

qPCR 2010 7 – 9th April 2010

Symposium & Exhibition

Main topic: The ongoing evolution of qPCR



www.qPCR2010-Vienna.net
University Vienna, Juridicum, Vienna City Center, Austria

Scientific coordination:

Michael W. Pfaffl
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Scientific board:

Stephen Bustin, School of Medicine, London, UK
Mikael Kubista, TATAA Biocenter, Sweden
Christine Mannhalter, Medizinische Universität Wien, Austria
Jo Vandesompele, CMGG, University of Ghent, Belgium
Michael W. Pfaffl, TUM, Germany

Location - Juridicum, University Vienna

Schottenbastei 10-16
1010 Wien (Vienna), Austria

Event organization:

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Last update on 18th March 2010

qPCR 2010 - Symposium Agenda

Tuesday, 6. April 2010

10:00 am - Industrial Exhibition – build-up
4:00 pm
4:00 pm - Early Registration
6:00 pm

Wednesday, 7. April 2010

7:30 am Registration

9:00 am **OPENING: qPCR 2010 Symposium & Industrial Exhibition**

Location: Lecture hall 10
Chair: Michael W Pfaffl & Martina Reiter

9:15 am **MIQE and QM strategies in qPCR**

- Location: Lecture hall 10
Chair: Michael W Pfaffl & Stephen Andrew Bustin

Session Content - The focus of this session will be placed on the MIQE guidelines and on quality management (QM) in qPCR. Following the MIQE guidelines (minimum information for publication of quantitative real-time PCR experiments) will encourage better experimental practice, allowing more reliable and unequivocal interpretation of qPCR results. QM strategies in real-time PCR to guarantee better and more valid results and allow reliable physiological conclusions.

9:15 – PLENARY: **Why the need for qPCR publication guidelines? - The case for MIQE**

Stephen Andrew Bustin
Barts and the London School of Medicine and Dentistry, United Kingdom

9:45 - **A Practical Approach to Assay Design for qPCR - Overcoming Difficult Assays, Designs and Optimizations while Conforming to the MIQE Guidelines**

Francisco Bizouarn
Bio-Rad Laboratories, United States of America

10:15 - **Standardization efforts of qPCR: Example - Quantitative Measurement of BCR-ABL Translocation**

Christine Mannhalter
Medical University Vienna, Austria

10:45 - **Dye spectra, dynamics and consequences**

Roderic Fuerst
IT-IS Life Science, Ireland

11:15 - Hydrolysis probes with improved quenching and performance

Mark Aaron Behlke
Integrated DNA Technologies, Inc., United States of America

11:45 - Advanced qPCR - one step ahead with next generation dyes

Alexander Rácz
Eurofins MWG Operon, Ebersberg, Germany

12:15 - New technologies for FFPE samples: Improved RNA isolation and novel cDNA priming for RT-qPCR and for microarray analysis

Guido Krupp¹, Susanne Quabius², Rolf Jaggi³
1: AmpTec GmbH, Hamburg, Germany; 2: Institute Immunology, UKSH Kiel, Germany; 3: Department of Clinical Research, University of Bern, Switzerland

12:30 - Zip Nucleic Acid hydrolysis and hybridisation probes for improving detection

Nathalie Lenne, Clément Paris, Valérie Moreau, Gaëlle Deglane, Patrick Erbacher
Polyplus-transfection, France

12:45 - Postmortem mRNA Profiling: Possibilities and Limitations

Marielle Heinrich¹, Antje Koppelkamm²
1: University of Freiburg, Germany; 2: University of Freiburg, Germany

13:00 – 14:00 Lunch

2:00 pm High throughput quantitative PCR – digital PCR

Location: Lecture hall 10

Chair: Mikael Kubista & Tania Nolan

Session Content - The focus of this session will be placed on miniaturizations and on high throughput qPCR: e.g. 384 and 1536 well applications, new high throughput platforms, droplet PCR, qPCR robotics, digital PCR, gene expression real-time RT-PCR arrays (mRNA and microRNA), quantitative multiplexing.

14:00 - PLENARY: Digital PCR and intra-cellular expression profiling

Mikael Kubista^{1,2}, Monika Sidova^{1,2}, David Svec^{1,2}, Radek Sindelka^{1,2}
1: TATAA Biocenter; 2: Institute of Biotechnology, Czech Academy of Sciences

14:30 - High-Throughput Gene Expression Analysis Using the LightCycler® Platform

Thomas Froehlich, Gregor Sagner, Armin Tgetgel, Gudrun Tellmann
Roche Diagnostics GmbH, Germany

15:00 - High-throughput Droplet PCR

Philip Day, Amelia MArkey, Stephan Mohr
University of Manchester, United Kingdom

15:30 - Detection of Related AKT Family Members using Solaris qPCR Gene Expression Assays

Ian Kavanagh¹, Zaklina Strezoska², Melissa Kelley²
1: Thermo Fisher Scientific, Epsom, Surrey, UK; 2: Thermo Fisher Scientific, Lafayette, CO, USA

16:00 – 16:30 Coffee Break

16:30 - Western-type diet affects the expression of genes known to be involved in human colorectal carcinogenesis in histologically normal mucosa of ApcMin/+ mice

Marjaana Pussila
University of Helsinki, Finland

17:00 - Fluidigm's BioMark System for Gene Expression, Genotyping, Digital PCR and other sample preparation applications using nanoliter reaction volumes

Leila Smith
Fluidigm Europe BV, The Netherlands

17:30 - Prognostic Impact of Gene Expression Analyses in Human Glioblastoma- MGMT expression analysis

Simone Kreth
LMU Munich, Germany

18:00 - Rapid Quantification of DNA libraries for Next Generation Sequencing

Raza Ahmed
Agilent Technologies, United Kingdom

18:30 – 21:00 Wine Reception in the Industrial Exhibition in “Juridicum”

8:30 am Thursday, 8. April 2010**1:00 pm RNAi - microRNA - siRNA Applications – miRNA normalisation**

Location: Lecture hall 10

Chair: Jo Vandesompele & Mirco Castoldi

Session Content - The focus of this session will be placed on the RNAi mechanism by microRNA. Following topics will be presented and discussed: microRNA extraction and microRNA quality control, apply MIQE guidelines to microRNA research, qRT-PCR technologies to detect microRNA, microRNA qPCR arrays, microRNA normalization strategies, siRNA applications in combination with qRT-PCR, microRNA targets and microRNA precursors, new siRNA manipulation and microRNA technologies.

8:30 - PLENARY: From reference genes to global mean normalization

Jo Vandesompele

Ghent University, Belgium

9:00 - MicroRNA dynamics in early neuronal differentiation with correlation to protein output

David Ruff

Life Technologies, United States of America

9:30 - Expression profiling of microRNA using real-time quantitative PCR, how to use it and what is availableMirco Castoldi^{1,2}

1: University of Heidelberg, Germany; 2: EMBL, Heidelberg, Germany

10:00 - microRNA profiling on challenging samples using LNA™ enhanced qPCRDitte Andreasen, Jacob Ulrik Fogh, William Biggs, Jesper Salomon, Adam Baker, Peter Mouritzen
Exiqon A/S, Denmark**10:30 – 11:00 Coffee Break****11:00 - Quantification of microRNAs – MIQE challenges and solutions**Michael W Pfaffl¹, Christiane Becker¹, Swanhild U Meyer¹, Sebastian Kaiser²

1: Physiology Weihenstephan, Technische Universität München, Germany; 2: Department of Statistics, LMU München, Germany

11:30 - Quantification of miRNA precursors in Mammalian Cells

Martin Kreuz

QIAGEN GmbH, Germany

12:00 - Establishing a set of "housekeeping RNA" genes for normalisation purposes in non-protein-coding RNA researchChenna R Galiveti¹, Timofey S Rozhdestvensky², Jürgen Brosius², Hans Lehrach¹, Zoltán Konthur¹

1: MPI for Molecular Genetics, Germany; 2: Institute of Experimental Pathology, ZMBE, University of Münster, Germany

12:15 - In search of underlying stress mechanisms using RNAi and gene expression profilingMichelle Plusquin¹, Katrien de Mulder², Peter Ladurner², Ann Cuypers¹, Tom Artois¹, Karen Smeets¹

1: Hasselt University, Centrum for Environmental Sciences, Belgium; 2: University of Innsbruck, Innsbruck, Austria

12:30 - MicroRNA expression in lung tissue and blood isolated from pigs suffering from bacterial pneumonia

Kerstin Skovgaard, Karin T. Poulsen, Peter M. H. Heegaard

Technical University of Denmark, Denmark

12:45 - New tools for efficient production of esiRNA and evaluation of their functionalitySonja Kärck¹, Johanna Pihlaja¹, Linda Degerth², Jaakko Kurkela¹

1: Finzymes, Finland; 2: Institute of Biotechnology & Department of Biological and Environmental Sciences, University of Helsinki

13:00 – 14:00 Lunch**2:00 pm Data Analysis: qPCR BioStatistics & Bioinformatics**

Location: Lecture hall 10

6:30 pm Chair: Ales Tichopad & Michael W Pfaffl

Session Content - The focus of this session will be placed on the post-qPCR data analysis. Following applications will be presented and discussed: new software applications, calculation of relative expression, real-time PCR efficiency determination, mathematical modelling, multivariate expression profiling, statistics in real-time PCR, data management, multi-way expression profiling, multiple regression analysis and 3D data visualization.

14:00 - Accurate and objective copy number profiling using real-time quantitative PCRJan Hellemans, Barbara Dhaene, Jo Vandesompele
University of Gent, Belgium**14:30 - Quality control for quantitative PCR based on amplification compatibility test**

Ales Tichopad

Technical University Munich Germany

15:00 - Expression profiling - clusters of possibilitiesMikael Kubista^{1,2}

1: TATAA Biocenter; 2: Institute of Biotechnology, Czech Academy of Sciences

15:30 - Bias in the Cq value observed with hydrolysis probe based quantitative PCR can be corrected with the estimated PCR efficiency value.Jan M Ruijter¹, Jari M Tuomi²

1: Heart Failure Research Center, Amsterdam, the Netherlands; 2: Department of Physiology & Pharmacology, London, Canada

16:00 – 16:30 Coffee Break**16:30 - Pros and cons of single curve efficiency algorithms**Stefaan Derveaux^{1,2}, Jo Vandesompele^{1,2}, Jan Hellemans^{1,2}

1: Center for Medical Genetics Ghent, Ghent University Hospital, Belgium; 2: Biogazelle, Ghent, Belgium

17:00 - Existing Methods and New Developments for RT-PCR Analysis in RSebastian Kaiser¹, Swanild U Meyer², Michael W Pfaffl²

1: LMU München, Germany; 2: TUM München, Germany

17:15 - DNA Melting and MathematicsBob Palais¹, Carl Wittwer²¹Mathematics Department, University of Utah; ²Pathology Departments, University of Utah;**17:30 - Quality Control in qPCR**

Mario Cunha, Luis Martins, Carmo Ornelas

Clinical Pathology, Lab. Virology, Portuguese Institute of Oncology, Lisbon, Portugal

17:45 - QPCR: Application for real-time PCR data management and analysisStephan Pabinger¹, Rene Snajder¹, Robert Rader¹, Heiko Eichhorn², Zlatko Trajanoski¹, Gerhard G. Thallinger¹

1: Institute for Genomics and Bioinformatics, Graz University of Technology, Austria; 2: Development Anti-Infectives Microbiology, Sandoz GmbH, Kundl, Austria

18:00 - Quantitative real time-PCR-assay for the analysis of gene-specific human influenza A virus transcription & replication dynamicsAntje Lagoda¹, Diana Hoffmann², Diana Vester¹, Claudius Seitz², Yvonne Genzel², Udo Reichl^{1,2}

1: Chair of Bioprocess Engineering: Otto-von-Guericke University, Magdeburg, Germany; 2: Max Planck Institute for Dynamics of Complex Technical Systems, Magdeburg, Germany

18:15 - Real-time Gene Expression Analysis as Monitoring Tool for Production of Recombinant ProteinsSabine Knappe¹, Christiana Cordes²

1: TU Dresden, Germany; 2: Hochschule Anhalt (FH)

20:00 – 24:00 Event Dinner downtown Vienna in “12 Apostelkeller”**8:30 am Friday, 9. April 2010****11:30 am High Resolution Melting - Epigenetics**

Location: Lecture hall 10

Chair: Carl T Wittwer & Jan Hellemans

Session Content - The focus of this session will be placed on the SNP analysis and on new HRM (high resolution melting) applications. Further the epigenetics, methylation markers, and the comparison of HRM platform will be discussed.

8:30 - PLENARY: High Resolution DNA Melting Analysis

Carl T Wittwer

University of Utah, United States of America

9:00 - Demonstrating the Utility of the Protein Thermal Shift Assay Using Applied Biosystems Real Time PCR Systems

Madeline O'Donoghue

Life Technologies, United States of America

9:30 - High Resolution Melting Analysis in Cancer Diagnosis

Claudio Orlando, Lisa Simi, Nicola Pratesi, Irene Mancini, Giulia Forni, Francesca Malentacchi

University of Florence, Italy

10:00 - HRM: an innovative technology for analysis of genetic variations - Advanced applications and critical success factors

Andreas Missel

QIAGEN GmbH, Germany

10:30 - Gene scanning by amplicon melting analysis and SNP detection by unlabeled probe melting analysisMaria Erali¹, David C. Pattison¹, Nancy H. Augustine², Harry R. Hill^{1,2}, Carl T. Wittwer^{1,2}

1: ARUP Institute for Clinical & Experimental Pathology, United States of America; 2: Department of Pathology, University of Utah, United States of America

10:45 – 11:15 Coffee Break**11:15 - Quantification of alternatively spliced transcripts by Real-time PCR using intercalating dyes**

Julia Meiser, Julia Frühwald, Stephan Philipp

Institute for Experimental and Clinical Pharmacology und Toxicology, Saarland University, Germany

11:30 - Rapid identification of multidrug-resistant Mycobacterium tuberculosis isolates by rpoB gene scanning using high-resolution melting curve PCR analysis

Ariane Tatjana Pietzka, Alexander Indra, Anna Stöger, Josef Zeinzinger, Miriam Konrad, Petra Hasenberger, Franz Allerberger, Werner Ruppitsch

Austrian Agency for Health and Food Safety, Vienna, Austria

11:45 - Quantitative one-step DNA methylation analysis using native genomic DNA as templateThomas von Kanel¹, Dominik Gerber¹, André Schaller¹, Alessandra Baumer², Eva Wey², Franziska M Gisler¹, Christopher B Jackson¹, Karl Heinemann³, Sabina Gallati¹

1: Division of Human Genetics, University of Bern, Switzerland; 2: Institute for Medical Genetics, University of Zurich, Switzerland; 3: Division of Medical Genetics, University of Basel, Switzerland

12:00 pm CNA - Circulating Nucleic Acids

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Location: Lecture hall 10

1:30 pm

Chair: Jim Francis Huggett & Pamela Pinzani

Session Content - The focus of this session will be placed on the analysis of circulating RNAs and DNA. A further focus is set on circulating microRNAs as diagnostic and prognostic marker.

12:00 - Cell-free circulating nucleic acids in cancer and pregnancy

Pamela Pinzani, Francesca Salvianti, Serena Vinci, Roberta Cascella, Claudio Santucci, Sara Zaccara, Mario Pazzagli, Claudio Orlando

Department of Clinical Physiopathology, University of Florence, Italy

12:30 - Diagnostic tools for measuring cell free nucleic acids; What can we expect from the next decade?

Jim Francis Huggett, Carole Foy

LGC, United Kingdom

13:00 - Targeting the human urine RNAome for tumor diagnostics by qPCR

Alfred Schöller

LK Weinviertel Mistelbach/Gänserndorf, Austria

13:30 – 14:30 Lunch**2:30 pm Single-cell qPCR**

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Location: Lecture hall 10

4:45 pm

Chair: Anders Stahlberg & Michael W Pfaffl

Session content - Single-cell sampling, pre-amplification techniques, laser micro-dissection, sub-cellular PCR, micro-manipulation of cell clusters, cellular micro injection, FACS spotting, single cell handling, pre-amplification...

14:30 - PLENARY: High Throughput Gene Expression Profiling of Single Cells

Ken Livak

Fluidigm Corporation, United States of America

15:00 - Single-cell gene expression profiling using reverse transcription quantitative real-time PCR

Anders Stahlberg

Gothenburg University, Sweden

15:30 - Analysis of Single Circulating Tumour Cells isolated from Gastro-Intestinal Cancer PatientsPetra Hartmann¹, Karin Görner¹, Claudia Holzauer¹, Jeannine Bachmann², Marc Martignoni², Marianna Alunni-Fabroni¹

1: Beckman Coulter Biomedical GmbH, Germany; 2: Klinikum rechts der Isar Technische Universität, Munich Germany

16:00 - Detection and characterization of single circulating tumor cells as chance to monitor and individualize chemotherapy

Stephanie Carl, Torsten Kroll, Katharina Pachmann

Friedrich Schiller University Jena., Germany

16:30 - Application of Microfluidic qPCR Arrays to the Profiling of miRNA Expression in Purified Hematopoietic Populations and in Single Cells

Oleh I. Petriv¹, Florian Kuchenbauer², Allen Delaney³, Veronique Lecault¹, Adam White¹, David G. Kent², Lindsay Laycock², Michael Heuser², Tobias Berg², Michael R. Copley², Jens Ruschmann², Sanja Sekulovic², Frann Antignano², Etsushi Kuroda², Victor Ho², Claudia Benz², Timotheus Y. F. Halim², Vincenzo Giambra², Gerald Krystal², Connie J. Eaves², Fumio Takei², Andrew P. Weng², James M. Piret⁴, Marco A. Marra³, R. Keith Humphries², Carl L. Hansen¹

1: University of British Columbia, Canada; 2: Terry Fox Laboratory, BC Cancer Agency, Vancouver, BC; 3: Genome Sciences Centre, BC Cancer Agency, Vancouver, BC; 4: Michael Smith Laboratories, University of British Columbia, Vancouver, BC

4:45 pm CLOSING: qPCR 2010 Symposium & Industrial Exhibition

- Location: Lecture hall 10

5:00 pm Chair: Michael W Pfaffl & Martina Reiter

5:00 pm

- Industrial Exhibition – booth removal

6:00 pm

General settings for presenter:

- Official event language is English. No translation will be provided.
- Plenary or invited talks will take 20-25 min with additional 5-10 min discussion - **in total 30 min.**
- Short talks will take 10-12 min with additional 3-5 min discussion - **in total 15 min.**
- Talks will be presented via PC using Microsoft Windows 2003 or 2007 and Microsoft PowerPoint 2003 or 2007.
- Please bring your presentation on a memory stick or on a CD.
- If you want to present on MAC please bring your own laptop with the appropriate software.
- Upload your presentations early in advance and check it for proper symbols, e.g. trademarks, copyright symbols, or Greek letters!
- Upload will be available from Tuesday afternoon near the registration desk or from Wednesday till Friday in the lecture hall no. 10.

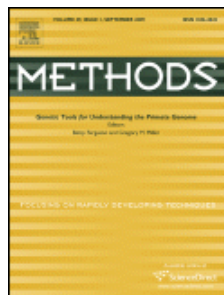
Event location:

- Juridicum der Universität Wien, Schottenbastei 10-16, 1010 Vienna, Austria
- Talks will be presented in lecture hall 10
- Industrial exhibition in the foyer and basement
- http://maps.google.com/maps?f=q&source=s_q&hl=en&geocode=&q=juridicum+wien
- <http://www.bioeps.com/qpcr2010/qPCR2010-google-earth-link.kmz>

Public transportation:

- Straßenbahn (tram): Line 1, 2, D (Stop: Börse), 37, 38, 40, 41, 42, 43, 44 (Stop: Schottentor)
- U-Bahn (underground): Line U2 (Stop: Schottentor-Universität)
- Bus: Line 1A (Stop: Helferstorferstraße), 3A, 40A (Stop: Börse)
- Detailed information about public transport in Vienna: <http://www.wienerlinien.at/wl/ep/home.do?tabId=0>

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