Research Article

Synthesis, Characterization, and Biological Activity Studies of Copper(II) Mixed Compound with Histamine and Nalidixic Acid

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Received 7 February 2009; Accepted 2 March 2009

Recommended by Virtudes Moreno

A mixed copper complex with deprotonated nalidixic acid (nal) and histamine (hsm) was synthesized and characterized by FTIR, UV-Vis, elemental analysis, and conductivity. The crystal structure of [Cu(hsm)(nal)H2O]Cl·3H2O (chn) showed a pentacoordinated cooper(II) in a square pyramidal geometry surrounded by two N atoms from hsm, two O atoms from the quinolone, and one apical water oxygen. Alteration of bacterial DNA structure and/or associated functions in vivo by [Cu(hsm)(nal)H2O]Cl·3H2O was demonstrated by the induction of a recA-lacZ fusion integrated at the amyE locus of a recombinant Bacillus subtilis strain. Results from circular dichroism and denaturation of calf thymus DNA (CT-DNA) suggested that increased amounts of copper complex were able to stabilize the double helix of DNA in vitro mainly by formation of hydrogen bonds between chn and the sugars of DNA minor groove. In vivo and in vitro biological activities of the chn complex were compared with the chemical nuclease [Cu(phen)(nal)H2O]NO3·3H2O (cpn) where phen is phenanthroline.

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1. Introduction

Since Lescher and col. prepared the nalidixic acid in 1962 [1], the synthesis of new quinolones continues (Figure 1). First generation antibiotics of quinolone family are effective against gram-negative bacteria usually found in light urinary diseases [2]; examples of these drugs are Nalidixic acid, Oxolinic acid and Cinoxacin. The fluoroquinolones, second generation, like ciprofloxacin are also effective against gram-positive bacteria; they can be used in urinary, skin, or respiratory infections [3]. Levofloxacin and sparfl Roxacin are examples of third generation quinolones, also known as fluoroquinolones, but they are more effective against gram-positives organism. They are used in treatment of pneumonia, bronchitis, sinusitis, and gonorrhea infections.

Fourth generation quinolones include the trovofloxacin with an effectiveness against anaerobic organism [4]. Quinolones inhibit the bacterial DNA synthesis [2], and there are several hypotheses to explain their mechanism of action. One of these hypothesis suggests the inhibition of subunit A of DNA-gyrase in presence of ATP [5–7]. Another hypothesis supports the existence of a cooperative bond between the quinolone–DNA–DNA-gyrase [8–11]. Also, it is suggested that quinolone may form coordination complexes with a transition metal ion present in the cytoplasm or with a metal biocomplex; this metal ion could be copper(II) [12].
Copper in biological systems is usually found surrounded by imidazole moieties from histidine residues [13, 14]. Copper concentration increases when a disease like arthritis or a neoplasia is present; therefore under the stress caused by the disease, copper may be available for coordination with some endogenic or exogenic compounds like peptides and drugs, respectively. With this in mind, the interactions of different quinolones with copper and other metal ions have been investigated for years [15]. The hsm-copper(II) system may be used to mimic the environment of this metal ion in some biological systems. The histamine molecule is a good ligand, which contains not only N atoms (from imidazole ring and aliphatic ammine) but also hydrogen atoms that are good for hydrogen bond formation and therefore are useful in molecular recognition. Because of these characteristics some histamine complexes with copper have been reported recently [16, 17]. In the present work we reported the synthesis, characterization, and biological activity results of a copper mixed complex (see Scheme 1), with hsm and nalidixic acid. This study contributes to get better knowledge how a metal ion is required to carry the quinolones to their site of action and also to clarify how metal surroundings affect the biological action of quinolones drugs.

2. Experimental

2.1. Materials and Physical Measurements. The histamine dihydrochloride, nalidixic acid (Sigma-Aldrich products), and CuCl₂ · 2H₂O (J. T. Baker products) were used as provided. Far-IR spectra were taken on a Bruker IFS-55 spectrophotometer as polyethylene pellets. Medium-IR spectra were carried out on Perkin-Elmer spectrophotometer model FT 1600 as KBr pellets. Electronic spectra were recorded on an Agilent 8453 UV-Vis spectrophotometer using water as
2.2. Synthesis of Mixed Complexes. [Cu(hsm)(nal)H2O]Cl · 3H2O: Nalidixic acid (232.2 mg, 1 mmol) was dissolved by Desert Analysis, Organic Microanalysis, Tucson AZ, USA. immediately before used. Elemental analyses were performed with NaOH (40 mg, 1 mmol) in 70 mL of water. This solution was added into a previously prepared equimolar mixture of histamine dihydrochloride (184.07 mg, 1 mmol) and CuCl2 · 2H2O (170.48 mg, 1 mmol) dissolved in a total volume of 15 mL of water. The final solution was brought to pH 7.5 and left for slow crystallization in a refrigerator (4°C). Purple crystals suitable for X-ray analysis were isolated. Anal. Calc. for C17H31CuN5O8Cl: C, 38.35; H, 5.87; N, 13.15. Found: C, 39.82; H, 5.50; N, 13.65%. IR (KBr, cm−1): 1634(s), 1607(m), 1522(m), 1501(m), 1469(s), 1388(s), 1287(s), 1222(s), 1207(s), 1154(s), 1117(s), 1047(s), 1032(s), 984(s), 958(s), 896(s), 872(s), 843(s), 786(s), 746(s), 703(s), 653(s), 619(s). Conductivity: 105 Ω−1 cm2 mol−1 in water 10−3 M.

[Cu(phen)(nal)H2O]NO3 · 3H2O was obtained as previously reference indicates [18].

2.3. Crystallographic Studies. A crystal specimen of 0.35 × 0.20 × 0.15 mm3 was selected and mounted on a Siemens P4/PC diffractometer using highly oriented graphite monochromatized Mo-Kα radiation, λ = 0.71073 Å, T = 293 K; none absorption correction was made. The structure was solved by the direct methods (SIR92) and difference Fourier maps and refined by the full-matrix least squares. C21H28Cu1Cl1N5O7, M = 513.43, Blue, regular prism, triclinic crystals, space group, P1, a = 10.4745(17) Å, b = 10.5001(16) Å, c = 11.1374(19) Å, α = 80.4080(10)°, β = 85.1840(10)°, γ = 72.5410(10)°, V = 1151.43(3) Å3, Z = 2, ρcalc = 1.481 Mg/m3, μ = 1.111 mm−1, 4796 reflections collected (1.86 < θ < 25.00°, Rint = 0.0226), Final R indices [I > 2σ(I)], R1 = 0.0455, wR2 = 0.1053, R indices (all data), R1 = 0.0655, wR2 = 0.1161. Selected bonds lengths and bond angles are presented in Table 1. All data are available at Cambridge Crystallographic Data Centre; see supplementary material.

2.4. Biological Test

2.4.1. Organism and Growth Conditions. B. subtilis strain YB-3001 carrying pCCR202 (a recA-lacZ fusion integrated in the amyE locus) was kindly provided by Dr. Ronald E. Yasbin

| Table 1: Selected bond lengths (Å) and bond angles (°) for [Cu(hsm)(nal)H2O]Cl · 3H2O. |
|-----------------|------------------|------------------|
| Bond lengths (Å) | Bond angles (°)  |
| Cu(1)–O(2)      | 1.934(3)         | O(2)–Cu(1)–O(3)  | 91.22(12) |
| Cu(1)–O(3)      | 1.961(2)         | O(2)–Cu(1)–N(3)  | 173.72(14) |
| Cu(1)–N(3)      | 1.966(3)         | O(3)–Cu(1)–N(3)  | 90.39(12)  |
| Cu(1)–N(8)      | 1.996(3)         | O(2)–Cu(1)–N(8)  | 84.84(14)  |
| Cu(1)–O(4)      | 2.344(3)         | O(3)–Cu(1)–N(8)  | 165.77(11) |
| N(3)–C(4)       | 1.385(4)         | N(3)–Cu(1)–N(8)  | 92.14(13)  |
| N(8)–C(7)       | 1.479(5)         | N(3)–Cu(1)–O(4)  | 93.47(13)  |
| O(1)–C(24)      | 1.241(4)         | O(3)–Cu(1)–O(4)  | 95.56(10)  |
| O(2)–C(24)      | 1.264(4)         | N(3)–Cu(1)–O(4)  | 92.41(12)  |
| O(3)–C(14)      | 1.271(4)         | N(8)–Cu(1)–O(4)  | 98.32(12)  |
| C(4)–C(6)       | 1.490(6)         |                  |           |
| C(6)–C(7)       | 1.510(6)         |                  |           |
| C(13)–C(14)     | 1.419(5)         |                  |           |
| C(13)–C(24)     | 1.484(5)         |                  |           |

| Table 2: Experimental melting temperatures (Tm) and difference with the CT-DNA Tm (ΔTm) values as determined from the thermal denaturation profiles of CT-DNA and its interactions with the [Cu(hsm)(nal) H2O]Cl · 3H2O or [Cu(phen)(nal)H2O]NO3 · 3H2O complexes. |
|-----------------|------------------|------------------|
| r               | [Cu(hsm)(nal)H2O]Cl · 3H2O / CT-DNA | [Cu(phen)(nal)H2O]NO3 · 3H2O / CT-DNA |
|                 | Tm (°C)          | ΔTm              | Tm (°C)          | ΔTm              |
| 0.0             | 82.7             | —                | 82.7             | —                |
| 0.096           | 83.5             | 0.8              | 83.4             | 0.7              |
| 0.28            | 84.9             | 2.2              |                   |                  |
| 0.48            | 84.6             | 1.9              | 87.5             | 4.8              |
| 0.77            | 86               | 3.3              | 83.7             | 1                |
| 0.96            | 86.9             | 4.2              |                   |                  |
(University of Nevada, Las Vegas). To propagate this strain, Luria Bertani (LB) medium was used. Chloramphenicol was added to the culture medium at a final concentration of 3 μg/mL.

2.4.2. Induction Experiments. B. subtilis YB-3001 was grown to an optical density of 0.3 at 600 nm, and at this point, the culture was split into 6 subcultures. One of the cultures was used as control, and the other five were supplemented with CuCl₂, nalidixic acid, [Cu(hsm)]₁²⁺, hsm, and [Cu(hsm)(nal)H₂O]Cl · 3H₂O complex to a final concentration of 300 μM. Samples of the culture were collected before and after 5 hours of addition of the compounds and they were processed for β-galactosidase activity as previously described [19, 20]. The β-galactosidase activity is reported in Miller units [21].

2.4.3. Nuclease Activity of Metal Complexes Against a 196 bp DNA Fragment. Experiments to characterize the nuclease activity of the metal complex were performed using as a substrate a 196 bp PCR fragment encompassing part of the open reading frame and the promoter regions of the ytk gene from B. subtilis [22]. Amplification of this DNA fragment was carried out using 0.1 μg of chromosomal DNA from B. subtilis 168 and the oligonucleotide primers 5′-GGGATAAACATGTACGAG-3′ (forward) and 5′-CTTCTGCGACTCCAT CGGCTCTAC-3′ (reverse). Amplification was performed with Vent DNA polymerase (New England Biolabs, Beverly, MA). The 196 bp DNA obtained was purified from low melting point agarose gels as previously described [23].

A typical reaction mixture contained in a final volume of 25 μL: DNA 375 ng, [Cu(hsm)(nal)H₂O]Cl · 3H₂O or [Cu(phen)(nal)H₂O]NO₃ · 3H₂O complexes, 100 μM, and Mercaptopropionic acid (MPA), 7 mM. The reaction mixture was incubated for 50 minutes at 37°C, diluted with loading buffer, which contained 50 mM Tris-acetate buffer, pH 7, glycerol 50% (v/v), and Bromophenol blue as a tracking dye, and loaded on a 2% agarose gel containing 50 mM Tris-acetate buffer, pH 7, and 1 mg/mL ethidium bromide. The gel was run in the same buffer at 90 V. The DNA on the gel was observed and photographed using an Eagle Eye gel documentation system.

2.4.4. Biophysical Studies. Sodium cacodylate hydrate and Calf Thymus DNA (CT-DNA) were purchased from Sigma-Aldrich Chemical Company. CT-DNA was dialyzed at 4°C at 7 mM. The reaction mixture was increasing, the absorbance changes at 260 nm were recorded on a Jasco—715 spectropolarimeter at room temperature under constant nitrogen flush. The wavelength range between 200 and 300 nm was monitored.

All CD spectra were carried out in 5 mM sodium cacodylate, 0.6 M NaCl, pH = 7.1 buffer, using a quartz cell. Similar experiments were made with [Cu(phen)(nal)H₂O]NO₃ · 3H₂O complex. The sodium cacodylate buffer was employed as background.

2.4.6. Melting Temperature Studies. Thermal denaturation experiments were performed in the same buffer as the CD spectra, using quartz cuvettes with an Agilent 8453 UV-visible spectrophotometer equipped with a Peltier system. The chn/CT-DNA molar ratio was r = 0.0, 0.096, 0.28, 0.48, 0.77, and 0.96. After 1 hour of incubation at 37°C, samples were continuously heated at 1°C min⁻¹. As the temperature was increasing, the absorbance changes at 260 nm were recorded. The investigated interval of temperature ranged from 37°C to 90°C. DNA concentration was equal to 1.03 × 10⁻⁴ M. Similar experiments were made with the cpn complex.

3. Results and Discussions

3.1. Structural and Spectroscopic Properties of Mixed Complexes. The molecular structure of [Cu(hsm)(nal)H₂O]Cl · 3H₂O complex of Figure 2 shows a distorted square pyramidal geometry around the copper ion as it is suggested by the distortions parameter that r. Tau-descriptor (r) for five coordination complexes expressed as the difference between the angles of the bonds O(2)–Cu(1)–N(3) and O(3)–Cu(1)–N(8) divided by 60 gives a value of 0.13, being the ideal values of 1 for a trigonal bipyramid and 0 for a square pyramid [25].

The base of the pyramid is formed by two oxygen atoms of the nalidixate ligand (one oxygen of the carboxylate group and other for the keto group, Cu(II)–O(2) = 1.934(3),
Cu(II)–O(3)=1.961(2) Å resp.) and two N atoms of the histamine ligand (one aliphatic nitrogen and other imidazole nitrogen, Cu–N(8) = 1.996(3) Å, Cu–N(3) = 1.966(3) Å resp.). The C(24)–O(1) bond length is longer than the C(24)–O(2) as expected for carboxylic metal coordination. Copper and O(3), O(2), and N(3) are almost coplanar, and they define the mean square plane of the pyramid base (0.6022(4)X + 0.5019(3)Y + 0.6208(3)Z = 16.1191(18)). The major deviations of those atoms are ~0.077 Å whereas the N(8), that is, also forming part of the pyramid base is about 0.244(3) Å above the plane. At apical position a molecule of water is coordinated (Cu–O(4) = 2.344(3) Å). The angle formed between the mean plane of the pyramid base and the apical ligand is 87.73(12)°. The amino group of histamine is coordinated in trans position to the keto group analogous to copper complex reported previously [26]. In Figure 3, it is possible to observe that the packing pattern is largely dictated by π–π stacking forces interaction between the aromatic rings of the nalidixate anion with a distance of 3.771 Å as well as hydrogen bonding interactions since

**Figure 3:** PLUTON plot showing the stacking between nalidixate rings and hydrogen bondings in the crystal of [Cu(hsm)(nal)H2O]Cl · 3H2O complex.

**Figure 4:** Activity of [Cu(hsm)(nal)H2O]Cl · 3H2O for cleavage of plasmid DNA. 375 ng of 196 bp DNA were incubated with (lanes 3, 4) or without (lanes 1, 2) [Cu(hsm)(nal)H2O]Cl · 3H2O (100 μM) or with (lanes 5, 6) [Cu(phen)(nal)H2O][NO3] · 3H2O (100 μM) in presence (lanes 2, 4, 6) or absence (lanes 1, 3, 5) of mercapto propionic acid, (MPA) (7 mM), for 50 minutes at 37 °C.

**Figure 5:** Maximum levels of recA-directed β-galactosidase induction obtained as response of the addition of the [Cu(hsm)(nal)H2O]Cl · 3H2O (chn), [Cu(phen)(nal)H2O][NO3] · 3H2O (cpn) complexes, or some of their molecular components on cultures of B. subtilis YB3001. Percentage indicated as comparison to the highest activity encountered (cpn = 100%).
crystal structure includes an uncoordinated chloride anion and three water molecules that provide crystalline stability through a hydrogen bond network.

The IR spectra of \([\text{Cu(hsm)}\text{(nal)}] \cdot 3\text{H}_2\text{O}\) complex are quite complex due to the presence of numerous functional groups in the molecules; selected signals are listed in Section 2. The mid-infrared spectrum showed bands corresponding to both ligands. A broad band around 3500 cm\(^{-1}\) can be assigned to the O–H stretching vibrations of lattice water molecules. Also between 3261 and 2661 cm\(^{-1}\) some medium bands appeared corresponding to amine and amide vibrations forms. A broad band between 1634 and 1501 cm\(^{-1}\) which is split and includes the vibrations \(v_\text{π(}\text{COO}])\) and \(v_\text{π(}\text{CO})\) is present, showing the interaction of these groups (the 4-oxo and to the 3-carboxylate groups) with the metallic ion. Similar results are observed for far infrared spectrum. At 538 and 503 cm\(^{-1}\) two bands assigned to Cu–NH\(_2\) combination modes appeared, as it had reported previously [26]. The UV-visible spectra showed a broad band centered around 625 nm, that is, observed due to the d-d transitions for Cu(II) corresponding to a typical square pyramidal copper(II) complex with two nitrogen atoms coordinated. In the UV region three intense bands appeared that correspond to the \(\pi−\pi\) transitions of the ligands as showed in similar hsm complex previously reported [26]. It is remarkable the similarity of chemical structure of \([\text{Cu(hsm)}\text{(nal)}] \cdot 3\text{H}_2\text{O}\) complex with \([\text{Cu(phen)}\text{(nal)}] \cdot 3\text{H}_2\text{O}\) complex [18]. While \text{cpn} complex has a desirable planarity due to phenanthroline ligand, on the other hand \text{chn} complex has the possibility to form hydrogen bonding due to histamine ligand.

3.2. Biological Activity Studies of \([\text{Cu(hsm)}\text{(nal)}] \cdot 3\text{H}_2\text{O}\) Complex with \([\text{Cu(phen)}\text{(nal)}] \cdot 3\text{H}_2\text{O}\). Comparing with \([\text{Cu(phen)}\text{(nal)}] \cdot 3\text{H}_2\text{O}\). The ability of the \([\text{Cu(phen)}\text{(nal)}] \cdot 3\text{H}_2\text{O}\) metal complex to interact with DNA in vivo and its capacity to promote the complete degradation of plasmid and chromosomal DNA under reductive conditions has been previously reported [27]. Therefore we investigated whether the \([\text{Cu(hsm)}\text{(nal)}] \cdot 3\text{H}_2\text{O}\) complex has similar biological activity. For this purpose, we investigated here whether \text{chn} complex behaves as a chemical nuclease by inducing the degradation of double stranded DNA under
both, reductive, and nonreductive conditions. As a positive control we used cpn complex at the same concentration. The results shown on Figure 4 revealed that the chn complex does not possess chemical nuclease activity even in the presence of Mercaptopropionic acid (MPA) (Figure 4, lanes 3 and 4). On the other hand, as previously reported the cpn complex behaved as a thiol-dependent chemical nuclease with a complete degradation of DNA at this concentrations (Figure 4, Lane 6) [27].

To investigate the interaction of chn with DNA we took advantage of the bacterial SOB response of the gram-positive microorganism Bacillus subtilis. This response, similar in several aspects to the SOS response of E. coli, is triggered by physicochemical agents which promote alterations in the structure of DNA and when B. subtilis is grown under conditions which induce genetic competence [27—29]. Thus the strain B. subtilis YB3001, containing a single copy of the recA-lacZ fusion integrated at the amyE locus, was treated with [Cu(hsm)(nal)H2O]Cl · 3H2O complex and with each of its components, (CuCl2, hsm, nal, and [Cu(hsm)]2+) [27]. As shown in Figure 5 the levels of β-galactosidase induced by the [Cu(hsm)(nal)H2O]Cl · 3H2O complex were 20% lower than those induced by the analogous [Cu(phen)(nal)H2O]NO3 · 3H2O complex [27]. However it is noticeable that none of the components of the [Cu(hsm)(nal)H2O]Cl · 3H2O complex were able to induce the β-galactosidase activity from the recA-lacZ fusion to levels comparable to those observed for the full complex, neither its activity can be interpreted as an additive effect of the independent components.

Therefore, we can conclude that the complex acts as a whole, being able to cross the cell membranes and interact with the DNA directly.

To investigate the way of [Cu(hsm)(nal)H2O]Cl · 3H2O DNA interaction, the in vitro interaction of chn and cpn with CT-DNA was analyzed by melting temperature and circular dichroism (CD). In Figure 6 it is shown the CD spectra of CT-DNA following additions of increasing amounts of [Cu(hsm)(nal)H2O]Cl · 3H2O.

Results reveal that this complex induces small CD changes. Similar behavior was found for complex [Cu(phen)(nal)H2O]NO3 · 3H2O. It is important to mention that both complexes are CD inactive. The observed changes in the CD spectra suggest that both complexes interact with DNA through the sugar-phosphate bone, in the minor groove. This result is in agreement with the increment in the melting point observed when the complex concentration increases, (see Figure 7) and suggests that the main interaction between the complexes and DNA may be through hydrogen bond interactions. The results showed that at low concentration both complexes increase the Tm of CT-DNA (Table 2). However at higher concentrations a different behavior between both complexes was observed.

This difference between both complexes should be related with the type of coordinated ammine. Being histamine able to form stronger hydrogen bonds, it is reasonable to speculate that when complex concentration increases, more hydrogen bonds will be formed and therefore more stable the double helix will be. On the other hand, when phenantrolmine is the diaminic at low concentration, it is possible that the main interaction between the complex and DNA is dominated by hydrogen bonds with the antibiotic, but when concentration increases, it is possible to have two types of interactions between the complex and DNA, one via hydrogen bonds as stated before and a second one weaker due to the intercalation of the phenanthroline rings, which will be reflected in a destabilization of the double helix. In conclusion, from this study it is possible to say that quinolones behave very similar as ligands; also it is observed that their coordination mode is relatively independent of the type of coordinated diaminmine. However the activity as chemical nuclease is strongly dependent of the diaminmine. Our work suggests that complexes of the quinolone family drugs with copper coordinated to other aminines may be active, even if the nuclease activity is not present as in those complexes with phenantrolmine. It seems that DNA-complex interaction is dominated by hydrogen-bond type, and therefore the design of new potential copper-based drugs should consider this.

References


