

## **MANUFACTURE AND DESIGN OF DNA MICROARRAYS FOR DIAGNOSIS**

Ramírez J., Chávez-González L., Guzmán-León S. and Santillán-Torres J. L.  
Microarrays Unit, Institute of Celular Physiology, UNAM. AP 70242, CP 04510  
México D.F. [jramirez@ifc.unam.mx](mailto:jramirez@ifc.unam.mx) <http://microarrays.ifc.unam.mx>

One of the uses for the information obtained from complete genomic sequences, has been the study of functional genomics with the DNA microarray technique. These studies had allowed identify discrete groups of genes, related to a phenomenon, a disease or a reaction to a pharmacological drug. This opens the possibility of using this technology as a tool for diagnosis.

With the development of new substrates for microarray printing it is possible to print up to 16 individual arrays in the same surface, with a maximum of 1000 different probes in each one. The probes can be printed even in several copies of each gene, allowing for more significant statistical analyses of the results. Unlike other tests in which genetic expression patterns are analyzed for each individual, where the possibility of maintaining the same conditions for all experiments are more complex and their normalization is not always ideal, with these micro arrays it is possible to determine changes in the genetic expression of up to 16 individual samples in one experiment, all of them under the same parameters, this allows us to obtain repeatable and comparable results between the study subjects. Additionally these substrates, allow us to reduce costs and open the possibility of studying large groups of individuals. It is also possible to study groups of pharmaceutical drugs, as well as different experimental conditions.

In this poster we show the new substrates, the procedures for the design of the probes and the printing of microarrays for diagnosis, using tools and techniques employed in a complete genome microarray manufacture. The capture of the images, fluorescence quantification and association with the data bases, as well as some facilities for the normalization and analysis of the results.