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Synthesis, Characterization, Crystal Structure and Antimicrobial Evaluation of a Novel –M–X–M–X– Type Infinite Chain 1D Cu(II) Complex with Eflornithine Hydrochloride Hydrate as Ligand

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Abstract A novel –M–X–M–X– type infinite chain 1D copper(II) complex of Eflornithine, Dichloro-[2-amino-5-ammonio-2-(difluoromethyl)pentanoate]copper(II) hydrate, $[Cu(C_6H_{12}F_2N_2O_2)Cl_2]\cdot H_2O$ **1** has been synthesized and characterized by elemental analysis, spectroscopic techniques (UV/Vis and FT-IR), TGA and X-ray diffraction. Single-crystal X-ray diffraction analysis of the complex **1** showed the structure to be monoclinic with space group *Cc*, a = 13.1295(15) Å, b = 12.1859(14) Å, c = 8.1927(9) Å, β = 118.359(3) Å, V = 1153.5(2) $Å^3$, Z = 4. The complex exhibits a quadratic planar coordination of the Cu-atom. The Cu(II) centre is coordinated by two chloride atoms, an oxygen atom of the carboxyl- and a nitrogen atom of the amino-group, respectively, forming a quadratic planar geometry. The terminal amino group of the ligand is protonated to form NH_3^+ while the carboxylic moiety is deprotonated to form Zwitterionic eflornithine ligand, with the coordination of the metal at the nitrogen atom of the second amino group. The compound has –M–X–M–X– infinite 1D chain polymeric structure. Two neigbouring Cu(EFL)Cl chain units are bridged by an Cl^- ion, forming a –Cu–Cl–Cu–Cl– linear chain structure along C-axis. The antibacterial activities of the complex on *Escherichia coli* (*E. coli*), *Staphylococcus aureus* (*S. aureus*) and *Pseudomonas aeruginosa* (*P. aeruginosa*) were investigated and found to be active at higher concentration than the parent ligand.

Keywords Eflornithine hydrochloride hydrate · Crystal structure · Zwitterions · TGA · Spectra · Antibacterial activity

1 Introduction

Human African trypanosomiasis is invariably fatal unless treated. The disease progresses from haemolymphatic infection (first stage disease), which is characterized by fever, headaches, joint pains and itching to meningoencephalitic (neurological phase) (second stage) which begins when the parasite invades the central nervous system. Disruption of the sleep cycle is a leading symptom of this stage [1]. Tryptophol is a chemical compound that induces sleep in humans and this is produced by the Trypanosoma in sleeping sickness [2]. Other neurological symptoms include confusion, tremor, general muscles weakness, paralysis of a limb [3]. Damage caused in the neurological phase is irreversible [4]. Most patients with second stage disease are treated with a series of intravenous injections of melarsoprol. This drug has been used since 1949 but is associated with severe toxic effects, in particular a reactive encephalopathy, which affects 5–10 % of patients, with 10–70 % of these cases dying [5, 6]. The encephalopathy cannot be predicted, prevented, or managed satisfactorily, despite half a century of investigations. Melarsoprol related death rates are about 6 % [7]. An additional concern is the increase in treatment failures with melarsoprol, as high as 30 %, reported in several foci in

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Uganda, Sudan, Democratic Republic of Congo, and Angola [8–10]. Eflornithine initially evaluated for the treatment of cancer, is the only alternative drug registered for the treatment of second stage human African trypanosomiasis especially West Africa form. The drug exerts a trypanostatic effect by inhibiting the parasite's ornithine decarboxylase, an enzyme needed for the synthesis of polyamines, themselves involved in cell multiplication and differentiation [11–13]. Adverse effects of Eflornithine include seizures, gastrointestinal disorders, and myelosuppression. A major disadvantage of the drug is the labour intense mode of its administration, requiring one intravenous infusion every 6 h for 14 days (56 infusions in total). Even though, Eflornithine is considered as the safer drug to treat Human African Trypanosomiasis (HAT), the difficulties in logistics as stated above actually necessitate urgent need for alternative therapy.

In search for a pharmacological control of HAT disease, metal complexes appear to be a promising new approach [14, 15]. The use of metal complexes as pharmaceuticals, particularly modification of existing drug by coordination to metal centre has shown promising results recently [16, 17]. The efficacy of therapeutic agent is known to be enhanced upon coordination to metal ion [18]. Metal ions are electron deficient, whereas most biological molecules such drug and protein are electron rich. The attraction between these opposite charges leads to a general tendency for metal ions to bind and interact with biological molecules [19]. Copper was chosen for its importance in biological and physiological activities that mediate a multitude of chemical reaction needed for life [20–22]. Copper complexes of various pharmaceutical active ingredients are reported in the literature [23–27]. It is interesting to state that little has appeared in the literature on antitrypanosomiasis metal complexes particularly Eflornithine hydrochloride.

In continuation of our studies coordination of metal with biologically important ligand, we report the first crystal structure of zwitterion novel copper complex containing Eflornithine hydrochloride hydrate as ligand (Fig. 1).

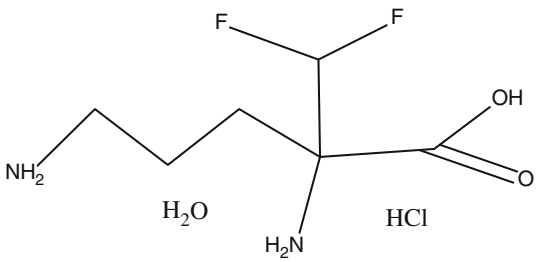


Fig. 1 Molecular structure of Eflornithine hydrochloride hydrate

2 Experimental Section

2.1 Materials

The Eflornithine hydrochloride hydrate was commercially obtained and used without further purification. Hydrated metal salts ($CuCl_2{\cdot}2H_2O$), used for complexation was obtained from British Drug House (BDH) Poole, England.

2.2 Synthesis of the Complex

*2.2.1 Synthesis of $[Cu(C_6H_{12}F_2N_2O_2)Cl_2]{\cdot}H_2O$ **1***

This complex was synthesized by adding to a solution of Eflornithine hydrochloride hydrate (0.2367 g, 1 mmol) in distilled water (10 ml), a solution of $CuCl_2{\cdot}2H_2O$ (0.1705 g, 1 mmol) in methanol (10 ml). The mixture was stirred for 1 h, the blue precipitate formed was separated out by filtration and washed with methanol (Scheme 1). Single blue crystal suitable for X-ray analysis was obtained by vapour diffusion at room temperature of methanolic solution of complex with hexane as antisolvent.

M. wt: 334.63 $gmol^{-1}$, Yield: 95.8 %, M. pt: 170–172 °C, Anal. Calc for $C_6H_{14}Cl_2CuF_2N_2O_3$ (%): C 21.54; H 4.22; N 8.37; Found %: C 21.46; H 4.30; N 8.29. IR (KBr pellet, cm^{-1}) 3,553, 3,491, 3,242, 3,142, 3,032, 2,936, 2,581, 2,481, 1,651, 1,600, 1,453, 1,373, 1,303, 1,281, 1,207, 1,119, 1,073, 1,042, 976, 897, 772, 664, 604, 569, 505, 434. Uv–Vis (distilled water) nm(cm^{-1}): 220(45,455), 348(28,736), 660(15,152).

2.3 Physical Measurement

The C, H and N analyses were performed on Carlo Erba Model EA1108 elemental analyzer from micro analytical laboratory of Medac Limited UK. IR spectra on the range of 4,000–400 cm^1 were obtained from samples in the form of KBr pellets using FTIR-8501 Schimadzu Spectrometer. Thermogravimetric analysis (TGA) was performed using a TA instrument TAQ-500. Sample of 1-2 mg was heated at 10 °C min^{-1} under nitrogen gas flow (50 ml min^{-1}).

Electronic absorption spectra (200–1,100 nm) were recorded using JENWAY 6405 Uv/Vis spectrophotometer. The melting points were determined on MPA100 Optimelt Automated Melting Point System.

2.4 Crystallographic Data Collection and Structural Analysis

For complex **1** single crystal suitable for X-ray crystallography were obtained by slow vapour diffusion of

Scheme 1 Synthesis of **1**

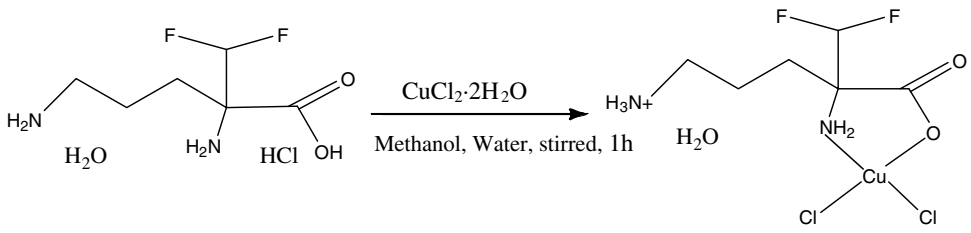


Table 1 Crystal data and structure refinement for **1**

Empirical formula	$C_6H_{14}Cl_2CuF_2N_2O_3$
Formula weight	334.63
Temperature/K	100.0
Crystal system	monoclinic
Space group	*Cc*
a/Å	13.1295 (15)
b/Å	12.1859 (14)
c/Å	8.1927 (9)
β/°	118.359 (3)
Volume/Å^3	1,153.5 (2)
Z	4
ρ_{calc} mg/mm^3	1.927
m/mm^{-1}	2.377
F(000)	676.0
Crystal size/mm^3	0.38 × 0.282 × 0.207
Radiation	MoKα (λ = 0.71073)
2θ range for data collection	4.858–77.6°
Index ranges	$-22 \le h \le 22$, $-21 \le k \le 21$, $-14 \le l \le 14$
Reflections collected	26,709
Independent reflections	6,101[R(int) = 0.0240]
Data/restraints/parameters	6,101/2/169
Goodness-of-fit on F^2	1.090
Final R indexes [I >=2σ (I)]	$R_1 = 0.0158$, $wR_2 = 0.0400$
Final R indexes [all data]	$R_1 = 0.0162$, $wR_2 = 0.0404$
Largest diff. peak/hole/e Å^{-3}	0.56/−0.47
Flack parameter	−0.010 (2)

Table 2 Selected bond length (Å) and angles (°) for complex 1

Cu1–Cl1	2.2324 (3)
Cu1–Cl2	2.2834 (3)
Cu1–O2	1.9469 (8)
Cu1–N1	2.0269 (9)
O1–C1	1.2376 (12)
O2–C1	1.2841 (12)
N1–C2	1.4830 (13)
N2–C5	1.4966 (15)
F1–C6	1.3673 (13)
F2–C6	1.3136 (14)
Cl1–Cu1–Cl2	94.903 (12)
O2–Cu1–Cl1	175.81 (3)
O2–Cu1–Cl2	86.21 (3)
O2–Cu1–N1	83.16 (3)
N1–Cu1–Cl1	95.39 (3)
N1–Cu1–Cl2	168.50 (2)
C1–O2–Cu1	117.81 (7)
C2–N1–Cu1	109.60 (6)
O1–C1–O2	124.54 (9)
O1–C1–C2	119.96 (9)
O2–C1–C2	115.36 (8)
N2–C5–C4	111.52 (9)
N1–C2–C1	109.13 (9)
N1–C2–C3	110.11 (8)
N1–C2–C6	111.20 (8)
C3–C2–C1	108.22 (8)
C6–C2–C1	108.59(8)
C6–C2–C3	108.50(8)
F1–C6–F2	105.84 (9)
F1–C6–C2	110.14 (9)
F2–C6–C2	109.80 (8)

methanolic solution of complex with hexane as antisolvent. Details of the crystal parameters, data collection and refinements were listed in Table 1. Data were collected on a Bruker D8 Venture Dual Source diffractometer equipped with a CMOS-detector using graphite-monochromated Mo Kα(γ = 0.71073 Å) radiation at 100 K. The structure was solved by Charge Flipping using SUPERFLIP [28] and refined by full-matrix least-squares methods based on F^2 using SHELXL [29]. Molecular graphics or complete structure solution, refinement and analysis program was achieved using OLEX2 [30]. Crystal data and refinement details are listed in Table 1. Table 2 lists selected molecular parameters.

2.5 Antibacterial Experiments

A total of three clinical bacteria isolates*: E.coli*, *S. aureus* and *P. aeruginosa* were collected from University of Ilorin Teaching Hospital (UITH), Nigeria for antibacterial screening. Standardized sensitivity text agar (Lab M, UK) was used for the antibacterial assay. The three clinical bacteria isolates were challenged with varying concentrations of the metal complex using the agar diffusion technique and zones of inhibition were interpreted using

standard recommendation National Committee for Clinical Laboratory Standards (NCCLS, 2006) [31].

2.5.1 Minimum Inhibitory Concentration MIC

MIC of the samples was determined using the broth dilution technique. Nutrient broth was seeded with standardized inocula of the test organisms. These were challenged with varying concentrations of the Copper II complex and Ligand (EFL) samples.

For the antimicrobial susceptibility testing, ten clinical antibiotics with their concentrations given in parentheses were used as control as recommended by the National Committee for Clinical Laboratory Standards (NCCLS, 2006) [31]. The antibiotics used to challenge *P. aeruginosa* and *E. coli* being gram negative organisms were ciprofloxacin (10 μg), gentamycin (10 μg), perfloxacin (30 μg) and tarivid (10 μg). Those used for *S. aureus* a gram positive organism were erythromycin (30 μg), gentamycin (10 μg), augumentin (30 μg), chloramphenicol (10 μg), cotrimoxazole (10 μg), streptomycin (30 μg) and ciprofloxacin (10 μg).

3 Results and Discussions

The preparation of EFL-copper(II) complex (EFL = $C_6H_{12}F_2N_2O_2$) can be represented by general scheme thus:

$$[(C_6H_{12}F_2N_2O_2)]\cdot HCl\cdot H_2O + CuCl_2\cdot 2H_2O \xrightarrow[[MeOH,H_2O]]{\text{stirred/reflux}} [Cu(C_6H_{12}F_2N_2O_2)Cl_2]\cdot H_2O$$

The complexes are generally soluble in distilled water and DMSO, but insoluble in common organic solvents. The elemental analysis result of the complex is in good agreement with the formula $[Cu(C_6H_{12}F_2N_2O_2)Cl_2]\cdot H_2O$ and confirmed by X-ray crystal structure of **1**.

Determination of stoichiometric ratio using Job's method suggested mole ratio 1:1 metal to ligand. The complex consists of metal ion which coordinates through the nitrogen atom of the amino and oxygen atom of the carboxylate groups of the ligand with two chloride ions to form tetrahedral structure.

The complex formed Zwitterionic structure. The terminal amino group of the ligand is protonated to form NH_3^+ while the carboxylic moiety is deprotonated to form Zwitterionic eflornithine ligand, with the coordination of the metal at the nitrogen atom of the second amino group. This finding is in agreement with our previous work on metal complex of quinine in which quinine ligand is protonated to form Zwitterionic ligand [32].

The structure can also be compared with a molecular L-histidinium trichlorozincate[L-histidine H^+] $ZnCl_3$. This is an example of protonation/deprotonation species N–H and O–H stretching [33]. Protonation at the amino group removes the free lone pair electron of the nitrogen atom and this limits the hydrogen bonding of the N-terminus to a donor only site [34].

Water is attached to one of the three hydrogen atoms of the protonated amino group. The formula of the structure gives a net formula charge of −1, the excess negative charge of −1 is then balanced by protonation of the Eflornithine ligand as given in the formula.

3.1 Infrared Spectra Characterization

The infrared spectra of the metal complex in the far IR region 4,000–400 cm^{-1} was compared with that of the ligand as shown in Fig. 2. The infra-red spectra of the complex was found to be different from that of the ligand and showed either a shift or disappearance of some characteristic frequencies and appearance of some new frequencies. In the ligand two amino groups are present. The terminal one is protonated and the second is involved in coordination with copper ion.

The absorption band at 3,242–3,142 cm^{-1} assigned to the N–H stretching is due to protonation of terminal amino group to form NH_3^+. This is evidenced by the appearance of two characteristic absorption bands between 1,600 and 1,453 cm^{-1}, one is at 1,600–1,512 cm^{-1} representing asymmetric bending vibration and another at 1,452–1,303 cm^{-1} representing symmetric vibration mode of NH_3^+ [35, 36]. The sharp and medium intensity based at 3,381 cm^{-1} (assigned to N–H stretching in the ligand) shifted to 3,491 cm^{-1}. This is

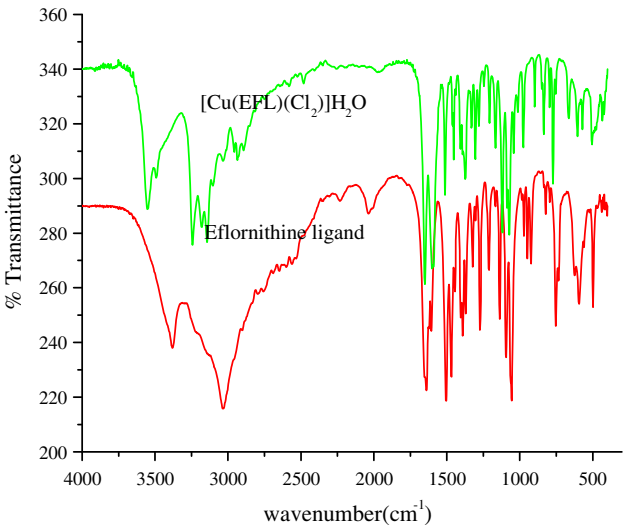


Fig. 2 FT-IR spectra of Eflornithine ligand and $[Cu(EFL)Cl_2]\cdot H_2O$ complex

probably due to the involvement of second NH_2 group in coordination with the copper ion [37].

A strong band observed at 3,553 cm^{-1} is assignable to $\sqrt{}$(OH) lattice water [38, 39] which is supported by the bending mode at 1,650 cm^{-1}. Hydrogen bonding between the NH of the NH_3^+ of the ligand and OH of the water shows peak at 2,581 and 2,481 cm^{-1}.

In the IR spectrum of the free, Eflornithine ligand there is a strong absorption band at 1,639 cm^{-1} for the COOH group. In the Cu (II) complex, this absorption band is absent due to deprotonation and the band due to asymmetric stretch vasym(COO^-) and the symmetric stretch vsym(COO^-) are observed at 1,651 and 1,373 cm^{-1} respectively [40]. The difference vasym(COO) and vsym(COO^-) being 278 cm^{-1} can be taken as a proof of unidentate coordination of the carboxylate group to the central atom [41]. This is in good agreement with the results obtained from X-ray diffraction measurements. The νC–O stretching frequency in C–O–H observed at 1,273 and 1,211 cm^{-1} in the free ligand has shifted to 1,280 and 1,246 cm^{-1} in the spectra of all complexes due to coordination of OH via deprotonation [42]. There is no change in position and intensity of absorption band at 1,281 cm^{-1} due to ν(C–F) in eflornithine ligand after coordination. This indicates that fluorine atoms are not involved in coordination to the metal. The peak position is the same in other fluorine containing compounds [19].

The low frequency skeletal vibration due to M–O, M–N and M-Cl stretching provide direct evidence for complexation. The bands in the 569, 505 and 434 cm^{-1} have been assigned to ν (M–O) and ν (M–N) vibrations respectively [43, 44].

3.2 Electronic Spectra

The UV–VIS spectrum of Eflornithine hydrochloride hydrate showed absorption peaks at wavelengths between 218 and 314 nm which are assigned to II–II*, n–II* inter ligand transition. This band is shifted to higher energy in the complexes. The low intense band (348–355 nm) found in complexes is assignable to ligand-to-metal charge transfer (LMCT) [45, 46] transition. The blue crystal of Cu (II) exhibited another broad band at 660 nm which is attributed to d–d transition ($^2T_2$–^2E) which is an evidence of distorted tetrahedral structure.

3.3 Thermogravimetric Analysis

Thermogravimetric analysis curve of the complex **1** is given in Fig. 3. Thermal analysis shows that the compound is stable at room temp. The thermal behavior of the complex was followed up to 400 °C. In the first stage of thermal decomposition the complex starts to lose one water molecule between 118 and 160 °C with the experimental loss of 5.89 % (calc. mass loss 5.39 %).

The second stage between 160 and 235 °C is related to the release of one eflornithine ligand (found = 55.58 %, calc. = 54.50 %). The experimental mass loss agrees with the calculated for the two decomposition stages.

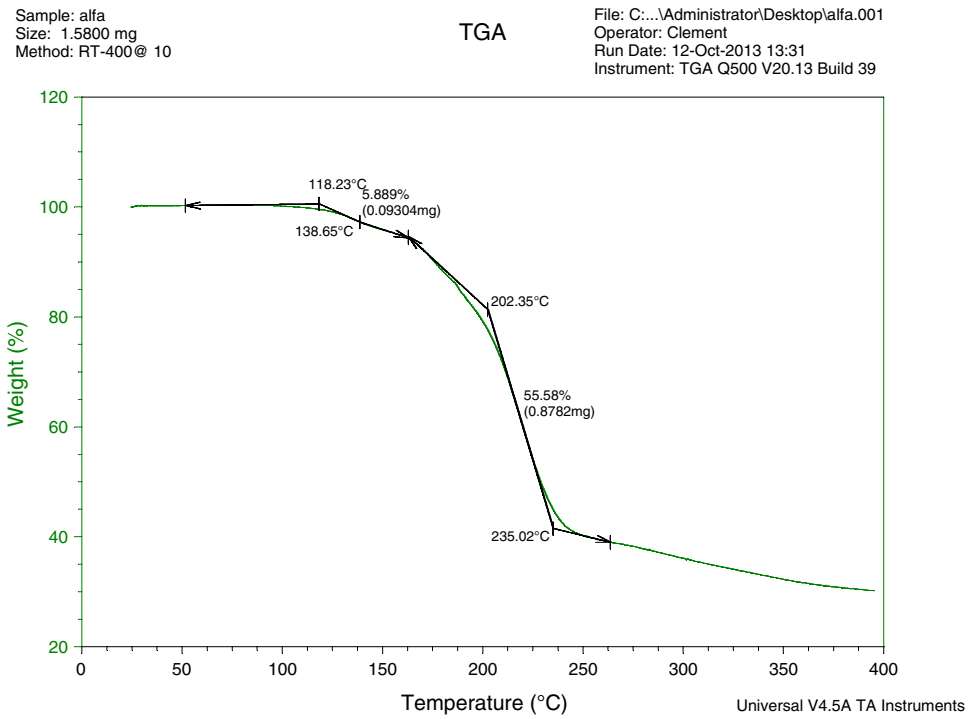


Fig. 3 The TGA curve of the $[Cu(C_6H_{12}F_2N_2O_2)Cl_2]\cdot H_2O$

3.4 Description of the Crystal Structure of Complex **1**

The Ortep representation of the structure of **1**, indicating atom numbering scheme, is shown in Fig. 4 and selected bond length and bond angles are listed in Table 2. The complex exhibits a quadratic planar coordination of the Cu-atom. The Cu(II) centre is coordinated by two chloride atoms [d = 2.2834(3) and 2.2324(3) Å], an oxygen atom [d = 1.9469(8) Å] of the carboxyl- and a nitrogen atom [d = 2.0269(8) Å] of the amino-group, respectively, forming a quadratic planar environment in the first coordination sphere. Another chloride ion of a neighboring complex molecule (1) is located at a distance of 2.948(3) Å from the copper atom, leading to a 4 + 1 coordination in a square-pyramidal fashion and interconnecting the complex molecules **1** to infinite linear chains running along the crystallographic c-axis (cf. Fig. 5). The crystal structure contains one water molecule, connecting three molecules of **1** via two oxygen atoms of the carboxyl-groups and one hydrogen-atom of the ammonium-group, respectively.

All hydrogen atoms attached to N were refined freely, the hydrogen atoms attached to C and O were refined with the riding model. The Cu–N (2.023 Å), Cu–O (1.947 Å) and Cu–Cl (mean = 2.257 Å) are normal and are similar to those observed for copper(II) complexes of related biological ligands [47–50]. As expected Cu–N (2.023 Å) bonds are larger than the Cu–O (1.947 Å) one, this observation is similar to the study reported earlier which involved coordination of copper via amino nitrogen and carboxylate oxygen atoms of the square planar [51]. All the planar angles are distorted to a slight extent, the square planar angles are Cl1–Cu1–Cl2 94.9 (12)°, O2–Cu1–Cl2 82.21 (3)°, O2–Cu1–N1 83.16 (3)° and N1–Cu1–Cl1 95.39 (3)° as compared to ideal square planar angle of 90°, indicating that the coordination geometry is quadratic planar [52]. The bonds O2–Cu1–Cl1 and N1–Cu1–Cl2 have angles of 175.81 (3)° and 168.50 (2)° respectively which are close to 180° in line with the quadratic planar arrangement. The compound is halogen-bridged metal complexes. It has –M–X–M–X– infinite 1D chain polymeric structure. Two neigbouring Cu(EFL)Cl chain units are bridged by an Cl^- ion, forming a –Cu–Cl–Cu–Cl– linear chain structure along C-axis (Fig. 5). The chain structure of MXM is stabilized with the ligand by hydrogen bonds between $–NH_3^+$ (ammonio ion) and oxygen atoms of water. This finding is in close agreement with similar studies by previous worker [53].

Protonation of N2 results in slight increase in N–C–C bond angle which are greater in protonated amine bond angles (N2–C5–C4111.52 (9)°) as compared with unprotonated amino group N1–C2–C1 109.13 (7)° probably due to shift of Ione pair electron of the nitrogen atoms towards their protons [54]. Furthermore, the N–C distances are slightly different. The N2–C5 (1.496 Å) of the protonated amine is >N1–C2 (1.4830 Å) of the unprotonated amino group, this may be due to electron withdrawing behavior of

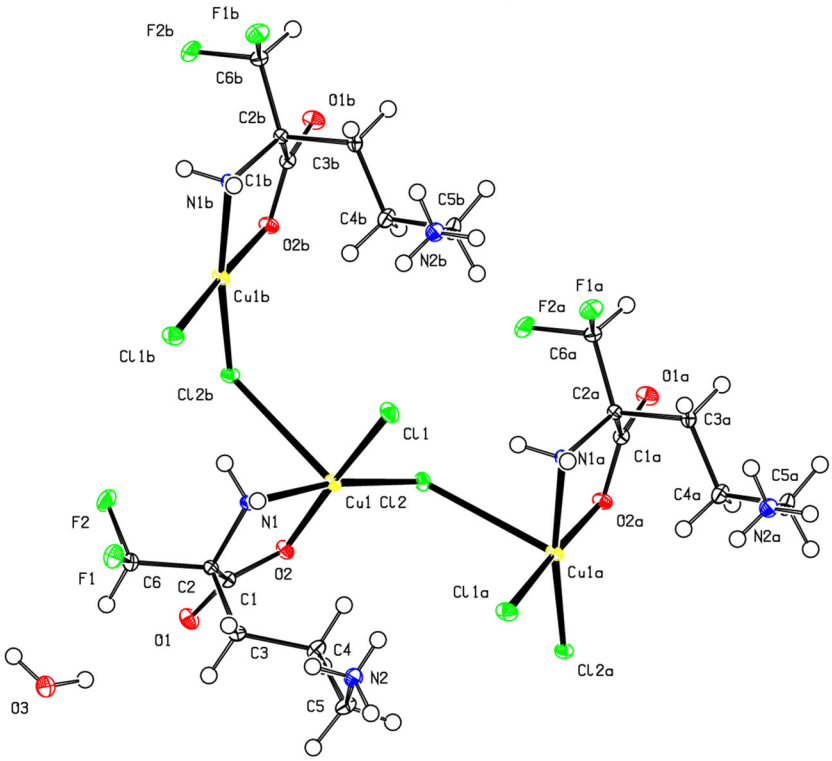


Fig. 4 Ortep diagram of molecular structure of 1 with numbering scheme adopted. *Ellipsoids* are shown at 50 % probability level

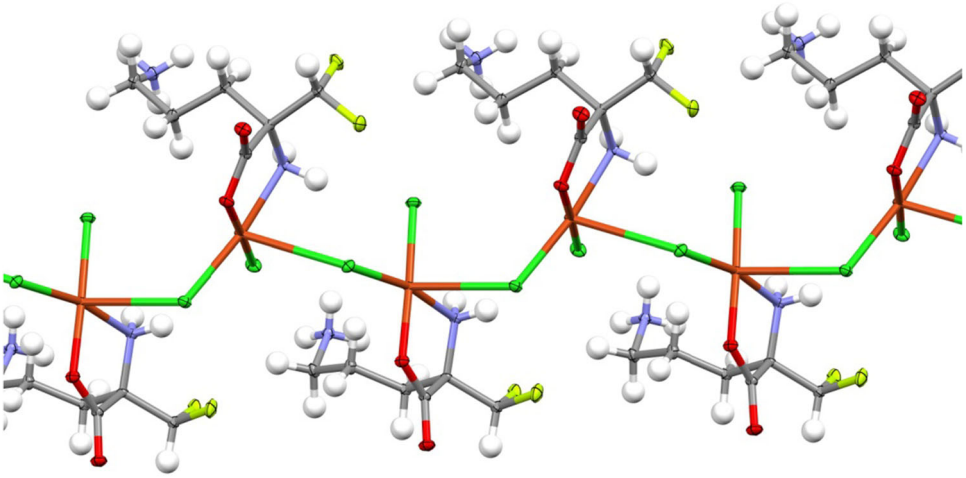


Fig. 5 Polymeric chains showing –Cu–Cl–Cu– infinite 1D structure of **1**

Table 3 Antibacterial activities of ligand (EFL) at different concentrations on test organisms

Concentration (gL^{-1})	Zones of inhibition (mm)		
	E. coli	*S. aureus*	*P. aeruginosa*
0.0001	0.0	0.0	0.0
0.001	0.0	0.0	0.0
0.01	0.0	0.0	0.0
0.1	1.2	1.0	1.2
1.0	1.8	1.2	1.4

Table 4 Antibacterial activities of Copper Complex at different concentrations on test organisms

Concentration (gL^{-1})	Zones of inhibition (mm)		
	E. coli	*S. aureus*	*P. aeruginosa*
0.0001	0.0	1.2	0.0
0.001	1.2	1.4	1.1
0.01	1.6	2.0	1.4
0.1	2.0	3.2	1.8
1.0	3.2	4.2	2.8

Table 5 Antibacterial activity of different antibiotics used as control on *P. aeruginosa and E.coli*

Antibiotic	Zone of Inhibition (mm)	
	P. aeruginosa	*E.coli*
Ciprofloxacin	19.3 ± 0.5	24 ± 0.8
Gentamycin	0.00	0.00
Pefloxacin	0.00	22.6 ± 1.2
Tarivid	0.00	19.7 ± 1.0

Table 6 Antibacterial activity of different antibiotics used as control on *S. aureus*

Antibiotic	Zone of inhibition (mm)
Erythromycin	17.0 ± 0.9
Gentamycin	18.0 ± 0.6
Augumentin	11.3 ± 1.1
Chloramphenicol	22.0 ± 0.7
Cotrimoxazole	18.0 ± 1.2
Streptomycin	17.6 ± 1.1
Ciprofloxacin	11.2 ± 1.0

the proton leading to increase of N–C–C angle and lengthening of the N–C bond [19].

3.5 Antibacterial Results

The results of the antibacterial screening as contained in Tables 3 and 4 show appreciable activity of the drug metal complexes compare to the ligand when challenged with test organisms at varying concentrations. Copper complex was effective at virtually all concentrations used except against *E. coli* and *P. aeruginosa* at 0.0001 gL^{-1}. Highest susceptibility to Copper complex was recorded by *S. aureus* with clearance zone of 4.2 mm at 1.0 gL^{-1}.

The results show that all the metal-drug complex possesses a measure of antibacterial activity against all the organisms tested. The results also agree with the findings of other researchers [55, 56] that antibacterial potency is usually concentration dependent.

The data as shown in Tables 5, 6 and 7 also revealed that the activity of the Ligand EFL was bacteriostatic against all the organisms tested, while the activity of the copper (II) complex was bacteriostatic against *E. coli* and *P. aeruginosa* but bactericidal against *S. aureus* at 0.0001 g/L concentration.

Table 7 Minimum inhibitory concentration of the copper (II) complex and ligand (EFL) samples against test organisms

Test organisms	Minimum inhibitory concentration (g/L)	
	Ligand EFL	Copper(II) Complex
Escherichia coli	0.04	0.0002
Staphylococcus aureus	0.03	0.00004
Pseudomonas aeruginosa	0.10	0.001

4 Conclusions

The complex **1** was synthesized by reacting eflornithine hydrochloride hydrate with $CuCl_2{\cdot}2H_2O$ in methanol/water. A quadratic planar structure was assigned to the complex by analyzing elemental analysis, FTIR, electronic spectra, TGA and X-ray crystallographic. To the best of our knowledge, the single X-ray crystal structure of copper complex obtained represents the first copper crystal structure of eflornithine hydrochloride hydrate which is zwitterionic with –M–X–M–X– infinite chain 1D structure. The screening data revealed that the complex exhibits more efficient antimicrobial activity than the free ligand. These findings may lead to development of novel metal based drugs.

5 Supporting Information Available

CCDC 969579 contains the supplementary crystallographic data for this paper. These data can be obtained free of charge via http://www.ccdc.cam.ac.uk/conts/retrieving.html (or from the Cambridge crystallographic Data Centre, 12, Union Road, Cambridge CB2 1EZ; fax +441223336033).

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