Synthesis and Characterization of Some Biologically Active Copper Complexes for Microbial Applications

By

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A thesis submitted in partial fulfillment of the requirements for the degree of Masters of Philosophy in Chemistry

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Declaration

This is to certify that the thesis work entitled **"Synthesis and Characterization of Some Biologically Active Copper Complexes for Microbial Applications"** has been carried out by Md. Ali Azam Khan in the Department of Chemistry, Khulna University of Engineering & Technology, Khulna, Bangladesh. The above thesis work or any part of this work has not been submitted anywhere for the award of any degree or diploma.

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Abstract

In this study, in order to verify our hypothesis amino acid base copper complexes have been prepared for biological application.

Reaction of tcydan and $Cu(ClO_4)_2 \cdot 6H_2O$ with nucleobases (adenine, hypoxanthine and theophylline) gave three tcydan–metal–amino-acid base complexes, $[Cu(tcydan)(ade)].ClO_4.2H_2O$ **(1)**, $[\{Cu(tcydan)\}_2(hypoxanth)]^+.(ClO_4)_3$ **(2)** and $[Cu(tcydan)(theophy)]_3.(ClO_4)_3.2H_2O$ **(3)**. The complexes were prepared in H_2O/CH_3OH or H_2O/CH_3CN media at room temperature under pH 8–9. The crystal structures were determined by X-ray diffraction.

In the structure of complex **1**, the square-pyramidal Cu^{2+} ion binds to an adenine ligand through the deprotonated N(9) and to four nitrogens of a tcydan ligand, and an interligand hydrogen bond is formed between the secondary amino nitrogen of tcydan and the ring nitrogen N(3) of the base.

In complex **2**, two square-pyramidal Cu^{2+} ions bind to a xanthine ligand, one through N(7) with the formation of a hydrogen bond between the exocyclic oxygen O(6) of the base and the secondary amino nitrogen of a tcydan ligand, and the other through the deprotonated N(9) with the formation of a hydrogen bond between N(3) of the base and the amino nitrogen of tcydan.

In the structure of complex **3**, the square-pyramidal Cu^{2+} ion binds to a theophyllinato ligand through N(7) and four nitrogens of a tcydan ligand with the formation of a hydrogen bond between O(6) of the base and amino group of tcydan, as observed in **2** and **3**.

In summary, the adenine complex **1** involves the metal-N(9) bonding with the formation of an intramolecular interligand N(tcydan)-H···N(3) hydrogen bond. On the other hand, the absence of the possible metal bonding to N(7) or N(1) of adenine might be due to a steric repulsion, between amino groups of tcydan and the N(6) amino group when the metal ion binds to N(7) or N(1) of the base.

Synthesized Cu-complexes are quite capable of removing Fecal coliform (FC) from water.

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INTRODUCTION

1.1 Amino Acids

Twenty percent of the human body is made up of protein. Protein plays a crucial role in almost all biological processes and amino acids are the building blocks of it. A large proportion of our cells, muscles and tissue are made up of amino acids, meaning they carry out many important bodily functions, such as giving cells their structure. They also play a key role in the transport and the storage of nutrients. Amino acids have an influence on the function of organs, glands, tendons and arteries. They are furthermore essential for healing wounds and repairing tissue, especially in the muscles, bones, skin and hair as well as for the removal of all kinds of waste deposits produced in connection with the metabolism.

Meirion Jones, a well-known BBC journalist, reported that contrary to years ago, many doctors have now confirmed that a supply of amino acids (also by way of nutritional supplements) can have positive effects.

Jones and Erdmann explain the changes in medical opinion in the following way: "Unfortunately, in the real world countless factors are working to prevent our bodies from receiving a full and balanced supply of these all-important substances. Among these factors are the pollution caused by burning fossil-fuels, the hormones fed to cattle, the intensive use of fertilizers in agriculture, and even habits such as smoking and drinking, all of which can prevent our bodies from fully using what we eat. Worse still is the amount of nutrition that is lost from our food through processing before we actually get to eat it...By providing the body with optimal nutrition, amino acids help to replace what is lost and, in doing so, promote well-being and vitality."

A recent study from Germany carried out by the DAK has revealed that older people in particular are more prone to suffering from malnutrition. "If the body is lacking in the

minimum energy and nutrients, the body cannot carry out its bodily and mental functions. Without the necessary vitamins, proteins (amino acids), trace elements and minerals, there is a risk of debilities and metabolic disorders which can have serious consequences."

Almost every disease caused by civilization is a result of imbalances in our metabolism. The amino-acid pool is jointly responsible for achieving a balanced metabolism. The amino acid pool describes the entire amount of available free amino acids in the human body. The size of the pool amounts to around 120 to 130 grams in an adult male. If we consume protein in the diet, the protein in the gastro-intestinal tract is broken down into the individual amino acids and then put back together again as new protein. This complex biological process is called protein biosynthesis. The entire amino acid pool is transformed, or 'exchanged' three to four times a day. This means that the body has to be supplied with more amino acids, partly by protein biosynthesis, partly by the diet or through consumption of suitable dietary supplements.

Nucleic acids are any group of organic substances found in the chromosomes of living cells and viruses that play a central role in the storage and replication of hereditary information and in the expression of this information through protein synthesis. In most organisms, nucleic acids occur in combination with proteins; the combined substances are called nucleoproteins. The two chief types of nucleic acids are DNA (deoxyribonucleic acid), which carries the hereditary information from generation to generation, and RNA (ribonucleic acid), which delivers the instructions coded in this information to the cell's protein manufacturing sites [1-3].

Deoxyribonucleic acid (DNA) is a nucleic acid that contains the genetic instructions used in the development and functioning of all known living organisms and some viruses. The main role of DNA molecules is the long-term storage of information. DNA is often compared to a set of blueprints or a recipe, or a code, since it contains the instructions needed to construct other components of cells, such as proteins and RNA molecules. The DNA chain is 22 to 26 Å wide and one nucleotide unit is 3.4 Å long [4]. Although each individual repeating unit is very small, DNA polymers can be very large molecules containing millions of nucleotides. For instance, the largest human chromosome, chromosome number 1, is approximately 220 million base pairs long [5]. In living organisms, DNA does not usually exist as a single molecule, but instead as a pair of molecules that are held tightly together [6]. These two long strands entwine like vines, in

the shape of a double helix. The nucleotide repeats contain both the segment of the backbone of the molecule, which holds the chain together, and a base, which interacts with the other DNA strand in the helix. The backbone of the DNA strand is made from alternating phosphate and sugar residues (Fig. 1.1) [7]. The sugar in DNA is 2-deoxyribose, which is a pentose sugar. The sugars are joined together by phosphate groups that form phosphodiester bonds between the third and fifth carbon atoms of adjacent sugar rings. In a double helix the direction of the nucleotides in one strand is opposite to their direction in the other strand. This arrangement of DNA strands is called antiparallel. The asymmetric ends of DNA strands are referred to as the 5′and 3′ends, with the 5' end being that with a terminal phosphate group and the 3' end that with a terminal hydroxyl group. One of the major differences between DNA and RNA is the sugar, with 2-deoxyribose being replaced by the alternative pentose sugar ribose in RNA.

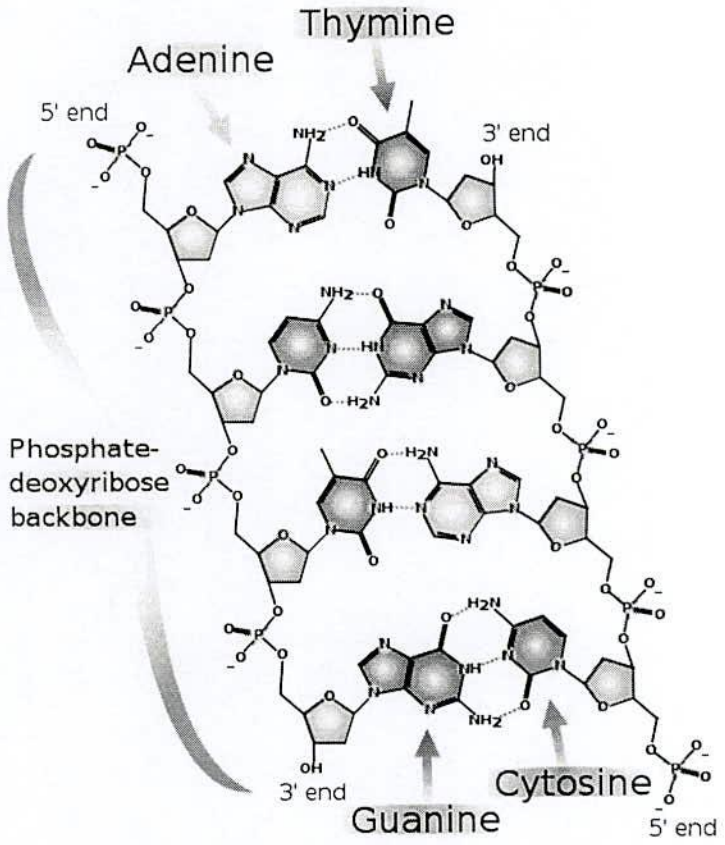


Fig. 1.1 Chemical structure of DNA.

Each type of base on one strand forms a bond with just one type of base on the other strand. This is called complementary base pairing. Here, purines form hydrogen bonds to pyrimidines, with A (adenine) bonding only to T (thymine), and C (cytosine) bonding only to G (guanine). This arrangement of two nucleotides binding together across the double helix is called a base pair. As hydrogen bonds are not covalent, they can be broken and rejoined relatively easily. The two strands of DNA in a double helix can therefore be pulled apart like a zipper, either by a mechanical force or high temperature [8]. As a result of this complementarity, all the information in the double-stranded sequence of a DNA helix is duplicated on each strand, which is vital in DNA replication. Indeed, this reversible and specific interaction between complementary base pairs is critical for all the functions. The two types of base pairs form different numbers of hydrogen bonds, AT forming two hydrogen bonds, and GC forming three hydrogen bonds. DNA with high GC-content is more stable than DNA with low GC-content, but contrary to popular belief, this is not due to the extra hydrogen bond of a GC basepair but rather the contribution of stacking interactions (hydrogen bonding merely provides specificity of the pairing, not stability) [9]. Long DNA helices with a high GC content have stronger-interacting strands, while short helices with high AT content have weaker-interacting strands [10]. DNA exists in many possible conformations that includeA-DNA, B-DNA, and Z-DNA forms, although, only B-DNA and Z-DNA have been directly observed in functional organisms [7].

Nucleotides are the building blocks of all nucleic acids. Nucleotides have a distinctive structure composed of three components covalently bound together: a nitrogen-containing "base" - a pyrimidine (one ring) or purine (two rings), a 5-carbon sugar - ribose or deoxyribose and a phosphate group (Fig. 1.2) [11]. Nucleotides also exist in activated forms containing two or three phosphates, called nucleotide diphosphates or triphosphates. If the sugar in a nucleotide is deoxyribose, the nucleotide is called a deoxynucleotide; if the sugar is ribose, the term ribonucleotide is used.

The structure of a nucleotide is depicted below. The structure on the left - deoxyguanosine - depicts the base, sugar and phosphate moieties. In comparison, the structure on the right has an extra hydroxyl group on the 2' carbon of ribose, making it a ribonucleotide - riboguanosine or just guanosine.

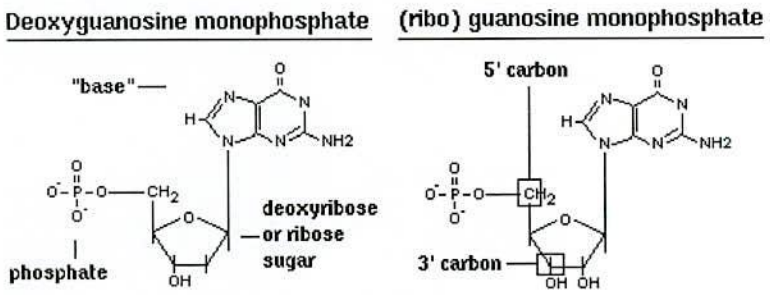


Fig. 1.2 Chemical structure of nucleotide

In the right-hand figure, note also the 5' and 3' carbons on ribose (or deoxyribose) - understanding this concept and nomenclature is critical to understanding polarity of nucleic acids. The 5' carbon has an attached phosphate group, while the 3' carbon has a hydroxyl group. The combination of a base and sugar is called a nucleoside.The system of a base covalently bound to the 1' carbon of a ribose or deoxyribose is called a nucleoside, and a nucleoside with one or more phosphate groups attached at the 5' carbon is called a nucleotide. The main nucleosides are adenosine, guanosine, cytidine, thymidine and uridine (Fig. 1.3).

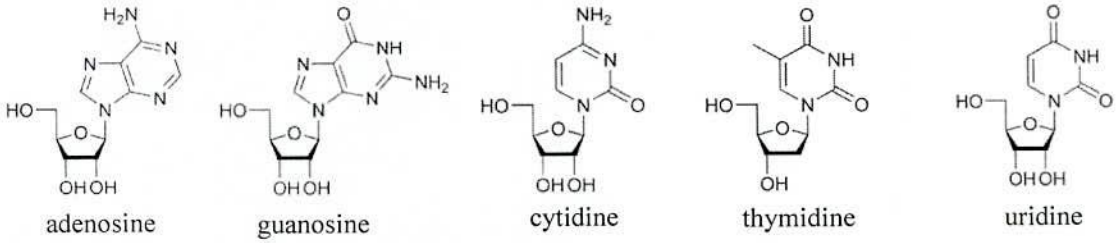


Fig. 1.3 Chemical structure of some amino acids

Nucleobases are the parts of DNA and RNA that may be involved in pairing. The main ones are cytosine, guanine, adenine (DNA and RNA), thymine (DNA) and uracil (RNA) (Fig. 1.4). They are usually simply called bases in genetics. Because A, G, C, and T appear in the DNA, these molecules are called DNA-bases; A, G, C, and U are called RNA-bases. Uracil replaces thymine

in RNA. These two bases are identical except that uracil lacks the 5' methyl group. Adenine and guanine belong to the double-ringed class of molecules called purines (abbreviated as R). Cytosine, thymine, and uracil are all pyrimidines (abbreviated as Y).

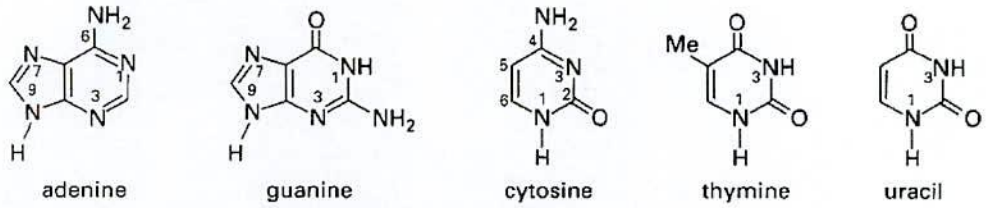


Fig. 1.4 Chemical structure of amino acids bases

Apart from adenosine (A), cytidine (C), guanosine (G), thymidine (T) and uridine (U), DNA and RNA also contain bases that have been modified after the nucleic acid chain has been formed. In DNA, the most common modified base is 5-methylcytidine (m5C). In RNA, there are many modified bases, including pseudouridine (Ψ), dihydrouridine (D), inosine (I), ribothymidine (rT) and 7-methylguanosine (m7G) [12].

Hypoxanthine and xanthine are two of the many bases created through mutagen presence, both of them through deamination (replacement of the amine-group with a carbonyl-group). Hypoxanthine is produced from adenine, xanthine from guanine [14]. Similarly, deamination of cytosine results in uracil. These are some of modified purine and pyrimidine bases are given bellow (Fig. 1.5).

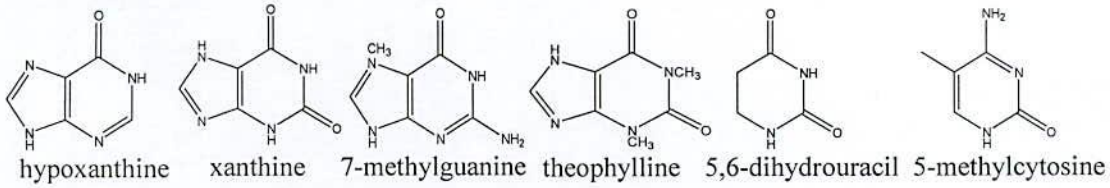


Fig. 1.5 Modified purine and pyrimidine bases

1.2 Amino Acids and Metal Ions

Metal-nucleic acid chemistry becomes highly relevant when the transition metal compounds are applied as chemical probes in the nucleic acid biochemistry or in chemotherapy. The significance of metal binding to nucleic acids and to enzymes involved in processes related to DNA

replication, transcription, messenger RNA translation has long been recognized [14-17]. The action of metal ions in these enzyme-catalyzed reactions and also in DNA and RNA degradation by nucleases is only partially understood. In the stability of the tertiary structure of tRNA, it is clearly documented that Mg(II) is important because it cross-links phosphate groups [18, 19]. Metal ions, however, can also have a destabilizing effect on DNA double helical structure if they interact with bases rather with phosphate groups. In the series Mg(II), Co(II), Ni(II), Zn(II), Cd(II), Cu(II), the affinity for base complexation relative to phosphate to binding increases from left to right. In RNA divalent metal ions like Cu(II), Zn(II) and Pb(II) can have an even more destructive consequence on structure in that they catalyze nonenzymatic phosphodiester cleavage [20-22].

Research on metal ion-nucleic acid complexes was advanced when anti-tumor activities of ci-dichlorodiammineplatinu(II) were discovered [23-25]. In vitro studies clearly demonstrated that this reagent attacks guanine at N(7) and also involves O(6) [26-28]. The exact mechanism of the in vivo action is still a matter of debate [29]; it is, however, well established that the template function of DNA is impaired and DNA synthesis inhibited. Owing to these properties, platinum(II) compounds are now being tested in the treatment of several forms of cancer [30, 31]. Active interest in metal ion-nucleic acid complexes has produced a number of review articles describing the stereochemistry of metal binding to bases, to nucleosides and, to nucleotides [15, 32-36].

The more recent developments in this field are characterized by the attempt to elucidate even very specific details of metal nucleic acid interaction, such as the significance of hydrogen bonding interactions between co-ligands of the metal and the nucleic acid target, and to understand fully the role of metal ions in catalytically active nucleic acids such as ribozymes: DNAzymes. On the other hand, there appears to be a tendency in many cases to bypass molecular details of metal-nucleic acid interactions and to concentrate primarily on functional

aspects of such complexes. Studies on 'metallized' DNA, to be used as conducting molecular wires, are an example.

1.3 Types of Interactions

Nucleic acids are excellent targets for metal ions and metal-containing compounds, in that they are negatively charged and provide a plethora of potential binding sites. These are the phosphate oxygen atoms, the various atoms of the heterocyclic nucleobases and to some extent even the hydroxyl groups of the sugars [37, 38].

The types of interactions between metal ions and nucleic acids can be roughly divided into two categories, namely non-covalent interactions and coordinative bonding. The first type of interaction refers to 'coordinatively saturated' metal species, irrespective of the nature of the metal ion and that of the ligands. The second type takes place directly between the metal and any of the donor sites of nucleic acids [39- 41].

Binding sites for metal ions offered by the four naturally occurring nucleotides are oxygen and nitrogen atoms, and both belong to class a, or hard ligands [42, 43]. Therefore, only certain types of metal ions are able to bind, viz., alkali, alkaline earth and transition metal ions. These are listed in Table 1.1, and correlated with most preferred nucleotide binding sites derived from crystalline complexes.

Table 1.1 Metal-ions interacting and co-crystallizing with nucleic acid constituents and preferred binding sites.

Alkaline	Li, Na, K, Rb and Cs
Alkaline earth	Mg, Ca, Sr and Ba
Transition metals	Mn(II), Ru(III), Os(VI), Co(III), Co(II), Ni(II), Pd(II), Pt(II), Cu(II), Ag(I), Au(III), Zn(II), Cd(II) and Hg(II)

Preferred binding sites

Base keto oxygen and ring nitrogen — Phosphate oxygen — Sugar hydroxyl

Transition metals

Alkaline and Alkaline Earth metals

The essential, structurally most interesting characteristics of feature of metal binding to nucleic acid are;

(a) Phosphate groups: These can binds to most of alkali, alkaline and transition metal ions to form salt-like complexes between positively charged metal ions and negatively charged phosphate oxygens.

(b) Sugar hydroxyls: These interact preferentially with alkaline and alkaline earth cations but not with transition metals. Exception thus so far known is Cd(II) complex of IMP in which Cd(II) binds to hydroxyl group. In all these complexes, the hydroxyl group enters the metal ion coordination sphere with the lone electron pair of the oxygen as observed in many other adducts between sugar hydroxyls and alkaline or alkaline earth cations [44, 45].

© Hetarocyclic nitrogens of bases: Since these atoms carry lone electron pairs, they are good ligands for alkali and transition metals and also for alkaline earth cations [45]. Coordination to purine bases with unsubstituted N(9) is preferentially first to N(9) (in bridge to N(3)), then to N(7) and then to N(1), with binding to the imidazole ring in general favored over binding to the pyrimidine moiety. Coordination to N(1) unsubstituted pyrimidine bases is first to N(1) rather than to N(3) in thymine and uracil, but for cytosine the reverse trend is found. In both purine and pyrimidine bases, metal ion binding shifts the proton tautomeric equilibrium toward one side, to N(7)-H for purines and to N(3)-H for pyrimidines, thymine, uracil. When glycosyl links are formed, N(9) of purines, binding to N(7) is then preferred over that to N(1) and over N(3). In pyrimidine derivatives, only cytidine can offer N(3) for complexation as uridine and thymidine have no ring nitrogen available.

(d) Base keto substituents: These are available to contribute to complex formation with metal ions. In pyrimidine nucleotides, metal ion bind to O(2) (cytosine) or O(2), O(4) (thymidine, uracil). In contrast, in the purine systems guanine and hypoxanthine, O(6) is generally not involved in direct metal binding, probably because N(7) is a better ligand and simultaneous coordination of N(7) and O(6) would lead to unfavourable geometry [46, 47]. The keto oxygen O(6) can accept hydrogen bonds from other ligands in the coordination sphere of the metal ion, and these interligand interactions indirectly contribute to complex formation.

(e) Base amino substituents: These are never involved in direct metal ion coordination because the lone electron pair is delocalized over the π-bonding system of the attached heterocycle and is not available for metal ion binding. Amino groups can act as hydrogen bond donors to other ligands of the metal ion thus indirectly facilitate complexation.

(f) N(7)-metal-N(6) and N(7)-metal-O(6) chelations: The formation of the N(7)/O(6) chelating ring for guanine derivatives has been substantiated in the Me_3Pt-theophyllinate complex [48], while the N(7)/N(6) chelation mode for adenine derivatives has not been proven. One can expect the N(7)/N(6) chelation mode, but only under conditions where the amino group can be deprotonated.

(g) Base thioketo substituents: In 6-mercaptopurine, in 2-thiocytosine and in 2- and 4-thiouracil these are soft groups and therefore very good ligands for transition metal ions [42, 43]. They are far better candidates than purine or pyrimidine nitrogen and oxygen atoms as could be demonstrated by the exclusive and strong affinity of mercury and platinum reagents to the only 4-thiuridine in tRNA [49].

(h) Coordination number vs binding sites of metal ion: In purines, N(7) is rather exposed and allows six fold or even higher coordination of the metal ion. In contrast, binding to N(3) in cytosine is sterically restricted due to the two flanking keto and amino groups which limit the available spatial volume and consequently lead to preference for lower, four- or fivefold coordination number. It is not always true, as substantiated by $[Rh_2(acetamidato)_4(1\text{-methylcytosine})_2].2H_2O$, where the cytosine base does bind to the axial position of the octahedral rhodium ion through N(3) with the formation of interligand N(4)-H...O(amidato) and N-H(amidato)...O(2) hydrogen bonds [50].

(i) Selective metal ion coordination of bases: It is clear that metal ion coordination to bases is rather specific. Thioketo substituents as soft ligands are very good candidates for coordination to transition metal ions and override hard ligands nitrogen and oxygen. Binding to base ring nitrogen atoms manifests subtle selectivity because N(3) of cytosine is sterically shielded by keto

and amino groups and is therefore a ligand for metal ions with coordination number lower than 6, whereas N(7) of purine bases can accommodate all kinds of alkaline and alkaline earth, and transition metal ions. Finally, interligand hydrogen bonding between N(6) amino group in adenine or O(6) keto group in guanine and other ligands of the metal ion adds another degree of selectivity.

(j) Interligand interactions as a factor affecting the site-specific metal binding: As mentioned above that exocyclic amino N(6) and keto O(6) substituents are not involved in direct metal bonding, but act as hydrogen bonding donor or acceptor respectively, while other ligands in the coordination sphere of the metal ion, and these type of interligand interactions could affect specific metal binding sites as well as stability of the complex formation. Typical examples include an observed trend in the reaction selectivity between nucleic acid derivatives and $Na[Co(acetylacetonato)_2(NO_2)_2]$, as adenine>cytosine>uracil=guanine, and the specific metal bonding to adenine but not to guanine in the reaction with $[Rh_2(acetate)_4]$. The preferential bonding of cis-$[PtCl_2(NH_3)_2]$ to guanine might reflect interligand interaction also.

CHAPTER II

Literature Review

Preferred metal binding sites, modes and factors affecting them have been major subjects to be elucidated. Gillert and Bau have pointed out a correlation between coordination number and metal binding site on nucleobases [51]. Marzilli and Kistenmacher have originally demonstrated the importance of stereospecific interligand interactions as factors that affect the specific metal binding to nucleic acid bases, involving hydrogen bonding, electrostatic repulsions, and steric constraints [35]. Marzilli and Kistenmacher [52] studied adenine specific $[Co(acetylacetonato)_2(NO_2)_2]^+$ species, and $[Rh_2(carboxylato)_4]$ was exposed by Bear et al. [53] which is also adenine-specific compound. Marzotto et al have reported the cystal structures of $[Cu(tren)(ade)].Cl.2H_2O$ [54] and $[Ni(tren)(ade)Cl].Cl$ [55]. Guanine specific $[Ni(dimethyltetraazabicycloheptadecapentaene)]^{2+}$ was elucidated by Burrows and Pokita[56], a discovery for oxo-purine base specific metal complex. Pyrimidine type nucleic acid bases like thymine (or uracil)- specific $[Zn(tcydan)(H_2O)]^{2+}$ was demonstrated by Kimura et al [57]. Aoki et al have confirmed the validity of the base- or site-specific metal bonding in the $[Rh_2$(carboxylato or amidato$)_4$(nucleobase or its derivative$)_2]$ system that could be rationalized by intramolecular interligand interactions [58-63].

It was showed that nta-capped $[Ni(nta)(H_2O)]^-$ species indeed binds exclusively to adenine through N(7) with the formation of intramolecular hydrogen bonds between the amino substituent N(6) and carboxylato oxygens of nta [64]. The interaction of $[Cu(tren)]^{2+}$ or $[Ni(tren)(H_2O)]^{2+}$ with nucleobases and derivatives was rationalized by Aoki and his group in terms of interligand interactions. Metal ions bind selectively for guanine derivatives over N(9) substituted adenine might be due to the formation of H-bond between the amino group of tren and the O(6) carbonyl group of an N(7)-metal bonded guanine while a steric repulsion between the amino group of tren and the N(6) amino group of an N(7)-metal bonded adenine. It is also observed that tren-capped two Cu^{2+} ions bind to a hypoxanthinate anion, one through N(9) and

the other through N(7) with the formation of interligand hydrogen bonds for each metal bonding [65] . However, $[Ni(tren)(H_2O)]^{2+}$ species bind to hypoxanthine through N(7) with the formation of intramolecular hydrogen bond between the keto substituent O(6) of the base and amino nitrogens of tren [66]. Structures of tren-metal ion-xanthine ternary complexes that involve the specific metal bonding to N(7) of xanthine, accompanying an intermolecular interligand H-bond between the amino group of tren and O(6) of the base [67].

Under alkaline condition $[Ni(tren)]^{2+}$, $[Zn(tren)]^{2+}$ and $[Cd(tren)]^{2+}$ bind to an ade ligand through N(9) as well as intramolecular interligand hydrogen bond was formed among amino group of the tren and N(3) of the base. In the case of hypoxanthine base tren capped Zn^{2+} ion binds to N(9) with the formation of hydrogen bond through O(6) of the base and amino group of the tren ligand as mentioned above. But two tren-capped Cd^{2+} ions bind to hypoxanthine, one through N(7) and the other through N(9) ligand and interligand H-bonds were formed for each metal bonding. In uracil complexes tren-capped Ni^{2+}ion or Cu^{2+} ion binds to N(1) of uracilato anion with the formation of intramolecular hydrogen bond through keto substituent O(2) of the base [68].

1.6 Aim of the Present Work

There has been a continued demand for the elucidation of factors that determine the metal binding sites on amino acid bases because of their biological demand. Amino acid-metal complexes are used as drugs in human system. So the specific aims of this research are:

i) to prepare the Cu-amino acid based complexes.

ii) to characterize the prepared complexes.

iii) to observe the biological applications of the complexes.

Chapter 3

EXPERIMENTAL

3.1 Materials and Instruments

The materials, methods and equipments used to carry out the experimental work in this study are described below;

3.1.1 Chemicals

All the chemicals and solvents used in this study are analar grade and commercially available. The various metal salts, solvents and other chemicals were used without further purification. The chemicals and solvents were purchased from various companies and those are mentioned in the following table.

Name of the compound	Name of the company
$Cu(ClO_4)_2.6H_2O$	Kishida Chemical & Co. Ltd., Japan
Adenine	Tokyo Kasei Kogyo Co. Ltd., Japan
Hypoxanthine	Sigma-Aldrich Chemie GmbH, Germany
Xanthine	Kanto Chemical Co., Inc., Japan
Theophylline	Nacalai Tesque Inc., Japan
Uracil	Kishida Chemical & Co. Ltd., Japan
Cytosine	Tokyo Kasei Kogyo Co. Ltd., Japan
1,4,7,10-tetraazacyclododacane.4HCl (tcydan.4HCl)	Tokyo Chemical Industry Co. Ltd., Japan
Tris(2-aminoethyl)amine (tren)	Sigma-Aldrich Chemie GmbH, Germany
CH_3OH	Kishida Chemical & Co. Ltd., Japan
CH_3CN	Wako Pure Chemical Industries Ltd., Japan

3.1.2 Instruments

The FT-IR spectra were recorded on a JEOL JIR-7000 spectrometer in the range of 400-4000 cm^{-1} using KBr plate in the Department of Chemistry, University of Dhaka. The X-ray diffraction data of all the complexes were collected on a Rigaku7R diffractometer with graphite-monochromated Mo Kα radiation (λ = 0.7107 Å) using an 18 kW rotating anode generator at Toyohashi University.

3.2 Preparation of the Complexes

3.2.1 Preparation of [Cu(tcydan)(ade)].ClO_4.$2H_2O$ (1)

An aqueous solution (4 mL) dissolving adenine (0.1 mmol) was added into a methanolic solution (4 mL) dissolving $Cu(ClO_4)_2.6H_2O$ (0.1 mmol), and the resultant light blue colored solution was treated with an aqueous solution (1 mL) of tcydan.4HCl (0.1 mmol). 5N NaOH solution was added up to pH about 9-10, and the deep blue colored solution was allowed to stand under room temperature for complex **1**, after four months blue plates like crystals were observed. The amount of yield is 30 mg (36.80%).

3.2.2 Preparation of [{Cu(tcydan)}$_2$(hypoxanth)].$(ClO_4)_3$ (2)

The complex **2** was prepared by adding an acetonitrilic solution (4 mL) dissolving $Cu(ClO_4)_2.6H_2O$ (0.1 mmol) into an aqueous solution (2 mL) dissolving hypoxanthine (0.1 mmol), then an aqueous solution (1 mL) of tcydan.4HCl (0.1 mmol) was added into the resultant light blue colored solution. The deep blue colored solution was treated with 5N NaOH solution up to pH about 7-8, and allowed to stand under room temperature. Blue columnar crystals were formed after two weeks. The amount of yield is 36 mg (43.64%).

3.2.3 Preparation of [Cu(tcydan)(theophy)]$_3$.$(ClO_4)_3$.$2H_2O$ (4)

To prepare complex **4** an aqueous solution (4 mL) of theophylline (0.1 mmol) was added into CH_3CN solution (4 mL) dissolving $Cu(ClO_4)_2.6H_2O$ (0.1 mmol), and then an aqueous solution (1 mL) of tcydan.4HCl (0.1 mmol) was mixed into it. The resultant blue colored solution was kept

under room temperature, after 5N NaOH solution (pH about 8) was added. Blue columnar crystals were formed after two months. The amount of yield was 32 mg (36.70%).

3.3 X-ray Data Collection and Crystal Structure Determination

To collect the X-ray diffraction data a suitable sized perfect single crystal of each complex was mounted on glass fiber. Reflection data were collected on a RASA-7R model diffractometer (Rigaku) with graphite-monochomated Mo Kα radiation (λ= 0.7107Å) using 18 kW rotating anode generator. The details data, data collection and structure refinement are mentioned in the next chapter. Intensity data were corrected for Lorentz and polarization effects for all the complexes. Empirical absorption correction based on ψ-scan method was applied for all the complexes.The programs used for the crystal structures determination are Oscail (SHELX-97, SHELXL-97-2 and ORTEX), Mercury 2.2 and Ortep3v2.

The structure were solved using direct methods and refined by full-matrix least squares methods, minimizing the function $\sum w(|F_o|-|F_c|)^2$. All the non-hydrogen atoms were refined anisotropically for **1**, **2**, **4** and **5**. In **1**, all of four hydrogen atoms attached to the adenine base were located in a difference Fourier map and the positions of all H-atoms belonging to tcydan were calculated. Their positional and isotropic thermal parameters were included in the least-squares refinements but fixed. In **2**, **4** and **5**, all H atoms were located in difference Fourier maps and refined isotropically. In **3**, because of a limited number of reflection data, all non-hydrogen atoms were refined isotropically except for the Cu and xanthine atoms which were anisotropically refined. No attempt was made to locate hydrogen atoms. The tcydan ligand is disordered into the two arrangements with occupancy factors estimated to be equal based their electron densities. There exist two ClO_4 anions, each of which rides on a two-fold axis, with estimated occupancy factors of 0.7 and 0.3, respectively. Among the six crystallization water molecules, one locates on an inversion center and two are disordered to be half occupied. This high disordering of the molecules causes the high R values.

3.4 Determination of Fecal Coliform (FC)

Membrane Filtration Method was pertained for the determination of fecal coliform in which the culture medium was used to grow colony and incubation temperature of 44.5±0.2 °C for selectivity and gives 93% accuracy in differentiating between coliforms from warm blooded animals and those from other sources. Developed Color of colony was blue.

3.4.1 Apparatus

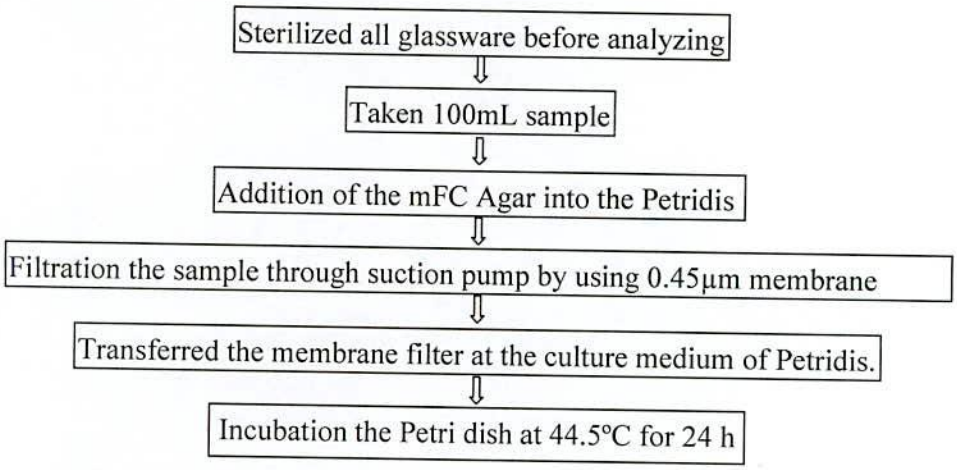
Apparatus which were used for measuring fecal coliform of water are Autoclave, Oven, Bacteriological unit, Petridis, Beaker, Cylinder, 0.45µm membrane filter, Colony counter, Forceps, Incubator, Glass rod, Conical flask, Electric Balance etc.

3.4.2 Reagents

M-FC Agar / m FC Broth Base, Sodium Chloride, Sodium hydroxide, Rosolic Acid, 1N HCl were used for measuring faecal coliform of the water samples.

3.4.3 Preparation of mFC Agar: 52g mFC agar was suspended in 1L purified water. To mix agar it was heated with frequent agitation and boiled until the powder dissolve completely. 10 mL of 1% solution of rosolic acid was added in 0.2 N NaOH. Heating was continued for 1 minute. pH was adjusted 7.4 with 1 N HCl, if necessary.

Flow Chart for FC Testing Procedure



3.4.4 Calculation: Fecal coliforms /100mL = (coliform colonies counted × 100) / (mL sample filtered)

3.5 Determination of Total Coliform (TC)

Membrane Filtration Method [83] was pertained for the determination of faecal coliform in which the culture medium was used to grow colony and incubation temperature of 36±1°C for 23±1hours. Developed Color of colony was Metallic (Golden) Red.

3.5.1 Apparatus

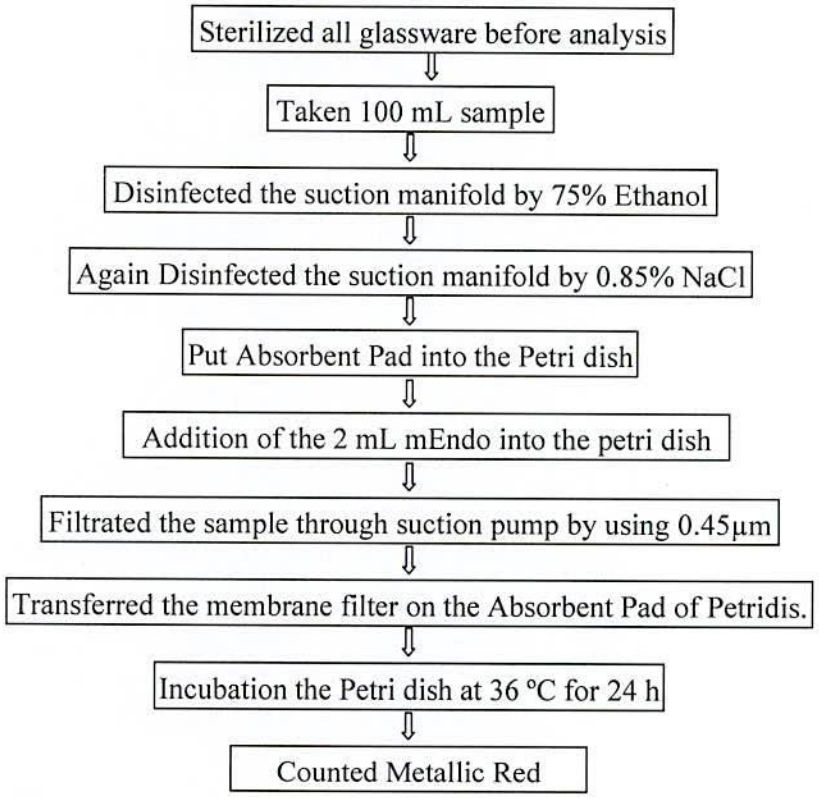
Apparatus which were used for measuring total coliform of water are Autoclave, Incubator, Bacteriological unit, Petri dish, Beaker, Cylinder, 0.45µm membrane filter, Colony counter, Pipette, Oven, Absorbent Pad, Forceps, Conical flask, Glass rod, Electric balance, etc.

3.5.2 Reagents

M-Endo Broth, Sodium Chloride, Ethanol were used for measuring total coliform of the water samples.

3.5.3 Preparation of m-Endo Broth: 4.8g of the powder (M-Endo) was dissolved in 100 mL purified water containing 2.0 mL of non denatured ethanol. The solution was heated to boil but avoid overheating. After preparation, it was keep for 96 hours in refrigerator. pH value of culture media was adjusted about 7.2.

Flow Chart for TC Test Procedure



3.5.4 Calculation

Total coliforms/100mL = (coliform colonies counted ×100) / (mL sample filtered)

Chapter 4

Results and Discussion

4.1 Structure of [Cu(tcydan)(ade)].ClO_4.$2H_2O$ (1)

The molecular formula of the ternary tcydan-Cu^{2+}-adenine complex is $C_{13}H_{28}ClN_9O_6Cu$; M = 505.43. The complex **1** consists of a $[Cu(tcydan)(ade)]^+$ cation, a perchlorate anion and two crystallization water molecules in the asymmetric unit, as shown in Fig. 3.1. 1.

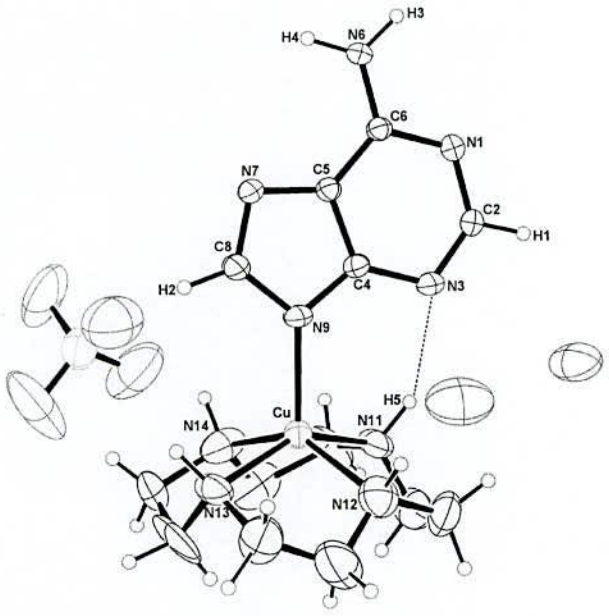


Fig. 4.1.1 Molecular structure of [Cu(tcydan)(ade)].ClO_4.$2H_2O$

Fig. 4.1.1 shows that in the structure of complex **1** the square-pyramidal Cu^{2+} ion binds to an ade ligand through the deprotonated N(9) and to four nitrogens of a tcydan ligand, with the equatorial positions occupied by four secondary nitrogen atoms of tcydan and the axial position by N(9) of adenine with the Cu-N(9) distance of 2.060(5) Å. An intramolecular interligand hydrogen bond is formed between the secondary amino nitrogen N(11) of tcydan and the ring nitrogen N(3) of the base (N(11)...N(3) = 3.21 Å and H(5)...N(3) = 2.5 Å). Among the four ring nitrogens N(1), N(3), N(7), and N(9) of adenine, N(9) is the most basic (pKa ca. 10 [69]) followed by N(1) (pKa ca. 4 [69]), and thus neutral adenine bears a proton at N(9). In accord with this view, N(9) is the most preferred metal binding site for unsubstituted adenine. The crystal data and structural

feature of complex **1** with its molecular dimensions are listed in Table 4.1.1, Table 4.1.2 and Table 4.1.3.

Fig. 4.1.2 shows the crystal packing of the complex and Table 4.1.4 lists hydrogen bonds and other short contacts. As shown in Fig. 4.1.3, each adenine moiety fully participates in hydrogen-bonding with two adjacent ones, one through N(6)-H(3)...N(7) and N(1)...H(4)-N(6) hydrogen bonds and the other through N(6)-H(4)...N(1) and N(7)...H(3)-N(6) hydrogen bonds, creating a sheet structure with an infinite adenine-adenine zig-zag molecular array.

Two crystallization water molecules exist in the asymmetric unit, forming two different hydrogen bonds with the tcydan moiety, one through N(12)-H(6)...O(5) (N(12)...O(5) = 2.95 Å and H(6)...O(5) = 2.0 Å), and the other through O(6)...H(7)-N(13) (O(6)...N(13) = 3.03 Å and O(6)...H(7) = 2.1 Å). The water molecule O(5) forms a network type structure in the crystal packing between the O(3) of the perchlorate anion and O(6) water molecule, by forming two more hydrogen bonds, one through O(5)...O(3) = 3.03 Å) and the other through O(6)...O(5) = 2.87 Å). O(6) water molecule forms a hydrogen bond with the ring nitrogen N(3) of the base (N(3)...O(6) = 3.12 Å). Perchlorate anion is linked with the tcydan moiety through O(1), forming a hydrogen bond between the N(14) of tcydan and O(1) of the perchlorate anion (N(14)...O(1) = 3.07 Å).

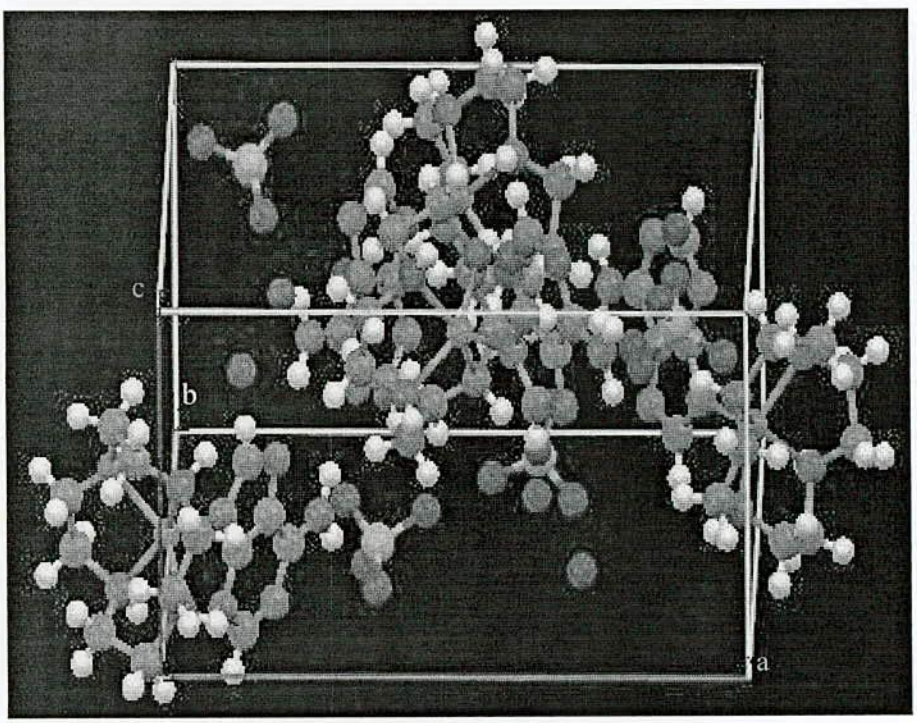


Fig. 4.1.2 View of the crystal packing in complex **1**

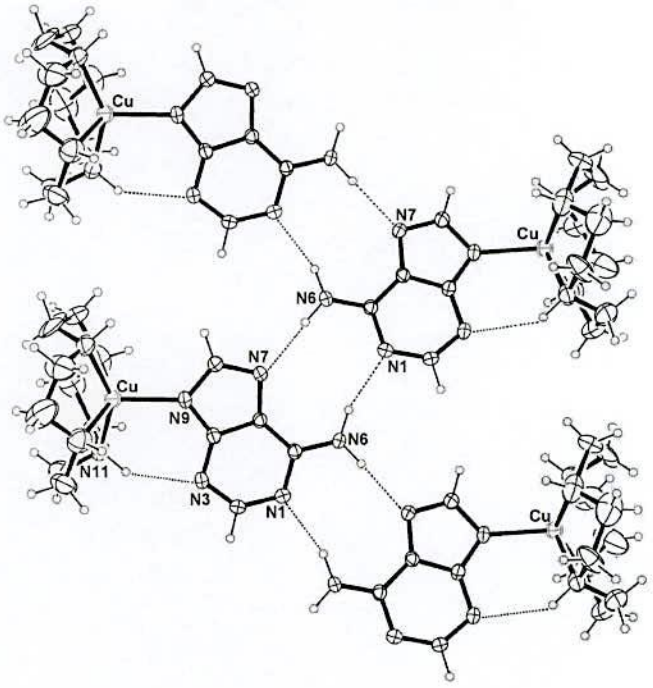


Fig. 4.1.3 Molecular sheet constructed by infinite hydrogen-bonded adenines in the zig-zag molecular array (broken lines denote hydrogen bonds) of complex **1**

Table 4.1.1 Crytal data and structure refinement for $[Cu(tcydan)(ade)].ClO_4.2H_2O$ **(1)**

Complex **(1)**	$[Cu(tcydan)(ade)].ClO_4.2H_2O$
Empirical formula	$C_{13}H_{28}N_9O_6ClCu$
Formula weight	505.43
Color of the crystal	Blue
Crystal size (mm)	0.5 X 0.2 X 0.2
Temperature (K)	293(2)
Wavelength	0.7107 Å
Crystal system	Orthorhombic
Space group	$P2_12_12_1$
Unit cell dimensions	a = 15.575(3) Å, b = 16.167(2) Å, c = 8.436(2) Å
Volume	2124.4(7) $Å^3$
Z	4
Crystal density (gcm^{-3})	1.580
Absorption coefficient (mm^{-1})	1.2043
$F(000)$	1052
Theta range for data collection	2.0 to 27.4956°

Scan technique	ω-2θ
Limiting indices	$0 \leq h \leq 20$, $0 \leq k \leq 20$, $0 \leq l \leq 10$
Reflections collected/unique	4026/2198
Completeness to theta	Full
Absorption correction	Empirical (ψ-scan)
Refinement method	Full-matrix least-squares on F
Reflection measured	4026
Data/restraints/parameters	2198/0/271
Goodness-of-fit	1.690
Final R indices [I>2σ(I)]	$R^a = 0.0540$, $R_w{}^b = 0.0550$
Max./ min. residual (e Å^{-3})	0.5697/-0.4139

[a] $R = \sum ||F_o| - |F_c|| / \sum |F_o|$.

[b] $R_w = [\sum w(|F_o| - |F_c|)^2 / \sum w|F_o|^2]^{1/2}$.

Table 4.1.2 Bond lengths of $[Cu(tcydan)(ade)].ClO_4.2H_2O$ **(1)**

Bond	Distance	Bond	Distance
Cu(1) – N(9)	2.060(5)	N(13) – H(7)	0.97
Cu(1) – N(11)	2.023(8)	N(14) – C(16)	1.58(2)
Cu(1) – N(12)	2.047(9)	N(14) – C(17)	1.37(2)
Cu(1) – N(13)	2.036(8)	N(14) – H(8)	0.97
Cu(1) – N(14)	2.052(10)	C(2) – H(1)	0.97
Cl(1) – O(1)	1.45(1)	C(4) – C(5)	1.41(1)
Cl(1) – O(2)	1.33(1)	C(5) – C(6)	1.386(9)
Cl(1) – O(3)	1.35(1)	C(8) – H(2)	0.97
Cl(1) – O(4)	1.38(1)	C(11) – C(12)	1.55(2)
N(1) – C(2)	1.348(9)	C(11) – H(9)	0.95
N(1) – C(6)	1.362(9)	C(11) – H(10)	0.96
N(3) – C(2)	1.317(9)	C(12) – H(11)	0.95
N(3) – C(4)	1.362(9)	C(12) – H(12)	1.00
N(6) – C(6)	1.339(8)	C(13) – C(14)	1.46(2)
N(6) – H(3)	0.95	C(13) – H(13)	0.94
N(6) – H(4)	0.96	C(13) – H(14)	0.97
N(7) – C(5)	1.376(8)	C(14) – H(15)	0.97
N(7) – C(8)	1.33(1)	C(14) – H(16)	0.96
N(9) – C(4)	1.359(10)	C(15) – C(16)	1.48(2)
N(9) – C(8)	1.365(10)	C(15) – H(17)	0.93
N(11) – C(11)	1.33(1)	C(15) – H(18)	0.96

N(11) – C(18)	1.55(2)	C(16) – H(19)	0.92
N(11) – H(5)	0.96	C(16) – H(20)	0.98
N(12) – C(12)	1.57(2)	C(17) – C(18)	1.56(2)
N(12) – C(13)	1.40(2)	C(17) – H(21)	0.97
N(12) – H(6)	0.97	C(17) – H(22)	0.96
N(13) – C(14)	1.54(2)	C(18) – H(23)	0.94
N(13) – C(15)	1.38(2)	C(18) – H(24)	0.98

Table 4.1.3 Bond angles of [Cu(tcydan)(ade)].ClO_4.$2H_2O$ **(1)**

Angle	Degree	Angle	Degree
N(9) – Cu(1) – N(11)	102.9(3)	C(12) – N(12) – C(13)	116(1)
N(9) – Cu(1) – N(12)	113.1(3)	C(12) – N(12) – H(6)	108
N(9) – Cu(1) – N(13)	109.7(3)	C(13) – N(12) – H(6)	110
N(9) – Cu(1) – N(14)	104.4(3)	Cu(1) – N(13) – C(14)	104.4(7)
N(11) – Cu(1) – N(12)	83.7(4)	Cu(1) – N(13) – C(15)	106.7(9)
N(11) – Cu(1) – N(13)	147.3(3)	Cu(1) – N(13) – H(7)	112
N(11) – Cu(1) – N(14)	85.0(4)	C(14) – N(13) – C(15)	109(1)
N(12) – Cu(1) – N(13)	85.9(4)	C(14) – N(13) – H(7)	112
N(12) – Cu(1) – N(14)	142.3(4)	C(15) – N(13) – H(7)	112
N(13) – Cu(1) – N(14)	84.6(5)	Cu(1) –N(14) – C(16)	104.2(7)
O(1) – Cl(1) – O(2)	105.4(9)	Cu(1) – N(14) – C(17)	108.6(8)
O(1) – Cl(1) – O(3)	109.7(10)	Cu(1) – N(14) – H(8)	113
O(1) – Cl(1) – O(4)	113(1)	C(16) – N(14) – C(17)	110(1)
O(2) – Cl(1) – O(3)	107(1)	C(16) – N(14) – H(8)	109
O(2) – Cl(1) – O(4)	107.2(9)	C(17) – N(14) – H(8)	112
O(3) – Cl(1) – O(4)	112.2(9)	N(1) – C(2) – N(3)	129.5(7)
C(2) – N(1) – C(6)	117.9(6)	N(1) – C(2) – H(1)	116
C(2) – N(3) – C(4)	112.4(6)	N(3) – C(2) – H(1)	115
C(6) – N(6) – H(3)	121	N(3) – C(4) – N(9)	127.4(7)
C(6) – N(6) – H(4)	120	N(3) – C(4) – C(5)	123.6(7)
H(3) – N(6) – H(4)	120	N(9) – C(4) – C(5)	109.1(6)
C(5) – N(7) – C(8)	102.8(7)	N(7) – C(5) – C(4)	108.8(7)
Cu(1) – N(9) – C(4)	127.2(5)	N(7) – C(5) – C(6)	132.4(7)
Cu(1) – N(9) – C(8)	129.2(5)	C(4) – C(5) – C(6)	118.8(6)
C(4) – N(9) –C(8)	102.6(5)	N(1) – C(6) – N(6)	117.7(6)
Cu(1) – N(11) – C(11)	111.1(8)	N(1) – C(6) – C(5)	117.9(6)
Cu(1) – N(11) – C(18)	105.0(7)	N(6) – C(6) – C(5)	124.3(6)
Cu(1) – N(11) – H(5)	112	N(7) – C(8) – N(9)	116.7(6)

C(11) – N(11) – C(18)	106(1)	N(7) – C(8) – H(2)	122
C(11) – N(11) – H(5)	111	N(9) – C(8) – H(2)	121
C(18) – N(11) – H(5)	110.6747	N(11) – C(11) – C(12)	104(1)
Cu(1) – N(12) – C(12)	104.8(7)	N(11) – C(11) – H(9)	111
Cu(1) – N(12) – C(13)	106.7(8)	N(11) – C(11) – H(10)	112
Cu(1) – N(12) – H(6)	110	C(12) – C(11) – H(9)	110
C(12) – C(11) –H(10)	110	N(13) – C(15) – H(18)	111
H(9) – C(11) – H(10)	108	C(16) – C(15) – H(17)	111
N(12) – C(12) – C(11)	111.6(9)	C(16) – C(15) – H(18)	107
N(12) – C(12) – H(11)	112	H(17) – C(15) – H(18)	110
N(12) – C(12) – H(12)	108	N(14) – C(16) – C(15)	110.6(10)
C(11) – C(12) – H(11)	111	N(14) – C(16) – H(19)	111
C(11) – C(12) – H(12)	109	N(14) – C(16) – H(20)	107
H(11) – C(12) – H(12)	106	C(15) – C(16) – H(19)	112
N(12) – C(13) – C(14)	109(1)	C(15) – C(16) – H(20)	108
N(12) – C(13) – H(13)	110	H(19) – C(16) – H(20)	109
N(12) – C(13) – H(14)	110	N(14) – C(17) – C(18)	104(1)
C(14) – C(13) – H(13)	109	N(14) – C(17) – H(21)	110
C(14) – C(13) – H(14)	108	N(14) – C(17) – H(22)	112
H(13) – C(13) – H(14)	109	C(18) – C(17) – H(21)	112
N(13) – C(14) – C(13)	111(1)	C(18) – C(17) – H(22)	111
N(13) – C(14) – H(15)	108	H(21) – C(17) – H(22)	107
N(13) – C(14) – H(16)	109	N(11) – C(18) – C(17)	109(1)
C(13) – C(14) – H(15)	111	N(11) – C(18) – H(23)	109
C(13) – C(14) – H(16)	111	N(11) – C(18) – H(24)	107
H(15) – C(14) – H(16)	107	C(17) – C(18) – H(23)	113
N(13) – C(15) – C(16)	106(1)	C(17) – C(18) – H(24)	111
N(13) – C(15) – H(17)	111	H(23) – C(18) – H(24)	108

Table 4.1.4 Hydrogen bonds in [Cu(tcydan)(ade)].ClO_4.$2H_2O$ **(1)**

Donor (D) – H	Acceptor (A)	D – H (Å)	D···A (Å)	H···A (Å)	D – H···A (°)
N(6) – H(3)	N(7)	0.95	3.02	2.0	177
N(6) – H(4)	N(1)	0.96	3.00	2.1	163
N(11) – H(5)	N(3)	0.96	3.21	2.5	135
N(12) – H(6)	O(5)	0.98	2.95	2.0	174
N(13) – H(7)	O(6)	0.97	3.03	2.1	162
N(14) – H(8)	O(1)	0.97	3.07	2.2	150
N(14) – H(6)	O(2)	0.97	3.51	2.8	128

O(5)	O(3)	3.03
O(5)	O(6)	2.87
O(6)	N(3)	3.12

4.2 Structure of [{Cu(tcydan)}$_2$(hypoxanth)].$(ClO_4)_3$ (2)

The complex **2** involves a $[\{Cu(tcydan)\}_2(hypoxanth)]^{3+}$ cation and three perchlorate anions in the asymmetric unit (Fig. 4.2.1). The molecular formula and molecular weight of the complex **2** are $C_{21}H_{43}Cl_3N_{12}O_{13}Cu_2$ and M = 905.02, respectively.

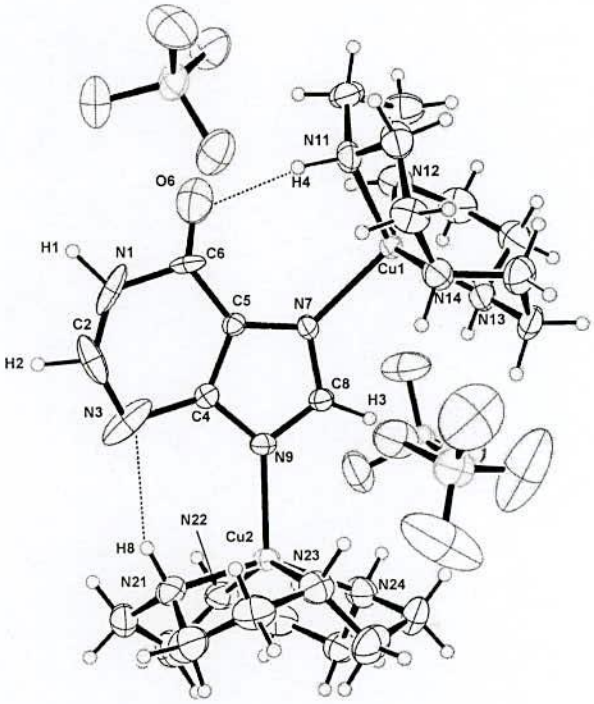


Fig. 4.2.1 Molecular structure of [{Cu(tcydan)}$_2$(hypoxanthinato)].$(ClO_4)_3$

In the structure of the $[\{Cu(tcydan)\}_2(hypoxanth)]^{3+}$ cation, two square-pyramidal Cu^{2+} ions bind to a hypoxanth ligand, one through N(7) (Cu(1)-N(7) = 2.111(6)(Å), and the other through deprotonated N(9) (Cu(2)-N(9) = 2.096(6)(Å). This is second X-ray example of a hypoxanthine in the anionic form; the first is observed in $[\{Cu(tren)\}_2(hypoxanth)]^{3+}$ [65]. Interestingly, intramolecular interligand hydrogen bonds are formed for each metal bonding: a hydrogen bond between the exocyclic O(6) of the base and secondary amino group of tcydan (O(6)...N(11) =

3.01 Å) and O(6)...H(4) = 2.3 Å) for the N(7)-metal bonding, and another hydrogen bond between the ring nitrogen N(3) of the base and amino group of tcydan (N(3)...N(21) = 3.15 Å and N(3)...H(8) = 2.4 Å) for the N(9)-metal bonding, as is the case for the adenine complex **1**. The crystal structure data and the molecular dimensions of the metal coordinations and of the tcydan ligands in the two $[Cu(tcydan)]^{2+}$ fragments are listed in Table 4.2.1, Table 4.2.2 and Table 4.2.3. The metal coordination effects on the molecular dimensions of the hypoxanthine molecule (listed in Table 4.2.2 and Table 4.2.3) are comparable with the literature value mentioned in [65], in which the hypoxanthine exists as a monvalent anion with both N(7) and N(9) deprotonated and the bond angles C(5)-N(7)-C(8) = 103.2(5)° and C(4)-N(9)-C(8) = 103.2(5) ° are essentially the same as those observed in $[\{Cu(tren)\}_2(hapoxanthinato)].(ClO_4)_3$ [65]. Fig. 4.2.2 shows the crystal packing and Table 4.2.4 lists hydrogen bonds. Two $[\{Cu(tcydan)\}_2(hypoxanth)]^{3+}$ cations associate across an inversion center to form a dimer structure (shown in Fig. 4.2.3) in which two hypoxanthine rings are stacked to each other with an average spacing of 3.25 Å, and a hydrogen bond is formed between the O(6) of hypoxanthine of one unit and the N(22) of tcydan of the another unit (O(6)...N(22) = 3.04 Å). These dimer structures are rather loosely packed in such a way that they do not directly contact with themselves but with perchlorate anions through weak hydrogen bonds. One of the perchlorate anion is linked with one of the tcydan moiety, forming a hydrogen bond between O(21) and N(14), (N(14)...O(21) = 3.05 Å and H(7)...O(21) = 2.1 Å).

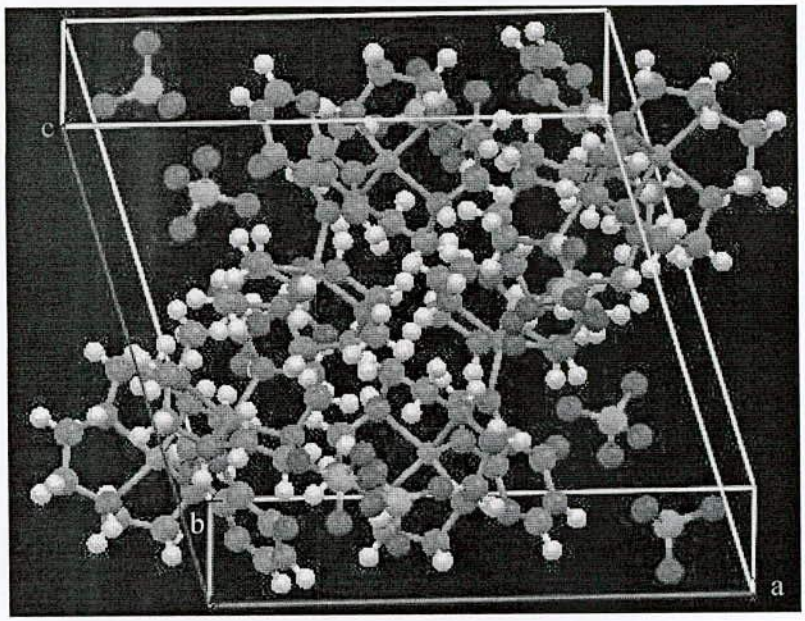


Fig. 4.2.2 View of the crystal packing in **2**

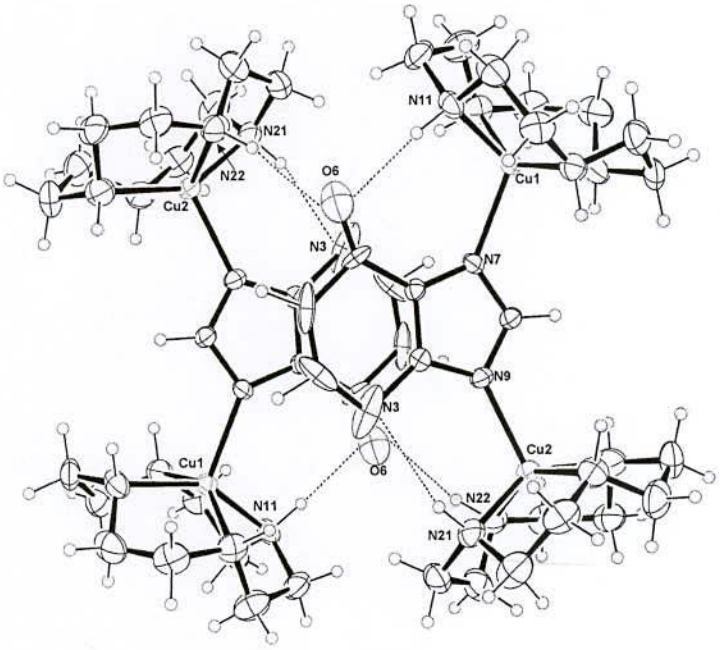


Fig. 4.2.3 The formation of a dimeric structure in **2**, composed of antiparallely self-stacked hypoxanthines across an inversion center. Broken lines denote hydrogen bonds.

Table 4.2.1 Crystal data and structure refinement for $[\{Cu(tcydan)\}_2(hypoxanth)].(ClO_4)_3$. **(2)**

Complex **(2)**	$[\{Cu(tcydan)\}_2(hypoxanth)].(ClO_4)_3$
Empirical formula	$C_{21}H_{43}N_{12}O_{13}Cl_3Cu_2$
Formula weight	905.02
Color of the crystal	Blue
Crystal size (mm)	0.4 X 0.3 X 0.2
Temperature (K)	293(2)
Wavelength	0.7107 Å
Crystal system	Monoclinic
Space group	$P2_1/a$
Unit cell dimensions	a = 16.281(2) Å, b = 15.009(4) Å, c = 15.389(2) Å
	β = 105.034(9)°
Volume	3632(1) $Å^3$
Z	4
Crystal density (gcm^{-3})	1.655
Absorption coefficient (mm^{-1})	1.4667
F(000)	1864
Theta range for data collection	2.0 to 27.4957°
Scan technique	ω-2θ
Limiting indices	$-11 \le h \le 21$, $-3 \le k \le 19$, $-19 \le l \le 19$
Reflections collected/unique	10365/4246
Completeness to theta	Full
Absorption correction	Empirical (ψ-scan)
Refinement method	Full-matrix least-squares on F
Reflection measured	10365
Data/restraints/parameters	4246/0/460
Goodness-of-fit	1.620
Final R indices [I>2σ(I)]	R^a = 0.0580, $R_w{}^b$ = 0.0600
Max./ min. residual (e $Å^{-3}$)	1.8862/-1.1334

[a] $R = \sum ||F_o| - |F_c|| / \sum |F_o|$.

[b] $R_w = [\sum w(|F_o| - |F_c|)^2 / \sum w|F_o|^2]^{1/2}$.

Table 4.2.2 Bond lengths of $[\{Cu(tcydan)\}_2(hypoxanth)].(ClO_4)_3$ **(2)**

Bond	Distance	Bond	Distance
Cu(1) – N(7)	2.111(5)	N(11) – H(4)	0.97
Cu(1) – N(11)	2.014(6)	N(12) – C(12)	1.42(1)
Cu(1) – N(12)	2.018(7)	N(12) – C(13)	1.52(1)
Cu(1) – N(13)	2.041(6)	N(12) – H(5)	0.98
Cu(1) – N(14)	2.032(7)	N(13) – C(14)	1.44(1)
Cu(2) – N(9)	2.096(6)	N(13) – C(15)	1.52(1)
Cu(2) – N(21)	2.003(7)	N(13) – H(6)	0.97
Cu(2) – N(22)	2.028(7)	N(14) – C(16)	1.44(1)
Cu(2) – N(23)	2.042(7)	N(14) – C(17)	1.50(1)
Cu(2) – N(24)	2.019(7)	N(14) – H(7)	0.97
Cl(1) – O(11)	1.421(7)	N(21) – C(21)	1.50(1)
Cl(1) – O(12)	1.416(7)	N(21) – C(28)	1.42(1)
Cl(1) – O(13)	1.429(7)	N(21) – H(8)	0.96
Cl(1) – O(14)	1.410(7)	N(22) – C(22)	1.43(1)
Cl(2) – O(15)	1.414(7)	N(22) – C(23)	1.50(1)
Cl(2) – O(16)	1.399(7)	N(22) – H(9)	0.96
Cl(2) – O(17)	1.395(6)	N(23) – C(24)	1.44(1)
Cl(2) – O(18)	1.415(7)	N(23) – C(25)	1.51(1)
Cl(3) – O(19)	1.30(1)	N(23) – H(10)	0.97
Cl(3) – O(20)	1.36(1)	N(24) – C(26)	1.45(1)
Cl(3) – O(21)	1.405(6)	N(24) – C(27)	1.51(1)
Cl(3) – O(22)	1.320(10)	N(24) – H(11)	0.97
O(6) – C(6)	1.17(1)	C(2) – H(2)	0.98
N(1) – C(2)	1.30(1)	C(4) – C(5)	1.386(9)
N(1) – C(6)	1.44(1)	C(5) – C(6)	1.378(9)
N(1) – H(1)	0.97	C(8) – H(3)	0.96
N(3) – C(2)	1.28(1)	C(11) – C(12)	1.50(1)
N(3) – C(4)	1.51(1)	C(11) – H(12)	0.98
N(7) – C(5)	1.366(8)	C(11) – H(13)	0.95
N(7) – C(8)	1.344(8)	C(12) – H(14)	0.96
N(9) – C(4)	1.365(8)	C(12) – H(15)	0.97
N(9) – C(8)	1.345(9)	C(13) – C(14)	1.51(2)
N(11) – C(11)	1.52(1)	C(13) – H(16)	0.97
N(11) – C(18)	1.43(1)	C(13) – H(17)	0.96
C(14) – H(18)	0.96	C(22) – H(31)	0.96
C(14) – H(19)	0.96	C(23) – C(24)	1.50(1)

C(15) – C(16)	1.49(1)	C(23) – H(32)	0.96
C(15) – H(20)	0.97	C(23) – H(33)	0.96
C(15) – H(21)	0.95	C(24) – H(34)	0.97
C(16) – H(22)	0.97	C(24) – H(35)	0.96
C(16) – H(23)	0.97	C(25) – C(26)	1.51(2)
C(17) – C(18)	1.50(1)	C(25) – H(36)	0.95
C(17) – H(24)	0.96	C(25) – H(37)	0.97
C(17) – H(25)	0.97	C(26) – H(38)	0.96
C(18) – H(26)	0.97	C(26) – H(39)	0.97
C(18) – H(27)	0.97	C(27) – C(28)	1.52(2)
C(21) – C(22)	1.51(1)	C(27) – H(40)	0.96
C(21) – H(28)	0.96	C(27) – H(41)	0.97
C(21) – H(29)	0.98	C(28) – H(42)	0.96
C(22) – H(30)	0.97	C(28) – H(43)	0.97

Table 4.2.2 Bond angles of $[\{Cu(tcydan)\}_2(hypoxanth)].(ClO_4)_3$ **(2)**

Angle	Degree	Angle	Degree
N(7) – Cu(1) – N(11)	107.6(2)	O(19) – Cl(3) – O(22)	117.5(9)
N(7) – Cu(1) – N(12)	114.3(3)	O(20) – Cl(3) – O(21)	109.4(7)
N(7) – Cu(1) – N(13)	105.5(2)	O(20) – Cl(3) – O(22)	101(1)
N(7) – Cu(1) – N(14)	99.3(3)	O(21) – Cl(3) – O(22)	112.3(6)
N(11) – Cu(1) – N(12)	85.9(3)	C(2) – N(1) – C(6)	123.6(8)
N(11) – Cu(1) – N(13)	146.4(3)	C(2) – N(1) – H(1)	119
N(11) – Cu(1) – N(14)	84.6(3)	C(6) – N(1) – H(1)	117
N(12) – Cu(1) – N(13)	85.5(3)	C(2) – N(3) – C(4)	101.2(9)
N(12) – Cu(1) – N(14)	146.4(3)	Cu(1) – N(7) – C(5)	131.3(4)
N(13) – Cu(1) – N(14)	84.9(3)	Cu(1) – N(7) – C(8)	123.8(4)
N(9) – Cu(2) – N(21)	103.5(3)	C(5) – N(7) – C(8)	103.2(5)
N(9) – Cu(2) – N(22)	111.9(3)	Cu(2) – N(9) – C(4)	131.1(5)
N(9) – Cu(2) – N(23)	110.1(3)	Cu(2) – N(9) – C(8)	125.4(5)
N(9) – Cu(2) – N(24)	102.1(3)	C(4) – N(9) – C(8)	103.2(5)
N(21) – Cu(2) – N(22)	86.0(3)	Cu(1) – N(11) – C(11)	106.6(5)
N(21) – Cu(2) – N(23)	146.2(3)	Cu(1) – N(11) – C(18)	107.2(5)
N(21) – Cu(2) – N(24)	85.0(3)	Cu(1) – N(11) – H(4)	110
N(22) – Cu(2) – N(23)	84.7(3)	C(11) – N(11) – C(18)	113.6(7)
N(22) – Cu(2) – N(24)	146.0(3)	C(11) – N(11) – H(4)	110
N(23) – Cu(2) – N(24)	84.8(3)	C(18) – N(11) – H(4)	109

O(11) – Cl(1) – O(12)	108.5(4)	Cu(1) – N(12) – C(12)	105.7(6)
O(11) – Cl(1) – O(13)	109.6(5)	Cu(1) – N(12) – C(13)	107.5(6)
O(11) – Cl(1) – O(14)	108.4(5)	Cu(1) – N(12) – H(5)	110
O(12) – Cl(1) – O(13)	110.8(5)	C(12) – N(12) – C(13)	113.3(8)
O(12) – Cl(1) – O(14)	111.4(5)	C(12) – N(12) – H(5)	109
O(13) – Cl(1) – O(14)	108.2(5)	C(13) – N(12) – H(5)	111
O(15) – Cl(2) – O(16)	107.0(5)	Cu(1) – N(13) – C(14)	105.2(6)
O(15) – Cl(2) – O(17)	111.0(5)	Cu(1) – N(13) – C(15)	106.6(5)
O(15) – Cl(2) – O(18)	108.4(5)	Cu(1) – N(13) – H(6)	111
O(16) – Cl(2) – O(17)	112.2(5)	C(14) – N(13) – C(15)	114.4(8)
O(16) – Cl(2) – O(18)	105.9(5)	C(14) – N(13) – H(6)	109
O(17) – Cl(2) – O(18)	112.1(5)	C(15) – N(13) – H(6)	111
O(19) – Cl(3) – O(20)	103(1)	Cu(1) –N(14) – C(16)	105.5(6)
O(19) – Cl(3) – O(21)	112.2(6)	Cu(1) – N(14) – C(17)	107.1(5)
Cu(1) – N(14) – H(7)	110	C(4) – C(5) – C(6)	120.4(7)
C(16) – N(14) – C(17)	115.8(7)	O(6) – C(6) – N(1)	115.8(8)
C(16) – N(14) – H(7)	109	O(6) – C(6) – C(5)	133.3(9)
C(17) – N(14) – H(7)	110	N(1) – C(6) – C(5)	110.0(7)
Cu(2) – N(21) – C(21)	107.0(5)	N(7) – C(8) – N(9)	115.6(6)
Cu(2) – N(21) – C(28)	107.8(6)	N(7) – C(8) – H(3)	122
Cu(2) – N(21) – H(8)	110	N(9) – C(8) – H(3)	122
C(21) – N(21) – C(28)	113.2(8)	N(11) – C(11) – C(12)	110.3(7)
C(21) – N(21) – H(8)	111	N(11) – C(11) – H(12)	109
C(28) – N(21) – H(8)	108	N(11) – C(11) – H(13)	110
Cu(2) – N(22) – C(22)	105.6(6)	C(12) – C(11) – H(12)	109
Cu(2) – N(22) – C(23)	107.7(5)	C(12) – C(11) – H(13)	111
Cu(2) – N(22) – H(9)	110	H(12) – C(11) – H(13)	107
C(22) – N(22) – C(23)	114.4(8)	N(12) – C(12) – C(11)	108.7(8)
C(22) – N(22) – H(9)	109	N(12) – C(12) – H(14)	109
C(23) – N(22) – H(9)	110	N(12) – C(12) – H(15)	111
Cu(2) – N(23) – C(24)	104.9(5)	C(11) – C(12) – H(14)	110
Cu(2) – N(23) – C(25)	108.2(5)	C(11) – C(12) – H(15)	111
Cu(2) – N(23) – H(10)	110	H(14) –C(12) – H(15)	107
C(24) – N(23) – C(25)	113.9(8)	N(12) – C(13) – C(14)	109.0(7)
C(24) – N(23) – H(10)	109	N(12) – C(13) – H(16)	111
C(25) – N(23) – H(10)	110	N(12) – C(13) – H(17)	111
Cu(2) – N(24) – C(26)	105.5(6)	C(14) – C(13) – H(16)	109
Cu(2) – N(24) – C(27)	107.5(6)	C(14) – C(13) – H(17)	110

Cu(2) – N(24) – H(11)	110	H(16) – C(13) – H(17)	107
C(26) – N(24) – C(27)	115.1(8)	N(13) – C(14) – C(13)	108.5(8)
C(26) – N(24) – H(11)	109	N(13) – C(14) – H(18)	110
C(27) – N(24) – H(11)	110	N(13) – C(14) – H(19)	111
N(1) – C(2) – N(3)	136(1)	C(13) – C(14) – H(18)	109
N(1) – C(2) – H(2)	110	C(13) – C(14) – H(19)	111
N(3) – C(2) – H(2)	114	H(18) – C(14) – H(19)	107
N(3) – C(4) – N(9)	122.1(6)	N(13) – C(15) – C(16)	109.9(7)
N(3) – C(4) – C(5)	128.9(6)	N(13) – C(15) – H(20)	110
N(9) – C(4) – C(5)	109.0(6)	N(13) – C(15) – H(21)	111
N(7) – C(5) – C(4)	109.0(6)	C(16) – C(15) – H(20)	108
N(7) – C(5) – C(6)	130.5(7)	C(16) – C(15) – H(21)	111
H(20) – C(15) – H(21)	107	C(24) – C(23) – H(32)	110
N(14) – C(16) – C(15)	107.2(7)	C(24) – C(23) – H(33)	108
N(14) – C(16) – H(22)	110	H(32) – C(23) – H(33)	108
N(14) – C(16) – H(23)	112	N(23) – C(24) – C(23)	107.6(8)
C(15) – C(16) – H(22)	109	N(23) – C(24) – H(34)	112
C(15) – C(16) – H(23)	111	N(23) – C(24) – H(35)	111
H(22) – C(16) – H(23)	107	C(23) –C(24) – H(34)	110
N(14) – C(17) – C(18)	109.5(7)	C(23) – C(24) – H(35)	109
N(14) – C(17) – H(24)	110	H(34) – C(24) – H(35)	107
N(14) – C(17) – H(25)	110	N(23) – C(25) – C(26)	108.0(7)
C(18) – C(17) – H(24)	110	N(23) – C(25) – H(36)	111
C(18) – C(17) – H(25)	110	N(23) – C(25) – H(37)	110
H(24) – C(17) – H(25)	107	C(26) – C(25) – H(36)	112
N(11) – C(18) – C(17)	107.1(7)	C(26) – C(25) – H(37)	109
N(11) – C(18) – H(26)	110	H(36) – C(25) – H(37)	108
N(11) – C(18) – H(27)	112	N(24) – C(26) – C(25)	108.5(9)
C(17) – C(18) – H(26)	110	N(24) – C(26) – H(38)	112
C(17) – C(18) – H(27)	111	N(24) – C(26) – H(39)	110
H(26) – C(18) – H(27)	107	C(25) – C(26) – H(38)	111
N(21) – C(21) – C(22)	110.4(7)	C(25) – C(26) – H(39)	109
N(21) – C(21) – H(28)	111	H(38) – C(26) – H(39)	107
N(21) – C(21) – H(29)	110	N(24) – C(27) – C(28)	109.2(7)
C(22) – C(21) – H(28)	111	N(24) – C(27) – H(40)	110
C(22) – C(21) – H(29)	108	N(24) – C(27) – H(41)	110
H(28) – C(21) – H(29)	106	C(28) – C(27) – H(40)	111
N(22) – C(22) – C(21)	107.7(8)	C(28) – C(27) – H(41)	109

N(22) – C(22) – H(30)	111	H(40) – C(27) – H(41)	108
N(22) – C(22) – H(31)	111	N(21) – C(28) – C(27)	107.1(9)
C(21) – C(22) – H(30)	111	N(21) – C(28) – H(42)	111
C(21) – C(22) – H(31)	110	N(21) – C(28) – H(43)	110
H(30) – C(22) –H(31)	107	C(27) – C(28) – H(42)	111
N(22) – C(23) – C(24)	109.0(7)	C(27) – C(28) – H(43)	110
N(22) – C(23) – H(32)	111	H(42) – C(28) – H(43)	107
N(22) – C(23) – H(33)	111		

Table 4.2.4 Hydrogen bonds in[{Cu(tcydan)}$_2$(hypoxanth)].$(ClO_4)_3$ **(2)**

Donor (D) – H	Acceptor (A)	D – H (Å)	D···A (Å)	H···A (Å)	D – H···A (°)
N(11) – H(4)	O(6)	0.97	3.01	2.3	132
N(11) – H(4)	O(11)	0.97	3.21	2.4	140
N(11) – H(4)	O(12)	0.97	3.17	2.6	117
N(13) – H(6)	O(15)	0.97	3.48	2.6	158
N(13) – H(6)	O(18)	0.97	3.27	2.4	147
N(14) – H(7)	O(21)	0.97	3.05	2.1	175
N(21) – H(8)	N(3)	0.96	3.15	2.4	132
N(22) – H(9)	O(6)	0.96	3.04	2.1	167
N(23) – H(10)	O(15)	0.97	3.23	2.3	162
N(23) – H(10)	O(16)	0.97	3.23	2.6	144
O(6)	O(11)		3.29		
O(6)	O(12)		3.16		
O(6)	O(14)		3.451		

4.3 Structure of $[Cu(tcydan)(theophy)]_3.(ClO_4)_3.2H_2O$ (4)

The complex **3** consists of three $[Cu(tcydan)(theophy)]^+$ cations (Mol. 1, Mol. 2 and Mol. 3), three perchlorate anions, and two crystallization water molecules in the asymmetric unit. Molecular formula and molecular weight of the complex **3** are $C_{45}H_{85}Cl_3N_{24}O_{20}Cu_3$ and M = 1579.34, respectively. In the structure of each $[Cu(tcydan)(theophy)]^+$ cation, the square-pyramidal Cu^{2+} ion binds to a theophy ligand through N(7) and four nitrogens of a tcydan ligand, as observed in complexes **2** and **3** (Fig. 4.3.1) .

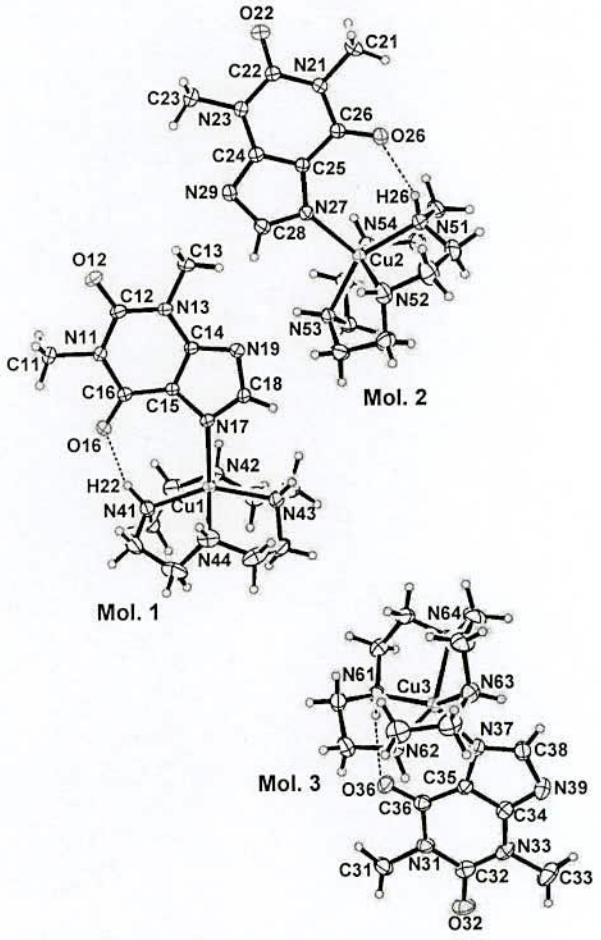


Fig. 4.3.1 Molecular structure of $[Cu(tcydan)(theophy)]_3^{3+}$ cation

In each $[Cu(tcydan)(theophy)]^+$ cationic structure, a deprotonated theophylline base coordinates axially to a Cu^{2+} ion at N(7) position, (Cu(1)-N(17) = 2.122(3) Å, Cu(2)-N(27) = 2.103(4) Å and Cu(3)-N(37) = 2.111(4) Å), while four nitrogens of tcydan ligand occupy the equatorial positions. Each $[Cu(tcydan)(theophy)]^+$ cation involves an intramolecular interligand hydrogen bond between the exocylic keto substituent O(6) of the base and one of amino nitrogen of tcydan ligand, (N(41)...O(16) = 2.85 Å, N(51)...O(26) = 2.80 Å and N(61)...O(36) = 2.91 Å). The crystal data with structure refinement and the molecular dimensions of the asymmetric unit are listed in Table 4.3.1, Table 4.3.2 and Table 4.3.3. Fig. 4.3.2 shows the crystal packing and Table 4.3.4 lists hydrogen bonds and other short contacts. In this structure Mol. 1 and Mol. 2 form two

hydrogen bonds through exocyclic keto oxygen of each base and one of the nitrogen of tcydan ligand (O(12)...N(54) = 2.89 Å and O(22)...N(42) = 2.88 Å). Mol. 1 forms another hydrogen bond with Mol. 3 through one of the nitrogen of tcydan ligand (N(44)...O(32) = 2.84 Å), (shown in Fig. 4.3.3), creating a trimeric structure. The $[Cu(tcydan)(theophy)]^+$ cation stacked along the c axis and further packed along b axis. The perchlorate counter anions occupy the voids created by the packing of $[Cu(tcydan)(theophy)]^+$ cations. N(43) of tcydan ligand forms a hydrogen bond with O(29) of perchlorate anion, while O(30) forms a H-bond with O(1) water molecule which is linked with O(2) water through hydrogen bonding.

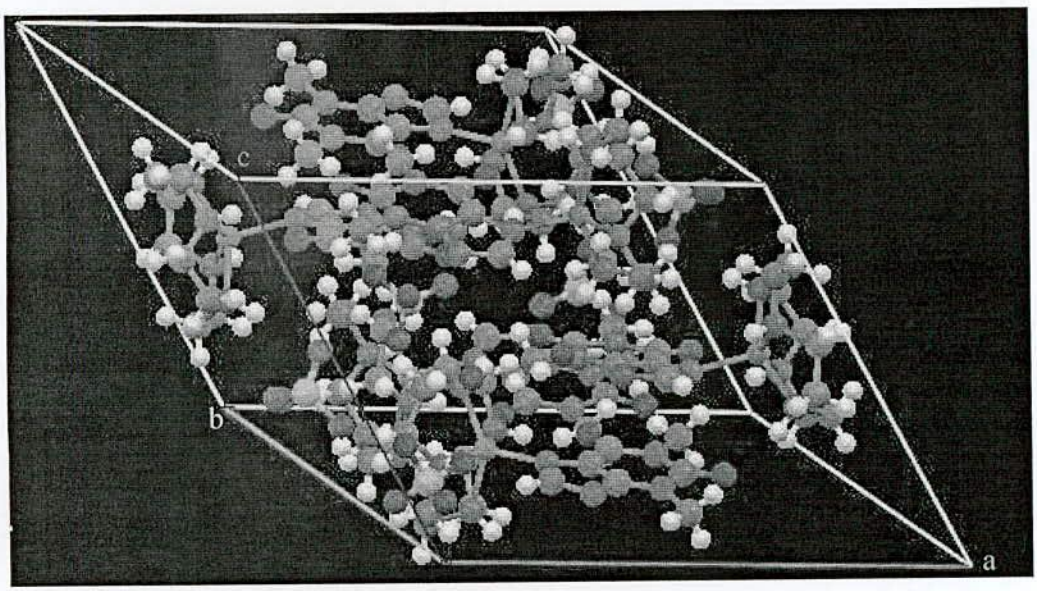


Fig. 4.3.2 View of crystal packing of complex **3**

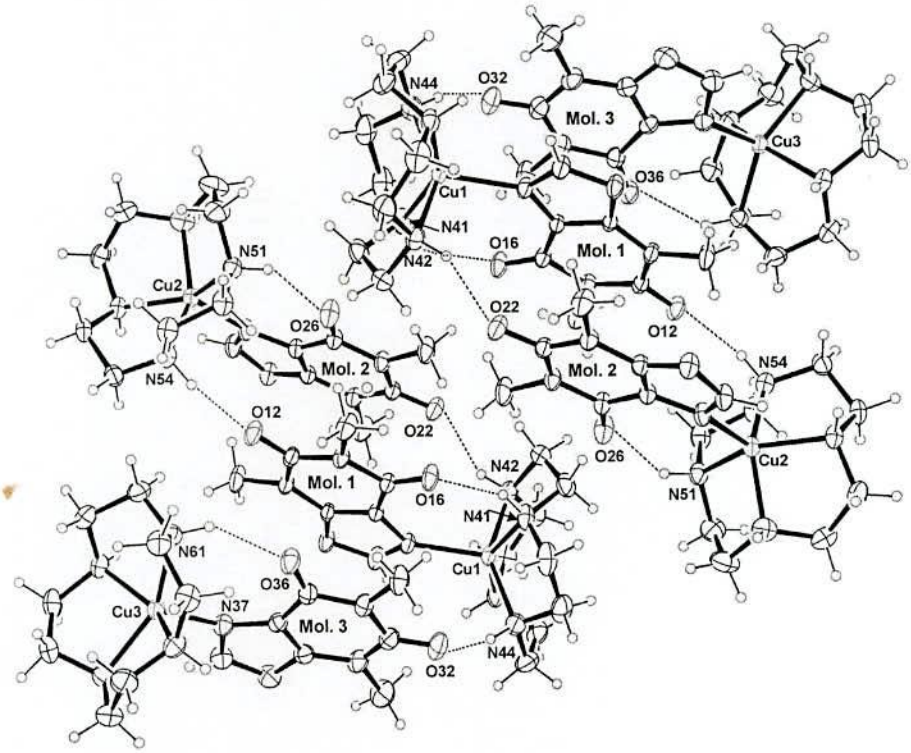


Fig. 4.3.3 Trimeric structure constructed by hydrogen bonded theophyllines (broken lines denote hydrogen bonds) of complex **3**

Table 4.3.1 Crytal data and structure refinement for $[Cu(tcydan)(theophy)]_3.(ClO_4)_3.\ 2H_2O$ **(3)**

Complex **(4)**	$[Cu(tcydan)(theophy)]_3.(ClO_4)_3.(H_2O)_2$
Empirical formula	$C_{45}H_{85}N_{24}O_{20}Cl_3Cu_3$
Formula weight	1579.32
Color of the crystal	Blue
Crystal size (mm)	0.5 X 0.4 X 0.3
Temperature (K)	298(2)
Wavelength	0.7107 Å
Crystal system	Triclinic
Space group	*P*-1
Unit cell dimensions	$a = 15.841(3)$ Å, $b = 16.639(2)$ Å, $c = 15.209(3)$ Å
	$\alpha = 95.007(13)°$, $\beta = 116.930(12)°$, $\gamma = 108.735(12)°$
Volume	3253.6(9) $Å^3$
Z	2

Crystal density	1.575 gcm^{-3}
Absorption coefficient	1.180 mm^{-1}
$F(000)$	1602
Theta range for data collection	2.50 to 27.50°
Scan technique	ω-2θ
Limiting indices	$-20 \leq h \leq 11$, $-20 \leq k \leq 21$, $-17 \leq l \leq 19$
Reflections collected/unique	14942/9652
Completeness to theta	Full
Absorption correction	Empirical (ψ-scan)
Refinement method	Full-matrix least-squares on F
Reflection measured	14942
Data/restraints/parameters	9652/0/856
Goodness-of-fit	0.922
Final R indices [I>2σ(I)]	$R^a = 0.0576$, $R_w{}^b = 0.1607$
Max./ min. residual ($e Å^{-3}$)	1.018/-0.651

[a] $R = \sum | |F_o| - |F_c| | / \sum |F_o|$.

[b] $R_w = [\sum w(|F_o| - |F_c|)^2 / \sum w |F_o|^2]^{1/2}$.

Table 4.3.2 Bond lengths of $[Cu(tcydan)(theophy)]_3.(ClO_4)_3.2H_2O$ **(3)**

Bond	Distance	Bond	Distance
Cu(1) – N(41)	2.016(4)	N(21) – C(22)	1.385(6)
Cu(1) – N(43)	2.038(4)	N(21) – C(26)	1.400(5)
Cu(1) – N(44)	2.040(4)	N(21) – C(21)	1.468(6)
Cu(1) – N(42)	2.074(4)	N(11) – C(12)	1.392(5)
Cu(1) – N(17)	2.122(3)	N(11) – C(16)	1.421(5)
Cu(2) – N(52)	2.021(5)	N(11) – C(11)	1.474(6)
Cu(2) – N(51)	2.027(4)	N(42) – C(43)	1.466(7)
Cu(2) – N(54)	2.045(4)	N(42) – C(42)	1.483(7)
Cu(2) – N(53)	2.063(4)	N(29) – C(24)	1.352(6)
Cu(2) – N(27)	2.103(4)	N(29) – C(28)	1.361(6)
O(16) – C(16)	1.221(5)	N(52) – C(53)	1.473(7)
N(27) – C(28)	1.334(6)	N(52) – C(52)	1.501(7)
N(27) – C(25)	1.394(5)	N(44) – C(47)	1.472(8)
N(54) – C(57)	1.472(6)	N(44) – C(46)	1.475(8)
N(54) – C(56)	1.476(6)	Cu(3) – N(61)	2.018(4)
N(17) – C(18)	1.331(5)	Cu(3) – N(62)	2.044(4)
N(17) – C(15)	1.390(5)	Cu(3) – N(63)	2.046(4)

O(26) – C(26)	1.238(5)	Cu(3) – N(64)	2.052(4)
O(22) – C(22)	1.232(5)	Cu(3) – N(37)	2.111(4)
N(53) – C(55)	1.477(6)	N(61) – C(61)	1.482(6)
N(53) – C(54)	1.486(6)	N(61) – C(68)	1.494(6)
O(12) – C(12)	1.221(5)	N(37) – C(38)	1.330(6)
N(23) – C(22)	1.368(5)	N(37) – C(35)	1.375(6)
N(23) – C(24)	1.382(5)	O(36) – C(36)	1.220(6)
N(23) – C(23)	1.458(6)	N(64) – C(67)	1.482(7)
N(41) – C(41)	1.467(7)	N(64) – C(66)	1.497(7)
N(41) – C(48)	1.487(8)	N(31) – C(32)	1.393(6)
N(13) – C(12)	1.368(6)	N(31) – C(36)	1.418(6)
N(13) – C(14)	1.375(5)	N(31) – C(31)	1.476(7)
N(13) – C(13)	1.462(6)	N(63) – C(65)	1.473(7)
N(43) – C(44)	1.467(7)	N(63) – C(64)	1.497(8)
N(43) – C(45)	1.480(7)	O(32) – C(32)	1.228(6)
N(51) – C(51)	1.444(7)	N(62) – C(63)	1.485(8)
N(51) – C(58)	1.485(7)	N(62) – C(62)	1.497(7)
N(33) – C(32)	1.353(7)	C(14) – C(15)	1.380(5)
N(33) – C(34)	1.385(6)	C(15) – C16)	1.415(6)
N(33) – C(33)	1.461(7)	C(24) – C(25)	1.366(6)
N(39) – C(34)	1.344(7)	C(25) – C(26)	1.419(6)
N(39) – C(38)	1.368(7)	C(34) – C(35)	1.376(6)
Cl(3) – O(37)	1.351(7)	C(35) – C(36)	1.425(6)
Cl(3) – O(39)	1.353(6)	C(41) – C(42)	1.504(8)
Cl(3) – O(40)	1.371(9)	C(43) – C(44)	1.503(9)
Cl(3) – O(38)	1.418(5)	C(45) – C(46)	1.492(9)
Cl(2) – O(27)	1.369(6)	C(47) – C(48)	1.488(9)
Cl(2) – O(28)	1.370(6)	C(51) – C(52)	1.493(9)
Cl(2) – O(29)	1.404(5)	C(53) – C(54)	1.518(8)
Cl(2) – O(30)	1.470(8)	C(55) – C(56)	1.502(7)
Cl(1) – O(18)	1.284(8)	C(57) – C(58)	1.503(7)
Cl(1) – O(20)	1.316(9)	C(61) – C(62)	1.502(8)
Cl(1) – O(19)	1.323(8)	C(63) – C(64)	1.520(9)
Cl(1) – O(17)	1.349(10)	C(65) – C(66)	1.525(9)
N(19) – C(14)	1.346(5)	C(67) – C(68)	1.519(8)
N(19) – C(18)	1.371(6)		

Table 4.3.3 Bond angles of $[Cu(tcydan)(theophy)]_3.(ClO_4)_3.2H_2O$ **(3)**

Angle	Degree	Angle	Degree
N(41) – Cu(1) – N(43)	146.56(16)	C(24) – N(23) – C(23)	121.4(4)
N(41) – Cu(1) – N(44)	85.56(19)	C(41) – N(41) – C(48)	114.2(4)
N(43) – Cu(1) – N(44)	84.91(19)	C(41) – N(41) – Cu(1)	105.6(3)
N(41)– Cu(1) – N(42)	84.28(17)	C(48) – N(41) – Cu(1)	107.3(3)
N(43) – Cu(1) – N(42)	84.73(18)	C(12) – N(13) – C(14)	120.0(3)
N(44) – Cu(1) – N(42)	143.78(17)	C(12) – N(13) –C(13)	118.3(4)
N(41) – Cu(1) – N(17)	110.94(15)	C(14) – N(13) – C(13)	121.5(4)
N(43) – Cu(1)– N(17)	102.06(15)	C(44) – N(43) – C(45)	114.4(4)
N(44) – Cu(1) – N(17)	115.76(16)	C(44) – N(43) – Cu(1)	107.9(3)
N(42) – Cu(1) – N(17)	100.33(15)	C(45) – N(43) – Cu(1)	104.1(3)
N(52) – Cu(2) – N(51)	84.77(17)	C(51) – N(51) – C(58)	113.8(4)
N(52) – Cu(2) – N(54)	144.43(18)	C(51) – N(51) – Cu(2)	108.0(3)
N(51) – Cu(2) – N(54)	84.37(16)	C(58) – N(51) – Cu(2)	109.4(3)
N(52) – Cu(2) – N(53)	85.25(17)	C(22) – N(21) – C(26)	126.3(4)
N(51) – Cu(2) – N(53)	145.84(15)	C(22) – N(21) – C(21)	116.3(4)
N(54) – Cu(2) – N(53)	85.03(15)	C(26) – N(21) – C(21)	117.2(4)
N(52) – Cu(2) – N(27)	106.93(18)	C(12) – N(11) – C(16)	126.6(4)
N(51) – Cu(2) – N(27)	107.17(15)	C(12) – N(11) – C(11)	115.6(4)
N(54) – Cu(2) – N(27)	108.64(16)	C(16) – N(11) – C(11)	117.7(4)
N(53) – Cu(2) – N(27)	106.99(14)	C(43) – N(42) – C(42)	114.6(4)
C(28) – N(27) – C(25)	101.9(3)	C(43) – N(42) – Cu(1)	105.2(3)
C(28) – N(27) – Cu(2)	123.4(3)	C(42) – N(42) – Cu(1)	108.2(3)
C(25) – N(27) – Cu(2)	133.5(3)	C(24) – N(29) – C(28)	101.1(4)
C(57) – N(54) – C(56)	114.7(4)	C(53) – N(52) – C(52)	116.3(5)
C(57) – N(54) – Cu(2)	104.4(3)	C(53) – N(52) – Cu(2)	104.6(3)
C(56) – N(54) – Cu(2)	108.0(3)	C(52) – N(52) – Cu(2)	108.8(3)
C(18) – N(17) – C(15)	102.7(3)	C(47) – N(44) – C(46)	114.5(5)
C(18) – N(17) – Cu(1)	123.7(3)	C(47) – N(44) – Cu(1)	105.5(3)
C(15) – N(17) – Cu(1)	132.7(3)	C(46) – N(44) – Cu(1)	108.0(4)
C(55) – N(53) – C(54)	113.6(4)	N(61) – Cu(3) – N(62)	84.99(17)
C(55) – N(53) – Cu(2)	104.2(3)	N(61) – Cu(3) – N(63)	147.28(17)
C(54) – N(53) – Cu(2)	107.8(3)	N(62) – Cu(3) – N(63)	85.35(19)
C(22) – N(23) – C(24)	119.5(4)	N(61) – Cu(3) – N(64)	85.70(16)
C(22) – N(23) – C(23)	119.2(4)	N(62) – Cu(3) – N(64)	145.71(17)
N(63) – Cu(3) – N(64)	84.91(18)	O(27) – Cl(2) – O(30)	102.2(6)

N(61) – Cu(3) – N(37)	106.47(16)	O(28) – Cl(2) – O(30)	97.3(5)
N(62) – Cu(3) – N(37)	106.44(17)	O(29) – Cl(2) – O(30)	107.7(5)
N(63) – Cu(3) – N(37)	106.24(17)	O(18) – Cl(1) – O(20)	115.2(9)
N(64) – Cu(3) – N(37)	107.85(16)	O(18) – Cl(1) – O(19)	114.5(8)
C(61) – N(61) – C(68)	115.2(4)	O(20) – Cl(1) – O(19)	112.0(9)
C(61) – N(61) – Cu(3)	105.6(3)	O(18) – Cl(1) – O(17)	102.4(10)
C(68) – N(61) – Cu(3)	108.4(3)	O(20) – Cl(1) – O(17)	109.9(9)
C(38) – N(37) – C(35)	102.6(4)	O(19) – Cl(1) – O(17)	101.4(9)
C(38) – N(37) – Cu(3)	125.0(4)	C(14) – N(19) – C(18)	101.2(3)
C(35) – N(37) – Cu(3)	128.5(3)	O(12) – C(12) – N(13)	122.0(4)
C(67) – N(64) – C(66)	113.8(4)	O(12) – C(12) – N(11)	121.1(4)
C(67) – N(64) – Cu(3)	104.6(3)	N(13) – C(12) – N(11)	116.9(4)
C(66) – N(64) – Cu(3)	108.0(3)	N(19) – C(14) – N(13)	126.1(4)
C(32) – N(31) – C(36)	126.0(4)	N(19) – C(14) – C(15)	111.8(3)
C(32) – N(31) – C(31)	116.8(4)	N(13) – C(14) – C(15)	122.1(4)
C(36) – N(31) – C(31)	117.2(4)	C(14) – C(15) – N(17)	107.5(3)
C(65) – N(63) – C(64)	113.6(5)	C(14) – C(15) – C(16)	122.1(4)
C(65) – N(63) – Cu(3)	103.7(3)	N(17) – C(15) – C(16)	130.4(4)
C(64) – N(63) – Cu(3)	107.5(3)	O(16) – C(16) – C(15)	128.5(4)
C(63) – N(62) – C(62)	113.8(5)	O(16) – C(16) – N(11)	119.4(4)
C(63) – N(62) – Cu(3)	105.4(3)	C(15) – C(16) – N(11)	112.0(3)
C(62) – N(62) – Cu(3)	108.4(3)	N(17) – C(18) – N(19)	116.7(4)
C(32) – N(33) – C(34)	119.9(4)	O(22) – C(22) – N(23)	121.2(4)
C(32) – N(33) – C(33)	119.5(5)	O(22) – C(22) – N(21)	121.5(4)
C(34) – N(33) – C(33)	120.6(5)	N(23) – C(22) – N(21)	117.3(4)
C(34) – N(39) – C(38)	101.0(4)	N(29) – C(24) – C(25)	111.6(4)
O(37) – Cl(3) – O(39)	117.8(5)	N(29) – C(24) – N(23)	126.2(4)
O(37) – Cl(3) – O(40)	103.0(8)	C(25) – C(24) – N(23)	122.2(4)
O(39) – Cl(3) – O(40)	97.7(7)	C(24) – C(25) – N(27)	108.1(4)
O(37) – Cl(3) – O(38)	116.8(5)	C(24) – C(25) – C(26)	121.3(4)
O(39) – Cl(3) – O(38)	113.3(4)	N(27) – C(25) – C(26)	130.2(4)
O(40) – Cl(3) – O(38)	104.5(5)	O(26) – C(26) – N(21)	119.4(4)
O(27) – Cl(2) – O(28)	119.9(6)	O(26) – C(26) – C(25)	127.4(4)
O(27) – Cl(2) – O(29)	114.2(4)	N(21) – C(26) – C(25)	113.2(4)
O(28) – Cl(2) – O(29)	112.6(4)	N(27) – C(28) – N(29)	117.2(4)
O(32) – C(32) – N(33)	122.0(5)	N(44) – C(47) – C(48)	107.5(5)
O(32) – C(32) – N(31)	120.4(5)	N(41) – C(48) – C(47)	110.3(4)
N(33) – C(32) – N(31)	117.6(4)	N(51) – C(51) – C(52)	109.6(5)

N(39) – C(34) – C(35)	111.6(4)	C(51) – C(52) – N(52)	109.7(5)
N(39) – C(34) – N(33)	125.9(4)	N(52) – C(53) – C(54)	108.3(4)
C(35) – C(34) – N(33)	122.4(4)	N(53) – C(54) – C(53)	109.3(4)
N(37) – C(35) – C(34)	108.1(4)	N(53) – C(55) – C(56)	108.2(4)
N(37) – C(35) – C(36)	130.9(4)	N(54) – C(56) – C(55)	109.9(4)
C(34) – C(35) – C(36)	121.1(4)	N(54) – C(57) – C(58)	107.9(4)
O(36) – C(36) – N(31)	119.2(4)	N(51) – C(58) – C(57)	109.3(4)
O(36) – C(36) – C(35)	127.9(4)	N(61) – C(61) – C(62)	108.0(4)
N(31) – C(36) – C(35)	112.8(4)	N(62) – C(62) – C(61)	110.3(4)
N(37) – C(38) – N(39)	116.8(5)	N(62) – C(63) – C(64)	106.8(5)
N(41) – C(41) – C(42)	108.7(4)	N(63) – C(64) – C(63)	109.3(5)
N(42) – C(42) – C(41)	110.2(4)	N(63) – C(65) – C(66)	107.4(5)
N(42) – C(43) – C(44)	107.8(4)	N(64) – C(66) – C(65)	109.6(4)
N(43) – C(44) – C(43)	110.7(4)	N(64) – C(67) – C(68)	107.7(4)
N(43) – C(45) – C(46)	107.7(4)	N(61) – C(68) – C(67)	108.7(4)
N(44) – C(46) –C(45)	111.4(5)		

Table 4.3.4 Hydrogen bonds in $[Cu(tcydan)(theophy)]_3.(ClO_4)_3.2H_2O$ **(3)**

Donor (D) – H	Acceptor (A)	D – H (Å)	D···A (Å)	H···A (Å)	D – H···A (°)
N(41) – H(22)	O(16)	0.91	2.85	2.0	151
N(42) – H(23)	O(22)	0.91	2.88	2.1	147
N(43) – H(24)	O(29)	0.91	3.00	2.1	161
N(44) – H(25)	O(32)	0.91	2.84	2.0	160
N(51) – H(26)	O(26)	0.91	2.80	2.0	148
N(52) – H(27)	O(2)	0.91	2.83	2.0	162
N(53) – H(28)	N(19)	0.91	3.05	2.3	137
N(54) – H(29)	O(12)	0.91	2.90	2.0	156
N(61) – H(30)	O(36)	0.91	2.90	2.1	144
O(1)	O(2)		2.83		
O(1)	O(30)		3.00		
O(2)	O(2)		2.85		
N(39)	O(2)		2.922		

Metal bonding properties of nucleobases and interligand intramolecular interactions that effect metal binding sites on nucleobases

4.5 Discussion of Tcydan-Cu^{2+}- Amino acid based Ternary Complexes

The present study shows that tcydan and Cu^{2+} ion form ternary metal complexes with nucleobases like N(9)-unsubstituted adenine and guanine derivatives. For adenine, Cu^{2+} ion binds at deprotonated N(9) position of adenine with the formation of intramolecular interligand hydrogen bond between secondary amino group of tcydan and ring N(3) of the base. Metal complexes of adenine base whose crystal structures have been determined are listed in Table 5.1.

Table 5.1 Metal coordination site(s) in metal complexes of unsubstituted adenine base

Complex	Geometry about metal	Protonation site(s) at ring nitrogens	Coordination site(s)	Ref.
$[Cu(tren)(ade)].ClO_4$	trig. bipyr.	none	N9	[65]
$[Cu(tcydan)(ade)].ClO_4.2H_2O$	sq. pyr.	none	N9	this work
$[Ni(tren)(ade)(ClO_4)].adenine$	sq. bipyr.	none	N9	[66]
$[Zn(tren)(ade)].ClO_4$	trig. bipyr.	none	N9	[67]
$[Cd(tren)(ade)].ClO_4$	trig. bipyr.	none	N9	[67]
$[Ni(tren)(ade)].ClO_4$	sq. bipyr.	none	N9	[67]
$[Cu(ade)(glygly)(H_2O)]$	sq. pyr.	N7	N9	[70]
$[Cu_2(ade)_4Cl_2].Cl_2.6H_2O$	sq. pyr.	N7	N3, N9	[71]
$[Cu_2(ade)_4(H_2O)_2].(ClO_4)_4.2H_2O$	sq. pyr.	N7	N3, N9	[72]
$[Cu_3(AdeH)_2(\mu\text{-}Cl)_4Cl_4].4H_2O$	oct. sq. pyr.	N1, N7	N3, N9	[73]
$[Cu(adeH)_2Cl_2].Cl_2$	tet.	N1, N7	N9	[74]
$[Cu(adeH)_2Br_2].Br_2$	tet.	N1, N7	N9	[75]
$[Cu_2(ade^-)_4(H_2O)_2].6H_2O$	sq. pyr.	none	N3, N9	[76]
$[Cu(ade^-)_2(dien)].H_2O$	sq. pyr.	none	N9	[77]
$[Cu(ade^-)(tren)].Cl.2H_2O$	trig. bipyr.	none	N9	[54]
$[Co(ade)_2(H_2O)_4].(adeH)_2.(SO_4)_4.6H_2O$	oct.	N7	N9	[78]
$[Co^{III}(ade^-)(en)_2Cl].Br.H_2O$	oct.	none	N9	[79]
$[Ni(ade^-)(tren)Cl].Cl$	oct.	N7	N3	[55]
$[Zn(adeH)Cl_3]$	tet.	N1, N9	N7	[80]
$[Zn(adeH)Cl_3].(adeH).Cl$	tet.	N1, N9	N7	[81]

$[Cd(adeH)(H_2O)(NO_3)_2]_2.(NO_3)_2$	oct.	N1, N7	N3, N9	[82]
$[Ag_2(adeH)_2](ClO_4)_4.2H_2O$	appr. lin.	N1, N7	N9	[83]
$[Au^I(ade^-)(Ph_3P)]$	appr. lin.	none	N9	[84]
$[\{(\eta^6\text{-}C_6H_6)Ru(ade)Cl\}_4].Cl_4$	9-coordinated	N1	N7, N9	[85]
$[\{(\eta^6\text{-p-cymene})Ru(ade^-)\}_4].(CF_3SO_3)_4$	9-coordinated	none	N6, N7, N9	[86]
$[(thiacyclophane)Pd(ade)].BF_4$	sq.pl.	none	N3	[87]
$[Pd(ade^-)_2\{(n\text{-}Bu)_3P\}_2].4MeOH$	sq.pl.	none	N9	[88]
$[Cu(\mu^2\text{-ade})(H_2O)(glycinato)(NO_3)]$	oct.	N7	N1, N9	[89]
$[Co(ade)(dien)_2Cl].(Cl)_2.H_2O$	oct.	N7	N9	[90]
$[Zn(ade)(H_2O)(iminodiacetato)]$	oct.	N7	N9	[91]
$[Mn(ade)_2(H_2O)_4].(ClO_4)_2$	oct.	N7	N3	[92]
$[Cu(Ade)(H_2O)(glycylglycinato)]$	trig. bipyr.	N7	N9	[93]

In most of the crystal structures, metal ion(s) binds to adenine preferentially through N(9), or N(9)+N(3) among its five nitrogen atoms, N(1), N(3), N(6), N(7) and N(9). The metal-N(3) bonding is exceptional and only few structures are available. The authors suggest that the steric effects around the metal ion, that is, the octahedral geometry moiety might be responsible to the metal bonding to N(3), while the N(9) might be the preferential binding site for trigonal-bipyramidal geometry with lower steric hindrance. The mononuclear metal-N(7) bonding for N(9)-unsubstituted adenine has been observed, and it is always accompanied by the formation of an intamolecular hydrogen bond(s) between N(6) of the base and hydrogen bonding acceptor ligand.

For guanine derivatives N(7) is the preferred metal binding site. We conclude that hypoxanthine specifically binds to metal ion at N(7) and N(9) as a monoanionic ligand with the formation of intramolecular interligand hydrogen bonds between the amino group of tcydan and N(3), or O(6) of the base. So far reported metal-hypoxanthine complexes are listed in Table 5.2.

Table 5.2: Metal coordination sites in metal complexes of unsubstituted hypoxanthine base

Complex	Geometry about metal	Protonation site(s) at ring nitrogens	Coordination site(s)	Ref.
$[\{Cu(tcydan)\}_2(hypoxanth)].(ClO_4)_3$	sq. pyr.	N1	N7, N9	this work
$[\{Cu(tren)\}_2(hypoxanth)].(ClO_4)_3$	trig. bipyr.	N1	N7, N9	[65]
$[\{Ni(tren)(H_2O)\}_2(hypoxanth)].(ClO_4)_3.1.5H_2O$	sq. bipyr.	N1	N7, N9	[66]
$[Ni(tren)(H_2O)(hypoxanth)].ClO_4.2H_2O$	sq. bipyr.	N1, N7	N9	[66]
$[\{Ni(tren)(H_2O)\}_2(hypoxanth)]_2.(NO_3)_6.4.5H_2O$	sq. bipyr.	N1	N7, N9	[66]
$[Cu_2(hypoxanthine)_2(H_2O)_4(SO_4)_2]$	oct.	N1, N7	N3, N9	[94]
$[Cu(hypoxanthine)(H_2O)(SO_4)]_n$	tri. bipyr.	N1, N9	N3, N7	[95]
$[Co(hypoxanthine)(H_2O)_5].(SO_4)$	oct.	N1, N9	N7	[95]
$[Co_2(hypoxanthine)_2(H_2O)_4(SO_4)_2]$	oct.	N1, N7	N3, N9	[96]
$[Ni(hypoxanthine)(H_2O)_5].(SO_4)$	oct.	N1, N9	N7	[95]
$[Zn_2(hypoxanthine)_2(H_2O)_4(SO_4)_2]$	oct.	N1, N7	N3, N9	[94]
$[Cd_2(hypoxanthine)_2(H_2O)_4(SO_4)_2]$	oct.	N1, N7	N3, N9	[94]
$[Ru(hypoxanthine)(NH_3)_5].Cl_3.3H_2O$	oct.	N1, N9	N7	[97]
$[Cu_2(hypoxanthine)_4Cl_2].Cl_2.6H_2O$	sq. pyr.	N1, N7	N3, N9	[98]
$[\{Cd(tren)\}_2(hypoxanth)].(ClO_4)_3.0.5H_2O$	tri. bipyr.	N1	N7, N9	[68]
$[Zn(tren)(hypoxanth)].ClO_4.H_2O$	tri. bipyr.	N1	N9	[68]

The crystal structures so far reported show that there are mainly two types of structures, one type involving the metal bonding through both N(3) and N(9), or N(7) and N(9), and the other involving solely through N(7) or N(9). In the present study two tcydan-capped Cu^{2+} ions bind to a hypoxanthinate anion, one through N(7) and the other through N(9).

In the case of the tcydan-Cu^{2+}-xanthine system, it is found that xanthine binds to metal specifically through N(7) with the formation of intramolecular interligand hydrogen bond between amino group of tcydan and O(6) of the base. Metal complexes of xanthine are listed in Table 5.3.

In most of the xanthine complexes, metal ion binds to N(7), and protanation sites are N(1) and N(3). N(7) site is the most suitable site to bind with metal through formation of intramolecular interligand hydrogen bond with O(6) of the base.

Another guanine derivative theophylline binds with Cu^{2+} ion through N(7) with the formation of intramolecular interligand hydrogen bond between the nitrogen of tcydan and O(6) of the base. So far reported crystal structures of metal-theophylline complexes are listed in Table 5.4. It is found that theophylline is bonded with metal ion preferentially through N(7) position and our result is also in accord with that results.

Table 5.3: Metal coordination site(s) in metal complexes of unsubstituted theophylline base

Complex	Geometry about metal	Protonation site(s) at ring nitrogens	Coordination site(s)	Ref.
$[Cu(theophylline)(H_2O)_2Cl_2]$	sq. pyr.	N9	N7	[107]
$[Cu(tcydan)(theophy)]_3.(ClO_4)_3.2H_2O$	sq. pyr.	none	N7	this wok
$[Zn(theophylline)_2(en)]$	tetr.	none	N7	[108]
$[Cu(theophylline)_2Cl_2]$	tetr.	N9	N7	[109]
$[Rh^{II}Rh^{III}(theophylline)_2(\mu^2\text{-acetamidato})_4].NO_3.H_2O$	oct.	N9	N7	[60]
$[\{Pt(CH_3)_3\}(\mu^2\text{-theophylline})]_6.CH_3Cl$	oct.	none	N7, N9, O6	[48]
catena-$[Hg(theophylline)_2(\mu^2\text{-}NO_3)].NO_3$	tetr.	N9	N7	[110]
catena-$[Hg(\mu^2\text{-theophylline})(H_2O)Cl]$	tetr.	none	N7, N9	[110]
$[Rh_2(theophylline)_2(\mu^2\text{-acetato})_4].2H_2O$	oct.	N7	N9	[58]
$[Cu(theophylline)_2(H_2O)_3].2H_2O$	tri. bipyr.	none	N7	[111]

In summary, the adenine complex **1** involves the metal-N(9) bonding with the formation of an intramolecular interligand N(tcydan)-H...N(3) hydrogen bond. On the other hand, the absence of the possible metal bonding to N(7) or N(1) of adenine might be due to a steric repulsion, around the crowded metal center, between amino groups of tcydan and the N(6) amino group when the metal ion binds to N(7) or N(1) of the base. Each of the three oxopurine complexes **2** and **3**

commonly involves the metal-N(7) bonding with the formation of an interligand N(tcydan)-H...O(6) hydrogen bond. In addition, N(9) of the base is involved in the metal coordination with the formation of an interligand N(tcydan)-H...N(3) hydrogen bond in the hypoxanthine complex **2**, while a steric repulsion between amino groups of tcydan and the proton attached to the ring N(9) of xanthine or the methyl group at N(3) of theophylline may preclude metal-N(9) bonding in the theophylline complex **3**. These observations all support our hypothesis that interligand interactions could affect the site-specific metal bonding to nucleobases.

5.6 Biological Applications

5 mL 1μM solution of complex 1 was pertained in 1 L water containing fecal coliform and total coliform for 1 hour. Fecal coliform (FC) and total coliform (TC) were counted before and after treatment as shown in figure 4.5.1 and 4.5.2. It is seen from the figure that after treatment water is FC and TC free. Similar results were obtained for other two complexes.

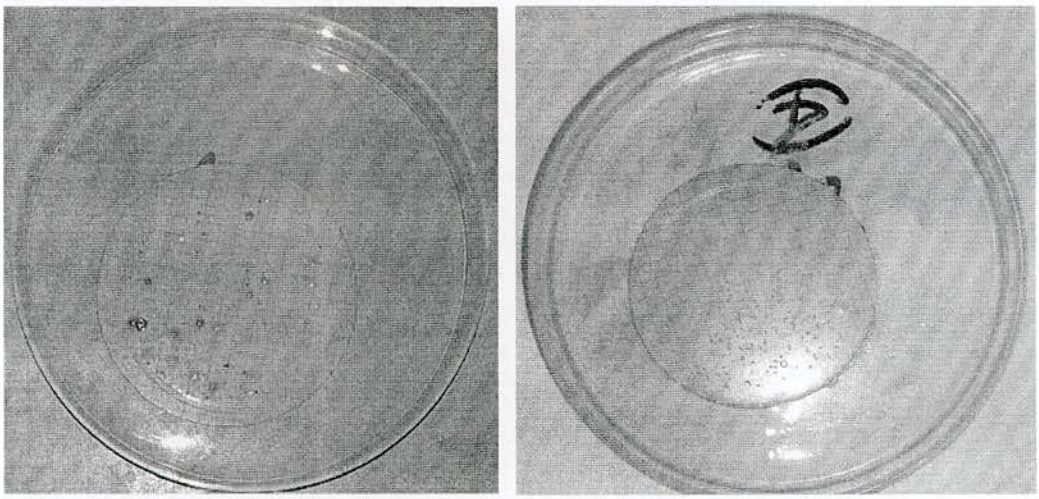


Figure 4.5.1: Fecal coliform before treatment (top left) and after treatment (top right)

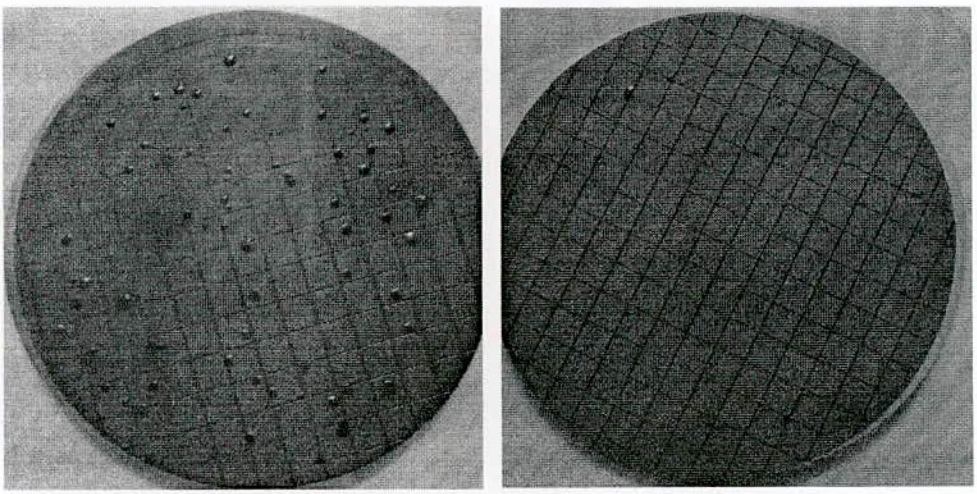


Figure 4.5.1: Total coliform before treatment (top left) and after treatment (top right)

Chapter 5

Conclusion

Amino acid ligand base copper complexes have been successfully prepared. In the present investigation, we deal with the tetradentate 1,4,7,10-tetraazacyclododacane (tcydan) ligand, where tcydan bears four secondary amine groups that could function as hydrogen-bonding donors only. Reaction of tcydan and $Cu(ClO_4)_2.6H_2O$ with nucleobases gave four ternary tcydan-metal-nucleobase complexes, $[Cu(tcydan)(ade)].ClO_4.2H_2O$ **(1)**, $[\{Cu(tcydan)\}_2$-$(hypoxanth)].(ClO_4)_3$ **(2)** and $[Cu(tcydan)(theophy)]_3.(ClO_4)_3.2H_2O$ **(3)**. The complexes were prepared in H_2O/CH_3OH or H_2O/CH_3CN media at room temperature under pH 8-9. The crystal structures were determined by X-ray diffraction.

The adenine complex **1** involves the Cu^{2+}-N(9) bonding with the formation of an intramolecular interligand N(tcydan)-H...N(3) hydrogen bond. On the other hand, the absence of the possible metal bonding to N(7) or N(1) of adenine might be due to a steric repulsion, around the crowded metal center, between amino groups of tcydan and the N(6) amino group when the metal ion binds to N(7) or N(1) of the base.

Each of the three oxopurine complexes **2**, and **3** commonly involves the Cu^{2+}-N(7) bonding with the formation of an interligand N(tcydan)-H...O(6) hydrogen bond. In addition, N(9) of the base is involved in the metal coordination with the formation of an interligand N(tcydan)-H...N(3) hydrogen bond in the hypoxanthine complex **2**, while a steric repulsion between amino groups of tcydan and the methyl group at N(3) of theophylline may preclude the metal-N(9) bonding in the theophylline complex **3**.

Fecal coliform (FC) and total coliform (TC) were removed from water by the complexes.

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