Title: 5547-Expression Profiling with Microarrays

Abstract: Microarrays are important tools for profiling gene expression, and are based on complementary binding between probes that are attached to glass chips and nucleic acids derived from samples. Using these arrays, scientists can simultaneously evaluate the expression of thousands of genes. In addition, the expression profiles of different cells or tissue types can be compared, allowing researchers to deduce how the expression of different genes change during biological processes, and thus gain insight into how the genes may function in pathways or networks.

Here, JoVE explains the principles behind microarrays. This is followed by a general protocol for performing a microarray experiment, and a brief introduction to analyzing microarray data. We end on a discussion of how scientists are currently using microarrays, for example to compare gene expression between different cell types derived from cancerous and non-cancerous tissues, to study important biological problems.

Application Videos:

1. MicroRNA Expression Profiles of Human iPS Cells, Retinal Pigment Epithelium Derived From iPS, and Fetal Retinal Pigment Epithelium **(Thumbnail 51589@ 0:44-cartoon showing microarray images pointing towards gene network diagram; take screenshot before any text appears)**

Description: Stem cells can be directed to form more specialized cell types, and are a popular tool in regenerative medicine research. This video demonstrates a protocol using microarrays to study the role of microRNAs (miRNAs) — small RNA molecules that can fine tune gene expression by inhibiting translation of target mRNAs — in the differentiation of stem cells into retinal cells. RNA collected from cell types representing different stages of retinal cell differentiation is labeled and hybridized to a miRNA array. The resulting expression profiles are then subjected to pathway analysis to identify networks of miRNA target genes that might be involved in retina development.

2. Biomarkers in an Animal Model for Revealing Neural, Hematologic, and Behavioral Correlates of PTSD **(Thumbnail 3361@7:40-heat map generated from microarray data, demonstrating green, black, and red squares)**

Description: Post-traumatic stress disorder (PTSD), as its name suggests, is an anxiety disorder that can manifest after a traumatic experience. Here, researchers used microarrays to assess changes in the expression of mitochondria-specific genes in brains dissected from a rodent model of PTSD. As mitochondria are the organelles that produce energy for the cell, researchers were able to use this data to evaluate how PTSD may affect energy consumption or production in different areas of the brain.

3. Microarray-based Identification of Individual HERV Loci Expression: Application to Biomarker Discovery in Prostate Cancer **(Thumbnail 50713@7:35-two microarray chips on white backdrop)**

Description: Over the evolutionary history of humans, viral genetic material has been incorporated into the human genome. Some of these “endogenous retroviruses” (ERVs) may still be actively expressed, and their products are suggested to be associated with certain cancers. The authors of this article used microarrays to assess expression from such ERVs in prostate cancer samples.

4. Profiling of Estrogen-regulated MicroRNAs in Breast Cancer Cells **(Thumbnail 51285@12:05-heatmap results from microarray analysis)**

Description: Compared to normal cells, cancer cells may respond differently to endogenous signals in the body. The authors of this article present a microarray-based protocol to compare the gene expression profile of human breast cancer cells exposed to the hormone estrogen for different lengths of time, specifically assessing levels of miRNAs. Changes in the expression levels of different miRNAs can provide insight into molecular pathways involved in the response of cancer cells to estrogen, and may lead to the discovery of potential therapeutic targets.

5.Single Cell Transcriptional Profiling of Adult Mouse Cardiomyocytes **(Thumbnail 3302@6:35-liquid being introduced onto expression array; remove text overlay)**

Description: An important application for gene expression profiling is to evaluate and compare gene expression in single cells, which can be used to characterize random expression differences among individual cells or genes, and identify populations of rare cells based on their expression profiles. In this video, researchers isolated individual mouse heart muscle cells and extracted their RNA. The sample was then subjected to whole transcriptome amplification, where the amounts of all expressed RNA in the cell was amplified in an unbiased fashion, before being labeled and hybridized to a mouse genomic array.

Related Science Education Videos:

5038 - Introduction to the Spectrophotometer

5333 - Induced Pluripotency

5428 - An Introduction to Modeling Behavioral Disorders and Stress

5546 – Introduction to Gene Expression