03.2.06 COMPLEXES OF THE Ag⁺ AND CH₃Hg⁺ IONS WITH METHYL DERIVATIVES OF CYTOSINE, THYMINE AND HYPOXANTHINE. By A. L. Beauchamp, F. Bélanger-Garléphy, J.-P. Charland, F. Guay and M. Sinard, Département de Chimie, Université de Montréal, Montréal, Canada.

The present work is part of a systematic study of the structures of Ag⁺ and CH₃Hg⁺ complexes with the purines and pyrimidines found in nucleic acids. We intend to clarify the role played by these metal ions when added to solutions of polynucleotides or nucleic acids and to provide basic chemical informations which could be extrapolated to the interactions of Pt anti-cancer drugs with DNA.

Chelate formation between N7 and the carbonyl oxygen of guanine is one of the model mechanisms used to explain the attack of Pt complexes on DNA. In order to assess the reactivity of 06 toward soft metal ions, silver complexes with 9-methylhypoxanthine (MHpx), a guanine-like ligand, were prepared. With AgClO₄, a complex of the formula [(MHpx)₂AgClO₄]·H₂O was obtained, in which Ag⁺ is linearly bonded to N7 atoms of two ligands, whereas 06 is involved only in H-bonding. The nitrate has the stoichiometry [(MHpx)₂AgNO₃]·H₂O. The solid consists of infinite chains in which the ligand bridges two Ag⁺ ions along the chain via N7 and the uncommon endocyclic N3 atom. The carbonyl group is free. The preference for the strained N3 position over the unhindered O6 group is an indication of the poor basicity of the latter site to the usual N3 site. By reacting an excess of NaN₃ with [CH₃Hg(MHpx)]Cl, addition compounds [CH₃Hg(MT)][ClN₃]·0.2H₂O could be obtained, in which CH₃Hg⁺ is linearly bonded to N7 atoms of two ligands, whereas 06 is involved only in H-bonding. The nitrate has the stoichiometry [(MHpx)₃AgNO₃]·H₂O. The solid consists of infinite chains in which the ligand bridges two Ag⁺ ions along the chain via N7 and the uncommon endocyclic N3 atom. The carbonyl group is free. The preference for the strained N3 position over the unhindered O6 group is an indication of the poor basicity of the latter site to the usual N3 site. By reacting an excess of NaN₃ with [CH₃Hg(MHpx)]Cl, addition compounds [CH₃Hg(MT)][ClN₃]·0.2H₂O could be obtained, in which CH₃Hg⁺ is linearly bonded to N7 atoms of two ligands, whereas 06 is involved only in H-bonding.

03.2.07 RESTRICTION OF PEPTIDE CONFORMATION BY α-METHYL SUBSTITUTION. Patrick Van Reusen, G. Drory, S. Steigman and William L. Duax, Medical Fdn. of Buffalo, Inc., 73 High St., Buffalo, NY 14203 and T. M. Balasubramanian and G. R. Marshall, Dept. of Physiology and Biophysics, Washington University, St. Louis, MO 63110.

The conformational space accessible to a peptide can be severely limited by α-methyl substitution on one or more of the constituent amino acids. All except one of the 22 crystallographic observations of α-aminoalobucrate (α-methylalanine) in linear peptides fall within a region which is midway between the conformations of an α and a 3-π helix and with an average value of φ=56.5° and ψ=-99.8°. The single exception is that of the conformation of the second Ab residue in the peptide BOC-AbH-AbH-06, for which the φ and ψ torsion angles are observed to be 31.6° and -138.5°, respectively. This lower value is about 12° from the φ value and therefore maintains the spatial relationship between the side chain methyl groups and the carbonyl oxygen atoms observed for the other Ab residues. The observed conformation of BOC-AbH-Val-06 is such that α-methyl substitution of amino acids other than alanine restricted the backbone conformation in a similar fashion. The observed values of the φ and ψ torsion angles of 59.0° and 33.3° for the α-methylphenylalanine residue nearly coincide with the average values for Ab residues. Furthermore, the restriction of the backbone conformation is accomplished without altering the conformation of the side chain or the remainder of the peptide. Research supported in part by Grant No. GM-19684 from the National Institute of General Medical Sciences, DHHS (PVR, OBS and ULD).

03.2.08 INFLUENCE OF THE HYDRATION ON THE REPLENISHMENT. S. Par A. Aubry et J. Prétet, Laboratoire de Minéralogie et Cristallographie, Case Officielle n°140, 54037 Nancy Cedex, France et G. Boussard, B. Vitoux et M. Marraud, Laboratoire de Chimie Physique Macromoléculaire, E.N.S. I.C., 1 Rue Grandville, 54000 Nancy, France.

Les structures cristallines des deux formes anhydre et hydratée de la N-pivaloyl-L-prolyl-N'-dimalyl-D-alaninine ont été résolues par diffraction des rayons X. Le dérivé anhydre présente un repliement de type III avec les angles conformationnels φ=-58°, ψ=136°, ϕ=-97° et ψ=19° stabilisé par la liaison hydrogène ω=2°-3° de longueur 2.97 Å. Dans le composé hydraté, la molécule d'eau vient se placer en pont entre les atomes O et N réalisant un système complexe de liaisons hydrogène entre les atomes O₆ et N₃ echantilloné 3-2,75 Å, N₃=0.19 Å, ω=18°, ω'-3° et ω'-2°. Les angles conformationnels sont alors ω=-6°, ω'=164°, ω'=139°, ω'=35°. Bien que les angles dièdres ψ et ϕ se soient respectivement une rotation d'environ 30° et 10°, la forme générale de la molécule est conservée. L'hydratation provoque donc une ouverture du repliement à 10 ème pour permettre l'insertion d'une molécule d'eau, le cycle passant ainsi à douze atomes. C'est la première fois qu'une molécule peptidique est étudiée à la fois sous forme anhydre et hydratée à l'état solide et c'est la première fois qu'une molécule d'eau a été mise en évidence dans une cellule dissection. Ce phénomène devra être pris en considération dans l'étude conformationnelle des polypeptides linéaires en solution aqureuse.
X-RAY STUDIES OF AMINO ACID - VITAMIN INTERACTIONS. THE CRYSTAL STRUCTURE OF LYСINE PANTOTHENATE. By D.M. Salunke and M. Vijayan, Molecular Biophysics Unit, Indian Institute of Science, Bangalore 560012, India.

Non-covalent interactions play a crucial role in the structure, binding and action of proteins. As part of an attempt to study, at the atomic resolution, the possible geometrical features of such interactions through the X-ray analysis of crystalline complexes of amino acids and short peptides among themselves as well as with other biomolecules (Acta Cryst. (1980) B36, 125-126, and the references therein), the crystal structure of a 1:1 complex between lysine and pantothenate has been determined. The complex crystallizes in the monoclinic space group P2₁ with two formula units in a cell of dimensions a = 5.883, b = 15.515, c = 10.024 Å and β = 106.8°. The structure, solved by the direct method, has been refined to a current R value of 0.039 for 1868 observed reflections. The zwitterionic positively charged lysine molecules in the structure exist in the fully extended conformation whereas the pantothenate anions have a somewhat folded structure. The unlike molecules aggregate into separate alternating layers in the crystal structure as in several other crystalline complexes involving amino acids. The packing of the molecules is due in the two compounds to hydrogen bonds, which are different in each structure.