

Sección temática: Genómica y Transcriptómica

Microarrays as a functional approach to the transcriptome

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Knowing a cell's transcriptome is a fundamental requisite in order to analyze its response to the environment. Microarrays have supposed a revolution on this field as they are able to yield an overview of gene expression at any environmental condition on a genome-wide scale.

This technique consists in the hybridisation of a nucleic acid sample, previously marked, with a probe (which might be made up of cDNA, oligonucleotides or PCR products) anchored to a solid surface (made of glass, plastic, silicon...) giving as a result a dot grid which reveals, after image analysis, which genes are being expressed. Nevertheless, this only can be achieved if information on the species genome has been generated.

Different kinds of expression microarrays exist attending to the probe's nature and the method used in its synthesis. In this poster two of these will be treated:

Spotted Microarrays, for which the probe is synthesised prior to its fixation to the array and allow the analysis of two targets simultaneously. They can be easily customized, but lack high reproducibility and sensitivity.

Oligonucleotide Microarrays, which are characterized by the direct printing of the probe on the array. In this case the probes consist on, invariably, oligonucleotides that are complementary to a small fraction of the gene it is representing at the microarray. Their application is somewhat restricted. This fact, however, makes them more reproducible.

Currently, the approach towards the transcriptome studies from the Next Generation Sequencing technologies offers a large volume of information in a short amount of time needing less previous information on the target organism than that needed by microarrays, but their expensive price limits their use. The versatility of the latter, together with their reduced costs in comparison to other techniques, makes them an interesting resource in applications that may need less complexity.