

PREFACE

The translation of mRNA is a complex, multi-step process involving a large number of RNA and protein components whose synthesis is carefully regulated to ensure efficient and accurate translation of an mRNA sequence into a polypeptide sequence. It also represents one of the key stages at which gene expression is regulated. Over the past twenty years detailed in vitro biochemical analysis has led to a basic understanding of the structural characteristics of the individual RNA and protein components together with some detail on their role in various intermediary reactions occurring during the initiation, elongation and termination phases of translation. What has been lacking is a concerted effort in applying genetic techniques to the study of the translation process.

With the recent exciting developments in recombinant DNA-based genetics, new approaches are now available that should provide us with a fuller understanding of the translation process - its components, mechanism, fidelity and regulation. This is particularly true for eukaryotic systems which have proven virtually intractable through classical genetic approaches, but upon which so much detailed biochemical work has been carried out. The time therefore seemed right to us to appraise these new genetic approaches, and to discuss how best to apply them in a study of the translational process taking into account what has been achieved to date by the classical genetic approaches in prokaryotes. It was, with this intention in mind, that we set out to organise this meeting.

With the generous financial assistance of NATO and the French Ministry of Research (MRES) we were able to bring together over 50 researchers, from both the USA and Europe, with our common interest. The meeting, held in the clear and invigorating air of Aussois, high in the French Alps, aimed to provide, for the first time, a forum for an open exchange of ideas and techniques with a view to identifying new approaches to the genetic analysis of translation, particularly bringing together the "old" and the "new" technologies of genetic manipulation. Rather than restricting ourselves to one particular aspect of translation (e.g.

ribosomes, tRNAs, etc.) we chose to attempt to cover all aspects of the process, with equal attention being paid to prokaryotic and to eukaryotic systems, since many of the approaches we foresaw would be widely applicable. In addition we felt it important that discussions should consider translation as a single co-ordinated process and not a collection of individual macromolecular species that just happen to be involved in translating mRNAs.

That the meeting worked so well is largely a testimony to the enthusiasm of the participants, all of whom contributed ideas, not only in their own specialised fields but to other aspects of translation. We hope that this volume will convey this enthusiasm to fellow researchers and funding bodies alike, and illustrate that indeed many new approaches are already being taken in the genetic dissection of the translational process.

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