Chapter 13
Study of Basic Concepts on the Development of Protein Microarray – Gene Expression Profiling: Protein Microarray

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ABSTRACT

The physical and biological activity of any organisms is mainly depended on the genetic information which stored in DNA. A process at which a gene gives rise to a phenotype is called as gene expression. Analysis of gene expression can be used to interpret the changes that occur at biological level of a stressed cell or tissue. Hybridization technology helps to study the gene expression of multiple cell at a same time. Among them microarray technology is a high- throughput technology to study the gene expression at transcription level (DNA) or translation level (Protein). Analysis the protein only can predict the accurate changes that happens in a tissue, when they are infected by a disease causing organisms. Protein microarray mainly used to identify the interactions and activities of proteins with other molecules, and to determine their function for a system at normal state and stressed state. The scope of this chapter is to outline a detail description on the fabrication, types, data analysis, and application of protein microarray technology towards gene expression profiling.

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INTRODUCTION

Molecular biology is study of biological activity of living organisms at molecular level, it also comprises the braches of biology, genetics, chemistry, and biochemistry. Molecular biology basically deals with the interactions between the various types of macromolecules. The two main types of macromolecules are nucleic acids (Deoxyribonucleic acid -DNA and ribonucleic acid- RNA) and proteins. Since the study of structure, function and relationship between these two types of macromolecules are called as molecular biology.

In 1957, Crick formulated the term the central dogma of molecular biology, which describes the information-flow in the replication of DNA and in the making of protein from DNA. In 1958 the mechanisms of replication were understood by the Meselson–Stahl experiment which predicts the double helical structure of DNA. The double helical structures are made up of sugar, phosphates and nucleotide or base pairs (adenine-A, thymine-T, guanine-G and cytosine-C).

In transcription process the genetic information from double strand DNA molecule was copied as a single stranded messenger ribonucleic acid (m-RNA) by the process of transcription (Figure 1.). The term m-RNA is called as codons. Codon is a sequence of three nucleotides which contains a message for specific amino acids. The information for the building of proteins is written in DNA using the genetic codes which consist of codon. In translation process at the initial stage m-RNA attaches to ribosomes, then the t-RNA (Transfer-RNA) attaches to m-RNA and releases the amino acids to produce proteins i.e. Poly peptides.

The study on synthesis of functional gene product by the process of m-RNA transcription is called as gene expression. Any changes in physiology characterization (structural mutation) of a cell or organisms are complemented by the changes in the configuration of gene expression (Nicole et al., 2000). Since analysis of gene expression is important to find the flow of genetic information from a gene which is used in the synthesis of protein (Functional gene product).

Methods like northern blot, quantitative reverse transcription PCR, serial analysis of gene expression, dot plot analysis are used to analysis the expression of particular gene (m-RNA) in a cell or organisms. All the above conventional analysis of gene expression was studied using one gene at a time, thus these methods are become inappropriate when analysis large numbers of functional gene products simultaneously. The limitation of above methods are overcome by hybridization array technology which is simultaneously generating the labelled copies of multiple sample RNAs and then hybridizing them to numerous different gene specific fixed DNA molecules (Willard et al 2000).

Figure 1. Central dogma of life