isber REGIONAL SYMPOSIUM
GRANADA, SPAIN
October 24-25, 2023

PROGRAM

isber 2023 BIOSPECIMEN SCIENCE REGIONAL SYMPOSIUM

GRANADA, SPAIN | OCTOBER 24-25, 2023

In partnership with

Biobanco del Sistema Sanitario Público de Andalucía
Consejería de Salud y Consumo

ISBER 2023
REGIONAL SYMPOSIUM

Granada, Spain Oct. 24-25, 2023

"Biospecimen Science, Research, and Innovation"

Vision

To be the leading network in the global biobanking and biorepository community.

Mission

ISBER advances the expertise and quality of biorepositories and biobanking science worldwide.

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APRIL 9-12, 2024
ANNUAL MEETING
Dreaming Beyond Barriers:
The Future of Biobanking
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General Information

Meeting Venue

Hospital Universitario Clínico San Cecilio
Av. del Conocimiento, s/n, 18016 Granada, Spain
Ground floor

Meeting Hotel

Hotel Abades Nevada Palace 4*, Granada
C. de la Sultana, 3, 18008 Granada, Spain
Phone Number: (+34) 958 80 99 99

Registration Hours

Tuesday, Oct. 24	8:00am – 6:00pm
Wednesday, Oct. 25	7:30am – 3:00pm

Meeting Registration

Registration Type	Regular Rate	On-Site Rate *(After Oct 20)*
ISBER member	$300	$400
Non-Member	$400	$500
Student/Technician	$300	$400

**Please note, all rates are subject to 21% VAT*

Full Conference Registration

Full conference registration includes participation in all scientific sessions and food and beverage during the symposium.

Exhibit Hall Pass

Exhibit hall pass includes access to the exhibit hall and conference meals served in the exhibit hall.

Certificates of Attendance

All attendees will receive a certificate of attendance after completing the meeting evaluation. A link to the evaluation will be sent out via email following the meeting.

Poster Presentations

POSTER SET-UP:
Tuesday, October 24, 2023 | 8:00am –10:15am

PRESENTATION TIME:
Tuesday, October 24 | 5:30pm – 6:30pm
**Please note that delegates are also encouraged to peruse the posters during session breaks.*

POSTER TAKEDOWN:
Wednesday, October 25, 2023 | 2:00pm – 5:00 pm

Exhibit

EXHIBIT INSTALLATION:
Tuesday, October 24 | 8:00am –10:00am

EXHIBIT HOURS:
Tuesday, October 24 10:00am – 4:00pm
Wednesday, October 25 9:00am – 2:30pm

EXHIBIT TAKEDOWN:
Wednesday, October 25 | 2:30pm – 4:00pm

Program Planning Task Force Members

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Bialystok, Poland

Stella Somiari
CSS Institute of Molecular Medicine
Windber, United States

Program-at-a-Glance

DAY 1 – TUESDAY, OCTOBER 24, 2023

9:00am – 9:15am	**Welcome and Opening Remarks** *Manuel Enrique Reyes Nadal – Director Gerente del Hospital Universitario San Cecilio de Granada* *Alison Parry-Jones – ISBER President* *José Manuel Puerta Puerta – Director Científico del Biobanco del SSPA* *Gonzalo Balbontín Casillas – Director Gerente de la Fundación Pública Andaluza Progreso y Salud* *Isaac Túnez Fiñana – Secretario General de Salud Pública e I+D+i en Salud*	*Conference Room*
9:30am – 10:15am	**Keynote Presentation: Standardising the Pre-analytical Reporting of Biospecimens to Improve Reproducibility in Extracellular Vesicle Research – A GEIVEX Study** *José Antonio López Guerrero, Instituto Valenciano de Oncología (IVO), Spain*	*Conference Room*
10:15am – 10:45am	Networking Break in Exhibit Hall	*Exhibit Hall*
10:45am – 12:15am	**Symposium 1, Part 1 – Human-Focused** *Chair: Fay Betsou* JFDI II: Contrived Materials and a Data Set for the Evaluation of Liquid Biopsy Tests *Adam Corner, Bio-Rad Laboratories, United Kingdom* Reproducibility of Biomarker Testing in Neurology *Eline Willemse, University Hospital Basel, Switzerland* Polygenic Risk Estimation of Human Diseases from Paraffin Embedded Archival Tissue: A Recipe for Chaos? *Omar Youssef, University of Helsinki, Finland*	*Conference Room*
12:15pm – 1:15pm	Lunch in Exhibit Hall	*Exhibit Hall*
1:15pm – 2:45pm	**Symposium 1, Part 2 – Human-Focused** *Chair: Fay Betsou* Samples Management and Traceability with CNAG LIMS *Lidia Agueda, Centro Nacional de Análisis Genómico (CNAG), Spain* Guidelines for Quality Control in Banking Human Induced Pluripotent Stem Cell Lines *Slaven Erceg, National Stem Cell Bank-Valencia Node, Spain* Standard Peripheral Blood Mononuclear Cell Cryopreservation Affects Detection of Clinically-Relevant T Cell Markers with Flow Cytometry *Feng He, Luxembourg Institute of Health, Luxembourg*	*Conference Room*
2:45pm – 3:15pm	Networking Break in Exhibit Hall	*Exhibit Hall*
3:15pm – 4:15pm	**Corporate Workshop** Breaking The Ice: A Game-Changing Approach to Room Temperature Biological Sample Storage *Mario Tenera Morgado, 300K Solutions, Portugal*	*Conference Room*

DAY 1 – TUESDAY, OCTOBER 24, 2023

4:30pm – 5:30pm	**Symposium 2 – Environmental-Focused** *Chair: Jennifer Ness* Seed Biobanking and Cryobiotechnologies: An Overview *Marcos Castellanos, Nottingham Arabidopsis Stock Centre, University of Nottingham, United Kingdom* Release of a Handbook on Biodiversity Biobanking Practices *Jonas Astrin, Leibniz Institute for the Analysis of Biodiversity Change, Museum Koenig, Germany*	*Conference Room*
5:30pm – 6:30pm	**Abstract Poster Presentations**	*Poster Room*

DAY 2 – WEDNESDAY, OCTOBER 25, 2023

8:00am – 8:45am	**Roundtable Discussions [CONCURRENT]** Topic 1: ISO 20387 & Biospecimen Science *Fay Betsou, Institut Pasteur, France* Topic 2: Field Collections & Ensuring Sample Integrity with Regulatory Compliance *Jennifer Ness, National Institute of Standards & Technology, USA* Topic 3: Tissue Pre-Analytics and Genomics *William Mathieson, Integrated Biobank of Luxembourg, Luxembourg*	*Biobank*
9:15am – 10:00am	**Keynote Presentation: Preanalytics and Fitness for Purpose of the Biospecimens: Perspective of the Clinical Biologist** *Giuseppe Lippi, University of Verona, Italy*	*Conference Room*
10:00am – 10:30am	Networking Break in Exhibit Hall	*Exhibit Hall*
10:30am – 12:00pm	**Symposium 3 – Microbial-Focused** *Chair: Eva Ortega* Is the Presence of Microorganisms in Liquid Nitrogen Storage Tanks a Challenge for Cryostorage? *Felizitas Bajerski, Leibniz Institute DSMZ - German Collection of Microorganisms and Cell Cultures GmbH, Germany* Unraveling the Impact of Freeze-Drying on Bacterial Viability During Long-Term Preservation *Jindrich Peiren, Ghent University - BCCM/LMG bacteria collection, Belgium* Proteotyping Bacteria and Fungi by Phylopeptidomics: Pre-analytical Factors Review and Potential *Jean Armengaud, Commissariat à l'Energie Atomique et aux Energies Alternatives (CEA), France*	*Conference Room*

DAY 2 – WEDNESDAY, OCTOBER 25, 2023

12:00pm – 1:00pm	**Symposium 4 – Microbiome-Focused** *Chair: Jose Antonio Carrillo Ãvila* Advancing Microbiome Analysis: Quality Control, Standardization, and Method Validation *Lorieza Neuberger-Castillo, Integrated BioBank of Luxembourg (IBBL), Luxembourg Institute of Health (LIH), Luxembourg* Bacteriophage Collection: Challenges and Promises *Laurent Debarbieux, Institut Pasteur, France*	*Conference Room*
1:00pm – 2:00pm	Lunch in Exhibit Hall	*Exhibit Hall*
2:00pm – 3:00pm	**Oral Abstract Presentations** Extracting DNA From Formalin-Fixed, Paraffin-Embedded Tissue Using Purigen Biosystems´ Isotachophoresis Robot: A Comparison With Silica Spin Columns And Magnetic Beads *William Mathieson, Luxembourg* Biospecimens from the SpaceX Inspiration4 Mission Constitute the First Commercial Aerospace Biobank: The Cornell Aerospace Medicine Biobank (CAMbank) *Eliah Overbey, United States* Architecture of a Zooplankton Biobank: Design, Data Flow and Sample Management *Helena Rodriguez, Spain* Ice Recrystallization Inhibitors Enable Efficient Cryopreservation of Induced Pluripotent Stem Cells: A Functional and Transcriptomic Analysis *Kathleen Mommaerts, Luxembourg*	*Conference Room*
3:00pm – 4:00pm	**Debate: Funding to Support Biospecimen Science Research** *Chair: Stella Somiari* *Begoña Oliver, Biomedical Research Institute of Malaga (IBIMA), Spain* *Vanessa Tumilasci, Azenta Life Sciences, United States* *Mihai Bragaru, Thermo Fisher Scientific, United Kingdom* *Rosana Cabello, Roche, Spain* Evidence-based knowledge is lacking on how pre-analytical factors experienced throughout the lifecycle of a biospecimen, affect sample integrity and quality. These factors include-collection vessel, time between collection and stabilization, stabilization methods, processing methods, arterial clamp time among others. Biospecimen Science Research studies should precede biomarker development studies with the goal of providing data on how different pre-analytical factors impact the molecular nature of the sample and the subsequent research outcome. Knowledge gained through BSR can allow pre-qualification of samples for an intended use (fit for purpose). We suggest that encouraging BSR in both public and private laboratories will generate evidence-based data which will enhance and accelerate reliable & reproducible research, and provide significant cost savings.	*Conference Room*
4:00pm – 4:15pm	**Closing Remarks**	*Conference Room*
4:30pm – 5:30pm	**Interactive Session @ Biobanco del Sistema Sanitario Público de Andalucía** *Pre-registration is recommended.*	*Biobank*

Presentation Summaries

Day 1 – October 24, 2023

Standardising the Pre-analytical Reporting of Biospecimens to Improve Reproducibility in Extracellular Vesicle Research - A GEIVEX Study

José Antonio López Guerrero, Instituto Valenciano de Oncología (IVO), Spain

The standardization of clinical studies using extracellular vesicles (EVs) has mainly focused on the procedures employed for their isolation and characterization; however, preanalytical aspects of sample collection, handling, and storage also significantly impact the reproducibility of results. Herein I present the results of a survey based on SPREC among GEIVEX members to explore how laboratories handled fluid biospecimens. The survey indicated that variability in preanalytical approaches reaches 94%. Moreover, in some cases, researchers had no access to all relevant preanalytical details of samples, with some sample aspects with potential impact on EV isolation/ characterization not coded within the current version of SPREC. Our study highlights the importance of working with common SOPs to control preanalytical conditions. The application of SPREC represents a suitable approach to codify and register preanalytical conditions. Integrating SPREC into the SOPs of laboratories/biobanks will provide a valuable source of information and constitute an advance for EV research by improving reproducibility and credibility.

JFDI II: Contrived Materials and a Data Set for the Evaluation of Liquid Biopsy Tests

Adam Corner, Bio-Rad Laboratories, United Kingdom

Liquid Biopsy Assays have significant potential in the management and maintenance of patients with cancer. BloodPAC, as a multidisciplinary community including academic, private and governmental/non-profit organisations is focused on accelerating the development, validation and clinical use of liquid biopsy assays. Two of the main focuses of BloodPAC to this end are guidelines for Recommended Data Element & Analytical methods and Evidence generation. RDEs have been published or are in process across the range of liquid biopsy workflows, including pre-analytical minimal technical data elements and RDE for clinical & patient context and MRD/MCED. Protocols for analytical validation of defined and custom liquid biopsy assays are published or in process currently. In parallel, the JFDI working group focuses on the role of contrived samples and bio-banked samples in liquid biopsy analysis, comparing different analytical methods.

Reproducilibility of Biomarker Testing in Neurology

Eline Willemse, University Hospital Basel, Switzerland

Where neuropathological examination of brain tissue can only be done after death, and MRI imaging is expensive and not always accessible, fluid biomarkers in brain fluid or blood provide powerful tools to aid the diagnosis of brain disorders. Fluid biomarkers are quantitative, cheap and easily accessible. Reproducibility of fluid biomarker results, however, is a complication that hampered the clinical application of these biomarkers. To illustrate, the road from discovery to clinical application of biomarker amyloid-beta, one of the hallmarks of Alzheimer's disease, took about 20 years. Since this biomarker can significantly aid patient management as well as drug development, we are in crucial need of speeding up this process. What factors caused these reproducibility issues? Which solutions were found? How were the learnings applied to novel developments in the field of biomarker development? And can we use AI to improve reproducibility issues in biomarker development?

Polygenic Risk Estimation of Human Diseases from Paraffin Embedded Archival Tissue: A Recipe for Chaos?

Omar Youssef, University of Helsinki, Finland

Germline variants play a crucial role in cancer predisposition. The conventional analysis of germline variants relies on DNA extracted from blood or saliva. However, Finnish biobanks and pathology archives host millions of formalin-fixed paraffin-embedded normal tissue (FFPE-NT) samples, often linked with extensive clinical follow-up information. These underutilized samples could provide a vital source for germline variants genotyping. In close collaboration with FinnGen (www.finngen.fi), we, at the University of Helsinki, managed to establish a methodology for accurate genotyping of FFPE-NT on genome-wide array. This enabled us to calculate polygenic risk scores (PRS) from FFPE-NT and achieve significant concordance with PRS calculated from matched blood-derived genotypes.

Samples Management and Traceability with CNAG LIMS

Lidia Agueda, Centro Nacional de Análisis Genómico (CNAG), Spain

After a short description of CNAG, Lidia will speak about how their in-house developed LIMS was created and is used to ensure traceability of all CNAG procedures, with a focus on stock DNA and RNA sample management.

Guidelines for Quality Control in Banking Human Induced Pluripotent Stem Cell Lines

Slaven Erceg, National Stem Cell Bank-Valencia Node, Spain

Standard Peripheral Blood Mononuclear Cell Cryopreservation Affects Detection of Clinically-relevant T Cell Markers with Flow Cytometry

Feng He, Luxembourg Institute of Health, Luxembourg

In his presentation, Dr. Feng He (Hefeng) will discuss systems immunology and its applications in various diseases. He will discuss the cryopreservation effects on the analysis of several clinically-relevant markers in PBMC in general. He will then extend his talk on how to apply multi-omics approaches in cryopreserved and fresh clinical samples to comprehensively investigate the peripheral immune systems in early-to-mid stage Parkinson's disease.

Seed Biobanking and Cryobiotechnologies: An Overview

Marcos Castellanos, Nottingham Arabidopsis Stock Centre, University of Nottingham, United Kingdom

The world needs to conserve its plant genetic resources as they are at risk of disappearing due to genetic erosion caused by climate change, habitat destruction, plant pathogens and changes in agricultural practices. Seed biobanks represent a powerful tool in the conservation and propagation of plant genetic resources. Conventional ex-situ germplasm banking strategies rely on slowing down seeds' metabolism without causing irreversible damage by controlling two key factors: moisture and temperature. But traditional protocols do not work with recalcitrant seeds as they cannot tolerate the drying and freezing process. Seed biobanking also cannot be applied to species that produce few or no seeds, or for which seeds are inaccessible for collecting. Because of this, the development of novel storage strategies as well as cryobiotechnologies such as cryopreservation and in-vitro techniques offer the potential for the long-term storage of seeds and other plant tissues. An integrated approach that combines the latest biobanking technologies with on-field expertise will be essential to broaden ex-situ conservation globally and to secure plant biodiversity for future generations.

Release of a Handbook on Biodiversity Biobanking Practices

Jonas Astrin, Leibniz Institute for the Analysis of Biodiversity Change, Museum Koenig, Germany

Confronted with global biodiversity decline, we need to ramp up efforts regarding ex-situ conservation and the archival of molecular samples. Environmental and biodiversity biobanks are key infrastructures in this process. However, information flow between the various biobank types has so far often been limited, hindering the harmonization of activities and products. Within the EU-funded SYNTHESYS+ NA3.1 project, we compiled extensive information on biobanking workflows for animals, plants, fungi, and protists, resulting in a comprehensive 270-page handbook with reference collections and links to online resources. "Biodiversity Biobanking - a Handbook on Protocols and Practices" is open access and available under: https://doi.org/10.3897/ab.e101876 The new resource concentrates on biodiversity-specific content and refers to the ISBER Best Practices regarding general information on biobank management. It offers guidance on field sampling, preservation, and storage of biomaterials (live, fixed, and DNA) along with management procedures.

Day 2 – October 25, 2023

Roundtable Discussion Topic 1: ISO 20387 & Biospecimen Science

Fay Betsou, Institut Pasteur, France

A discussion around the link between biospecimen science and ISO biobank accreditation. We will discuss how biospecimen science can support biobank accreditation and method validation. We will also discuss on potential limits imposed by accreditation on biospecimen science inside the biobank.

Roundtable Discussion Topic 2: Field Collections & Ensuring Sample Integrity with Regulatory Compliance

Jennifer Ness, National Institute of Standards & Technology, USA

The Field Collections and Nagoya Protocol Roundtable will be in two parts. Part I will discuss the unique challenges

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posed by collecting samples outside of standard laboratory or hospital settings and how to maintain the highest sample integrity. This discussion will feature stories and experience from both human and non-human biobanks. Part II will discuss implementation of the Nagoya protocol and the global challenges and benefits, therein.

Roundtable Discussion Topic 3: Tissue Pre-analytics and Genomics

William Mathieson, Integrated Biobank of Luxembourg, Luxembourg

A discussion focused on biospecimen research in the context of genomic analyses, both in respect of patient diagnosis and genomic research.

Preanalytics and Fitness for Purpose of the Biospecimens: Perspective of the Clinical Biologist

Giuseppe Lippi, University of Verona, Italy

After decades of research in the area of overall quality of laboratory diagnostics, it has become quite clear that the preanalytical phase is the most vulnerable part of the entire testing process, where errors are most likely to occur, compromising test reliability and jeopardizing patient safety. The Working Group for the Preanalytical Phase (WG-PRE) was officially established by the European Federation of Clinical Chemistry and Laboratory Medicine (EFLM) in 2013. The main goal of this WG is to reduce the impact of preanalytical variability on test quality and to improve harmonization of the still manual labor-intensive activities associated with biospecimen collection, handling, transport, storage, and preparation. Since its inception, the WG-PRE has completed many valuable projects, including a final definition of fasting status and harmonization of patient and blood tube identification, color coding of blood collection tubes, sequencing of blood tubes during blood collection, the, serum indices, but has also participated in the project of developing reliable quality indicators for the preanalytical phase. Other projects of WG-PRE include the development of phlebotomy guidance.

Is the Presence of Microorganisms in Liquid Nitrogen Storage Tanks a Challenge for Cryostorage?

Felizitas Bajerski, Leibniz Institute DSMZ - German Collection of Microorganisms and Cell Cultures GmbH, Germany

High-quality long-term storage of valuable living materials is essential for future research, public health and the bioeconomy. Therefore, cryostorage is often performed in the vapor or liquid nitrogen (LN) phase at temperatures below -150 Â°C. To assess the potential risk of microbial cross-contamination during cryostorage, we conducted an extensive literature review and a brief survey among different culture collections to raise awareness of microbial contamination of storage containers. Furthermore, we systematically examined tanks in different biobank facilities for the presence of bacteria, fungi, plant, and human cells at different phases of LN storage in a culture-independent approach. In identifying potential contaminants, their sources, and evaluating their potential harms, we found that the samples themselves, the LN, the human microbiome, and the environment are all potential routes of contamination. The freshly produced LN is usually not the source of contamination, and only a few studies provided evidence of a risk of microbial cross-contamination. Most biobanks prevent potential contaminations by using sealed devices or -150Â°C freezers.

Unraveling the Impact of Freeze-Drying on Bacterial Viability During Long-Term Preservation

Jindrich Peiren, Ghent University - BCCM/LMG bacteria collection, Belgium

Freeze-drying or lyophilization is widely used as long-term preservation technique for bacteria in industry and in biological resource centres (BRCs). Although freeze-drying is a very complex physical process affected by many parameters requiring specific equipment and trained personnel, a properly freeze-dried bacterial strain can still reveal a viable culture after 30 years of storage or more. In this presentation the freeze-drying process and its impact on bacterial viability is explained step by step.

Proteotyping Bacteria and Fungi by Phylopeptidomics: Pre-analytical Factors Review and Potential

Jean Armengaud, CEA, France

High-throughput identification of microorganisms is key for clinical diagnostics and microbiology in general. Mass spectrometry for proteotyping microorganisms has been shown efficient because rapid and low cost. Recent studies have demonstrated the discriminative power of proteotyping based on tandem mass spectrometry. As this technology can quickly identify the most probable taxonomical position of

any microorganism, even if not yet previously characterized in terms of taxonomy, and discriminate closely related strains, its application on environmental isolates, new emergent threats, or large collections has been promoted. Here, I will introduce the phylopeptidomics methodology with striking examples, its potential to be multiplexed and thus applicable on thousands of samples, and review the pre-analytical factors required for its application. The potential and perspectives of this methodology will be also commented, as it apply even on mixtures of microorganisms and complex microbiota. The methodology is thus applicable on collections of more complex samples.

Advancing Microbiome Analysis: Quality Control, Standardization, and Method Validation

Lorieza Neuberger-Castillo, Integrated BioBank of Luxembourg (IBBL), Luxembourg Institute of Health (LIH), Luxembourg

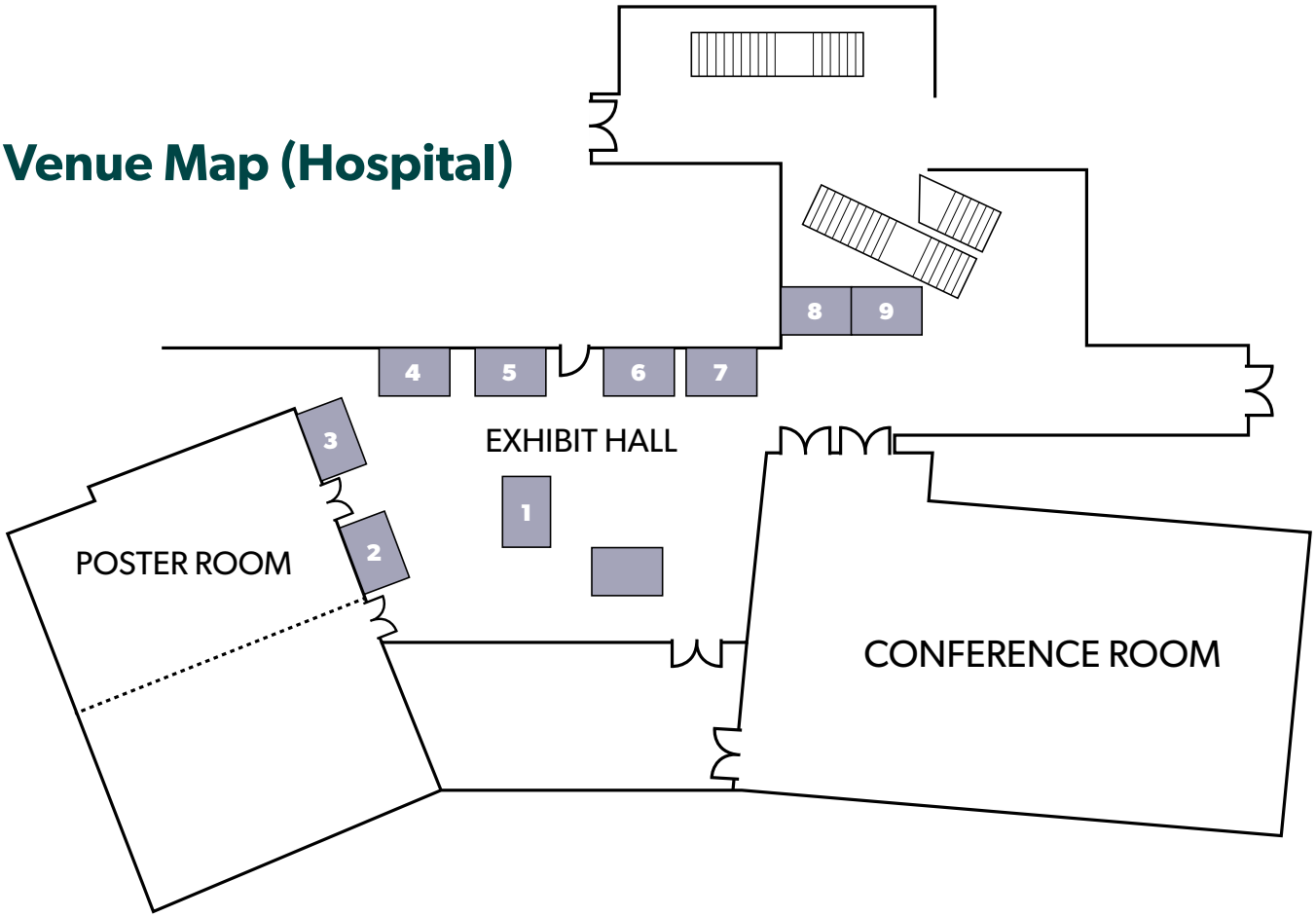
In the rapidly evolving field of microbiome, ensuring data accuracy, reliability and comparability across studies is of paramount importance. This presentation delves into the critical aspects of microbiome research. We will explore the significance of routine internal control samples in microbiome analyses and their role in enhancing data quality. Additionally, we'll discuss an evaluation of available QC materials, shedding light on the quest for consistency and reproducibility in this field. Method validation will be addressed, focusing on the extraction of DNA from human stool samples for downstream microbiome analysis. This step is crucial for generating reliable microbiome data. Lastly, collaborative studies with the National Institute of Standards and Technology (NIST) and the Medicines and Healthcare products Regulatory Agency (MHRA, UK) aim to address variability, bias, and the establishment of global standards for microbiome analysis. Collectively, these efforts underscore the significance of rigorous practices, cooperation and the pursuit of standardized methodologies in advancing microbiome research and its potential for transformative insights into human health.

Bacteriophage Collection: Challenges and Promises

Laurent Debarbieux, Institut Pasteur, France

Bacteriophages, viruses infecting bacteria, are present in all environment where bacteria thrive, including animals body. Discovered in the early 20th century, bacteriophages were first used to treat human bacterial infections before the use of antibiotics. Next, they were used as models to uncover major biological mechanisms and gave birth to the discipline of molecular biology. Quite surprisingly, while bacterial collections have emerged in many countries towards the entire 20th century, only three bacteriophage collections were established. Nowadays, the worldwide issue of increasing antibiotic resistance of bacterial pathogens has revived the interest in the therapeutic use of bacteriophages, namely phage therapy. While a number of private and public laboratories are engaged in building bacteriophage collections there is not yet specific guidelines on procedures to be followed to secure the reliability and sustainability of such collections that hold promises of multiple applications beyond phage therapy.

Venue Map (Hospital)



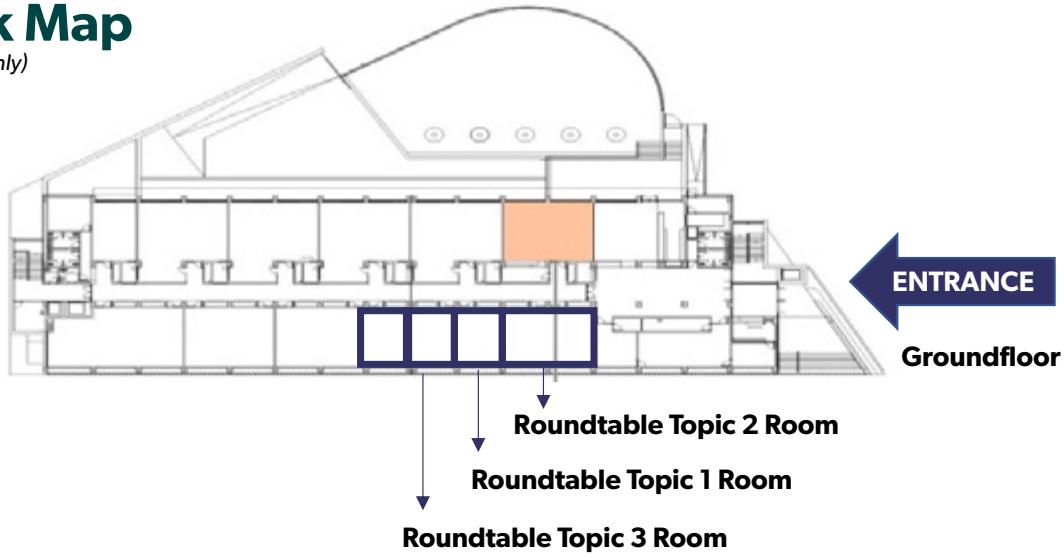
Exhibitors

Booth	Company
1	Azenta Life
2	Liconic
3	Thermo Fisher Scientific
4	300K Solutions
5	Modul Bio

Booth	Company
6	Hamilton Storage GmbH
7	DeltaLab Nirco SL (LVL Technologies)
8	Angelantoni Life Sciences S.r.l.
9	DiData

Biobank Map

(For Roundtables Only)



Exhibitor Listing

300K

300K Solutions is a biotech company founded in 2019 dedicated to develop and provide solutions for the storage and shipment of biospecimens at room temperature. 300K Solutions is developing its solution for nucleic acids, integer cells, liquid biopsy and solid tissues stored in Blood Banks and Biorepositories, Research, Genetic Analysis and Pathology Labs. Find a new way to store biological samples with 300K Solutions and see how to maximize your space and safety for stored biospecimens.

Angelantoni Life Sciences S.r.l.

Angelantoni Life Science manufactures a wide range of cold storage rooms used to preserve vaccines, drugs and other products for the Pharmaceutical Healthcare Industry.

Azenta Life Sciences

Azenta Life Sciences provides unrivaled sample exploration and management solutions to help our customers accelerate discovery, development, and delivery to bring impactful breakthroughs and therapies to market faster. We are the global leader in automated compound management for drug discovery, biological storage, and sample processing solutions. Azenta understands the importance of sample integrity and provides a comprehensive range of solutions across our leading capabilities of genomic services, sample repository services (SRS), consumables and instruments, data management and informatics, sample sourcing, and automated ultra-cold storage.

DeltaLab Nirco SL (LVL Technologies)

Deltalab is a leading company in design and manufacturing of labware.

Wherever DELTALAB reaches it does so with commitment to quality, service, and ethically-driven responsibility at an international level.

Talent, ethics and enthusiasm are the basis of this international referral company. DELTALAB provides solutions to any specific need, be it processing, application, or use, while always complying at the highest standards of quality, sustainability criteria, economic efficiency, and relying on our strategy of reinvestment and permanent research.

DiData

DiData is a ready-to-use and flexible web-based platform to integrate your scientific data such as clinical projects, laboratory, biobanks, and more

Hamilton Storage GmbH

Hamilton Storage is the global leader in automated sample management systems, benchtop devices and labware. We

are offering a comprehensive portfolio of automated sample management systems for biological and compound samples, from room temperature down to the ULT range. Our sample storage solutions, benchtop devices, and consumables are designed for sample integrity, flexibility, and reliability for life science applications.

Liconic USA

LiCONiC specializes in the design and manufacture of automated sample storage solutions used in laboratories and applications with special climate requirements. We are experts in sample management and tracking for the biorepository, blood banking, and compound storage markets. Our 30 years of leadership in this field has led to an installation base of several thousands of systems in operation worldwide. Liconic's built-for-purpose approach provides users with state-of-the-art storage solutions.

Modul-Bio

Modul-Bio specialises in IT solutions for biological sample management, implementing barcode systems, Biobank Information Management Systems (BIMS) and collaborative tools for tracking, managing and sharing biospecimen collections. We deploy software dedicated to biobanking for Biological Resource Centres, national cohort projects, biotech companies and biorepositories.

Thermo Fisher Scientific

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Oral Abstracts

WEDNESDAY, OCTOBER 25 | 2:00pm – 3:00pm

Abstract #	Title	Topic	Presenter	Country
O1	Extracting DNA From Formalin-Fixed, Paraffin-Embedded Tissue Using Purigen Biosystems´ Isotachophoresis Robot: A Comparison With Silica Spin Columns And Magnetic Beads	Validation of Processing Methods / Method Comparison	William Mathieson	Luxembourg
O2	Biospecimens from the SpaceX Inspiration4 Mission Constitute the First Commercial Aerospace Biobank: The Cornell Aerospace Medicine Biobank (CAMbank)	Other	Eliah Overbey	United States
O3	Architecture of a Zooplankton Biobank: Design, Data Flow and Sample Management	Other	Helena Rodriguez	Spain
O4	Ice Recrystallization Inhibitors Enable Efficient Cryopreservation of Induced Pluripotent Stem Cells: A Functional and Transcriptomic Analysis	Cell Preservation and Cryobiology	Kathleen Mommaerts	Luxembourg

O1: Extracting DNA From Formalin-Fixed, Paraffin-Embedded Tissue Using Purigen Biosystems´ Isotachophoresis Robot: A Comparison With Silica Spin Columns And Magnetic Beads

Camille Bellora [1], Glenn Nohar [2], William Mathieson [1]
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Background: DNA extracted from formalin-fixed, paraffin-embedded (FFPE) blocks is inherently low in yield and fragmented compared with that from frozen tissue. Maximizing yields and integrities is therefore critical. Most extraction methods involve the binding of DNA to silica, either in the form of spin-columns or magnetic beads. However, yield-loss occurs because neither the binding nor elution of DNA from silica is 100 % efficient. We evaluated a new, automated DNA extraction method from Purigen Biosystems that uses an isotachophoresis robot to isolate DNA entirely in the liquid phase based on its ionic mobility, which avoids yield-loss due to DNA failing to bind to or elute from silica.

Methods: DNA was extracted from 14 FFPE tissue blocks using the Purigen reagents and robot, a manual silica spin column method (QIAamp FFPE kit, Qiagen) and an automated silica magnetic bead method (Chemagic FFPE kit run on a Chemagen 360 robot, both Perkin Elmer). Each method used 2 sections of 10 µm. Deparaffinisation and Proteinase K digestion was as per each method`s protocol (user optimized for Chemagen). DNA yield was assessed using pico green fluorometry, purity by OD 260:280 and 260:230 and integrity by DNA Integrity Numbers (DINs) and qPCR (Illumina FFPE QC Assay). Purigen extractions were performed at GC Biotek (Purigen`s European representative), but all remaining work was done independently.

Results: Median DNA yields were 1.4 µg (Purigen), 1.6 µg (Chemagen) and 1.0 µg (QIAamp). The difference between Purigen and QIAamp was statistically significant ($p = 0.002$) with the percent additional yield in Purigen higher in lower-yielding samples. The difference in yield between Purigen and Chemagen was not statistically significant, but due to a lower elution volume, DNA concentrations were higher in Purigen (mean 49 ng/µl compared to 38 ng/µl, $p = 0.002$). Mean DNA purity was poorer in Purigen than either Chemagen or QIAamp ($p < 0.05$): 1.49, 1.71 and 1.81 (260:280) and 0.78, 1.69 and 2.0 (260:230) respectively. The difference in DIN between the methods was not statistically significant but Purigen returned lower ΔCq in qPCR (denoting less fragmented DNA) than the other methods: median 1.50 (Purigen), 1.58 (Chemagen) and 1.53 (QIAamp), $p < 0.05$.

Conclusion: The Purigen system performed either better

than or as well as the silica columns kit or the silica magnetic bead method in respect of DNA yield, concentration and integrity, but DNA purity was poorer.

O2: Biospecimens from the SpaceX Inspiration4 Mission Constitute the First Commercial Aerospace Biobank: The Cornell Aerospace Medicine Biobank (CAMbank)

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Historically, access to biospecimen samples collected from astronauts has been incredibly limited. Commercial space missions, such as the SpaceX Inspiration4 mission, have provided a new avenue for astronaut biospecimen collection and the opportunity to establish the first commercial aerospace medicine biobank. The Cornell Aerospace Medicine Biobank (CAMbank) has been created to make biospecimen samples from spaceflight accessible to the scientific community and to serve as a long-term storage mechanism for astronaut samples.

As reported in Overbey, et al. 2023[1],the inaugural cohort of biospecimen samples were collected from the four SpaceX Inspiration4 crew members longitudinally before (Launch: L-92, L-44, L-3 days), during (Flight Day: FD1, FD2, FD3), and after (Return: R+1, R+45, R+82, R+194 days) spaceflight, spanning a total of 289 days across 2021-2022. The collection process included venous whole blood, capillary dried blood spot cards, saliva, urine, stool, body swabs, capsule swabs, SpaceX Dragon capsule HEPA filter, and skin biopsies. Venous whole blood was further processed to obtain aliquots of serum, plasma, extracellular vesicles and particles, and peripheral blood mononuclear cells (PBMCs). In total, 2,911 sample aliquots were shipped to our central lab at Weill Cornell Medicine for downstream assays and biobanking.

Since its creation, CAMbank now includes samples from the Polaris Dawn and Axiom-2 crews. Additionally, the biobank is expanding to include ground control cohorts to provide control samples matched to the crews it houses. An aerospace biobank will significantly increase the accessibility of astronaut biospecimens and expand the field of those studying the effects of spaceflight on the human body. In this presentation, we will discuss the breadth of samples collected, the challenges of collecting at multiple samples sites across the USA (Los Angeles, Houston, Cape Canaveral, New York, and home collections), our methodology for sample preservation, and how these samples have been used in downstream genomic and biomarker assays.

[1]Collection of Biospecimens from the Inspiration4 Mission Establishes the Standards for the Space Omics and Medical Atlas (SOMA). In Revision, Nature Communications. bioRxiv: https://doi.org/10.1101/2023.05.02.539108

O3: Architecture of a Zooplankton Biobank: Design, Data Flow and Sample Management

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Background: Zooplankton has a keyrole in marine ecosytem biodiversity and services, and climate change has increased the research activity on this animal component due to its role in ocean´s biological pump, marine food web and disease transmission. Surveys aimed at collecting zooplankton originate a large number of samples, with many associated data. Marine Ecology and Biodiversity Group (IIM-CSIC), have collected 1780 zooplankton samples. Thus, it was necessary to store and manage those samples following quality criteria and ensuring their traceability.

Methods: Zooplankton samples were obtained by using different nets with 200 µm mesh size. When the volume of samples were greater than 250 ml, a Folsom splitter was used to obtain a smaller but representative subsample. A Rossete sampler equipped with Niskin bottles and CTD was used to obtain oceanographic parameters.

Information from these samples fuels the metadata, which became part of the Biobank system (Bio-e-Bank platform from Vitrosoft) at the Technical Biobank Unit (UTB). All the sampling information was included in an extraction questionnaire and all the associated samples were identified by a Bank code. These samples, in 250 ml plastic bottles and preserved with ethanol, were stored in security cabinets, following biocontainment measures. Each zooplankton sample was analysed (morphological and molecular methods) to determine the structure and composition of zooplankton community.

Results: A zooplankton biobank was created, by designing the software architecture and defining each phase: questionnaires, TFC (Type, Format, Conservation) and processing plan (storage). The flow of samples and data were determined, ensuring sample traceability and quality in the process.

The samples (N=1780) and metadata (50 parameters per sample and zooplankton results) were introduced and stored in the Zooplankton Biobank. In addition, we have received samples from other zooplankton monitoring programs that have been also included in Biobank system.

Conclusion: Biobanks are playing an increasing role in marine research. The creation of this zooplankton biobank allowed us, not only to storage that kind of samples and data with all the guarantees of traceability and security of a biobank, but also to manage all the processes of receiving and transferring samples. This would increase the number of end users who could benefit from this platform, by acceding and banking zooplankton samples from different monitoring programs.

O4: Ice Recrystallization Inhibitors Enable Efficient Cryopreservation of Induced Pluripotent Stem Cells: A Functional and Transcriptomic Analysis

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Background: The successful use of human induced Pluripotent Stem Cells (iPSCs) for research or clinical applications requires the development of robust, efficient, and reproducible cryopreservation protocols. After cryopreservation, the survival rate of iPSCs is compromised and cell line-dependent. Ice recrystallization inhibitors (IRIs) have the potential to enhance cryopreservation outcomes by maintaining small crystal size within a frozen solution unlike conventional cryoprotective agents (such as DMSO) that do not shield cells from ice recrystallization. We assessed the use of IRIs for cryopreservation of human iPSCs.

Methods: A screening study was first performed to assess optimal concentrations of specific small-molecule carbohydrate-based IRIs to minimize toxicity. Then, a cryopreservation study compared the cryoprotective efficiency of 15 mM IRIs in 5 % or 10 % DMSO-containing CryoStor® solution ("IRI-5" and "IRI-10") with the commercial CryoStor® CS10 (BioLife Solutions). Three iPSC lines were cryopreserved as single-cell suspensions in the cryosolutions then post-thaw characteristics, including pluripotency and differential gene expression, were assessed. RNA librairies were created, QC-checked (RiboGreen® RNA Assay and RNA Integrity Numbers (RINs)) then sequenced on a NovaSeq 6000 using the TruSeq Stranded mRNA kit (both Illumina). RNA sequencing analysis compared 24 h post-thaw cells and their freshly isolated (non-frozen) iPSC sister samples.

Results: The cryosolution IRI-5 exhibited higher post-thaw mean recovery (57.7 %, $p < 0.035$) and viability (85.3%, $p = 0.037$ with IRI-10) while the cryosolution CS10 exhibited the lowest number of differentially expressed genes (DEGs) and deregulated pathways in the mRNA sequencing analysis. The cryosolution IRI-10 was the least efficient, as demonstrated by the lowest post-thaw recovery (46.7%) and viability (80.7%), lowest survival rate, and highest number of DEGs and deregulated pathways in the mRNA sequencing analysis. Similar expression levels of stemness gene markers were obtained for all cryosolutions.

Conclusion: We demonstrate the fitness-for-purpose of 15 mM IRI in 5 % DMSO-containing CryoStor® solution (IRI-5) as an efficient cryoprotective solution for iPSCs in terms of post-thaw recovery, viability, pluripotency, and transcriptomic changes. IRIs can reduce DMSO concentrations and its associated toxicities, thereby improving the utility, effectiveness, and efficiency of cryopreservation.

Poster Abstracts Presentation Schedule

Abstract #	Abstract Title	Category	Presenter		Country
P1	Ice Slice Baby; Exploring the Use of Ice Embedding for Frozen Sectioning in Biobanking	Validation of Processing Methods / Method Comparison	Paola	Foulkes	United Kingdom
P2	Filter-Biobanking: Possibility in Waste Water Based Epidemiology (WBE)	Other	Koh	Furuta	Japan
P3	DNA Quality Controls in the HCB-FRCB-IDIBAPS Biobank	Quality Control Methods	Teresa	Botta-Orfila	Spain
P4	Preservation of Viable Human Tissue for Translational Biomedical Research in HUB-ICO-IDIBELL Biobank	Cell Preservation and Cryobiology	Claudia	Garcia Roca	Spain
P5	Undertaking Routine Monitoring For Nuclease Contamination Of Laboratory Equipment And Consumables: A Biobank's Experience	Quality Control Methods	William	Mathieson	Luxembourg
P6	Improving Yields in Multi-analyte Extractions by Utilizing Post-Homogenized Tissue Debris	Validation of Processing Methods / Method Comparison	William	Mathieson	Luxembourg
P7	Does Controlling Fixation Time with More Stringency Result in Formalin-Fixed, Paraffin-Embedded Tissue Blocks with Improved Amenability to Next Generation Sequencing?	Quality Control Methods	William	Mathieson	Luxembourg
P8	Improving Yield and Integrity in Automated DNA Extractions from Formalin-Fixed, Paraffin-Embedded Tissues by Optimizing the Manufacturer`s Deparaffinisation and Proteinase K Digest Protocol	Validation of Processing Methods / Method Comparison	William	Mathieson	Luxembourg
P9	Quality Control Program in the WMU Biobank-the Only One ISO 20387:2021-01 Accredited Biobank in Poland	Quality Control Methods	Joanna	Glenska-Olender	Poland
P10	Tissue Microarrays: Turning Hidden Resources in Research Gems	Other	Daniel	Catchpoole	Australia
P11	Validation of Laboratory Data for Research Purposes in a Cancer Hospital in Upper Egypt	Validation of Processing Methods / Method Comparison	Ahmed	Abdelhafiz	Egypt
P12	Standard Preanalytical Code (SPREC) version 4.0: Optimizing Sample Quality and Biospecimen Research	Quality Control Methods	Lalita	Wadhwa	United States
P13	Retrospective Review of 15 Years of Biospecimen Collections for Respiratory Assay Development	Other	Karen	Howe	Switzerland
P14	Harnessing the Power of Multiomics from a Single Sample with Advanced Automation for Sample Handling and Processing	Validation of Processing Methods / Method Comparison	Vanessa	Tumilasci	Canada
P15	Stool as a Bioresource for Biomedical Research Studies in the Era of Precision Medicine: Importance of Biobanks	Other	Carmen	Canadas	Spain
P16	Comparison of Peripheral Blood Mononuclear Cell (PBMC) Isolation Methods : With or Without Whole Blood Dilution	Validation of Processing Methods / Method Comparison	Emmanuel	Roux	France
P17	Optimization and Standardization of Procedures to Obtain High-Quality Saliva Samples in a Biobank Context	Validation of Processing Methods / Method Comparison	Daniel	Alba Olano	Spain
P18	Proficiency Testing Program 12th anniversary: Past, Present and Future	Validation of Processing Methods / Method Comparison	Sabrina	Saracino	Luxembourg
P19	Importance of Quality Evaluation in Assessing Conditions of Tissue Processing	Quality Control Methods	Olga	Kofanova	Luxembourg

Abstract #	Abstract Title	Category	Presenter		Country
P20	Assessing Biological Risks in a Marine Biobank Technical Unit	Other	Andrea	Ramilo	Spain
P21	Challenges and Solutions for the Implementation of the Sample PREanalytical Code (SPREC) for the Coding of Samples in the Biobank Information Management System (BIMS)	Other	Ana Maria	Sánchez-López	Spain
P22	A Pilot Study to Repurpose Biological Material from Glass Slides	Validation of Processing Methods / Method Comparison	Ainara	Egia	Spain
P23	Data Quality Control in a Marine Parasite Biobank	Quality Control Methods	Helena	Rodriguez	Spain
P25	Measurement Protocol for Quality Assessment Studies of Blood Samples Using Raman Spectroscopy	Quality Control Methods	Maria Gabriela	Fernandez Manteca	Spain
P26	Assessing the Quality and Integrity of FFPE Blocks in an Indian Network Biobank, Prepared from Different Formalin Fixation Times Using Immunohistochemistry and DNA Isolation Techniques	Validation of Processing Methods / Method Comparison	Shaji	Ayillath	India
P27	From TPP to TSP, a New Concept in Infectious Disease Biobanking for Diagnostic Applications	Other	Fay	Betsou	Switzerland
P28	Characterization of Organoids as Guarantee of Quality of these Recent Models	Quality Control Methods	Juan David	Rejón	Spain
P29	Novel Dry Technology for Stabilization and Room Temperature Storage of Whole PB Samples	Validation of Processing Methods / Method Comparison	Marta	Martin Ayuso	Spain
P30	Use of Freeze-Dried Cell Lines as Controls for Next-Generation Sequencing Studies	Validation of Processing Methods / Method Comparison	Marta	Martin-Ayuso	Spain
P31	IVO Biobank experience in Biospecimens and External Quality Assurance (EQA) Programs	Quality Control Methods	Jose Antonio	Lopez Guerrero	Spain
P32	Quality Assessment of Blood Samples with Raman Spectroscopy	Quality Control Methods	Maria Gabriela	Fernandez Manteca	Spain
P33	Feasibility of DNA Extraction Directly from Freeze-dried and Frozen Bacterial Strains for Whole Genome Sequencing	Validation of Processing Methods / Method Comparison	Dominique	Clermont	France
P34	Expand the Horizon, Sharpen the Vision: A Comprehensive Approach to Develop ISBER Best Practices Fifth Edition	Other	Emma	Snapes	Ireland

Poster Abstracts

P1: Ice Slice Baby; Exploring the Use of Ice Embedding for Frozen Sectioning in Biobanking

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Background: The standard procedure for sectioning frozen tissue specimens at the biobank for quality assurance (QA), involves embedding samples in optimal cutting temperature compound (OCT). OCT produces artefact in frozen tissue samples. This artefact can interfere with downstream processing, morphology assessment and QA of frozen tissue samples. We received a project application that requested frozen sections of pancreatic tissue to be cut using water and no embedding media. To assess the feasibility of this request, a study was performed where fresh frozen kidney samples were sectioned without OCT embedding.

Methods: Two frozen kidney tumour samples from the same patient were selected. Sample 1 was cut according to the routine biobank standard operating procedure for cutting frozen sections. The tissue was embedded in OCT on the cutting chuck, sectioned at 4µm at -29oC and placed onto a Superfrost microscope slide. Sample 2 was fixed to the cutting chuck by partially embedding in 1ml frozen distilled water, sectioned at 4µm, and placed onto a Superfrost microscope slide. Sections were stained with H&E and reviewed by a pathologist.

Results: Sample 2 remained adhered to the chuck and adequate sections were obtained for QA. More folding was seen in sections from sample 2, but the sections were morphologically better than that of sample 1 due to the absence of embedding media artefact. Additionally, the morphology of sample 2 was more comparable to the morphology of FFPE processed tissue than that of the OCT embedded frozen sections. The quality of the cellular morphology of the tissue was still high, despite the tissue having been cryopreserved for 18 years.

Conclusions: These results demonstrate that partially embedding tissue in ice offers an effective alternative to OCT. The absence of OCT artefact also provides better quality sections for QA purposes. Embedding fresh frozen tissue in ice submits the tissue to a freeze thaw cycle. This is a significant limitation for biobanks where the preservation of sample integrity for future processing and analysis is crucial. Securing samples to the cutting chuck via partially embedding with OCT may offer the advantage of preserving tissue integrity and removing embedding artefact from sections. As this study only focused on kidney tumour tissue, further research is needed to establish whether this embedding technique would translate to other tissue types.

P2: Filter-Biobanking: Possibility in Waste Water Based Epidemiology (WBE)

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Statement of the problem: COVID-19 put all of us in very difficult situation in this couple of years. At the same time, experiences in these difficulties provided opportunities for various innovations. Development of various online communication technologies is the one big example. Another intriguing example could be added to this list, such as pathogen detection by using waste water samples.

During this pandemic, people realized the difficulty of detecting the timing when pathogens invade into the community. Some of this author group proposed to utilize waste water as a resource of pathogen detection. They were successfully confirmed that analyses of waste water samples have indicated not only proof of the current infection but also an early sign of prevalence in the community. Then the group revealed the pathogens were in the real world and interacted with other pathogens. This needs longitudinal analyses of diverse pathogens, such as biobanking-"Filter-Biobanking".

Proposed solution: In May 2020, a part of this author group started analyses of SARS-CoV-2 detection by using waste water samples. The outcome was remarkable and the result was reported (Ref 1). One unique feature of this group is using filters for analyzing waste water. For testing possibilities of longitudinal analyses, they utilized archived filters.

Method for archived electronegative membranes:

The waste water samples collected between October 2018 and April 2020 were originally intended for the detection of enteric viruses and thus concentrated with an electronegative membrane method with acid rinse followed by alkaline. 100 mL of each sample supplemented with 25 mM MgCl2 was filtered through electronegative membranes, followed by filtration of 200 mL of 0.5 mM H2SO4 and 10 mL of 1 mM NaOH (pH 10 to 11).

Validation of the detection methods:

Concentrations of viral RNA in waste water collected between October 2018 and January 2023 were determined with two variations method. To validate these two, for the quantification of viral RNA in waste water, a seeding experiment was conducted.(Ref 3)

Impact on downstream analyses:

During these procedures, the group concluded that archiving these filters as a part of samples was useful and important. These archived samples could be utilized for detection of divers pathogens including variants.

Conclusions and possibilities: Waste water biobanking provides opportunities for analyses of samples retrospectively to obtain important public health insights at the population level; for example, when a pathogenic virus invades or emerges in a community, how effective public health interventions work for mitigating the prevalence of infectious disease, or whether the characteristics of infectious disease (e.g., epidemic level, genetic distribution, seasonality) change compared to the previous seasons.

Various innovative technologies have already introduced into this field of WBE. The group confirmed importance WBE with filter-biobanking, although "Filter-biobanking" in WBE needs further innovation.

"Filter-biobanking" may have tremendous potential, if filters in general can be transported and/or stored in ambient temperature and/or dry. This may open the door for utilization of this technology into the resourceless environment including LMICs. One of this author group has some clues in this direction such as "Effect of protective agents on long-term preservation of LDH protein for preserving desiccated clinical analytes at room temperature"(Ref 6-7).

References:

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P3: DNA Quality Controls in the HCB-FRCB-IDIBAPS Biobank

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Statement of the problem: Biobanks must ensure the optimal quality and traceability of the human samples processed, stored and subsequently procured to investigators in order to achieve high-quality research. The HCB-FRCB-IDIBAPS Biobank currently conducts periodic quality controls on DNA samples, which are divided in three different procedures to ensure: (i) quality of the samples stored in the biobank for a long period of time; (ii) correct functioning of the system and proper performance; and (iii) optimal quality before sample procurement. Parametrically, the three controls assess concentration and purity, integrity and traceability. During 2023, all the procedures and protocols related with these controls were reviewed and updated for the transition to the new ISO 20387:2020.

Proposed solution: In the HCB-FRCB-IDIBAPS Biobank, purity is determined simultaneously with concentration using a spectrophotometer. These allow calculation of the concentration and Abs260/Abs280 ratio. Furthermore, to determine DNA integrity, two different techniques are employed: firstly, an electrophoresis of the genomic DNA in a low percentage agarose gel and secondly, if the result of the genomic DNA electrophoresis is not conclusive, a PCR amplification of a long fragment (KIT gene). In both techniques, the observation of a defined high-weight molecular band in the gel stands for an unharmed DNA sample. Moreover, to guarantee sample traceability, biological sex of the sample donor, which is previously registered in the database, is determined performing a PCR amplification of ZFX and ZFY genes. Both genes show difference in length due to an Alu element inserted in ZFX and the PCR product electrophoresis allows the differentiation of female and male individuals. In 2021 a new protocol based on short tandem repeats (STRs) amplification was optimized using five different STRs. Therefore, currently it is possible to discriminate samples that come from different individuals with the same biological sex.

Conclusion: One of the controls carried out during the first half of 2023 showed that 99,6% of the samples processed in

the Biobank were pure and 99,6% non-fragmented, ensuring that the extraction process is suitable for the sample and technical performance is optimal. Therefore, evaluation of the purity, integrity and traceability of a DNA sample ensures an optimal performance of the experiments and thus, ultimately aids to foster the translational research field.

P4: Preservation of Viable Human Tissue for Translational Biomedical Research in HUB-ICO-IDIBELL Biobank

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Background: HUB-ICO-IDIBELL Biobank is a hospital-based biobank committed to the duty of responding to the needs of its scientific and research environment. The availability of viable human tissue has become necessary for translational biomedical research. The main objectives of this study were:

1. To identify the researchers needs in order to prioritize tissues with the most scientific interest.
2. To analyze the effect of cryopreservation in cell viability.
3. To create a Standard Work Procedure of tissue cryopreservation technique and establish it as a service on demand.

Methods: To identify the researchers needs, we contacted the biobank internal committee. Two fresh lymph nodes (G1-lymphoma and G2-prostate metastasis) and two fresh glioblastomas (N1 and N2) were fragmented and cryopreserved in 90% Fetal Bovine Serum (FBS) + 10% Dimethyl Sulfoxide (DMSO) or a commercial storage solution. The samples were submitted to slow-freezing (1ºC/min) at -80ºC for 24h and preserved at -196ºC afterwards. After 5 months, the 4 cryopreserved samples were thawed and a dissociation protocol was performed, using a commercial enzyme kit for each type of tissue.

Results: The study identified the lymph node and glioblastoma as tissues of interest for IDIBELL researchers. The dissociation protocol was effective in all cases except for G2 sample, which could not be dissociated into cell suspension due to the presence of marked fibrosis. Tissue fragment size was bigger for N1. Cell viability was >90% for G1, 66% for N1 and 72% for N2, suggesting that cell viability might be related to fragment size, as a more fragmented tissue may allow better cryopreservation medium penetration.

Conclusion: It was observed that for more fibrotic tissues (G2) the protocol may need specific enzymes and incubation time readjustments. Also, FBS + DMSO and the commercial storage solution were good cryopreservation mediums for both types of tissue and cell viability and population remained stable even after 5 months of cryopreservation. Consequently, a preliminary Standard Work Procedure of tissue cryopreservation was created.

Our further objective is to include fresh cryopreserved tissue in the biobank collections, allowing the availability of viable, well-characterized tissue samples with the final histopathological diagnosis. In this regard, our next step is to expand the protocol to other types of tissue for organoid and patient-derived xenograft models' generation and biobanking.

P5: Undertaking Routine Monitoring For Nuclease Contamination Of Laboratory Equipment And Consumables: A Biobank`s Experience

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Background: Nucleases as contaminants have catastrophic potential because they rapidly degrade nucleic acids but retain high resilience to inactivation. Laboratories undertake rigorous precautions to prevent nuclease contamination of reagents and consumables, but such measures are not infallible. We therefore implemented routine nuclease testing to monitor and control for nuclease contamination in our laboratory processes, equipment and consumables.

Method: Laboratory Test Items (consumables from in-use boxes on lab benches, blanks from nucleic acid extraction robots, elution buffers, spectrophotometer microplates, MilliQ water and ice) are tested for RNase and DNase using cleavable, fluorescent DNA and RNA substrates. Assay sensitivity was determined using doubling dilutions of nucleases of known activity. A Test Item is considered "Contaminated" if it returns double the fluorescence of the Negative Control.

Results: In 8 years and 17 rounds of testing (30 Test Items/round), 1.1 % of RNase and 0.2 % of DNase tests returned a "Contaminated" result, enabling us to take remedial action. Contamination is ⇢ 2.90 x 10-9 U RNase or ⇢ 2.56 x 10-4 U DNase. Despite our adoption of rigorous precautions, there is a propensity for RNase contamination to occur in areas where it is used in DNA extractions and DNase contamination to occur where it is used in RNA extractions. Spectrophotometry microplates are also vulnerable. Despite being plumbed into external sources of deionized water, our ice machine and MilliQ water supply, like our in-use boxes of consumables, have consistently been nuclease-free.

Conclusion: The testing regimen enables us to quantify the risk of nuclease contamination in our laboratories, identify higher-risk activities and design our workflows such that risk is minimized. Testing also helps us fulfill our obligations for ISO 20387:2018 General Requirements for Biobanking and ISO 17025 Testing and the Calibrations Laboratory Standards. These both stipulate that laboratory environmental conditions must be monitored with defined quality control criteria. In no instance was an elevated nuclease level consequential in terms of its impact on sample quality. DNA extractions should be performed in spatially separate areas (ideally different laboratories) from RNA extractions and use dedicated equipment. Likewise, downstream nucleic acid work should also be spatially separated from where extractions are performed. We encourage others to adopt a similar regimen.

P6: Improving Yields in Multi-analyte Extractions by Utilizing Post-Homogenized Tissue Debris

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Background: In multi-analyte extractions from frozen biospecimens, tissue is homogenized in lysis buffer, centrifuged, then DNA, RNA, and protein are purified from the supernatant. However, DNA and protein yields are usually lower than in single-analyte extractions. We assessed whether yields in simultaneous extractions can be improved by revisiting the post-homogenized, post-centrifuged tissue debris that is normally discarded. We subjected said debris to additional multi-analyte extractions (Method A) or DNA-only extractions (Method B).

Methods: Simultaneous DNA, RNA and protein extractions were performed from 36 frozen endometrium tissue blocks using the AllPrep kit (Qiagen) as per the kit`s protocol, except the post-homogenized tissue debris was frozen at -80 °C, not discarded. For Method A, the tissue debris from 12 blocks was thawed then subjected to three additional simultaneous extractions, each further homogenizing the debris from the previous extraction. For Method B, the tissue debris from 24 blocks was thawed, digested with Proteinase K then applied to DNA-only extractions, using either a silica spin-column (n = 12) or an alcohol precipitation protocol (n = 12). Method B was then validated using a new cohort of 65 tissue blocks.

Results: Method A yielded no additional RNA, 13 % additional DNA (which became progressively more degraded with each homogenization) and 162 % additional protein (which changed in proteome with each additional homogenization when analyzed using SDS-PAGE). Method B yielded 27 % additional DNA with the silica spin-column protocol and 204 % additional DNA with the precipitation protocol. The DNA was not compromised in integrity (assessment by long-range PCR, DNA Integrity Numbers, and size at peak fluorescence of electropherogram). In the validation cohort, Method B yielded 32 % and 55 % additional DNA with the silica spin-columns and alcohol precipitation protocols respectively.

Conclusion: We do not recommend Method A because applying additional homogenizations to tissue debris caused DNA degradation and changes in the recovered proteome. However, users can adopt Method B by freezing tissue debris from a simultaneous extraction at -80 °C rather than disposing of it. Then, should a sample fail QC on account of insufficient DNA yield, a Proteinase k digest followed by a DNA-only extraction can be applied to said debris. The rescued additional DNA is of similar integrity as that from the initial simultaneous extraction.

P7: Does Controlling Fixation Time with More Stringency Result in Formalin-Fixed, Paraffin-Embedded Tissue Blocks with Improved Amenability to Next Generation Sequencing?

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Background: Formalin-fixed, paraffin-embedded (FFPE) tissue blocks are optimal for patient diagnosis because tissue architecture is preserved excellently. However, DNA extracted from FFPE blocks is fragmented, which is challenging for Next Generation Sequencing (NGS). Excessive formalin fixation is detrimental to DNA, so controlling fixation times more stringently than current recommendations (6 – 72 hrs., College of American Pathologists) might generate FFPE blocks with improved amenability to NGS. We apply stricter controls to a cohort of "Genomic" FFPE blocks, which we compare with blocks prepared using a standard protocol ("Std" blocks) in respect of DNA yield, integrity and amenability to NGS.

Methods: Genomic and Std FFPE blocks (n = 39 of each) were prepared from patient-matched cancer tissue (10 tissue types). Std blocks were fixed and processed using the hospital`s routine workflow: variable block sizes and 27 – 174 hrs. fixation. Genomic blocks were 5 mm3 with 27 – 34 hrs. fixation. DNA was extracted from 10 x 4 µm sections using the QIAamp FFPE kit (Qiagen), quantified (pico green) and assessed by qPCR (Illumina FFPE QC Assay) and DNA Integrity Numbers (DINs). DNA libraries were created from 80 ng

DNA, QC-checked (pico green and DNA 1000 chips) then 9 pM sequenced on a MiSeq using the AmpliSeq Cancer Hotspot Panel (all Illumina).

Results: Differences between Genomic and Std blocks were not statistically significant for either DNA yield or integrity by qPCR, but DINs were higher in Genomic blocks than Std blocks (mean DIN 5.9 and 4.7 respectively, $p < 0.001$). DNA purity was slightly higher in Genomic blocks (260:280 of 1.80 compared to 1.75, $p = 0.03$). Libraries were equally successfully created in all blocks. NGS coverage was similar in Genomic and Std blocks (median 1879 x and 1903 x respectively, $p = 0.71$), as was the number of mapped reads (median 400,000 in both, $p = 0.61$). Genomic blocks had slightly lower error rates (median 0.17 compared to 0.20 % per base, $p < 0.001$) and properly paired reads (mean 87.9 compared to 91.1 %, $p = 0.004$).

Conclusion: Controlling fixation times and tissue block sizes with greater stringency than current clinical guidelines returned FFPE blocks that yield DNA that is slightly less degraded. For NGS, in the FFPE-friendly AmpliSeq cancer hotspot panel we used, the improvement in DNA integrity was inconsequential and the existing Std FFPE processing workflow is fit for purpose.

P8: Improving Yield and Integrity in Automated DNA Extractions from Formalin-Fixed, Paraffin-Embedded Tissues by Optimizing the Manufacturer's Deparaffinization and Proteinase K Digest Protocol

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Background: Automation is a requisite when labs perform large numbers of DNA extractions. However, DNA yield and/or integrity can be poorer in automated compared to manual extractions. We optimized the manual deparaffinisation and proteinase K digest steps in our automated DNA extraction protocol for formalin-fixed, paraffin-embedded (FFPE) tissue.

Methods: Our starting point was the manufacturer`s protocol of the Chemagic FFPE DNA kit, run on a 96-sample Chemagen MSM1 robot (all Perkin Elmer). We sequentially optimized the no. of sections/extraction, the volume of proteinase K, digest time, temperature and thermomixing during digestion, using 12 FFPE tissue blocks. We also evaluated adding a break point after the digest. DNA was quantified (pico green fluorometry), purity-assessed (photometry) and integrity-assayed by qPCR (Illumina FFPE QC Assay), multiplex PCR (100, 200, 300 and 400 bp amplicons of GAPDH) and DNA Integrity Numbers (DINs). The optimized protocol was then validated using a new cohort of 24 FFPE blocks and compared to the manual QIAamp FFPE DNA extraction kit (Qiagen).

Results: The optimized protocol returned a median yield that was 25.7 times higher than the manufacturer`s protocol (1284 compared to 50 ng DNA, $p < 0.001$). The difference in 260:230 was not statistically significant but the optimized protocol had slightly poorer 260:280 (median 1.67 and 1.84 respectively, $p = 0.024$). The optimized protocol had lower ΔCq by qPCR (i.e., improved integrity): median 0.7 compared to 3.2, $p < 0.001$. DINs were higher in the optimized protocol (also denoting improved integrity): median 4.9 compared to 2.0, $p = 0.045$. In multiplex PCR, 75 % of the samples in the optimized protocol returned the 400 bp amplicon with the other 25 % returning the 300 bp amplicon. A break point can be added between the proteinase k digest and the DNA extraction (with samples stored at -80 °C) without losing yield or integrity. Compared with the manual kit, DNA extracted using the optimized, automated protocol was higher in yield (mean 1.6 compared to 0.7 µg DNA, $p < 0.001$), the difference in DIN was not statistically significant but slightly poorer in integrity by qPCR (mean ΔCq 0.90 compared to 0.65, $p = 0.001$).

Conclusion: The performance of a high-throughput robot that extracts DNA from FFPE inefficiently can be radically improved by optimizing the deparaffinisation and proteinase k digest steps. Users should not assume the manufacturer`s protocol is optimal.

P9: Quality Control Program in the WMU Biobank-the Only One ISO 20387:2021-01 Accredited Biobank in Poland

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Background: Wroclaw Medical University Biobank (WMU) is a modern biobanking unit for long-term storage and processing of human biological samples and associated data, ISO 20387 accredited. The scope of accreditation No. BB 001 covers human biological material such as: peripheral blood, urine, saliva, feces, nasal swab, breast milk, tissues, cerebrospinal fluid stored in various temperature conditions (from - 65° C to -86° C; -20° C to -30° C; 15° C to 30° C; below - 150° C).

The quality management system (QMS) covers all activities of the WMU Biobank and ensures quality of the biological

material/data according to the highest international standards. Special attention is concentrated on dedicated quality control criteria for biological resources and related data for specific fit for purpose with particular emphasis on point 7.8 and Annex B of ISO 20387.

Methods: Quality control in Biobank WMU is carried out in three ways: internal quality control activities performed during routine work, on an ongoing basis; internal, periodic quality control and participation in external quality control, including proficiency schemes. QC is subject to biological material, data linked to biological material and processes directly affecting the quality of biological material and related data to measure adherence to protocols and sample integrity. Furthermore, Biobank establishes a 4-year Proficiency Testing Participation Plan. This plan specifies the proficiency testing programs in which the biobank obligatorily participates (e.g., IBBL).

Results: Before the accreditation WMU Biobank has designed and performer a QC program. This program includes measurements and evaluation of the selected parameters like integrity, uniformity, purity, volume, availability, identification, time and temperature and some biochemical parameters of BM samples that indicate that the biobanking process is carried out in accordance with the assumed acceptance criteria. The correctness of the data created in Biobank is verified once every three months. All created Excel files are subject to verification for data compliance. For this purpose, we verify the file on the computer and the file from the saved copy from the external drive and the server (according to good practice 3-2-1). In addition, we generate an excel file with the records of boxes and samples from the BBMS system and we check the correctness of data from the system and from backup copies from the disk and from the server. Currently, Biobank is improving the existing QC program and expanding the program in line with the expectations of the accreditation body. New program involves the measurements of biochemical parameters from whole blood, plasma, serum , saliva, urine, feces and tissue before and after long storage. At the beginning the parameters will be checked after 3 months, after half a year and then after a year.

Conclusion: The QC program developed by WMU Biobank focuses on continuous improvement and validation of quality control methods and procedures for selected parameters. Biobank's quality control is an approach to ensure that the research and development work carried out in the laboratory provides accurate, repeatable and reliable results, minimizing errors and removing duplicates.

P10: Tissue Microarrays: Turning Hidden Resources in Research Gems

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It is expected that biobanks provide critical tissue resources to researchers to conduct fundamental investigation into disease states and to ensure the best research use of all tissue biospecimens by linking them to key questions being asked in research. Recognizing the rarity of childhood cancers, small tumour specimen volumes, and the burgeoning need for tissue-directed research we describe here the impact of a research focused biospecimen resource The Tumour Bank at The Children's Hospital at Westmead (TB-CHW) has initiated alongside the main source of all such tissue, our histopathology department. In 2012 we leveraged the hospital's formalin fixed paraffin embedded tissue (FFPE) tissue block archive to commence a tissue microarray (TMA) construction program. Our purpose was to provide rationalised access to FFPE tissue whilst not impacting on the availability of blocks for future diagnostic or medico-legal review. Construction of the TMAs that represented a single childhood cancer subtypes required a deep dive into the block archives with blocks selected covering sample collected over a couple of decade long period or more. This resulted in a tissue resource where enough rare paediatric tumours representing all patient seen at a single centre are drawn together to provide meaningful results in their own right. The TB-CHW TMA selected blocks from the past two or more decades, establishing a workable pipeline for the construction of TMAs involving block selection, pathologist review, block construction and QA processes, staining and review, digital microscope and downstream image analyses. The program constructed 25 TMAs which has subsequently supported 21 international studies with a total of 828 individual slides released novel technical evaluation, image analyses and biological assessment that have shifted beyond routine chromogenic and immunohistochemical staining into spatial assessment of targeted regions for protein and gene expression activity as well as deep learning and artificial intelligence.

P11: Validation of Laboratory Data for Research Purposes in a Cancer Hospital in Upper Egypt

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Background: Biobanking is about collection of high quality samples and associated data. Laboratory data are among the most important clinical data for human biobanks, especially in cancer biobanks. Validation of laboratory results is essential to ensure their fitness for purpose in both clinical and research purposes. Shefa Alorman is a recently established oncology hospital in Upper Egypt that treats both pediatric and adult patients. In this study, we aimed to validate the results of several analytes before incorporating them into the biobank database.

Methods: We used the Dimension® EXLTM 200 Integrated Chemistry System to assess the accuracy, precision, and trueness of six representative clinical chemistry analytes (ALT, AST, total bilirubin, uric acid, glucose, and phosphorus). Five controls were measured for each level of quality control for five days (5 × 5; total 25). We then calculated the coefficient of variation to compare this value to within-subject biologic variation according to Westgard biological variation data to measure precision. To measure accuracy, we calculated the recovery of analytes (Mean/Target × 100%) and evaluated it against the acceptable range. For trueness, we calculated the bias% and calculated total error and compared them to the total allowable error. If any deviation was noted, the process was repeated after the cause had been investigated.

Results: After three rounds of evaluation, the six analytes showed acceptable performance, ensuring their trueness, precision, and accuracy.

Conclusion: The evaluation of the clinical performance of laboratory analytes is an essential step to ensure the reliability of their results for both clinical and research purposes. These data are used in basic and clinical research to understand the pathogenesis of diseases, establish new correlations, and identify new biomarkers. Biobanks that collect these data should ensure that this process is carried out effectively through communication with laboratory and/or quality personnel who are responsible for them.

P12: Standard Preanalytical Code (SPREC) version 4.0: Optimizing Sample Quality and Biospecimen Research

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The International Society for Biological and Environmental Repositories (ISBER) Working Group on Biospecimen Science has recently updated the Standard Preanalytical Code ('SPREC') for clinical specimens (version 1.0 Cancer Epidemiol Biomarkers Prev 2010; 19:1004–1011). This biospecimen 'barcode' provides information about the pre-analytical processing of samples, which takes place between specimen collections to the point of their experimental use in analysis and research. Biospecimen science has emerged in the healthcare sector to identify the contribution of cellular and molecular alterations that occur in biospecimens because of their process history, rather than the intrinsic differences attributed to specimens per se. The rationale is, that the more precision afforded to recording a sample's process history the more accurate and explicit the information that can be gained from biospecimen research, especially when it involves multiple different collaborating institutions and biobanks. Thus, tracing and understanding the impacts of pre-analytical variables is important as they can potentially affect sample quality and lead to deviation in experimental results that may be difficult to attribute and identify. The clinical SPREC was designed to meet the increasing demands of the end users of healthcare biobanks, especially those using sensitive analytical technologies, undertaking molecular/omics research, and engaging in large consortia projects that require equivalence across sample processing. The categorical nature of the clinical SPREC greatly facilitates the assessment of equivalence in sample processing as contrasted with detailed

narratives that are cumbersome and laborious to decipher. The clinical SPREC version 4.0 builds on the previous version 3.0 (Biopreservation and Biobanking 2018; 16:9) and adds new elements and options based either on supplementary biospecimen types or on the latest technological developments. The SPREC version 4.0 remains a simple, seven-element-long code, formulated using existing laboratory management tools and technical protocols (e.g. sample preparation, centrifugation, cryoprotection, freezing, and storage regime). Importantly, additions of new elements or options do not alter in any way previous versions of SPREC codes.

P13: Retrospective Review of 15 Years of Biospecimen Collections for Respiratory Assay Development

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Background: Biospecimens play a pivotal role in the advancement of medical research and assay development. With a growing emphasis on personalized medicine and diversity-inclusive research, in order to continually improve assay development methods it is important to understand the diversity of demographic subgroups in biospecimen collections as it may have an impact on product quality and effectiveness.

Methods: Retrospective sample information from Roche's biospecimen archive database was collected from nearly 40 respiratory projects spanning: research & development, clinical development, medical affairs, and proactive biospecimen collection. The clinical and epidemiological data information, including gender, race, and geographic location, of each biospecimen was reviewed where available. Specific demographics of collection locations were used as benchmarks to compare the collected data against in order to identify potential biases.

Results: Our review identified discernible trends in the gender, racial, and geographic demographics of biospecimen collections. The results of this analysis demonstrate evident biases, with both over- and underrepresentation of certain demographic groups, bringing to light that improved attention should be paid to these factors during biospecimen collection where possible.

Conclusion: The integrity and applicability of assay results are inherently tied to the diversity and inclusivity of the biospecimens from which they are developed. Complex factors, such as local regulations and disease epidemiology, play a role in the availability and collection of biospecimens. One factor where significant improvement can be achieved is in recognizing and addressing biases in biospecimen collections. Based on our findings, we will leverage this study to influence our approach to biospecimen collections and emphasize the need for rigorous quality control in the acquisition of the clinical data. Ensuring comprehensive representation of all demographic subgroups in biospecimen collections is crucial to developing accurate and universally effective assays.

P14: Harnessing the Power of Multiomics from a Single Sample with Advanced Automation for Sample Handling and Processing

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Background: The omics era has greatly expanded the repertoire of approaches available for researchers and clinicians to unravel the complexity underpinning human health: Next Generation Sequencing (NGS) approaches can characterize genomes, epigenomes, transcriptomes and proteomes. Advanced DNA barcoding and automated microfluidics can take this to the next level, enabling multiomic characterization of single cells. Peripheral blood mononuclear cells (PBMCs) offer a window into the immune system that, when combined with these omics tools, can provide a near holistic view of immune processes across patient cohorts.

Methods: Here we detail a workflow using a single blood draw to rapidly produce a diverse set of multiomics results including genomics, epigenomics, transcriptomics and proteomics. This starts with automated sample handling and processing of the primary blood draw to ensure high viability and yield of PBMCs, along with simultaneous plasma separation and collection. These samples are then aliquoted and simultaneously processed for automated and semi-automated whole exome sequencing, single cell RNA sequencing, epigenetic characterization and Olink proteomic assays.

Results: With this robust workflow and advanced robotics for sample handling and processing to minimize potential batch effects, genomic, epigenomic, transcriptomic and proteomic results can be produced within days of primary sample collection using minimal sample amounts. Along with this comprehensive workflow, standalone and integrated -omics results will be presented.

Conclusion: High throughput integrative omics workflows, as described here, drive greater insights in human health, allowing for a rapid combined approach to address the biological questions at hand.

P15: Stool as a Bioresource for Biomedical Research Studies in the Era of Precision Medicine: Importance of Biobanks

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In the last decade advances in biomedical research and personalized medicine have been very important. During these years, a new bioresource used to improve clinical and diagnostic information about existing pathologies, as well as search for new therapies has been stool. This bioresource has gained great importance in biomedical research in recent years, with biobanks playing a key role in the stool strategic collections creation, which can be used to the research community. In the provincial node of Malaga within the Biobank of the Public Health System of Andalusia (BBSSPA), since 2019 stool samples collection circuits have been established to support various research projects. The demand for this bioresource has been constantly increasing among the biomedical research community. Since that date, our biobank has activated more than 5 sample collection circuits, providing services to a wide range of research projects. An analysis of the procedures carried out during this period, as well as the strategies adopted to provide excellent service to the requests received in the biobank, has been conducted. This study highlights the increasing importance of stools in our provincial node and the actions which have been undertaken to generate these new sample collections to give support to the biomedical projects management by biobank. Similarly, an analysis has been conducted to highlight the technical requirements and challenges associated with processing and storing this sample based on its ultimate use in biomedical research. The study reveals that initially, the samples were collected for microbiota studies, but today, various studies can be conducted ranging from metagenomics to mass spectrometry. Therefore, the technical considerations for processing the bioresource have evolved over the years to accommodate each specific request. In conclusion, we could observe that the process optimization and work protocols in biobanks is essential for establishing collection circuits and creating stools collections which are of great interest for the research community. These efforts enable high- quality research in precision medicine and position biobanks as reference repositories for this type of bioresource.

P16: Comparison of Peripheral Blood Mononuclear Cell (PBMC) Isolation Methods : With or Without Whole Blood Dilution

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Peripheral blood mononuclear cells (PBMC) are elements of interest to the research community, particularly in the fields of immunology and tumor biology. The methods used for their isolation and freezing vary significantly between different biobank laboratories with subsequent variability in the quality attributes of the PBMCs. These include the yield of cells isolated from whole blood, their viability, as well as the conservation of cell sub-populations so that they are as close as possible to the physiological state.

In the process of validating our SepMate isolation method, we assessed one understudied preanalytical parameter, the dilution of whole blood in PBS1X, before PBMC isolation. To do this, paired blood samples were collected from 3 healthy donors. For each of the two method protocols, the one with and the one without predilution, we measured the PBMC viability with a Muse® equipment and compared the results by ANOVA. Flow cytometry analyses were carried out on CytoflexS® to verify the effective preservation of specific sub-populations, such as Leukocytes (CD45), T lymphocytes (CD3/CD4), B lymphocytes (CD19), Monocytes (CD14), Natural killer (CD56), and finally any contamination by granulocytes (CD66b).

Our results suggest that the average PBMC isolation yield is improved without whole blood dilution (diluted: 8.85 x10^6 PBMC, undiluted: 9.40 x10^6 PBMC). No significant difference in overall PBMC viability (diluted: 95,6%, undiluted: 94,1%), or significant contamination by granulocytes (diluted: 0,5%, undiluted: 0,4%), was observed between the two protocols. However, CD45+ early apoptosis levels were higher when blood was not diluted before PBMC isolation (diluted: 22,6%, undiluted: 25,4%).

We conclude that the two protocols have overall equivalent performance. Interestingly, plasma from the initial separation of undiluted blood can be collected for other applications. Thus, the manufacturer recommendation to pre-dilute SepMate whole blood needs to be considered relative to the expected PBMC end uses (phenotyping, genotyping, functional tests) and the need to conserve paired plasma for other analyses.

P17: Optimization and Standardization of Procedures to Obtain High-Quality Saliva Samples in a Biobank Context

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Standardization of the processes involved in the collection, transport, processing and storage of samples is fundamental and a particularly complex challenge for biobanks. Our study is aimed at trying to define and, if possible, control the pre-analytical variables that affect different primary samples, in order to optimize the conditions of collection and processing, ensuring the highest quality of the samples stored in biobanks and, therefore, the reproducibility of the studies carried out with them. This will allow the design of longitudinal cohorts of high-quality samples for future research uses, which will allow the analysis of a wide range of analytes.

In this part of the study, four standardized methods and commercial saliva collection tubes were compared through the subsequent extraction and quantification of both cortisol, as a model analyte, and human and bacterial DNA. Samples were obtained from healthy volunteer donors, from whom saliva samples were collected under all experimental conditions on the same day. Samples were immediately aliquoted and frozen at -80°C.

Cortisol was quantified by ELISA assay. DNA was extracted using a commercial kit and afterwards, 16S rRNA and 18S rRNA were analyzed by real-time PCR (qPCR). No major differences were observed between the cortisol levels obtained from the different methods of sample collection. However, two of the experimental conditions tested showed a significant decrease in the amount of human and bacterial DNA recoverable from their samples, compared to the other two conditions. This indicates that two of the saliva collection methods are less efficient than the others and are therefore not optimal for use in the context of a biobank.

Our results show the importance of controlling preanalytical variables, which effect is clearly dependent on the determination to be made on the samples. Further studies will be necessary to try to better define these pre-analytical variables, in order to establish a saliva collection procedure that allows obtaining reliable results in different types of studies, which is key to optimize the use of samples in the context of a biobank.

P18: Proficiency Testing Program 12th anniversary: Past, Present and Future

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Statement of the problem: High quality biobank laboratories play a crucial role in the context of multi-center clinical trials, basic and applied research, by providing and enhancing the translational link within transversal and personalised medicine initiatives. By minimizing the number of sample processing errors and increasing the reproducibility of pre-clinical and clinical studies, biobank laboratories will also improve and speed up biomarker discovery.

Proposed solution: As a part of biobank quality management system, Proficiency Testing (PT) program has been introduced for biobank processing laboratories by IBBL 12 years ago. The aim was to provide an independent assessment of a laboratory's overall quality performance, on top of the pre-existing quality controls that each laboratory could independently establish and integrate internally.

Starting from just 2 PT schemes in 2011, the PT program has since evolved and nowadays it comprises an array of up to 22 schemes, encompassing both analytical and pre-analytical phases. The PT schemes correspond to routine workflows carried out in a laboratory and include the most widespread commonly applied assays used across biobanks. In the future, as additional and novel biospecimen quality control assays are developed, they will be progressively implemented into new schemes. Information on the PT program can be found following the link: https://www.lih.lu/en/biospecimen-proficiency-testing/

The overall progression of the PT program has demonstrated global participation, with participants hailing from over 40 different countries worldwide. On average, more than 70% of participants have achieved satisfactory proficiency test results across all schemes. Laboratories that have participated in PT schemes consistently over several years have seen a global improvement in their performance in terms of their z-scores. A statistical analysis conducted on all data collected during the first decade of the annual PT program provides evidence and highlights the most critical preanalytical variables and the specificity of their impact on the applied processing methods.

Conclusions: The annual PT program serves multiple purposes, including supporting the development of biobank quality assurance, providing unique evidence-based insights into the impact of pre-analytical factors, evaluating the comparative performance of different processing methods and kits, while aiding laboratories in validating their processing methods.

P19: Importance of Quality Evaluation in Assessing Conditions of Tissue Processing

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Background: Effective processing protocols are essential for the successful outcome of sample downstream analyses, for both fundamental and clinical research studies. The application of vacuum technology at the starting point of tissue collection enables biospecimen management in relation to sample transport, fixation or freezing time for biobanking and further processing. Also, it is important to be able to qualify samples and stratify collections by quality at any time. At IBBL we established a workflow to monitor the quality of different biospecimens. In this study we present the results of such qualification applied to human tissue samples, following the application of vacuum seal technology for samples received from LNS Pathology.

Methods: Colon tissues were transported fresh from a surgery room and vacuum-sealed with the SealSAFE automated system. All tissues were kept at 4°C for different periods (15', 30', 60' and 2, 4, 6, 24, 30, 48h) and then snap-frozen in liquid nitrogen. All aliquots were transferred for secondary processing and IBBL quality control (QC). Single and simultaneous DNA/RNA/protein extractions were applied. The molecular derivatives were evaluated in terms of yield, purity, integrity, gene expression and amplifiability.

Results: When analyzing different vacuum fixation times, no specific trends were observed for DNA/RNA yields, purity and integrity. However, we obtained higher dsDNA yields when single DNA extraction was used compared to the simultaneous extraction. Single DNA extraction also returned dsDNA percentage above our QC threshold of 70%. Higher purity values were obtained when the simultaneous extraction was applied, versus the single DNA extraction. DNA amplification of small and large fragments was successful irrespective of the treatment. We observed a high variability, but sufficient RNA yields for all samples. 92.6% of RNA samples had purity above 1.6. For all samples RINs were higher than 6. The size-range reverse PCR resulted in 942 bp amplicon for all samples. MicroRNA presence and stability measured in all samples under different conditions were detected with no specific trends.

Conclusion: Our results confirmed the previously published data on the suitability of vacuum technology for tissue logistics from surgery to biobanks, thus increasing the collection time without a sharp loss in sample quality. Obtained QC results could be used as a guide for future collections and processing for the examined tissue types.

P20: Assessing Biological Risks in a Marine Biobank Technical Unit

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Statement of the problem: Marine samples take part in an ecosystem which includes, not only animals, plants and their environment, but also other organisms such as parasites, viruses, bacteria and fungi. Many of these microscopic organisms are pathogens for marine flora and fauna, causing significant economic losses in the productive sector. Moreover, an important number of them are zoonotic pathogens which are spread through food, water and the environment. Thus, as stated in the One Health approach (World Health Organization) there are a clear link between animal health, human health and environment. It is therefore essential a holistic vision aimed to prevent, detect, contain and minimize the potential public and animal health risks. However, the marine biological risks are therefore not taken into account in sampling, handling and analysis of marine samples by research centers and private companies. Additional efforts need to be undertaken to identify zoonotic pathogens from marine samples, carry out the risk assessment and preventive actions in order to ensure workers safety and hygiene.

Proposed solution: The Biobank Technical Unit (UTB-CSIC) is a traceable high-quality sampling platform, which include marine organisms, their DNAs and associated data. Nowadays, the priority objective of UTB-CSIC is to contribute to identify and assess on marine biological risks. Thus, during the last year we focused on generating an environmental DNA (eDNA) Biobank from marine water that provides different ecosystem services. As a first approximation to evaluate the genetic diversity and identify potential zoonotic pathogens, DNA metabarcoding libraries for parasites, bacteria and fungi were constructed and sequenced in Illumina PE250 platform. Bioinformatic analysis will allow to know the identity of microorganisms included in each type of water and categorize and assess the risk for each biological agent. Standardized procedures and protocols will be developed, including preventive measures for handling of each type of water.

Conclusion: Biobanked eDNA will be useful for researching of wide variety of organisms and for deepening both in studies of animal and human health, as well as, in food safety. This information will be essential to assess the risk of manipulating marine samples in research centers, and to carry out preventive actions in order to ensure workers safety.

P21: Challenges and Solutions for the Implementation of the Sample PREanalytical Code (SPREC) for the Coding of Samples in the Biobank Information Management System (BIMS)

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Statement of the problem: The impact of the preanalytical variables on the quality of the biological samples and their effect on the analytical results has been widely studied. Therefore, a Sample PREanalytical Code (SPREC) has been proposed to trace the preanalytical variables in order to facilitate and harmonize the use of biological samples for research, especially when the samples are obtained from different sites or biobanks. In the Andalusian Public Health System Biobank (SSPA Biobank) the SPREC coding is planned to be automatically done through the information registered in their biobank information management system (BIMS), nSIBAI.

Proposed solution: To achieve this objective, an analysis of the preanalytical information registered in the BIMS and their correlation with the SPREC code was carried out. Correspondence tables were prepared identifying the following challenges: a) some of the preanalytical variables are not being currently registered in the BIMS and b) there is not always a direct correspondence between BIMS data and SPREC code.

So, different solutions were identified respectively: a) the design of specific questionnaires for the registration of these preanalytical variables in the BIMS and b) the establishment of a correlation between SPREC and multiple information registered in the BIMS. Finally, those variables which will not be automatically coded were identified and further analysis will be required to find a solution to trace them.

Conclusions: The study carried out has allowed to configure a structure and add the tool in the BIMS to automatically assign the SPREC to biological samples registered when the necessary information is available. This structure is customized and maybe updated with future versions of SPREC.

P22: A Pilot Study to Repurpose Biological Material from Glass Slides

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Background: The availability of human biological specimens is a mayor limitation for biomedical research. Therefore, it is important to maximize the use of biological material, and repurpose it whenever possible.

Objective: This work stems from the need to repurpose tissue from glass slides that didn´t present property compatible with immunohistochemical procedures.

Methods: We set to evaluate a scenario where human tissue (tonsil) from an exhausted paraffin block had been adhered onto a super frost glass slides that was incompatible with a specific IHC procedure, so that it needed to be transferred to a Superfrost PLUS microscope slide. The procedure needed to be robust, reproducible and should preserve the histological properties and IHC compatibility of the material.

We tested different solutions and conditions to detach the tissue from Superfrost slides. Heated water, at different temperatures and times, or high pH solutions used in the IHC protocols. It was just with this last solution (Ultra Cell Conditioning Solution, ULTRA CC1, from Ventana-Roche - routinely used in the unmasking procedure) that resulted in the immediate release of the tissue from the slide, allowing us to place it into a new surface (Superfrost PLUS). The procedure could be repeated, and the macroscopic structure of the biological material remained unaffected.

We proceeded with a detailed histological characterization of the transferred tissue before releasing it to the researchers. To this end, we stained the original and the repurposed tissue with a Hematoxoline & Eosine, following the clinical procedure of the pathology service. A pathologist confirmed that the tissue architecture of the repurposed material was acceptable.

Lastly, we tested the immunohistochemical properties of the repurposed tissue. Superfrost PLUS glass slides were subject to IHC in an automated protocol. The tissue integrity was generally well-retained, just some parts of the edges were slightly bended sometimes, but there were no detaching issues and the immunoreactivity obtained in the tissue complied with the required standards.

Conclusion: This pilot study opens the possibility of repurposing tissue slides that are incompatible with specific

staining procedures, and in the future, to also redirect usage of tissue slides for other molecular biology strategies such as nucleic acid purification.

P23: Data Quality Control in a Marine Parasite Biobank

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Statement of the problem: Evidence of Anisakidae larvae in a high and rising number of fish species of commercial interest around the world has remarkably increased. The importance of fish infection by Anisakidae lies in their repercussion on seafood safety and quality, increasing awareness about anisakids as a re-emergent risk in fish-eating consumers.

Parasite Biobank was implemented at the UTB-CSIC in 2013. Until now, it managed more than 100000 parasite samples (mainly Anisakidae) from almost 25000 extractions. Furthermore, during that period a BoB (EpiData, software Bio-o-Bank Vitro®) was generated, with all the traced information for any extraction and sample. Those data showed to be an invaluable asset for evaluating and monitoring the Anisakidae presence in fisheries and aquaculture systems, but also for other significant objectives, such as developing risk management tools.

From 2018 to 2022, as part of several collaborative projects between CSIC and the Spanish Seafood industry, a technological support task was designed to develop new strategies for anisakid risk management. Fish industry operators made the inspection and banked the results. As data was the banked "golden" items, we developed a quality control process to ensure their quality and traceability.

Proposed solution: Data collection: Detection method is a key step. Operators evaluated the presence of zoonotic Anisakidae following the UV-Press inspection method, as described in ISO 23036-1:2021. Operators were trained at the UTB, which also provided mentoring, advising and technical assistance regarding the inspection process as well as the data traceability within the Biobank platform tool.

Verification plan: In order to ensure that the inspection method was properly implemented according to ISO 23036-1:2021 standard, pressed portions of fish, randomly selected and previously inspected by operators, were sent to UTB (i.e. verifier), where they were re-examined by highly specialised laboratory staff.

Validation: As UTB act as verifier and their results were stablish as the "gold standard", we designed an internal quality control to validate our own performance on the ISO 23036-1:2021.

Conclusion: Data quality is a measure of the condition of data based on factors such as accuracy, completeness, consistency and reliability. We (UTB-CSIC) developed a normalized protocol to routinely assess on these parameters of quality for banked data provided by registers (fish inspectors) during collection processes.

P25: Measurement Protocol for Quality Assessment Studies of Blood Samples Using Raman Spectroscopy

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Background: Raman spectroscopy has become increasingly important as an analytical technique in haematological studies over the last few decades. This non-invasive optical technique is fast and requires no sample preparation, making it a valuable tool in a wide range of applications. The versatility of Raman spectroscopy instrumentation allows precise configuration of parameters such as exposure time, number of accumulations, laser power and diffraction slit sizes. One promising application is the identification of spectral markers to assess the quality of samples based on the time between extraction and storage in a biobank. Achieving the highest quality and precision in Raman spectra requires a meticulous experimental setup that takes into account all relevant parameters.

The main objective of this study is to determine the optimal measurement conditions for the development of a quality control method for serum and plasma samples using Raman spectroscopy. We aim to optimise several measurement parameters, both in terms of the sample and the instrumentation.

Methods: We used dried drops of pooled blood serum and plasma. The acquisition was performed using a JASCO NRS-4500 confocal Raman microscope. As the distribution of the analytes after drying is an unpredictable factor affecting the quality of the spectra, we paid particular attention to the conditions under which the samples were dried. Measurements were taken over the entire surface of the dried drops using automated spatial sweeps.

Results: The optimal measurement parameters were determined by evaluating the advantages and limitations of each modification. The combination of these optimisations resulted in Raman spectra with minimal noise.

Conclusions: This work has allowed us to define a rigorous

measurement protocol for quality control of serum and plasma samples to be used in future studies.

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P26: Assessing the Quality and Integrity of FFPE Blocks in an Indian Network Biobank, Prepared from Different Formalin Fixation Times Using Immunohistochemistry and DNA Isolation Techniques

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Background: 64 Codon is a network biobank working in India, collecting Indian Asian Ethnic Human Biological Samples (HBS) with the mission of supporting collaborative research. In our model of a network biobank, we collect formalin-fixed paraffin-embedded (FFPE) tissue blocks made out of remnant tumor tissue from a network of our pathology lab partners. Since tissue collection protocols are not uniform across our country about formalin fixation time, there is a need for formalin fixation time as part of our quality control process. We are conducting a pilot study to assess the quality and integrity of FFPE tissue blocks prepared at different formalin fixation times, which is crucial for ensuring reliable results in downstream applications such as IHC and DNA isolation techniques.

Method: This prospective study compared the effect of two different formalin fixation periods on immunohistochemistry and DNA isolation. This study was performed according to the guidelines and approval of the Institute Ethics Committee (IEC). Tissue samples were obtained from remnant tumor tissue from chemonaive breast cancer patients who had undergone surgery and whose tumor tissue had been grossed by Pathologists as part of their clinical management. The standard group had a 10% neutral buffered formalin fixation time of less than 72 hours, while the comparator arm had prolonged formalin fixation of 240 hours. Patients who had either Her 2 Neu IHC score of 1+ or 3+ were included as part of the study. The samples were then converted to FFPE blocks and Her 2 Neu IHC was performed in paired samples from standard and comparator arms. IHC scoring was performed by a single pathologist who was blinded to the samples. DNA Isolation included 24 samples of 12 cases. IHC results were analysed using the Paired Sample Sign Test and DNA Isolation results by the Wilcoxon Signed Rank Test, $p<0.05$ was considered statistically significant.

Results: For the IHC study, 32 samples were included, 16 of them being Her2Neu 1+ and 16 being Her2Neu 3+. There was a statistically significant difference in IHC score between the 72-hour and 240-hour groups (Sign test Neg differences = 16, positive difference=0, ties = 16, $p<0.001$). The difference was seen entirely in IHC3+ samples which showed reduced expression on prolonged exposure to formalin. There was no change in IHC 1+ samples irrespective of formalin fixation time. Similarly, the quantity of DNA isolated was significantly higher in 72 hours compared to the 240 hours group (Wilcoxon Signed Rank test $p = 0.006$).**Conclusion:** Prolonged formalin fixation of tissue in biorepository samples adversely affects immunohistochemistry and DNA isolation for downstream applications. Every effort must be made by biorepositories to collect and process formalin-fixed samples within 72 hours to prevent deterioration in the quality of tissue.

P27: From TPP to TSP, a New Concept in Infectious Disease Biobanking for Diagnostic Applications

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Background: A target product profile (TPP) refers to a set of specifications that any new diagnostic kit is expected to fulfil (https://www.who.int/observatories/global-observatory-on-health-research-and-development/analyses-and-syntheses/target-product-profile/who-target-product-profiles). Developers of diagnostic kits follow TPPs in their development and validation pipelines to ensure an end-product meets expectations, for example in terms of diagnostic sensitivity and specificity. The development and validation of diagnostic kits requires biospecimens and associated data. To assist with this, we have introduced the concept of a target specimen profile (TSP). A TSP corresponds to the required characteristics of the panel(s) of specimens needed in the development and evaluation pipeline of a new diagnostic kit, taking into consideration the TPP.

Methods: We developed a standardized TSP template, including all of the qualitative and quantitative characteristics a specimen panel must possess to enable the (i) identification of new diagnostic biomarkers, (ii) validation of identified diagnostic biomarkers, (iii) production of quality control materials to be used in the kit, and (iv) production of quality control materials to be used in external quality assurance programs for the diagnostic kit. This concept was applied to ten neglected tropical diseases: human African trypanosomiasis, dengue, cutaneous and visceral leishmaniosis, leprosy, lymphatic filariasis, onchocerciasis, schistosomiasis, soil transmitted helminthiasis, and trachoma.

Results: A TSP for a given specimen panel includes the following specifications that the sample panel must fulfil information about the types of specimens, their necessary annotations, their preanalytical specifications, their geographical origins, their reference characterizations, their volumes and quantities, and the numbers of the various categories of patients and donors. These specifications have been developed for each context in which new diagnostic kits may be used, such as disease elimination, disease surveillance, confirmation of suspected cases, and screening in high or low endemic areas.

Conclusion: The TSP is a concept that is anticipated to help diagnostic developers in selecting the most appropriate sample panels to assist in their product development and evaluation; TSPs should also be useful in guiding biobanks in the prospective collection of sample panels to support the development and validation of diagnostics.

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P28: Characterization of Organoids as Guarantee of Quality of these Recent Models

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Statement of the problem : Thanks to recent advances in stem cells cultures, it has been possible to generate 3D in vitro biomodels known as organoids. These organoids simulate the structures of tissues and organs, allowing the interaction between different cell types in a more physiological manner compared to conventional monolayer or suspension cultures. Recent studies have demonstrated that organoids can be used to understand organ development and diseases, offering a wide range of applications. However, during the generation of organoids, alterations may occur not reflecting the same characteristics than the original tissue.

Proposed solution: To guarantee the organoids suitability as biomodels, different techniques currently used in the Andalusian Public Health System Biobank (BBSSPA) have been optimized for organoids characterization:

- G-Karyotiping: Cells from organoids have been collected and treated with colcemid to arrest the mitosis process. After to expose the cells to hypotonic solution, to separate and fix the chromosomes on slides using methanol and acetic acid, stained chromosomes staining were visualized under the microscope. The mitotic images were captured with a camera, and a software allowed us to analyze the karyotype to identify chromosomal abnormalities.
- Traceability control: Short Tamdem Repeats (STRs) analysis was performed following the ASN-0002-2022 standard by the ATCC Standards Development Organization recommendation. This document advises for authentication of human cell lines and organoids, by analysis of at least 13 STRs loci in addition to amelogenin. The required 13 STRs loci are included in the 16 STRs loci analyzed by CLA, AmpFISTR Identifiler Plus kit and fragment analysis procedures used by the BBSSPA.
- Morphological characterization is a crucial step in the investigation of organoids. Organoids were characterized through haematoxylin and eosin-stained slides. Organoids were fixed, cryoprotected and embedded in OCT. Finally, 20 mm sections were stained with haematoxylin and eosin to assess organoid morphology. **Conclusion:** The validation of organoid characterization methodologies allows to the BBSSPA to carry out exhaustive quality control of the organoids transferred to different research projects. These characterization processes are mandatory assays for the deposit of organoids in banks and the publication of results in scientific journals.

P29: Novel Dry Technology for Stabilization and Room Temperature Storage of Whole PB Samples

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Peripheral Blood (PB) is a widely used biospecimen in the field of biobanking since it plays a key role in clinical research. Its various components provide a multitude of possible applications such as immune profiling, proteomics, genomic studies, among others. With such versatility in its uses, it is desirable that blood be optimally collected and stored since applications such as Immune profiling by flow cytometry, which requires fresh blood samples for accurate results, is not always possible due to time or transport constraints. Although there are several commercially available solutions to preserve cells fixed for some days the most common choice is the cryopreservation of PBMC, where samples can be collected during the recruitment and be further analyzed. This requires specialized ultra-low freezer facilities, complex

shipment procedures, and no exempt from the possibility of losing the samples. Moreover, there are studies describing the selective cell loss during PBMNCs isolation together with the variability in the recovery after thawing the samples that may induce a bias in subpopulation distribution.These limitations can be addressed with optimal storage conditions of whole PB in a standard process that minimizes the pre-analytical variation. The technique here proposed includes an innovative approach consisting of stabilizing the sample with a precision drying technique. We evaluated the suitability and applicability of this stabilization system with a proof of concept where PB samples were processed in fresh, part was stored at -80ºC and part of the sample was dried and stored at room temperature. When compared in the same samples (fresh, frozen, and dried) the frequency of the different subsets by Flow cytometry showed a similar recovery that frozen and thawed samples and the frequency of the populations remained stable for the main subsets which were B, T NK, monocytes, and neutrophils with an r2>0.9. In terms of nucleic acids, DNA extraction was performed both in fresh, frozen, and dried aliquots, showing a similar quality and functional profile following the ISBER standards for quality control assurance.The alternative here evaluated offers the possibility of stabilizing and storing whole PB at room temperature to be used for a wide range of downstream applications, including Flow cytometry, protein analysis or genomic techniques such as NGS. This implies that precision drying is an innovative, sustainable, and accurate choice for the room temperature PB storage in biobanks.

P30: Use of Freeze-Dried Cell Lines as Controls for Next-Generation Sequencing Studies

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The rise of Next-Generation Sequencing (NGS) technologies has had a profound impact in the study of hematological neoplasias, leading to a better understanding of these malignancies. However, there is a lack of standardization in terms of quality control to ensure the use of these techniques in the clinical field. In this context, is extremely important the availability of samples with known biomarkers and alterations to be used as controls in these genomic studies. Moreover, these samples should have long-term stability and its analysis must be replicable, both through time and in different laboratories.

To face this challenge, 300K Solutions is developing a disruptive and innovative technology to allow room temperature (RT) storage of cell lines currently used as controls in NGS studies. Thus, this type of storage could potentially guarantee the standardization needed to implement these cutting-edge techniques in clinical diagnostics. Here, we show that our stabilization solution offers protection during the freeze-drying process resulting in long-term stability at RT. Moreover, it enables the extraction of DNA with optimal quality from 4 different lymphoblastic cell lines (H929, CA46, RS4;11 and REH) used as controls in the EuroClonality-NGS DNA capture (EuroClonality-NDC) assay for the study of lymphoproliferative disorders. This quality control assessment followed the Proficiency Standards stablished by the International Society for Biological and Environmental Repositories (ISBER) and includes a variety of molecular biology techniques to address DNA purity, integrity, and functionality. Importantly, using the genetic material obtained from the H929 cell line we have demonstrated its adequacy for this specific NGS assay. Finally, preliminary results show that our stabilization technology could allow the extraction of high-quality RNA.

All together, these results strongly suggest that the use of freeze-dried samples as controls for genomic studies could provide the standardization required to ensure its clinical application.

P31: IVO Biobank experience in Biospecimens and External Quality Assurance (EQA) Programs

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Background: The EQA programs are considered a valuable tool that provides information of the effectiveness of the laboratory standard operating protocols (SOP).

Participating in these programs allows to determine the capacitation, being objectively evaluated by a third party. The participation in EQA programs is a widespread practice in diagnostics laboratories. However, it was only after the publication the ISO 20387 standard that it began to have relevance in biobanks setting. Moreover, the EQA program offer have been developed and increased recently

The IVO biobank has been pioneering in being accredited with the ISO20387, its participation in EQA programs since 2020 being one of the milestones to comply with the standard. IVO Biobank staff has a wide experience in the participation in this type of assessments, since the Laboratory of Molecular Biology and the Department of Pathology, services on which the biobank operation depends, have been participating in different EQA programs since 2009.

Methods: IVO biobank has participated in seven programs through different entities (IBBL, National DNA Bank-ISCIII and EMQN). The selection of the program is made defining a strategic plan according to the scope of accreditation. According to this we have participated in the following programs: RNA y DNA Integrity; DNA and RNA extraction from whole blood; DNA extraction from FFPE; cfDNA extraction from plasma; RNA purity by spectrophotometry. For 2023 IVO biobank is enrolled in the following programs: DNA and RNA extraction from frozen tissue; and isolation and aliquoting plasma.

Results: A command matrix was set up to organize and schedule the participation of the IVO Biobank in the different EQA programs, which has been defined according to the strategic incorporation of new SOPs as well as the availability of resources to cover the costs of this participation. The results obtained during these years were satisfactory, indicating the effectiveness of the different SOP workflows.

Conclusión: The SOPs can be considered effective, robust and provide a high level of confidence in the results obtained. EQA programs provides a technical improvement and demonstrate the ability to detect possible errors, such as inadequate qualification of personnel, incomplete validation of the test procedure or a punctual error in the operation of the equipment, etc. All this information supports the daily management of the biobank as well as its strategic planification.

P32: Quality Assessment of Blood Samples with Raman Spectroscopy

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Background: The development of quality control processes must be thoroughly realized with scientific rigor and be easily implemented in the pipeline of a biobank. Given its high speed and specificity, this work proposes the usage of Raman spectroscopy, combined with dimensionality reduction and machine learning classification techniques to detect the deterioration of blood serum and plasma left at ambient temperature.

Methods: We took pooled samples of serum and plasma that were kept at ambient temperature until their spectra were measured at different points in time after extraction. Raman spectroscopy usually requires a pre-processing pipeline to be applied to the spectra before obtaining any result. Therefore, we performed intensity normalization and outlier detection before the analysis.

PCA is then applied to reduce the dimensionality of the data and extract the most relevant information in it. It selects those linear combinations of wavenumbers that keep as much variance from the original dataset as possible, and then uses them as eigenvectors that define a new latent space. Linear Support Vector Machine (LinSVM) and a Multi-Layer Perceptron (MLP) were the used classifiers to detect the deterioration on the latent space.

Results: Using two principal components was enough to keep more than 99% of the original variance, both for serum and plasma. We trained the LinSVM and MLP models on the training dataset for each type of sample and evaluated their performance based on the accuracy of the predictions for the test dataset. LinSVM and MLP yielded similar results, with an accuracy of ~79% for the serum and ~90% for the plasma.

Conclusion: The suggested pipeline was able to correctly predict how much time the samples spent in unsuitable conditions.

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P33: Feasibility of DNA Extraction Directly from Freeze-dried and Frozen Bacterial Strains for Whole Genome Sequencing

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Background: With the aim of carrying out high-throughput genomic sequencing, the purpose of this study was to show the feasibility of DNA extraction from freeze-dried and cryopreserved bacterial strains without going through a prior culture step, by comparing three extraction methods.

Methods: Eleven freeze-dried or cryopreserved Gram-positive or Gram-negative bacteria belonging to different species and cultivated on different media with different culture times were used. DNA extraction was performed using 2 Qiagen extraction kits, the DNeasy® Blood and Tissue Kit (BT) and the DNeasy® PowerSoil® Kit (PS) used with the Qiacube instrument and the NucleoMag DNA Bacteria Kit (Macherey-Nagel) (KF) used with a King Fisher Flex extraction equipment. Moreover, DNA extraction from 12 Escherichia coli strains was done with both the NucleoMag DNA Bacteria Kit (Macherey-Nagel) (KF) used with the King Fisher Flex extractor, and the PDQeX nucleic acid extractor (MicroGEM).

The criteria used to compare the different kits were the total

and double stranded DNA concentration and DNA purity, the success of whole genomic sequencing and the detection of the plasmid harbored by the strain CIP 65.8.

Results:

- DNA extraction directly from freeze-dried and cryopreserved bacteria was efficient regardless of the kit and the extraction equipment used.
- Genomic sequences were successfully obtained, and genomic identification of the strains was accurate.
- The plasmid DNA was detected in the strain concerned regardless of the kit and the extraction equipment used.
- Yield of double stranded DNA may be different with different extraction methods for freeze dried and cryopreserved specimens.

Conclusion: DNA extracted directly from freeze-dried and cryopreserved bacterial strains, without prior reculturing, is fit for purpose for whole genome sequencing.

P34: Expand the Horizon, Sharpen the Vision: A Comprehensive Approach to Develop ISBER Best Practices Fifth Edition

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Statement of the problem: Repository management operates within a constantly evolving landscape influenced by the changing fields of biospecimen science, technology, legal requirements, and ethical considerations — a dynamic further amplified by unprecedented challenges, both local and global in nature. The recently published Fifth Edition of the International Society for Biological and Environmental Repositories (ISBER) Best Practices signifies a pivotal milestone in navigating these complexities. Creating this new edition required a comprehensive approach capable of delivering a focused resource reflecting the expanding horizon of its diverse users. The document is testament to the collective efforts of many dedicated individuals who have built upon the foundations of prior editions.

Proposed solution: Our presentation introduces the process taken to shape this Fifth Edition, inspired by the need to broaden perspectives while maintaining precision and focus. Extensive user feedback on the prior edition was elicited and systematically analyzed by a Gap Analysis Task Force to identify areas for improvement. This facilitated the gathering of multifaceted perspectives to formulate key elements of the revision scope. The Editorial Board guided a diverse group of contributors with expertise across various relevant specialties in updating the document structure and content. The writing team integrated new material with existing content upholding the tradition of providing recommendations and best practices across all major aspects of repository operations. Reviewers played a critical role, objectively assessing the document's merit and providing suggested revisions to align it with the quality of prior editions. This collaborative effort ensured the gradual emergence of a strong and robust resource over iterative write/review phases. The use of a formal evaluation tool with well-defined criteria enabled further refining of the best practices.

Conclusion: The outlined approach ensures that the new ISBER Best Practices remains relevant and credible by following a transparent and inclusive process. Our presentation not only shares the process but also highlights the outcomes of this collective endeavor, along with scenarios for effectively translating content into practice. We invite you to delve into our experiences and insights in shaping the future of repository management to meet the evolving demands in the biospecimen scientific landscape.