BOOK REVIEWS

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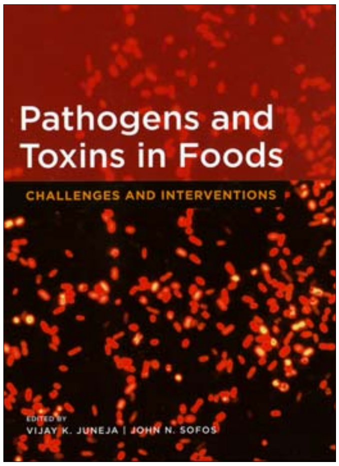

Pathogens and toxins in foods. Challenges and interventions

VIJAY K. JUNEJA, JOHN N. SOFOS (EDS)

2009. ASM Press,
Washington, USA
512 pp, 22 × 28.5 cm
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Recent scandals in which the widespread consumption of food contaminated with particular microorganisms or microbial products resulted in serious illness and even death have served to highlight the importance of food safety. The situation is further complicated by difficulties in regulating foods that are imported from all over the world, and by the increasing demand by consumers for natural, minimally processed foods, prepared with a minimum of preservatives. *Pathogens and toxins in foods. Challenges and interventions* will contribute significantly to improving the detection of food pathogens and to reducing the risk of food contamination.

The book is organized in thirty chapters, fifteen of which focus on food-borne microorganisms (pathogenic bacteria, viruses, prions, and parasites). Seven chapters describe chemical-toxic agents, including natural toxins in fungi, plants, and seafood as well as chemical residues and food allergens. Six chapters deal with the development and implementation of safety measures, specifically, the HACCP (hazard analysis and critical control point) system, which is widely used by the food industry. Two chapters describe appropriate detection methods.

The food-borne pathogens singled out for discussion are *Bacillus cereus* and other *Bacillus* spp.; *Campylobacter jejuni* and other campylobacters; *Clostridium botulinum*; *C. perfringens*; diarrheagenic *Escherichia coli*; *Listeria monocytogenes*; *Salmonella*; *Staphylococcus aureus* and other staphylococci; *Shigella*; pathogenic vibrios in seafood; *Yersinia enterocolitica* and *Y. pseudotuberculosis*; other bacterial pathogens, including *Aeromonas, Arcobacter, Helicobacter*, *Mycobacterium*, *Plesiomonas*, and *Streptococcus*; human pathogenic viruses in food; food-borne parasites; prions and prion-mediated diseases. However, the book does not take the standard approach to describing pathogenic microorganisms, but, after briefly summarizing the symptoms, it focuses specifically, and exhaustively, on the ecophysiology of each microorganisms in the particular environment the it finds.

Each food-borne organism or group of organisms is the subject of a single chapter, For each pathogen, an overview of its food-related characteristics is followed by a discussion of its incidence in the environment and in food, its survival and growth in food products, recent advances in control measures used in food processing that influence the number and spread of the organism, current biological, chemical, and physical interventions to guard against contamination, as well as discriminative detection methods to confirm these pathogens and to trace-back contaminated food products. In considering all possible sources of food contamination, the book does not limit its discussion to microorganisms but also addresses potentially toxic chemical agents or molecules, including seafood toxins, fungal and mushroom toxins, naturally occurring toxins in plants, and biogenic amines in food. It also provides a critical evaluation of the uncertainties in gluten testing; the hazards posed by chemical residues (especially in the United States); and European food safety perspectives on residues of veterinary drugs and growth-promoting agents.

Toxic compounds that can enter the human food chain as contaminants are derived from natural as well as synthetic sources. They include products resulting from the metabolic processes of the animals, plants, or microorganisms from which the food is derived; biological and chemical contaminants from air, water, and soil; intentionally introduced food additives; and compounds formed during food processing. These toxicants and their toxic effects can be measured and quantified by several techniques derived from analytical chemistry, bioassays, and applied mathematics.

Food allergy has also emerged as a major public health concern due to its increasing prevalence in the general population, and especially in children. It represents an adverse immune response to proteins present in food that is mediated usually by immunoglobulin E (IgE) but also by non-IgE (cellular) mechanisms. For example, peanut allergy, which is relatively common, is IgE-mediated whereas celiac disease is a cellular response. The development and implementation of reliable food-allergen detection and quantification methods are necessary to ensure consumer protection.

The chapter on HACCP focuses on all levels of the food production process in what the book describes as a “farm-to-table approach.” Thus, interventions for hazard control during the pre-harvest, harvest, food processing, retail-handled ready-to-eat, and food-service stages are described. The authors emphasize that each participant in the food chain, from farmer to processor to retailer to consumer, has some responsibility for food safety.

In the pre-harvest stage, i.e., when a food commodity—be it a crop or livestock—is growing, biological hazard prevention measures are aimed at minimizing pathogen contamination. While several methods for hazard control can reduce the pathogen load in foods of different origin, these decontamination methods are no substitute for proper agricultural or manufacturing practices during the harvest and production of food commodities. The ultimate success of food safety measures at the retail and food service levels depends on the maintenance and effective implementation of food safety management systems. Employees must be thoroughly trained to handle and prepare food according to the operation's food safety rules, such as those addressing correct hand washing and personal hygiene, the cleaning of equipment and all food preparation and handling facilities, pest control, and other service-related procedures.

Pathogens and toxins in foods is obligatory reading for anyone involved in food production but it also provides essential information for all those interested in the field of food microbiology, as its subject matter pertains to microbial ecology, clinical microbiology, and modern molecular techniques.

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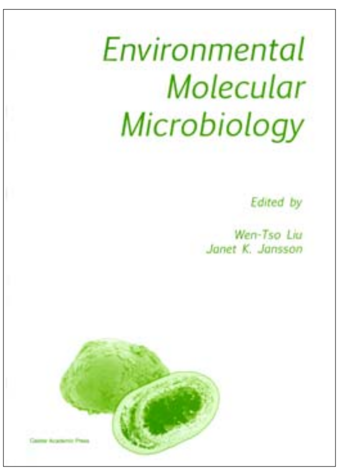

Environmental molecular microbiology

WEN-TSO LIU,
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2010. Caister Academic Press,
Norfolk, UK
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Throughout life's evolution, microorganisms have been responsible for maintaining the biosphere. Microbial communities are central to health, sustainable cities, agriculture, and most of the planet's geochemical cycles. Prokaryote communities are also potential reservoirs for new drugs and metabolic processes. Exploring microbial diversity has become equivalent to the exploration of outer space. There are more than 10^{16} prokaryotes in only a ton of soil, compared to 10^{11} stars in our galaxy.

Although measuring the reservoir of prokaryotic diversity is not a trivial task, fortunately, microbial ecology is currently benefiting from a technological boom with respect to the rapid development of molecular techniques, in general, and "omics" technologies in particular (genomics-metagenomics, proteomics-metaproteomics, transcriptomes). These techniques and their applications are the subject of *Environmental molecular microbiology*, which provides a state-of-the-art molecular toolbox to study microbial ecology. The book is divided into two principal thematic blocks. The first, with five chapters, describes the basis of the different molecular approaches that can be applied to study microbial diversity and the functions that it represents. Genomics and metagenomics, metaproteomics, microarrays, and molecular fingerprinting approaches are discussed at length in these chapters. The second block, with six chapters, focuses on the application of these molecular approaches to the study of microbes in different environments, such as soil, marine water, plants, the human body, wastewater, and biofilms.

Microbes are the largest component of biodiversity, but appropriate techniques to quantify that diversity, either in laboratory models or in natural communities, is lacking. The enrichment and isolation approach establishes artificial conditions under which only the "fittest" of microorganisms will successfully compete. Furthermore, the conditions that allow microbial growth in vitro are not easily determined—not only ability and persistence on the part of the researcher, but also a fair amount of luck are needed to identify them. To avoid this obstacle, in 1986, two articles were published that set the tone for a new era in microbial ecology: one by Olsen et al. [*Annu Rev Microbiol* 40:337-365] and the other by Pace et al. [*Adv Microbial Ecol* 9:1-55]. Those authors proposed a framework around which the study of microbial diversity and community structure could proceed outside the confines of the agar plate. The central tenet was that all cellular organisms could be detected and potentially identified in situ based solely on their rRNA, even organisms that have yet to be isolated in axenic culture. As a result of these two papers, over the past three decades there has been an exponential increase in the amount of environmental sequence data reported (Chapter 1).

Since the debut of whole-genome sequencing, in July 1995 (*Haemophilus influenzae*), until November 2009, the genomes of 962 *Bacteria*, 70 *Archaea*, and 122 *Eukarya* have been published. Genomics (in the case of single microbial species) has revealed both differences between closely related microorganisms and variability in genetic content (~ 40% on average) within species that carry mobile elements such as prophages, plasmids, insertion sequences, and transposons. The application of metagenomics (in the case of whole communities) to different environments has provided significant information regarding the genetic potential of microbes present in those habitats.

Reverse transcription of mRNA followed by PCR amplification was for many years the method of choice for monitoring the expression of biomarkers, over time and space, directly from the environment. But there are several difficulties with this strategy, including the rapid turnover of mRNA, the general instability of mRNA, and the fact that mRNA levels often do not directly correlate with the level of protein expression. Proteomics is the study of the entire suite of proteins expressed by a cell type, an organism, or a community (i.e., metaproteomics). Proteomics developed as an extension and alternative to genomics; however, it remains plagued by sever technical limitations, for example, its inability to detect proteins of low abundance in a complex sample.

Microarrays are another current methodology of interest and diverse application, including the characterization of microbial diversity of selected environments and the study of functional gene diversity as well as microbial activities in the environment. A microrray consists of multiple DNA oligonucleotide probes that, under high stringency conditions, hybridize only to specific complementary nucleic acid sequences (targets); a fluorescent signal indicates the presence of genetic regions of interest (Chapters 2–5).

Vast fields of exploration are opening up in microbiology. Exciting questions whose answers were largely inaccessible due to the limitations of classical approaches can now be tackled by the additional use of molecular and genomic tools. How many microbial species are there? What is the real extent of this diversity? What does all that microbial biodiversity do? How do ecosystems ultimately work? The first, albeit very preliminary, step in answering these questions is to identify the different components of the various communities. The resulting information must then be complemented with data about community function (metabolism, lifestyle), interactions, spatial and temporal dynamics, and the response to environmental variables. Molecular analysis of different habitats has thus far revealed different levels of microbial diversity. For instance, 42 bacterial phyla were recorded in the microbial mats of Guerrero Negro (Baja California, Mexico); agriculture soil can contain more than 20 bacterial phyla; approximately 12 phyla are present in the waters of the Sargasso Sea (Atlantic); the adult human gastrointestinal tract, with 8 phyla, and healthy human skin, also with 8 phyla, are the environments that contain the lowest number of phyla, although they appear to be highly diverse at the strain and species levels (Chapters 6–9).

Understanding the ecology of microorganisms is inarguably one of the most compelling intellectual challenges facing contemporary ecology. *Environmental molecular ecology* is highly recommended to students and researchers interested in microbial diversity and ecology. The knowledge and methodologies described in the book offer invaluable research tools with which to meet this challenge.

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