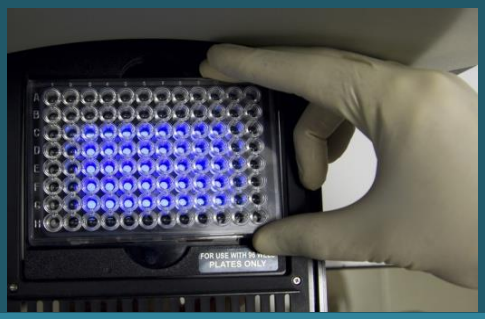
11-12 July 2016, Philadelphia, USA

www.globalengage.co.uk/digital-and-qpcr.html



2nd qPCR and Digital PCR Congress: USA

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

Global Engage is pleased to announce the American leg of our successful qPCR & Digital PCR series, which will be co-located with our Microfluidics Congress on 11-12 July 2016 in Philadelphia.

Bringing together over 150 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, infectious diseases, vaccines, prenatal diagnostics, clinical applications, microbiology, food microbiology, environmental testing and other novel applications.

With increasing numbers of real-time PCR users purchasing digital PCR due to the reduction in its 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 five separate tracks covering

Confirmed Speakers Include:

Jerald Radich
Director the Molecular Oncology Lab and Member of Clinical Research Division, Fred Hutchinson Cancer Center, Professor of Medicine, University of Washington School of Medicine

Joel Tellinghuisen
Emeritus Professor of Chemistry, Vanderbilt University

G. Mike Makrigiorgos
Professor of Radiation Oncology, Dana Farber Cancer Institute and Harvard Medical School

Conference Synopsis

Day 1 – Stream One

Digital PCR: Applications & Possibilities

- Introduction, benefits, future development of dPCR
- Comparing dPCR to qPCR
- Converting to dPCR and choosing your system
- Validation of dPCR
- Complimenting digital PCR with other technologies including NGS
- Multiplexing in digital PCR
- Detection of patient-specific mutations
- Applications for precision medicine

Day 1 – Stream Two

qPCR: Strategies & Developments

- Developments in qPCR methods
- MIQE guidelines & standardisation
- qPCR/RT-PCR assay design, optimisation & validation
- Sample preparation & quality control methods
- Detection, quantification and sequencing of RNA
- Automation of qPCR methods
- Bioinformatics and data analysis
- Multiplexing
- Parallel sequencing

Day 2 - Stream One

Healthcare Case Studies

- Clinical/Diagnostic applications
- Oncology (rare variant detection, monitoring therapy response, early relapse detection.)
- Neurological disorders
- Prenatal diagnostics
- Infectious diseases
- Biomarker discovery
- Micro RNA/ncRNA/siRNA applications
- Gene expression and synthesis
- Single cell analysis
- Liquid Biopsies

Day 1 and 2

Plant, Food and Environmental Case Studies

- Environmental Sampling
- Water contamination analysis with dPCR and qPCR
- qPCR in plant research
- 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

2nd qPCR & Digital PCR Congress: USA – 11-12 July 2016, Philadelphia, USA

Confirmed Speakers:

Fred Kramer
Professor of Microbiology, Biochemistry and Molecular Genetics, Public Health Research Institute, Rutgers University

Patricia Silveyra
Assistant Professor, Pennsylvania State University

Anubhav Tripathi
Professor of Engineering, Molecular Pharmacology, Physiology and Biotechnology, Brown University

Derek Ostertag
Head of R&D Diagnostics, Tocagen

Shu Chen
Research Scientist and Manager, Agriculture and Food Laboratory, University of Guelph

Valerie Taly
Group Leader, University of Paris Descartes

Hendrik Viljoen
Professor and Chair of Chemical and Bimolecular Engineering, University of Nebraska-Lincoln

Bob Dorazio
Research Statistician, US Geological Survey

Greg McCollum
Research Plant Physiologist, US Department of Agriculture

Katia Sol-Church
Director Nemours Biomolecular Core Lab Alfred I. duPont Hospital for Children

Stream Chair: Sanjiv Shah
Microbiologist, US Environmental Protection Agency

John Thomas Bradshaw
Senior Development Scientist, Artel

Suzanne Fuqua
Professor, Baylor College of Medicine

Wayne Barnes
Associate Professor, University of Washington St Louis

Joel Tellinghuisen
Emeritus Professor of Chemistry, Vanderbilt University

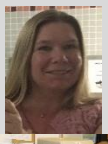
Rachel Noble
Professor and Director of Institute for the Environment, University of North Carolina Institute of Marine Sciences

Jerald Radich
Director the Molecular Oncology Lab and Member of Clinical Research Division, Fred Hutchinson Cancer Center

Mojca Milavec
Senior Research Specialised Associate National Institute of Biology, Slovenia

John Griffith
Principal Scientist & Coordinator of Molecular Technology, Southern California Coastal Water Research Project

Sandra Koseoglu
Senior Scientist, Pharmacology and Cellular Pharmacology, Merck Laboratories



Tigst Demeke
Program Manager of Grain Biotechnology Research, Canadian Grain Commission

Tiong Gim Aw
Research Associate, Michigan State University

Erica Romsos,
Forensic Scientist, Biomolecular Measurements Division, Applied Genetics, National Institute of Standards and Technology

Konrad Faulstich
Director of Business Development, BioNTech

Martin Chilvers
Assistant Professor, Department of Plant, Soil and Microbial Sciences, Michigan State University

Maria Mayda
Senior Scientist, ATCC

Sandhya Parshionikar
Acting Associate Division Director, Water Supply and Water Resources Division, US Environmental Protection Agency

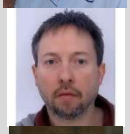
Nick Papadopoulos
Professor and Director of Translational Genetics, Johns Hopkins

Ronald Rabin
Chief, Laboratory of Immunobiochemistry, US Food and Drug Administration

Piotr Garstecki
Associate Professor, Institute of Physical Chemistry, Polish Academy of Sciences

G. Mike Makrigiorgos
Professor of Radiation Oncology, Dana Farber Cancer Institute and Harvard Medical School

Musaddeq Hussain
Principal Scientist, Merck Laboratories



Guillaume Pavlovic
Head of Genetic Engineering and Model Validation Department, Mouse Clinical Institute, France

Anne Eischeid
Research Scientist, US Food and Drug Administration, Center of Food Safety and Applied Nutrition

Rachel Tam
Senior Scientific Researcher, Genentech

Mary Bronner
Professor of Pathology, University of Utah and Co-Division Chief, Anatomic Pathology and Oncology, ARUP Laboratories

Jean Beagle Ristaino
William Neal Reynolds Distinguished Professor, North Carolina State University

Chetan Bettegowda
Assistant Professor of Neurosurgery, Johns Hopkins University

Jackie Woods
Research Microbiologist, US Food and Drug Administration

Stream Chair: Sony Agrawal
Senior Scientist, Merck Laboratories

Sarmitha Sathiamoorthy
Scientist, Sanofi Pasteur, Canada

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Agenda: Day One – Monday 11th July 2016

08.00-08.50	**Registration & Coffee**		
08.50-09.00	**Global Engage Welcome Address** **Stream Chair's Opening Remarks**		
09.00-09.35	**Keynote Address: Title TBC** Confirmed: **Nickolas Papadopoulos, Professor of Oncology and Director of Translational Genetics, Sidney Kimmel Comprehensive Cancer Center, Johns Hopkins University**		
09.35-10.05	**Types I and II Interferons at the Respiratory Epithelial Barrier** Confirmed: **Ronald Rabin, Chief, Laboratory of Immunobiochemstry, US Food and Drug Administration**		
10.05-10.35	**Solution Provider Presentation** RESERVED FOR PLATINUM SPONSORS For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk		
10.35-11.45	**Morning Refreshments** **Poster Presentation Sessions and One-to-One Networking Meetings**		
	Track 1 – Digital PCR: Possibilities & Opportunities	**Track 2 – qPCR: Strategies & Developments**	**Track 3 – Plant, Food and Environment Case Studies**
11.45-12.10	**Color-Coded Molecular Beacons for Multiplex Digital PCR Assays** Every droplet of a digital PCR assay can contain as many as 35 different highly specific molecular beacon probes that are each tagged with a different combination of three out of seven available fluorescent colors. All of the molecular beacons remain dark except for those whose probe sequence is exactly complementary to a target sequence within the amplicons that are generated in a droplet. Because each droplet is a screening assay, as many as 35 rare mutations (for example, mutations relevant to cancer diagnosis, prognosis, and treatment that may be present in a "liquid biopsy") can be simultaneously and accurately quantitated with an instrument that can distinguish the fluorescent colors that are present. Confirmed: **Fred Kramer, Professor of Microbiology, Biochemistry and Molecular Genetics, Public Health Research Institute, Rutgers University**	**Techniques for sampling for HIV– Title TBC** Confirmed: **Anubhav Tripathi, Professor, Brown University, USA**	**A single-codon mutation that converts PCR enzymes Taq and Klentaq1 to be able to catalyze RT-PCR, LAMP, and RT-LAMP, and be resistant to chocolate and blood** Confirmed: **Wayne Barnes, Associate Professor, Department of Biochemistry and Molecular Biophysics, Washington University in St Louis, USA**
12.10-12.35	**Clinical Application of ddPCR to Cancer Therapy, Monitoring and Diagnosis: Lung cancer and melanoma as paradigms** • Understand how ctDNA will likely be a disruptive entity in the practice of molecular pathology and clinical oncology. • Learn about ddPCR testing of EGFR T790M mutation in lung adenocarcinoma and BRAF mutations in melanoma. • Understand the concept of tumor heterogeneity and how ctDNA may be able to circumvent this in tumor molecular diagnosis. Confirmed: **Mary Bronner, Professor of Pathology, Division Chief, Anatomic Pathology and Molecular Oncology, University of Utah and ARUP Laboratories, USA**	**Developing automated absolute qPCR capabilities to evaluate antiviral potencies** Confirmed: **Sandra Koseoglu, Senior Scientist, Pharmacology, Cellular Pharmacology, Merck Research Labs**	**Use of real-time PCR for E coli and Listeria analysis – Title TBC** Reserved: **Kendra Nightingale, Associate Professor of Food Safety and Public Health, International Center for Food Industry Excellence, Texas Tech University**

12.35-13.00	**Ultra-sensitive mutational analysis in cell-free DNA by Digital PCR** Cell-free DNA in plasma offers a non-invasive approach to monitor tumour molecular profiling in real-time, detection of emerging genomic alterations associated with drug resistance, clarifying cancer prognosis and diagnosis of cancer progression. We developed an ultra-sensitive ddPCR approach to detect actionable mutations in cfDNA. We will show the validation of this ddPCR platform using commercially available DNA controls, FFPE tissues and cfDNA matched samples and compared this approach to other orthogonal technologies, including qPCR and NGS and achieved 100% concordance across these platforms. DdPCR can detect mutations down to 0.03% allele frequency with 100% sensitivity and specificity. DdPCR platform enables the development of a non-invasive method to overcome existing challenges to provide molecular understanding of patient's tumour evolution and aid in the development of personalized cancer therapies. Confirmed: **Rachel Tam, Senior Scientist, Genentech**	**Better qPCR through statistics** • Scale-independent markers for the quantification cycle C_q, like the second-derivative maximum or relative threshold, perform better than the absolute threshold. • For small copy number N_0, the dispersion of C_q in replicate experiments is dominated by Poisson statistics , making it possible to estimate N_0 directly from the C_q variance; the method is useful for N_0 in the range 10-200, with relative precision $(2/n)^{1/2}$ (20% for 50 replicates). • Relative expression is commonly estimated using the $\Delta\Delta C_q$ method, or the $\Delta\Delta C_{q,adj}$ method, where in the latter, there is allowance for variability in the amplification efficiency AE; for the often-use "standard curve" design, nonlinear least squares can be used to estimate $\Delta\Delta C_{q,adj}$ and its uncertainty, with automatic inclusion of uncertainty in the AEs. Confirmed: **Joel Tellinghuisen, Emeritus Professor, Vanderbilt University, USA**	**Applications of Droplet Digital™ PCR in Food and Feed Testing: Challenges and Solutions** Confirmed: **Shu Chen, Research Scientist, Manager, Agriculture and Food Laboratory, University of Guelph**
13.00-13.30	Solution Provider Presentation **Title To Be Confirmed** Confirmed: **Remi Dangla – CEO of Stilla Technologies**		Solution Provider Presentation **Accuracy Matters When Transferring a Quantitative, Bench-top Assay to Automation: Understanding Method Transfer Pitfalls** • Assays are usually performed on the benchtop using handheld pipettes before they are transferred to an automated liquid handling platform • The manual assay should be directly compared to the automated assay for consistencies in pipetting performance. • Undetected differences in accuracy will impact the integrity of the assay as the automation process continues. Confirmed: **John Thomas Bradshaw, Senior Development Scientist, Artel**
13.30-14.30	**Lunch and One-to-One Networking Meetings**		
14.30-14.55	**ddPCR Developments for Breast Cancer Mutation Detection– Title TBC** Confirmed: **Suzanne Fuqua, Professor, Baylor College of Medicine**	**Opportunities for expedited isothermal PCR** • Review of the Recombinase Polymerase Amplification (RPA) process and identification of the rate limiting steps. Experiments are shown in which DNA amplification occurs under conditions of rotational turbulent flow. A mathematical model is used to demonstrate how to use RPA for qPCR applications. • Two utilities of expedited RPA are discussed: the use of super paramagnetic nanoparticles (SPMNPs) to retrieve target DNA from the lysate onto the mechanical stirrer and the collection of cells by SPMNPs from a clinical sample for analysis by RPA. • New opportunities for expedited RPA. Some applications in agriculture and medicine will be discussed as well as the development of a system for unmanned aerial vehicle applications. Confirmed: **Hendrik Viljoen, Professor and Chair of Chemical and Biomolecular Engineering, University of Nebraska, USA**	**Enteric Viruses in Clinical, Wastewater and Environmental Samples: Research Perspective and Outbreak Analysis** • Detection and quantification of enteric viruses in environmental samples • Characterization of enteric viruses in environmental samples • Virus and bacterial indicators in environmental samples Confirmed: **Jackie Woods, Research Microbiologist, US Food and Drug Administration**

14.55-15.20	**dPCR metrology – Title TBC** Confirmed: **Erica Romsos, Forensic Scientist, Biomolecular Measurements Division, Applied Genetics, National Institute of Standards and Technology**	**Digital PCR assays for the use in Point-of-Care systems and on standard Real-Time devices.** • Digital PCR assays introduced absolute quantitation yet, in the classic format they require massively large number of partitions of the sample. • Here we describe two innovative approaches that maximize the information gain from each partition and reduce the required number of compartments by orders of magnitude. • An explicit algorithm for designing multi-volume/dilution assays allows to independently tailor the precision and dynamic range to the particular application. • We also describe the first synergistic digital-analogue assay, that can be run on standard Real-Time PCR devices, with multiple tests fitted on a single well-plate, combining absolute quantitation with high precision and dynamic range. • Both methods are described in terms of ready-to-use explicit design and analysis formulas and open up new grounds for the use of digital assaying technologies. Confirmed: **Piotr Garstecki, Associate Professor, Institute of Physical Chemistry, Polish Academy of Sciences, Poland**	**Quantifying pathogenic viruses and bacteria using digital droplet PCR in complex water samples** Digital droplet PCR (ddPCR)-based quantification of viral and bacterial pathogens in complex water and shellfish samples has the power to revolutionize monitoring and surveillance. For example, in recreational waters, quantification of norovirus and adenovirus at detection limits relevant to swimmers and surfers was previously not possible. However, with the advent of improved capture and detection techniques detection limits relevant to human health are attainable. We have analyzed a range of complex water and shellfish samples for specific viral and bacterial pathogens and will illustrate the possibilities for improved future water quality management using ddPCR, including hazard identification, QMRA, and improved notification. The importance of attention to detail for sample processing, quantification of standards, and assessments of recovery and inhibition will be featured. Confirmed: **Rachel Noble, Professor and Director of the Institute for the Environment, University of North Carolina Institute for Marine Sciences, USA**
15.20-15.45	**Digital PCR for biological and synthetic standards** Biological and synthetic nucleic acid standards are a particular form of standardized nucleic acids that can be used for multiple applications such as controls, checking the metrological traceability of DNA/RNA products, validating analytical measurement methods, and for calibration of instruments. Given the intended use of these nucleic acids, a precise, reliable and reproducible quantification process is vital to define them as standards. This presentation will discuss the benefits and challenges of digital PCR and how this technology has been used at ATCC for absolute quantification of Nucleic acid-based products. Confirmed: **Maria Mayda, Senior Scientist, ATCC**	**Designing, developing qPCR assays for validation– Title TBC** Confirmed: **Sarmitha Sathiamoorthy, Scientist, Sanofi Pasteur, Canada**	**Detection limits of digital PCR assays and their influence in presence-absence surveys of environmental DNA** The digital PCR (dPCR) assay can potentially be used to estimate low concentrations of nucleic acids with greater accuracy and precision than other assays. This potential is particularly important in the quantification of environmental DNA (eDNA), which is often used to identify the presence of an animal species not easily detected by traditional survey methods. In this application it is essential to establish an unambiguous reference point (or detection limit) for the presence of eDNA. We developed a statistical model for estimating dPCR-based limits of detection from serial dilution experiments with known standards. We illustrated the benefits of this approach by analyzing samples of grass carp eDNA collected in ponds known to contain different numbers of grass carp. Confirmed: **Robert Dorazio, Research Statistician, US Geological Survey**
15.45-16.15	Solution Provider Presentation **Title To Be Confirmed** Confirmed: **Senior Representative, RainDance Technologies**		**Solution Provider Presentation** For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk
16.15-17.05	**Afternoon Refreshments** **Poster Presentation Sessions and One-to-One Networking Meetings**		

17.05-17.30	**Innovative methods in quantitating host residual DNA in biologic drugs** • Host residual DNA as impurity in a biologic drug is currently quantified by DNA extraction followed by qPCR • We have developed methods for direct qPCR without DNA extraction from mAb drugs • We have applied direct methods in digital PCR based residual DNA quantification Confirmed: **Musaddeq Hussain, Principal Scientist, Merck Laboratories**	**Effects of DNA-related factors on droplet digital PCR for absolute quantification of genetically engineered traits** • Low levels of genetically engineered traits were analyzed with RainDance droplet dPCR system • The effects of source of DNA and treatment of DNA on droplet dPCR results were investigated • Absolute quantification of GE traits in non-target DNA was investigated using droplet dPCR Confirmed: **Tigst Demeke, Research Scientist. Canadian Grain Commission, Grain Research Laboratory**
17.30-17.55	**Exploring the potential of dPCR for the development of reference measurement procedure** • Comparison of one qPCR and two dPCR platforms for quantification of CMV • Quantification of CMV by dPCR (without quantification) • Inter-laboratory comparison of methods for quantification of CMV (4 laboratories, 3 dPCR platforms) Confirmed: **Mojca Milavec, Senior Research Specialised Associate, Department of Biotechnology and Systems Biology, National Institute of Biology, Slovenia**	
17.55	**Chair's Closing Remarks and End of Day 1**	
17.55-19.00	**Networking Drinks Reception**	

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

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08.00-08.35	**Registration, One-to-One Networking Meetings, & Coffee**	
08.35-08.40	**Global Engage Welcome Address** **Stream Chair's Opening Remarks: TBC**	
08.40-09.10	**Keynote Address:** **Novel methods for enrichment of mutations and differentially methylated sequences from tumor and liquid biopsy DNA** Circulating DNA is poised to become a widely used tool for repeated assessment of cancer mutation and methylation status during the course of therapy. Removing the high excess wild type DNA fraction from circulating DNA allows enrichment of variant DNA and boosts the potential of all endpoint detection technologies, including sequencing. We present Nuclease-assisted Mutation Enrichment, NaME, a simple and powerful approach to remove wild type DNA from large gene pools simultaneously, in order to focus sequencing on clinically relevant DNA alterations. This single-step approach retains current sample preparation protocols almost unchanged and combines seamlessly with downstream technologies such as HRM, COLD-PCR, ddPCR and next generation sequencing. Application in clinical samples and liquid biopsies will be presented. Confirmed: **Mike Makrigiorgos, Professor of Radiation Oncology, Dana Farber Cancer Institute and Harvard Medical School, USA**	
09.10-09.40	**Solution Provider Presentation** RESERVED FOR PLATINUM SPONSORS For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk	
	Track 1 – Healthcare Case Studies	**Track 2 – Plant, Food and Environmental Case Studies**
09.45-10.15	**Tumor Derived Cell Free DNA as a Diagnostic Tool for Human Malignancies** Human malignancies shed molecules of cell free DNA into the bloodstream and adjacent bio-fluids. These molecules of cell free tumor DNA can be distinguished from the background normal DNA by the presence of somatic mutations. Using sensitive digital approaches, we are now able to detect and track tumor DNA levels over time. Such an approach can theoretically be applied for applications related to screening, disease monitoring and treatment response. Confirmed: **Chetan Bettegowda, Assistant Professor of Neurosurgery, Johns Hopkins University, USA**	**Automated Environmental Sampling and Testing by dPCR – Title TBC** Confirmed: **John Griffith, Principal Scientist and Coordinator of Molecular Technology, Southern California Coastal Water Research Project, USA**
10.15-11.25	**Morning Refreshments** **Poster Presentation Sessions and One-to-One Networking Meetings**	
11.25-11.55	Solution Provider Presentation **Title To Be Confirmed** jnmedsys Confirmed: **Senior Representative, JN Medsys**	**Solution Provider Presentation** For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk
11.55-12.20	**Aneuploidy screening of embryonic stem cell clones by metaphase karyotyping and droplet digital polymerase chain reaction** The successful germ line transmission of a mutated allele in embryonic stem (ES) cells depends on karyotypic integrity. Classical methods for the identification of aneuploidy involve cytological analyses that both are time consuming and require rare expertise to identify mouse chromosome. We validated a PCR based method as an alternative to classical karyotype analysis that enables laboratories that are non-specialist or work with large numbers of clones to precisely assess ES cells for the most common aneuploidy found in ES cells prior to microinjection to maintain high level of germ line transmission potential. This method can be applied to any other cell line (iPS, human cells …) to evaluate the karyotypic integrity. Confirmed: **Guillaume Pavlovic, Head of Genetic Engineering and Model Validation Department, Mouse Clinical Institute, France**	**Using Quantitative PCR and Digital PCR for Fecal Pollution Source Tracking in Environmental Waters** The detection of the origin of fecal pollution in complex watersheds is beginning to take a prominent place in hazard identification and risk management policies. Microbial source tracking (MST) is a field that has developed molecular methods to differentiate various sources of fecal contamination from humans and animals. Most of the MST methods utilize genetic markers, which are host-specific, or library independent, and rely mainly on quantitative PCR without cultivation of the microorganisms. This presentation will focus on the use of qPCR- and digital PCR-based MST for determining the sources of fecal pollution in watersheds in Michigan Confirmed: **Tiong Gim Aw, Research Associate, Department of Fisheries and Wildlife, Michigan State University**
12.20-12.45	**Digital PCR: A tool for clinical investigations of pediatric-onset genetic disorders** • Establishments of new digital PCR services for bench to bedside translational research, a core lab perspective • Copy number variation in Spinal Muscular Atrophy, dPCR as a tool for genotype/phenotype correlation • Complex genomic rearrangements at the PLP1 locus, dPCR as a deliverable for breakpoint studies Confirmed: **Katia Sol-Church, Director Nemours Biomolecular Core Lab Alfred I. duPont Hospital for Children**	**PMA RT-qPCR for water quality analysis – Title TBC** Confirmed: **Sandhya Parshionikar, Acting Associate Division Director, Water Supply and Water Resources Division, US Environmental Protection Agency**

12.45-13.10	**Identification of miRNA biomarkers for pediatric lung disease using PCR profiling** • Using miRNAs as biomarkers and diagnostic tools for human lung diseases: selecting the best sample source. • Bronchopulmonary dysplasia and Pulmonary Hyperternsion in the preterm infant, using miRNA profiling to identify patients and risk and therapeutic targets. • Common technical challenges when profiling by PCR, strategies for data analysis and interpretation. Confirmed: **Patricia Silveyra, PhD Assistant Professor, Department of Pediatrics, The Pennsylvania State University College of Medicine, USA**	**Quantitative Real-time PCR for Detection of Food Allergens** QPCR is a highly sensitive and specific detection method for allergenic foods. This talk will focus on development of qPCR methods for detection of crustacean shellfish. For this work, group-specific assays were developed for shrimp, crab, and lobster using mitochondrial 12S and 16S gene sequences. The method was evaluated for detection of crustaceans at concentrations from 0.1 to 10^5 ppm (mg/kg) in a variety of food matrices and processing conditions, including foods with inherently low DNA content, acidic pH, and foods treated with high temperature and pressure. With the exception of combined conditions of high temperature, high pressure, and acidic pH, the assays were linear over 6-8 orders of magnitude, with high reaction efficiencies and detection limits of approximately 0.1 to 1 ppm. Confirmed: **Anne Eischeid, Research Scientist, US Food and Drug Administration, Center for Food Safety and Applied Nutrition**
13.10-14.10	**Lunch**	
14.10-14.35	**MammaTyper – Making Breast Cancer Stratification Reproducible** Breast cancer has been recognized as multiple diseases, each subtype requiring a different therapy. Correct determination of the subtype of breast cancer is therefore crucial to therapeutic choice and patient's prognosis on survival. MammaTyper, a CE/IVD marked test, combines proven medical principles with state-of-the art RT-qPCR measurement technology to conclude the subtype of breast cancer. The test determines the gene expression level of markers, which are recommended by guidelines and provides results with highest precision and reproducibility. Analytical and clinical validation data are provided and precision as well as clinical utility in adjuvant and neo-adjuvant setting is discussed. A CE/IVD certified optimized and simplified process for sample preparation from FFPE tissue material is also revealed. Confirmed: **Konrad Faulstich, Director of Business Development and Project Management, BioNTech**	**Food Case Study** Invitation to:
14.35-15.00	**The use of digital detection in leukemia** Digital detection allows for the detection of rare transcripts or leukemia cells, which is important in the quantification of residual disease, as well as understanding clonal selection and expansion. This talk we describe the various ways digital analysis can be used in the research and management of leukemia patients, especially in the context of discontinuation strategies in chronic myeloid leukemia. Confirmed: **Jerald Radich, Director the Molecular Oncology Lab and Member of Clinical Research Division, Fred Hutchinson Cancer Center, Professor of Medicine, University of Washington School of Medicine, USA**	**Late Blight: A reemerging plant disease that threatens global food security** • Plant pathogens cause losses estimated to be as high as $30 billion per year and the risk of spread of pathogens globally with trade requires continued monitoring and improved diagnostic capabilities. • Late blight caused by *Phytophthora infestans* causes a devastating disease of potato and tomato and was responsible for the Irish potato famine. • Her work on the population genetics of historical epidemics of the pathogen and the population structure of present day late blight outbreaks will be discussed as well as the pioneering research techniques on 150-year-old historic herbarium specimens. Confirmed: **Jean Beagle Ristaino, William Neal Reynolds Distinguished Professor, North Carolina State University**
15.00-15.25	**Droplet digital PCR, liquid biopsies and patient follow-up** Droplet digital PCR allows for analysis of specific genetic markers with high sensitivity and precision Analysis of liquid biopsies by digital PCR is a highly pertinent tool for patient follow up and treatment management Illustrative examples will be presented both for different markers and different cancer types. Confirmed: **Valerie Taly, Group Leader, University of Paris Descartes, France**	**qPCR assay development for Fusarium virguliforme analysis in soybean – Title TBC** Confirmed: **Martin Chilvers, Assistant Professor, Department of Plant, Soil and Microbial Sciences, Michigan State University**

15.25-15.50	**Biomarker Identification and Viral Tracking of Cancer-Selective Immunotherapy Drug Product in Recurrent High Grade Glioma Clinical Trials** Toca 511 (vocimagene amiretrorepvec) is an investigational retroviral replicating vector that encodes the transgene cytosine deaminase. Toca 511 can be delivered by multiple routes and selectively infects and spreads in tumor cells. Subsequent oral administration of investigational 5-fluorocytosine (Toca FC) results in formation of the antineoplastic drug 5-fluorouracil within infected tumors. Thus, clinically, treatment with Toca 511 and extended-release 5-FC (Toca FC) is designed to selectively destroy tumor cells within the body, while leaving healthy cells unharmed. This presentation will focus on the viral drug monitoring program and biomarker identification program using real time and digital PCR assays to support current phase I and II clinical trials. Confirmed: **Derek Ostertag, Head of R&D Diagnostics, Tocagen Inc**	**Digital PCR detection of Candidatus Liberibacter species in citrus and Asian citrus psyllids** • Worldwide citrus production is being devastated by Huanglongbing (HLB), a disease associated with Candidatus Liberibacter sp. (CLas) a bacterial pathogen, vectored by insects known as citrus psyllids (ACP). Confirmation of CLas infection has important regulatory consequences and is an essential component of HLB management. • Currently, CLas infection can only be confirmed via PCR technology, and quantitative real time PCR is the USDA APHIS approved protocol for survey. Suspect samples must be confirmed by conventional PCR. Digital PCR may provide a more sensitive assay for confirmation of infection. • We have compared detection of CLas via digital PCR with quantitative real time PCR and conventional PCR. Our results indicate digital PCR may serve as alternative to conventional PCR for confirmation of CLas infection. Confirmed: **Greg McCollum, Research Plant Physiologist, USDA Agricultural Research Service**
15.50-16.20	**Afternoon Refreshments** **Poster Presentation Sessions**	
16.20	**Chair's Closing Remarks and Conference Close**	

Venue

Hilton Philadelphia City Avenue
4200 CITY AVENUE,
PHILADELPHIA, PENNSYLVANIA,
19131, USA

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.

The 2nd qPCR and Digital PCR Congress USA is co-located with:

The Microfluidics Congress USA

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