



**Functional Plant Genomics.** J. F. Morot-Gaudry *et al.* (eds). Science Publishers, An Imprint of Edenbridge Ltd, British Isles, P.O. Box 699, Enfield, New Hampshire 03748, USA. 2007, 699 pp. Price: US\$ 66.90.

This book is a revised and updated English edition of the original book entitled *La Genomique en Biologie Vegetale* published in 2004. I read the book with great interest as there was a lot for me to learn. I do not want to keep the reader waiting for my recommendation. Just order a copy of this book if you are in the area of plant genomics or have any intention to take up work in this field in the near future. The reason for my recommendation is that this book educates you on the techniques and experiments that are in vogue today to understand the structure, function and application of genomics. The basis and explanation of experimentation is given with great clarity. There are many of us who have entered the field of genomics without having undergone any formal training or exposure. In this book each author has done a great job of not only giving information on the subject, but providing experimental details. Also, in many chapters the excitement of participants in various genomics projects has been brought out in a lucid manner.

This book has 699 pages which are classified into 32 chapters and are arranged sequentially to take the reader from genome architecture to genomics and technology. The chapters are grouped into four sections, viz. structural genomics and *in silico* analysis, functional genomics, plant models in genomics, and genetic variability and plant breeding.

The science of genomics is driven by techniques, tools and instrumentation. The last decade has seen a spurt of information in plant biology. It is possible on the one hand to look at the behaviour

and function of an individual protein using various microscopic techniques and gene-engineering technologies, and on the other hand, one can decode the genomic-level changes that are foremost in analysing complex developmental traits and behaviour. This book, as mentioned above, describes many such techniques and shows how information can be generated if the tools are intelligently deployed.

The first chapter by Delseny *et al.* gives an overall concept of plant-genome organization and the methods that have been employed to elucidate the physical organization of plant genomes. The authors start with cytogenetic tools, like Giemsa staining, to analysing DNA using denaturation/renaturation kinetics, to physical organization by cloning and organization, and by assembling YAC or BAC clones into series of overlapping clones named contigs and finally on the use of ChIp (chromatin immunoprecipitation) methods to understand the heterogeneity and dynamics of chromatin. The next chapter by Choisey *et al.* describes how the bold decisions of sequencing entire genomes of various organisms, including *Arabidopsis* were taken and how the concept of International Consortiums to handle such large projects came up. The chapter coherently describes the whole technology behind sequencing. It gives an account of how different groups were assembled to sequence the *Arabidopsis* genome that was completed by 2000. This initiative was followed by rice genome sequencing. Compared to *Arabidopsis* (130 Mb), rice has a bigger genome (430 Mb) and hence the task was difficult. However, with the participation of many countries, the project was completed. India was also a partner in this project and now has joined in the tomato genome sequencing project too. The chapter describes how the experience and confidence has now led to the sequencing of other genomes like maize, two legumes, Medicago and Lotus, a tree plant, poplar; tomato, grape vine and finally wheat which has a large genome. A list of other plants whose genomes are being sequenced is also given. Among these, the genome of a moss, *Physcomitrella* is now complete (*Science*, 13 December 2007). In fact a comparison of *Physcomitrella* with other genomes is in progress to gain an insight into the evolutionary aspects of how the plants got adapted on land.

A major task for the present biologist is how to make best use of the information

that is flowing into databases at a rapid rate. Chapters 3 and 4 by Chiapello and Rodolphe respectively, give an idea about various databases that are available and the bioinformatic tools that one can use. In chapter 5, Nicolas and Chapello give details about how to use the database and the tools to predict genes, and the benefits and limitations of the currently available gene-prediction models.

Having predicted the number of genes an organism has, the next step is to find out the function of the encoded proteins. The chapters by Gibrat and Martin, and by Risler *et al.* illustrate that an initial attempt can be made to predict the function of a protein using *in silico* analysis. One could get an idea about its localization by finding out if the protein has TM domains and any cell-sorting signals. It should be possible to find out using various bioinformatic programs the nature of the proteins, i.e. the alpha and beta structure, and presence of known motifs. Large-scale comparison at the protein sequence level, rather than at the nucleotide level, can also give information about function. This information can then be used to develop clusters. These chapters have also highlighted the weakness of certain programs and therefore the researcher has to make his/her best choice and proper judgement.

While information obtained by *in silico* analysis is useful, confirmation and validation through experiments is required in most cases. The next section having 11 chapters, deals with the experimental part of functional genomics. The chapter by Chupeau and Davey deals with various techniques used for the transfer of genes in plants and studying their functions in either a homologous or heterologous system. This is usually done by overexpressing or underexpressing the gene and looking for a phenotype in normal and other conditions. There are two chapters on the analysis of the expression of genes. One by Doumas *et al.* deals with the use of DNA microarrays. They describe different techniques to make microarrays, like contact printing, jet printing and direct DNA synthesis on the chip, the *in situ* probe synthesis. Experimental designs for microarray have also been discussed. While this chapter has listed various software tools that are currently used for gene expression data analysis, the chapter by Riva *et al.* deals with various statistical tools that need to be employed to derive meaningful inference from the

analysis of gene expression data. This chapter is not easy to understand for classical molecular biologists having little knowledge of mathematics and statistics. One of the ways to look for gene function is by disrupting the gene and then looking for a phenotype. Later, using genome walking technology, one can find out the nature of the gene that was disrupted. The chapter by Granier and Bouchez gives details of the various ways to get mutants using transposons, T-DNA insertion, Ac/Ds and En/spm system, etc.

It is becoming amply clear that changes in the transcript profile in any tissue or in response to external factors need not reflect on the carbon-copy changes in the protein levels, either qualitatively or quantitatively. This has led to the development of the field of proteomics; analysis of total protein components in a specific situation. The technology of proteomics is discussed in detail in a chapter by Zivy *et al.* This chapter also discusses how the drawbacks of the classical proteomics using 2D gels followed by the identification of proteins have been taken care of by the use of different techniques like ICAT (Isotope Coded Affinity Tag) or SILAC (Stable Isotope Labeling by Amino acids in Cell culture), etc. Currently many other methods like 2D-LC or 2D-LC-MS/MS are also being used. Addendum to this chapter importantly describes how post-translational modification of proteins, especially phosphorylations can be analysed, what is now termed as phosphoproteome maps.

What finally matters for the growth and development of a plant is the change in the profile of different metabolites. During the last few years, a major emphasis has been to profile the changes in the total metabolites as brought about by the catabolic and anabolic activities of the proteins, and consequently an area of metabolomics has emerged. Realizing the importance of this area, the book devotes four chapters (over 70 pages) on this topic. Krapp *et al.* take the reader through various analytical techniques used for separation and identification of metabolites and the use of statistical and bioinformatics tools. It is emphasized that to get the proof of equivalence in transgenic plants generated through gene transformation, comparison of metabolite profile is the most desirable and convincing. Moing *et al.* describe the use of different NMR spectroscopy techniques for metabolite identification and fingerprinting.

Use of isotope labelling in the analysis of metabolic fluxes is presented by Dieuaide-Noubhani. The fourth chapter on this topic gives an account of the mathematical way of representing metabolic networks, where intermediate metabolites become links in other reactions of other networks, thus forming a matrix. The last chapter of the book also deals with metabolic fingerprinting and describes the principles and application of MID-FT-IR (Middle Fourier Transformed InfraRed) technique for high throughput screening. It has now become important to know the function of a protein in a specific cell type and find out its interacting partners. It is becoming clear that it is the interaction that is important to elicit a specific response rather than the presence of the proteins per se.

There are two chapters in the functional genomics section by Brown *et al.* and Bolte *et al.* respectively, which deal with different microscopic techniques (electron, confocal), reporters, probes, application of GFP, FRET and other technologies to study the localization, movement and interaction of proteins. Both these chapters give the techniques and theory behind the use of various equipment and probes in a comprehensive style.

Having described various tools and techniques used in functional genomics, a section is devoted to describe a few plant models where such applications have led to the generation of important knowledge about genes and their role in plant growth and development. The work on *Arabidopsis* is described by Johnson and Bouchez, rice by Delseny, *Medicago truncatula* by Journet and Gamas, tomato by Stevens *et al.* grapes by Adam-Blondon *et al.* and sugarcane by Hoarau *et al.* In organizing this section the editors have included a simple genome like that of *Arabidopsis* and also a complex genome as that of sugarcane, and also covered both monocot and dicot species. Currently many groups are also checking the sequences of different ecotypes and recently, it was found in *Arabidopsis* that there can be a difference of even up to 3–4% between two ecotypes. In each of these chapters the efforts that are being made to generate more resources, like that of developing TILLING populations in rice, tomato, etc. and use of the genomics information with respect to the biology of the plant have also been covered. For example, it has been discussed that in *Medicago*, it would be of interest to

find the genes involved in nitrogen fixation, and in tomato, the resistance genes to different pathotypes can be studied.

The use of different genetics and genomics tools and techniques in mapping genetic diversity and in plant breeding programmes has been covered in the last major section. The basis behind the selection of different molecular markers is described by Falque and Santoni. Use of transposable elements to analyse plant diversity is covered by Tam *et al.* In crop plants some of the important agronomic and yield traits are controlled by many genes. Using *Arabidopsis* as a case study, Loudet and Daniel-Vedele bring out the use of quantitative genetics at the molecular level to understand complex characters, and Stevens *et al.* describe the characterization of QTLs. Manicacci *et al.* bring out the concept of molecular evolution. The practical way to use genomics in plant breeding is covered by Hirel *et al.* using maize and wheat as case studies.

One chapter that apparently seems to stand alone is that by Planchot *et al.* entitled 'From genomics to self-assembly'. Here the concept proposed is to look at different levels of cellular assembly and organization in order to comprehend the molecular recognition phenomena.

As mentioned above, this book is a valuable resource for all those who wish to learn about various techniques that can be employed in the field of structural, functional and application genomics. The diagrams, tables and especially flow charts to give data and explain the basics of techniques employed are an additional strong point of the book. However, the editors could have added another chapter on comparative and evolutionary genomics and also a chapter on small non-coding RNA, microRNA, siRNA, etc. Techniques like atomic force microscopy and live cell imaging could have also been included. Nevertheless this is a book that should be on the shelf of all libraries in the departments of genetics, molecular biology and biotechnology. It is also useful for those working in non-plant areas as the techniques described in the book can also be used to understand their genome, proteome and metabolome.

S. K. SOPORY

*International Centre for Genetic Engineering and Biotechnology, Aruna Asaf Ali Road, New Delhi 110 067, India e-mail: sopory@icgeb.res.in*