Synthesis, a case of isostructural packing, and antimicrobial activity of silver(I)quinoxaline nitrate, silver(I)(2,5-dimethylpyrazine) nitrate and two related silver aminopyridine compounds

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The synthesis and low temperature crystal structures of $[Ag(quinoxaline)]_n(NO_3)_n$, **1**, $[Ag(2,5\text{-dimethylpyrazine})(NO_3)]_n$, **2** and $[Ag_4(3\text{-aminopyridine})_4(NO_3)_4]_n$ **3** are presented. The quinoxaline compound forms a 1D coordination polymer with the characteristic linear 2-coordination figure of silver(I), the N–Ag–N angle being 164.2(1)°, and only weak silver–nitrate interactions. In addition there is an interaction giving pairs of parallel chains as the main structural theme. The 2,5-dimethylpyrazine compound has approximately trigonal-planar coordination, also binding one nitrate at the relatively short Ag–O distances 2.444(3) Å and 2.484(3) Å, respectively, for the two crystallographically different silver atoms. This also results in a 1D coordination polymer that, despite the large differences in the Ag(I) coordination environment, is isostructural with **1**. $[Ag_4(3\text{-aminopyridine})_4(NO_3)_4]_n$ **3** forms a 2D coordination polymer by bridging nitrate ions. The antimicrobial activity of **1–3**, and also of $[Ag_3(2\text{-aminopyridine})_4](NO_3)_3$, **4** was screened for 13 different pathogens and substantial activity was shown for **1** against *Escherichia coli* and *Pseudomonas aeruginosa* (MIC 4 μg cm^{-3}) and somewhat lower activity was registered against *Sarcina lutea* and *Salmonella typhi* for **1**, *Bordetella bronchiseptica* for **2**, *Salmonella typhi* and *Pseudomonas aeruginosa* for **3**, and *Escherichia coli* and *Shigella sonnie* for **3** (MIC 8 μg cm^{-3}). Only low activity was shown against the yeast *Candida albicans* for **1**, **2** and **4** whereas no activity against this pathogen was registered for **3**.

Introduction

Anyone who has eaten a boiled egg with a silver spoon can testify that silver has a direct effect on biological molecules. The foul tasting (or rather smelling) sulfur compounds released in this process make this a very unpleasant memory.[1] It is therefore probably not so surprising that silver has some biological activity and it has indeed been used as an antimicrobial agent for a long time both in metallic form and as various Ag(I) salts.[2]

Although there is much interest currently in the addition of silver to medical instruments and in wound (especially burns) dressings to avoid infections,[3–7] in general the use of Ag(I) compounds for medical purposes seems to be on the decline, for example the compulsory dropping of $AgNO_3$ solutions in the eyes of newly born babies has been abolished in Sweden since 1986.[8] On the other hand, it should be noted that there is a significant and increasing sale of non-prescribed drugs and "alternative" preparations based on silver and its compounds which has led to some concern for the development of silver resistant bacterial strains.[2,9,10]

Nevertheless, there is some current interest in investigating and applying new and more sophisticated Ag(I) compounds for their antimicrobial activity.[3,11–23] The exact mode of action of these compounds is unknown on a molecular level, but interference with electron transport, binding to DNA, and interactions with cell membranes have each been proposed.[24] Furthermore, there seem to be very few clear correlations between the chemical properties, structure and connectivity of the tested compounds and their antimicrobial activity (which may vary widely). Nomiya and co-workers have suggested that the most important factors are the type of atoms directly bound to the Ag(I) ion (O being better than N and S, which are in turn significantly better than P) and the ease of ligand replacement.[13] The study of the antimicrobial activity of Ag(I) complexes with pyridyl type ligands seems, however, to have been largely restricted to the ligands 1,10-phenanthroline, 1,10-phenanthroline-5,6-dione and bipyridine.[23,25,26]

Structural aspects of such compounds are clearly biologically relevant as well as being of considerable interest in the areas of coordination polymers, supramolecular chemistry and crystal engineering.[27] A somewhat controversial subject in the latter area, especially for Ag(I) coordination polymers, is the character of the nitrate ion: is NO_3^- solely a spectator ion or do coordinated nitrate ions play a profound role in determining the dimensionality and structure of the coordination polymer?

Here we present the synthesis and structure of the coordination polymers $[Ag(quinoxaline)]_n(NO_3)_n$, **1**, $[Ag(2,5\text{-dimethylpyrazine})(NO_3)]_n$, **2** and $[Ag_4(3\text{-aminopyridine})_4(NO_3)_4]_n$ **3**, and the screening of the antimicrobial activity of these and the related compound $[Ag_3(2\text{-aminopyridine})_4](NO_3)_3$, **4** for 13 different pathogens (see Scheme 1).

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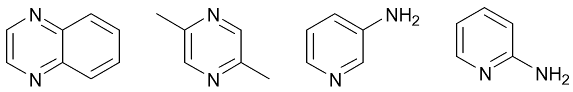
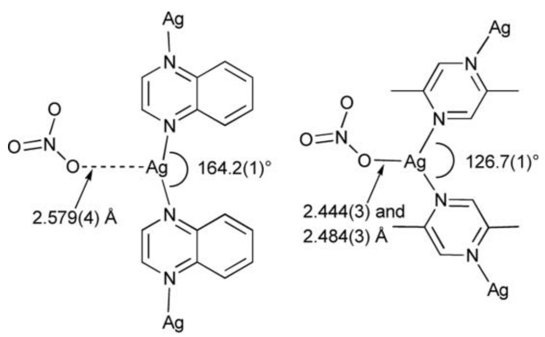


Scheme 1 The pyridyl ligands quinoxaline, 2,5-dimethylpyrazine, 3-aminopyridine and 2-aminopyridine used to prepare compounds **1–4**.

Results

The synthesis of **1–4** is a fairly straightforward combination of the starting materials but the structural chemistry of **1** and **2** is more interesting since the distinctively different coordination environment around Ag(I), linear two-coordinated in **1** and trigonal-planar for **2** (see Scheme 2), still gives rise to an isostructural packing of the so-formed 1D coordination polymers. Compound **3** on the other hand forms a somewhat unusual tetrameric silver complex as part of a 2D coordination polymer network. Crystal data are given in Table 1.



Scheme 2 The distinctively different coordination environment around Ag(I): linear two-coordinated in **1** and trigonal-planar for **2**.

Structure description

$[Ag(quinoxaline)]_n(NO_3)_n$ 1. Relevant geometric data are found in Table 2. In this compound there is imposed *m*-symmetry, with the Ag and nitrate groups on a mirror plane and the quinoxaline moiety lying across a mirror plane. The silver complexes in **1** form slightly wobbly chains with N–Ag–N angles of 164.2(1)°. An ORTEP-type drawing is shown in Fig. 1 accompanied by the crystal packing in Fig. 2.

Table 2 Selected bond lengths and angles for **1**. Symmetry transformations used to generate equivalent atoms: (i): $x, 1/2 + y, z$

Bond	Distance/Å	Bond Angle	Angle/°
Ag1–N1	2.267(3)	N1–Ag1–N1^{i}	164.2(1)
Ag1···O3	2.579(4)	N1–Ag1–O3	94.47(7)
		O1–Ag1–O3	45.32(7)

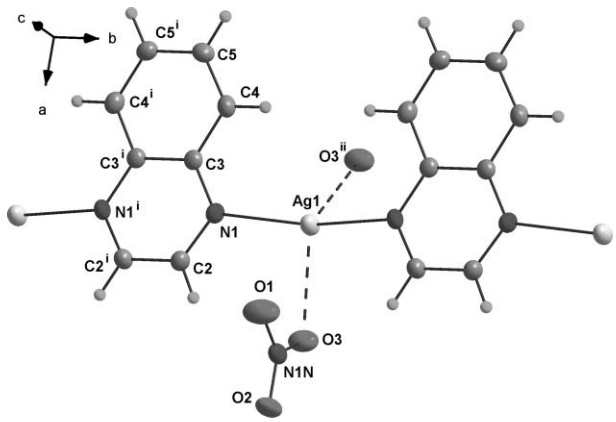


Fig. 1 A numbering scheme with thermal ellipsoids drawn at 50% probability level for **1**. The symmetry codes are (i): $x, -1/2 - y, z$, (ii): $x - 1/2, 1/2 - y, 1/2 - z$.

The crystal packing of the chains is characterised by a pairwise association of parallel chains separated by stacks of nitrate ions. There is no π-stacking between the parallel chains because the chains are displaced such that the aromatic groups do not face each

Table 1 Crystal data for **1–3**

Compound	1	2	3
Ligand	Quinoxaline	2,5-Dimethylpyrazine	3-Aminopyridine
Formula	$C_8H_6AgN_3O_3$	$C_{12}H_{16}Ag_2N_6O_6$	$C_5H_6AgN_3O_3$
M	300.03	556.05	264.00
Crystal syst.	Orthorhombic	Monoclinic	Triclinic
Space group	*Pnma*	$P2_1/c$	*P*1
a [Å]	9.1400(2)	13.1291(2)	7.5269(1)
b [Å]	7.3099(1)	14.0159(1)	10.4241(1)
c [Å]	13.0487(3)	9.0890(1)	11.0236(1)
α [°]	90	90	68.994(1)
β [°]	90	90.101(1)	71.029(1)
γ [°]	90	90	89.920(1)
V [Å^3]	871.82(3)	1672.52(3)	757.065(14)
Z	4	4	4
μ/mm^{-1}	2.300	2.387	2.630
ρ/g cm^{-3}	2.286	2.208	2.316
Measured refl.	8503	29180	13403
Unique refl.	878	5999	9843
R_{int}	0.0550	0.1315	0.0209
R (I > 2σ)	0.0233	0.0403	0.0233
wR_2(all)^a	0.0653	0.0968	0.0580
Flack param.	—	—	−0.018(15)

^{a} $w = [\sigma^2(F_o^2) + (aP)_2 + bP]$; $P = (|F_o|^2 + 2|F_c|^2) / 3$, $a = 0.0428, 0.0273, 0.0277$, and $b = 0.5179, 0.0136, 0.087$ for **1**, **2** and **3**, respectively.

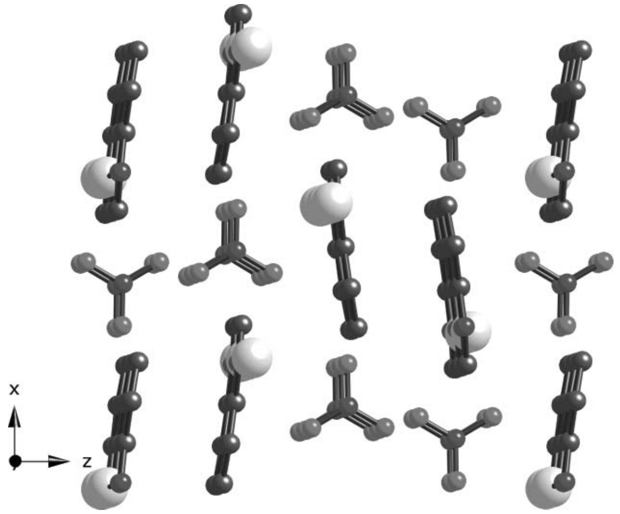


Fig. 2 Crystal packing in **1**. Note the displacement of the pair-wise packed chains that make Ag ions face the aromatic groups.

other but instead face the silver ions from the neighbouring chain, although without any significant Ag···C or Ag···H interactions. However, in between the pairs of chains there are some closer contacts, C–H···C; 3.15 Å and C···C; 3.390(3) Å, although these chains are not parallel (21° tilt). In the packing diagram, we see that the Ag(I) complexes tend to associate and the nitrates are clearly separated from these units.

[Ag(2,5-dimethylpyrazine)(NO$_3$)]$_n$, 2. Crystal data for **2** are given in Table 1 and relevant geometric data in Table 3. This structure is non-merohedrally twinned and simulated the orthorhombic system. The twin-volume ratio refined to 0.564(1) : 0.436(1). The silver complexes in this compound form zig-zag chains with N–Ag–N angles of 126.7(1)°, nevertheless, this results in a linear arrangement of the dimethylpyrazine ligands. An ORTEP-type drawing is shown in Fig. 3 accompanied by the crystal packing in Fig. 4.

As in **1** there is a pair-wise association of parallel chains with a similar displacement of the chains, again making the aromatic groups face the silver ions from the neighbouring chain without π-stacking. However, in between the pairs of chains there are some closer contacts between methyl groups and an aromatic carbon C–H···C; 2.91–3.11 Å. Overall, this results in a very similar packing to **1**, as demonstrated by a comparison of Fig. 2 and 4. In Fig. 5 the arrangement of two parallel and co-planar chains are compared for the two compounds.

Table 3 Selected bond lengths and angles for **2**. Symmetry transformations used to generate equivalent atoms: (i): $x - 1,y,z$ (ii): $x, -y + 1/2,z + 1/2$

Bond	Distance/Å	Bond Angle	Angle/°
Ag1–N1B	2.295(4)	N1B–Ag1–N1A	126.69(12)
Ag1–N1A	2.312(5)	N1B–Ag1–O13	118.05(15)
Ag1–O13	2.444(3)	N1A–Ag1–O13	115.25(15)
Ag2–N4B	2.289(4)	N4B–Ag2–N4A^{i}	126.66(11)
Ag2–N4A^{i}	2.306(4)	N4B–Ag2–O22^{ii}	115.24(14)
Ag2–O22^{ii}	2.484(3)	N4Ai–Ag2–O22^{ii}	118.06(14)

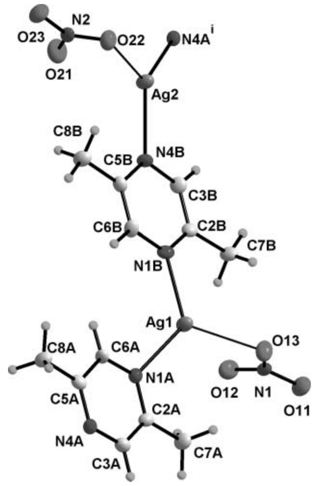


Fig. 3 An ORTEP-type drawing with thermal ellipsoids drawn at 50% probability level of **2** The symmetry code is: (i): $x - 1, y, z$.

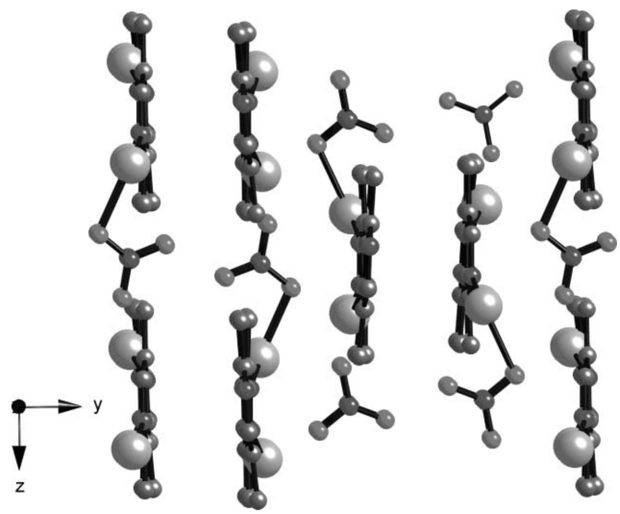


Fig. 4 Crystal packing in **2**.

[Ag$_4$(3-aminopyridine)$_4$(NO$_3$)$_4$]$_n$ 3. The silver complex in this compound is tetranuclear and a thermal ellipsoid drawing is shown in Fig. 6. Bond lengths and angles are given in Table 4. Note that the tetranuclear unit is further supported by intramolecular hydrogen bonds.

The 2D-coordination polymer formed by the bridging nitrates is indicated in Fig. 7, in which another important structural feature is also shown, namely, the stacking of the tetranuclear units. The centroid–centroid distances (3.71–3.86 Å) and tilt angles of two adjacent aromatic rings (5.8–9.0°) are indicative of interactions between the π-systems, but there may also be some Ag(I)–Ag(I) interactions to account for.

Antimicrobial activity

The compounds were dissolved in dimethylsulfoxide (DMSO) and tested against four Gram positive as well as eight Gram negative bacteria and one yeast. The antimicrobial activity of **1–4** is presented in Table 5.

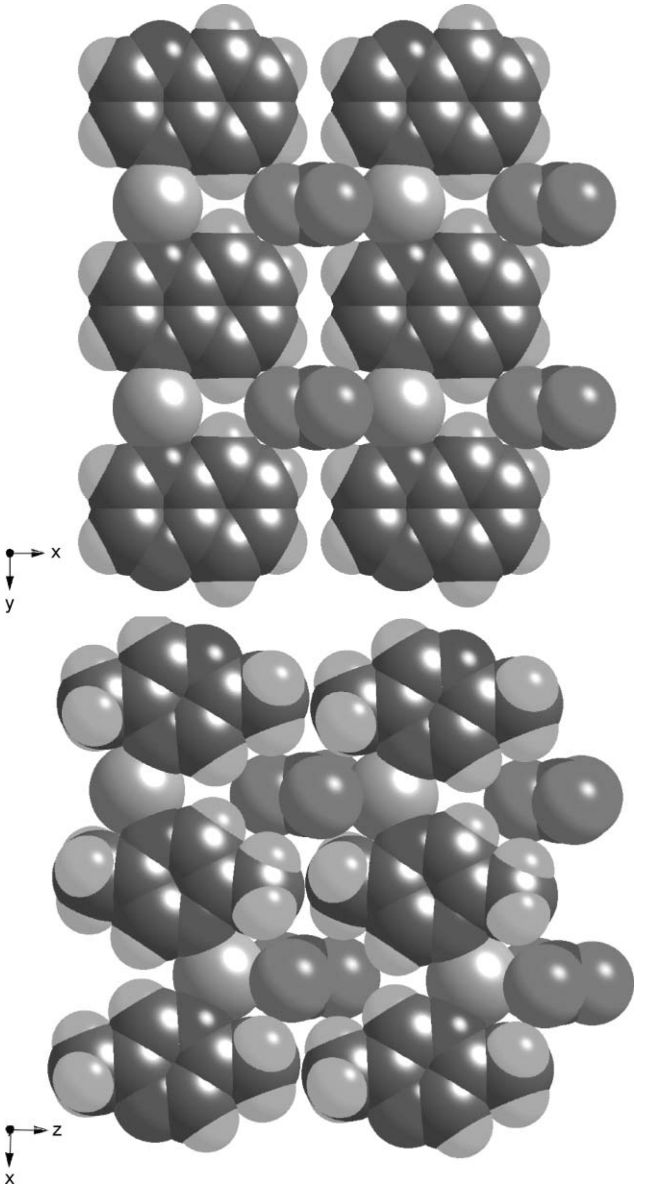


Fig. 5 Comparison of the chain structures in **1** and **2** using space-filling models. Note that despite the radically different coordination geometry around silver, the overall arrangement is isostructural (compare also Figs. 2 and 4). The dimensions of the ligands as judged from the 6.349 Å and 6.432 Å H-to-H "lengths" are very close.

Complex 1 exhibited a broad spectrum against Gram positive and negative bacteria and yeasts. The highest activity against a Gram positive bacteria was recorded with *Sarcina lutea*, and for Gram negative bacteria *Escherichia coli* and *Pseudomonus aeruginosa*, followed by *Salmonella typhi* and *Proteus mirabilis*, while *Bacillus subtilis*, *Bordetella bronchiseptica*, *Serratia marcescens* and *Shigella sonnie* bacteria were found to be resistant to this compound.

Complex 2 on the contrary showed only weak activity against most Gram positive and negative bacteria, the exception being *Bordetella bronchiseptica*, for which it was the most active compound in this study. It also proved to be the most effective compound against the yeast *Candida albicans*.

Table 4 Selected bond distances and angles for **3**

Bond	Distance/Å	Bond Angle	*Angle*/°
Ag1–O1B	2.562(3)	N1A–Ag1–N1C	140.07(8)
Ag1–O2B	2.643(2)	N3C–Ag2–N3H	126.32(11)
Ag2–O1D	2.445(3)	N3F–Ag3–N3A	124.98(10)
Ag2–O1E	2.463(2)	N1H–Ag4–N1F	146.94(8)
Ag3–O1G	2.456(3)	N3A–H31A–O2D	148(4)
Ag3–O2E	2.463(2)	N3C–H31C–O2G	171(5)
Ag4–O2E	2.570(2)	N3C–H31C–O3G	134(4)
Ag4–O1E	2.582(2)	N3F–H31F–O2D	154(4)
Ag1–N1A	2.216(2)	N3H–H31H–O3G	162(5)
Ag1–N1C	2.228(2)		
Ag2–N3C	2.297(2)		
Ag2–N3H	2.340(2)		
Ag3–N3F	2.317(2)		
Ag3–N3A	2.369(3)		
Ag4–N1H	2.207(2)		
Ag4–N1F	2.216(2)		
Ag1–Ag4	3.5094(3)	(intramol.)	
Ag1–Ag4	4.0415(3)	(intermol.)	
N3A···O2D	3.135(4)		
N3C···O2G	3.129(4)	N3A–H32A–O2B	150(5)
N3C···O3G	3.179(4)	N3C–H32C–O3B	168(4)
N3F···O2D	3.068(4)	N3F–H32F–O3B	167(5)
N3H···O3G	3.011(4)	N3H–H32H–O1B	132(4)
N3A···O2B	3.087(3)		
N3C···O3B	3.184(4)		
N3F···O3B	3.174(3)		
N3H···O1B	3.118(3)		
Centr.C-centr.H[a]	3.7135(17)	(intramol.)	
Centr.A-centr.F[a]	3.7926(17)	(intramol.)	
Centr.C-centr.H[a]	3.8572(17)	(intermol.)	
Centr.C-centr.F[a]	3.7470(17)	(intermol.)	

[a] Centr. = pyridyl centroid, letters denote rings according to Fig. 6.

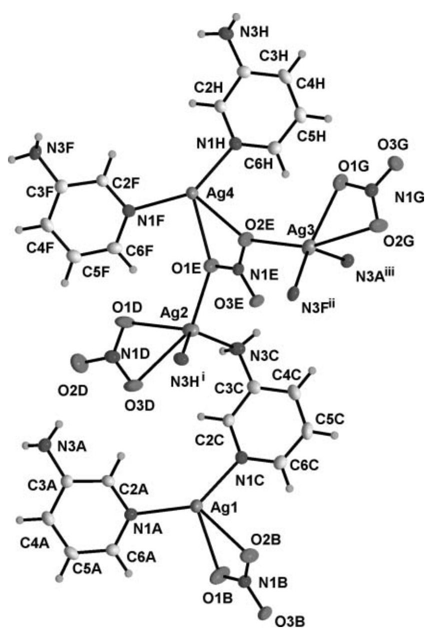


Fig. 6 ORTEP-type drawing of compound **3**. Thermal ellipsoids are shown at 50% probability level. The symmetry code is: (i): $x - 1, y, z$.

Complex 3 is moderately anti-Gram positive, more active against Gram negative bacteria and inactive against *Candida albicans.* The highest activity recorded for **3** was recorded against *E. coli* and *Shigella sonnie*.

Table 5 Screening of antimicrobial activity of compounds **1–4**

	1 MIC[a]/μg cm^{-3}	**2** MIC[a]/μg cm^{-3}	**3** MIC[a]/μg cm^{-3}	**4** MIC[a]/μg cm^{-3}
Gram positive bacteria				
Bacillus subtilis	128	256	64	256
Micrococcus luteus	16	64	32	128
Sarcina lutea	8	128	64	64
Staphylococcus aureus	32	256	32	128
Gram negative bacteria				
Bordetella bronchiseptica	256	8	16	32
Escherichia coli	4	32	8	16
Klebsiella pneumoniae	32	64	16	32
Proteus mirabilis	16	32	32	16
Salmonella typhi	8	32	64	8
Serratia marcescens	256	256	32	256
Shigella sonnie	256	256	8	256
Pseudomonas aeruginosa	4	16	16	8
Fungal pathogen				
Candida albicans	32	16	256	32

[a] MIC = Minimum Inhibitory Concentration, is the lowest concentration of the compound that 100% inhibits the growth of the microorganism.

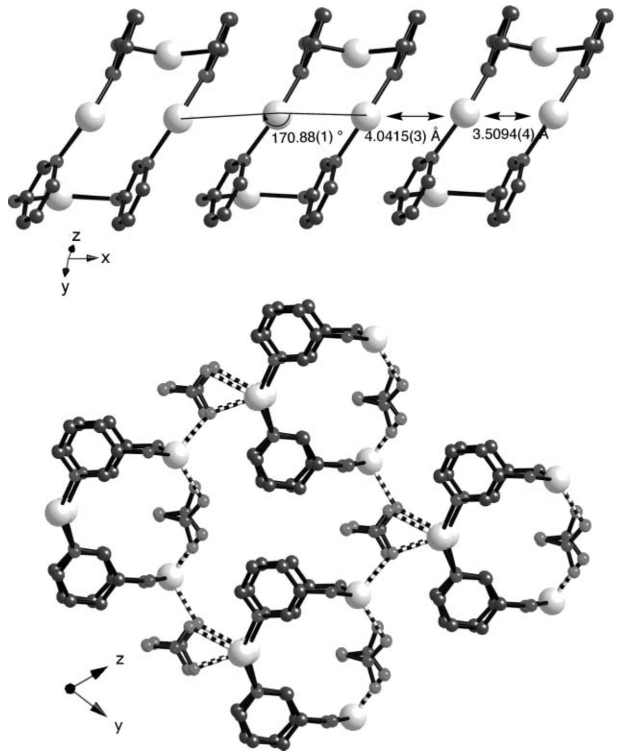


Fig. 7 Top: The stacking of the tetranuclear Ag(I) complexes in **3** (hydrogen atoms and coordination to nitrates omitted for clarity). Bottom: the layers formed by Ag(I)–nitrate bonds.

Complex 4 is inactive against the tested Gram positive bacteria but active against most of the tested Gram negative bacteria, with highest activity against both *Salmonella typhi* and *Pseudomonas aeruginosa*. It is inactive against *Serretia marcescens* and *Shigella sonnie.* In addition, it showed some modest anti-yeast activity.

Discussion

Structures of 1 and 2

Nitrate coordination. **1** and **2** clearly have a different coordination environment around Ag(I) as can be seen in Scheme 2 and Fig. 1 and 3. Both bond lengths and N–Ag–N angles suggest an Ag–O bond present in **2** but absent in **1**. However, it is not completely clear where the limits for an Ag–O bond should be set. In Fig. 8 we have compiled data from the Cambridge Structural Database (CSD)[28–30] for two-coordinated AgN_2 units with one additional Ag–O interaction and three-coordinated $AgN_2(ONO_2)$ units where the authors have thus defined an Ag–O bond. Intuitively, one would expect the N–Ag–N angle to decrease as the Ag···O distances decrease, and this is demonstrated in Fig. 8. We also see that the normal "cut-off" value used is around 2.6 Å and that there are regions around 2.2–2.4 Å where the Ag–O bond seem unambiguous, and likewise over 2.7 Å where a coordinative (dative) Ag–O bond seems unlikely.

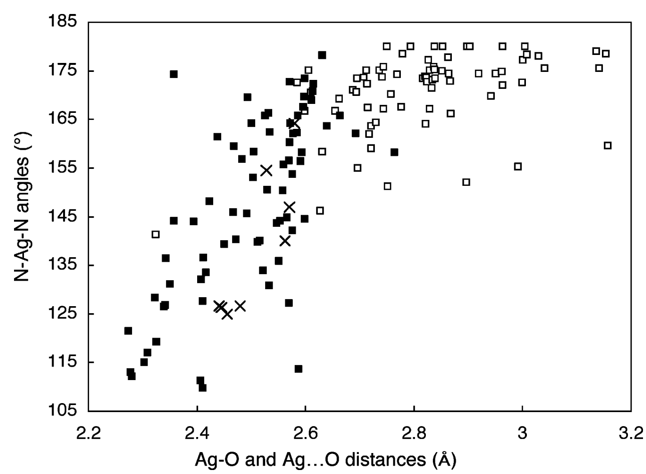


Fig. 8 The population of N–Ag–N angles plotted against shortest Ag–O (■) and Ag···O (□) distances for Ag-complexes with two nitrogens coordinated. × denotes compounds **1–4**.

However, between 2.4 Å and 2.7 Å there is a "grey" area where structures have to be scrutinized in more detail before a judgment can be passed. This data analysis is of course very crude and, for example, does not take into account if the nitrate is unidentate or bidentate, or if many nitrates are within close proximity of the Ag ion.

In **2** we have preferred to assign a bond for the shorter interaction (2.44–2.48 Å) since the coordination figure then becomes very regular trigonal-planar, but in **1** we believe the interaction is too weak for a bond as judged by the longer distance (2.579(4) Å) and the larger angle (164.2(1)°).

Chain packing in 1 and 2. It is important to bear in mind that the bond lengths do not necessarily mirror the energetics of the interaction, and it is quite likely that any Ag–nitrate interaction is rather weak. A clear indication of this is that the chain packing in **1** and **2** is similar. In fact, when we look at the intermolecular interactions in detail we see significant differences, and it is not only the Ag(I) coordination that changes. However, if we take one step back and look globally, there is no doubt that the two compounds are isostructural (see Fig. 2, 4 and 5).

This prompted an investigation of the packing patterns of similar Ag(I) 1D coordination polymers based on pyrazine-type ligands, in order to ascertain whether this packing pattern is found in other compounds. Of the 16 compounds found from the CSD, 15 had parallel chains and could roughly be divided into the four categories presented in Fig. 9.

The 16th compound (CSD reference code TOZGUK, pyrazine, OH^-, PF_6^-) had chains running perpendicular and could thus not be classified in this way. In Table 6 we present the results of this analysis, and clearly the most common packing pattern is alternating 1D polymers and stacks of anions (square alternating packing). A pattern resembling that in **1** and **2** is also found for two coordination polymers with 2,3-diphenylpyrazine derivatives.[31]

Structure of 3

The main features of this structure have already been noted, namely, a 2D coordination polymer with bridging nitrates where the Ag(I)–O distances fall in the uncontested region of Fig. 7. The "π–π" interactions are somewhat long according to the study by Janiak,[32] and the pyridyl rings are not completely co-planar.

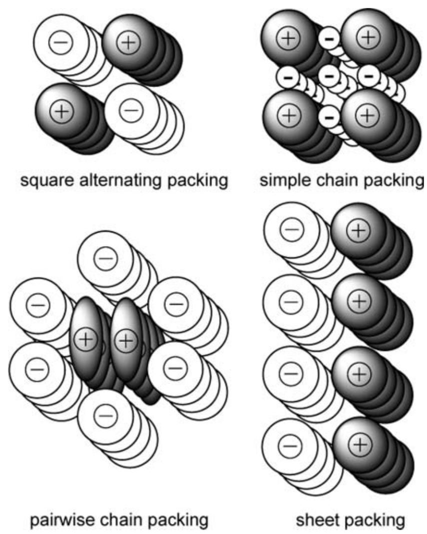


Fig. 9 Schematic of the different modes of packing for 1D coordination polymers based on Ag(I) and pyrazine units. Shaded shapes represent the coordination polymer viewed along the chain axis and circles with minus signs are stacks of anions. The smaller circles represent more diffuse spreading of the anions.

Moreover the intermolecular Ag(I)–Ag(I) distances (4.0415(3) Å) are rather long compared to twice the van der Waals radii (3.44 Å[33]). Thus, although the pillar formation is striking, there seem to be only weak interactions within the stack. On the other hand, even though this can be classified as a 2D-coordination polymer, it can also be seen as a "sheet packing" according to Fig. 9.

We note that the analogous 2-aminopyridine compound, **4**, forms a 2D network through hydrogen bonding between amino groups and nitrates,[34] however, the 4-amino compound gives a two-fold interpenetrated hydrogen bonded 3D-net of the $(8^3)(8^6)_2$-tfa type.[35]

Table 6 Schematic chain packings for pyrazine type 1D Ag(I) coordination polymers, see Fig. 9. The exact nature of ligands and anions for each compound is given in the footnote

#^{a}	CSD ref. code	Square alternating packing	Pair-wise chain packing	Simple chain packing	Sheet packing
1	ACOHIJ	X			
2	EQOYIS		X		
3	EQOYOY		X		
4	EQOYUE			X	
5	HOQFAU	X			
6	IHIYED				X
7	IHIYIH				X
8	IXACOZ	X			
9	OGAVOH	X			
10	OGAVUN	X			
11	OGAWAU	X			
12	QEGCUA			X	
13	SURBAI	X			
14	VANMAY	X			
15	YUNZUC	X			
16	**1**		X		
17	**2**		X		

^{a} **1**: pyrazine, CF_3COO^- **2**: 2,3-diphenylpyrazine, BF_4^- **3**: 2,3-bis(3′,5′-dimethylphenyl)pyrazine, $CF_3SO_3^-$ **4**: 2,3-bis(3′,5′-dimethylphenyl) pyrazine, CF_3COO^- **5**: pyrazine, NO_2^- **6**: 1,4-diazatriphenylene, BF_4^- **7**: diazatriphenylene, ClO_4^- **8**: 2-methylpyrazine, CF_3COO^- **9**: trimethylpyrazine CF_3COO^- **10**: 2,6-dimethylpyrazine CF_3COO^- **11**: 2,5-dimethylpyrazine, CF_3COO^- **12**: (a C_2-symmetric di-camphor derivative of pyrazine), NO_3^- **13**: pyrazine, PF_6^- **14**: quinoxaline, ClO_4^- **15**: pyrazine, BF_4^-

Antimicrobial activity

The different pattern of activity towards the tested micro-organisms are illustrated in Fig. 10 together with data for [Ag(*R*-(+)-2-pyrrolidone-5-carboxylic acid)]$_n$ ([Ag(*R*-othf)]$_n$), which is one of the most antimicrobial active Ag(I) complexes found to date.[36]

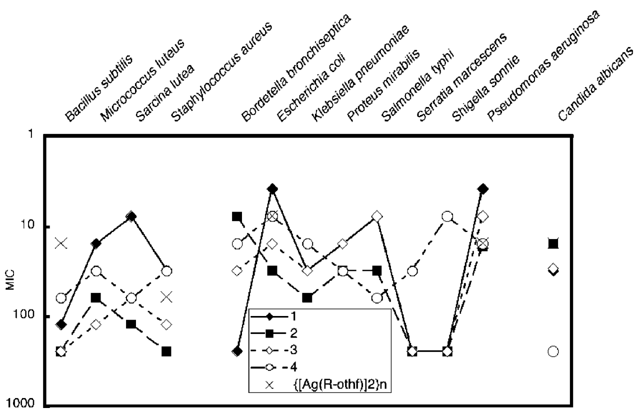


Fig. 10 A graphical presentation of the "spectrum" of antimicrobial activity (logarithmic scale) of compounds **1–4** and of [Ag(*R*-othf)$_2$]$_n$, one of the most antimicrobial active Ag(I) complexes found to-date.

As far as the activity of the compounds is concerned, the values are not remarkable. Compound **1** is both better and worse than ([Ag(*R*-othf)]$_n$) for some bacteria and also the general difference in MIC value by factors of 10–30 against different bacteria have also been found in similar studies.[36] Against the yeast *Candida albicans*, **2** seems to be almost as active as [Ag(1,10-phenanthroline)$_2$]ClO$_4$, but far less active than [Ag(1,10-phenanthroline-5,6-dione)$_2$]ClO$_4$, which has a reported MIC value of 0.3 μg cm^{-3}.[25] We also note that the present compounds do not perform worse than the oxygen donor compounds or histidine derivatives of Nomiya *et al.*[14,37]

For structure–activity correlations we were restrained by the low solubility of our compounds, which made speciation studies in solution difficult. (Such studies should also preferably be performed at a chloride concentration close to the physiological value 0.15 M,[38] a fact that complicates the issue because of precipitation of very insoluble AgCl(s)).

However, we might argue the following points: The stoichiometry of **1** and **2** makes the formation of the neutral species [AgCl(quinoxaline)] and [AgCl(dimethylpyrazine)] likely, or alternatively the corresponding charged aqua complex. Higher coordination numbers may also be possible but the geometry of these ligands make complexes with higher nuclearity improbable. As can be seen from Fig. 10, the "activity spectrum" of **1** and **2** are also similar, except for notable differences against *Bordetella bronchiseptica* and *Sarcina lutea*. (Note, however, that the *x*-axis is arbitrary and two sets of data may look more or less similar depending on the order of the data-points.)

Compounds **3** and **4** may on the other hand form polynuclear species resembling those found in the solid state (given by the stoichiometry in the formulae). The implications of this for the activity are unclear, but we note that for **3** and **4** the difference in activity patterns is much larger than between **1** and **2**.

It is also necessary to take into account that the distribution of these compounds dissolved in DMSO might enhance the activity, as reported by McCann *et al.*[18]

Conclusions

It is debatable whether the best way to analyse the 1D coordination polymers **1** and **2** is to account for all the specific atom–atom interactions and then work upwards in scale, eventually rationalising the overall packing. For each structure this is surely something that has to be carried out, but we hope to have shown the advantage of looking on a larger scale and searching for similarities and patterns. Thus, for compounds **1** and **2**, both the coordination around Ag(I), and the various intermolecular interactions differ significantly but the overall structure is the same and related to other cases of 1D silver coordination polymers.

In addition, we have shown that this set of compounds with six-ring aromatic nitrogen type donors are as active against a test selection of potential pathogens as previously investigated compounds based on, for example, carboxylates, and imidazoles.

Experimental and computational details

Materials and methods

All chemicals were reagent grade and used without further purification. [Ag$_3$(2-aminopyridine)$_4$](NO$_3$)$_3$, **4**, was prepared as earlier reported.[34] In the preparations of **1–3** an excess ligand was used in a futile attempt to force a higher coordination number on silver(I).

X-Ray crystallography

Crystallographic measurements were made on a Siemens Smart CCD diffractometer with graphite monochromated Mo-Kα radiation at 173 K. The structures were solved by direct methods and subsequent full-matrix least-squares refinement, including anisotropic thermal parameters for all non-hydrogen atoms. Hydrogen atoms were refined isotropically using geometrical constraints. The calculations were carried out with the SHELXTL program package.[39]

CCDC reference numbers 265755, 290465 and 265754.

For crystallographic data in CIF or other electronic format see DOI: 10.1039/b516723j

Search of the Cambridge Crystallography Database

The Conquest software (version 1.6) was used for each run and the retrieved structures all had *R* values <10% and were error-free. An N–Ag–N unit and a nitrate unit were created and the Ag–N bonds specified as "no ring". Then one run was made where an Ag–O bond was created and the coordination at Ag was specified as three. These are the filled data points in Fig. 8. Subsequently another run was made where an intermolecular contact between Ag and O replaced the Ag–O bond and, consequently, the coordination at Ag was specified as two. These are the unfilled data points in Fig. 8.

Synthesis of [Ag(quinoxaline)]$_n$(NO$_3$)$_n$ (1). To a 10 ml aqueous solution of silver nitrate (0.20 g, 1.18 mmol), 0.26 g (2.0 mmol) of quinoxaline in 15 ml ethanol were added. Further, 2–3 drops of 0.1 M nitric acid were added with continuous stirring. The solution became clear and was filtered off 2 or 3 times and allowed to stand for at least 3 weeks. Yellowish crystals suitable for X-ray measurement were collected and dried in air, producing a yield of about 65%. Analytical data (%): Calc.: C, 32.03; H, 2.01; N, 14.01; Ag, 35.95. Found: C, 31.98; H, 2.11; N, 14.14; Ag, 35.89. IR, KBr disc (cm^{-1}): 3439w, 3079m, 3048m, 2925w, 2630w, 2394w, 2352w, 2327s, 1941m, 1860m, 1743m, 1676m, 1643m, 1627m, 1609m, 1552m, 1535m, 1517m, 1498vs, 1382vs, 1204s, 1124s, 1029vs, 954vs, 867vs, 849w, 812s, 756vs, 663w, 612brw, 524w, 460w, 394vs, 367s, 343s, 317s, 294s, 271vs.

Synthesis of [Ag(2,5-dimethylpyrazine)(NO_3)]$_n$ (2). This complex was prepared by mixing silver nitrate (0.16 g, 1.0 mmol) in 30 cm^3 water with a solution of 2,5-dimethyl pyrazine (0.20 g, 2.0 mmol) in 15 cm^3 ethanol. A few drops of HNO_3 (0.01 N) were added dropwise with continuous stirring. The mixture was allowed to stand for several days at room temperature. Grey crystals of the complex suitable for X-ray measurements were collected and dried in air, producing a yield of about 40%. Analytical data (%): Calc.: C, 25.92; H, 2.90; N, 15.11; Ag, 38.79. Found: C, 26.03; H, 2.82; N, 15.36; Ag, 38.63. IR, KBr disc (cm^{-1}): 2397m, 1809m, 1763m, 1514sh, 1488s, 1432sh, 1382vs br, 1328sh, 1261sh, 1155s, 1061s, 1036s, 985w, 928w, 889w, 824s, 426w, 407m, 390w, 366w, 343w, 316m, 295m, 274m.

[Ag_4(3-aminopyridine)$_4$(NO_3)$_4$]$_n$ (3). To a 10 ml aqueous solution of silver nitrate (0.20 g. 1.18 mmol), 0.19 g. (2.0 mmol) of 3-aminopyridine in 15 ml ethanol were added. Further, 2–3 drops of 0.1 M nitric acid were added with continuous stirring. The solution became clear and was filtered off 2 or 3 times and allowed to stand for at least 3 weeks. Yellowish crystals suitable for X-ray measurement were collected and dried in air, producing a yield of about 85%. Analytical data (%): Calculated: C, 22.74; H, 2.29; N, 15.91; Ag, 40.86. Found: C, 22.62; H, 2.33; N, 16.00; Ag, 40.90. IR, KBr disc (cm^{-1}): 2898w, 2321s, 2257w, 2137w, 2122w, 2079w, 2009w, 1936w, 1915w, 1861w, 1764vs, 1744s, 1711s, 1694s, 1677s, 1659vs, 1625vs, 1585s, 1553s, 1468s, 1429w, 1388s br, 1299br, 1259s, 1195s, 1133s, 1093w, 1046s, 1017s, 896s, 824m, 799vs, 754vs, 701w, 681vs, 664s, 631vs, 532s, 496s, 388s, 366s, 344s, 330s, 317s 294w, 271vs.

Testing of antimicrobial activity

Antimicrobial activities of **1–4** were determined according to the recommendations of NCCLS[40] by the use of a broth microdilution method. Minimum inhibitory concentrations (MICs) for the tested compound were conducted using five standard Gram-positive bacteria (*Bacillus subtilis* ATCC 31324, *Micrococcus luteus* ATCC 10240, *Sarcina lutea* ATCC 10773, *Staphylococcus aureus* ATCC 6538) and eight Gram-negative bacteria (*Bordetella bronchiseptica* ATCC 4617, *Escherichia coli* ATCC 8739, *Klebsiella pneumoniae* ATCC 15050, *Proteus mirabilis* ATCC 12453, *Salmonella typhi* ATCC 3112, *Serratia marcescens* ATCC 13880, *Shigella sonnie* ATCC 11060, *Pseudomonas aeruginosa* ATCC 9027) in addition to one yeast (*Candida albicans* ATCC 8731).

The test materials were dissolved in DMSO. The highest concentration used was 256 μg cm^{-3}. The inoculum was 10^5 cfu ml^{-1} for bacteria and 10^4 CFU/ml for the yeast. Bacteria were cultured in Mueller Hinton Broth (MHB) for 24 h at 35 °C and the yeast in Glucose Peptone Broth (GPB) for 48 h at 30 °C. The MIC value corresponds to the lowest concentration that inhibited bacterial growth.

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