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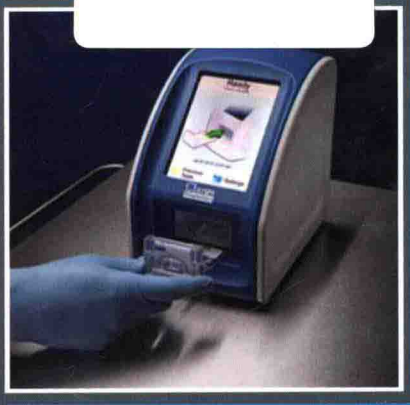

Biological Identification

DNA Amplification and Sequencing, Optical Sensing, Lab-on-chip and Portable Systems

Edited by R. Paul Schaudies

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Number 59

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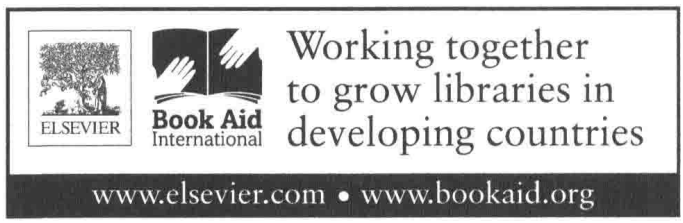

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Preface

The need to accurately identify and characterize biological organisms in a rapid fashion pervades almost all aspects of our life. The safety of the life essentials of food and water requires that we be able to identify and eliminate contamination at all levels of collection and distribution. Zoonotic infections, introduced either deliberately or through natural exposure, pose a cross-species threat to human life. The rise of emerging infectious diseases exacerbated by widespread international travel adds the requirement for not only rapid discovery and test distribution, but also improved treatment methods. Hospitals have become reservoirs of infectious organisms, leading to the now pervasive term 'hospital acquired infections' (HAI). HAIs are accounting for a growing percentage of infections leading to sepsis and frequently death. Then there is concern over the deliberate release of infectious organisms into a densely populated environment. The US Government has spent significant resources on the BioWatch program designed to protect our major population centers from a biological warfare attack.

The diversity of biological microorganisms presents a challenge almost as great as their ability to defend themselves against our attempts to kill them, or at least inhibit their replication. The diversity of replication mechanisms and the ability to use host mechanisms for replication only complicate our attempts to selectively inhibit the invader. All of the diverse approaches for the identification and characterization of microbiological organisms share the requirement to differentiate the target from the environment it is part of. This may involve attempts to isolate the target from the environment, frequently termed 'sample preparation'. Sample preparation is the ultimate driver for sensitivity, as the material must be extracted and concentrated and transferred into a matrix that is compatible with the identification strategy. The ability to rapidly and accurately identify microorganisms, especially those that cause disease in man, is paramount in all regions where people live. This work provides highlights of a multitude of scientific approaches to both identifying and characterizing biological material by exploiting the characteristics that are unique to an organism and differentiate it from its environment.

Part I of this book concentrates on the genetic elements of DNA and RNA for the identification and characterization of biological organisms. The DNA or RNA from an organism provides the blueprint from which activities are derived. The presence of a specific genetic element does not guarantee expression, but the

absence of a specific gene does indicate an absence of activity associated with that genetic element. The chapters begin with Next Generation Sequencing (NGS) in complex matrices and how these technical approaches identify both known and previously undiscovered organisms. While NGS is becoming much more affordable and the data analysis time is decreasing, there is still a pressing need to ask and answer much simpler and specific questions using the amplification of specific smaller regions of nucleic acids. The following chapters include classical polymerase chain reaction methods and isothermal amplifications as well as bead arrays for the analysis of amplified nucleic acid fragments. The need to make identification systems portable resulted in Part II of the book.

Part II, Lab-on-chip and portable systems for biodetection and analysis, is a collection of diverse approaches and technologies, not limited to nucleic acid signatures, to make systems efficient and smaller. Small systems require different approaches to fluid movement than bench-top systems, as well as unique power requirements. Smaller assay volumes require highly efficient sample preparation and detection methods because the small volume frequently requires higher concentrations than larger-volume detection approaches. This second part of the publication provides an in-depth overview of multiple approaches for specific signal generation based on the structural recognition of biological signatures. This section is followed by Part III, which focuses on optical approaches for recognition and identification.

Optical identification methods either detect modifications after an optically active molecule interacts with the target or take advantage of unique electromagnetic spectral properties of the organism itself. Most optical approaches have the advantage of being non-destructive and thereby preserving the sample for either culture or further analytical examination. The final section of the book describes a unique approach to sample preparation utilizing charge and mass differences to concentrate material of interest. The final chapter documents some very promising approaches for biological identification based on mass spectrometry.

I would personally like to thank all of the authors, as well as the individuals at Woodhead Publishing for their professionalism and dedication in producing this work.

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