



**November 1-4, 2010**  
**Clarion Hotel San Francisco Airport, Millbrae, CA**

qPCR, also known as Real-time PCR is a modification of standard Polymerase Chain Reaction, which is often compared to the photocopying of nucleic acid (DNA or RNA). The process involves the alternate heating and cooling of a small sample containing a segment of nucleic acid molecules dozens of times over several hours. Throughout this process, copies of these DNA molecules are "amplified" or exponentially increased so that the nucleic acid can be more readily analyzed. The method is called "real time PCR" because the amplified DNA can be detected during the PCR process, in real time, rather than at the end of the process. This ensures more accurate and precise quantification of nucleic acid.

The real time PCR reaction proceeds automatically without user intervention, providing increased productivity and reduces human error, resulting consistent and reproducible results. The application of real-time PCR is vast in life science industry, healthcare, diagnostics, Forensics, Food, air and water safety, Point of care in physician offices, clinics and local labs and in bio-defense. The same has extensive usage in research on Biomarkers, Stem Cells, Single Cell, siRNA, miRNA, Diagnostics, Immunology and Expression Profiling.

The most relevant topics of the qPCR field are:

**Preanalytics – Sample preparation, extraction and purification**

The quality of the qPCR data depends on the meticulous isolation of the starting RNA. Expert scientists will present on the on the latest refinements for controlling this critical phase of the experiment.

**Standardization and quality control**

The qPCR technique is now the gold standard for the analysis of gene expression and is practiced on an industrial scale. Therefore, universal standards are critically required. Learn from highly experienced professionals about the use of controls, such as synthetic RNA or RNA templates from known sources, to monitor the quality of the reverse transcriptase reaction.

**High throughput expression profiling – digital PCR, integration and workflow**

Since its commercialization in 1996, real-time PCR using the 5' nuclease assay has been the gold standard for high-throughput mRNA profiling. The technique uses an endogenous reference and a calibration standard to calculate the delta delta  $C_T$ —which typically gives a two fold distinction in copy number. Today, an alternative technique known as digital PCR provides exponentially higher resolution and sensitivity. This presentation will address how digital PCR expands the application of PCR as well as its integration into today's laboratory.

**Epigenetics, mutation analysis and copy number variation**

New classes of variants have emerged as promising for translating the vast amount of genetic data coming out of disease research laboratories into clinically useful knowledge. These new markers will require validation against a small set of samples and subsequently against much

larger sample sets to establish their statistical association with disease states. Emerging technologies for this next era of association studies and mutation analysis will be discussed.

### **Molecular diagnostics of complex diseases – detection and profiling of tumor cells**

Complex diseases, such as cancer, show a wide spectrum in the number and frequency of alleles related to disease, both within populations and at different stages of the disease progression. Therefore, scientists need screening techniques that are highly sensitive yet that have the throughput to survey thousands of tumor biopsies to understand the range of variation that may be useful in diagnosis and treatments. Discussions will cover recent advances in this challenging field.

### **Single-cell and sub-cellular expression profiling**

Recent advances in quantitative PCR have enabled the measure of mRNA copies at the single-cell and sub-cellular levels rather than as an average of the expression within a population of cells. This important advance reveals differences among individual cells so that the standard deviation of gene expression levels – not an average – can be compared among different cell populations. Experts will present on the current state of the science and technology.

### **Non coding RNAs**

Recent developments have shown that non coding RNAs are important in directing post-transcriptional regulation of gene expression or in guiding RNA modifications. Non coding RNAs can be difficult to analyze by real-time PCR because of their small size and potential for secondary structures. This presentation will cover new strategies and chemistries to address the unique challenges.

### **Next Generation Sequencing (NGS) techniques – complement or competitor to qPCR?**

Scientific progress often depends on the affordability of the technologies needed for basic and applied research. Some experts predict that NGS platforms--capable of reading millions of DNA sequences in a single run--will one day provide the most inexpensive and comprehensive method to validate discoveries. Discussions will cover the scope and pace of NGS adoption in context of the performance improvements on the horizon for qPCR.

### **qPCR, Next Generation Sequencing experimental design and data mining**

While next generation sequencing achieves dramatic reductions in the cost per base and produces giga-base results per day, the technology faces barriers to widespread adoption without automated solutions for library preparation. Here qPCR has shown its broad scientific utility, enabling large cohort studies that require preparation of many 100s of samples. The presentation will survey the various qPCR methods for NGS sample preparation and clarify issues with experimental design and post sequencing data mining.

### **Clinical applications of qPCR and Next Generation Sequencing**

This decade will witness continuing improvements in the efficiency of qPCR and NGS, opening new opportunities for molecular medicine: point-of-care diagnostics, in which tumor samples can be harvested and tested for mutations at the patient's bedside; the identification of infectious disease in the field; non-invasive prenatal diagnostics; and many others. The emphasis is on quickly and cost-effectively obtaining clinically relevant information. Our panel will discuss the innovations that are shaping the field.