PREFACE

This volume contains contributions from the speakers at the NATO Advanced Research Workshop on "3D Structure and Dynamics of RNA", which was held in Renesse, The Netherlands, 21 - 24 August, 1985.

Two major developments have determined the progress of nucleic acid research during the last decade. First, manipulation of genetic material by recombinant DNA methodology has enabled detailed studies of the function of nucleic acids *in vivo*. Second, the use of powerful physical methods, such as X-ray diffraction and nuclear magnetic resonance spectroscopy, in the study of biomacromolecules has provided information regarding the structure and the dynamics of nucleic acids. Both developments were enabled by the advance of synthetic methods that allow preparation of nucleic acid molecules of required sequence and length.

The basic understanding of nucleic acid function will ultimately depend on a close collaboration between molecular biologists and biophysicists. In the case of RNA, the ground rules for the formation of secondary structure have been derived from physical studies of oligoribonucleotides. Powerfull spectroscopic techniques have revealed more details of RNA structure including novel conformations (e.g. left-handed Z-RNA).

A wealth of information has been obtained by studying the relatively small transfer RNA molecules. A few of these RNAs have been crystallized, enabling determination of their three-dimensional structure. It has become apparent that "non-classical" basepairing between distal nucleotides gives rise to tertiary interactions, determining the overall shape of the molecule. Independent evidence for the 3D folding stems from high resolution proton NMR studies of dissolved molecules. Newly started molecular dynamics calculations promise to provide us with a detailed knowledge of the atomic motions in these molecules. Details of the structures and of the interaction with ligands are also derived from data obtained by a variety of spectroscopic techniques. When these are combined with results of (bio)-chemical analysis it is possible to arrive at a clear picture of structure and function of this class of RNA molecules.

In most cells the bulk of RNA is present in ribosomes. The three classes of ribosomal RNA, 5S RNA, 16S RNA and 23S RNA have been studied extensively, although not in such detail as transfer RNA. For all three classes "consensus" secondary structures have been derived These are primarily based on phylogenetic data, but are supported by experiments using (bio)-chemical approaches. Unfortunately, it has as yet not been possible to crystallize a ribosomal RNA (or part of it) and the molecules are too large to be studied by NMR at its current state of the art. However, some progress has been made with fragments of ribosomal RNA. Similarly, through the use of a variety of techniques, including recombinant DNA methods, functional areas in ribosomal RNAs have been mapped.

Important information has also been obtained regarding the folding of viral RNA. Here, some novel folding principles have been introduced which might also play a role in other RNA molecules.

A recent finding that RNA molecules, like enzymes, have catalytic properties, has attracted much attention. The auto-catalytic selfsplicing of RNA appears to depend on a precise folding pattern of the RNA near the splice junction.

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Finally it should be mentioned that the success of the meeting and the high scientific standard of this volume are the result of the enthousiastic co-operation of the participants. There is clearly a need for meetings devoted to RNA at regular intervals in the future.

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