BIOLOGICALLY IMPORTANT TERNARY COORDINATION COMPLEX. CRYSTAL AND MOLECULAR STRUCTURES OF ADENINE-GLYCYLGLYCINE-COPPER(II) COMPLEX.

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SUMMARY: The crystal and molecular structures of an adenine-glycylglycine-copper(II) complex have been determined by X-ray diffraction. The chelating atoms, amino and amide nitrogen atoms, the carboxyl oxygen atom of the dipeptide, N(9) of adenine and one water molecule form a square-pyramid. The hydrogen-bonded adenine base-pairs stack with a distance of 3.8Å, while the dipeptides contact each other by N-H---O hydrogen bond to form a dimer.

Ternary coordinate complexes play an important role in biological processes. In many instances, enzymes are well known to be activated by metal ions[1]. On the other hand, a number of metal ions have been also shown to have a crucial effect on the biological activity of nucleic acids. Moreover, DNA or RNA polymerase, ribosome and so on should have substantial interactions between nucleic acid, protein and metal ion. Therefore, it is of considerable interest in stereochemistry to elucidate the precise molecular dimensions of a ternary coordinate complex between nucleic acid, protein and metal ion in the crystalline state. In this communication, we report briefly the crystal and molecular structures of an adenine-glycylglycine-Cu(II) complex which are so far the first case of a biologically important ternary complex determined by the X-ray diffraction method.

The single crystal of this complex was obtained by the following procedure; glycylglycine-Cu(II) and adenine were dissolved in 30% aqueous ethanol in a 1:1 mol ratio. After reacting at 60°C for thirty minutes, the powdered sample was obtained by slow evaporation at room temperature[2]. The very small blue plate crystal obtained by recrystallization in aqueous solution was used for X-ray diffraction analysis. The space group is $P\bar{1}$ with two formula units in the unit cell: a = 6.93(1)Å, b = 12.07(1)Å,

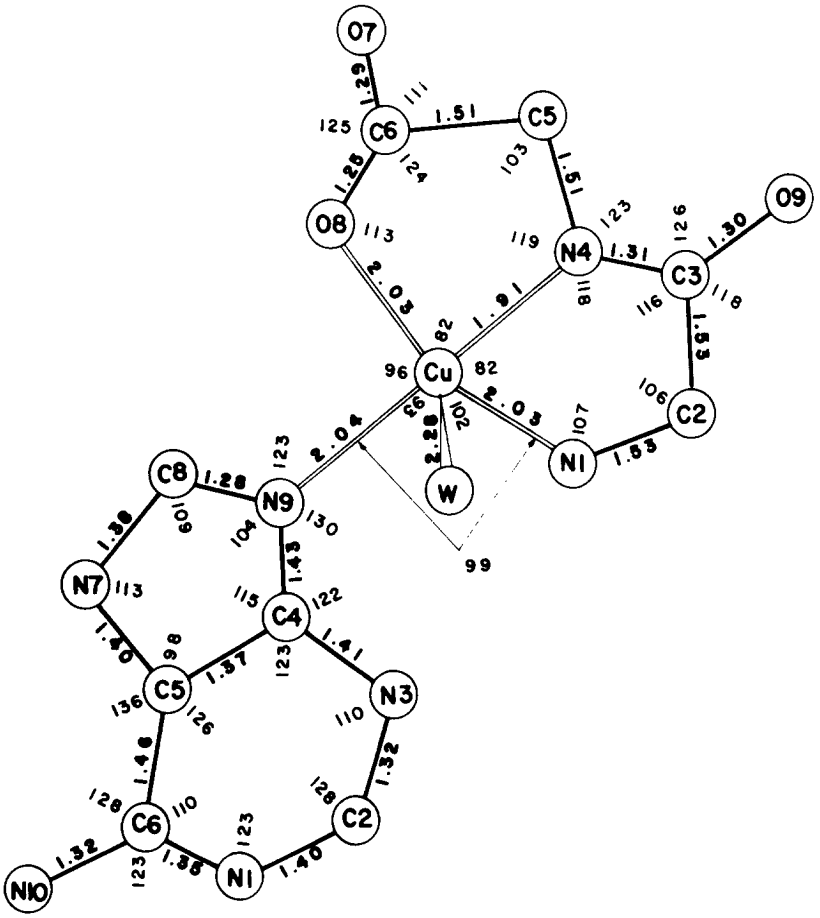

Fig. 1.

c = 7.62(2)Å, α = 92.9(1)°, β = 94.7(1)° and γ = 95.0(1)°. The intensities of 799 independent reflections were collected by the film method. The structure was solved by the heavy atom method and refined to an R-factor of 0.13 by a block-diagonal least-squares procedure applying anisotropic temperature factors to all non-hydrogen atoms.

The coordination around the copper atom is shown in Fig.1 with the bond lengths and angles. The chelating atoms, N1, N4 and O8 of the glycylglycine molecule and N9 of the adenine molecule occupy the corners of a square from which the copper atom is moved by 0.19Å towards the loosely bound water molecule(W). As also reported on the crystal structure of copper-glycylglycine trihydrate[3], the peptide C3-N4 bond(1.31Å) is apparently shorter than the usual C-N bond and this indicates that the peptide bond

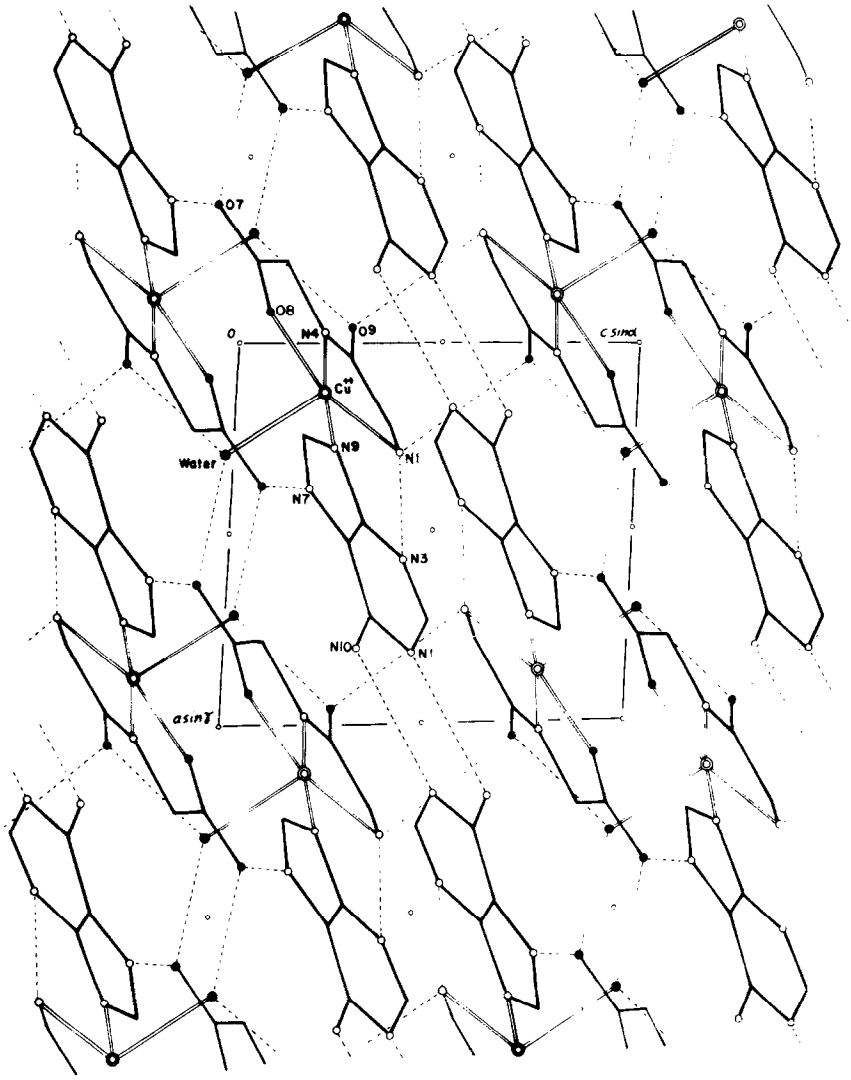

Fig. 2.

is strengthened by the replacement of hydrogen by copper and the amide carbonyl C3-O9 bond length is somewhat longer than that found in many peptide molecules. The similar situation also occurs in the adenine molecule, that is, a hydrogen atom attached to the N9 atom is replaced by copper and the C8-N9 bond(1.28Å) is obviously shorter than the other C-N bonds in the adenine molecule. It is probably true that this liberated hydrogen atom is covalently bound to N7 and participates in the intermolecular hydrogen bond[4].

The mode of interaction between adenine, glycylglycine and copper ion found in this X-ray analysis is profound biological

significance. As shown in Fig.2, the adenine molecule is dimerized by two N-H---N hydrogen bonds related by a center of symmetry, and each base-pair stacks one by one with a distance of 3.8Å to elongate along the a-axis, while the glycylglycine molecules contact each other by the N-H---O hydrogen bond between amino nitrogen and carbonyl oxygen of the adjacent dipeptide molecule to form a dimer. The copper ion, N-H---N and N-H---O hydrogen bonds mediate between adenine and glycylglycine molecules. The water molecule contacts with carboxyl and amide oxygen atoms by hydrogen bonds. Full detailed data of the structure will be published elsewhere in the near future.

This complex is the simplest model compound for the investigation of a nucleic acid-protein-metal complex and now we are preparing somewhat complicated ternary coordination complexes.

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