.

The succinate dianion is located on another inversion center and thus displays a planar carbon skeleton. The succinate dianions bridge neighboring Mn^{II} atoms through terminal carboxyl groups to form a 'succinate-bridged' polymeric chain; the chains are nearly perpendicular to the 'water-bridged' polymeric chains shown in Fig. 2.

 $O{-}H{\cdots}O$ hydrogen bonding between carboxylate ligands and coordinated water molecules and $N{-}H{\cdots}O$ hydrogen

bonding between carboxylate and benzimidazole (Table 2) stabilize the polymeric structure.

 π - π stacking interactions are usually found in the structures of metal complexes with benzimidazole (Li *et al.*, 2005); however, no such π - π stacking between benzimidazole rings is observed in (I).

Experimental

 $MnCl_2 \cdot 4H_2O$ (0.20 g, 1 mmol) was added to an aqueous solution (20 ml) containing succinic acid (0.12 g, 1 mmol) and NaOH (0.08 g, 2 mmol). After the solution was refluxed for 2 h, an aqueous solution (10 ml) of benzimidazole (0.12 g, 1 mmol) was added to the above solution. The solution was refluxed for a further 3 h and filtered. After cooling to room temperature, the solution was filtered once more. Single crystals of (I) were obtained from the filtrate after two weeks.

 $D_x = 1.611 \text{ Mg m}^{-3}$

Mo $K\alpha$ radiation Cell parameters from 5996

reflections

 $\mu=0.79~\mathrm{mm}^{-1}$

T = 295 (2) K

Chunk, colorless

 $0.41 \times 0.35 \times 0.20 \text{ mm}$

 $\Delta \rho_{\rm min} = -0.30 \text{ e } \text{\AA}^{-3}$

 $\theta = 2.1 - 27.2^{\circ}$

Crystal data

 $\begin{bmatrix} Mn(C_4H_4O_4)(C_7H_6N_2)_2(H_2O) \end{bmatrix} \\ M_r = 425.30 \\ Monoclinic, C2/c \\ a = 13.0071 (5) Å \\ b = 13.9756 (6) Å \\ c = 9.7024 (4) Å \\ \beta = 96.042 (2)^{\circ} \\ V = 1753.92 (12) Å^3 \\ Z = 4 \end{bmatrix}$

Data collection

Rigaku R-AXIS RAPID 1994 independent reflections 1859 reflections with $I > 2\sigma(I)$ diffractometer $R_{\rm int} = 0.017$ ω scans $\theta_{\text{max}}^{\text{int}} = 27.4^{\circ}$ $h = -16 \rightarrow 16$ Absorption correction: multi-scan (ABSCOR; Higashi, 1995) $T_{\min} = 0.745, T_{\max} = 0.850$ $k = -18 \rightarrow 18$ 7988 measured reflections $l = -11 \rightarrow 12$ Refinement $w = 1/[\sigma^2(F_o^2) + (0.0431P)^2]$ Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.027$ + 1.0253P] where $P = (F_0^2 + 2F_c^2)/3$ $wR(F^2) = 0.075$ $(\Delta/\sigma)_{\rm max} < 0.001$ S = 1.11 $\Delta \rho_{\rm max} = 0.25 \ {\rm e} \ {\rm \AA}^{-3}$ 1994 reflections

Table 1

130 parameters

Selected geometric parameters (Å, °).

H-atom parameters constrained

Mn-O1 Mn-N1	2.1217 (9) 2.2295 (11)	Mn-O3	2.4982 (3)
O1-Mn-N1 O1-Mn-O3	87.60 (4) 90.82 (4)	N1-Mn-O3	89.28 (3)

Table 2

Hydrogen-bonding geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$N2 - H2 \cdot \cdot \cdot O2^i$	0.86	1.96	2.7992 (16)	163
$O3-H3A\cdots O2$	0.90	1.82	2.6845 (14)	160
6	. 1 1.			

Symmetry code: (i) $\frac{1}{2} + x$, $\frac{1}{2} - y$, $\frac{1}{2} + z$.

The water H atoms were located in a difference Fourier map and isotropically refined by riding in their as-found positions relative to

the atom O3. Other H atoms were placed in calculated positions with C-H = 0.93 (aromatic) or 0.97 Å (methylene) and N-H = 0.86 Å, and included in the final cycles of refinement in the riding model, with $U_{\rm iso}({\rm H}) = 1.2U_{\rm eq}$ of the carrier atom.

Data collection: *PROCESS-AUTO* (Rigaku, 1998); cell refinement: *PROCESS-AUTO*; data reduction: *CrystalStructure* (Rigaku/ MSC, 2002); program(s) used to solve structure: *SIR92* (Altomare *et al.*, 1993); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *ORTEP-3 for Windows* (Farrugia, 1997) and *XP* (Siemens, 1994); software used to prepare material for publication: *WinGX* (Farrugia, 1999).

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