

RESEARCH AT THE MACROMOLECULAR CHEMISTRY GROUP IN BARCELONA

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NUCLEAR PROTEINS, PEPTIDE MODELS AND THEIR COMPLEXES WITH DNA

Spermatozoa provide a source of unique nuclear proteins which vary tremendously in different species, ranging from identity with somatic nuclei to a large variety of compositions as reviewed elsewhere.¹ In our group we have characterized the proteins present in many organisms, with special emphasis on echinoderms,²⁻¹⁰ molluscs,¹¹⁻¹⁷ some fish¹⁸⁻²⁰ and other vertebrates.²¹⁻²⁴

Our structural studies have shown that when histones predominate the chromatin fiber acquires a partially regular shape which we have characterized both by X-ray diffraction^{25,26} and electron microscopy.²⁷⁻³¹ Unfortunately the degree of order of chromatin fibers is not sufficient to allow a complete resolution of the structure. Our work shows³² that the X-ray data can be interpreted by the interference of a few closely packed nucleosomes placed with their flat faces parallel to the axis of the fibers, but no useful information can be extracted on the long range organization of chromatin fibers.

In parallel studies we established the organization of crystalline complexes of DNA and protamines, finding that hexagonal packing is found in most cases, with different protein sizes and amino acid compositions.³³ The exact localization of the amino acids on DNA can not be established with certainty.³⁴ In fact we have recently proposed a new model³⁵ which may reconcile the contradictory proposals of previous investigations.

In order to learn more about the different possibilities of protein-DNA interaction we have also studied model peptides which interact with DNA,^{36,37} with the finding of new types of structural associations between polypeptide chains and DNA³⁸ and general rules for the behaviour of DNA in the presence of amino acids.³⁹

PEPTIDES

In order to improve our knowledge of basic proteins we decide to investigate in a systematic way several basic peptides, since very few of them had been previously studied. As a result we crystallized and solved the structure of several di- and tri-peptides which contain the amino acids lysine and arginine. In one of the accompanying papers (Verdaguer et al., this volume) a recent structure is presented and compared with previous structures studied in our group. A review of all these studies has been recently presented.⁴⁰

OLIGONUCLEOTIDES

In order to increase our understanding of nucleic acid structures we have studied polynucleotides in fiber form⁴¹⁻⁴³ and crystallized several oligonucleotides and determined their structure.⁴⁴⁻⁴⁶ An example of current work is given in one of the papers which follow (Tabernero, this volume). One of the most interesting structures which we have recently studied is the dodecamer CCCCCGCGGGG. It crystallizes as a double helix in the A form, which is thus the longest molecule which has been crystallized in this conformation. Its detailed structure indicates that the local geometry depends strongly on the interactions of DNA. We also find that the CpG sequence is very versatile, a result of considerable interest since this sequence is very rare in higher organisms and through its methylation appears to be involved in the process of cell differentiation.

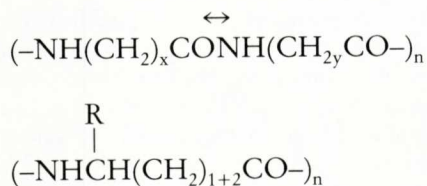
PROTEINS

Quite recently our laboratory has been engaged in the determination of protein structures by X-ray diffraction. The resolution of several proteins is currently in progress. In the paper by Tormo et al (this volume) we present the first protein from which a structure has been determined in our laboratory.

POLYAMIDES

Several years ago we decided to study the structure of polyamides which might have a conformation intermediate between the classical ny-

lons, which form sheet structures, and the proteins, which often have helical structures. We are thus studying two groups of polymers with the following general formulae:



In the first type of structure either x or y are unity and the central amide group may be inverted. The presence of a single CH_2 group between two peptide residues corresponds to a glycine or related residue and gives rise to helical structures similar to polyglycine II. However the exact geometry varies in different polymers so that we are presently comparing the structure of polyamides of the types $2/n$, $1,n$ and $n,3$. In some cases a γ structure is found. A theoretical analysis of these polymers is presented by Bella in this volume. References to previous work are given there.

The second family of polymers contains side groups. We have shown that these polymers can form a variety of helices⁴⁷⁻⁵¹ with a structure similar to the classical α helix found in polypeptide chains. What is interesting is that in this case the same polymer chain may form different types of helices, which are also analyzed by Bella in this volume. The helical structure of these polyamides allows the formation of liquid crystals⁵² and the polymers show piezoelectric properties.⁵³

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ABSTRACT

The Macromolecular Chemistry group was established in the Department of Chemical Engineering of the Universitat Politècnica de Catalunya about twenty years ago as a joint venture with the Consejo Superior de Investigaciones Científicas, which has supported the group at various levels during this time. In this period about 230 publications have been produced and 41 students have obtained a PhD in the group. About 80% of them are now in academic positions.

The group concentrates in structural studies such as electron microscopy, infrared spectroscopy, calorimetry and, more specifically, in X-ray diffraction. Several generators provided with pinhole and low angle cameras are available. The most recent acquisition is a GX-21 rotating anode generator provided with a CAD4 automatic diffractometer.

The main lines of endeavour are described below and a few examples of our current work are given in the accompanying papers.

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