High quality biological resources are critical pre-requisite for research and clinical diagnosis. Evidence-based practices in biological resources research have been promoted by research institutions and programs such as the US NCI Biospecimen Research Network (BRN), and SPIDIA, a consortium funded by the European Union. These projects and programs identified major questions of methodology and pre-analytical variables that could influence the quality of samples. They also resulted in significant findings that should promote best practices for biological resources use in clinical and basic research programs.

The aim of this meeting is to disseminate evidence-based practices, and promote integration of the results of such studies into research and clinical practice.

Attendees

Researchers from European and Asian biobanks.

The meeting will be followed by a two days practical laboratory course on pre-analytical sample processing in biobanks.

The meeting will deal with quality control of

- Tissue samples
- Brain samples
- Tumors
- Liquid samples
- Nucleic acids
- Proteins
- Cell cultures
Biobanking National Infrastructures meeting
17-19th May 2016 - Nice, France

Speakers

BECKER Karl Friedrich  Universitäts-München-Institut für Pathologie, Germany
BJÖRKMAN Jens  TATAA Biocenter - Göteborg, Sweden
BONNET Jacques  Inserm U916, Bordeaux, France
CLEMENT Bruno  Inserm UMR 991, Rennes, France
DAGHER Georges  Inserm US13, Paris, France
DAIDONE Maria Grazia  Instituto Tumori, Milan, Italy
DUYCKAERTS Charles  Inserm U106, Paris, France
ERB Gilles  Roche diagnostics, France
GERLIER Denis  CIRI, Lyon, France
HASLACHER Helmuth  BBMRI, Wien, Austria
HOFMAN Paul  Inserm1081, CHU Nice, France
HUPPETZ Berthold  Medical Graz University, Austria
JUNOT Christophe  CEA, Paris, France
LAVITRANO Maria Luisa  Milan Bicocca Univ, Italy
LAWLOR Rita T.  ARC-NET Research Centre, Italy
LITTON Jan-Eric  Karolinska Institute - Sweden
LOIBNER Martina  Medical University of Graz, Austria
LUNDEBERG Joakim  Karolinska Institute - Sweden
MATHIESON William  Integrated BioBank of Luxembourg, Luxembourg
METSPALU Andres  Estonian Genome Center, Estonia
MOORE Helen  National Cancer Institute, USA
MORENTE Manuel  Spanish National Cancer, Spain
NAIMI Ben Youssef  Anygenes, Paris, France
OELMUeller Uwe  QIAGEN, Germany
OLLIER Bill  CIGMR, UK
PARODI Barbara  IRCCS AOU San Martino – IST, Genoa
RUAN Liangliang  Shanghai Clinical Research Center
STANTA Giorgio  Trieste University, Italy
TURANO Paola  Magnetic Resonance Centre, Florence, Italy
VACHER Coralie  Illinum, UK
VAUGHT Jim  ISBER, USA
WANG Peng  Beijing Capital University, China
WATSON Peter  BC Cancer Agency, Vancouver Island Center, Canada
WICHMANN Erich  Helmholtz Zentrum Muenchen, Germany
YUILLE Martin  CIGMR, UK
ZAOMI Myriam  Inserm US013, Paris, France
ZATLOUKAL Kurt  Medical Graz University, Austria

The construction and operation of national biobanking infrastructure

Georges DAGHER  The French National infrastructure for biobanking
Maria Luisa LAVITRANO  The Italian National infrastructure for biobanking
Kurt ZATLOUKAL  The Austrian National infrastructure for biobanking
Manuel MORENTE  The Spanish National infrastructure for biobanking
# Preliminary Program

## TUESDAY MAY 17, 2016

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Speaker</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:00</td>
<td><strong>Welcome &amp; Opening Remarks</strong></td>
<td>G. DAGHER</td>
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<tr>
<td>10:00</td>
<td><strong>Session 1 : Controlling Preanalytical factors</strong></td>
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<td>Why it is mandatory to control the pre analytical phase in biobanking activity associated with personalized medicine projects?</td>
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<td>Standardized improved pre-analytical workflows: the bridge to good quality samples for reliable analytical test results.</td>
<td>U. OELMUELLER</td>
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<td>11:00</td>
<td>Developing evidence-based preanalytical procedures in metabolomics.</td>
<td>P. TURANO</td>
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<td>11:30</td>
<td>Using tissue samples for quantitative protein and phosphoprotein analysis – critical considerations</td>
<td>K.-F. BECKER</td>
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<td>12:00</td>
<td>How to define sample quality in rapidly developing field?</td>
<td>K. ZATLOUKAL</td>
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<td>12:30</td>
<td>U.S. perspective on developing biospecimen evidence-based practices</td>
<td>H. MOORE</td>
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<td>13:00</td>
<td><strong>Lunch break</strong></td>
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<tr>
<td>14:30</td>
<td><strong>Session 2. The present and future of biobanking</strong></td>
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<td>14:30</td>
<td>Pan European infrastructure BBMRI-ERIC.</td>
<td>J. E. LITTON</td>
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<td>15:00</td>
<td>The Austrian national infrastructure.</td>
<td>K. ZATLOUKAL</td>
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<td>15:20</td>
<td>The French National Infrastructure.</td>
<td>G. DAGHER</td>
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<td>15:40</td>
<td>The Italian National infrastructure.</td>
<td>M.-L. LAVITRANO</td>
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<td>16:00</td>
<td>The Spanish National infrastructure.</td>
<td>M. MORENTE</td>
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<td>16:20</td>
<td>The Beijing infrastructure.</td>
<td>P. WANG</td>
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<td>16:40</td>
<td><strong>Break</strong></td>
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<td>17:00</td>
<td><strong>Next Generation Biobanking.</strong></td>
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<td>17:00</td>
<td>Precision Public Health: the essential role of healthcare-integrated biobanks .</td>
<td>B. OLLIER</td>
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<td>M. YUILLE</td>
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<td>17:40</td>
<td>Next generation histology using next generation sequencing.</td>
<td>J. LUNDEBERG</td>
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<td>18:00</td>
<td>Next Generation Biobanking.</td>
<td>P. HOFMAN</td>
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<td>18:20</td>
<td>Sustainability of biobanking.</td>
<td>B. CLEMENT</td>
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<td>18:40</td>
<td>Open discussion.</td>
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<td>20:00</td>
<td><strong>Cocktail reception &amp; Dinner</strong></td>
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WEDNESDAY MAY 18, 2016

9:00  Session 3. Quality control in Genomics

9:00  Quality control for the quantification of gene expression biomarkers.  J. BJÖRKMAN
9:30  The importance of quality biobanking in the development of Cancer Care.  R. T. LAWLOR
10:00  Total genomic solution for Biobanks, maximize the value of your specimen.  C. VACHER
10:30  Upcoming title.  B. NAIMI
11:00  Coffee break
11:30  Quality Control standard for nucleic acids.  J. BONNET
12:00  RNA in Archive Tissues: Degradation Causes and Extraction Precautions.  G. STANTA
12:30  Discussion.
13:00  Lunch

15:00  Session 4. Quality control in Biobanks

15:00  Evidence-based biobanking practices.  J. VAUGHT
15:30  Quality control in a Brain Bank.  C. DUYCKAERTS
16:00  Phenotypes and samples in the Estonian Biobank: ensuring the quality and control.  A. METSPALU
16:30  Molecular biology-based quality control program: High-quality biobanking in China.  L. RUAN
17:00  Free time
18:15  BIOBANQUES SAB meeting
<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Title</th>
<th>Presenter</th>
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<tbody>
<tr>
<td>9:00</td>
<td>Session 5.</td>
<td>Good practices in cell culture.</td>
<td>B. PARODI</td>
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<td>9:30</td>
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<td>Quantitative detection of Mycoplasma by Real-Time PCR of a 1.5 kb fragment using degenerate universal primers targeting 16S rDNA.</td>
<td>D. GERLIER</td>
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<td>10:00</td>
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<td>Pre-analytic processing of liquid samples in population cohorts in Germany.</td>
<td>E. WICHMAN</td>
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<td>10:30</td>
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<td>Challenges in using liquid biopsies for precision medicine.</td>
<td>M.-G. DAIDONE</td>
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<td>11:00</td>
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<td>Coffee break</td>
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<td>11:30</td>
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<td>Topic to be defined.</td>
<td>G. ERB</td>
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<td>12:00</td>
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<td>Metabolomics of tissues.</td>
<td>P. TURANO</td>
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<td>12:30</td>
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<td>Liquid biopsies for metabolomics (To be confirmed).</td>
<td>C. JUNOT</td>
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<td>13:00</td>
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<td>Discussion.</td>
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<td>Lunch</td>
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<td>15:00</td>
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<td>Storage of paraffin tissues: Increasing sample retrieval rates by automation.</td>
<td>B. HUPPETZ</td>
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<td>15:30</td>
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<td>Quality assurance programs and tools to disseminate biobanking standards.</td>
<td>P. WATSON</td>
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<td>16:00</td>
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<td>Implementing quality management in French Biobanks: Lessons from 10 years of experience.</td>
<td>M. ZAOMI</td>
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<td>16:30</td>
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<td>Towards a national cross-auditing system.</td>
<td>H. HASLACHER</td>
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<td>17:00</td>
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<td>Internal and External Quality Control at the Integrated Biobank of Luxembourg.</td>
<td>W. MATHIESON</td>
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<td>17:30</td>
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<td>Discussion.</td>
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<td>End of meeting</td>
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TUESDAY MAY 17, 2016

Paul HOFMAN. Why it is mandatory to control the pre analytical phase in biobanking activity associated with personalized medicine projects?

Summary: The onset of several targeted therapies and of new immunotherapy programs has dramatically changed the taking care of cancer patients. In this context, many molecules are currently under development targeting different receptors (located at the membrane, at the cytoplasm or at the nucleus) or targeting different intracellular pathways. The assessment of these different cellular targets is now strongly mandatory before treatment. Thus, the drug administration to the cancer patient is directly link to the presence or to the absence of the molecular target detected into the cancer tissue. These so called “companion diagnostic test” concern the establishment of different tests looking for genomic alteration or protein expression. The biological samples used in this context are variable and can be some tissue, cytological and blood (circulating tumor cells or circulating free DNA) samples. These different samples need to be very well managed for patients taking care. It is noteworthy that the databases associated with the biobanks integrate now more and more information concerning genomics data and companion diagnostic tests results in order to analyze these biomarkers according to the follow up of patients and to their treatment. The quality of the results depends greatly of the management of samples by controlling the different pre analytical parameters. The final goal is then to reduce the false negative and the false positive results. This presentation will explain the main pitfalls occurring during the management of samples during the pre-analytical steps and the potential consequences in both biopathology and biobanking activities.

Uwe OELMUELLER. Standardized improved pre-analytical workflows: the bridge to good quality samples for reliable analytical test results.

Summary: Molecular in vitro diagnostics and biomedical research have allowed great progress in medicine. Further progress is expected by new biomarker tests analyzing cellular biomolecule profiles such as nucleic acids, proteins, and metabolites. However, profiles of these molecules can change significantly during sample collection, transport, storage, archiving and processing, caused by post collection cellular changes such as gene inductions, gene down regulations, biomolecules modifications or degradation. This can make the outcome from diagnostics or research unreliable or even impossible because the analytical test will not determine the situation in the patient but an artificial bioanalyte profile generated during the pre-analytical process. High quality clinical samples with preserved bioanalyte profiles are therefore critical to biobanking, research and diagnostics. The EU FP7 SPIDIA consortium could achieve significant progress by developing new pre-analytical workflow technologies and by generating evidence for developing new standards. The European Committee CEN/TC 140 “In vitro Diagnostic Medical Devices” has released first 9 Technical Specification documents addressing pre-analytical workflows for different blood, other body fluids and tissue based molecular applications. They are currently under further development to International Standards within the ISO/Technical Committee 212 “Clinical Laboratory Testing and In Vitro Diagnostic Test Systems”. The presentation will give an overview about SPIDIA’s and thereon build other international project’s achievements and future work.

Paola TURANO. Developing evidence-based preanalytical procedures in metabolomics.

Summary: Urine, serum, plasma, and saliva are commonly used biofluids for metabolomics analyses. Their content in small molecules provides a strong metabolic signature of the individual phenotype, called the metabotype, which can be stable over a long time scale (up to 10 years). Significant metabotype drifts are observed upon onset of pathophysiological conditions. Metabolomic fingerprinting is therefore used for disease diagnosis and prognosis and to evaluate the individual response to treatment. These approaches, however, require that the measured metabolic profile reflects as closest as possible the original individual metabolome. We have extensively used NMR to identify changes induced by
preanalytical procedures and to develop evidence-based SOPs for sample collection and handling. NMR-based metabolomics can also be applied for the evaluation of the quality of biobanked biofluids.

Karl Friedrich, BECKER. Using tissue samples for quantitative protein and phosphoprotein analysis – critical considerations.

Summary: Proteomics methods are very slowly or not at all translated into current clinical workflows for tissue analysis. Collecting human tissue samples is a complex process that varies between hospitals or even within single institutions. Standardization of the entire workflow from test ordering to the report of the proteomic assay, with special emphasis on the pre-analytical phase, is crucial for successful integration of proteomic studies in the clinic as protein and phosphoprotein profiles may change due to sample processing before the analytical test is performed. The goals of personalized medicine to offer more effective drugs to patients cannot be reached until the research community, funding organizations, journal editors, biobanks managers, in vitro diagnostic developers, and many others adopt and follow common international standards. The aim of this presentation is to highlight the progress of proteomic studies with human tissues and to discuss the challenges that must be understood and addressed for successful integration of proteomics methods to clinical practice.

Kurt ZATLOUKAL. How to define sample quality in a rapidly developing field?

Summary: There is general acceptance that even the best analytical technology cannot deliver reliable results when the quality of the samples analysed is not appropriate. The problem in reproducing scientific data is increasingly recognized a major issue resulting in major financial losses of R&D spendings and potential harm for patients. There are several reasons for lack of reproducibility identified, such as shortcomings in study design and lack of experimental details, particularly detailed description of identity and quality of biological samples analysed. This generates a major need for better standardization and description of pre-analytical details essentially in all fields of biological and medical research. This need has been boosted by recent developments in personalized medicine. The European commission has funded under its framework programme 7 the project SPIDIA (Standardization and improvement of generic pre-analytical tools and procedures for in-vitro diagnostics) to develop the scientific basis for reliable performance of molecular test and to translate this into standards and norms. The work of SPIDIA has led to several new CEN Technical Specifications (TS) for molecular in vitro diagnostic examinations – specifications for the pre-examination processes, which are addressing specific pre-analytical quality requirements for human blood and tissue samples as well as the most relevant analytes (i.e., DNA, RNA, proteins, metabolites). The TS are developed for molecular in vitro diagnostic laboratories but give explicit reference also to biobanks and developers of diagnostics. The TS are defining all critical steps of sample pre-analytics from collecting the sample from the patient to transport, processing, storage (biobanking) and isolation of the analyte. They do not deal with issues of analytical technologies, medical diagnosis or patient treatment. TS have to be generally applicable and may not refer to specific products; therefore, TS do not refer to the same level of technical detail as Standard Operating Procedures (SOPs). Nevertheless TS define critical issues to be further specified in SOPs. The CEN TS for molecular in vitro diagnostic examinations – specifications for the pre-examination processes provide a series of useful definitions, few concrete recipes (e.g., for Standard Formalin Solution) and a long list of documentation requirements of quality relevant parameters. These TS will also gain relevance in the context of the upcoming European regulatory framework for in vitro diagnostic (EU IVD Regulation), which requests validation of several key pre-analytical parameters in the development of molecular diagnostics.

Helen MOORE. U.S. perspective on developing biospecimen evidence-based practices.

Summary: The U.S. National Cancer Institute (NCI) has played a leading role in developing Best Practices for Biospecimen Resources, sponsoring new research in Biospecimen Science, and building groundbreaking research biospecimen collections including postmortem biospecimens for the NIH GTEx program. The ultimate goal of these efforts is to increase the reproducibility of basic and clinical research. The field has greatly advanced since the launch of the NCI Best Practices and the NCI Biospecimen Research Network (BRN) in 2007. This presentation will address the following questions: What have we learned from the BRN? How can we move from biospecimen science research data to biospecimen evidence-based practices? What’s the difference between evidence-based practices and SOPs? What new research funding programs do we need to carry this work forward? What will we do in the U.S. to build evidence-based practices? How can...
we work internationally to collaboratively review and consider the weight of various sources of biospecimen science research data?

**Joakim LUNDEBERG.** Next generation histology using next generation sequencing.

**Summary:** Histological analysis with different staining techniques first established the basic structural organization of healthy organs and the changes that take place in common pathologies more than a century ago. Yet these histological techniques are limited by low throughput, being restricted to the analysis of single or few markers in individual tissue sections. With the introduction of next generation sequencing more global and quantitative measurements can be achieved. In this presentation a new approach will be demonstrated that combines histology and RNA sequencing denoted Spatial Transcriptomics. This allows for visualization and quantitative analysis of the transcriptome with spatial resolution in individual tissue sections.

**Peng WANG** Beijing Biobank of Clinical Resources, BBCR.

**Summary:** In May 2009, Beijing Municipal Science and Technology Commission launched the project “Beijing Clinical Data and Specimen Resources for Ten Major Diseases (hereinafter referred to as Beijing Biobank of Clinical Resources, BBCR)” and funded the project. Capital Medical University was commissioned as the project leader. BBCR is characterized by having multiple disease categories, large scale participating hospitals, which brought great challenges for unified standardization and bioinformatics management. The project team strictly implemented the idea of “1-2-3 rule”, which means unified standards, two-level management and the third-party supervision, thereby accumulating experiences and providing these useful experiences for the future similar projects.

**Bill OLLIER, Martin YUILLE** Precision Public Health: the essential role of healthcare-integrated biobanks.

- First talk: Precision Public Health and an “engine” for health improvement
- Second talk: From theory into practise

**Summary:** Precision Public Health (PPH) builds on the concept of Predictive Preventive Personalised Participatory (P4) medicine by applying it in the field of Public Health implemented via primary care. PPH aims at prevention (preventing or delaying risk factor exposure) using individual risk profiles developed for all members of the population. Whereas Precision Medicine in the UK refers to the development of more precisely targeted medicines including new medicines, PPH refers to the development of Public Health policy and practice to achieve universal prevention by including new tools such as biomarkers in order yo specify individualised health improvement interventions. For practical reasons, a PPH pathfinder project starts with a selective prevention strategy but the goal is universal prevention. While P4 medicine is also preventive in its intentions, it is seen as being driven by the consumer. PPH is driven by public policy. It therefore has a good prospect of achieving improved population health regardless of socio-economic and educational status. The universal principles of the UK national Health Service provide a critical policy element that allows PPH. We are developing a PPH pathfinder project for Greater Manchester (GM). Recent decentralisation of national health funding to GM will facilitate evidence-based population health improvement by enabling greater integration across local government services (health, Public Health, social care but also education, transport, housing). A key policy driver will be the adoption of obesity onto the Community Risk Register. An obesity epidemic exists in the UK and, by recognising this on the risk register, policies and practices across the range of local government responsibilities can be reviewed and modified to address the epidemic. The PPH pathfinder project should be implemented in one part of GM (Salford) where the essential infrastructure for PPH already exists. This infrastructure comprises a hospital-based high-throughput quality-managed biobank, integrated electronic health records across all of primary and secondary care and a suite of health improvement interventions. For the pathfinder, about 10,000 participants (18 -49 years old) will be recruited via family doctors to the project. They will consent to research, provide a sample, undergo a health check and receive feedback. This feedback will use biomarker and other data to calculate an individual’s current risk of chronic disease including obesity-related disease. This risk information will be provided along with education on suitable preventive action and offers of access to health improvement interventions. Taken together, the project will reduce exposure to risk factors and thus improve health. It will also provide a platform for basic, translational and implementation research for improved PPH and, simultaneously, for Precision Medicine.
WEDNESDAY MAY 18, 2016

Jens BJÖRKMAN. Quality control for the quantification of gene expression biomarkers.

**Summary:** Measuring an RT-qPCR signal with an assay targeting a transcript of interest is easy and the data generated often look good, but it is a different story if the signal truly reflects the amount of targeted transcript that actually were present in the sample in vivo. This has to be validated to greatest extent possible by performing relevant controls. I will describe quality control measures to test for degradation of RNA, inhibition, genomic DNA background and also provide means to compensate for interplate variation.

Rita T. LAWLOR. The importance of quality biobanking in the development of Cancer Care.

**Summary:** The essence of personalized lies in the ability to effectively diagnose disease, determine whether the disease is likely to progress, identify the drug most likely to be effective, evaluate side effects or whether further therapy can be avoided for each individual. This requires a sufficient number of high quality materials (qualified and molecularly characterized) and information be available for validation of these tests and for drug development initiatives to validate drugs on models derived from the original disease biomaterial, selected according to the appropriate target group, before being moved to clinical trials. The procurement of high quality cancer samples is the critical first step where the quality of the sample pertains to the vitality of the sample, the quality of the neoplastic component, the quality of the molecular components. This pre-analytical information provides vital insight into potential discrepancies in genomic data due to sample collection and handling processes. However, associated clinical/pathological data permits the correlation of the genomic data with the disease being investigated and the quality of this data is also important. The potential for variability is immense and requires evidence based best practices to reduce the variability and conjugate the term quality at each step of the process.

Coralie VACHER. Total genomic solution for Biobanks, maximize the value of your specimen.

**Summary:** Illumina’s mission is to improve Human health by unlocking the power of the genome, from genome-wide discovery to targeted validation and beyond. The presentation will cover all aspects of the genetic analysis workflow for biobanks; from characterization of specimen, to QC, in depth genetic profiling and data analysis.

Jacques BONNET. Quality Control standard for nucleic acids.

**Summary:** In order to be suitable for the analyses and manipulations for which they have been prepared, nucleic acids must obey certain quality standards. Low quality can also lead to nucleic acids instability during storage. Various quality control tests have been developed. The basic principles of these tests are universally accepted and applied. However the common techniques may have some drawbacks and limitations despite constant improvements of the equipments. Here I shall describe, without attempting to be comprehensive, the principles of some existing techniques, their limitations and possible adjustments and developments.

Giorgio STANTA. RNA in Archive Tissues: Degradation Causes and Extraction Precautions.

Jim VAUGHT. Evidence-based biobanking practices.

**Summary:** Methods for collecting, processing, storing and analyzing biospecimens have been developed with little consideration for standardization or long-term quality management. Various pre-analytical variables can affect the quality of biospecimens. There is the potential for: incorrect diagnoses; incorrect treatment; irreproducible results; and the
Potential for misinterpretation of artifacts as new biomarkers. The future development of international collaboration in biobanking will require evidence-based biobanking practices in order to exchange samples and data of consistent quality.

**Peter Watson.** Quality assurance programs and tools to disseminate biobanking standards.

**Summary:** Development of evidence-based standards and their implementation through internationally accepted best practices in biobanking is critical to address and improve quality in research. However, human research biobanking is a very diverse activity involving researchers as well as professional biobanks, and the need, depth, and relevance of distinct aspects of quality vary in different phases of research. Therefore, a spectrum of quality assurance programs is needed to communicate a staircase of standards to researchers as well as biobankers. This talk will highlight one of several quality assurance programs available internationally, the Canadian Tissue Repository Network (CTRNet) Certification Program (accessible through www.biobanking.org).

**Andres Metspalu.** Phenotypes and samples in the Estonian Biobank: ensuring the quality and control.

**Summary:** The presentation is an overview of how the Estonian Biobank designed in order to ensure the quality of the data collection, sample handling and quality control. Several specific steps were taken to achieve the maximum quality. First, due to the fact that we used the primary care providers and physicians and senior nurses in hospitals as recruitment personnel, we had to standardize everything and use the computer-assisted questionnaire. Second, special monitoring unit was set up at the biobank to oversee the incoming questionnaires and diagnoses were validated using the different eHealth databases, like EMR and eHealth database, hospital databases and national registries. Thirdly, LIMS system was developed for the sample handling and CSPro quality standard was obtained for the genotyping/sequencing facility. Finally ISO 9001:2008 quality management systems have been in place from the beginning. At the end I’ll give few examples how the quality really matters.

**Liangliang Ruan** Molecular biology-based quality control program: High-quality biobanking in China.

**Summary:** Biobanking has been considered as a cornerstone for translational medicine. The top priority of biobanking is to ensure high quality of biospecimens and associated data. Method validation is one of crucial processes for a quality-based biobank. However, there are no routine guidelines specially designed for such studies. Therefore, in line with the need for competence in testing and calibration, the ISO concept has been introduced to biobanking as a model for Quality Management Systems (QMS) in this field. In this study, we focused on the validation of DNA quantitation by spectrophotometry, a basic bio-analytical method in molecular biology. This simple validation model for DNA quantitation has been part of the sampling program for biospecimen quality control in China Biobanking Network.

**William Mathieson.** Internal and External Quality Control at the Integrated Biobank of Luxembourg.

**Charles Duyckaerts, Sabrina Leclere-Turbant, Marie-Claire Artaud-Botte** Quality control in a Brain Bank.

**Summary:** Brain often suffers much in the peri-mortem period. Markers of the quality of the tissue have been proposed: the pH of the cerebrospinal fluid has been considered one of those but its use remains limited. As for other tissues, the quality of the RNA may be tested by RIN. Western blots may help to analyze the integrity of the protein. However, one crucial question in neuropathology is the topography of the sample: for the cortex, for instance, the quantity of white matter present in the sample may drastically modify the quantity e.g. of cholesterol. The concentration in neuromediators is highly dependent on the region which is sampled. The distribution of the lesions is also discrete and highly regionalized: the examples of Alzheimer and Parkinson diseases are particularly illustrative. The control of the topography of the sample is thus one of the major difficulties in neuropathological research and has been variously solved. The expertise in...
neuroanatomy of the person performing the sample is a prerequisite that should be ascertained. The morphological examination of the sample before its use is certainly the safest technique.

**THURSDAY MAY 19, 2016**

**Barbara PARODI.** Good practices in cell culture.

**Summary:** Authenticity and purity of human and animal cell lines used in research is essential in order to guarantee reproducibility, reliability and proper application of any results produced. Internationally available guidelines and good practices for cell culture will be discussed, for development of new cell lines, authentication, preparation of master and working banks, cryopreservation, exchange between laboratories, microbial contamination and misidentification. The activities of the International Cell Line Authentication Committee (ICLAC) will also be presented.

**Denis GERLIER.** Quantitative detection of Mycoplasma by Real-Time PCR of a 1.5 kb fragment using degenerate universal primers targeting 16S rDNA.

**Summary:** The ever-growing usage of cell lines to understand every biological process at the molecular and cellular level and the ability of microbes and parasites to invade them put these tools under stringent quality scrutiny to ensure unbiased interpretation of cell-based experiments. One of the major recognized pitfalls in cell culture is the adventitious contamination by Mollicutes, usually referred as mycoplasma, Mycoplasma being a major subgroup of the Mollicutes within the Tenericutes taxa. Several techniques have been developed to detect mycoplasma but they are either cumbersome, difficult to interpret and/or limited to the detection of only a limited range of species. We have adapted and extended a PCR that amplifies a long DNA fragment using universal degenerate primers so as to detect Mycoplasma 16S rDNA by Real-Time PCR (RT-PCR) followed by a sequencing-based identification step. We will report the advantages of this technique by comparison of three other methods, Hoechst DNA labelling, MycoAlert® and PlasmoTest® in detecting and identifying mycoplasma contamination in cell cultures including in BSL1 to BSL4 virus stocks. This work was supported by a grant from the French BioBanques Infrastructure, IBISA and ANR.

**Erich WICHMANN.** Pre-analytic processing of liquid samples in population cohorts in Germany.

**Summary:** Linkage of high quality biosamples with detailed data from medical examinations, questionnaires and interviews offers great opportunities for research. This is particularly true for large scale prospective epidemiological studies with long observation periods, like the KORA Cohort in Augsburg and the German National Cohort (GNC). For the GNC 200.000 randomly selected adults will be recruited by 18 study centers and will be followed-up for 20-30 years. In addition to the extensive basic examination protocol, followed by reassessment examinations and follow-up questionnaires, the biorepository is a cornerstone of the GNC. The GNC biorepository will comprise more than 20 million aliquots of plasma, serum, erythrocytes, lymphocytes, urine, saliva, nasal swabs and stool. Preanalytics and aliquoting are performed locally in the study centers and are highly standardized and extensively automated. All samples are stored at -80°C and -180°C respectively. A laboratory information system documents all processing steps and storage locations. Access to data and biosamples will be granted to researchers within and outside Germany. Experience with already existing epidemiological biobanks like KORA shows impressive results, especially with regard to genetic research as well as post-genomics (e.g. transcriptomics, metabolomics, epigenomics). Previous success stories explain the strongly increased demand for data and biosamples from the population. These resources will become even more important for biomedical research in the future.

**Maria Grazia DAIDONE.** Challenges in using liquid biopsies for precision medicine.

**Summary:** For cancer management, predicting and monitoring response to treatment and disease progression longitudinally is crucial due to changes in tumor biology and therapy responsiveness over time. However, solid tumors are usually sampled only at time of initial diagnosis, as obtaining tissue biopsies is an invasive procedure with associated risks. Thus, there is a pressing need for approaches able to serially detect function-related reliable biomarkers reflecting treatment response and/or disease progression through easy noninvasive procedures, amenable for longitudinal analysis of tumor molecular features. Recent evidences indicate that blood and other body fluids could replace invasive surgical
biopsies and represent a "liquid biopsy" containing cells and nucleic acids released by primary and metastatic lesions, reflecting their biological features and allowing identification of clinically useful biomarkers and treatment-induced cancer adaption processes. The development of new and highly sensitive technologies that allow to detect and characterize circulating tumor cells, to identify cell-free nucleic acids (circulating tumor-associated microRNAs and cancer-specific mutations in circulating DNA) and to measure their eventual dynamic changes represents therefore a major achievement for disease monitoring. However, notwithstanding preliminary findings support the prognostic and/or predictive role of this new generation of biomarkers, there are a number of technical and biological caveats that still require additional studies to demonstrate and validate their clinical utility. Critical issues are represented by nonuniform sample choice, handling, and processing, as well as by blood cell contamination in sample preparation and lack of consensus for nucleic acid data normalization. The exciting potential of liquid biopsies as source of specific and sensitive cancer biomarkers could confer an important advance in the disease management, but their clinical significance might not be proven without a global consensus of procedures and standardized protocols for their accurate detection.

**Paola TURANO.** Metabolomics of tissues.

**Summary:** Tissues are particularly informative biospecimens in metabolomics because they directly report the metabolome of the diseased organ, where biomarker variations with respect to a healthy status are the most evident. However, the metabolome might be influenced by preanalytical procedures during and after medical intervention, as well as during storage. Here, we report about the use of NMR metabolic profiles to evaluate the effect of warm and cold ischemia on human liver tissues.

**Manuel MORENTE.** Quality as an ethical requirement.

**Summary:** Biobanking is more than a technical platform or activity. Biobanks are is the crossroad between individuals (donors), users (scientific community) and society (the final goal of every biomedical research and main funders of research and biobanks). In this whole context, quality of samples managed by biobanks is more than a technical issue and acquire an ethical dimension in order to respond to the altruist donation from subjects, the compromise with researchers and the perspective of the social value of our activity.

**Peter WATSON.** Quality assurance programs and tools to disseminate biobanking standards.

**Summary:** Development of evidence based standards and their implementation through internationally accepted best practices in biobanking is critical to address and improve quality in research. However human research biobanking is a very diverse activity involving researchers as well as professional biobanks, and the need, depth, and relevance of distinct aspects of quality vary in different phases of research. Therefore a spectrum of quality assurance programs is needed to communicate a staircase of standards to researchers as well as biobankers. This talk will highlight one of several quality assurance programs available internationally, the Canadian Tissue Repository Network (CTRNet) Certification Program (accessible through www.biobanking.org).
BECKER, Karl-Friedrich
Prof. Becker is Head of the Laboratory for Experimental Pathology at the Technical University of Munich, Germany. As partner of the European large-scale project SPIDIA (www.spidia.eu) and the m4 Munich Cluster of Excellence (www.m4.de) he analysed the variability of protein and phosphoprotein levels in clinical tissue specimens during the pre-analytical phase. Prof. Becker is expert and project leader of CEN/Technical Committee 140 (In-vitro Diagnostic Medical Devices) Working Group 3 and ISO/TC 212 (Clinical Laboratory Testing and In vitro Diagnostic Test Systems) Working Group 4.

BONNET, Jacques
Jacques Bonnet was initially trained as a chemical engineer (Strasbourg, 1967). His Science Thesis was about transfer RNA sequencing and interactions with aminoacyl-tRNA synthetases (1975). A two year postdoc stay (School of hygiene, Baltimore) brought him to work on the structure and expression of the hamster genome. In 1980 he was appointed professor at the Bordeaux University to teach nucleic acids physico-chemistry and molecular biology while working on gene expression in normal and pathologic nervous system and in cancer cells. In parallel, he has been and is still involved in various research and development projects in relation with academia and industry such as PCR detection of pathogens or the creation and scientific direction of Imagine Company. He is now emeritus Professor at Bordeaux University.

CLEMENT, Bruno
After a Ph.D. in Cellular and Molecular Biology, Bruno Clément joined the NIH in Bethesda, as a post-doctoral fellow for 3 years. In 1985, he was appointed at Inserm, and in 1992, he headed a group focused on liver cancer and the tumor microenvironment, in the “Liver Research” Inserm unit, in Rennes. He was member of the editorial board of Hepatology in 1997-2007. From 1998 to 2003, Bruno Clément was appointed at the Ministry of Research as a counselor and deputy-director of the Biotechnology Department. He was involved in the implementation of the Law on Innovation, the Biological Ressources Centres program, and the Biotechnology clusters. He was member of several international committees on biobanks and biotechnology, e.g. in OECD and in the European Commission. From 2003 to 2007 he was appointed counselor of the general director of Inserm for biobanks and biotechnology development, and scientific director of INSERM-Transfert, the TTO subsidiary of Inserm. He is currently CSO of the national BIOBANQUES infrastructure. In 2010 he was appointed Director of the Inserm unit n°991 “Liver, Metabolisms and Cancer”. Bruno Clément has published 130 papers in international peer-reviewed journals in the field of liver physiopathology, the role of the microenvironment in tumor progression and the development of innovative diagnosis and therapeutic tools for the treatment of liver cancers. More: http://cvscience.avesan.fr/cv/1179/bruno-clement

DAGHER, Georges
Georges Dagher, senior investigator at Inserm (Paris, France) accomplished most of his career in pathophysiological and clinical research at Necker Hospital (1979-1984), College de France (1985-1993) and Faculty of medicine Broussais-Hotel Dieu (1994-2004). He joined the Physiological Laboratory (Cambridge, UK) for a post doc fellowship (1983-85) and was a special guest to Physiological laboratory (Harvard Medical School, Boston, US, 1982, 1984). Georges Dagher published 90 papers in international peer-reviewed journals on hypertension, arterial hypertrophy, obesity and lipid metabolism, manic depression, renal physiology and trans-membrane ion transport. He is currently the Director of BIOBANQUES infrastructure a French infrastructure that regroups 85 biobanks (Inserm US 13), and Vice Chair of the pan-European infrastructure BBMRI-ERIC. He was the director of clinical research infrastructures at Inserm (2006-2009) and the deputy director of the department of clinical research at the Public Health Institute, Inserm, France (2009-2011). He was also a member of the ethics committee and the Institutional Review Board (IRB) at Inserm.
DAIDONE, Maria-Grazia
Graduated in Biological Sciences and Certified Board in Biostatistics at the University of Milan. She started her scientific career at Istituto Nazionale Tumori in Milan, where she is currently Head of the Biomarkers Research Unit and Director of the Department of Experimental Oncology and Molecular Medicine. She served the EORTC as Chairperson of the PathoBiology Group, and is currently in the Scientific Committee of BBMRI.it. Her scientific interests are dealing with: a) biomolecular characterization of solid lesions and liquid biopsies from several tumor types; b) identification and validation of biomarkers associated with cell proliferation, apoptosis and cell survival; c) relationship between gene expression profiles and clinical progression and/or treatment resistance in breast cancer; d) isolation, characterization and propagation of tumor-initiating cells obtained from human solid tumors; e) coordination of quality control studies for cancer biomarkers and proposition of guidelines for the clinical use of biomarkers; f) biobanking research.

DUYCKAERTS, Charles
Charles Duyckaerts, MD, PhD, born on December 16, 1951 in Liège, Belgium, is professor of Pathology at the University of Paris VI and head of the neuropathology laboratory at La Salpêtrière hospital. He has co-directed, at ICM (Institut du Cerveau et de la Moelle), the Inserm team “Alzheimer & Prions diseases” from 2009 to 2014, and is currently senior investigator. He has been the administrator of the National Brain Bank NeuroCEB since 2005. He has been co-chair of the scientific committee of the Alzheimer Association International Conference in Vancouver (2012). He has received the Henry Wisniewski Award for lifetime achievement in Alzheimer research (2006). He is doctor honoris causa of the University of Louvain (2014).

HOFMAN, Paul
Hospital-related Biobank (BB-0033-00025) University of Nice Sophia Antipolis and Inserm U10181 UMR CNRS 7284, IRCAN, Faculty of Medicine and FHU OncoAge, Pasteur Hospital, Nice, France
Paul Hofman is Professor of Pathology at the Nice Sophia Antipolis University, France. He did post doc trainings in Pathology at the Brigham and Women’s Hospital (Harvard Medical School USA) and at the Max Planck Institute (Tübingen, Germany). He heads the Laboratory of Clinical and Experimental Pathology, Pasteur Hospital, University of Nice Sophia Antipolis, France. He is the director of the FHU OncoAge at Nice Sophia Antipolis and of the Hospital-related biobank (BB-0033-00025) located in the Comprehensive Cancer Center and in the Hospital of Nice. He is the director of the Inserm U10181/UMR CNRS 7284 (IRCAN team 3) aiming to decipher the mechanisms occurring during the cross talk between inflammatory and cancer cells. IRCAN and OncoAge Centers (www.oncoage.org) aim to better understanding the different processes linking ageing process and cancer diseases. He published 487 papers (pubmedNCBI January 2016).

LAVITRANO, Maria Luisa
Marialuisa Lavitrano is professor of Pathology, director of Molecular Medicine Lab and pro-rector for international affairs at the Milano-Bicocca University. She participated to the preparatory phase of the European Biobanking and Biomolecular Resource Research Infrastructure (BBMRI) as Italian member state representative and she has been recently appointed BBMRI-IT Node Coordinator. For four years she developed the international strategies for the Ministry of Health and coordinated the Italian participation in the BioMedical Sciences ESFRI roadmap. Prof. Lavitrano is actively involved in research in molecular medicine with a translational approach for the transfer of the scientific results to the clinical practice. She also founded a university spin off for the development of tumour markers and of modulator compounds of drug resistance in epithelial tumours. Moreover, she is interested in bioethical aspect of science and research and participated at Bioethic Commissions of the Council of Europe, of the Vatican and of the Italian government.

LAWLOR, Rita T.
Rita T. Lawlor is a Computer Science graduate of Trinity College Dublin but works in Verona where she was the co-founder and project manager of the ARC-Net (www.arc-net.it) cancer research centre at the University of Verona, Italy and is completely a doctorate in Oncological Pathology. She runs the ARC-Net biobank and coordinates the biobank activities for the national AIRC SX1000 funded project on early diagnosis and risk assessment of pancreas cancer. She also project manages the Italian effort within the International Cancer Genome Consortium (www.icgc.org) for pancreas cancer and is co-PI for the European funded project on “Integrative Analysis of Gene Functions in Cellular and Animal Models of Pancreatic Cancer” (http://www.cam-pac.eu/) and “Biomarkers of tumour recurrence in pancreatic cancer” (Bio-Pac). She is part of the working group to define the standards for Research Biobanks of the Veneto Regional Government of
Italy and is part of the coordinating group to create a regional biobank network. She has participated in the joint AIOM-SIAPEC working group, scientific Italian societies of Oncology and Pathology, to define biobanking for cancer research. Her current research interests are in molecular diagnostic markers and therapeutic targets and the role of cancer heterogeneity and molecular characterization of samples in the application of individualized medicine.

**LUNDEBERG, Joakim**
Professor Joakim Lundeberg heads the division of Gene Technology, KTH Royal Institute of Technology and has a long experience in molecular technology development. His research group is located at the Science for Life Laboratory (SciLifeLab), a national center for molecular biosciences with focus on health and environmental research. The center combines frontline technical expertise with advanced knowledge of translational medicine and molecular bioscience. JL also heads the National Genomics Infrastructure (NGI), together with Profs Syvänen and Gyllensten, that provides Swedish researchers access to state of the art instrumentation for massively parallel sequencing and NGI is currently one of the largest sequencing centers in Europe.

**MOORE Helen**
Dr. Helen Moore leads the NCI Biorepositories and Biospecimen Research Branch (BBRB). As Chief she sets the direction and strategic vision for the Branch and oversees a complex set of projects related to biobanking, including: Biospecimen Science research conducted under the Biospecimen Research Network (BRN); acquisition of biospecimens for the NIH Genotype-Tissue Expression (GTEx) Program; the Biospecimen Research Database, a Web-based Biospecimen Science literature database; biobanking economics research; the NCI Best Practices for Biospecimen Resources. Dr. Moore is a molecular biologist with a broad background in research and development.

**MORENTE, Manuel M.**

**OELMUELLER, Uwe**
Uwe Oelmüller joined QIAGEN in 1995. He is currently heading the technology center ”Sample Preparation Technologies” within the global Molecular Diagnostics Development Department. The center involves technology and product development projects for clinical sample collection, cellular biomolecule profile preservation, sample storage, transport and archiving, and the isolation and analysis of human and pathogen nucleic acids. At the QIAGEN / Becton Dickinson joint venture company PreAnalytiX he is QIAGEN’s management committee co-chair. PreAnalytiX develops and sells integrated and standardized systems for pre-analytical workflows. Dr. Oelmüller is the convener of the ISO/TC 212 (Clinical Laboratory Testing and In Vitro Diagnostic Test Systems) Working Group 4 focusing on molecular diagnostics and microbiology. He is a member and project leader of the CEN/TC 140 (In vitro Diagnostic Medical Devices) Working Group 3 currently focusing on pre-analytical workflows. He is the coordinator of the European FP7 Collaborative Grant Project SPIDIA. Prior to QIAGEN, Dr Oelmüller headed a research group at the Clinical Microbiology Center, University of Goettingen, Germany, working on the AIDS disease stage relevant HIV RNA expression pattern.

**OLLIER, Bill**
Bill Ollier is Professor of Immunogenetics at Manchester University and Co-Director of the Centre for Integrated Genomic Medical Research in the University of Manchester Institute for Population Health. He is Director of Research and Development at Salford Royal Hospital NHS Trust. He is Honorary Professor at the University of Salford. He was educated at University College of Wales, Aberystwyth and the University of London. He became a Fellow of the Royal College of Pathologists in 2000. He was Chairman of the British Society for Histocompatibility and Immunogenetics (1994-9).
He has a focus on the genetic basis of common complex disorders (inflammatory and autoimmune conditions). CIGMR offers a comprehensive facility for the analysis of complex diseases by combining epidemiological, statistical and genetic approaches with contemporary genomic screens.

PARODI, Barbara
Barbara Parodi, born in Genoa, March 22nd, 1956. In 1983 degree in Medicine and Surgery, University of Genoa, Italy. Since 1984, employee at the National Cancer Institute (IST) of Genoa (now IRCCS AOU San Martino – IST); responsible of the core facility “Biological Bank and Cell Factory”.
Research activity: Studies on T - B cell interaction in the immune response, role of HLA in the immune response. Expertise: management, quality assurance and quality control in biobanks / Biological Resource Centres; Good Laboratory Practices (GLP) and Good Manufacturing Practices (GMP).
Institutional role: Executive manager of the institutional Biological Resource Centre. Member of the Governance Committee and Project manager of the Italian Node of BBMRI-ERIC, responsible of the Quality common service of the Node; chair of the subgroup “Parameters” of the international working group “BioResource Impact Factor”; member of the Scientific Advisory Board of - Telethon Genetic Biobank Network; - VAS (Vascular independent research and education European organization) European Teaching Panel; - CHRIS (Cooperative Health Research in South Tyrol) Study. Member of the Regional network of biobanks of Liguria. Coordinator of the Italian participation to the BBMRI preparatory phase. Qualified person for the production of cells for therapy, nominated by the Italian Agenzia del Farmaco (decree N. AIDT – 9/2004, L. 178/91). Delegate of the Italian Minister of Research at the OECD Task Force on BRCs. Compilation of the OECD Best Practice Guidelines for Biological Resource centres. Co-author of 3 international guidelines, 56 scientific publications on national and international Journals.

RUAN, Liangliang
Dr. Ruan was graduated from Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences in 2012. After initially working as a manager of biobank at SCRC in 2013, he is currently the director of technology and operation, responsible for developing technical and support team to ensure the efficiency and quality of deliverables, including molecular diagnostics, analytical chemistry, biobank and cell biology, as well as sample management, custom service and logistics. Dr. Ruan has developed Quality Management System for biobanking at SCRC, managed the sampling project for biospecimen quality control in China Biobank Network, and published more than 10 papers and been granted 5 patents. Dr Ruan is now Director of Technology and Operation, Shanghai Clinical Research Center (SCRC).

STANTA, Giorgio
Professor Giorgio Stanta is head of the Molecular Histopathology Lab at the University of Trieste, and he is interested in molecular analysis in clinical tissues. Coordinator of the European group IMPACTS, interested in molecular analysis in AT. Chairman of the “Biobanking and Molecular Pathobiology WG” of the OECI. Chairman of the “Molecular Pathology WG” of the ESP. Chairman of the “Archive Tissue WG of BBMRI-ERIC”. Member of the ESMO faculty for the Cancer Genetics group. Member of the managing board of BBMRI.IT and coordinator of the Italian network of archive tissue biobanks (NIPAB). Part of the Committee of CEN (European Committee for Standardization) for Molecular in-vitro diagnostic examinations — Specifications for pre-examination processes for fresh tissues, FFPE tissues, blood for DNA, RNA and proteins, technical specifications to ISO 15189. Selected by the Directorate General for Health and Consumer Protection of the European Commission to be part of the European Commission Initiative on Breast Cancer - Quality Assurance Scheme Development Group (QASDG).

TURANO, Paola
PAOLA TURANO is Associate Professor of General and Inorganic Chemistry at University of Florence and member of CERM, the Magnetic Resonance Center of the same university (www.cerm.unifi.it). Her main research interest is NMR in Life Sciences, with applications ranging from structural biology to metabolomics. As partner of the FP7 project SPIDIA, she evaluated the effect of pre-analytical procedures on the metabolomics analysis of urine, serum, plasma and tissues. Paola Turano is member of the CEN/Technical Committee 140 (In-vitro Diagnostic Medical Devices) Working Group 3. She is involved in the consortium EXCEMET (Expert Center in Metabolomics), aimed at strengthening the relationships between the metabolomics community and biobanks and offering services to help biobanks developing increasingly higher standards for their sample quality.
VACHER, Cora
Cora Vachet is the large scale genotyping and biobanks market development manager at Illumina for Europe, Middle East and Africa, working with the community to develop solutions to meet the specific requirements.

VAUGHT, Jim
Dr. Jim Vaught spent 14 years at the U.S. National Cancer Institute (NCI), most recently as the Chief of the Biorepositories and Biospecimen Research Branch (BBRB). He has been working in the field of biorepository and biospecimen science for over 20 years. He was one of the founding members of the International Society for Biological & Environmental Repositories (ISBER). He serves on a number of biobank advisory groups including the Telethon-Italy Genetic Biobank Network; the Biobanques Network (France) Scientific Board; and the Provia Labs (Boston) Advisory Board. He is Senior Biobank Advisor to the Shanghai Clinical Research Center. He is the author of over 70 peer-reviewed articles and book chapters. From 2006 to 2012 he was Senior Editor for Biospecimens and Biorepositories for the AACR journal Cancer Epidemiology, Biomarkers and Prevention. In 2012 he became Editor-in-Chief of Biopreservation and Biobanking, the official journal of ISBER. He is currently a Senior Research Fellow at the International Prevention Research Institute (Lyon), and a consultant for a number of international biobanking activities. Dr. Vaught is the President of ISBER for 2015-2016.

WANG, Peng
Since 2013, Peng Wang is director of the Administrative office at the Biobank of Clinical Resources in Beijing, China. After a B.M. obtained in 1982 at the China Medical University in Shenyang, Liaoning Province, in 1996, he graduated a PhD degree at the department of Pharmacology/Toxicology of the Medical College of Virginia, Richmond, USA. He pursued his career as IRTA Fellow at the Laboratory of Immunology of NEI, NIH in Bethesda Maryland, USA. Back to China in 2004, he headed first the Clinical Research Lab at the Peking Union Medical College Hospital in Beijing, before joining the Biobank of Clinical Resources.

WATSON, Peter H.
Dr. Peter H. Watson obtained his medical degree at the University of Cambridge, UK and completed his specialty training in Anatomic Pathology at the University of Manitoba, Canada in 1988. He is currently a Professor of Pathology BC Cancer Agency and University of British Columbia, and Chief Physician British Columbia Cancer Agency’s Vancouver Island Cancer Centre. In his biobanking roles he is the Director of the Tumor Tissue Repository program at the Cancer Agency, the Office of Biobank Education and Research at the University of British Columbia, and principle investigator co-leading the national Canadian Tissue Repository Network CTRNet. He also serves on the executive of the national NCIC clinical trials group Correlative Sciences and Tumor Banking committee, and he is deputy editor for the ISBER journal ‘Biopreservation and Biobanking’. Dr. Watson combines a clinical practice as a breast pathologist with a cancer research program, and has published over 150 research papers on elucidating mechanisms of tumor progression, the role of the intratumoral immune response, and biomarkers to guide response to cancer therapies. Websites: UBC-OBER: http://pathology.ubc.ca/education-resource/ober/. CTRNet: http://www.ctrnet.ca

WICHMANN, Erich
Prof. Erich Wichmann, MD, PhD, has been trained in physics and medicine, before he started working in the field of epidemiology. From 1990 to 2011 he was Director of the Institute of Epidemiology at the Helmholtz Center Munich and from 1995 to 2011 he held the Chair of Epidemiology at University of Munich. His main research activities have been in population-based epidemiology, especially addressing environmental and genetic influences on diabetes/metabolic diseases, cardiovascular diseases and lung diseases/allergies. Since many years he is active in the field of biobanking. He has contributed to the “OECD Guidelines on Human Biobanks and Genetic Research Databases”, has been Work Package Leader of the European Biobanking and Biomolecular Research Initiative BBMRI PP and BBMRI-LPC on large biobanks and PI of the Biobank Alliance of the Munich m4 Spitzencluster “Personalized medicine and target-orientated therapies”. He has played a major role in the initiation and set-up of the German National Cohort (GNC) including 200,000 participants and in the installation of the Biorepository of the GNC for 20 million liquid biosamples.
YUILLE, Martin
Dr Yuille was educated at the universities of Oxford, Edinburgh and Stanford. He is Reader in Biobanking at the University of Manchester and Co-Director of the Centre for Genomic Medical Research in the University of Manchester Institute for Population Health. He became a Fellow of the Royal College of Pathologists in 2004. His work in biobanking started in 2002 with the funding by the Medical Research Council of the UK DNA Banking Network. He was Associate Coordinator of the BBMRI Preparatory Phase. He sits on a number of work groups in BBMRI.UK. He has contributed biobanking expertise to FP7, IMI and nationally-funded projects and networks. He has a strong interest in the application of LIMS and ISO management tools to enable quality improvement and network development. Other research interests include haematological oncology and public health.

ZATLOUKAL Kurt
Kurt Zatloukal, M.D. is professor of pathology at the Medical University of Graz, Austria and is director of the Christian Doppler Laboratory for Biospecimen Research and Biobanking Technologies. His research focusses on molecular pathology of diseases as well as biobanking and related technologies. He coordinated the preparatory phase of the European biobanking and biomolecular research infrastructure (BBMRI) and is now director of the Austrian national node of BBMRI-ERIC. He led in the development of new European standards and norms for pre-analytical processing of tissue samples for molecular diagnostics. He is involved in developing the ethical and legal framework for Austrian medical research and health care. He is member of the Austrian Arzneimittelbeirat and the scientific board for genetic testing and human gene therapy at the Austrian Ministry of Health, and member of the Austrian Standards Institute. He has published 191 scientific papers and was co-inventor of 15 patents.