



Expression of Gene Profiling In Human Cells

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INTRODUCTION

Gene expression profiling is the measurement of the activity of thousands of genes at once in molecular biology to create a global picture of cellular function. These profiles can, for example, differentiate between cells that are actively dividing or show how cells respond to a specific treatment. Many experiments of this type measure an entire genome at the same time, that is, every gene present in a specific cell. A variety of transcriptomics technologies can be used to generate the data required for analysis. Sequence-based techniques, such as RNA-Seq, provide information on gene sequences in addition to expression levels. After sequencing a genome, expression profiling is a logical next step: the sequence tells us what the cell could possibly do, whereas the expression profile tells us what it is actually doing at a given point in time.

DESCRIPTION

Genes contain the instructions for making messenger RNA (mRNA), but each cell produces mRNA from only a subset of the genes it carries at any given time. If a gene produces mRNA, it is considered "on," otherwise "off." Many factors influence whether a gene is turned on or off, including the time of day, whether the cell is actively dividing, its surrounding environment, and chemical signals from other cells. Skin cells, liver cells, and nerve cells, for example, turn on slightly different genes, which is part of what distinguishes them. As a result, an expression profile can be used to deduce a cell's type, state, environment, and so on. The relative amount of mRNA expressed in two or more experimental conditions is frequently measured in expression profiling experiments. This is because changes in the levels of a specific mRNA sequence indicate a change in the need for the protein coded by the mRNA, which could indicate a homeostatic response or a pathological condition. Higher levels of mRNA coding for alcohol dehydrogenase, for example, indicate that the cells or tissues under study are responding to increased ethanol levels in their environment. Similarly, if

breast cancer cells express more mRNA associated with a specific transmembrane receptor than normal cells, this receptor may play a role in breast cancer. A drug that inhibits this receptor may be used to prevent or treat breast cancer. When developing a drug, gene expression profiling experiments may be performed to help assess the drug's toxicity, possibly by looking for changes in the expression of cytochrome P450 genes, which may be a biomarker of drug metabolism. Gene expression profiling has the potential to become an important diagnostic test. The human genome contains approximately 25,000 genes that work together to produce approximately 1,000,000 distinct proteins. This is due to alternative splicing, as well as the fact that cells make important changes to proteins after they are constructed, so a given gene serves as the basis for many possible versions of a particular protein. In any case, a single mass spectrometry experiment can identify approximately 2,000 proteins, or 0.2 percent of all proteins. While knowing which proteins a cell produces is more important than knowing how much messenger RNA is produced by each gene, gene expression profiling provides the most comprehensive picture in a single experiment.

CONCLUSION

Proteomics methodology, on the other hand, is improving. Other species, such as yeast, can identify over 4,000 proteins in just over an hour. Sometimes a scientist already has an idea of what's going on, a hypothesis, and conducts an expression profiling experiment to potentially disprove this hypothesis. In other words, the scientist is making a specific prediction about expression levels that may turn out to be incorrect. More often than not, expression profiling occurs before enough is known about how genes interact with experimental conditions to form a testable hypothesis. There is nothing to disprove if there is no hypothesis, but expression profiling can help identify a candidate hypothesis for future experiments. Most early expression profiling experiments, as well as many current ones, take this class discovery form.

Received:	30- March -2022	Manuscript No:	IPBM-22-13517
Editor assigned:	01- April -2022	PreQC No:	IPBM-22-13517 (PQ)
Reviewed:	15- April -2022	QC No:	IPBM-22-13517
Revised:	20- April -2022	Manuscript No:	IPBM-22-13517 (R)
Published:	27- April -2022	DOI:	10.35841/2472-1646-8.4.128

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Citation Kong Qiu (2022) Expression of Gene Profiling In Human Cells. Biomark J 8:128.

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