02. STRUCTURAL MOLECULAR BIOLOGY


The full understanding of the process of protein biosynthesis still awaits a structural model. To this end we have attempted crystallographic studies on ribosomes.

Three dimensional crystals of intact 50S ribosomal particles from B. stearothermophilus have been obtained by us. These crystals grow in vitro, within several weeks, by a modified version of the vapour diffusion technique. They grow reproducibly, each dimension of 1x0.2x0.1 mm and are rather fragile. Preliminary X-ray diffraction patterns of native and cross-linked single crystals have been obtained, mainly with synchrotron radiation (DORIS/X11 at EMBL/DESY). These extend to 2.5 Å resolution and indicate packing that accords with that of the single crystals.

X-ray diffraction data from samples containing large number of micro crystals show sharp rings, among them some with spacings that agree well with those of gels and of solutions of ribosomes. The low resolution "powder" diffraction patterns indicate packing that accords with that of the single crystals.

02.8-3 THE STRUCTURE OF RIBOSOMAL PROTEINS FROM A THERMOPHILIC BACTERIUM. By K.Appelt, S.J. White, and K.S.Wilson* of Max-Planck Institute for Molecular Genetics, Abt. Wittenberg, Hennestraße 63-73, 1000 Berlin 33.

We have been studying the crystal structures of ribosomal proteins from the thermophilic subtilisin in relatively small unit-cells, reasonable degree of internal order and adequate stability in the X-ray beam. Three dimensional crystals of intact 50S ribosomal particles from B. stearothermophilus have been obtained by us. These proteins are extracted from the ribosome by mild methods with 1 or 2 molar salt solutions to avoid denaturation of the molecule. Site specific differences from the cesium ions are calculated to be -16% for 4585 significant reflexions (F>2σF).

Granicidin A, a linear polypeptide antibiotic, forms channels in phospholipid membranes which are specific for monovalent cations. Dimers of this hydrophobic molecule adopt very different conformations in membranes and in organic solvent. Different crystal forms have been prepared in the presence and absence of ions and/or lipid molecules [Wallace, Biopolymers 22, 397 (1983)]. These crystals of one granicidin/ion complex which diffract to 1.5 Å have been prepared from a CsCl solution in methanol (Kimball and Wallace, Ann. N. Y. Acad., in press). This crystal form (space group P2_12_1, a=32.11, b=52.10, c=37.16 Å) contains 2 dimers per asymmetric unit. Because of the high cesium content in these crystals, the Bijvoet differences from the cesium ions are calculated to be +15% with a Cs^- partial structure contribution of 71% in F, so it was possible to calculate a 1.8 Å electron density map using single wavelength anomalous scattering for phasing. This preliminary map reveals the helical structure of the molecule and the cation-binding sites. Attempts to fit the polypeptide chain are now underway.

Supported by NSF Grants PCM 80-20063 and PCM 82-15109.