

BOOK REVIEWS

The Molecular and Cellular Biology of the Potato

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The title of the book is somewhat confusing if seen outside the framework of the series as a part of which it was published. The focus of the research presented in the book is laid upon improvement of resistance of potato plants and tubers against various physiological stresses and pests, and not as much on a complete description of the molecular and cellular biology of the potato. However, if seen as a part of the series *Biotechnology in Agriculture* this focus seems appropriate. The book is divided into six sections, which all deal with different aspects of current potato research. The first section describes the evolution of the potato germplasm. The first chapter deals with a short description of the origin of the germplasms of the potato cultivars that are used nowadays, and also stresses the importance of the continued use of newly discovered potato germplasms for strain improvement, even now when rDNA techniques are available. The second chapter gives an account of the use of RFLPs in genetic mapping of the potato genome and its importance for future genetic engineering.

The second section deals with the process of tuberization in potato, which gives the potato its nutritional and commercial value. A better understanding of this process should result in better use of molecular methods in potato improvement.

The third and largest section of the book describes the research on stress responses and disease resistance. In Chapter 5, the expression of the Proteinase Inhibitor II gene is studied. This gene is constitutively expressed in tubers, but in other parts of the plant (e.g., stem, leaves), only upon physical wounding. The protein causes inhibition of growth and

development in insect larvae that feed on potato. The gene expression is studied very thoroughly and includes an interesting analysis of the Proteinase Inhibitor II gene promoter. Other chapters in this section deal with physiological and environmental stresses that reduce the commercial value of potato tubers. The functional properties of proteinase II gene inhibitor protein upon insect larvae are studied in Chapter 8, and the results look very promising. In Chapter 6, the problem of "soft rot" of potato tubers is addressed. This disease is being caused by *Erwinia* bacteria in tubers subject to wounding and hypoxic stress. Hypoxic stress causes a global override of aerobic gene expression, which makes it more difficult to confer resistance by genetic engineering. A solution might be offered by placing a bacterial resistance gene under the control of a hypoxia-inducible promoter, such as ADH. Chapter 10 contains an overview of the current knowledge on several potato viruses and resistance of potato against these viruses. Research in this field is being hindered by the fact that the viral genomes, as well as the potato genes conferring resistance to these viruses, are not known at this moment.

The fourth section draws attention to the carbohydrate metabolism in tubers, which is an important (and difficult) subject. Advances in this field may lead to future improvement of the overall productivity of the potato. This section also describes research on another problem that is linked to carbohydrate metabolism, i.e., the undesirable sweetening process that takes place in cold-stressed tubers. This problem has enormous commercial impact on the potato industry. No attention is being paid, however, to recent efforts to change the starch composition of potato tubers, in order to increase their value for the starch industry.

The most interesting section in my view (the fifth section) covers the subject of genetically engineering resistance of potatoes against insects, using bacterial genes (*B. thuringiensis* proteins) and engineered resistance of potato against bacteria and fungi, using insect genes. These genes code for several types of polypeptides that show very potent bacteriocidal and fungicidal properties, especially when used simultaneously. Using the basic molecular framework laid down by these naturally produced polypeptides, "designer" polypeptides have been synthesized that possess even more powerful bacteriocidal and fungicidal properties. However, an important drawback for practical use is the observation that these toxins are probably lethal to mammals in high doses. In addition, this section contains a summary of modern methods for potato transformation and regeneration, showing the enormous progress that has been made in this field in the past eight years.

This last section of the book contains chapters on the certification procedure for the introduction of transgenic plants into the environment (field trials) and on the prospects of wider use of potatoes in developing countries, where wider use of potato as a food crop is obstructed by the occurrence of even more pests than in the industrialized countries.

In general, this book gives an excellent overview of the current biotechnological research on potato, written by specialists in the various disciplines. The major problems and pests encountered by potato producers are addressed and possible solutions to these problems are explored. This book offers a good introduction in this field for researchers without prior knowledge. The chapters are well written and address the subjects in a clear and complete (if possible) manner. It seems likely that in the future, the large research efforts will pay off and will improve the use of this important food crop throughout the world.

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Sequence Analysis Primer

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As technology improves, our ability to obtain sequence information from DNA, RNA, and protein has become quicker and easier. Sequences can potentially provide the scientist with much information about the structure, function, and evolution of a molecule. Gleaning that knowledge from the sequence, however, may be a much trickier task than actually doing the sequencing.

In *Sequence Analysis Primer*, the authors have attempted to give the beginning sequencer a reference book on the different computer programs available to aid in sequence analysis. Besides giving examples of how different programs function, the principles behind the theory are briefly described. The book is divided into four chapters. The first two chapters deal with the computer analyses that may be done on DNA, RNA, and proteins. The third chapter explores the questions of similarity and homology, and the fourth chapter presents a case study of the analysis of the *Notch* gene from *Drosophila*.

The first chapter starts out with a listing of the different computer programs available to aid in DNA sequence analysis. The chapter continues with different strategies to get the correct assembly of your sequence, using the programs to help you. Unfortunately, the only program that is given any more than a cursory mention is the Genetics Computer Group program, so unless you have that program, much of the information is irrelevant. The chapter does give a good overview on the identification of transcriptional signals and coding regions and on RNA structure.

The second chapter reviews the techniques used to assess the various physical and structural properties of proteins. The explanations of the different techniques and the assumptions made in using them are quite useful. This chapter also contains a detailed description on the profile method of determining motifs and provides a step-by-step procedure on how to produce one.

The third chapter deals with sequence comparison and the different tools available to perform this operation. The chapter is divided into three

parts: dot matrix methods, dynamic programming methods, and scoring systems. The section on dot matrix analysis consists of an introduction to the method and then gives many examples on how it has been used to examine various proteins. The derivation of the mathematical description of the dynamic programming alignment is somewhat difficult to understand, a problem that is compounded by a typographical error in one of the equations. A simple example of an alignment is given and examples of more difficult alignments are provided. The chapter concludes with descriptions of different scoring systems for sequence analysis.

The last chapter is probably the most useful for the beginning sequencer. This section describes the way in which the *Drosophila Notch* gene was characterized, starting with the DNA sequence analysis and moving on to the protein analysis and comparison to other proteins. Necessary terms whose definitions were lightly glossed over in the first three chapters of the book were finally explained clearly. The lesson about using caution when using computer programs to analyze data was driven home in this chapter by comparing the results of a homology search using different programs. Overall, this chapter was well written and contained much useful and practical information about how to analyze a sequence.

In general, *Sequence Analysis Primer* serves as a useful guide in addressing questions relating to sequence analysis. The many examples and figures help a great deal in making the text more understandable. The appendices to the book contain some very useful information, including addresses to the many databases and formats for submitting sequences electronically to the appropriate databases.

There are problems with the book, however. It is quite clear that each chapter was written by different authors because there is very little continuity throughout the book. Basic definitions that should have appeared early in the book are finally supplied in the final chapter and much information was repeated in different chapters. Finally, typographical errors were frequent and proved to be distracting when trying to understand an equation or searching for the last half of a misplaced paragraph.

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