Title: Introduction to Gene Expression

Abstract: Gene expression is the complex process where a cell uses its genetic information to make functional products. This process is regulated at multiple stages, and any misregulation could lead to diseases such as cancer.

This video highlights important historical discoveries relating to gene expression, including the understanding of how distinct combinations of DNA bases encode the amino acids that make up proteins. Key questions in the field of gene expression research are explored, followed by a discussion of several techniques used to measure gene expression and investigate its regulation. Finally, we look at how scientists are currently using these techniques to study gene expression.

Application Videos:

1. Profiling Individual Human Embryonic Stem Cells by Quantitative RT-PCR (**51408 Thumbnail@3:02-talent introducing liquid into well of PCR plate)**

Description: Individual cells—even those comprising the same tissue or organ—can exhibit subtle gene expression differences. This video demonstrates a protocol that uses quantitative reverse transcription PCR (qRT-PCR)—which gives an accurate, “real time” measurement of RNA levels—to evaluate gene expression in single cells. This technique is applied to compare gene expression between individual human embryonic stem cells from a single culture.

1. Genome-wide Analysis Using ChIP to Identify Isoform-specific Gene Targets (**2101 Thumbnail@4:32-talent pipetting from tubes on magnetic rack)**

Description: Protein variants that are alternatively spliced from the same gene transcript, known as isoforms, are often predicted to perform different functions. Here, researchers use chromatin immunoprecipitation, which isolates a protein of interest with antibodies in order to identify the DNA that it interacts with, to understand the different mechanisms of action of two isoforms of a gene regulatory protein.

1. Identifying Targets of microRNAs with the LightSwitch Luciferase Assay System Using 3′ UTR-reporter Constructs and a microRNA Mimic in Adherent Cells (**3343 Thumbnail@5:42-talent inserting plate into “luminometer”)**

Description: A class of small regulatory RNAs known as microRNAs can inhibit the expression of specific genes by binding to the 3′ untranslated region (UTR) of their transcripts. In this article, scientists cotransfected microRNAs into cells along with candidate gene 3’ UTRs that are coupled to a luminescent reporter construct. By observing for loss of luminescence signal in treated cells, researchers were able to identify novel gene targets of the microRNAs.

4. Non-Laser Capture Microscopy Approach for the Microdissection of Discrete Mouse Brain Regions for Total RNA Isolation and Downstream Next-Generation Sequencing and Gene Expression Profiling (**3125 Thumbnail @8:56-talent pipetting into spectrophotometer)**

Description: Integral to many methods of assessing gene expression, such as sequencing the transcriptome—or all of the expressed RNA in a cell—is the successful isolation of sufficient amounts of high-quality RNA. Researchers here demonstrate a protocol to extract RNA from small, distinct regions in the rodent brain.

5. Comprehensive Analysis of Transcription Dynamics from Brain Samples Following Behavioral Experience (**51642 Thumbnail@6:29-talent pipetting from strip-tube into PCR plate)**

Description: Studying gene expression changes in the brain is of major interest in understanding the neurological basis of behavior. The authors of this article treated mice with cocaine and then isolated the nucleus accumbens, the region of the brain involved in motor function. They then used a microfluidics system to perform high-throughput qRT-PCR, simultaneously evaluating the expression dynamics of hundreds of candidate genes.

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