03-Crystallography of Biological Macromolecules

03.10 – Macromolecular Assemblies

PS-03.10.01 STUDY OF GUANOSINE DERIVATIVES BY X-RAY DIFFRACTION

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Guanosine derivatives in water solution have been shown to self-associate forming macroaggregates in both isotropic (I) and liquid crystalline states (P. Mariani et al, J. Am. Chem. Soc., 1989, 111, 6369-6373; 1991, 113, 5809-5816; Liq. Crystals, 1991, 10, 495-506) (L.Q. Amaral et al, Liq. Crystals, 1992, 12, 913-919). The common structural unit is a planar disc-shaped tetramer formed by four hydrogen bonded guanosine residues. Self-association through stacking of the tetramers produces rod-shaped chiral aggregates leading to cholesteric N* and hexagonal H liquid crystalline phases with decreasing water content.

In a recent paper on the H phase in a micellar system (L.Q. Amaral et al, Phys. Rev. A, 1992, 46, 3548-3550) we analysed the distance "a" between cylinder axes in the H phase as a function of the volume concentration of solute c_v obtaining $a \alpha c_v^{-1/3}$, typical of finite cylinders, while $a \alpha c_v^{-1/2}$ is expected for infinite cylinders. This method of analysis is now used to study a series of guanosine derivatives, with following results:

- the dinucleoside phosphate G2 presents a N* - H transition and a change of functional behavior $a \alpha c_v^{-n}$ at the transition (n = 1/3 in N* phase and n = 1/2 in H phase), evidencing cylinder grow.

- the derivatives G1, G3 and G6 show instead n = 1/3 in the H phase, evidencing smaller aggregation process.

- the derivative G2 cyclic presents n = 1/2 in H phase.

- results obtained in folic acid salt, that forms aggregates similar to the four-stranded helices given by guanosine derivatives, evidence a direct I - H transition and n = 1/3 in H phase.

These results are discussed in terms of differences in the aggregation process of the several derivatives and the phase transitions analysed in terms of recent statistical mechanical theories that take self-association into account (M.D. Taylor and J. Herzfeld, Phys. Rev., 1991, A43, 1892-1905).

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COLLAGEN FIBRIL STRUCTURE AND MINERAL CRYSTAL GROWTH IN NORMAL AND PATHOLOGICAL BONES

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The major vertebrate hard tissues bone, dentin and mineralized tendon are composed of crystals of carbonate apatite (dahllite) in a matrix of type I collagen fibrils, together with small amounts of other macromolecules and water. The crystals are small plates organized in parallel layers along grooves through the collagen fibrils. These grooves arise from contiguous collagen 'gap' regions and are separated by the 67nm D repeat along the length of the fibrils and some 4nm in the orthogonal direction.

In mineralized turkey tendon and bone the crystals form initially in the gap regions, appearing as short needles near the surface of the collagen fibrils at the 'e' bands. The needles grow along the length of the fibrils till temporarily constrained by the boundaries of the grooves. They then grow laterally to form belts, and ultimately push their way out of the grooves into the 'overlap' regions.

The mineralized collagen fibrils with their 3-dimensionally ordered arrays of flat crystals may be regarded as building blocks, assembled in various ways in different mineralized tissues. In turkey tendon they are all generally parallel to the tendon axis, and there is a tendency for adjacent fibrils to be coherently aligned so that their crystals are coplanar. This is even more pronounced in cortical bone where crystals from many fibrils grow together to form continuous planes, but only within the confines of the lamellar sub-structures. In alternate lamellae the orientations of the collagen fibrils and the crystal planes are very different, giving the bone a kind of plywood structure. The relative widths and orientional relations between lamellae appear to vary with the bones mechanical functions.

Preliminary studies have been made of bones from patients affected by osteogenesis imperfecta (O.I.) a condition generally atttributed to mutations in the collagen. Some of the mineralized fibrils appear to have quite normal structures even in severe forms of O.I. However, others have small poorly aligned crystals, sometimes encrusted onto seemingly normal fibrils. Fused crystal aggregates, apparently unrelated to any collagen fibrils, were also seen. These observations could be attributed to a scarcity of collagen in the extracellular matrix rather than to the presence of structurally abnormal molecules, which are less likely to be extruded by the cells than the normal collagen.

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DATA COLLECTED AND EVALUATED FROM CRYSTALS OF RIBOSOMAL PARTICLES. by I. Agmon[1], H. Bartels[2], W.S. Bennett[2], Z. Berkovitch-Yellin [1,2,*], K. von Bohlen[2], A. Dribin[1], M. Eisenstein[1], F. Franceschi[3], H.A.S. Hansen[2], J. Harms[2], G. Kryger[1], I. Levin[1], F. Schlunzen[2], R. Sharon[1], J. Thygesen[2], N. Volkmann[2], A. Yonath[1,2] and A. Zaytzev-Bashan[1]. [1] Dept. of Structural Biology, Weizmann Institute, Rehovot, Israel. [2] Max-Planck-Research-Unit for Ribosomal Structure, Hamburg, Germany. [3] Max-Planck-Institute for Molecular Genetics, Berlin, Germany.

X-ray diffraction data have been collected at cryotemperatures, using intense synchrotron radiation sources, from crystals of ribosomes, their complexes with components of protein biosynthesis and their natural, mutated, selectively depleted and modified subunits, as well as from ribosomal particles specifically labelled with a gold cluster (composed of 11 gold atoms). The best crystals, those of the large subunit (50S) from Haloarcula marismortui, diffract to almost atomic resolution (2.9Å). The best resolution to date of the whole ribosome (70S) is 15Å and that of the small subunit (30S) is 7.3Å, both from Thermus Thermophilus.

Crystals of ribosomal particles exhibit special features: large unit cells, high mosaicity, extremely weak diffraction, beam sensitivity, a limited internal order and an extremely steep descent of the intensities of the reflections as a function of resolution.

