

Preface

The last decade has witnessed major changes that will affect the way in which much of biological research is carried out. Until recently, one could study only one or a few genes at a time and it took quite long – about three years – even in well-equipped laboratories to understand the structure and function of a gene. It was not possible rapidly to work out how different gene-products interacted physically and functionally. Now, due to the advent of high throughput sequencing methods and advances in computational techniques, it is possible to ‘look’ at the genome in its entirety. Along with improvements in sequencing technology, there have been major advances in the way the expression of genes is measured or, mutations in genomes are mapped. High throughput methods allow one to analyse large number of genes within a short period. What does all this mean for the average biologist working in our country? Has he or she become redundant-swept aside by the strong currents of high technology? Many of us feel helpless looking at the sheer scale of the present-day research and are not sure how we can contribute significantly any more.

Despair, however, can quickly turn to enthusiasm if one realizes that the amount of information available today can help anyone to conceive projects involving molecular tools as long as an access to the Internet is available. For example, one does not have to spend years trying to clone a specific DNA fragment: full genomic sequences of a large number of organisms are already available and a PCR reaction can result in the desired fragment. Databases and bioinformatics tools available on the Internet allow a researcher to find mutations, build three-dimensional structures of encoded proteins, get the relevant information and literature related to genes of interest and so on. Genome sequencing projects eventually throw up lists of genes with predicted functions with different degrees of certainty. A list usually contains a sizable number of genes that have unknown functions. Traditional genetic and biological methods may have to be used to investigate and confirm the putative functions. This is particularly relevant for the vast majority of genes whose products do not work in isolation. After all, genetic circuits consisting of interacting gene products are the basis of cellular functions. Unfortunately, many organisms are not amenable to biological approaches and their genetic systems have not been defined (though their genome may have been sequenced). Exploitation of the genomic data in these organisms may not be feasible due to the lack of amenable systems to study the functions of their genes *in vivo*. Small laboratories can contribute significantly by developing such genetic approaches such as methods for transfection, knockouts, expression blocking, etc., for different organisms. Judicious use of bioinformatics tools coupled with an insight into the biological properties of the system will help us to exploit genomic information. Any laboratory, however small or big, can contribute significantly.

In this issue of the *Journal of Biosciences* a collection of papers on different aspects of genomics have been included. The papers pertain to analysis of genomes and application of genomic information in basic biology, diagnosis and clinical research. They give us a glimpse of what is going on in this area, mainly in India.

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