Supplementary data for this paper are available from the IUCr electronic archives (Reference: MU1344). Services for accessing these data are described at the back of the journal.

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Potassium Tartronate and Ammonium Tartronate

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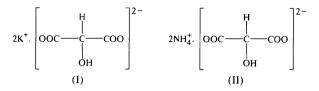
Abstract

Potassium tartronate (dipotassium hydroxypropanedioate, $2K^+.C_3H_2O_5^{--}$), (I), crystallizes in the monoclinic space group $P2_1/n$, with Z = 4, and ammonium tartronate (diammonium hydroxypropanedioate, $2NH_4^+.-C_3H_2O_5^{--}$), (II), crystallizes in orthorhombic space group $Pna2_1$, with Z = 4. There are two symmetryindependent cations in both (I) and (II). The coordination number of the K⁺ ion in (I) is seven, and the number of hydrogen bonds around the NH $_4^+$ ion in (II) is four. This difference arises from the fact that the hydrogen bonding governs the number of O atoms around NH $_4^+$ in (II), in contrast to the electrostatic interactions in (I).

Comment

Potassium hydrogen tartronate, (III) (Kroon & Kanters, 1982; Kanters & Kroon, 1976; Roelofsen *et al.*, 1978), and ammonium hydrogen tartronate, (IV) (Taka *et al.*, 1998), crystallize in the same space group, $P2_1/c$, and the crystal structures of (III) and (IV) are similar to each other. The differences in these structures are

interpreted in terms of the nature of the interactions around the cations (Taka *et al.*, 1998), *i.e.* electrostatic for K⁺ and hydrogen bonding for NH[‡]. The K⁺ ion in (III) is coordinated by eight O atoms, while the NH[‡] ion in (IV) forms six N—H···O hydrogen bonds, including two bifurcated hydrogen bonds. The present study was undertaken in order to obtain information on the interactions between the cation and the O atoms of the anion for the title salts of tartronic acid, *i.e.* potassium tartronate, (I), and ammonium tartronate, (II).



The asymmetric unit is composed of two cations and one tartronate anion in the crystals of both (I) and (II) (Fig. 1). The hydroxy group in (I) forms an intramolecular hydrogen bond [O1—H1O 0.70 (3), H1O···O4 2.07 (3), O1···O4 2.586 (3) Å and O1—H1O···O4 131 (4)°], while that in (II) forms an intermolecular hydrogen bond [O1—H1O 0.80 (3), H1O···O5^{iv} 2.17 (3), O1···O5^{iv} 2.921 (2) Å and O1—H1O···O5^{iv}

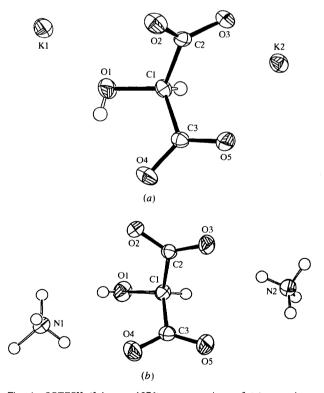
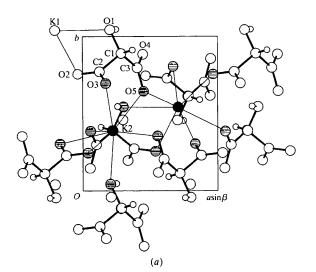


Fig. 1. ORTEPII (Johnson, 1976) representations of (a) potassium tartronate, (I), and (b) ammonium tartronate, (II), with the atomic numbering of the asymmetric units. Displacement ellipsoids are shown at the 50% probability level for non-H atoms and H atoms are drawn as spheres with $B_{\rm iso} = 1.0$ Å².

156 (3)°; symmetry code: (iv) -x, 2-y, $z-\frac{1}{2}$, as in Table 2]. Significant differences in the molecular geometries of the tartronate anions in (I) and (II) are observed only with respect to the conformations; O1—C1—C2—O2 and O1—C1—C3—O4 are 41.9 (3) and 15.2 (3)° in (I), while these torsion angles are 17.3 (2) and -26.1 (2)°, respectively, in (II).

As shown in Fig. 2, each K^+ ion in (I) is coordinated by seven O atoms, while each NH_4^+ ion in (II) participates in four $N-H\cdots O$ hydrogen bonds. Geometric parameters of the coordination in (I) and the hydrogen bonding in (II) are listed in Tables 1 and 2, respectively. The number of O atoms around each NH_4^+ ion in (II) is restricted by the hydrogen bonding, as found in (IV). The number in (II) is smaller than that around each K^+ ion in (I) because of the restriction due to the hydrogen bonding.



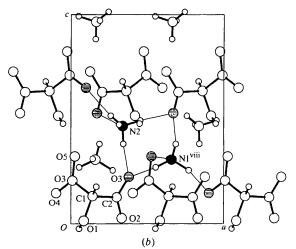


Fig. 2. (a) The coordination around the K^{*} ions in (I) viewed down the c axis. (b) The hydrogen bonds with the NH \ddagger ions in (II) viewed down the b axis. [Symmetry code: (viii) $\frac{1}{2} - x, \frac{1}{2} + y, \frac{1}{2} + z.$]

Experimental

Crystals of (I) were grown by slow evaporation from an aqueous solution containing equimolar amounts of tartronic acid (SIGMA T-0657) and potassium carbonate. Crystals of (II) were grown by slow evaporation from an aqueous solution containing tartronic acid and ammonia in a molar ratio of 0.5:1.

Compound (I)

Crystal data

$2K^+.C_3H_2O_5^{2-}$	Mo $K\alpha$ radiation
$M_r = 196.24$	$\lambda = 0.71073 \text{ Å}$
Monoclinic	Cell parameters from 20
$P2_1/n$	reflections
a = 6.933 (4) Å	$\theta = 9.5 - 11.0^{\circ}$
b = 7.826(4) Å	$\mu = 1.459 \text{ mm}^{-1}$
c = 11.969(7) Å	T = 295 K
$\beta = 104.05(5)^{\circ}$	Prismatic
V = 630.0 (6) Å ³	$0.45 \times 0.40 \times 0.35$ mm
Z = 4	Colourless
$D_x = 2.069 \text{ Mg m}^{-3}$	
D_m not measured	

Data collection

Rigaku AFC-5*R* diffractometer $\omega/2\theta$ scans Absorption correction: none 1563 measured reflections 1447 independent reflections 1307 reflections with $l > 2\sigma(l)$

Refinement

Refinement on F R = 0.031 wR = 0.034 S = 1.961307 reflections 99 parameters All H atoms refined $w = 1/\sigma^2(F)$

$R_{\rm int} = 0.024$
$\theta_{\rm max} = 27.5^{\circ}$
$h = 0 \rightarrow 8$
$k = 0 \rightarrow 10$
$l = -15 \rightarrow 15$
3 standard reflections
every 97 reflections
intensity decay: none

$(\Delta/\sigma)_{\rm max} = 0.01$
$(\Delta/\sigma)_{\rm max} = 0.01$ $\Delta\rho_{\rm max} = 0.52 \text{ e } \text{\AA}^{-3}$
$\Delta \rho_{\rm min} = -0.24 \ {\rm e} \ {\rm \AA}^{-3}$
Extinction correction: none
Scattering factors from Inter-
national Tables for X-ray
Crystallography (Vol. IV)

Table 1. Selected geometric parameters (Å) for (I)

K1···O1	2.853 (3)	K2· · · O1`'	2.786 (2)
K1···O2	2.822 (2)	K2· · ·O2 ^{∨n}	2.875 (2)
K1···O2 ¹	2.749 (2)	K2· · · O3	2.856 (2)
K1···O3 ^μ	2.959 (2)	K2···O3 ^{vn}	2.782 (2)
K1···O3 ¹⁰	2.989 (2)	K2···O4 ^{vin}	2.675 (3)
K1···O4 ^ι	2.816(2)	K2· · · O5	2.739 (2)
K1···O5`	2.860(2)	К2∙ ∙ ∙ О5'*	2.695 (3)

Symmetry codes: (i) $-\frac{1}{2} - x$, $\frac{1}{2} + y$, $\frac{1}{2} - z$; (ii) $x - \frac{1}{2}$, $\frac{3}{2} - y$, $z - \frac{1}{2}$; (iii) -x, 2 - y, 1 - z; (iv) x - 1, y, z; (v) $\frac{1}{2} - x$, $\frac{1}{2} + y$, $\frac{1}{2} - z$; (vi) x, y - 1, z; (vii) -x, 1 - y, 1 - z; (viii) $\frac{1}{2} - x$, $y - \frac{1}{2}$, $\frac{1}{2} - z$; (ix) 1 - x, 1 - y, 1 - z.

Compound (II)

Crystal data	
$\begin{array}{ll} & 2\mathrm{NH}_{4}^{\prime \mathrm{n}} \mathrm{C}_{3}\mathrm{H}_{2}\mathrm{O}_{5}^{2-} & \mathrm{Mo} K\alpha \\ & M_{r} = 154.12 & \lambda = 0.7 \end{array}$	radiation

Cell parameters from 25

 $0.40\,\times\,0.37\,\times\,0.14$ mm

reflections

 $\theta = 10.5 - 12.5^{\circ}$

T = 295 K

Colourless

 $R_{\rm int} = 0.038$

 $\theta_{\rm max} = 34^{\circ}$ $h = 0 \rightarrow 12$

 $k = 0 \rightarrow 12$ $l = -1 \rightarrow 16$

3 standard reflections

every 97 reflections

intensity decay: none

Prismatic

 $\mu = 0.146 \text{ mm}^{-1}$

Data collection

Rigaku AFC-5*R* diffractometer $\omega/2\theta$ scans Absorption correction: none 1808 measured reflections 1418 independent reflections 1186 reflections with $l > 2\sigma(l)$

Refinement

 $\Delta \rho_{\rm max} = 0.18 \ {\rm e} \ {\rm \AA}^{-3}$ Refinement on F $\Delta \rho_{\rm min} = -0.22 \ {\rm e} \ {\rm \AA}^{-3}$ R = 0.039wR = 0.038Extinction correction: S = 1.26 $I_{\rm corr} = I_o(1 + gI_c)$ 1186 reflections Extinction coefficient: 131 parameters $g = 1.42 \times 10^{-5}$ All H atoms refined Scattering factors from Inter $w = 1/\sigma^2(F)$ national Tables for X-ray $(\Delta/\sigma)_{\rm max} = 0.07$ Crystallography (Vol. IV)

Table 2. Hydrogen-bonding geometry (Å, °) for (II)

D—H···A	D—H	$\mathbf{H} \cdot \cdot \cdot \mathbf{A}$	$D \cdot \cdot \cdot A$	D — $\mathbf{H} \cdots \mathbf{A}$			
NI—H1NI···O2'	0.87 (3)	2.02 (3)	2.847 (2)	158 (3)			
N1—H2N1···O3"	0.97 (3)	1.86 (3)	2.786(2)	160 (2)			
N1—H3N1···O4 ^m	1.14 (4)	1.72 (4)	2.796 (3)	154 (3)			
N1—H4N1···O5"	0.80(4)	2.30(4)	3.082 (3)	167 (3)			
N2—H1N2· · · O2`	0.91 (3)	1.93 (3)	2.843 (2)	173 (3)			
N2H2N2···O3	0.86 (3)	1.94 (3)	2.795 (3)	172 (2)			
N2—H3N2···O4`'	0.93 (3)	1.99 (3)	2.869 (3)	158 (2)			
N2—H4N2···O2`"	0.98 (3)	1.97 (3)	2.888 (2)	155 (2)			
Symmetry codes: (i) $x - \frac{1}{2}, \frac{3}{2} - y, z$; (ii) $\frac{1}{2} - x, y - \frac{1}{2}, z - \frac{1}{2}$; (iii)							
$-\frac{1}{2} - x, y - \frac{1}{2}, z - \frac{1}{2}$; (iv) $-x, 2 - y, z - \frac{1}{2}$; (v) $1 - x, 2 - y, \frac{1}{2} + z$; (vi)							
$-x, 2 - y, \frac{1}{2} + z;$ (vii) $\frac{1}{2} - x, y - \frac{1}{2}, \frac{1}{2} + z.$							

Data collection and cell refinement were carried out with *RASAII* (Rigaku Corporation, 1990). The structures of (I) and (II) were solved by direct methods using *MITHRIL* (Gilmore, 1984) and refined by full-matrix least squares using *TEXSAN* (Molecular Structure Corporation, 1985). H atoms were located from difference Fourier maps and refined isotropically. The displacement ellipsoid plots were made with the aid of *ORTEPII* (Johnson, 1976). The calculations were performed on a VAX 3100 computer using *TEXSAN* at the X-ray Laboratory of Okayama University.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: AV1017). Services for accessing these data are described at the back of the journal.

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Acta Cryst. (1998). C54, 1259-1261

μ -Acetato- μ -aqua- μ -hydroxo-bis[(1,4dimethyl-1,4,7-triazacyclononane- $\kappa^3 N$)copper(II)] Diperchlorate

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Abstract

The structural characterization of the title complex, $[Cu_2(OH)(C_2H_3O_2)(C_8H_{19}N_3)_2(H_2O)](ClO_4)_2$, provides only the third example of a binuclear copper complex containing a bridging water molecule. The three bridging groups (aqua, acetato and hydroxo) are all different, a rare feature for spontaneous self-assembly reactions. The resulting geometry about the two Cu atoms is distorted octahedral, with the Cu—O(H) distance of 1.963 (2) Å distinguished from the Cu—O(H₂) distance of 2.737 (5) Å. The cation has crystallographically imposed mirror symmetry.

Comment

A triangular trinuclear arrangement of Cu atoms is necessary for the four-electron reduction of dioxygen to water for the blue copper oxidases (BCOs). This biologically unique arrangement has been structurally characterized for one member of the BCOs, ascorbate oxidase (Messerschmidt *et al.*, 1992). However, structural evidence in the form of intermediates supporting the proposed mechanism during enzymic activity remains elusive. The title complex, (I), addresses this deficit, providing a structural model complex for the Type 3 binuclear site [the Cu atoms are classified according to their spectroscopic properties as Type 1,