

Book review

S. FOSTER & V. E. TYLER [ed.]: Tyler's Honest Herbal. A Sensible Guide to the Use of Herbs and Related Remedies.

The Haworth Herbal Press, an Imprint of The Haworth Press, Inc., 10 Alice Street, Binghamton, NY, 1999, 442 pp., ISBN 0-7890-0705-3

This book is the fourth edition Tyler's Honest Herbal, providing essential botanical information as well as folkloric background of herbal remedies in a accessible style. It is viewing more than 120 herbs from a scientific standpoint too.

Unlike the other herb books, this book gives a serious evaluation of both the positive and negative features of the use of the most important herbs for therapeutic purposes. The amount of the useful information is contained in the write-ups on individual drugs which follow the introductory sections. Each write-up includes descriptive information on the source of the plant, its traditional uses, and an evaluation of the relevant and current literature which helps to support or disprove intended uses of the plant.

Most of them are organized according to a similar plan: a brief description of the drug and its proper nomenclature, as well as that of the plant from which it is derived, and precede comments on its alleged used. Then follows a nontechnical discussion of chemistry and pharmacology (when known) of the active principles of the drug. Next part is an evaluation based on all evidence known to the author which offers a judgment about the probable utility of the herb. The information on the various herbs has been arranged in alphabetical order by common name for the convenience of the readers.

This new edition contains valuable informations not found in the previous edition:

- research and information about cat's claw, celery, garcinia, grape seed, kava, pygeum, and wild yam
- informations about trials on many bestselling herbs, including black cohosh, echinacea, garlic, ginkgo, ginseng, St. John's wort, and saw palmetto
- hundreds of new supporting references from scientific studies on herbs and other dietary supplements.

A. PRUŽINSKÁ

Book reviews

H. D. BURGESS [ed.]: Formulation of Microbial Biopesticides. Beneficial Microorganisms, Nematodes and Seed treatments.

Kluwer Academic Publishers, P. O. Box 17, 3300 AA Dordrecht, The Netherlands, 1998, 383 pp., ISBN 0-412-62520-2

The book deals specifically with the formulation of beneficial microorganisms and nematodes.

This important title brings together a huge wealth of information within the covers of one book. This volume goes back to basics, i. e. ecological and biological knowledge, to analyse the special requirements when formulating microorganisms and to build up a detailed account of modern formulation technology. The disciplines involved are entomology, botany, microbiology, virology, nematology, chemistry and equipment design.

The book is broadly divided into five sections and spanning 10 chapters, covering principles of formulation, organisms with peroral and contact modes of action, organisms with the power of search and future trends. The microorganisms are divided into six groups: (1) microbial insecticides; (2) microbes that destroy, inactivate or compete with plant pathogens; (3) microbial herbicides; (4) beneficial organisms that improve plant nutrition; (5) microbes applied to seed; and (6) entomophilic nematodes.

General principles of formulation are established in Part 1 of this book. It describes types of application machinery common for many groups of organisms and for chemical too. This chapter elaborates the four basic functions of a formulation (stabilization, handling and application, environmental persistence, improvement of action) and how they affect formulation approach: it also reviews the main formulation types suitable for use with organisms. Both function and type are interrelated. General principles and approaches are discussed, and descriptions of particular products used for different organisms are covered in ensuing chapters.

In subsequent parts, the arrangement of organisms in groups is around mode of action. It dictates the formulator's ultimate objectives and, therefore is used as the basis for three separate parts in the book.

Some organisms, such as insect pathogenic bacteria and viruses, act through the gut and must be eaten to take effect; these are dealt with in Part 2. Part 3 covers others - such as insect pathogenic fungi, bacteria and fungi that control plant pathogens and weeds, *Rhizobium* inoculants and avirulent strains of plant pathogens - which act, infect or colonize after contact with external surfaces of the pest or plant.

Part 4 deals with entomophilic nematodes, which have a power of search before infecting. Thus the formulator must concentrate on encouraging the pest to be eaten by the organisms, or on facilitating contact between the organism and the external surfaces of pest and plant, or on preserving search mobility, as well as providing a food base for proliferation of the organisms in their new surrounds.

Each chapter considers research needs for the future, that are then reviewed, compared and discussed in Part 5.

The book also includes three very useful appendices cataloguing formulation additives, spray application criteria and terminology in alphabetical order for easy reference. Attention is directed to a series of recipe - type tables which explain how to make specimen formulations. There is a bewildering array of most sorts of additives, only those actually tried with organisms are included, not only those that have been successful, but also those that have failed, together with information on harmful effects or unexpected beneficial effects.

This book is designed for a wide readership.

A. PRUŽINSKÁ

R. DeSALLE & B. SCHIERWATER [eds.]: Molecular approaches to ecology and evolution

Birkhäuser Verlag, PO BOX 133, CH-4010 Basel, Switzerland, ISBN 0-8176-5725-8

The last ten years an explosion of activity in the application of molecular biological techniques to evolutionary and ecological studies has been seen. This volume attempts to summarise advances in the field and place into context the wide variety of methods available to ecologists and evolutionary biologists using molecular techniques. Both the molecular techniques and the variety of methods available for the analysis of such data are presented in the text.

The book has three major sections - populations, species and higher taxa. Each of these sections contains chapters by leading scientists working at these levels, where clear and concise discussion of technology and implication of results are presented.

The focus of the first three papers in section one is on the questions investigated in certain model systems (birds, insect) by means of appropriate molecular tools. The final two chapters deal with the molecular techniques themselves, and discuss the potential and application of the most prominent techniques currently in use.

Part two – Species – has six chapters, four of them use explicit tree-building approaches to examine problems at the interface of populations and species, the next two chapters discuss the species problem as a problem of diagnosis, and both are therefore attempts to make a direct connection to conservation biology.

Section three is concerned with five areas of modern systematics that are problematic in data analysis (alignment, data combination as it pertains to robustness of phylogenetic inference, computational difficulty of analysing large number of taxa, biogeographic analyses and developmental considerations in systematics).

The volume is intended for advanced students of ecology and evolution and would be a suitable textbook for advanced undergraduate and graduate student seminar courses.

P. KUŠNIRIKOVÁ

S. MOHAN JAIN, D. S. BRAR & B. S. AHLOOWALIA [eds.]: Somaclonal Variation and Induced Mutations in Crop Improvement.

Kluwer Academic Publishers, P. O. Box 989, 3300 AZ Dordrecht, The Netherlands, 1998, 500 USD, ISBN 0-7923-4862-1

The book is 32 volume of the book series Current Plant Science and Biotechnology in Agriculture. This volume deals not only with plant science and biotechnology but also with animal and food science, and microbiology.

The topic of the book is genetic variability, the basic process in plant breeding. The conventional breeding methods are not sufficient for the desirable rapid improvement and development of new cultivars. Therefore, plant breeders look for new technologies to create more genetic variability, reduce the time and improved yield.

The book is divided into three sections. The first one is dedicated to somaclonal variation in crop plants, cereals, forage grasses, ornamental plants, forest trees, banana and Solanaceous medicinal plants, it describes the mechanisms and chromosomal basis of somaclonal variation. The second section discuss the importance of the induced mutations and apomixis in plant breeding, and the usage of transpozons for the isolation of apomictic mutants. The last part deals with molecular basis of genetic variation and describes molecular methods for identification of somaclonal variation, RAPD markers, and transgene expression.

The book presents the „hot“ topics in the modern plant breeding to highlight the recent developments in mutagenesis and *in-vitro* induced variation.

R. BRUTOVSKÁ

R. Durbin, S. Eddy, A. Krogh, G. Mitchison: Biological sequence analysis. Probabilistic models of proteins and nucleic acids.

Cambridge University Press, The Edinburgh Building, Cambridge CB2 2UR, UK, ISBN 0-521-62971-3

The emerge of modern molecular genetics has changed the face of biology. The great acceleration in the accumulation of biological knowledge began with today's genome projects. The need to understand the biological data is driving forward the newly-created and explosively expanding research area of computational biology, or bioinformatics.

This book provides up-to-date and tutorial-level overview of sequence analysis methods, with particular emphasis on probabilistic modelling. It is structured into four parts covering problems in pairwise alignment, multiple alignment, phylogenetic trees and RNA structure. These parts are divided into 11 chapters. Chapter one is concerned with problem of deciding if a pair of sequences are evolutionary related or not. Here authors examine traditional pairwise sequence alignment and comparison methods which use dynamic programming, however, after introducing all the basic HMM algorithms and theory in chapter two, in the next chapter we revisit pairwise alignment from this new view. In chapter five authors consider the problem of finding sequences which are homologous to a known evolutionary family or superfamily. Beside standard approach to this problem we can learn about profile HMM for modelling protein and DNA sequence families based on multiple alignments. Third part of the book (chapter 7, 8) is devoted to questions of phylogeny. Here we find an overview of some popular methods for inferring evolutionary trees and also application of probabilistic modelling to this problem. Last part of book deals with RNA structure analysis using stochastic context-free grammar theory, which is clearly explained in the chapter 9. Because some chapters are more mathematically detailed the final chapter covers some topics in probability theory that are relevant to much of the earlier material.

I recommend this excelent book with many examples and exercises to all graduate or advanced undergraduate students with a background in molecular biology, mathematics, computer science or physics.

P. KUŠNIRIKOVÁ