Comparative analysis of the oestrogen-responsive gene expression profile of breast cancer cells with three different microarray platforms

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The DNA microarray is a technique which makes it possible to analyze the expression patterns of tens of thousands genes in a short time. The widespread use of this technique and the rapidly improving different technologies available by commercial and academic providers has led to the publication of thousands of results, extremely heterogeneous in terms of technology used and analysis subsequently applied to data. This leads to a difficulty in collaborating and exchange data between groups with common research interest, whereas collaborations would be extremely useful due to the high cost of this techniques and to the consideration that an experiment carefully designed could bring results relevant to different groups, each focusing on a different aspect of a main biological problem. So the awareness for the need of common standards or, at least, comparable technologies is emerging in the scientific community, as shown by the effort of the Microarray Gene Expression Data (MGED) Society, which is trying to set up at least experimental methodology, ontology and data format standards.

In addition, it is important the ability of being able to compare newly produced data with preceding experiments, so to ensure of keeping high the value of results produced with equipment of the old generation.

We thus started this work with the aim of evaluating the technical variability between three commonly used microarray platforms, such to adapt the first part of the analysis to the peculiarity of each technique, and the feasibility of a common subsequent analysis path, thus taking advantage of the different data-extraction abilities of the three. The chips used to study the gene expression profiles of hormone-responsive breast cancer cells with and without stimulation with estradiol are:

i) the Incyte 'UniGEM V 2.0' microarrays, containing over 14,000 PCR-amplified cDNAs, corresponding to 8286 unique genes, spotted at a high density pattern onto glass slides;

ii) the Affymetrix technology, based on 25 nucleotide-long oligonucleotides directly synthesized on a GeneChip® array, representing more than 39,000 transcripts derived from approximately 33,000 unique human genes;

iii) the Agilent 'Human 1A Oligo' Microarray consisting of 60-mer, *in situ* synthesized oligonucleotide probes for a total of about 18000 different genes.

The same samples were used to generate fluorescent targets to be hybridized on the different slides, with balanced dye swap when applicable for competitive hybridizations.

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