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Salts of 2-amino-5-iodopyridinium

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Reaction of 2-amino-5-iodopyridine (5IAP) with concentrated HBr at room temperature yielded 2-amino-5-iodopyridinium bromide, $C_5H_6N_2$ ⁺·Br⁻ or (5IAPH)Br. The complex formed pale-yellow crystals, which exhibit significant hydrogen bonding between the amino and pyridinium N—H donors and bromide ion acceptors. Halogen bonding is also observed. Similarly, reaction of 5IAP with cobalt(II) chloride in mixed HCl/HBr in 1-propanol yielded 2-amino-5-iodopyridinium (2-amino-5-iodopyridine-*�N*¹)bromido/chlorido(0.51/2.48) cobalt(II), $(C_5H_6IN_2)[COBr_{0.51}Cl_{2.48}(C_5H_5IN_2)]$ or $(5-IAPH)[(5IAP)Co Cl_{2,48}Br_{0.51}$, as blue block-shaped crystals. Two of the three halide positions exhibit mixed occupancy $\text{[C} \cdot \text{Br} = 0.797 \cdot (5) : 0.203 \cdot (5)$ and 0.689 (6):0.311 (6)], while the third position is occupied solely by a chloride ion. Extensive hydrogen and halogen bonding is observed.

1. Chemical context

The effects of randomness have been of particular interest in physics and chemistry. In particular, they have been considered regarding quantum information (Khrennikov, 2016), band theory (Coey *et al.*, 2005) and perturbation of the crystal lattice (Mackenzie, 1964; Anderson, 1958). With respect to magnetism, studies have looked at the relationship between randomness and spin glasses (Toulouse, 1986), amorphous magnets (Coey, 1978) and valence-bond solids (Kimchi *et al.*, 2018).

Superexchange in magnetic systems can be studied through the production of families of closely related compounds where small changes in the structure can be correlated with their effects on the magnetic properties of the materials. We have looked at the production of such complexes, especially those based upon salts of subsituted 2-aminopyridine for some time (Araujo-Martinez *et al.*, 2023; Coffey *et al.*, 2000; Landee *et al.*, 2001; Woodward *et al.*, 2002). One such compound, 2-amino-5 iodopyridine, has been involved in the production of a magnetic ladder (Landee *et al.*, 2001) and a family of Cu^{II} halides complexes (Huynh *et al.*, 2023).

One difficulty in the studies of randomness in such materials is the introduction of randomness into an otherwise ordered system. Crystallization is intrinsically a self-purifying process and attempts to introduce randomness through introduction of dopants into a system may be frustrated by exclusion of the 'impurity' during crystallization (Fujiwara *et al.* 1995). We have recently discovered a system, based upon 2-amino-5 iodopyridine (5IAP), where randomness can be introduced to the system *via* introduction of a mixture of halide ions; $(5IAPH)₂[CoCl_{4-x}Br_x]⁺H₂O$ (Mukda *et al.*, 2024) where 5IAPH is 2-amino-5-iodopyridinium. In the course of those investigations, we isolated the related compound

 $(5IAPH)[(5IAP)CoCl_{3-x}Br_x]$ and here report its structure and the structure of the related salt (5IAPH)Br.

2. Structural commentary

(5IAPH)Br (1) crystallized in the triclinic space group $\overline{P1}$ and comprises one 5IAPH cation and one bromide anion in the asymmetric unit (Fig. 1). The 5IAPH ring is planar (mean deviation of constituent atoms = 0.012 Å) with the amino substituent lying $0.070(1)$ Å out of that plane. The iodine atom is displaced significantly further out of the plane, $0.199(1)$ Å, toward the same face. The amino substituent deviates only slightly from sp^2 -hybridization [sum of \angle s = 360 (2) \degree]. The plane of the NH₂ group is nearly co-planar with the 5IAPH ring $[6.8 (15)°]$ as expected due to conjugation.

 $(5IAPH)[(5IAP)CoCl_{3-x}Br_x]$ (2) crystallized in the monoclinic space group $P2_1/n$. The asymmetric unit is shown in

Figure 1

The asymmetric unit of **1** shown as 50% probability ellipsoids (hydrogen atoms are shown as spheres of arbitrary size). Only those hydrogen atoms whose positions were refined are labeled.

Figure 2

The asymmetric unit of **2** shown as 50% probability ellipsoids (hydrogen atoms are shown as spheres of arbitrary size). Only those hydrogen atoms whose positions were refined are labeled.

Table 2

Hydrogen-bond geometry (\mathring{A}, \circ) for **1**.

Symmetry codes: (i) $-x, -y + 1, -z$; (ii) $x, y + 1, z$.

Fig. 2 and comprises one 5IAPH cation and one [(5IAP) $CoCl_{3-r}Br_r$] anion. The 5IAPH cation is nearly identical to that observed in **1**, with a high degree of planarity in the ring $(\pm 0.007 \text{ Å})$, the sum of the angles about the amino nitrogen atom being $359(2)^\circ$ and the amino group being nearly coplanar with the 5IAPH ring [deviation = 8.9 (16)^o]. As with **1**, the amino nitrogen atom $[0.013(5)$ Å and iodine atom [0.086 (1) \AA] are displaced slightly from the plane of the ring, again both toward the same face. The anionic unit comprises one Co^H ion with a 5IAP ring coordinated through the pyridine nitrogen atom and three coordinated halide ions. The halide ions are mixed Cl/Br with refined occupancies of Cl1/ Br1 [0.797 (5)/0.203 (5)] and Cl3/Br3 [0.689 (6)/0.311 (6)]. Attempts to refine the position of Cl2 as mixed Cl/Br resulted in an occupancy of Cl2 of 1.0 within error; no bromide ion was included in that position in the final refinement. The Co—*X* bond lengths are all similar (\sim 2.3 Å) regardless of halide ion (Table 1). The Co^H ion is only slightly distorted from tetrahedral with bond angles ranging from 105.1 (3) to 116.9 (3) $^{\circ}$. The 5IAP ring is comparable to the 5IAPH ring in terms of planarity (mean deviation = 0.006 Å) and displacement of N12 and I15 $[0.09 (1)$ Å and $0.077 (1)$ Å, respectively]. The amino group is again planar, but inclined 17 $(2)^\circ$ relative to the 5IAP plane, likely to accommodate the intramolecular $N12-H12A\cdots$ Cl2 hydrogen bond $[D\cdots A = 3.282(6) \text{ Å};$ Table 3].

3. Supramolecular features

Compound **1**. Extensive hydrogen (Table 2) and halogen bonding with the bromide ion as acceptor are present in the

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Figure 3

Halogen and hydrogen bonding in **1** (atoms are shown as spheres of arbitrary size). Dashed lines represent hydrogen and halogen bonds. Only those atoms involved in halogen or hydrogen bonding are labeled. Symmetry codes: Br1A = $-x$, 1 – y , $-z$; Br1B = x , $y + 1 z$; N12B = $-x$, $2 - y$, $-z$; I15C = 1 - *x*, *y*, *z* - 1.

structure (Fig. 3). The hydrogen bonds are typical with $D \cdot \cdot \cdot A$ distances ranging from $3.2136(12)$ to $3.4924(13)$ Å and D —H \cdots *A* angles of 150.8 (18) to 165.5 (18)^o. Each bromide ion serves as an acceptor of three hydrogen bonds from the pyridinium N—H and both protons on the amino group. The latter generates inversion-related pairs of 5IAPH ions bridged by the bromide ions (Fig. 3). A Type II halogen bond is also present with parameters $d_{\text{II}5C\cdots \text{Br}1}$ = 3.88 (1) A and

Figure 4

The structure of **1** viewed parallel to the *b* axis (atoms are shown as spheres of arbitrary size). Dashed lines represent hydrogen and halogen bonds.

Figure 5

Halogen and hydrogen bonding in **2** (atoms are shown as spheres of arbitrary size). Dashed lines represent hydrogen and halogen bonds. Only those atoms involved in halogen or hydrogen bonding are labeled. Symmetry codes: N12A = $\frac{1}{2} - x$, $y + \frac{1}{2}$, $-z - 0.5$; N21E/N22E = 1 - x, $2 - y$, $-1 - z$; N22C = $x - \frac{1}{2}$, $\frac{3}{2} - y$, $z + 0.5$; I15B = $-x$, $2 - y$, $-z$.

 \angle C15–I15*C* \cdot ··Br1 = 154.6 (4)°. Further halogen bonding is observed in the packing structure (Fig. 4). Sheets of 5IAPH and bromide ions are linked parallel to the *a* axis by Type I halogen bonds between inversion-related iodine atoms; $d_{115\cdots115A}$ = 3.81 (1) Å and $\angle_{C15-115\cdots115A}$ = 130.6 (3)^o [symmetry code: (A) $1 - x$, $1 - y$, $1 - z$].

Compound **2**. As with **1**, **2** exhibits multiple hydrogen (Table 3) and halogen bonds (Fig. 5). The hydrogen bonds are typical with $d_{D\cdots A} = 3.282$ (6)–3.341 (10) Å and $\angle_{D-H\cdots A} =$ 151 (5)–176 (5) $^{\circ}$. Type II halogen bonds are also observed between both the 5IAP ligand $[d_{115\cdots C11} = 3.464(3) \text{ Å},$ $\angle_{C15-I15\cdots C11}$ = 171.8 (3)^o] and the 5IAPH cation $[d_{125\cdots C11}$ = 3.511 (3) A^{\angle} \angle _{C15} \angle ₁₁₅ \angle . C₁₁ = 175.5 (4)^o. Unlike **1**, no I \cdots I halogen bonds are observed. Similar to **1**, the structure forms layers of hydrogen and halogen bridged ions parallel to the *ac* face diagonal (Fig. 6). Unlike **1**, there are no direct linkages between those layers.

Figure 6

The structure of **2** viewed parallel to the *b* axis (atoms are shown as spheres of arbitrary size). Dashed lines represent hydrogen and halogen bonds.

Table 4 Experimental details.

	1	$\overline{2}$		
Crystal data				
Chemical formula	$C_5H_6IN_2$ ⁺ Br^-	$(C_5H_6IN_2)[COBr_{0.51}Cl_{2.48}(C_5H_5IN_2)]$		
$M_{\rm r}$	300.93	629.20		
Crystal system, space group	Triclinic, P1	Monoclinic, $P2_1/n$		
Temperature (K)	100	100		
a, b, c(A)	$5.2152(2)$, $7.8039(3)$, $10.1294(4)$	9.6998 (7), 13.5527 (8), 13.8518 (11)		
	93.3762 (12), 104.1108 (11), 96.4297 (12)	90, 107.336 (3), 90		
$\alpha,\,\beta,\,\gamma$ (°) $V\left(\overset{\circ}{\mathbf{A}}{}^3\right)$	395.71(3)	1738.2(2)		
Z	2	4		
Radiation type	Mo $K\alpha$	Mo $K\alpha$		
μ (mm ⁻¹)	9.01	6.10		
Crystal size (mm)	$0.24 \times 0.21 \times 0.08$	$0.11 \times 0.07 \times 0.06$		
Data collection				
Diffractometer	Bruker D8 Venture dual wavelength Mo/Cu	Bruker D8 Venture dual wavelength Mo/Cu		
Absorption correction	Multi-scan (SADABS; Krause et al., 2015)	Multi-scan (SADABS; Krause et al., 2015)		
T_{\min} , T_{\max}	0.605, 0.746	0.413, 0.492		
No. of measured, independent and observed $[I > 2\sigma(I)]$ reflections	13418, 2412, 2346	15915, 4318, 3139		
$R_{\rm int}$	0.025	0.048		
$(\sin \theta/\lambda)_{\text{max}}$ (A^{-1})	0.714	0.668		
Refinement				
$R[F^2 > 2\sigma(F^2)], wR(F^2), S$	0.012, 0.029, 1.11	0.040, 0.090, 1.09		
No. of reflections	2412	4318		
No. of parameters	91	216		
No. of restraints	Ω	6		
H-atom treatment	H atoms treated by a mixture of independent and constrained refinement	H atoms treated by a mixture of independent and constrained refinement		
$\Delta \rho_{\text{max}}$, $\Delta \rho_{\text{min}}$ (e \AA^{-3})	$0.48, -0.50$	$1.22, -0.78$		

Computer programs: *APEX4* and *SAINT* (Bruker, 2022), *SHELXS2014* (Sheldrick 2008) and *SHELXL2019/2* (Sheldrick, 2015).

4. Database survey

The structures of a few salts of 5-IAPH have been reported. Copper(II) complexes include $(5IAPH)[CuCl₃(H₂O)₂]Cl$ (Abdalrahman *et al.*, 2013), two polymorphs of $(5IAPH)_{2}$ - $[CuCl₄]$ (Giantsidis *et al.*, 2002) and $(5IAPH)₂[CuBr₄]H₂O$ (Landee *et al.*, 2001). Several Hg and Zn salts of 5IAPH have also been reported (Khavasi et al., 2020), along with an Mn^{II} salt (Carnevale *et al.*, 2021). Copper complexes of 5IAP itself are also known including $[(5IAP)_2CuX_2]$, $X = Cl$, Br, $[(5IAP)_2CuBr_2]_2$, $[(5IAP)_3CuCl_2]$, $(Huynh$ *et al.*, 2023) and [(5IAP)2CuBr(OMe)]2 (Araujo-Martinez *et al.*, 2023).

Compound **1** may be most conveniently compared to its corresponding hydrate and chloride analogue (Polson *et al.*, 2013). The C—N bond lengths in **1** are slightly shorter than observed in the hydrated salt $(\sim 0.01 - 0.12 \text{ Å})$ and chloride analogue. Bond angles in 1 vary $\pm 2^{\circ}$ compared to the hydrated bromide salt, but not in any regular fashion, while they are comparable to those observed in the chloride complex within error.

With respect to compound **2**, although there no related compounds of 5-IAP, there are a number of reported structures including the $[LMX_3]$ ⁻ ion where *L* is a pyridine-based ligand. Several of these involve Pt^H (Adams *et al.*, 2005; Bel'skii *et al.*, 1990; Rochon & Melanson, 1980; Melanson & Rochon, 1976) or Co^{II} (Bogdanovic *et al.*, 2001; Crane *et al.*, 2004). The closest comparisons appear to be compounds of Cu^H (Healy *et al.*, 1985; Savariault *et al.*, 1988) or Co^H (Hahn *et al.*, 1997) with the formulae $(LH)[LMX_3]$ (L = phenazine or

quinoline for Cu, pyridine for Co). Similar hydrogen bonding is observed in all three compounds, but the absence of the iodine atom on the L group eliminates the halogen bonding observed in both **1** and **2**. Only in the quinolinium trichloridocuprate compound (Savariault *et al.*, 1988) are all of the aromatic rings approximately parallel, but even so the overall structure is that of dimers, rather than the extended sheet structure seen in **1** and **2**. With respect to the geometry at the metal ion, only the cobalt complex is similar with its slightly distorted tetrahedral geometry (as compared to the two strongly Jahn–Teller-distorted Cu complexes) and slightly shorter Co—Cl bond lengths (average $= 2.24 \text{ Å}$).

5. Synthesis and crystallization

Compound **1**: 2-Amino-5-iodopyridine (0.842g, 3.83 mmol) was dissolved in 10 mL of 9 *M* HBr and left to evaporate. After about one month, crystals of **1** were isolated by filtration $(0.623g, 56\%)$.

Compound **2**: HCl (0.0415 g, 12 *M*) and HBr (0.242 g. 9 *M*) were added to 2-amino-5-iodopyridine (0.439 g) creating a yellow solid. The solid was dissolved in 15 ml of 1-propanol and then cobalt(II) chloride hexahydrate (0.245 g) was added creating a dark-blue solution. After ten days, blue crystals were recovered by filtration. The crystals were predominantly lighter blue plates of $(5IAPH)_{2}[CoCl_{4-r}Br_{x}]\cdot H_{2}O$ (Mukda *et al.*, 2024), with a few dark-blue rhombic prisms mixed in. The

dark-blue prisms were separated by hand and identified as compound **2** by X-ray diffraction.

6. Refinement

Crystal data, data collection and structure refinement details are summarized in Table 4. All non-hydrogen atoms were refined anisotropically. Hydrogen atoms bonded to carbon atoms were placed geometrically and refined with a riding model and $U_{\text{iso}}(H) = 1.2U_{\text{eq}}(C)$. Hydrogen atoms bonded to nitrogen atoms were located in a Fourier map and their positions refined with $U_{\text{iso}}(H) = 1.2U_{\text{eq}}(N)$. Occupancies of the mixed halogen sites (*X*1 and *X*3) in **2** were allowed to refine freely. Mixed occupancy at the *X*2 site in **2** was initially assumed, but the bromide occupancy refined to zero within experimental error and the potential bromide ion was removed in the final refinement. Pseudo-isotropic restraints (ISOR) were applied to the lower occupancy ion, Br1.

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supporting information

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Salts of 2-amino-5-iodopyridinium

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Computing details

2-Amino-5-iodopyridinium bromide (1)

Crystal data

 $C_5H_6IN_2$ ⁺·Br[−] $M_r = 300.93$ Triclinic, *P*1 $a = 5.2152(2)$ Å $b = 7.8039(3)$ Å $c = 10.1294$ (4) Å α = 93.3762 (12)^o β = 104.1108 (11)^o $γ = 96.4297(12)°$ $V = 395.71(3)$ Å³

Data collection

Bruker D8 VENTURE dual wavelength Mo/Cu diffractometer Radiation source: microfocus sealed X-ray tube, Incoatec I*µ*s 3.0 HELIOS double bounce multilayer mirror monochromator *φ* and *ω* scans Absorption correction: multi-scan (SADABS; Krause *et al.*, 2015)

Refinement

Refinement on *F*² Least-squares matrix: full $R[F^2 > 2\sigma(F^2)] = 0.012$ $wR(F^2) = 0.029$ $S = 1.11$ 2412 reflections 91 parameters 0 restraints Primary atom site location: structure-invariant direct methods

Z = 2 $F(000) = 276$ $D_x = 2.526$ Mg m⁻³ Mo *Kα* radiation, $\lambda = 0.71073$ Å Cell parameters from 9950 reflections θ = 2.6–30.5° μ = 9.01 mm⁻¹ $T = 100 K$ Block, yellow $0.24 \times 0.21 \times 0.08$ mm

 $T_{\text{min}} = 0.605, T_{\text{max}} = 0.746$ 13418 measured reflections 2412 independent reflections 2346 reflections with $I > 2\sigma(I)$ $R_{\text{int}} = 0.025$ $\theta_{\text{max}} = 30.5^{\circ}, \theta_{\text{min}} = 2.1^{\circ}$ $h = -7 \rightarrow 7$ $k = -11 \rightarrow 11$ $l = -14 \rightarrow 13$

Secondary atom site location: difference Fourier map Hydrogen site location: mixed H atoms treated by a mixture of independent and constrained refinement $w = 1/[\sigma^2 (F_o^2) + 0.2575P]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{\text{max}} = 0.002$ $\Delta\rho_{\text{max}} = 0.48$ e Å⁻³ $\Delta\rho_{\rm min}$ = −0.50 e Å⁻³

Special details

Experimental. Data collections for compounds **1** and **2** were carried out with a Bruker D8 Venture Photon III diffractometer employing Mo-K*α* radiation (*λ* = 0.71073Å). The data were collected using Bruker Instrument Service v8.5.0.27 & APEX4 v2022.10-1 and reduced using Bruker SAINT v8.40b (Bruker, 2022). Absorption corrections were performed using SADABS (Krause, 2015). The structure was solved using SHELXS-2014 (Sheldrick, 2008) and refined using SHELXL-2019 (Sheldrick, 2015).

Geometry. All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds involving l.s. planes.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (Å²)

Atomic displacement parameters (Å2)

	U^{11}	I/22	U^{33}	I/I^2	U^{13}	U^{23}
N ₁₁	0.0168(5)	0.0103(5)	0.0141(5)	$-0.0016(4)$	0.0035(4)	$-0.0002(4)$
C12	0.0149(6)	0.0121(5)	0.0118(5)	0.0003(4)	0.0051(4)	0.0005(4)
N ₁₂	0.0150(5)	0.0149(5)	0.0171(5)	0.0000(4)	0.0008(4)	0.0008(4)
C13	0.0167(6)	0.0106(5)	0.0145(6)	0.0010(4)	0.0029(5)	0.0020(4)
C14	0.0149(6)	0.0127(6)	0.0147(6)	$-0.0005(4)$	0.0023(5)	0.0007(5)
115	0.01575(5)	0.01769(5)	0.01789(5)	0.00603(3)	0.00364(3)	0.00494(3)
C15	0.0154(6)	0.0144(6)	0.0136(6)	0.0035(5)	0.0053(5)	0.0033(5)
C16	0.0193(6)	0.0125(6)	0.0145(6)	0.0029(5)	0.0063(5)	0.0029(5)
Br1	0.01538(6)	0.01065(6)	0.01964(7)	$-0.00109(4)$	0.00095(5)	0.00055(5)

Geometric parameters (Å, º)

Hydrogen-bond geometry (Å, º)

Symmetry codes: (i) −*x*, −*y*+1, −*z*; (ii) *x*, *y*+1, *z*.

Crystal data

2-Amino-5-iodopyridinium (2-amino-5-iodopyridine-*κN***¹)bromido/chlorido(0.51/2.48)cobalt(II) (2)**

Special details

Geometry. All esds (except the esd in the dihedral angle between two l.s. planes) are estimated using the full covariance matrix. The cell esds are taken into account individually in the estimation of esds in distances, angles and torsion angles; correlations between esds in cell parameters are only used when they are defined by crystal symmetry. An approximate (isotropic) treatment of cell esds is used for estimating esds involving l.s. planes.

Fractional atomic coordinates and isotropic or equivalent isotropic displacement parameters (Å2)

supporting information

Geometric parameters (Å, º)

supporting information

Hydrogen-bond geometry (Å, º)

Symmetry codes: (i) −*x*+1/2, *y*−1/2, −*z*−1/2; (ii) *x*+1/2, −*y*+3/2, *z*−1/2; (iii) *x*+3/2, −*y*+3/2, *z*−1/2; (iv) −*x*+1, −*y*+2, −*z*−1.