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View Point

Should microarrays technology be included in medical curriculum?

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Microarray is a silver of glass or silicon robotically studded with two dimensional orderly arrangements of thousands of DNA spots. It provides a medium for matching known and unknown-DNA samples based on base-pairing rules (hybridization) and automating the process of identifying the unknowns. They may be used to assay gene expression within a single sample, or to compare gene expression in different cell types or tissue samples, both in healthy and diseased tissue[1]. The current literature on microarray is grossly inadequate for the medical students and research scholars. Since a microarray can be used to examine the expression of hundreds or thousands of genes at once, it promises to revolutionize the way scientists can examine gene expression[2]. Medical students should realize that the power of DNA microarray technology in medical applications relies principally on observing a common change in gene expression pattern in patients with the same type of diseases.

Despite the recent flood of new biological data from the human genome sequencing, scientists are struggling to answer many basic questions. There is a need to accelerate figuring out which genes are active, not by tackling one gene one experiment at a time, but implementing a massively parallel process. Microarrays allow researchers to get information on thousands of genes simultaneously—a dramatic increase in thorough output, from months to days, and benefits include—gene discovery, gene expression, disease diagnosis, drug discovery and toxicology.

Major applications of microarrays in the medical field include the following:

1. Genotyping—Genomic DNA, extracted from blood or other body fluids of a subject, is amplified by the polymerase chain reaction and applied to the microarray. This has the potential in risk assessment, both in research and clinical practice. As relevant genes are identified, the mutations and polymorphisms that underlie susceptibility to a range of common diseases will become direct predictors of susceptibility (***e.g.***, diabetes, hypertension, coronary heart disease, cancer susceptibility, and susceptibility to adverse and favourable drug responsiveness, etc).

2. Gene Expression Profiling—Through gene expression profiling, the function of genes is now being discovered almost as a matter of routine. The identification of new metabolic pathways and pathogenetic mechanisms, and new drug targets are likely to be discovered in many diseases in the next few years and would start to enter clinical practice with new treatment strategies. For individual patients, more precise diagnosis and risk assessment based on expression profiles are already achievable for certain conditions, leading to more accurate determination of prognosis and more individually tailored treatment. Oncology has taken the front seat in this area, and expression profiles in leukaemia/lymphoma, melanoma, and breast cancer have led to new methods for disease staging and classification. Microarrays that detect gene sequences in the genomes of different pathogens (***Mycobacterium tuberculosis***, HIV, etc) have been developed[3,4]. A major advantage is that these tests can be undertaken rapidly (in <24 h) without the need for cultures. If such tests are brought into clinical practice, they will lead to earlier, more targeted treatment, presently determined only after lengthy analysis by other methods.

3. DNA Sequencing—Thousands of base pairs of DNA, whose normal sequence is already known, can be screened on a single microarray for mutations in specific genes. This would greatly increase the scope for precise molecular diagnosis in a single gene and genetically complex diseases. These have already been used to screen entire genes for pathogenic mutations, such as, in the cancer susceptibility genes BRCA1 and p53[5].

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In general, undergraduate students in medical sciences are unaware about the microarray technology. Even most of the post-graduate students know about it in only theoretical aspects, and very few are aware of its application and utility in research and patients care. One of the reasons for this is that it is not covered in any of their curriculum. Given the rapid progress in the field of microarray and medical research, it should be the privilege of all the students to know about this technology and its applications. Despite many advantages, there are many drawbacks of microarray that medical students should also know, and these include—lack of standardization (because of absence of a unified 'language' for exchange of microarray data between different groups), inadequate computer tools (lack of turnkey bioinformatics models and tools inhibit quick and efficient analysis of the large data sets created, as well as statistical problems ranging from image analysis to pattern discovery and classification exists), fidelity of gene expression data, and cost (the entire process is cost prohibitive)[6]. Moreover, like any other new diagnostic tool, they will have to be rigorously appraised for sensitivity, specificity, and predictive value and licensing by regulatory bodies.

To conclude, microarray is still in its infancy, but given the large potential gain in clinically relevant information for individual patients and their diseases, the technology is likely to reach most large hospitals and institutes in the next few years. In our view, the undergraduate students need to know the basics and applications of microarray technology, whereas postgraduate and PhD or research students should know the details of the process including the application. Moreover, biomedical research evolves through the compilation of knowledge generation of new technologies. That's why this technology should be included in the medical curriculum at the university level for the betterment of science.

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