

Introduction

Most cells in an organism have a very similar genome yet mRNA expression (called the expression profile) can vary dramatically. These expression differences give rise to specialized cellular phenotypes and functioning. As analysis of the proteome is still quite difficult and doesn't provide high sensitivity, analysis of the transcriptome provides a surrogate that can be viewed as the functional potential of the cell/tissue. This is the case as a protein can only be made if the RNA is expressed. Characterization of expression profiles has evolved and matured over the years moving from Northern Analysis, through PCR to microarrays and now the current application of NextGen sequencing (RNA-Seq). RNA-Seq methodologies permit sequence characterization and abundance measurements for all RNAs from a sample even as small as a single cell, in an unbiased manner. The advent of RNA sequencing (RNA-Seq) based transcriptomic's eliminates the requirement to choose sequences for investigation (as with PCR or microarray analysis), as there is no need to choose targets or probes. Sequencing can provide a greater depth of information regarding transcript variants and gives a more complete picture of the transcriptome and in turn cellular phenotype.

Transcriptomic analysis has provided fundamental insights into cell biology including showing the existence of many alternatively and noncanonically spliced mRNAs from multiple genes expressed within a tissue sample. These variant splice forms are not limited to exonic coding region differences as previously undescribed retained introns have been found for a number of cytoplasmic mRNAs in various tissues. It is important to note that these results are not unexpected as much previous data on mRNA transcript sequence is based upon the most easily detectable (most abundant) isoforms present in cells, which then serve to define what we think of as canonical exons, introns, UTRs and gene boundaries. Further, transcriptome analysis has enabled the discovery of large numbers of distinct noncoding and small RNAs within tissues including the CNS. The discovery of variant splice forms of mRNA and other classes of RNA have encouraged extensive and continuing experimentation into the role of these RNAs in cellular function.

With regard to the CNS, transcriptomic analysis has been used to investigate the impact of behavior and drug responsiveness upon normal and disease associated brain and peripheral nerve functioning in a variety of organisms. This short course will highlight advances in understanding of CNS function enabled by transcriptomic analysis while emphasizing the complexities of data and functional analysis.