

Microarrays and macroconsequences

The National Human Genome Research Institute of the National Institutes of Health is delighted to sponsor this special supplement of *Nature Genetics*. Within these pages the reader will find a series of state-of-the-art reviews of the technology for production of nucleic acid microarrays in various formats. Examples of their utilization to address interesting biological problems are provided, as is a consideration of the challenging informatics problems presented by the collection of a great deal of data in a short period of time.

As the Human Genome Project hurtles towards completion of the first finished human sequence (now scheduled for 2003), microarray technology offers the potential to open wide new windows into the study of genome complexity. Applied to expression analysis, this approach facilitates the measurement of RNA levels for the complete set of transcripts of an organism. Applied to genotyping, microarrays usher in the possibility of determining alleles at hundreds of thousands of loci from hundreds of DNA samples, allowing the contemplation of whole genome association studies to determine the genetic contribution to complex polygenic disorders. Applied to mutation screening of disease genes with pronounced allelic heterogeneity, the use of microarrays is likely to move the possibility of genetic

testing for disease susceptibility of individuals, or even entire populations, into the realm of practical reality.

Advances reported herein are already having a substantial effect on the kinds of questions that can be asked and answered, particularly for model organisms whose genomes are already completely characterized. Their widespread application is anticipated, and will be yet another manifestation of the conclusion that there will be no 'post-genome' era, at least not any time soon. Instead, it seems that a 'genome perspective' is likely to characterize many areas of biomedical research on an accelerating scale.

It is still too early to predict what the ultimate impact of microarrays will be on our understanding of biology. Will this technical advance ultimately rival PCR or the development of recombinant DNA technology as a major quantum leap forward? Or will microarrays take their place alongside other substantial technical advances, such as the automation of DNA sequencing or the development of large insert cloning vectors? There are many critically important questions about this new field that are yet unaddressed. By the publication of this special set of articles, it is hoped that the technology of microarrays will be opened up and demystified, and that additional opportunities for creative exploration will be catalyzed.

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