mation should serve as valuable feedback for policy makers and rice scientists to reorient their future research and development priorities.

The excellent and the first-of-its-kind publication covering all aspects of the least known germplasm of great potential, is not without deficiencies. Part II for instance, is devoted exclusively to aromatic rices, and while giving emphasis to the popularly known *basmati* and *jasmine* rices should have included a chapter on aromatic rices of Afghanistan, Iran, and Iraq, which are known to have their own traditional basmati-like scented varieties and on varieties like 'Paw San Honue' of Myanmar. More than one chapter each on Indian and Pakistani *basmati* rices deal with largely similar issues/aspects on crop improvement, looks duplication and this could most certainly have been avoided in order to make the chapter on breeding more comprehensive. A single chapter each on crop management including the production-protection package would have been adequate instead of their being split into separate chapters. In small pockets in India and other countries, preferred varieties of different flavour and grain quality (not of basmati aroma and quality) are being nurtured. Also, varieties of medicinal value are known since long. Exclusive chapters on them under Part III would have enhanced further the value of this otherwise informative publication.

Rice, the staple food for more than one half of the global population, is the maximum researched crop with a wealth of scientific literature on all its aspects. All the information we have so far is about common varieties, and our knowledge on uncommon rices is incomplete. This book is a concerted effort on the part of sixty rice experts from fifteen countries worldwide, who attempt to fill this gap. The credit for bringing out this educative and exhaustive compendium on the least-known varieties goes to the editors and the publishers. Needless to mention that a rare publication of this kind should find a place in all the institutions/laboratories engaged in rice research.

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Prokaryotic Genomics. Michel Blot (ed.). Birkhauser Verlag, P.O. Box 133, CH 4010, Basel, Switzerland. 2002. 208 pp. Price not mentioned.

The genome revolution, which began in the last decade, has resulted in the complete sequencing of several genomes of important prokaryotic and eukaryotic organisms. The availability of completely sequenced genomes has facilitated quick *in silico* based predictions of gene identity and function; identification of drug targets; study of metabolic pathways and elucidation of disease susceptibility, etc. In the midst of this huge euphoria over *in silico* genomics, the equally important (if not more) physical aspect of studying the genome seems to have taken a back seat. In this respect, this book comes as a refreshing change. The book is a part of the *Methods and Tools in Biosciences and Medicine Series* and explains in an easy-to-understand language, various techniques for the physical mapping and analyses of prokaryotic genomes. Important techniques including PFGE, microarrays, microsatellite analyses, genetic footprinting, proteomics, etc. have been dealt with. The book begins with an obituary to Michel Blot, who unfortunately died in an accident in 2002, at the young age of 42 years.

The first chapter by Coline Dale, Howard Ochman and Wendy Smith from the University of Arizona, USA, discusses the physical mapping of bacterial chromosomes. The ability to determine the molecular size of bacterial chromosomes was revolutionized by the advent of the PFGE technique. The description given in this chapter can be used for sizing any bacterial genome. Important information for separation of co-migrating bands as well as other experimental details have been included. The second chapter by Joseph Casadesus and Eva M. Camacho from the Universidad de Sevilla, Spain, deals with two specific genetic mapping approaches to study the *Salmonella typhimurium* genome, viz. conjugation and phage-transduction. Based on the presentation, both techniques can be easily adapted to study other bacterial genomes. Details of the techniques and a troubleshooting guide, have also been included. The third chapter by Dominique Schnieder and Michel Blot from the Universite Joseph Fourier, France, describes the importance of insertion elements in studying prokaryotic genomes. These elements and transposons provide a wonderful tool to generate mutations. However, the chapter is very short and does not include several important aspects such as their use in generating gene knockouts in pathogenic bacteria such as *Mycobacterium tuberculosis*. The fourth chapter by David Metzgar from the Scripps Research Institute, USA, discusses the use of microsatellite sequences in bacterial strain typing. The microsatellite repeats are more common in eukaryotes than in prokaryotes, probably due to the constraint on genome size in bacteria which results in repeat contraction rather than repeat expansion. The chapter is very short and does not provide enough details, probably underscoring the relative unimportance of microsatellite markers to analyse bacterial genomes due to their lower abundance. The fifth chapter by Richard D'Ari and Daniel Vinella from the Institut Jaques Monod, Paris, France, describes the technique for generating gene duplications or deletions *in cis* and the methodology to generate the duplication/deletion at precise chromosomal locations.

The sixth chapter by Anne Thierauf and Stanley Maloy from the University of Illinois and San Diego State University, USA, respectively, describes the popular 'ancient' technique of generalized transduction. The protocol for generalized transduction using the P2 and the P22 phages of *Salmonella typhimurium* have been described in detail and transduction in other bacteria have also been dealt with. The various uses of generalized transduction have also been documented. The next chapter by Lu Zhou, Soo-Ki Kim, Larisa Avramova, Kirill A. Datsenko and Barry L. Wanner from the Purdue University, USA, discusses the use of conditional–replication integration and modular (CRIM) plasmids to generate *lacz*-reporter fusions. The chapter includes an introduction of the importance of reporter fusions and describes the basic features of a CRIM vector before describing the use of this vector in construction of reporter gene fusions. The technique is described in lucid detail and includes a list of all bacterial strains, consumables and equipment needed to carry out the experiment. One section on troubleshooting and another on applications of the technique are also included and it is probably, the best written chapter in the book. The eighth chapter by Scott S. Walker, from the Schering–Plough Research Institute, USA and Chad Houseweart and Teresa J. Kenney from the Genome Therapeutics Corporation, USA, describes the use of transposon-based mutagenesis in bacterial functional genomics. The next chapter by Bruno Tinland from Monsanto Europe Africa, Belgium, discusses gene transfer to plants through bacterial vectors. The *Agrobacterium*-mediated gene transfer has been an important tool for plant molecular biologists for the past twenty years. The chapter briefly describes the protocol for gene transfer and also includes the applications of the technique and troubleshooting. The tenth chapter by Simon Swift from the University of Auckland, New Zealand, discusses the signal sensing and signalling genes for Quorum sensing. Quorum sensing is a term used to define the signalling mechanisms in bacteria through which they sense population density and respond to it. Since it is a newly discovered phenomenon, it is gratifying to note that the authors have given details of the methodology, troubleshooting and applications. Details of bacterial strains and plasmids, different sensor genes, etc. have been neatly elucidated in the form of tables.

No book on genomes can be complete without a discussion of microarrays. The eleventh chapter by Michael T. Laub from Harvard University, and R. Frank Rosenzweig from the University of Montana, USA, discusses the use of microarrays in studying transcriptional profiling in bacteria. The rapid sequencing of bacterial genomes (more than sixty bacterial genomes have been sequenced) has necessitated the development of high throughput technologies to study functional genomics. Despite the immense popularity of the technique, the chapter is very brief and does not provide details for the bioinformatics component of microarrays. The next chapter is by Cecile Jourlin–Castelli and Francois Denizot from the Laboratoire de Chimie Bacterienne, IBSM-CNRS, France, and Philippe Bouloc from Laboratoire de Reseaux de Regulations, Institut de Genetique et Microbiiologie, Universite Paris-Sud, France. The chapter discusses transcriptome analysis by macroarrays and describes a radioactivity-based technique for comparing the transcriptome of bacteria grown under special conditions or to compare mutant strains. The useful feature of this chapter is the inclusion of details about RNA isolation from bacteria including the precautions that need to be taken. This is important for any gene expression-based analysis. The thirteenth chapter by Cecile Lelong from the Plasticite et Expression des Genomes Microbiens, France and Thierry Rabilloud from DRDC/BEPC, France, describes the important technique of proteomics and focuses mainly on the immensely popular 2D-gel electrophoresis. It also includes details on protein extraction from bacteria. The next chapter by Shaorong Chong and Francine B. Perler from New England Biolabs, USA, discusses the interesting technique of intein-mediated protein purification. This technique provides an attractive alternative to conventional recombinant protein purification tags such as MBP, GST, etc. Since the technique is relatively new and not well known, sufficient details regarding the principle and the materials required, have been included. The technique itself has been explained lucidly. The final chapter by Gustavo Di Lallo, Patrizia Ghelardini and Luciano Paolozzi from the Dipartimento di Biologia, Universita di Roma 'Tor Vergata', Italy, discusses the efficient two-hybrid assay in *E. coli*. The *E. coli* system presents several advantages over the yeast system, not the least being the ease of manipulation. This system can be used efficiently at least to study bacterial protein–protein interactions.

The book is basically a practical handbook on different techniques to analyse prokaryotic genomes. So, it may be disappointing for someone who is looking for theoretical knowledge. Some chapters lack important details; it might have been a better idea to have covered less topics so that sufficient details could have been included. The text uses very simple language. The subject that the book addresses is extremely important and relevant, given the importance of genomic studies in bacteria. The book is softbound, not too bulky and easy to carry with an attractive cover. All in all, a good guide for anyone starting on bacterial genomics.

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Constructed Wetlands for Wastewater Treatment in Cold Climates. U. Mander and P. Jenssen (eds). 11 Advances in Ecological Sciences, WIT Press, Southampton, Boston, UK. 2003, 325 pp. Price: $179.

Constructed treatment wetlands (CTW) are defined as engineered wetlands that utilize natural processes involving wetland vegetation, soil, and their associated microbial assemblages to assist, at least partially, in treating wastewater or other polluted water resources. The number of constructed treatment wetlands receiving wastewater from municipal, industrial, agricultural, and storm water sources has increased to more than 8000 sites across the world. The success story of CTWs depends upon appropriate design, siting, pre-treatment, operation and maintenance. These man-made systems are glaring examples of ecotechnology wherein integration of ecological functions provide the option of wastewater treatment, its recycling through conservation, enhancing wildlife abode, and offsetting significant losses in the wetland area. These provide effective wastewater treatment at moderate prices which are simple to maintain for individual residences, cluster of residences, resorts, restaurants, and other businesses that depend upon on-site systems for wastewater treatment.

This edited book consists of seventeen selected papers presented at two international conferences on wetland ecosystems for wastewater treatment: the Symposium 'Perspectives of Constructed Wetlands for Wastewater Treatment in Cold Climates' organized by the editors of this book and the 4th International Conference in Ecological Engineering on 'Managing the Wastewater Resource', organized by the Agricultural University of Norway and the Norwegian Center for Soil and Environmental Research (Jordforsk). In addition, the book included relevant case studies from USA, Poland and Czech Republic presented at an International workshop on 'Nutrient Cycling and Retention in Natural and Constructed Wetlands' held at the Czech Republic, and at an International Conference on 'Wetland Systems for Water Pollution Control', held at Florida, USA. From a large variety of constructed wetlands the subsurface flow wetland systems treating municipal or farm wastewater have been included in this book. The main focus of the seventeen up-to-date articles has been on the potential, and use