20-21 October 2015, London, UK

Global Engage Ltd

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3rd qPCR and Digital PCR Congress

DEVELOPMENTS & POTENTIAL OF qPCR & dPCR AS A TOOL FOR PROGRESSING MOLECULAR BIOLOGY RESEARCH

Following on from last year's sell-out event, Global Engage is pleased to announce the 3rd qPCR & Digital PCR Congress, which will be held on 20-21 October in London, United Kingdom at the Radisson Blu Heathrow Hotel and co-located with our 2nd Synthetic Biology Congress & inaugural Microfluidics Congress.

Bringing together over 300 industry and academic experts working in areas such as molecular biology/diagnostics, gene expression, genomics, biomarkers, pathogen detection, GMO, mRNA, NGS, bioinformatics and data management, the congress will examine the latest developments, opportunities and applications of both dPCR and qPCR through case studies across diverse areas such as oncology, virology, infectious diseases, vaccines, prenatal diagnostics, clinical applications, microbiology, food microbiology, microfluidics and other novel applications.

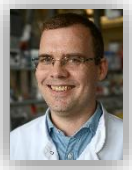
With increasing numbers of real-time PCR users purchasing digital PCR due to its reduction in cost, absolute quantification, improved sensitivity, precision and greater robustness; and with the gene amplification market predicted to grow to $2.2 billion by 2017, this conference provides a timely opportunity to learn first-hand about dPCR whilst also keeping up to date with latest developments and strategies in qPCR.

The conference will provide an interactive networking forum to both further develop and answer your queries through a vibrant exhibition room full of technology providers showcasing their technologies and other solutions, poster presentation sessions, expert led case study presentations and interactive Q&A panel discussions from a 50-strong speaker faculty examining topics on four separate tracks covering:

Confirmed Speakers Include:

Nickolas Papadopoulos
Professor, Department of Oncology & Director of Translational Genetics, Sidney Kimmel Comprehensive Cancer Center, Johns Hopkins University

Jim Huggett
Science Leader, Nucleic Acid Metrology, Molecular & Cell Biology, LGC



Boris Fehse
Professor, Department of Stem Cell Transplantation, Research Dept. Cell and Gene Therapy, University Medical Center (UMC) Hamburg-Eppendorf, Germany

Conference Synopsis

Day 1 – Stream One

Digital PCR: Applications and Possibilities

- Introduction, benefits, future development of dPCR
- Converting to dPCR from qPCR
- Oncology (rare variant detection, monitoring therapy response, early relapse detection, biomarkers for cancer detection etc.)
- Verifying accuracy of dPCR data
- Complimenting digital PCR with other technologies
  - o NGS v dPCR – Advantages over NGS
- Detection of patient-specific mutations
- Multiplexing in digital PCR
- Applications of precision medicine

Day 1 – Stream Two

qPCR: Strategies & Developments

- MIQE guidelines & standardisation
- qPCR/RT-PCR assay design, optimisation & validation
- Sample preparation & quality control
- Detection, quantification and sequencing of RNA
- Precise quantification of nucleic acids
- Amplification curve analysis/automated analysis of qPCR data/challenges & new solutions for data analysis
- Bioanalytics
- Single cell analysis

Day 2 - Stream One

qPCR & Digital PCR Case Studies

- Clinical/Diagnostic applications
- dPCR & its effect on patient care
- qPCR/dPCR in diagnosis of neurological disorders
- Molecular diagnostics
- Micro RNA/ncRNA/siRNA applications
- Infectious diseases/vaccines/environmental sampling
- Non-invasive prenatal diagnostics
- Gene expression
- Microfluidics and Lab-on-a-Chip
- Microfluidic design and flow control

Day 2 – Stream Two

Plant, Food and Environmental Case Studies

- qPCR in plant research
- Applications on plant breeding
- Detection and identification of plant and food pathogens
- Gene expression analysis
- qPCR in food research
- GMO quantification in food

For more information please contact Steve Hambrook, Conference Director, Global Engage Ltd.

steve@globalengage.co.uk **+44 (0) 1865 849841**

Confirmed Speakers

Tim Forshew
Senior Research Associate, Cancer Institute, University College London, UK

Marta Prado
Staff Researcher, INL - International Iberian Nanotechnology Laboratory, Portugal

Karen Kempsell
Senior Project Team Leader, Public Health England, UK

Paul Dark
Associate Professor in Inflammation and Repair, University of Manchester, UK

Thomas Barry
Lecturer, Nucleic Acid Diagnostics Research Laboratory, National University of Ireland, Galway

David Dobnik
Researcher, Department of Biotechnology and Systems Biology, National Institute of Biology, Slovenia

Christa Noehammer
Senior Scientist, Molecular Diagnostics, Austrian Institute of Technology (AIT), Austria

Evi Lianidou
Professor of Analytical Chemistry - ACTC Lab, University of Athens, Greece

Jorg Tost
Head, Laboratory for Epigenetics and Environment (LEE), CNG - Centre National de Génotypage, CEA - Institut de Génomique, France

Andrew Brooks
Chief Operating Officer, RUCDR Infinite Biologics and Director of the Bionomics Research and Technology Center, Rutgers University, USA

Petr Obrdlik
Functional Lead, Novartis Biologics Process R&D

Nickolas Papadopoulos
Professor of Oncology & Director of Translational Genetics, Sidney Kimmel Comprehensive Cancer Center, Johns Hopkins University, USA

Olivier Thas
Professor in Statistics, Ghent University, Belgium and University of Wollongong, Australia

Ann Cuypers
Professor, Centre for Environmental Sciences, Hasselt University, Belgium

Marcus Frohme
Professor, Technical University of Applied Sciences Wildau, Germany

Paul Moss
Professor of Haematology & Head of School of Cancer Sciences, University of Birmingham, UK

Sofia Forssten
Senior Scientist/Docent, DuPont/University of Turku, Finland

Boris Fehse
Professor, Department of Stem Cell Transplantation, Research Dept. Cell and Gene Therapy, University Medical Center (UMC) Hamburg-Eppendorf, Germany

Sílvia Coimbra
Professor, Department of Biology, University of Porto, Portugal

Susanna Engberg
Senior Research Scientist, AstraZeneca, Sweden

Marie Follo
Head of Core Facility, Department of Medicine, Freiburg University Medical Center, Germany

Jacqui Shaw
Professor of Translational Cancer Genetics, University of Leicester, UK

Jim Huggett
Science Leader, Nucleic Acid Metrology, Molecular & Cell Biology, LGC

Lakis Liloglou
Senior Lecturer, Institute of Translational Medicine, Dept of Molecular & Clinical Cancer Medicine, University of Liverpool, UK

Attila Lorincz
Professor of Molecular Epidemiology, Wolfson Institute of Preventive Medicine, UK [Session Chair]

Bert Niesters,
Professor in Molecular Diagnostics. Director, Laboratory of Clinical Virology, University Medical Center Groningen, The Netherlands

Petra Wolffs
Assistant Professor & Head of Unit Molecular Diagnostics, Maastricht University Medical Center, The Netherlands

Paul Dear
Team Leader, Single Molecule Genomics Group, MRC Laboratory of Molecular Biology, Cambridge, UK

Hege Russness
Researcher/Senior Consultant, Institute for Clinical Medicine/Dept. of Pathology, Oslo University Hospital, Norway

Špela Baebler
Research Associate, Department of Biotechnology and Systems Biology, National Institute of Biology, Slovenia

Also Speaking:

Tho Huu Ho, Senior Researcher, Department of Genomics and Cytogenetics, Biomedical Pharmaceutical Applied Research Centre, Vietnam Military Medical University, Vietnam

Senior Representative, Bio-Rad Laboratories

Senior Representative, RainDance Technologies

Ward De Spiegelaere, Post-Doctoral Fellow, University of Gent, Belgium

Mary Alikian, Research Assistant, Department of Medicine, Imperial College London, UK

Senior Representative, Formulatrix

Senior Representative, Integrated DNA Technologies

Jon West, Senior Research Scientist, Plant Biology & Crop Science, Rothamsted Research, UK

Senior Representative, Agilent Technologies

Jean Ruelle, Researcher, UCL - Université Catholique de Louvain, Belgium

Antoon Lievens, Researcher, Molecular Biology and Genomics Unit, European Commission - Joint Research Centre, Italy

Eric Abachin, Head, Microbiology R&D, Sanofi Pasteur, France [RESERVED]

Senior Representative, Thermo Fisher Scientific

Stefan Rödiger, Group Leader, BTU Cottbus – Senftenberg, Germany

Blanca Landa, Research Scientist, Institute for Sustainable Agriculture (IAS), CSIC, Spain

Senior Representative, Stilla Technologies

Pascale Tomasini, Assistance Publique Hôpitaux de Marseille, France

Senior Representative, Agilent Technologies

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TECHNE

For more information please contact Steve Hambrook, Conference Director, Global Engage Ltd.

steve@globalengage.co.uk +44 (0) 1865 849841

08.00-08.50	**Registration & Coffee**	
08.50-09.00	**Global Engage Welcome Address & Chairperson's Opening Remarks** **Chairperson:** Stefan Rödiger, Group Leader, BTU Cottbus – Senftenberg, Germany	
09.00-09.35	Keynote Address: **Detection of Rare Mutations in Biological Fluids in the Management of Cancer** Somatic mutations are cancer specific biomarkers. Detection of such mutations present in circulating tumor DNA and DNA derived from biological fluids has shown great promise for the development of non-invasive diagnostic tests that aid in the management of cancer patients. However, there are both technical and biological challenges for the development of noninvasive DNA-based diagnostic tests. The number of tumor DNA molecules with somatic mutations present in biological fluids is very low compared to that of DNA molecules with sequence from non-tumor cells and requires very sensitive methods for their detection. To this end, we have developed a method called SafeSeqS that addresses this issue. The presence and amount of tumor derived DNA in biological fluids can vary between different tumor types. To address this, we performed a survey for the detection of circulating tumor DNA in plasma from patients with different tumor types. We present data on different applications of liquid biopsy. Finally, we will present data on the detection of somatic mutations in other biological fluids and their clinical applications. CONFIRMED: **Nickolas Papadopoulos, Professor of Oncology & Director of Translational Genetics, Sidney Kimmel Comprehensive Cancer Center, Johns Hopkins University, USA**	
09.35-10.05	Solution Provider Presentation: **Title To Be Confirmed** CONFIRMED: **Senior Representative, RainDance Technologies**	Platinum Sponsor RainDance Technologies

	Digital PCR Congress	qPCR Congress
10.05-10.10	**Stream Chair:** Stefan Rödiger, Group Leader, BTU Cottbus – Senftenberg, Germany	**Stream Chair:**
10.10-10.35	**Title To Be Confirmed** Digital PCR For Cancer Detection CONFIRMED: **Andrew Brooks, Chief Operating Officer, RUCDR Infinite Biologics and Director of the Bionomics Research and Technology Center, Rutgers University, USA**	**Title To Be Confirmed** CONFIRMED: **Jacqui Shaw, Professor of Translational Cancer Genetics, University of Leicester, UK**
10.35-11.45	**Morning Refreshments and Poster Presentation Session** **One-to-One Networking Meetings**	
11.45-12.10	**GEF-dPCR: A new digital-PCR technique to assess gene-editing frequencies after designer-nuclease treatment** Genome editing using designer nucleases such as TALEN or CRISPR/Cas9 is an emerging technology in basic but also applied research. Whereas generation of gene knockouts has thus become very straightforward, quantification of actual k.o. rates remains a bottleneck, in particular, if the product of a targeted gene cannot be easily detected. To address this problem we devised a novel gene-editing frequency digital PCR (GEF-dPCR) that simultaneously quantifies numbers of edited and non-edited alleles. To this aim, PCR amplicons contain binding sites for two differently labeled Taqman probes, where the first probe binds away from the designer-nuclease cutting site and is thus NHEJ insensitive, whereas the second probe corresponds to the Indel region and is therefore NHEJ sensitive. We have shown that GEF-dPCR facilitates fast, easy, reliable and sensitive assessment of gene knock-out rates after designer-nuclease treatment. CONFIRMED: **Boris Fehse, Professor, Department of Stem Cell Transplantation, Research Dept. Cell and Gene Therapy, University Medical Center (UMC) Hamburg-Eppendorf, Germany**	**From Serum to Saliva Diagnostics – Comparative Studies on DNA-methylation and micro-RNA Biomarkers** The aim of our research activities at AIT, the Austrian Institute of Technology, is to define reliable biomarkers suitable for early and non-invasive disease diagnosis and prognosis. To this end we have been establishing and optimizing a whole range of multiplex capability technologies (e.g. microarrays, quantitative PCR, Luminex bead technology) to meet the special demands and challenges of diagnostic biomarker discovery - and validation in body fluids. Using this specific technology expertise we e.g. successfully discovered autoantibody- as well as DNA methylation -based diagnostic marker panels for the big 4 cancer entities (breast, colon, prostate, lung) in serum or plasma. Based on these success stories and the evident advantages of saliva as a diagnostic matrix our recent special interest is to go for saliva diagnostics and to evaluate saliva for its suitability for circulating biomarker-based diagnostics. Along these lines we will report on first results from comparative studies in serum and saliva on a selection of DNA methylation – as well as microRNA markers in a breast cancer cohort. In addition we will share our experiences made along the evaluation of various saliva sample collection systems, exosome isolation kits as well as qPCR-based microRNA assay formats with respect to microRNA expression profiling in saliva. Last but not least we will present first results which we obtained when comparing microRNA expression in plasma - and saliva-derived exosomes. CONFIRMED: **Christa Noehammer, Senior Scientist, Molecular Diagnostics, Austrian Institute of Technology (AIT), Austria**

12.10-12.35	**Practical Application of Droplet Digital PCR in Hematology/Oncology** We have used droplet digital PCR with the Bio-Rad QX100 system in a clinical setting to: • Develop assays for the detection of circulating tumor DNA (ctDNA) using tumor-specific SNP mutations for patients with solid tumors and to follow these patients over time • Detect JAK2 in patients with myeloproliferative syndromes at the time of first diagnosis, and then followed up with these patients after chemotherapy or transplantation • Measure levels of SRY to detect chimerism in female patients which have received hematopoietic cells from male donors to correlate the detected levels with clinical outcomes	**Title To Be Confirmed** qPCR Standardisation
	CONFIRMED: **Marie Follo, Head, Core Facility, Dept. of Medicine I (Hematology, Oncology and Stem Cell Transplantation), University Medical Center Freiburg, Germany**	CONFIRMED: **Marcus Frohme, Professor, Technical University of Applied Sciences Wildau, Germany**
12.35-13.00	**Digital PCR Analysis of Circulating Tumour DNA in Sarcoma and Childhood Brain Tumours** • Background of circulating tumour DNA analysis • dPCR optimisation for ctDNA analysis • ctDNA results from a large Sarcoma cohort	**qPCR Diagnostics Assay Development for Infectious Disease – Working with Industry - an Academics Perspective** • Research at the NADRL • NADRL qPCR Assay Design and Development Strategies • Benefits and Downsides to Working with Industry • Current qPCR Diagnostics Assay Development
	CONFIRMED: **Tim Forshew, Group Leader, Cancer Institute, University College London, UK**	CONFIRMED: **Thomas Barry, Lecturer, Nucleic Acid Diagnostics Research Laboratory, National University of Ireland, Galway**
13.00-13.30	Solution Provider Presentation: **Title To Be Confirmed** Platinum Sponsor BIO-RAD	Solution Provider Presentation: **Title To Be Confirmed** Platinum Sponsor IDT INTEGRATED DNA TECHNOLOGIES
	CONFIRMED: **Senior Representative, Bio Rad Laboratories**	CONFIRMED: **Senior Representative, Integrated DNA Technologies**
13.30-14.30	**Lunch**	
14.30-14.55	**Title To Be Confirmed**	**Title To Be Confirmed** qPCR & Digital PCR Assays for Vaccine Research
	CONFIRMED: **Jim Huggett, Science Leader, Nucleic Acid Metrology, Molecular & Cell Biology, LGC, UK**	Reserved: **Eric Abachin, Head, Microbiology R&D, Sanofi Pasteur, France**
14.55-15.20	**ddPCR-based Detection of DNA Methylation in Plasma for Early Diagnosis of Lung Cancer** DNA methylation is a fundamental epigenetic modification affecting the expression of mammalian genes and its role in human disease has been clearly illustrated, opening novel diagnostic and therapeutic routes. A large number of PCR-based detection techniques have been developed. From a clinical point of view, the challenge is to enable specific detection of abnormal methylation in clinical samples carrying very few abnormal copies in a high dilution of normal DNA. Digital PCR currently seems to fulfil a lot of the desired analytical characteristics for this task. We developed Droplet Digital methylation specific PCR (ddMSP) assays for a number of targets to be used in plasma, sputum and bronchial washings for early detection of lung cancer. The performance is higher of qMSP. The methodology with key assay design points as well as data on the clinical validation of these assays are presented.	**Highly Sensitive Quantification of Residual DNA in Biotech Products without need for DNA Extraction ("Direct PCR")**
	CONFIRMED: **Lakis Liloglou, Senior Lecturer, Institute of Translational Medicine, Department of Molecular & Clinical Cancer Medicine, University of Liverpool, UK**	CONFIRMED: **Petr Obrdlik, Functional Lead, Novartis Biologics Process R&D**

15.20-15.45

Data Analysis of Droplet Digital PCR with Generalised Linear Mixed Models

Target quantification with droplet digital PCR (ddPCR) depends heavily on the Poisson assumption which makes the data analysis less straightforward than for RT-qPCR. In this talk we demonstrate how a specific class of Generalised Linear Mixed Models (GLMM) can be used for the analysis of ddPCR data. The GLMM statistical modelling framework is very flexible and allows for analysing many experimental designs, including correctly dealing with replicates, run or plate effects and one or more references. The method can be used for absolute quantification, CNV and gene expression, and it allows for standard error and confidence interval calculation and hypothesis testing. Understanding the statistical model may help in improving designs for ddPCR experiments. GLMMs are available in many statistical software. We illustrate the flexibility of the framework using the R software

CONFIRMED:
Olivier Thas, Professor in Statistics, Ghent University, Belgium and University of Wollongong, Australia

MiddleWare Solutions in Molecular Diagnostics: improved Connectivity, Quality Control and LEAN Processes

During the last decades, laboratories have invested large amounts into equipment for molecular diagnostics. However, connectivity between this equipment as well to the Laboratory Information System (LIS), can still be cumbersome. MiddleWare systems are developed to facilitate this connectivity to ensure a proper data management, assist in quality assurance and finally contribute to patient safety. In this presentation, the contribution of a bottom-up developed system, called FlowG, is presented, enabling connectivity of equipment from different companies. Developments of software can be implemented in line with ISO15189:2012 guidelines. With the idea in mind that "the only limitation is your imagination", more ideas and add-ons are implemented into the FlowG concept, with text messaging for critical data, as well as an application (app) to get on-line status updates of equipment. In this presentation, recent developments of MiddleWare solutions will be presented.

CONFIRMED:
Bert Niesters, Professor in Molecular Diagnostics. Director, Laboratory of Clinical Virology, University Medical Center Groningen, The Netherlands

15.45-16.15

Solution Provider Presentation:
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Senior Representative, Formulatrix

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Senior Representative, Agilent Technologies

16.15-17.05

Afternoon Refreshments and Poster Presentation Session
One-to-One Networking Meetings

17.05-17.20

Short Talk/Young Investigator's Presentation:
Considerations for Low Level DNA Detection with dPCR, Quantifying the HIV Reservoir Markers

HIV remains an incurable disease due to the persistence of a small reservoir of latently infected cells despite effective antiretroviral treatment. In order to develop strategies for an HIV Cure, there is a demand for quantitative markers to monitor the size and dynamics of this viral reservoir. In this presentation the application of digital PCR will be described to assess different HIV reservoir markers, i.e. total HIV DNA, episomal HIV DNA, cell associated HIV RNA using ddPCR, in addition a custom nested digital PCR method will be discussed to quantify integrated HIV DNA. In addition to this, a new data driven method for threshold setting in ddPCR, using extreme value theory to enable low level template quantification will be described.

CONFIRMED:
Ward De Spiegelaere, Post-Doctoral Fellow, University of Gent, Belgium

Short Talk/Young Investigator's Presentation:
Heat Pulse Extension PCR for Unbiased Amplification of Nucleic Acids

We have introduced multiple heat pulses in the extension step of a PCR cycling protocol to generate a novel amplification technology (HPE-PCR), which temporarily destabilize secondary structures, in order to enhance DNA polymerase extension over GC-rich sequences. These secondary structures have been thought to block the DNA polymerase during the extension step, leading to decreased amplification efficiency. Different GC rich target sequences in the human genome, extremely long Fragile X GGC repeats and Myotonic Dystrophy type 1 CTG repeats have been used as models to develop and validate this novel technology. The HPE-PCR also improves the balance of amplification efficiencies between different sequences in a nucleic acid library, such as in library amplification for Next Generation Sequencing.

CONFIRMED:
Tho Huu Ho, Senior Researcher, Department of Genomics and Cytogenetics, Biomedical Pharmaceutical Applied Research Centre, Vietnam Military Medical University, Vietnam

17.20-17.45

Title To Be Confirmed
Use of dPCR for Detection of Chronic Viral Infection

CONFIRMED:
Paul Moss, Head of School of Cancer Sciences, Professor of Haematology, University of Birmingham, UK

Finding Needles in a Haystack with qPCR – Identification of Rare and Subclonal Mutations and their impact on Personalized Cancer Treatment using E-*ice*-COLD-PCR

We present a modified version of the *ice*-COLD-PCR assay called Enhanced-*ice*-COLD-PCR for *KRAS, BRAF and NRAS* mutation detection and identification, which allows the enrichment of the most frequent mutations. This assay permits the reliable detection of down to 0.1 % mutated sequences in a wild-type background. In contrast to other COLD PCR variants, the assay is simple to set-up especially when using qPCR thermocyclers with a gradient function. A single genotyping assay of the amplification product by pyrosequencing directly following the Enhanced-*ice*-COLD-PCR is performed to identify the mutated base. This developed two-step method is rapid, cost-effective and requires only a small amount of starting material (frozen, FFPE or plasma) permitting the sensitive detection and sequence identification of mutations within three hours. This method has been applied to different collections of cancer samples and enables detection of mutations in samples, which appear as wild-type using standard detection technologies.

CONFIRMED:
Jorg Tost, Head, Laboratory for Epigenetics and Environment (LEE), CNG - Centre National de Génotypage, CEA - Institut de Génomique, France

17.45-18.10	**Quantification of HIV Low-level Viremia with ddPCR** Plasma viral load (VL) is a useful biological marker for the clinical follow-up of HIV-positive patients. Commercial ultrasensitive VL assays based on qRT-PCR can detect low-level viremia below the current clinical threshold of 50 copies/mL. The relevance of measuring such residual viremia is still unclear and is currently investigated, particularly in strategies aiming at HIV cure. But the analytical variability in qPCR results is high at low DNA/RNA copy numbers: we developed digital PCR assays enabling more precision and reproducibility, using the ddPCR QX200 platform. We will present the main validation steps of an HIV-1 VL assay as well as another HIV-2 specific assay where low viremia is very common, in an ISO15189-accredited environment. We will then discuss the gaps remaining for dPCR use in routine clinical practice, and its interest for the study of complex clinical cases in combination with resistance testing and drug level monitoring. CONFIRMED: **Jean Ruelle, Researcher, UCL - Université Catholique de Louvain, Belgium**	**The Challenges of Delivering Precision Medicine to Improve Sepsis Recognition and Patient Outcome** In the setting of sepsis, microbiological cultures do not always provide high diagnostic accuracy for infection in a timely manner, routinely taking several days before a positive result is available. The time between initial clinical suspicion and confirmation of infection, results in the early use of empirical broad spectrum antimicrobial drugs because treatment delay is associated with substantial increases in mortality. Unnecessary and/or prolonged broad spectrum antimicrobial use is an inevitable consequence, which is associated with the development of drug resistant pathogens, *Clostridium difficile* infections, a range of avoidable adverse effects, as well as high costs. Therefore, I will describe the urgent global challenge that has emerged to develop techniques, including qPCR-based approaches, that could provide accurate diagnostic information within a short timeframe of clinical signs appearing and so allow more informed use of antibiotic therapy at an early stage. Highlighting examples of evidence from new large scale clinical diagnostic trials, I will consider how new rapid markers of infection may or may not contribute to developing more effective integrated care for patients with suspected sepsis. I will conclude by highlighting the key technological challenges that have emerged as we are applying new rapid diagnostic platforms to patients with sepsis. CONFIRMED: **Paul Dark, Associate Professor in Inflammation and Repair, University of Manchester, UK**
18.10	**Day 1 Close**	
18.10-19.10	**Drinks Reception**	

Co-Located with the **Microfluidics Congress**

Attracting experts working in microfluidic development and application, including point-of-care diagnostics, single cell analysis, lab-on-a-chip applications, droplet microfluidics and next generation microfluidics, the conference will examine the latest developments in the technologies and techniques being used for progressing medical **research** in areas such as disease monitoring, diagnostics, organ-on-a-chip and synthetic biology

www.globalengage.co.uk/microfluidics.html

Co-Located with the **2nd Synthetic Biology Congress**

With a focus on Synthetic Biology in the healthcare/drug discovery and agricultural sector, this interactive meeting will provide the opportunity to take home cutting edge research, strategies, case study examples and methods to allow you to keep up to date with the latest advancements, novel methods and applications of Synthetic Biology within your field.

www.globalengage.co.uk/synthetic-biology.html

Venue

Radisson Blu Heathrow Hotel
140 Bath Road,
Hayes,
Middlesex
UB3 5AW

A discounted group rate is available to all attendees. Details of how to book are available on registration. Space is limited and accommodation is available on a first come basis.

08.00-08.40	**Coffee & Networking Meetings**	
08.35-08.40	**Stream Chair Welcome Address:** Attila Lorincz, Professor of Molecular Epidemiology, Wolfson Institute of Preventive Medicine, UK	
08.40-09.10	Keynote Address: **Title To Be Confirmed** Invite to:	
09.10-09.40	Solution Provider Presentation: **Title To Be Confirmed** Gold Sponsor ThermoFisher SCIENTIFIC CONFIRMED: **Senior Representative, Thermo Fisher Scientific**	**Solution Provider Presentation** For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk
	qPCR & Digital PCR Case Studies	**Plant, Food and Environmental Case Studies**
09.40-09.45	**Stream Chair:** Attila Lorincz, Professor of Molecular Epidemiology, Wolfson Institute of Preventive Medicine, UK	**Stream Chair:**
09.45-10.10	**The Liquid Biopsy Approach: Following the Tumour in Peripheral Blood** CONFIRMED: **Evi Lianidou, Professor of Analytical Chemistry – Clinical Chemistry Laboratory of Analytical Chemistry Analysis of Circulating Tumor Cells (ACTC) Lab, University of Athens, Greece**	**qPCR calculator: A Tool for Accurate Quantification of Plant Transcripts and miRNAs** Due to several factors that can influence the final result, quantitative analysis and interpretation of qPCR data is not trivial. We have developed "qPCR calculator", a web-based tool for robust quantification of qPCR data using standard curve. It is designed as a workflow that guides the user through quality control and calculation steps. It deals with all the issues of qPCR related calculations from data consistency, pipetting errors, standard curve parameters, individual sample efficiencies/inhibition, range of quantification and normalization to one or several reference genes. Plant material often contain PCR reaction inhibitors which can be controlled by analysing serial dilutions of individual samples. Application of plant gene and miRNa expression analysis using "qPCR calculator" will be presented. CONFIRMED: **Špela Baebler, Research Associate, Department of Biotechnology and Systems Biology, National Institute of Biology, Slovenia**
10.10-11.00	**Morning Refreshments and Poster Presentation Sessions One-to-One Networking Meetings**	
11.00-11.30	Solution Provider Presentation: **Title To Be Confirmed** STILLA TECHNOLOGIES CONFIRMED: **Senior Representative, Stilla Technologies, France**	**Solution Provider Presentation** For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk
11.30-11.55	**Are dPCR Tests Suitable for Therapy Monitoring in Breast Cancer?** Breast cancer is a heterogeneous disease both at the clinical and molecular level. Detection and quantification of ctDNA in liquid biopsies is a promising tool for monitoring treatment response and disease progression of many cancer types. By designing patient specific test to detect ctDNA by dPCR is important, but tumor heterogeneity is a challenge. Very few somatic mutations are highly recurrent in breast cancer, in addition some tumors show a high cellular diversity. To be able to trace the dynamics of subpopulations will be of importance. The talk will give insight into the challenges and some examples of cases. CONFIRMED: **Hege Russnes, Researcher/Senior Consultant, Institute for Clinical Medicine/Dept. of Pathology, Oslo University Hospital, Norway**	**Arabinogalactan Proteins' Gene Expression Analysis in *Arabidopsis thaliana* and *Quercus suber*** Arabinogalactan Proteins (AGPs) are hydroxyproline rich glycoproteins that undergo several post-translation modifications. It has been shown that AGPs can be used as molecular markers for reproductive development (Coimbra *et al*. 2007). We have been studying the AGPs present in the male and female tissues, in order learn their biological roles during plant reproduction. Most of the AGPs were selected for analysis using microarray data available (Geneinvestigator, Arabidopsis eFP Browser). In order not only to validate the microarray data but also to check the different levels of AGPs expression in different tissues of two species, *Arabidopsis thaliana* and *Quercus suber*, quantitative RT-PCR analysis was carried out in male and female organs from both species. CONFIRMED: **Sílvia Coimbra, Professor, Department of Biology, University of Porto, Portugal**

11.55-12.20	**Applications of Digital Droplet PCR in Drug Discovery** Historically, cancer cell lines have been the tissue culture workhorse within the pharmaceutical industry, particularly in early drug discovery. However, despite yielding decades of fruitful research, breakthroughs in stem cell research and the growing push towards personalised medicine have highlighted the need for data to be generated in more physiologically relevant systems that translate better into human patients. Here, I will describe how we have leveraged state of the art technologies, including ddPCR, to generate modified cell lines specific for drug discovery research at AstraZeneca. As part of our resourceful molecular toolbox, ddPCR has allowed us to analyse copy number variations, detect rare events and monitor viral infections, thereby strengthening our drug discovery pipeline. CONFIRMED: **Susanne Engberg, Senior Research Scientist, AstraZeneca, Sweden**	**qPCR for the Detection of Allergenic Ingredients in Food Products** To ensure the compliance with food labeling and to improve consumer protection, reliable analytical methods for the detection and quantification of allergenic food ingredients are required. Among commonly used markers, DNA targets are interesting for quantification purposes and for methods where a high sensitivity is required due to their ubiquity, thermal stability, the possibility of amplifying the number of copies of the initial DNA target by PCR, and the possibility of using quantitative PCR (qPCR). Advantages and disadvantages of using DNA markers would be highlighted, jointly with qPCR, dPCR and other molecular biology based methods. Our latest developments in the field of qPCR applications for the detection of allergenic ingredients in food products will be discussed, as well as the advantages that nanotechnology can bring to molecular biology based analysis. CONFIRMED: **Marta Prado, Staff Researcher, INL - International Iberian Nanotechnology Laboratory, Portugal**
12.20-12.40	Short Talk/Young Investigator's Presentation: **Title To Be Confirmed** Digital PCR in Lung Cancer CONFIRMED: **Pascale Tomasini, Assistance Publique Hôpitaux de Marseille, France**	Short Talk/Young Investigator's Presentation: **From Real Time PCR to Digital PCR: Method Transfer Guidelines and Performance Parameters in the Field of Food Testing** In the field of food and feed related GMO testing real time PCR has been the gold standard for over a decade. A well-documented framework for scientific assessment and validation of real time PCR reference methods has been established. With the advent of digital PCR to many food-testing laboratories the EURL GMFF (European Union Reference Laboratory for GM Food & Feed) and ENGL (European Network of GMO Laboratories) are preparing a similar structure for the use of digital PCR: method optimisation in dPCR, establishing the performance of an assay, how much 'rain' is acceptable, threshold placement, etc. The presentation will give an overview of the underlying experiments and the progress in the development of these guidelines. CONFIRMED: **Antoon Lievens, Researcher, Molecular Biology and Genomics Unit, European Commission - Joint Research Centre, Italy**
12.40-13.10	Solution Provider Presentation: **Title To Be Confirmed** Gold Sponsor nanoString TECHNOLOGIES CONFIRMED: **Senior Representative, Nanostring Technologies**	**Solution Provider Presentation** For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk
13.10-14.10	**Lunch**	
14.10-14.35	**Title To Be Confirmed** PAnDA is a fast and accurate method of determining the chromatid content of human oocytes, prior to in vitro fertilization. It works by analysing the content of the polar bodies (daughter-cells of the oocyte), leaving the oocyte itself undamaged. Using this method, we are able to identify and reject aneuploid oocytes (which are very common in patients undergoing IVF) and significantly increase pregnancy rates. CONFIRMED: **Paul Dear, Team Leader, Single Molecule Genomics Group, MRC Laboratory of Molecular Biology, Cambridge, UK**	**Towards Real-time Detection of Airborne Spores to Control Crop Diseases** Air sampling integrated with DNA analysis methods is being used to monitor genetic changes in plant pathogen populations, such as those conferring virulence to crop varieties or resistance to a class of fungicide. For diseases that develop from airborne inoculum, timing of disease control methods can also be improved using automated air sampling devices, integrated with appropriate diagnostic methods. Current projects are integrating air sampling with isothermal DNA-based diagnostics and wireless reporting. We can expect a new approach to precision agriculture to emerge from this technology – farm-based devices that give precision on when to apply fungicides and when to omit applications. The technology could also be adapted for forecasting human allergens and pathogens. CONFIRMED: **Jon West, Senior Research Scientist, Plant Biology & Crop Science, Rothamsted Research, UK**

14.35-15.00	**Title To Be Confirmed** qPCR and Digital PCR for Examining Intestinal Microbiota CONFIRMED: **Sofia Forssten, Senior Scientist/Docent, DuPont/University of Turku, Finland**	**Helping Farmers to Grow Healthier Crops: Use of qPCR to Monitor Plant Resistance to Fungal Pathogens and Select Healthy Seed Lots** Fusarium and Verticillium wilts caused by fungal pathogens and Downy Mildews caused by Oomycetes are some of the most destructive plant diseases that can be best managed by risk assessment and use of resistant cultivars. The aim of our research is to develop reliable real-time quantitative polymerase chain reaction (q-PCR) protocols that allow quantifying those pathogens in plant root and stem tissues and seed lots that can contribute to implementation of those disease management strategies. We will present success stories and practical examples of q-PCR assays that we have developed to quantify *F. oxysporum* f. sp. *ciceris* in chickpeas, *Verticillium dahliae* in olive, and *Peronospora somniferi* in cultivated opium poppy. These protocols were developed following the MIQE guidelines providing the minimum information required for a qPCR experiment to quantify those pathogens ensuring their relevance, accuracy, correct diagnosis, and repeatability. Those protocols have allowed us to: i) clearly differentiated susceptible from resistant plant reactions to the pathogens as well as the degree of virulence between pathogen races; ii) quantify the pathogen in asymptomatic plant tissues at early stages of the infection process; iii) and certify the use of pathogen-free seed stocks for field sowings. The use of this type of protocols can be of great value for plant breeders and for epidemiological studies in growth chambers, greenhouses and field-scale plots and currently some of them are being implemented to select healthy seed lots before sowing. CONFIRMED: **Blanca Landa, Research Scientist, Institute for Sustainable Agriculture (IAS), CSIC, Spain**
15.00-15.25	**Title To Be Confirmed** qPCR and Digital Platform Comparison CONFIRMED: **Mary Alikian, Research Assistant, Department of Medicine, Imperial College London, UK**	**Title To Be Confirmed** Reliable Gene Expression Analysis by Reverse Transcription-Quantitative PCR CONFIRMED: **Ann Cuypers, Professor, Centre for Environmental Sciences, Hasselt University, Belgium**
15.25-15.55	**Afternoon Refreshments and Poster Presentation Sessions**	
15.55-16.20	**Identification of Disease Biomarkers: the Ins and Outs of Validation, Selection and Diagnostic Test Development** Selection and validation of biomarker candidates from big datasets for sensitive and specific diagnostic test development is a dynamic and evolving process. We are still developing an understanding of the most appropriate methods and pathways to enable this development pipeline. We discuss the outcome from two clinical studies of biomarker validation for development of next generation 'point of care' tests for Tuberculosis and Sepsis and the technical matters surrounding their translation onto diagnostic devices for near patient use CONFIRMED: **Karen Kempsell, Senior Project Team Leader, Public Health England, UK**	**Multiplex Quantification of Approved GMOs with Digital Droplet PCR** In EU regulation for labelling of GMOs the threshold for GMO content is set per ingredient (plant species), but is usually measured as single events and summed up for final result. To reduce the number of reactions needed for quantification of all present events, two multiplex assays were developed for Bio-Rad's Droplet Digital PCR. Setup and in-house validation of these multiplex assays for quantification of 12 approved maize lines will be presented. This will include the results of initial testing and comparisons with singleplex assays and further assessment of several performance parameters of multiplex assays (e.g. sensitivity, specificity, cost-effectiveness). Additionally, other multiplexing options would be discussed. CONFIRMED: **David Dobnik, Researcher, Department of Biotechnology and Systems Biology, National Institute of Biology, Slovenia**
16.20-16.45	**Title To Be Confirmed** CONFIRMED: **Petra Wolffs, Assistant Professor & Head of Unit Molecular Diagnostics, Maastricht University Medical Center, The Netherlands**	**Title To Be Confirmed** Invite to:
16.45	**Chairperson's Closing Remarks & Conference Close**	

Course Organiser:

tataabiocenter

Following on from last year's MIQE course run after the 2nd qPCR & Digital PCR Congress, we are pleased to announce that TATAA Biocenter will be running two training courses after the congress.

Course Details:

Course 1: qPCR Data Analysis Workflow: From Instrument to Data Interpretation (Instructor: Robert Sjöback)

Please note you will be required to bring your own laptop computer

Course 2: Digital PCR – Applications and Analysis (Instructor: Kristina Lind)

Cost per course:

Academic Rate: £495.00 + VAT

Industry Rate: £595.00 + VAT

Venue:

The training courses will take place at the conference venue (Radisson Blu Heathrow Hotel)

Outline of Courses:

A full outline of each course can be found below. To book your place on either course please contact Global Engage.

For more information please contact Scott Taylor, Operations Director, Global Engage Ltd.

scott@globalengage.co.uk **+44 (0) 1865 849841**

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2 Day Course: qPCR Data Analysis Workflow: From Instrument Data to Interpretation

This training course is aimed at those working with real-time qPCR and would like to learn how appropriate statistics shall be selected and applied correctly to get the most out of the qPCR data. It is a comprehensive course teaching the basics of statistics including the most common methods to analyse qPCR data generated both in large and small studies. Participants are expected to have knowledge and experience of the qPCR method. The course includes extensive computer based exercises using the software GenEx (MultiD Analyses) so bring your laptop computer.

The first day of the course focuses on the principles of statistics going through the terminology used in statistics and how to approach statistics when analysing qPCR data. Day one will describe the most common terms used in descriptive statistics and the most frequently used statistical tests to extrapolate from sample to population. It will also discuss how to setup qPCR experiments to be able to make statistical analysis of the data.

In addition day one focuses on the ability to detect difference and factors that influence the power analysis that can be made to optimize an experiment. The last part will discuss the pre-treatment that is required before analysing qPCR data, how to use relative quantification to compare samples and the use of reference genes to normalise between samples. Day one will also discuss the importance of controlling for genomic DNA contamination in gene expression analysis and how we can correct for gDNA presence using NoRT controls or ValidPrime.

Day two of this course focuses mainly on two things. The first is absolute quantification using standard curves that is used to quantify unknown samples. To do this in a proper way one need to know the limits between which we can make a good detection and quantification. How to identify limit of detection (LOD), limit of quantification (LOQ) and the dynamic range of a qPCR test will be handled.

Second main topic of the day is gene expression profiling where more than one gene is analysed in many samples. Analysing many genes in many samples often mean that the analysis cannot be performed with a single plate, to account for this a proper design is vital for your multi-plate experiment and analysis. We will finally discuss the most common multivariate methods used in expression profiling where samples (or genes) are classified based on the similar response of different genes (or samples)

- **Principles of Statistics**
  - Introduction to the basic principles of statistics
  - What do the basic terms mean?
- **Design of Experiments**
  - How should they be designed?
  - How to do statistical hypothesis testing
- **Statistical Tests**
  - Overview of the most common statistical tests
  - How do we apply the different tests and when are they valid?
- **Ability to Detect a Difference (Power Testing)**
  - How to define the power of a test
  - How to test the null hypothesis
  - Type I and type II errors
- **Relative Quantification**
  - How are the calculations for relative quantification performed?
  - How should qPCR data be pre-treated before comparison?
- **Multiplate Measurements**
  - How do we get Cq-values, what is delta-Cq and delta-delta-Cq?
  - How should we plan the experiment to analyse multi-plate measurements in the best way?
  - How do we use interpolate calibrators?
- **Absolute Quantification**
  - How is absolute quantification performed?
  - How to interpret standard curves
- **Limit of Detection**
  - How to calculate LOD and LOQ
  - How to identify the source of variance in experiments
- **Reference Genes**
  - How to find and validate optimal reference genes
- **Expression Profiling**
  - How can gene expression profiling be performed?
  - How to classify genes or samples with scatter plots and dendograms
  - How to handle missing data in multivariate analysis
  - Practical computer-based training in principal component analysis, self-organising maps and clustering analysis

Course Leader: Robert Sjöback, R&D Manager and Vice President TATAA Biocenter

Robert Sjöback is currently working as RnD Manager and Vice President at TATAA Biocenter. He received his PhD degree in Physical Chemistry from Chalmers University of Technology where he studied the fluorescent properties of DNA binding dyes and contributed to the development of the LightUp probes. Sjöback worked several years with research and product development of both PCR and ELISA based kits for food diagnostics. Since 2005 Sjöback has worked at TATAA Biocenter being responsible for the company research and product development, and the application and coordination of the company's externally financed research projects, including EU projects within FP6, FP7 and Horizon H2020 programs, as well as being lead instructor in the company training course program.

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2 Day Course: Digital PCR – Applications and Analysis

This course gives an overview of digital PCR and its applications. The course is theoretical and will focus on the different applications where digital PCR is advantageous, different instruments available and how the analysis is performed.

The course content includes:

- **Introduction to Digital PCR**
  - What is digital PCR
  - How does it work?
  - When is digital PCR useful?
- **Applications**
  - How to use digital PCR for absolute quantification
  - How is Copy Number Variation, CNV, analysis performed?
  - The advantage of digital PCR for rare mutant detection
  - How to do linkage analysis with digital PCR
  - How to use digital PCR for analysis of next generation sequencing libraries
  - Gene expression analysis with digital PCR
- **Basic Statistics for Digital PCR Analysis**
  - What is Poisson distribution?
  - What is the error in our measurement?
  - What is it that affects the precision?
  - What is it that affects the accuracy?
  - Which controls are needed?
- **Instrumentation**
  - Which instruments are available?
  - How do they work?
  - Which are the differences?
- **The Digital PCR Reaction**
  - What to think about when designing assays for digital PCR
  - Optimization of digital PCR
  - Trouble shooting
- **The Digital MIQE Guidelines**
  - What is specific in the digital MIQE guidelines?
  - Which information is important from a digital PCR experiment?

Course Leader: Kristina Lind, Lead Instructor, TATAA Biocenter

Kristina Lind received her PhD in Molecular Biotechnology from Chalmers University of Technology, Gothenburg, in 2007. Her PhD project included development of the protein quantification technique immuno-qPCR. She has held courses in TATAAs regime since 2001 and is now responsible for the course program and core facility at TATAA Biocenter. She is also leading a group that is involved in the commissioned services at the company and is project manager for a number of customer projects. As assistant quality manager she is deeply involved in the quality control and how to work with qPCR according to the MIQE guidelines.

For more information please contact Scott Taylor, Operations Director, Global Engage Ltd.

scott@globalengage.co.uk **+44 (0) 1865 849841**

3rd qPCR & Digital PCR Congress – October 20-21, 2015, London, UK

How To Register

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United Kingdom

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Conference Fees

qPCR/dPCR Congress	Industry rate:	£799 + vat	Discount Code:	
qPCR/dPCR Congress	Academic rate:	£499 + vat	Discount Code:	
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TATAA qPCR Course 2	Academic	£495 + vat	Industry rate:	£595 + vat

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