Metagenomics: Current Innovations and Future Trends

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Book Review

Future Microbiology

The current revolution in microbiology has been primarily driven by advances in technology and, in particular, by the development of the PCR and parallel sequencing platforms. The need to incorporate these technologies into the everyday thinking of microbiologists, and especially those studying the role microbes play in the environment, has been driven by the inability to culture the majority of microbes from an ecosystem and the logistics of using a myriad of media and culturing conditions to capture those that can be grown *in vitro*. To this end, the development of culture-independent methods has provided the scientific community with paradigm shifting revelations and opened up the world of the microbe to much more intense interrogation. One such approach, developed by Delong's group, involved shotgun cloning of large genomic DNA fragments into a fosmid vector background and maintenance of this vector in an *Escherichia coli* surrogate host [1]. The fosmid library could subsequently be screened and sequenced to obtain partial genomic information on microbes for which no cultured isolates existed. This approach was later given the neologism of 'metagenomics' by Jo Handelsman [2] and is now a major method being used in a variety of ways to explore whole microbial communities in order to determine the range of functions that are present without ever culturing the microbes. Since the development of the shotgun methods to generate metagenomic libraries in surrogate hosts, second-generation sequencing has provided us with another 'flavor' of metagenomics, namely sequence-based metagenomics, which bypasses the need to clone the metagenomic DNA. Together, these methods are transforming the way in which we carry out microbiology. Hence, it is very timely that we should have a book dedicated to the subject area, which is now well into its second decade and has amassed over 2100 publications with the word metagenom* (and wildcard variations thereof in SCOPUS) in the title or abstract since 1998. The current title, edited by Diana Marco, is somewhat

different to the previous books on this subject in as much as it is much more of a review of the current status of the field and does not provide practical protocols or methods to follow and perform metagenomics. Therefore, it is squarely aimed at those who would not be overly familiar with the subject and would be looking to be provided with a primer as to what is being undertaken in the area and to obtain a better understanding of the scope of the field. There are no standard operating procedures or flowcharts of how to perform metagenomics, so do not be disappointed if this is what you are seeking; instead, it provides an in-depth analysis of the 'state of the union' and some vision of where the field is heading. In addition, it does explore the limits and pitfalls of modern metagenomics, for example in chapter 7, which discusses single-cell genomics, and chapter 13, which explores *E. coli* and its efficacy as a surrogate host in functional metagenomics.

The book is divided into 15 chapters and covers a wide range of metagenomic topics including: viral – chapters 3 and 9; fungal – chapter 10; human/bacterial – chapters 4 and 11; environmental – chapters 12 and 15; functional – chapters 4 and 13; bioinformatic analysis – chapter 8; specific methods – chapters 5, 6, 7 and 12 (chapter 12 also deals with bioremediation); bacteria–host communications – chapter 13; bacterial genealogy – chapter 2; and the opening introductory chapter 1. Each chapter is written as a standalone essay on the current status in that area and they all provide some vision of where the topic is heading. The level of detail is high in each chapter and will provide sufficient background for any scientist who wishes to delve into the topic further. However, the one area where I felt the book needed more input and more breadth would be in the data handling/analysis. The chapter on next-generation sequencing approaches (chapter 5) does explore some of the other approaches that are available, while chapter 8 specifically deals with the Community Cyberinfrastructure

for Advanced Microbial Ecology Research and Analysis (CAMERA) pipeline. This issue is the most significant facing researchers undertaking metagenomics using next-generation sequencing platforms and the data analysis bottleneck will only get worse as the third-generation platforms such as the Ion Proton (up to 660 million reads per run) and Oxford Nanopore Technologies' MinION and GridION platforms start to deliver their proposed output.

In conclusion, I think that this book covers a wide range of areas in which metagenomics has made an impact and provides the reader with sufficient scope to see how this approach can be used. It should show any reader that the method

is highly applicable to any complex microbial community for which it is either not possible or practical to access the different organisms and isolate them for further analysis.

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