DNA Microarrays: Applications, Future Trends, and the Need for Standardization

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Abstract Microarray technology allows high-throughput analysis of tens or even hundreds of thousands of genes in a single experiment, and has been applied broadly to address a wide variety of questions in basic and applied sciences. The applications of the microarray technology range from gene-expression profiling and genotyping to DNA–protein interactions and genome sequencing, and the list of applications keeps growing, especially when combined with other technologies such as proteomic technologies. However, many steps are involved in each microarray experiment and a number of microarray platforms exist, each with its unique features. The challenge is how to standardize the methods and materials to allow intra- and inter-comparison of microarray data collected.
in the same or different set of experiments. With the challenge in mind, we address the need for standardization for each step of the microarray experiments with emphasis on quality control of array fabrication and scanner calibration and verification. The proposed standards are designed for checking the quality of mRNA, fabricating slides, hybridization, and collecting, analyzing, and storing data. By implementing standards for each step of the microarray process, the full potential of the microarray technology will be realized, especially in the area of disease diagnosis and drug development.

**Keywords**  Bead-based arrays · cDNA arrays · Expression profiling · External RNA control · Genotyping · Oligonucleotide arrays · Scanner performance validation

**Abbreviations**

- bp Base pair
- CCD Charged-coupled device
- cDNA Complementary deoxyribonucleic acid
- CGH Comparative genomic hybridization
- ChIP Chromatin immunoprecipitation
- DLBCL Diffuse large B-cell lymphoma
- EST Expressed sequence tags
- EB Ethidium bromide
- MAQC Microarray quality control
- MIAME Minimal information about a microarray experiment
- MIAPE Minimal information about a proteomics experiment
- NIST National Institute of Standards and Technology
- NRO Nuclear run-on
- ORFs Open reading frames
- PCR Polymerase chain reaction
- PMT Photo-multiplier tube
- RNA Ribonucleic acid
- aRNA Antisense RNA
- mRNA Messenger RNA
- SNP Single nucleotide polymorphisms
- TF Transcription factor

### 1 Introduction

Genomic sequences have been determined for a number of organisms from single-cell organisms to human beings [1–8]. For the human genome alone, at least 20,000 genes have been predicted to be expressed in human cells [4]. This enormous amount of sequence information has presented tremendous (but challenging) opportunities for basic research to study biological processes at the genomic level and for business such as disease diagnosis and drug development. The microarray technology responds to this genomic challenge allowing researchers to simultaneously analyze tens of thousands of genes or samples at the genome level in a single experiment [9]. One of the first genome-