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Introduction

There is no question that the progress made in recent years in the field of biology, particularly after the completion of the Human Genome Project, has transformed cancer research radically and provided new perspectives for the diagnosis and therapy of cancer.

Nevertheless, the results obtained are far from satisfactory, as illustrated by epidemiological data that indicates that cancer still represents a major cause of death in Europe and the United States.

Much progress has been made for tumours that are well characterised in terms of their pathogenesis at the molecular level, e.g. chronic myeloid leukaemia, not only in the development of specific diagnostic tools, but also for the identification of selective and effective therapies. The results obtained in some molecularly well characterised tumours represent a paradigm that can be followed in future research in to less well known and more complex neoplastic diseases. The molecular pathogenesis of most human solid tumours seems to be much more complex than that of leukaemias and is not fully elucidated. In addition, the heterogeneity of solid malignant tumours makes most of the traditionally used approaches of limited value.

We are confident that the rapid and significant advances made in recent years in the field of biology together with the extraordinary technological advances in other disciplines, e.g. proteomics, bioinformatics etc. will result in a tangible improvement in the near future, in the diagnosis and therapy of most tumours.

It may be noted that in the past many relevant therapeutic achievements have been made, applying empirical approaches that required nothing more than routine clinical and pathological expertise and the help of biostatisticians.

For example, the polychemotherapy regimens used in the treatment of some leukaemias and lymphomas were successfully developed by combining compounds with different modes of action, monitoring the antitumour activity and the toxicity and then fine-tunning dosageschedules on the basis of the results obtained. Instead, some of the novel approaches will require that clinical researchers work in close collaboration with experts of different disciplines, including those in the fields of biology, chemistry, bioinformatics and physics.

Already some of the molecularly targeted therapies require the appropriate selection of patients who can benefit from the therapy because their tumour exhibits the qualitative or quantitative alterations of the target required to elicit a therapeutic response. This means that the clinician must know the molecular biology of the tumour, be familiar with the techniques used to assess the alterations of a gene or a set of genes that are involved in the pathogenesis of the disease and in the response to the therapy, as well as be able to interpret the laboratory results correctly. The complexity seems to increase more and more, when patterns of different genes and proteins are considered and analysis of these data requires bioinformatics and mathematical skills. In order to work together, scientists and clinicians should be able to understand each other and scientific communication will play an important role in facilitating the collaborative interdisciplinary effort.

The reason for the preparation of this Special Issue of European Journal of Cancer "Gene Transcription and Cancer, from the Genome Project to Practical Achievements" is to illustrate important changes that are occurring in the current diagnostic and therapeutic approaches. We have invited some distinguished scientists to overview different aspects of contemporary cancer research, providing examples of results recently obtained that, hopefully, will soon be exploited clinically. However, it is important to underline that many scientifically attractive ideas and approaches still lack a rigorous validation and in order to evaluate their impact in oncological practice further clinical investigation will be required. We believe that the exploitation of the novel approaches, exemplified and discussed in this volume, once validated by appropriate statistical analysis methodologies, will have an

important impact on the survival and quality of life of cancer patients in the next decade. Thus, we hope that reading this volume will not only be an interesting intellectual experience, but will stimulate further research and ideas of scientists and clinicians to help speed up the urgent need to alleviate suffering due to cancerous diseases.

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