

Microarray

A microarray is a collection of microscopic features (most commonly DNA) which can be probed with target molecules in order to produce either quantitative (gene expression) or qualitative (diagnostic) data.

From: [Molecular Medical Microbiology \(Second Edition\), 2015](#)

Related terms:

[Messenger RNA](#),
[Sequencing, DNA](#)
[microarray](#),
[Transcriptome](#),
[Downregulation and upregulation](#), [Gene expression profiling](#),
[Microarrays, Methylation](#),
[Hybridization](#)

Microarray Technology

J. Read, S. brenner, in [Encyclopedia of Genetics](#), 2001

Microarray technology is a powerful technique used to compare differences in gene expression between two mRNA samples. Comparing RNA prepared from diseased cells and normal cells can lead to the identification of sets of genes that play key roles in diseases. Genes that are overexpressed or underexpressed in the diseased cells often present excellent targets for therapeutic drugs. The process uses [microarray](#) chips, prepared commercially, which comprise numerous wells, each of which contains an isolated gene. mRNA is extracted from the 'normal' sample, and a fluorescent labeled cDNA probe is generated, representing all of the genes expressed in the reference sample. A second cDNA probe is generated using a different-colored fluorescent label and mRNA extracted from the 'affected' cells. These may be cells exposed to a drug or toxic substance, taken from a tumor or diseased patient, or cells removed at a different time to the 'normal' sample. The two fluorescent probe samples are simultaneously applied to a single [microarray](#) chip, where they competitively react with the arrayed cDNA molecules. Each well of the [microarray](#) is scanned for the fluorescence intensity of each probe, the intensity of which is proportional to the expression level of that gene in the sample. The ratio of the two fluorescent intensities provides a highly accurate and quantitative measurement of the relative gene expression level in the two cell samples.

The Human Transcriptome: Implications for the Understanding of Human Disease

Matthias E. Futschik, ... Christine Sers, in [Molecular Pathology](#), 2009

Microarray Databases

Microarray experiments produce massive quantities of gene expression data. Therefore, it has become good practice to deposit generated [microarray](#) data in publicly accessible databases. This practice is typically requested by journal editors prior to publication of the data. This allows independent researchers not only to scrutinize data obtained by others for their own interests, but also to validate the original analyses. In fact, the practice of sharing [microarray](#) data has allowed the community of bioinformaticians and statisticians to develop new methods and compare them with existing ones based on publicly accessible data sets. Such comparisons have been extremely valuable, since results from [microarray](#) experiments rely not only on the raw data, but to a

substantial part on the applied computational methods. However, the interpretation of microarray experiments requires a common forum providing various types of information on the examined samples and experimental conditions, arrayed genes, microarray platforms, and applied computational approaches. Therefore, standards for publishing microarray data have been established. The most important one is the Minimum Information About a Microarray Experiment (MIAME) standard [25]. This standard requires deposition of raw microarray data, normalized data, sample annotation, experimental design, description of the microarray, and experimental conditions. Additionally, the development of large central microarray databases has facilitated data sharing. One of the first repositories was the Stanford Microarray Database (<http://genome-www5.stanford.edu/>), including a large collection of two-color array experiments. Currently, the two major public microarray databases are Gene Expression Omnibus provided by the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/geo/>) and Array Express () provided by the European Bioinformatics Institute. Both databases follow the MIAME standard and provide several options to users for depositing their own microarray data and for accessing information from others.

Laboratory Methods in Epigenetics

Yu Liu, ... Qianjin Lu, in [Epigenetics and Dermatology](#), 2015

2.5.1.1 Microarray

miRNA microarray is a tool based on nucleic acid hybridization to explore the expression profiling of miRNAs. The ready-to-use miRNA microarray consists of glass slides immobilized with 5' amine-modified oligonucleotide probes which are antisense to miRNAs. The isolated miRNAs are labeled with fluorescent dye and then hybridized with the miRNA microarray. The biotinylated miRNAs are then captured on the microarray at different positions by oligonucleotide probes in hybridization. Consequently, the specific miRNAs and their relative quantities can be evaluated by analyzing the fluorescence signal data [74].

The small size of miRNAs poses difficulties using the above methodology. New microarray platforms based on locked nucleic acid (LNA)-modified, Tm-normalized capture probes spotted onto N-hydroxysuccinamide (NHS)-coated glass slides have been successfully introduced into miRNA profiling microarray detection.

Guide to Yeast Genetics: Functional Genomics, Proteomics, and Other Systems Analysis

Gregg B. Whitworth, in [Methods in Enzymology](#), 2010

Abstract

Microarray experiments offer a potential wealth of information but also present a significant data analysis challenge. A typical microarray data analysis project involves many interconnected manipulations of the raw experimental values, and each stage of the analysis challenges the experimenter to make decisions regarding the proper selection and usage of a variety of statistical techniques. In this chapter, we will provide an overview of each of the major stages of a typical yeast microarray project. We will focus on providing a solid conceptual foundation to help the reader better understand each of these steps, will highlight useful software tools, and will suggest best practices where applicable.

Molecular Evolution: Producing the Biochemical Data

Katja Metties, Linda Medlin, in [Methods in Enzymology](#), 2005

Concluding Remarks

Microarray technology has various potential applications for biodiversity assessment at all levels. The biodiversity of natural complex microbial samples can be addressed in terms of species numbers and composition without a cultivation step by the application of microarrays that contain hierarchical sets of molecular probes like rRNA probes, which allow the quantification of representatives from very broad to circumscribed phylogenetic groups in a systematic fashion. Gene expression profiles should provide insights into how organisms interact with their environment and how they respond to environmental changes. Biodiversity in terms of genetic diversity at the subspecies level can be addressed with microarrays that target molecular markers, such as RAPDs, AFLPs, or microsatellites. A microarray that contains random oligonucleotides could be used to generate fingerprints of populations that can be easily interpreted. A polymorphism in genomic DNA content of organisms of one species can be visualized by a microarray that targets whole genomes of organisms. Usually, however, this kind of microarray is most widely used to generate expression profiles of organisms. A protocol for the application of DNA microarrays in biodiversity assessment was described in detail in this chapter.

Molecular Diagnosis of Thyroid Cancer

Furio Pacini, Silvia Cantara, in [Genetic Diagnosis of Endocrine Disorders \(Second Edition\)](#), 2016

Microarray

Microarray measures the expression of a large number of genes simultaneously by hybridization of cDNA to an array of short DNA probes specific for genes of interest. Microarray-based gene expression profiles are available for malignant thyroid tumors (follicular thyroid carcinoma and papillary thyroid carcinoma) and for benign lesions and show good sensitivity and high negative predictive value. The most used platform for microarray analysis is the Affymetrix GeneChips (Affymetrix), which provides comprehensive coverage of the transcribed human genome on a single array. Despite the potential of the method, microarray shows some limitations due to costs, lack of validation of data analysis methods, and a strong association with sample quality (i.e., sample collection, storage condition), which may vary the expression levels of many genes altering the functional status of the cells and, consequently, the results.

Genetic Profiling in Colorectal Cancer

Debashish Bose, Nita Ahuja, in [Early Diagnosis and Treatment of Cancer Series: Colorectal Cancer](#), 2011

Microarray Analysis

Microarray analysis of gene expression has developed into a powerful tool for the characterization of many pathophysiologic processes. The basic idea is that RNA isolated from tissue is hybridized to probes for specific genes that are fixed in a grid in small microscopic spots. Figure 20-2 provides a schematic that shows a typical arrangement of a microarray. Depending on the design of the experiment, the signal intensity of the hybridization is normalized to internal controls and other tissues to yield a result for each gene that tells the investigator whether a particular gene has an increased, decreased, or normal expression. The result for the sample, then, is an answer for each gene included in the microarray as to whether the gene is up- or downregulated; the composite data represent a gene expression profile for the sample. When a large number of samples are thus tested, depending on the experimental design, the use of microarrays makes possible the establishment of gene expression profiles for any given disease state, the comparison of subsets to determine molecular predictors of clinical behavior, and so on (Fig. 20-3). As the technology has advanced, the sophistication of microarray analysis has likewise provided increasingly powerful ways of discriminating the molecular characteristics of disease states, including the identification of methylation status of genes (an epigenetic modification of expression) and alternative splicing.

In colorectal cancer studies, microarray studies have provided a great deal of data in terms of genetic profiles.

Table 20-3 provides a partial list of studies that identified expression profiles that correlate with features of disease that the studies were designed to query. Some studies are listed to highlight molecular subsets that may be clinically significant. The table illustrates the use of microarray analysis to ask critical questions, including primary site of origin, prognosis, response to therapy, methylation status, and even diagnosis. Microarray analysis also exhibits particular robustness in that a properly designed and validated array can be derived from the analysis of a relatively small number of probes. This is hoped to make microarray analysis a potentially low-cost and easily reproducible assay that could be readily put into clinical practice.

The cost of development of microarray assays is relatively high in the case of colorectal cancer and requires a large investment before the establishment of clinical significance. First, as a surgical and oncologic disease, the development of clinically meaningful assays requires the collection of tissue from surgical specimens and subsequent long-term follow-up on a large number of patients. Some of this cost may be mitigated by developing assays using existing tissue banks and patient databases, but expression analysis may be problematic if significant mRNA degradation has occurred in banked specimens. Second, after validation and testing (see text that follows), the assay must be supported by a clinical trial that demonstrates its value to the management of patients. Until a specific microarray assay emerges as particularly significant in the potential management of colorectal carcinoma, we will not be able to specifically perform cost-benefit analysis, but, under the assumption that improved patient care and selection for treatment will result, an overall savings would be expected. Such analysis has been performed for the use of microarray analysis in breast cancer.

Bacterial Infections

Yurong Zhang, ... Vance G. Fowler, in [Genomic and Personalized Medicine \(Second Edition\)](#), 2013

Introduction

Microarray analysis of genome-wide transcriptional profiling is increasingly employed in the study of host-pathogen interactions in bacteremia. To date, these techniques have had three primary applications in the area of bacterial pathogenesis: class comparison (contrasting expression profiles of various classes of specimen), prognostic prediction (using expression profiles combined with other factors to predict clinical outcomes), and class discovery (in which important subtypes of specimens are distinguished by class (Simon et al., 2002). Initially, microarray technologies were used to identify the unknown function or regulation of target genes in microorganisms (pathogens). Extending this to a host-based approach, a number of studies have been conducted to identify new target genes or function of genes both *in vitro* and *in vivo*. In this chapter, we describe *in vitro* and *in vivo* microarray studies targeting host responses to bacterial pathogens at the whole-genome transcriptome level.

Cytokines and Interferons in Lupus

Mary K. Crow, ... Kyriakos A. Kirou, in [Dubois' Lupus Erythematosus and Related Syndromes \(Eighth Edition\)](#), 2013

Use of Microarray to Study Cytokine Effects

Microarray analysis, a system in which thousands of oligonucleotide sequences are spotted on a solid substrate, usually a glass slide, and RNA-derived material from a cell population is hybridized to the gene array, is an innovative technology that permits a global view of the profile of genes expressed in a cell population at a point in time, including genes in the cytokine pathways. Applying microarray analysis to heterogeneous cell populations in peripheral blood from patients with autoimmune diseases raises technical challenges. The variable proportions of different cell populations in each subject, each making variable contributions to the mRNAs in the blood sample, adds complexity to the comparison of study groups. Additionally, the statistical

analysis of thousands of gene sequences studied in multiple individuals is daunting. Investigations have now demonstrated that in spite of these technical challenges, significant and useful microarray data can be derived from complex cell samples, including peripheral blood mononuclear cells stimulated in vitro and peripheral blood preparations from patients with autoimmune disease. The view that IFN- α might play a central pathogenic role in SLE has only lately gained momentum with the completion of several large-scale studies of gene expression profiling with microarray technology. Multiple groups have used this powerful technology to demonstrate that mRNAs encoded by IFN-regulated genes are among the most prominent observed in peripheral blood cells of patients with lupus (Figure 7-1). This coordinate overexpression of multiple IFN- α -induced transcripts is what would be expected following ligation of the type I IFN receptor by IFN- α , and this molecular footprint has been called an “IFN- α signature.”

It should be emphasized that microarray is a screen to identify genes potentially altered in expression in a cell preparation or disease state. Microarray data should be confirmed by more quantitative techniques, such as real-time PCR, and data derived from patient samples should be confirmed in additional patient cohorts.

Pain

V.E. Scott, ... P. Honore, in [The Senses: A Comprehensive Reference](#), 2008

5.14.1 Introduction

Microarray gene chip technology is a powerful tool to evaluate changes in multiple transcript levels simultaneously in different tissue preparations. In the pain field, efforts have focused on characterizing gene transcript changes that occur in chronic pain states such as neuropathic pain () and this will be the main focus of this chapter. Neuropathic pain is initiated or caused by a primary lesion or dysfunction of the nervous system. As this technology emerged, it was anticipated that it could be used to determine the key molecular players in both the development and maintenance of neuropathic pain, which would enhance our understanding of this disease and provide insights into the identification of potential therapeutic targets for the treatment of pain. Prior to microarray approaches, studies were limited to evaluation of a set of specific preselected genes/proteins in samples from animal pain models or human tissues using techniques such as quantitative reverse transcriptase polymerase chain reaction (RT-PCR), Western blot analysis, and immunocytochemistry. Dependent upon the gene chips used, this analysis permits evaluation of both known and unknown gene transcripts (expressed sequence tags (ESTs)) using relatively small amounts of RNA. In each of the studies highlighted in this chapter a wealth of transcriptional information was obtained. However, determination of which gene product would offer the best therapeutic potential will require extensive additional follow-up studies. Microarray studies are clearly just the starting point. This chapter will be divided into sections detailing the studies that have been reported evaluating gene expression changes from neuropathic pain models using microarray gene chip analysis, including discussion in each section on study design, sample selection, isolation of RNA, choice of microarray gene chip platforms, and data analysis. The follow-up to microarray studies outlining the expectations and limitations of these studies will also be described. Lastly, the use of microarray gene chips for pinpointing genetic variation in disease states that will direct suitable therapeutics based upon genetic predispositions for specific patient populations will be discussed.

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