

15<sup>th</sup>-17<sup>th</sup> November 2010, Radisson Edwardian, Heathrow, London  
Accelerating Discovery & Clinical Development

## INTRODUCTION TO THE 2010 MEETING

Oxford Global Conferences is proud to present the 2<sup>nd</sup> Annual qPCR Congress ([www.qpcr-congress.com](http://www.qpcr-congress.com)), which is to be held on the 15<sup>th</sup> & 16<sup>th</sup> November 2010 at the Radisson Edwardian Heathrow in London. The congress is the single most focused event in Europe dedicated to key technological and scientific trends & advances in qPCR in the pharmaceutical and biotech industry, as well as academic institutions. There is also a post conference workshop on Experimental Design and Quality Control in qPCR Experiments on the 17<sup>th</sup> November. The Congress is to be held in conjunction with the 2<sup>nd</sup> Next Generation Sequencing Congress ([www.nextgenerationsequencing-congress.com](http://www.nextgenerationsequencing-congress.com)) & the Analytical Genomics Congress ([www.analyticalgenomics-congress.com](http://www.analyticalgenomics-congress.com))

This conference explores effective strategies, technologies and applications of qPCR in accelerating drug discovery and the development of clinical diagnostics. Over three days, the event will attract over 120 senior-level decision makers working in qPCR, gene expression, micro RNA, biomarkers, genomics, discovery, molecular biology, and clinical & diagnostics development and bioinformatics & data management from the UK, Europe and US. This prestigious event provides a forum for practitioners and researchers to learn more about key solutions being provided to their industry, network with their peers, and address key industry concerns through a series of cutting edge conference presentations in a professional yet relaxed environment.

## THE EVENT

In keeping with Oxford Global's highly successful life sciences series, an expert panel of 45 speakers will present a full conference programme covering the following key topics including:

### Day One – 15<sup>th</sup> November

#### qPCR Applications, Technology and Data Management

- Successful Gene Expression Analysis using real-time PCR
- Profiling technologies
- Other technologies: High resolution melt, Immuno PCR, Methylation sensitive PCR, SNP analysis, microRNA detection and Multiplex technologies
- Copy Number Variation
- Data Management / Bioinformatics : software applications, data mining, data visualization, biostatistics, multivariate statistics

### Day Two – 16<sup>th</sup> November

#### qPCR in Drug Discovery, Development, Molecular Diagnostics and the Clinic

- Novel uses of qPCR
- Single cell qPCR
- Assay optimisation and validation strategies
- qPCR in Biomarkers, Stem Cells, Oncology, HIV, Infectious & neurodegenerative diseases
- Development of clinical diagnostics and clinical Development

### Day Three – 17<sup>th</sup> November

#### Post Conference Workshop - Experimental Design and Quality Control in qPCR Experiments

## WHO ATTENDS?

Delegates are pre-qualified dependent on budget, responsibility and seniority. Delegates are senior-level decision makers, from major pharmaceutical, biotech companies and research institutions based in Europe and typically include VPs, Directors, Managers and Heads of:

Drug Discovery	Biomarkers	Bioinformatics	Clinical Diagnostics
Principal Investigation	Molecular Profiling	Clinical Development	qPCR
Toxicology	Gene Expression	Biochemistry	Genomics
Biostatistics	High throughput Technologies	Data Management	Cell Biology

## YOUR NETWORKING OPPORTUNITIES

Meet face-to-face with leading solution providers and senior-level industry peers through a series of formal and informal networking opportunities. Using our online appointment system, you are able to view the full profiles of all solution providers before the event. In addition you have the chance to pre-arrange one-to-one meetings with them, giving you the opportunity to discuss technologies, services and solutions that address your key business needs. Categories of solution providers include:

qPCR Technologies	Real-Time PCR Reagents & Instrumentation	RNAi Applications
Gene Expression Services	Bioinformatics/Biostatistics Solutions	Sampling Technologies
Multimarker Diagnostics	High Throughput Sequencing	Data Management Methods
Multiplex Technologies	Molecular & Expression Profiling	Screening Technologies

## Confirmed Speakers 2010

- Roman Artymyshyn, Principal Scientist, Target Discovery and Assessment, Lundbeck Research
- Nirmala Nanguneri, Director, Head of Biomarker Analysis and Informatics, Biomarker Development, Translational Sciences, Novartis Institutes for Biomedical Research
- Mikael Kubista, Head of Gene Expression Laboratory, Institute of Biotechnology
- Anders Stahlberg, Department of Chemistry and Biosciences, Chalmers University of Technology, Gothenburg University
- Fanny Schmidt, Post-Doctoral Fellow, MerckSerono SA
- Paola Rossatto, Lab. Researcher – Biology QC Department, Merck Serono
- Jan .M. Ruijter, Researcher, Dept. Anatomy, Embryology & Physiology, Academic Medical Centre, Amsterdam
- Pavel Neuzil, Korean Institute of Science and Technology, (KIST)
- Yiu-Lian Fong, Director, Diagnostic Development, Novartis Molecular Diagnostics
- Barbara D'haene, Center for Medical Genetics Ghent (CMGG), Ghent University Hospital
- Frank McCaughan, MRC Laboratory of Molecular Biology
- Philip Zimmermann, Group Leader at ETH Zurich (Swiss Federal Institute of Technology)
- Victor Turcanu, Lecturer in Paediatric Allergy, King's College London and Honorary Lecturer in Allergy, Guy's and St Thomas' NHS Foundation Trust, London
- Benaissa EL Moulaj, Laboratory of Human Histology-CRPP, Institute of Pharmacy-CHU
- Afif Abdel Nour, Research Scientist, Molecular Biotechnology, Institut Polytechnique LaSalle Beauvais
- Karen Smeets, Research Group Zoology: Biodiversity and Toxicology, Centre for Environmental Sciences, Hasselt University
- Susan Baigent, Avian Oncogenic Virus Group, Institute for Animal Health
- Marco Tomasetti, Investigator, Department of Molecular Pathology and Innovative Therapies, Polytechnic University of Marche, Ancona, Italy
- Ales Trichopad, Co Founder and CTO, Labonnet
- Senior Representative, Exiqon

## Reserved Speakers 2010

- Gregory L. Shipley, Asst. Professor, Director, Quantitative Genomics Core Laboratory Department of Integrative Biology and Pharmacology The University of Texas Health Science Center – Houston

### SPONSORED BY





# 2nd Annual qPCR Congress

15th – 17th November 2010, Radisson Edwardian, Heathrow, London

[www.qpcr-congress.com](http://www.qpcr-congress.com)

Day 1 – Monday 15th November 2010

08.00 – 09.00	<b>REGISTRATION &amp; COFFEE</b>
	<b>qPCR Applications, Technology and Data Management</b>
09.00 – 09.10	<b>Chairman's Opening Address</b>
09.10 – 09.40	<p><b>Keynote Address</b>  <b>Confounding Factors in the Microarray Profiling of Peripheral Blood</b></p> <ul style="list-style-type: none"> <li>• Various confounding factors when analyzing the gene expression in whole blood collected in clinical trials</li> </ul> <p>CONFIRMED:  <b>Nirmala Nanguneri, Director, Head of Biomarker Analysis and Informatics, Biomarker Development, Translational Sciences, Novartis Institutes for Biomedical Research</b></p>
09.40 – 10.10	<p><b>Solution Provider Presentation</b>  <b>Title to be Confirmed</b>  <b>Senior Representative, Exiqon</b></p> <p style="text-align: center;">Sponsored by  </p>
10.10 – 10.35	<p><b>Differential Gene Expression in Drug Target Discovery: From Genome Wide-Expression Studies to Target-Specific Inhibitors</b></p> <ul style="list-style-type: none"> <li>• q-PCR as validation tool, focusing on a specific gene family</li> <li>• Use of micro-arrays and qPCR on disease-related samples</li> <li>• Overlaying DGE data from converging phenotypic studies</li> </ul> <p>CONFIRMED:  <b>Fanny Schmidt, Post Doctoral Fellow, MerckSerono SA</b></p>
10.35 – 11.05	<b>MORNING REFRESHMENTS</b> <b>POSTER PRESENTATION SESSION</b>
11.05 – 11.30	<p><b>Using qPCR and RNA Microarrays to Dissect the Immunological Mechanisms that Underlie Peanut Allergy</b></p> <ul style="list-style-type: none"> <li>• Peanut allergy and conversely peanut tolerance are maintained by T lymphocytes that circulate in the blood. By isolating these lymphocytes and characterising their gene expression using mRNA microarrays and qPCR we shall identify biomarkers that reflect the allergy and tolerance states.</li> <li>• The use of these biomarkers should bring to light the natural processes of allergic sensitization that occur before a food allergy is fully developed. Thus the biomarkers might define the temporal 'window of opportunity' when preventive interventions are most likely to be successful as well as the groups of patients who would benefit most from such interventions.</li> <li>• These biomarkers could also be used to monitor interventions aimed at treating established food allergies, for example by defining their endpoint i.e. they would reveal the emergence of T lymphocytes that can maintain peanut tolerance.</li> </ul> <p>CONFIRMED:  <b>Victor Turcanu, Lecturer in Paediatric Allergy, King's College London and Honorary Lecturer in Allergy, Guy's and St Thomas' NHS Foundation Trust, London</b></p>
11.30 – 11.55	<p><b>Analysis of Circulating miRNA Biomarker in Serum Using Quantitative Reverse Transcription-PCR (qRT-PCR)</b></p> <p>Recently, finding miRNA in the blood has suggested the potential for miRNA-based blood biomarkers in cancer detection. It was hypothesised that the levels of specific circulating miRNA species may be used to detect and monitor the pathological development associated with agent-induced tissue injuries. Prerequisite to developing circulating miRNA as diagnostic biomarker is the ability to measure absolute amount of molecular biomarkers from plasma and/or serum with sufficient sensitivity and precision to be clinically effective. These challenges have been met by innovative solutions based on quantitative RT-PCR (qRT-PCR). The clinic effectiveness of circulating nucleic acid as biomarkers is affected by a range of variable including pre-analytic factors involved into specimen collection and processing factors influencing RNA extraction efficiency and the technical issues involved in successful qRT-PCR and data analysis. Therefore, a standardized method is required for clinic applications. A optimised method for RNA extraction will be described. As well, a synthetic miRNA probe will be used for normalization and the accuracy and precision of analysis evaluated.</p> <p>CONFIRMED:  <b>Marco Tomasetti, Investigator, Department of Molecular Pathology and Innovative Therapies, Polytechnic University of Marche, Ancona, Italy</b></p>
11.55 – 12.20	<p><b>Title to be Confirmed</b></p> <p>CONFIRMED:  <b>Pavel Neuzil, Korean Institute of Science and Technology, (KIST)</b></p>

12.20 – 12.50	<p style="text-align: center;"><b>Solution Provider Presentation</b></p> <p style="text-align: center;">Sponsored by Thermo Fisher Scientific</p>
12.50 – 13.50	<b>LUNCH</b>
13.50 – 14.20	<p style="text-align: center;"><b>Solution Provider Presentation</b></p> <p style="text-align: center;">For sponsorship opportunities please contact  <a href="mailto:sponsorship@oxfordglobal.co.uk">sponsorship@oxfordglobal.co.uk</a></p>
14.20 – 14.45	<p><b>Methylation Analysis Using qPCR Compared to LC/MS</b></p> <p>CONFIRMED:  <b>Atif Abdel Nour, Research Scientist, Molecular Biotechnology, Institut Polytechnique LaSalle Beauvais</b></p>
14.45 – 15.10	<p><b>Gene Copy Number qPCR Development and Validation on CHO/NS0 Recombinant Cell Lines</b></p> <ul style="list-style-type: none"> <li>• Gene copy number determination is one of the most challenging tests required for Genotypic Characterization studies of recombinant cell lines</li> <li>• We developed and validated a real time qPCR method for the determination of the expression construct copy number present in the cell banks. Normally the determination is performed using Southern blot based techniques that are time consuming and mostly inaccurate to determine an absolute quantification, in particular when low copies of the vector are inserted</li> <li>• The validation of a reference gene used to circumvent extraction variability has been also performed</li> </ul> <p>CONFIRMED:  <b>Paola Rossatto, Lab. Researcher – Biology QC Department, Merck Serono</b></p>
15.10 – 15.40	<p><b>Solution Provider Presentation</b>  <b>Experiment Design, Data Analysis and Quality Control in qPCR Assays</b></p> <div style="text-align: right;"></div> <p>CONFIRMED:  <b>Ales Trichopad, Co Founder and CTO, Labonnet</b></p>
15.40 – 16.10	<b>AFTERNOON REFRESHMENTS POSTER PRESENTATION SESSION</b>
16.10 – 16.35	<p><b>Molecular Copy-Number Counting (MCC) - Multilocus Interrogation of Archived Clinical Biopsies in Basic Research and the Delivery of Personalised Medicine</b></p> <ul style="list-style-type: none"> <li>• Multiplex analysis of subnanogramme quantities of DNA</li> <li>• Application to clinical biopsies - basic research</li> <li>• Application to clinical biopsies - developing personalised medicine using MCC</li> <li>• Integrating multilocus sequence analysis into the MCC protocol</li> </ul> <p>CONFIRMED:  <b>Frank McCaughan, MRC Career Development Fellow, MRC Laboratory of Molecular Biology</b></p>
16.35 – 17.00	<p><b>Accurate and Objective Copy Number Profiling Using Real-Time Quantitative PCR</b></p> <ul style="list-style-type: none"> <li>• Advantages and disadvantages of qPCR based copy number screening</li> <li>• Setting up qPCR based copy number screening</li> <li>• Workflow of qPCR based copy number screening <ul style="list-style-type: none"> <li>○ Pipetting and qPCR runs</li> <li>○ Calculations and quality control</li> <li>○ Interpretation</li> </ul> </li> <li>• qPCR based copy number screening in a clinical setting</li> </ul> <p>CONFIRMED:  <b>Barbara D'haene, Center for Medical Genetics Ghent (CMGG), Ghent University Hospital</b></p>
17.00 – 17.30	<p><b>Handling qPCR Data Resulting from Monitoring PCR Cycling with DNA-Binding Dyes or Hydrolysis Probes</b></p> <ul style="list-style-type: none"> <li>• Cumulative versus non-cumulative fluorescence</li> <li>• Baseline correction</li> <li>• PCR efficiency estimation</li> <li>• Cq-shift correction</li> </ul> <p>CONFIRMED:  <b>Jan .M. Ruijter, Researcher, Dept. Anatomy, Embryology &amp; Physiology, Academic Medical Centre, Amsterdam</b></p>

17.30 – 17.55	<p><b>The Context-Specific Choice of Reference Genes Significantly Improves RT-qPCR Data Normalization</b></p> <ul style="list-style-type: none"> <li>• Most scientists use commercial gene panels to normalize data. These panels contain 10-20 genes supposed to be stable; however, more than 100 publications indicate that these genes are not generally suitable.</li> <li>• We hypothesized and demonstrated experimentally that gene expression stability is context-dependent, and that the choice of reference genes should be context-driven</li> <li>• Using the GeneSinger database of more than 40,000 Affymetrix arrays, we identified genes that are highly stable in selected tissues and organisms, and validated these new candidates against commonly used reference genes from commercial gene panels. The newly identified genes performed significantly better as normalizers.</li> <li>• The results showed that related tissues have similar sets of optimal reference genes</li> <li>• We built a novel tool called RefGene to search for context-specific reference genes and have made it publicly available.</li> </ul> <p>CONFIRMED:  <b>Philip Zimmermann, Group Leader at ETH Zurich (Swiss Federal Institute of Technology)</b></p>
17.55	<b>END OF DAY ONE &amp; NETWORKING DRINKS</b>

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Day 2 – Tuesday 16th November 2010

	<p><b>Single Cell Profiling &amp; qPCR Case Studies in Drug Discovery, Development, Molecular Diagnostics and the Clinic</b></p>
08.45 – 09.15	<p><b>Keynote Address</b>  <b>High Performance High Throughput qPCR</b></p> <p>CONFIRMED:  <b>Mikael Kubista , Head of Gene Expression Laboratory, Institute of Biotechnology</b></p>
09.15 – 09.40	<p><b>Understanding Cell Heterogeneity Using Single-Cell Gene Expression Profiling</b></p> <ul style="list-style-type: none"> <li>• Gene expression in single cells</li> <li>• Methodology considerations: possibilities and limitations</li> <li>• Experimental data from single astrocytes, embryonic stem cells and beta-cells</li> <li>• Data interpretations: How to use and understand single-cell gene expression data, especially stem cells</li> </ul> <p>CONFIRMED:  <b>Anders Ståhlberg, Research Scientist, Lundberg Laboratory of Cancer Research, Department of Pathology, Sahlgrenska Academy at University of Gothenburg, Gothenburg, Sweden</b></p>
09.40 – 10.10	<p style="text-align: center;"><b>Solution Provider Presentation</b></p> <p style="text-align: center;"><b>Reserved</b></p> <p style="text-align: center;"><b>Qiagen</b></p>
10.10 – 10.35	<p><b>Peripheral Blood Gene Expression Profiles Identify Subjects with Major Depression: Moving Toward Transcription Based Diagnostics and Patient Segmentation</b></p> <ul style="list-style-type: none"> <li>• Our goal is to develop diagnostics and patient segmentation strategies for neuropsychiatric disorders.</li> <li>• Patients diagnosed with major depressive disorder (MDD) represent a heterogeneous population with respect to underlying disease biology.</li> <li>• Segmentation based on readily accessible biomarkers may aid the development of more targeted and effective treatments.</li> <li>• To define disease-relevant biomarkers, we evaluated gene transcription patterns in peripheral blood samples using qPCR. from depressed patients (enrolled in clinical trials for depression) vs. healthy controls.</li> <li>• A focused approach was used to assess transcription of a limited number of genes associated with diverse physiological processes.</li> <li>• Gene transcription patterns to classify depressed patients (vs controls) have been identified.</li> </ul> <p>CONFIRMED:  <b>Roman Artymyshyn, Principal Scientist, Target Discovery and Assessment, Lundbeck Research</b></p>
10.35 – 11.05	<p><b>MORNING REFRESHMENTS</b>  <b>POSTER PRESENTATION SESSION</b></p>

11.05 – 11.35	<p><b>Approaches for Analytical Validation of a PCR-based Molecular Diagnostic Test to Support Drug Development</b></p> <p>The presentation will outline effective approaches and strategies for analytical validation of a PCR-based IVD test and discuss the major differences between assay qualifications for biomarker development and analytical validations for IVD, especially for companion diagnostics</p> <p>CONFIRMED  <b>Yiu-Lian Fong, Director, Diagnostic Development, Novartis Molecular Diagnostics</b></p>
11.35 – 12.05	<p style="text-align: center;"><b>Solution Provider Presentation</b></p> <p style="text-align: center;">For sponsorship opportunities please contact  <a href="mailto:sponsorship@oxfordglobal.co.uk">sponsorship@oxfordglobal.co.uk</a></p>
12.05 – 12.30	<p><b>Development &amp; Validation of Real-Time PCR Assays to Differentiate Between and Quantify, Vaccine and Virulent Strains of Marek's Disease Virus</b></p> <p>CONFIRMED:  <b>Susan Baigent, Avian Oncogenic Virus Group, Institute for Animal Health</b></p>
12.30 – 13.00	<p style="text-align: center;"><b>Solution Provider Presentation</b></p> <p style="text-align: center;">For sponsorship opportunities please contact  <a href="mailto:sponsorship@oxfordglobal.co.uk">sponsorship@oxfordglobal.co.uk</a></p>
13.00 – 14.00	<b>LUNCH</b>
14.00 – 14.25	<p><b>Title to be Confirmed</b></p> <p>RESERVED:  <b>Gregory L. Shipley, Asst. Professor, Director, Quantitative Genomics Core Laboratory Department of Integrative Biology and Pharmacology The University of Texas Health Science Center – Houston</b></p>
14.25 – 14.55	<p><b>Use of qPCR in Combination with RNAi to Screen for Toxicological/Carcinogenic Biomarkers</b></p> <p>CONFIRMED:  <b>Karen Smeets, Research Group Zoology: Biodiversity and Toxicology, Centre for Environmental Sciences, Hasselt University</b></p>
14.55 – 15.25	<p><b>Can Aptamers Rival with Antibodies in Immuno-PCR?</b></p> <p>CONFIRMED:  <b>Benaissa EL Moulaj, Laboratory of Human Histology-CRPP, Institute of Pharmacy-CHU</b></p>
15.25	<b>CLOSE OF DAY TWO</b>

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Day 3 – Wednesday 17th November 2010

## Post Conference Workshop - Experimental Design and Quality Control in qPCR Experiments

**Course Tutor: Mikael Kubista, TATAA Biocenter & Institute of Biotechnology at the Czech Academy of Sciences**

Mikael was among the pioneers who developed real-time PCR. Starting in 1991 his laboratory developed dyes and probes for real-time PCR and founded LightUp Technologies as Europe's first company focusing on real-time PCR based human infectious disease testing. His team then developed experimental approaches for accurate measurements of expression levels, and they pioneered the fields of single cell expression profiling and multidimensional expression profiling by real-time PCR. Mikael also developed methods and approaches to analyze gene expression data and co-founded MultiD Analyses that develops the popular software GenEx for processing of real-time PCR data. Working as advisor for Unesco he introduced real-time PCR in Africa and in the Middle East. In 2001 Mikael founded the TATAA Biocenters as global leading service providers and organizers of hands-on training in real-time PCR. Regular training courses are held all over Europe, Africa, Asia and in the US. The TATAA courses world-wide are supported by leading instrument manufacturers and reagents suppliers in the real-time PCR field. Currently Michael's work focuses on circulating tumor cells and the development of guide lines, where he recently co-authored the MIQE guidelines, and quality control for qPCR analysis and the pre-analytical steps, which is done within SPIDIA. Mikael is also advisor to several biotech and pharmaceutical companies.

### 1 Day Experimental Design and Quality Control in qPCR Experiments

9am – 5pm including Lunch and refreshments

■ The key to successful qPCR analysis is arguably quality experimental design that balances statistical significance and experimental cost. Performing a fully nested pilot study GenEx estimates the variance contributions from the different experimental steps, advising you which steps may be improved to enhance data quality and where technical replicates shall be performed. It also indicates the number of subjects needed to achieve a desired resolution. Too few subjects and you may not be able to prove or disprove your hypothesis, while too many subjects may improve resolution beyond what is practically relevant and money is wasted. Further requirement for success is high performance of the equipment being used. Mal-performing dispensers or qPCR instruments may compromise a study. This can be avoided by using proper standard operating procedures including quality controls. Finally, data shall be reported according to the Minimum Information for Publication of Quantitative Real-Time PCR Experiments (**MIQE**) guidelines such that results can be properly evaluated and easily reproduced.

- Absolute quantification, qPCR standard curve, Reverse calibration, Limit of detection
- Experimental design, Noise contributions to RT-qPCR analysis (nested ANOVA), cost-performance optimization of experiments
- Sample size estimations (Power testing)
- Selecting reference genes (geNorm, Normfinder)
- qPCR data pre-processing, Outlier detection. Relative quantification, Comparison of groups (parametric and non-parametric methods)
- Expression profiling, missing data treatment, scaling of data, Un-supervised clustering of genes and samples (hierarchical clustering, self-organized maps, Principal Component Analysis), Supervised clustering of samples (Artificial neural network)
- Standard operating procedures and quality control
- The MIQE guidelines
- Exercises