



qPCR & NGS 2015 **23rd – 27th March 2015**
Symposium & Exhibition & Workshops

*Advanced Molecular Diagnostics
for Biomarker Discovery*

@TUM, Freising-Weihenstephan, Germany



Event Agenda

qPCR & NGS 2015

7th international qPCR & NGS Symposium
Industrial Exhibition & Application Workshops

**“Advanced Molecular Diagnostics
for Biomarker Discovery”**

Scientific coordination: Michael W. Pfaffl
Physiology, Freising – Weihenstephan
TUM School of Life Sciences
Weihenstephaner Berg 3
Technical University Munich (TUM)
85354 Freising
Germany

www.qPCR-NGS-2015.net

qPCR & NGS 2015 Event Agenda Overview

online agenda HTML => <http://agendaHTML.qPCR-NGS-2015.net>

online agenda PDF => <http://agendaPDF.qPCR-NGS-2015.net>

	Lecture Hall no. 14 (HS 14)	Lecture Hall no. 15 (HS 15)	Foyer & Seminar Rooms S1 & S2
Sunday 22 nd March			12:00 – 18:00 Industrial Exhibition Built up
			15:00 – 18:00 Arrival & Registration
Monday 23 rd March	10:00 – 10:30 Opening of the Symposium Welcome by Michael W. Pfaffl		8:00 – 10:00 Arrival & Registration & Poster Setup in Foyer lower level
	10:30 – 12:30 Adv. Molecular Diagnostics 1		10:00 – 21:00 Industrial Exhibition in Foyer
	12:30 – 14:00 Lunch		
	14:00 – 18:00 Adv. Molecular Diagnostics 2	14:00 – 18:00 Next Generation Sequencing 1	
	18:00 – 22:00 Reception at the Industrial Exhibition		18:00 – 22:00 Evening Poster Session in Foyer lower level
Tuesday 24 th March	8:30 – 10:30 Digital PCR	8:30 – 10:30 Next Generation Sequencing 2	8:30 – 14:00 Industrial Exhibition in Foyer
	11:00 – 12:30 Non-coding RNA 1	11:00 – 12:30 NGS Data Analysis	
	12:30 – 14:00 Lunch		12:30 – 14:00 Lunch Poster Session in Foyer lower level
	13:00 – 14:00 Life Technologies: Lunch-time seminars	13:00 – 14:00 Agilent Technologies: Lunch-time seminars	
	14:00 – 18:30 Biomarker Discovery & Circulating Nucleic Acids	14:00 – 18:30 MicroGenomics & Single-Cell Diagnostics	
19:30 – 24:00 Symposium Gala Dinner Location: Bräustüberl Weihenstephan, Weihenstephaner Berg 10, 85354 Freising European – Bavarian - Asian Buffet, Music & Dancing & Cocktails			
Wednesday 25 th March	8:30 – 12:50 Optimisation, MIQE & QC in qPCR	8:30 – 12:30 qPCR BioStatistics & Bioinformatics	8:30 – 14:00 Industrial Exhibition in Foyer
	12:30 – 14:00 Lunch		12:30 – 14:00 Lunch Poster Session in Foyer lower level
		12:30 – 13:30 BDQ Editors Meeting	
		13:45 – 14:00 BDQ Poster Awards	
	14:00 – 16:30 Non-coding RNA 2	14:00 – 16:30 Molecular Diagnostics Agi, Vet, Food & Env	14:00 – 17:00 Poster Take Down in Foyer lower level
16:30 – 17:00 Closing of the Symposium Michael W. Pfaffl			
Thursday 26 th March	Seminar rooms S1 - S3 & Computer seminar rooms PU26, PU34A & PU36 9:00 - 17:00		
Friday 27 th March	qPCR, dPCR & NGS Application Workshops: <ul style="list-style-type: none"> • Basic real-time qPCR Application Workshop (2-days) hosted by TATAA Biocenter • qPCR Data Analysis Workflow: from instrument data to interpretation (2-days) hosted by TATAA • digital PCR (2-days) hosted by Bio-Rad • NGS data analysis workshop (2-days) hosted by Genomatix • “Sample to Insight” Analyzing and interpreting the biological meaning in NGS data (2-days) hosted by Qiagen 		

Agenda - qPCR & NGS 2015

Sunday 22nd March 2015

- 12:00 – 18:00 Built-up for Industrial Exhibition
- 15:00 – 18:00 Arrival & Registration
Poster Setup

Monday 23rd March 2015

Welcome & Opening of the Symposium Lecture hall HS 14

08:00 – 10:00 Built-up for Industrial Exhibition
Arrival & Registration

09:00 – 10:00 Welcome Coffee & Tea

10:00 Welcome & Opening of the Symposium

Michael W. Pfaffl
Scientific coordinator of the qPCR & NGS Event

Stephen A. Bustin
Editor in Chief – Biomolecular Detection & Quantification

Advanced Molecular Diagnostics 1

Monday, 23/Mar/2015: *Location:*
10:30am - 12:30pm Lecture hall 14
Session Chair:
Stephen Andrew Bustin
Michael W. Pfaffl

Presentations

- 10:30 Keynote Lecture:**
PCR in less than 30 seconds: Efficient, specific amplification with increased primer and polymerase.
Jared S Farrar¹, Carl T Wittwer²
¹Virginia Commonwealth University; ²University of Utah; carl.wittwer@path.utah.edu
- 11:00 Laser-driven PCR for ultrafast DNA detection**
Lars Ullerich, Federico Bürsgens, Joachim Stehr
GNA Biosolutions GmbH, Germany; ullerich@gna-bio.com
- 11:30 Keynote Lecture:**
Digital PLA (Proximity Ligation Assay)
Harvinder Singh Dhillon¹, Christina Greenwood¹, Gemma Johnson¹, Mark Shannon², Doug Roberts³, Stephen Bustin¹
¹Anglia Ruskin University, Chelmsford, Essex, United Kingdom; ²Thermo Fisher Scientific, Sunnyvale, CA, USA; ³Formulatrix, Bedford, MA, USA; stephen.bustin@anglia.ac.uk
- 12:30 New advances in sequencing-based technology in Clinical Application and Molecular Diagnosis**
Fang Chen, Ya Gao, Hui Jiang, Yanyan Zhang
BGI-Shenzhen, China, People's Republic of; fangchen@genomics.cn

12:30 – 14:00 Lunch in the student cafeteria

Advanced Molecular Diagnostics 2

Monday, 23/Mar/2015: *Location:*
2:00pm - 6:00pm Lecture hall 14
Session Chair:
Justin O'Grady
Mikael Kubista

Presentations

- 14:00 Pathogen DNA enrichment strategies for nanopore sequencing based infectious diseases diagnostics.**
Justin O'Grady
University of East Anglia, United Kingdom; justin.ograde@uea.ac.uk
- 14:30 Differentiation of Identical Twins using Next Generation Sequencing**
Burkhard Rolf
Eurofins, Germany; BurkhardRolf@eurofins.com
- 15:00 Mobile applications for qPCR**
Jo-Ann Stanton
Ubiquitome, New Zealand;
jo.stanton@anatomy.otago.ac.nz
- 15:30 "NanoString - The Next Step After NGS"**
Michael Rhodes
NanoString Technologies; mrhodes@nanosttring.com

16:00 – 16:30 Coffee break & Networking

- 16:30 Optimized Targeted NGS With Multiplex Competitive PCR Amplicon Libraries for Reliable Diagnostic Testing of Cancer FFPE Samples**
Jiyoun Yeo², Erin Crawford², Tom Morrison¹, Xiaolu Zhang², Luke Stewart³, James Willey^{1,2}
¹Accugenomics, Inc., United States of America; ²University of Toledo College of Medicine; ³Fluidigm, Inc.; james.willey2@utoledo.edu
- 17:00 Whole Exome Sequencing for Detection of Genetic Variants to Predict Chronic Lung Allograft Dysfunction**
Markus Schmitt
GATC Biotech AG, Germany; m.schmitt@gatc-biotech.com
- 17:30 Single Cell Analysis of Nuclear Receptor Transcription**
Michael Mancini
Baylor College of Medicine, United States of America; mancini@bcm.edu

18:00 – 22:00 Evening Poster Session

18:00 – 22:00 Networking
Reception in Industrial Exhibition

NGS 1: Next Generation Sequencing 1

Monday, 23/Mar/2015: *Location:*
2:00pm - 6:00pm *Lecture hall 15*
Session Chair:
Jan Hellemans
Steve Lefever

Presentations

14:00 Keynote Lecture:

Next-Generation RNA-Seq

Gary Schroth

Illumina, United States of America; gschroth@illumina.com

14:30 Targeted resequencing and variant validation using pxlence PCR assays

Steve Lefever^{1,2}, Frauke Coppiepers^{1,2}, Daisy Flamez³, Jo Vandesompele^{1,2}

¹Ghent University, Center for Medical Genetics Ghent, Ghent, Belgium; ²pxlence, Dendermonde, Belgium; ³Ghent University, Biomarked, Ghent, Belgium; steve.lefever@ugent.be

15:00 Customized Solution Hybridization Enrichment Panels: From A Single Gene To An Entire Exome- Design, Usage, And How To Increase Your Odds For A Successful Outcome

Scott Rose

Integrated DNA Technologies, United States of America; srose@idtdna.com

15:30 High-Throughput Single-Cell Sequencing Library Generation Using Nextera And The LabCyte ECHO 525

Stephan Lorenz

Wellcome Trust Sanger Institute, United Kingdom; sl11@sanger.ac.uk

16:00 – 16:30 Coffee break & Networking

16:30 Inferring Ribosome Dynamics From mRNA Degradome Sequencing.

Vicent Pelechano¹, Wu Wei^{2,3}, Lars M Steinmetz^{1,2,3}

¹European Molecular Biology Laboratories, Genome Biology Unit, Germany; ²Stanford Genome Technology Center, Stanford University, USA; ³Department of Genetics, Stanford University School of Medicine; pelechan@embl.de

17:00 Sample to Insight - analysis, visualization and interpretation of next generation sequencing and gene expression data

Anne Arens

QIAGEN GmbH, Germany; anne.arenis@qiagen.com

17:30 High resolution NGS-based HLA-typing using in-solution targeted enrichment

Michael Wittig¹, Jarl Andreas Anmarkrud^{2,3,4}, Jan Christian Kässens⁵, Simon Koch⁶, Michael Forster¹, Eva Ellinghaus¹, Johannes E.R. Hov^{2,4,7}, Sascha Sauer⁸, Manfred Schimmler⁵, Malte Ziemann⁹, Siegfried Görg⁹, Frank Jacob⁶, Tom Hemming Karlsen^{2,4,7}, Andre Franke¹

¹Christian-Albrechts-University Kiel, Institute of Clinical Molecular Biology, ²Norwegian PSC Research Center, Department of Transplantation Medicine, ³K.G. Jebsen Inflammation Research Center, Institute of Clinical Medicine, ⁴Research Institute of Internal Medicine, ⁵Christian-Albrechts-University of Kiel, Department of Computer Science, ⁶Muthesius Academy of Fine Arts and Design, ⁷Section of Gastroenterology, Department of Transplantation Medicine, ⁸Max-Planck Institute for Molecular Genetics, Berlin; ⁹University of Lübeck, Institute of Transfusion Medicine, Lübeck, Germany; m.wittig@mucosa.de

18:00 – 22:00 Evening Poster Session

18:00 – 22:00 **Networking Reception in Industrial Exhibition**

Tuesday 24th March 2015

Digital PCR

Tuesday, 24/Mar/2015: *Location:*
8:30am - 10:30am *Lecture hall 14*
Session Chair:
Jim Francis Huggett
Tim Forshew

Presentations

8:30 Keynote Lecture:

How could digital PCR benefit clinical analysis?

Jim Francis Huggett

LGC, United Kingdom; jim.huggett@lgcgroup.com

9:00 Rapid and Ultra-Sensitive Single-Cell Transcript Profiling with Droplet Digital PCR (ddPCR™): Application to neural induction

Svilen Tzonev

Digital Biology Center, Bio-Rad, United States of America; Svilen_Tzonev@bio-rad.com

9:30 NGS and dPCR Analysis of Circulating Tumour DNA and Their Potential Uses in Cancer Patient Care

Tim Forshew

UCL, United Kingdom; t.forshew@ucl.ac.uk

10:00 Droplet generation for NGS library preparation and for digital PCR on the same instrument

Sabit Delic, Manja Meggendorfer, Niroshan Nadarajah, Wolfgang Kern, Torsten Haferlach

MLL Münchner Leukämie Labor GmbH, Germany; sabit.delic@mll.com

10:30 – 11:00 Coffee break & Networking

Non-coding RNAs 1

Tuesday, 24/Mar/2015: *Location:*
11:00am - 12:30pm *Lecture hall 14*
Session Chair:
Jo Vandesompele
Robert Sjöback

Presentations

11:00 Keynote Lecture:

Updated evaluation of quantitative miRNA expression platforms in the microRNA quality control (miRQC) study

Pieter Mestdagh, Jo Vandesompele

Ghent University / Biogazelle, Belgium (on behalf of the microRNA quality control study consortium); joke.vandesompele@ugent.be

- 11:30 MicroRNA profiling using a rapid, highly sensitive qPCR panel**
Simon Baker¹, Lihan Zhou², Florent Chang Pi Hin¹, Ruiyang Zou², Heng-Phon Too²
¹Bioline Reagents Ltd, United Kingdom; ²MIRXES Pte. Ltd, Singapore; Simon.Baker@bioline.com
- 12:00 Fast and flexible bioinformatics analysis of RNA seq data to provide biological insight**
Jesper Culmsee Tholstrup
 EXIQON, Denmark; jet@exiqon.com

12:30 – 14:00 **Lunch in the student cafeteria**

12:30 – 14:00 **Lunch Poster Session**

Life Technologies: Lunch-time seminars

Tuesday, 24/Mar/2015: *Location:*
1:00pm - 2:00pm **Lecture hall 14**
Session Chair:
Thomas Schild

Presentations

- 13:00 Digital PCR analysis of tumor-specific mutations from peripheral blood in ER positive breast cancer samples**
Atocha Romero
 Hospital Universitario Puerta de Hierro, Spain; atocha10@hotmail.com
- 13:30 Highly sensitive amplicon-based RNA quantification by Ion Torrent Proton semiconductor sequencing.**
Ulrich Certa
 Hoffmann-La Roche AG, Switzerland; ulrich.certa@roche.com

Biomarker Discovery & Circulating Nucleic Acids

Tuesday, 24/Mar/2015: *Location:*
2:00pm - 6:30pm **Lecture hall 14**
Session Chair:
Stephen Andrew Bustin
Michael W. Pfaffl

Presentations

- 14:00 Keynote Lecture:**
Mass Spectrometry Based Draft Of The Human Proteome
Bernhard Kuster
 TU München, Germany; kuster@tum.de
- 14:30 CircRNA: a new class of non-coding ribonucleic acid molecules**
Stanislas Werfel
 Technische Universität München, Germany; werfel@ipt.med.tum.de
- 15:00 From Serum to Saliva Diagnostics – Comparative Studies on Circulating Biomarkers**
Manuela Hofner, Florian Sammer, Linda Stöger, Isabella Riegler-Stocker, Suzana Ilic, Johana Luna-Coronell, Veronika Triebel, Klemens Vierlinger, Andreas Weinhäusel, Christa Nöhammer
 AIT Austrian Institute of Technology, Austria; christa.noehammer@ait.ac.at

- 15:30 Proximity Ligation Assay for the specific detection of *Aspergillus* species**
Gemma Johnson¹, Mark Shannon², Christopher Thornton³, Samir Agrawal⁴, Cornelia Lass-Flörl⁵, Wolfgang Mutschlechner⁵, Stephen Bustin¹
¹Postgraduate Medical Institute, Faculty of Medical Science, Anglia Ruskin University, UK; ²Thermo Fisher Scientific, USA; ³School of Biosciences, University of Exeter, UK; ⁴Blizard Institute of Cellular and Molecular Science, Queen Mary University, London, UK; ⁵Division of Hygiene and Medical Microbiology, Innsbruck Medical University, Innsbruck, Austria; gjohnson82@gmail.com

16:00 – 16:30 Coffee break & Networking

- 16:30 Extracellular Vesicles As Disease Biomarkers?**
Mercedes Tkach^{1,2}, Joanna Kowal^{1,2}, Clotilde Thery^{1,2}
¹Institut Curie Section recherche, Paris, France; ²INSERM U932, Paris, France; mercedes.tkach@curie.fr
- 17:00 Cell to Cell Communication via extracellular RNA and Exosomes**
Michael W Pfaffl
 TUM, Germany; michael.pfaffl@wzw.tum.de
- 17:30 Exosomes – A novel approach to biomarker identification**
Constanze Kindler¹, Jonathan Shaffer²
¹QIAGEN GmbH, Germany; ²QIAGEN Sciences; constanze.kindler@qiagen.com
- 18:00 RT-qPCR based screening of blood-circulating microRNAs for the identification of biomarkers and novel drug targets**
Matthias Hackl¹, Sylvia Weilner¹, Susanna Skalicky¹, Rita Reynoso², Natalia Laufer³, Heribert Stoiber⁴, Peter Dovjak⁵, Peter Pietschmann⁶, Johannes Grillari^{1,2}
¹TAmiRNA GmbH, Muthgasse 18, 1190 Vienna, Austria; ²Department of Biotechnology, University of Natural Resources and Life Sciences Vienna, Vienna, Austria; ³CONICET, Buenos Aires, Argentina; ⁴Division of Virology, Innsbruck Medical University, Innsbruck, Austria; ⁵Salzkammergutklinikum Gmunden, Austria; ⁶Department of Pathophysiology and Allergy Research, Medical University Vienna, Austria; matthias.hackl@tamirna.com

19:30 – 24:00 Symposium Gala Dinner

Location: **Bräustüberl Weihenstephan**
 Weihenstephaner Berg 10
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 Music & Dancing & Cocktails
www.Braeustueberl-Weihenstephan.de



Tuesday 24th March 2015**Next Generation Sequencing 2**

Tuesday, 24/Mar/2015: *Location:*
 8:30am - 10:30am **Lecture hall 15**
Session Chair:
 Karen E. Nelson
 Michael W. Pfaffl

Presentations

- 8:30 Keynote Lecture:**
Next Generation Sequencing Applications to the study of human and animal Microbiomes.
Karen E. Nelson
 J. Craig Venter Institute, United States of America; karennel@gmail.com
- 9:00** **DNA-based Food Authenticity and Safety Control using Advanced Barcoding by Next Generation Sequencing**
Ilka Haase, Christine Käppel, Elmar Schilling
 Eurofins Genomics, Germany; ilkaahaase@eurofins.com
- 9:30** **Integrative Analyses of Primary and Relapse Tumor Samples Identifies Genomic Changes During Cancer Progression**
Alexander Schramm
 University Hospital Essen, Germany; alexander.schramm@uni-due.de
- 10:00** **Microbiomes via sequencing: Challenges and opportunities**
Thomas Clavel
 Junior Research Group Intestinal Microbiome, TU München, Germany; thomas.clavel@tum.de

10:30 – 11:00 **Coffee break & Networking**

NGS data analysis

Tuesday, 24/Mar/2015: *Location:*
 11:00am - 12:30pm **Lecture hall 15**
Session Chair:
 Robert P. Loewe
 Michael W. Pfaffl

Presentations

- 11:00** **Benchmarking of RNA-seq data processing pipelines using whole transcriptome qPCR expression data**
Jan Hellemans¹, Jo Vandesompele^{1,2}, Pieter Mestdagh^{1,2}
¹Biogazelle, Belgium; ²CMGG, UGent, Belgium; jan.hellemans@biogazelle.com
- 11:30** **Chances and challenges in RNA-Seq analysis**
Matthias Scherf, **Martin Seifert**
 Genomatix, Germany; seifert@genomatix.de
- 12:00** **RNAseq data analysis: getting more insight by combining it with public RNAseq experiments**
Philip Zimmermann
 Nebion AG, Switzerland; phz@nebion.com

12:30 – 14:00 **Lunch in the student cafeteria**

12:30 – 14:00 **Lunch Poster Session**

Agilent Technologies: Lunch-time seminars

Tuesday, 24/Mar/2015: *Location:*
 1:00pm - 2:00pm **Lecture hall 15**
Session Chair:
 Raza Ahmed
 Bernd Martin

Presentations

- 13:00** **High Resolution Melting – How To Produce Highly Reproducible Measurements**
Robert P. Loewe
 GeneWake GmbH, Germany; robert.loewe@genewake.com
- 13:30** **Total Confidence qPCR – The New AriaMX Real-Time PCR System**
Bernd Martin
 Agilent Technologies, Germany; bernd.martin@agilent.com

Microgenomics & Single-Cell Diagnostics

Tuesday, 24/Mar/2015: *Location:*
 2:00pm - 6:30pm **Lecture hall 15**
Session Chair:
 Anders Ståhlberg
 Mikael Kubista

Presentations

- 14:00** **Keynote Lecture:**
Expression Profiling of Circulating Tumor Cells: a Prognostic and Predictive Biomarker in Cancer.
Mikael Kubista^{1,2}, Robert Sjöback¹, Marie Jindrichova², Eva Rohlova¹, Vendula Novosadová^{1,2}, Siegfried Hauch³, Katarina Kolostova⁴, Bahriye Aktas⁵, Mitra Tewes⁵, Maren Bredemeier⁵, Sabine Kasimir-Bauer⁵
¹TATAA Biocenter, Sweden; ²Institute of Biotechnology, CAS, Czech Republic; ³AdnaGen; ⁴Charles University; ⁵University Hospital Essen; mikael.kubista@tataa.com
- 14:30** **Analyzing Function And Gene Expression Of Individual Dopamine Neurons - Form Mice To Men.**
Birgit Liss
 Birgit Liss, Department of Applied Physiology, University of Ulm, Albert Einstein Allee 11, 89081 Ulm, Germany.; birgit.liss@uni-ulm.de
- 15:00** **From Cultures to Results in One Day: A New Workflow for Accurate and Reproducible Large Scale qPCR Expression Analysis from Limited Samples in Stem Cell Research**
Mark Kibbschull¹, Stephen Lye^{1,2,3}, Steven Okino⁴, Haya Sarra⁵
¹Lunenfeld-Tanenbaum Research Institute, Mount Sinai Hospital, Toronto, Canada; ²Departments of OBS/GYN, Physiology, and Medicine, University of Toronto, Toronto, Canada; ³Fraser Mustard Institute for Human Development, University of Toronto, Toronto, Canada; ⁴Gene Expression Division, Life Science Group, Bio-Rad Laboratories, Hercules, United States; ⁵Gene Expression Division, Life Science Group, Bio-Rad Laboratories, Mississauga, Canada; kibbschull@lunenfeld.ca

15:30 Feasibility of a workflow for the molecular characterization of single Circulating Tumor Cells by Next Generation Sequencing.

Francesca Salvianti¹, Giada Rotunno², Francesca Galardi³, Francesca De Luca³, Marta Pestrin³, Alessandro Maria Vannucchi², Angelo Di Leo³, Mario Pazzagli¹, Pamela Pinzani¹

¹Department of Clinical, Experimental and Biomedical Sciences, University of Florence, Florence Italy.; ²Department of Clinical and Experimental Medicine, University of Florence, Florence Italy; ³Sandro Pitigliani Medical Oncology Department, Hospital of Prato, Istituto Toscano Tumori, Prato, Italy; p.pinzani@dfc.unifi.it

16:00 – 16:30 Coffee break & Networking

16:30 Single-cell analysis of Myxoid liposarcoma reveals novel subpopulations and dysfunctional cell cycle regulation

Anders Ståhlberg

University of Gothenburg, Sweden; anders.stahlberg@gu.se

17:00 From a ton of RNA to a single cell - Challenges for a Sequencing core lab to achieve robust Transcriptome Profiling

Andreas Dahl¹, Sylke Winkler², Sylvia Klemroth¹, Annekathrin Kränkel¹, Yannick Dupont^{1,2}, Susanne Reinhardt¹, Mathias Lesche¹

¹BIOTEchnology Center, Technische Universität Dresden, Germany; ²Max Planck Institute for Molecular Cell Biology, Dresden; andreas.dahl@biotec.tu-dresden.de

17:30 G&T-seq: Separation and parallel sequencing of the genomes and transcriptomes of single cells

Iain Macaulay¹, Wilfried Haerty², Parveen Kumar³, Yang Li², Tim Hu², Mabel Teng¹, Niels van der Aa³, Paul Coupland¹, Chris Ponting^{1,2}, Thierry Voet^{1,3}

¹Sanger Institute, United Kingdom; ²MRC Functional Genomics Unit, Oxford; ³KU Leuven; im2@sanger.ac.uk

18:00 Intracellular molecular gradients within *Xenopus laevis* oocytes prepare the cell for asymmetric division

Radek Sindelka, Monika Sidova, Mikael Kubista
IBT AS CR, Czech Republic; sindelka@ibt.cas.cz

19:30 – 24:00 Symposium Gala Dinner

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Wednesday 25th March 2015

Optimisation, MIQE & QC strategies in qPCR

Wednesday, 25/Mar/2015:

Location:

8:30am - 12:50pm

Lecture hall 14

Session Chair:

Tania Nolan

Afif M. Abdel Nour

Presentations

8:30 Keynote Lecture:

Variability of the Reverse Transcription Step: Practical Implications

Stephen Bustin^{2,1}, Harvinder Dhillon², Sara Kirvell², Christina Greenwood², Michael Parker², Gregory Shipley^{4,1}, Tania Nolan^{1,3}

¹The Gene Team, United Kingdom; ²Postgraduate Medical Institute, Anglia Ruskin University, Cambridge, UK; ³Institute of Population Health, University of Manchester, Manchester UK; ⁴Shipley Consulting, LLC, Austin, Texas, USA; tania.nolan@geneteamconsultants.com

9:00 qScript XLT cDNA SuperMix: overcoming the common pitfalls of cDNA synthesis as applied to relative quantification and RT-qPCR.

David Mark Schuster, Yun Feng

Quanta BioSciences, United States of America; dave.schuster@quantabio.com

9:30 New tools for quality assessment of RNA in Molecular Diagnostics

Jens Björkman¹, David Švec^{1,2}, Robert Sjöback¹, Emelie Lott¹, Mikael Kubista^{1,2}

¹TATAA Biocenter AB, Sweden; ²Laboratory of Gene Expression, Institute of Biotechnology, Academy of Sciences of the Czech Republic, Prague, Czech Republic; jens.bjorkman@tataa.com

10:00 – 10:30 Coffee break & Networking

10:30 ThermaStop™: Properties and Benefits

Alexandra Isabel Over¹, Lawrence Wagh²

¹Biosearch Technologies, United States of America; ²Brandeis University, USA; AlexOver@brandeis.edu

11:00 Engineered DNA Polymerases

Ramon Kranaster

myPOLs Biotec UG (haftungsbeschränkt), Universitätsstr. 10, 78457 Konstanz, Germany, www.mypols-biotec.com, T +49(0)7531 884654; ramon.kranaster@mypols.de

11:30 Reducing time and error rates by automating qPCR workflows

Matjaz Hren¹, Kristina Gruden², Klemen Zupančič¹, Nataša Mehle², Manca Pirc^{1,2}, Urška Čepin¹, Maja Ravnikar²

¹BioSistemika LLC, Slovenia; ²National Institute of Biology, Slovenia; matjaz.hren@biosistemika.com

12:00 Middleware Solutions To Improve Molecular Diagnostics; Connectivity, Quality Control And Lean Processes

HGM Niesters¹, F Klein¹, J Poodt²

¹Department of Medical Microbiology, Division of Clinical Virology, UMC Groningen; ²LabHelp, Bladel, The Netherlands; h.g.m.niesters@umcg.nl

12:30 Digital publication: how making the MIQE guidelines easier to follow.**Afif M. Abdel Nour¹, Michael W. Pfaffl²**¹Bio-Rad, United Arab Emirates; ²TUM Physiology, Freising, Germany; iBook@bioMCC.com12:30 – 14:00 **Lunch in the student cafeteria**12:30 – 14:00 **Lunch Poster Session****Non-coding RNAs 2****Wednesday, 25/Mar/2015:****2:00pm - 4:30pm***Session Chair:***Pieter Mestdagh****Robert Sjöback***Location:***Lecture hall 14****Presentations****14:00 Keynote Lecture:****Decoding lncRNA functions using high-throughput pathway perturbation.****Pieter Mestdagh, Jan Hellemans, Ariane De Ganck, Jo Vandesompele**Biogazelle, Belgium; pieter.mestdagh@biogazelle.com**14:30 New sensitive and specific method for microRNA analysis****Robert Sjöback¹, Lukáš Valihrach², Mikael Kubista^{1,2}**¹TATAA Biocenter AB, Sweden; ²Institute of Biotechnology, CAS, Czech Republic; robert.sjback@tataa.com**15:00 MiRNA Profiling In Tumor Tissue, Body Fluids And Exosomes - A Combinational Techniques Approach Of NGS And QPCR.****Robert P. Loewe**

GeneWake GmbH,

Germany; robert.loewe@genewake.com**15:30 Development and Optimisation of PCR Assays to Analyse MicroRNAs and their Target Genes****David Arthur Simpson**Queen's University Belfast, United Kingdom; david.simpson@qub.ac.uk**16:00 Improved Small RNA Library Preparation Workflow for Next Generation Sequencing****Sabrina Shore, Jordana Henderson, Anton McCaffrey, Gerald Zon, Richard Hogrefe**TriLink Biotechnologies, United States of America; sshore@trilinkbiotech.com**Closing of the Symposium****Lecture hall HS 14**16:30 **Closing of the Symposium & Farewell**

Michael W. Pfaffl

Sylvia Pfaffl

Wednesday 25th March 2015**qPCR BioStatistics & Bioinformatics****Wednesday, 25/Mar/2015:****8:30am - 12:30pm***Session Chair:***Jan Ruijter****Stefan Rödiger***Location:***Lecture hall 15****Presentations****8:30 Removal of Between-Plate Variation in qPCR with Factor Correction: Completion of the Analysis Pipeline Supported by RDML.****Jan Ruijter¹, Jan Hellemans², Adrian Ruiz-Villalba¹, Maurice van den Hoff¹, Andreas Untergasser³**¹Academic Medical Center, the Netherlands; ²Biogazelle, Belgium; ³Heidelberg University, Heidelberg, Germany; j.m.ruijter@amc.uva.nl**9:00 Unexpected System-specific Periodicity In Quantitative Real-Time Polymerase Chain Reaction Data And Its Impact On Quantification****Andrej-Nikolai Spiess¹, Stefan Rödiger², Thomas Volksdorf³, Joel Tellinghuisen⁴**¹Department of Andrology, University Hospital Hamburg-Eppendorf, Germany; ²Faculty of Natural Sciences, BTU Cottbus – Senftenberg, Cottbus, Germany; ³Department of Dermatology, University Hospital Hamburg-Eppendorf, Germany; ⁴Department of Chemistry, Vanderbilt University, Nashville, Tennessee, USA; a.spiess@uke.de**9:30 The PrimerBank database: an analysis of high-throughput primer validation.****Athanasia Spandidos^{1,2,3}, Xiaowei Wang^{1,2,4}, Huajun Wang^{1,2}, Brian Seed^{1,2}**¹Center for Computational and Integrative Biology, Massachusetts General Hospital, Boston, MA; ²Department of Genetics, Harvard Medical School; ³Current address: 1st Department of Pathology, National and Kapodistrian University of Athens, Athens, Greece.; ⁴Current address: Division of Bioinformatics and Outcomes Research, Department of Radiation Oncology, Washington University School of Medicine, St Louis, MO.; a.spandidos@gmail.com10:00 – 10:30 **Coffee break & Networking****10:30 Occurrence of unexpected PCR artefacts warrants thorough quality control****Adrián Ruiz-Vilalba¹, Bep van Pelt-Verkuil², Quinn Gunst¹, Maurice van den Hoff¹, Jan Ruijter¹**¹Department of Anatomy, Embryology and Physiology, Academic Medical Centre (AMC), Amsterdam, The Netherlands; ²Department of Innovative Molecular Diagnostics, University of Applied Sciences, Leiden, the Netherlands; a.ruizvilalba@amc.nl**11:00 Impact of Smoothing on Parameter Estimation in Quantitative DNA Amplification Experiments****Stefan Rödiger¹, Andrej-Nikolai Spiess², Michal Burdukiewicz³**¹BTU Cottbus - Senftenberg, Senftenberg, Germany; ²University Medical Center Hamburg-Eppendorf, Hamburg, Germany; ³University of Wroclaw, Wroclaw, Poland; Stefan.Roediger@b-tu.de**11:30 RDML qPCR Data Format - Ready For The Next Level?****Andreas Untergasser¹, Steve Lefever², Jasper Anckaert², Jan M Ruijter³, Jan Hellemans⁴, Jo Vandesompele^{2,4}**¹University of Heidelberg, Heidelberg, Germany; ²Ghent University, Ghent, Belgium; ³Academic Medical Center, Amsterdam, The Netherlands; ⁴Biogazelle, Zwijnaarde, Belgium; andreas@untergasser.de**12:00 RDML Consortium Meeting****Andreas Untergasser** and coworkers

On behalf of the RDML consortium

12:30 – 14:00 [Lunch in the student cafeteria](#)

12:30 – 14:00 [Lunch Poster Session](#)

BDQ Editors Board Meeting

Wednesday, 25/Mar/2015: *Location:*
 12:30pm – 1:30pm **Lecture hall 15**
Session Chair:
 Stephen Andrew Bustin
 Helen Habernickel

BDQ Poster Awards

Wednesday, 25/Mar/2015: *Location:*
 1:45pm - 2:00pm **Lecture hall 15**
Session Chair:
 Stephen Andrew Bustin
 Helen Habernickel

Molecular Diagnostics in Agriculture, Veterinary Medicine, Food & Environmental Science

Wednesday, 25/Mar/2015: *Location:*
 2:00pm - 4:30pm **Lecture hall 15**
Session Chair:
 Irmgard Riedmaier-Sprenzel
 Michael W. Pfaffl

Presentations

14:00 Comparison of Different RNA Sources to Examine the Lactating Bovine Mammary Gland Transcriptome using RNA-Sequencing

Angela Canovas¹, Claudia Bevilacqua², Gonzalo Rincon¹, Pauline Brenaut², Alma Islas-Trejo¹, Russell C. Hovey¹, Marion Boutinaud³, Caroline Morgenthaler², Monica K. VanKlombenberg¹, Juan F. Medrano¹, **Patrice D. Martin²**

¹Department of Animal Science, University of California-Davis, One Shields Avenue, Davis, 95616, CA, USA; ²Institut National de la Recherche Agronomique,

UMR 1313 Génétique animale et Biologie intégrative, F-78350 Jouy-en-Josas, France; ³INRA, AGROCAMPUS OUEST, UMR1348 PEGASE, F-35590 Saint-Gilles, France; patrice.martin@jouy.inra.fr

14:30 Optimized library preparation for sequencing of whole bacterial genomes and low density microbiota by Illumina-based NGS

Mareike Wenning, Christopher Huptas, Manuela Schreiner, Siegfried Scherer

Lehrstuhl für Mikrobielle Ökologie, Zentralinstitut für Ernährungs- und Lebensmittelforschung, Technische Universität München; mareike.wenning@wzw.tum.de

15:00 Transcriptomic Biomarkers in Food Safety: RNA Biomarkers against the abuse of growth promoters

Irmgard Riedmaier-Sprenzel, Melanie Spornraft, Michael, W. Pfaffl

TUM Physiology, Germany; irmgard.riedmaier@wzw.tum.de

15:30 Challenges in Detection of Genetically Modified Organisms

Mojca Milavec, David Dobnik, Jana Žel

National Institute of Biology, Slovenia; mojca.milavec@nib.si

16:00 A Transcriptomic Approach To Ascertain Insights Into The Etiology Of Brown Trout Syndrome

Marc Young¹, Jens-Eike Taubert¹, Juergen Geist², Michael W. Pfaffl³, Ralph Kuehn¹

¹Unit of Molecular Zoology, Chair of Zoology, Department of Animal Science, TUM; ²Aquatic Systems Biology Unit, Department of Ecology and Ecosystem Management, TUM; ³Physiology Weihenstephan, Department of Animal Sciences, TUM; marc.young@tum.de

Closing of the Symposium **Lecture hall HS 14**

16:30 **Closing of the Symposium & Farewell**
 Michael W. Pfaffl
 Sylvia Pfaffl

Thursday 26th March & Friday 27th March 2015

The workshops are aimed at giving participants a deep and objective understanding of real-time quantitative PCR, Next Generation Sequencing, biostatistics, expression profiling, digital-PCR, and its applications. The courses are intended for academic or industrial persons considering working with qPCR and/or NGS or scientists currently working with these technologies seeking a deeper understanding. All qPCR workshops offer extensive hands-on training by qPCR or NGS experts in the field. The qPCR workshops on 26th and 27th March (9 am – 5 pm) are hosted by TATAA Biocenter (www.TATAA.com) or Bio-Rad (www.Bio-Rad.com). The NGS data analysis workshop on 26th and 27th March (9 am – 5 pm) are hosted by Genomatix (www.Genomatix.com) and Qiagen (www.Qiagen.com).

Workshop topics:

- **Basic real-time qPCR Application Workshop** (2-days)
hosted by TATAA Biocenter (Seminar room – S3)
- **qPCR Data Analysis Workflow: from instrument data to interpretation** (2-days)
hosted by TATAA Biocenter (Computer seminar room – PU26)
- **digital PCR** (2-days)
hosted by Bio-Rad (Seminar room – S1)
- **NGS data analysis workshop** (2-days)
hosted by Genomatix (Computer seminar room – PU26A - GIS room)
- **“Sample to Insight” Analyzing and interpreting the biological meaning in NGS data** (2-days)
hosted by Qiagen (Computer seminar room – HU34A)



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