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Transcriptional Profiling: An Effective Tool of Modern Biology

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Today a multitude of research problems are being tackled using transcriptional profiling as a tool. Functional genomics experiments, particularly quantitative gene expression studies rely heavily on transcriptome profiling. This allows for knowing which genes, and at what level, are being expressed in the given cell type(s) under the defined experimental situation. Gene expression studies allow the biologist to tackle the problem at hand with a holistic view.

There are many situations where a biologist would like to know what alterations are there in his test sample as compared to the control, with respect to gene expression. For example, transcriptome profiling can help characterizing the host response to a particular infection. Since the first report (in the year 1998) regarding the use of DNA microarrays to monitor the host transcriptional response to human cytomegalovirus, many more such studies have been published covering most of the important viral infections [1]. This technique covering the whole set of expressed genes in a given organism has also been applied fruitfully to various bacteria such as *Helicobacter pylori, Vibrio cholerae, Mycoplasma pneumoniae, Salmonella enterica, Pseudomonas syringae,* etc. Genome-wide studies of bacterial gene expression seem to be slowly shifting from microarray technology to second generation sequencing platforms. RNA-seq offers certain advantages over conventional hybridization-based techniques, such as annotation independent detection of transcription, better sensitivity and increased dynamic range. Applicability of the RNA-seq approach has also been demonstrated for whole environments, resulting in development of techniques for sampling the metatranscriptomes of soil and marine communities [2]. Bacterial whole transcriptome studies hitherto have enjoyed a high success rate of ncRNA discovery.

Our lab is presently engaged in two different areas of research, both of which are amenable to gain important insights from the appropriate use of transcriptional profiling. *First*, we are investigating anti-virulence (mainly anti-quorum sensing) properties of various natural products. Quorum-sensing in bacteria is known to regulate expression of a large number of genes, e.g. those associated with pigment production, toxin release, biofilm formation, etc. [3]. Many of the potent natural extracts can exert their anti-quorum sensing effect by targeting multiple genes of the test pathogen simultaneously; a comparative gene expression analysis -of the bacterial culture exposed to the extract, and the unexposed control- can provide useful information about mode of action of the given extract. *Second,* we are working on cell-sound interaction. We have already shown that sound stimulation can significantly alter microbial growth and metabolism [4]. Now, through a research grant sanctioned to us by *Gujarat Council on Science & Technology (GUJCOST)*, we shall be applying comparative transcriptome analysis (i.e. comparing gene expression of sound stimulated *test* culture with that of *control*, which is not exposed to sound) to elucidate the molecular basis of microbial response to sound. Besides answering certain fundamental questions regarding how microbes receive and respond to audible sound, information thus gained can open new possibilities with practical implications such as improvement in productivity of useful products through the culture of microorganisms by playing appropriate music while fermentor vessels are in operation. Transcriptome profiling is very much likely to help answering many more interesting biological questions in future.

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