

Microarray Technology and Its Applications

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Preface

It has been stated that our knowledge doubles every 20 years, but that may be an understatement when considering the Life Sciences. A series of discoveries and inventions have propelled our knowledge from the recognition that DNA is the genetic material to a basic molecular understanding of ourselves and the living world around us in less than 50 years. Crucial to this rapid progress was the discovery of the double-helical structure of DNA, which laid the foundation for all hybridization based technologies. The discoveries of restriction enzymes, ligases, polymerases, combined with key innovations in DNA synthesis and sequencing ushered in the era of biotechnology as a new science with profound sociological and economic implications that are likely to have a dominating influence on the development of our society during this century. Given the process by which science builds on prior knowledge, it is perhaps unfair to single out a few inventions and credit them with having contributed most to this avalanche of knowledge. Yet, there are surely some that will be recognized as having had a more profound impact than others, not just in the furthering of our scientific knowledge, but by leveraging commercial applications that provide a tangible return to our society.

The now famous Polymerase Chain Reaction, or PCR, is surely one of those, as it has uniquely catalyzed molecular biology during the past 20 years, and continues to have a significant impact on all areas that involve nucleic acids, ranging from molecular pathology to forensics. Ten years ago microarray technology emerged as a new and powerful tool to study nucleic acid sequences in a highly multiplexed manner, and has since found equally exciting and useful applications in the study of proteins, metabolites, toxins, viruses, whole cells and even tissues. Although still relatively early in its evolution, microarray technology has already superseded PCR technology not only in the breadth of applications, but also in the speed with which this evolution has taken place. Note that the literature dealing with microarrays has increased dramatically from its humble beginnings in the mid-nineties to reach more than 2000 articles and almost 300 reviews in 2004 alone (Fig 1). Although a saturation point may have been reached - not surprisingly given that there is

still a limit to the number of laboratories that have access to this technology—its impact is truly remarkable, especially when compared, for example, to the emerging and much touted field of Nanotechnology.

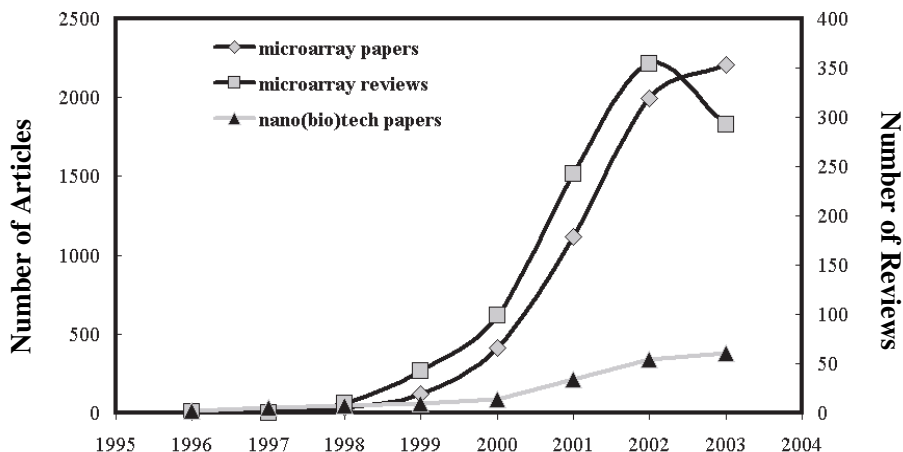


Fig. 1. Comparative evolution of publications regarding microarrays and nanobiotechnology

Amidst the pace of such rapid knowledge expansion, there is a challenge in trying to compose a book that does not face obsolescence by the time of its first publication. Alas, the breadth of this field is driving the growing knowledge base into many new directions, generating the need for different books at different levels and each with a different and unique focus.

As early participants in the development of microarray technology the editors have learned to appreciate the need for contributions from many different areas in the basic sciences and engineering that were crucial to its birth and continued healthy growth. In turn we have observed how the involvement in this particular scientific endeavour has affected many careers, turning physicist into oncologists, physicians into bioinformaticians, and chemists and biologists into optical engineers. Provided the diverse nature of backgrounds that are required to further propel this field, we thought it appropriate to aggregate this book around three aspects of microarray technology: *fundamentals*, designed to provide a scientific base; *fabrication*, which describes the current state of the art and compares ‘old’ and new ways of building microarrays; and *applications*, that are aimed to highlight only the amazing variety and options provided by these techniques. As an aid to the practitioner we have also asked the authors to provide a detailed method section wherever appropriate.

Part 1, General Microarray Technologies, opens with an overview on microarray formats. Chapters 2 and 3 cover the fundamentals of the physico-chemical aspects of immobilizing biomolecules on different substrates, while

Chaps. 4 and 5 describe the principal techniques used for array manufacture. Chapter 6 explores the limits of miniaturization with nanoarrays, and Chap. 7 illuminates various aspects of microfluidics for automation. Finally, Chaps. 8 and 9 deal with the principles of labelling and detection methodologies. The next parts are concerned with application of these fundamental techniques toward the development and use of specific types of microarrays. Part 2 describes DNA based microarrays in 4 chapters, covering SNP detection, high sensitivity expression profiling, comparative genomic hybridization, and the analysis of regulatory circuits. Part 3 contains 3 chapters that deal with microarrays for protein and small molecule detection, describing array technology for antibodies, aptamers, and lipid bound proteins, respectively. The final part comprises 4 chapters that introduce the most esoteric arrays, those that contain high information content in each feature (whole cells or tissues), and the capability of performing biological reactions, such as transfections. How the combination of these types of arrays generates new insights into the molecular basis of normal and malignant cell function is summarized in the last chapter.

It appears that given the dynamics of microarray technology any book would be a ‘work in progress’. Rather than fighting this, the editors and the authors of this book embrace this concept: chances are that this book will grow in time in line with the new developments in microarray technology.

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