Editorial

Dear authors and readers,

While writing the introduction to this issue of *FEBS Letters*, it is not clear (at least to me) how close we have come to a complete coverage of the sequence of the human genome and how many gaps are still left to be filled after all the available sequence information has been assembled. As important as these details may be, they are still just details. No doubt that much more valuable sequence information is going to be produced in the years to come by both public and private efforts. Genome sequencing, however, is no longer the main challenge. The focus has now changed from determining DNA sequences to interpreting the functional information contained in these monotonous strings of nucleotides.

Everybody anticipates that this second endeavor will be much tougher than the first. In 1990 not many of us would have bet that most of the sequencing of the human genome could have been completed in less than two years. Even at that time, however, one could imagine a flow diagram of the necessary steps to achieve this goal. The discussion revolved around the desire to invest heavily in this project rather than to focus on its feasibility. At that time, the main techniques to carry out the project had already been established. Despite several attempts to develop revolutionary approaches that, in principle, could have speeded up the acquisition of sequence information, the dideoxy method of Fred Sanger has persisted as the main sequencing method, with only minor modifications to make it compatible with automation.

Genomic sequence information has a value per se. This is clearly understood by groups working with yeast who, in the past 3 years, have experienced the value of entering WEB sites that contain the entire genome of their favorite organism organized in a user friendly database. In other words, the availability of the sequence of an entire genome speeds up the traditional and still very much needed approaches that address the function of one or few genes. However, if we limited our effort to what we are currently doing, albeit at a higher speed, we would not exploit all the potential of this wealth of information.

A Medline search for the keywords 'protein' and 'interaction' returns approximately 500 articles published in 1999. This provides a rough estimate of the number of new entries/year in the protein interaction database. At this pace, even with the most optimistic prediction (each of these publications describes a new protein interaction), it would take the entire scientific community more than 200 years to discover the partners of the estimated 100 000 peptides encoded in a single mammalian genome. Clearly, more general, faster and, at the same time, reliable approaches are needed. At the turn of the Millennium, reports utilizing novel approaches have appeared, which describe hundreds to thousands of new interactions with a limited number of experiments and time investment.

The purpose of this issue is to provide an overview of these emerging technologies. Some of these are already well established and have found their important niche in functional genomics. Others are still being developed. It is clear that no single technique is likely to have the same impact on functional genomics that the dideoxy sequencing method has had on the initial phase of the sequencing project. In fact, one of the major and most difficult challenges will be the integration of data obtained through very different techniques.

When we started to think about a collection of short reviews on functional genomics, we contemplated covering all the possible areas. By looking at the contents' page, it is clear, despite the high interest in the topics covered, that many important approaches are missing. These could form the basis for a new collection of reviews to be published in a forthcoming issue.

All contributions but one are from European groups. This does not reflect the European chauvinism of the editor but is perhaps a higher appeal, from a European journal of good tradition, for a European group. In addition, this also reflects the leadership of some European groups in the development of methods for functional genomics. Europe has contributed substantially to the first phase of genomics, the *Saccharomyces cerevisiae* sequencing project being one of the first examples in biology of a large collaboration among several laboratories.

Recently we have witnessed a worldwide change in the scale of the efforts and a flourishing of new genomic programs and genomic centers, very few of which are in Europe. It is not possible to generalize, however, since Europe is not a single country. We have countries such as Italy, where no integrated program has been running in the last few years, and where the few isolated genome projects are supported by charities such as AIRC (Italian Association for Cancer Research) and Telethon. Alternatively, we have countries such as Britain and small countries like Denmark that possess relatively strong programs. The feeling, however, is that Europe in general risks to lag behind in this important phase of the genome project unless decisions about investment in this field are taken soon by the national governments and the European Commission. We hope that the publication of this issue will give a contribution towards this goal.

Gianni Cesareni

Note from the *FEBS Letters* Editorial Office

As demonstrated by this issue dedicated to reviews on functional genomics, *FEBS Letters* is now interested in publishing three or four Special Issues per year in addition to our normal weekly publication. Special Issues could consist of manuscripts focused on either (1) opportune topics of sufficient general interest or (2) coverage of significant meetings/conferences. Please contact Connie Lee (lee@embl-heidelberg.de) at the *FEBS Letters* Editorial Office in Heidelberg if you have ideas or suggestions for future Special Issues in our journal.

0014-5793/00/$20.00
PII: S0014-5793(00)01770-1