Oral Abstract

O1 An AI Assessment Model for Cancer Tissues Frozen H&E Sections before Distribution in Biobanks

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Background: High-quality tumor biospecimens are the cornerstone of precision medicine and cancer research. Morphological quality control of preserved tumor samples before distribution is essential to ensure the downstream studies. However, the current reliance on manual pathological assessment in biobanks might give rise to subjectivity, low efficiency, and a shortage of pathological expertise, which significantly hinders this important process. To address these challenges, we integrated artificial intelligence (AI) into the morphological assessment of frozen H&E sections.

Methods: Frozen H&E sections were prepared from the same tissue selected for distribution. Utilizing whole slide imaging (WSI) technology and AI tools, we annotated, trained, and validated an AI-based morphological assessment model using over 400 scanned images of frozen breast cancer H&E sections. The model automatically quantifies tumor cells, immune cells, tumor area percentage, and necrotic area percentage in H&E sections. These results were compared with assessments by pathologists to proof the reliability of the AI assessment. A final morphological assessment report form will be generated for the downstream study group.

Results: 1. The AI model objectively identified parenchyma, stroma, and cellular subpopulations in frozen H&E sections, providing quantitative data on tumor area percentage, necrotic area percentage, tumor cell percentage, and immune cell percentage. 2. Based on the analytical data, quality control results were categorized as "Excellent", "Qualified", or "Candidate". 3. Comparisons between AI and pathologist assessments showed a correlation of 90% to 97%. 4. The morphological assessment reports automatically generated by AI system will be available.

Conclusions: This study demonstrates that the application of AI models for morphological assessment of frozen tumor sections has showed its power. It provides a solution for morphological assessment without requiring the direct involvement of pathologists, addressing the critical shortage of pathologists in biobanks. This approach enhances efficiency and accuracy, offering objective and precise morphological data for breast cancer samples prior distribution to the study. This ensures downstream research with reliable and reproducible results, serves as virtual pathological images for reference in downstream research. Ultimately, this approach upgrades tumor samples from being merely "usable" to being "precisely applicable".

O2 A MBirSA Statement on Benefit Sharing in Biobanking in South Africa

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Background: Benefit sharing has become a key principle in research and biobanking, particularly in low- and middle-income countries where concerns about equity, exploitation, and historical injustice persist. In South Africa, these issues are amplified by its role in generating globally significant biological and genomic data from underrepresented communities. Yet ambiguity remains about what constitutes a "benefit," how benefits should be shared, and whether such practices are permissible under South African law.

Objective: This paper discusses the principles and legality of benefit sharing in South Africa and outlines the development of a national consensus statement by the Medical Biorepositories of South Africa (MBiRSA). The aim is to clarify the legal position, identify gaps, and propose a principled, practical framework for benefit sharing in biobanking.

Methods: MBiRSA is convening an interdisciplinary group of legal scholars, ethicists, researchers, policymakers, regulators, and community representatives to deliberate on the legal and ethical dimensions of benefit sharing. Through workshops and consultations, participants are mapping relevant laws, analysing interpretive ambiguities, and exploring feasible benefit-sharing models that align with ethical and legal principles.

Results: The consensus statement concludes that benefit sharing is not prohibited under South African law, provided it aligns with regulatory and ethical requirements. It identifies beneficence, equity, transparency, solidarity, distributive justice, and reciprocity as core guiding principles. Benefits may include capacity strengthening, infrastructure development, access to data and results, and community engagement, rather than direct financial returns. The statement recommends incorporating benefit-sharing arrangements into governance frameworks, material transfer agreements, and community engagement plans, with ethics committees actively reviewing such provisions.

Conclusion: The MBiRSA consensus statement provides nationally grounded clarity on the legality and principles of benefit sharing in genomics and biobanking. It clarifies ethical obligations for researchers, institutions, and ethics committees. Embedding benefit sharing within governance processes promotes fairness, accountability, and trust, positioning South Africa as a regional leader in responsible and sustainable biobanking governance.

O3 A Study on the Sharing Mechanism under the General Hospital Biobanks from the Perspective of the Principle of Solidarity

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Currently, there are many challenges such as inefficiency and ethical dilemmas when the people are trying to practice data and sample sharing in the general hospitals, so that people needs a fair and reasonable sharing mechanism to avoid on individual-centered consent and governance models that limit trust, reciprocity, to achieve the maximum capacity on sustained, equitable resource sharing. Therefore, constructing an ethical framework based on the principle of solidarity becomes necessary to promote responsible, sustainable sharing practices in general hospital biobanks.

This study proposes a governance framework guided by the principle of solidarity. It advocates for a shift from a transactional logic toward a model of shared responsibility and mutual benefit. Drawing on Durkheim's social solidarity concept and Prainsack & Buyx's tripartite model, the study further constructs a solidarity-based ethical framework for biobank sharing:

(1) Interpersonal solidarity—based on ethical reciprocity: participants voluntarily contribute samples for collective benefit, with biobanks ensuring transparency and benefit feedback.
(2) Group solidarity—functions through participatory co-governance. Ethics committees comprising patients, researchers, and regulators jointly deliberate on consent models, data reuse, and risk management.
(3) Institutional solidarity—manifests in shared accountability. Biobanks implement layered consent, data traceability, and transparent risk-sharing to protect all contributors.

This framework translates solidarity from a moral ideal into actionable governance. It redefines the biobank's role as ethical "bridges" and "guarantors" that link individual contributions to public-health goals through clear policies, feedback, and risk-mitigation measures.

Integrating the principle of solidarity into biobank governance provides a feasible pathway to enhance transparency, strengthen public trust, and unlock greater collaborative value in biomedical research. By operationalizing solidarity through multi-level mechanisms of reciprocity, co-governance, and institutional accountability, the biobank evolves from a passive repository into a dynamic ethical infrastructure—bridging individuals and communities, transforming voluntary contribution into shared social value. In doing so, it builds a sustainable, participatory, and ethically coherent sharing ecosystem that safeguards contributors while advancing collective health goals.

O4 AI-Driven Framework for Full-Lifecycle Management of Biobank Dry Repositories

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Problem: The biobank dry repository (i.e., a multimodal, sample-centered biomedical data repository) serves as a core infrastructure for precision medicine and translational research. Unlike general medical multimodal datasets, it emphasizes sample-centric integration, where all data layers—ranging from clinical, omics, and imaging to textual annotations—are directly linked to specific biological samples. Such repositories must ensure long-term preservation, traceability, standardization, and reusability across research contexts. However, current dry repositories face major challenges including fragmented management, weak data linkage, inconsistent quality control, and inadequate support for knowledge-driven research, resulting in low utilization efficiency and limited innovation capacity.

Proposed Solution: To address these challenges, we propose an integrated five-dimensional framework incorporating full-process management, knowledge integration, data governance, AI-driven intelligence, and model-based applications. A Sample Lifecycle Management System achieves traceable, standardized, and transparent operations. A disease-centered knowledge graph links samples with clinical and omics data, enabling semantic integration and knowledge discovery. A secure data governance system ensures compliance through classification, desensitization, and controlled access. AI agents using NLP and multimodal analytics automate metadata extraction, quality assessment, and relationship reasoning. A domain-specific large model built on Retrieval-Augmented Generation (RAG) mechanisms provides intelligent research assistance and decision support.

Conclusions: This framework enhances the management, interoperability, and research value of biobank dry repositories, transforming them from passive data stores into intelligent infrastructures that drive biomedical discovery and precision healthcare.

O5 Morphology-Guided Zonal Sampling Protocol for Colorectal Cancer: A Histology-Based Strategy to Enhance Biobank Specimen Quality

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Objective: The quality of colorectal cancer specimens in biobanks directly impacts molecular testing and translational research. Uneven tumor cell distribution across anatomical regions often causes sampling bias. This study aimed to characterize tumor cell distribution within distinct histological zones and develop a morphology-guided sampling protocol integrating macroscopic observation with microscopic validation to optimize tissue selection.

Methods: Seven surgically resected colorectal cancer specimens, including tumor and adjacent tissue, were analyzed. Based on gross morphology, tumors were classified as elevated ($n = 4$) or ulcerative ($n = 3$). A three-zone model was applied: Zone A (central necrosis, excluded), Zone B (intermediate transition from core to margin), and Zone C (tumor–normal interface). Formalin-fixed, paraffin-embedded sections were stained with HE and independently evaluated by two pathologists. Tumor cell percentages were compared using two-way ANOVA.

Results: Marked anatomical heterogeneity was observed. In ulcerative-type tumors, Zone B contained significantly higher tumor cell percentages than Zone C ($70.3 \pm 6.5\%$ vs. $40.7 \pm 7.2\%$, $p = 0.008$). Grossly, Zone B appeared gray-white to gray-red with moderate firmness, representing the optimal sampling

area. In elevated-type tumors, no significant difference was found between Zones B and C (78.1 ± 5.6% vs. 73.4 ± 7.3%, p = 0.12). These tumors appeared dark-red, moist, and soft; deeper red, softer areas (typically in Zone B) yielded higher tumor representation, whereas mucinous or degenerative regions showed reduced density.

Conclusion: This study proposes a morphology-based, subtype-specific sampling strategy for colorectal cancer biobanking. For ulcerative-type tumors, sampling the intermediate Zone B ensures higher tumor enrichment; for elevated-type, selecting deep-red, soft regions provides optimal yield. This morphology-guided protocol links gross features with histopathology, offering a reproducible framework to standardize tissue collection and improve biobank sample quality for molecular and biomarker studies.

O7 A Comparative Evaluation of Different Cooling Strategies for Cryopreserving Mouse Liver Tissue: Assessing Viability, Structure, Metabolism, and Regenerative Potential

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Objective: Conventional cryopreservation often induces cellular damage. To explore a superior long-term preservation method that mimics fresh tissue physiology, this study systematically evaluated vitrification against programmed freezing, direct liquid nitrogen plunging, and fresh tissues across multiple key parameters, aiming to assess its superiority in maintaining tissue biological integrity.

Methods: Mouse liver tissues were subjected to vitrification, programmed freezing, or direct liquid nitrogen plunging, with fresh tissues as control. Assessments included: cell viability (flow cytometry and AO-PI staining); morphology and ultrastructure (HE staining and scanning electron microscopy); nucleic acid integrity (UV spectrophotometry, microfluidic chip and agarose gel electrophoresis); ATP content (chemiluminescence assay); and long-term function (organoid culture).

Results: The post-thaw cell viability in the vitrification group (64.37%) was slightly lower than that of fresh tissues (72.4%) but significantly higher than both programmed freezing (12.1%) and direct plunging (9%) groups. Vitrified tissues showed minimal histological alterations and well-preserved nuclear/mitochondrial morphology, comparable to fresh controls. Programmed freezing reduced mitochondrial count, while direct plunging caused severe damage (nuclear rupture, mitochondrial swelling). DNA integrity was similar across all groups. RNA integrity in the vitrification group was comparable to fresh controls, but declined in the other cryopreserved groups. ATP content and organoid formation/proliferation efficiency in the vitrification group were not significantly different from fresh tissues.

Conclusion: Vitrification surpasses conventional methods by more effectively maintaining cell viability, structural integrity, and molecular and functional competence of liver tissues, establishing it as a highly effective and reliable strategy for long-term tissue preservation.

O8 A Serum Metabolomics Signature for Early Detection and Molecular Stratification in Head and Neck Squamous Cell Carcinoma

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Background: Head and neck squamous cell carcinoma (HNSCC) is the sixth most common malignancy worldwide, with nearly 60% of patients diagnosed at advanced stages. Current diagnostic approaches lack sufficient sensitivity for early detection, highlighting the urgent need for reliable and minimally invasive biomarkers to improve early diagnosis and patient stratification.

Materials and Methods: We performed comprehensive serum metabolomics profiling in 669 participants (338 HNSCC, 331 healthy controls) across discovery and external validation cohorts using liquid chromatography-tandem mass spectrometry (LC-MS/MS). Machine learning-based feature selection was applied to develop a diagnostic model. Multi-omics integration incorporating transcriptomics and spatial transcriptomics was conducted to explore mechanisms underlying metabolic alterations and clinical heterogeneity.

Results: Systematic profiling revealed coordinated reprogramming of arginine metabolism, characterized by arginine depletion and ornithine accumulation. An 8-metabolite diagnostic signature achieved high accuracy, with internal validation area under curve(AUC) of 0.990 (sensitivity 91.3%, specificity 97.1%) and multicenter external validation AUC of 0.986 (sensitivity 95.6%, specificity 93.8%). Diagnostic performance remained high for stage I disease. Integrative analyses identified two metabolically defined molecular subtypes: C1 (immune-active, favorable prognosis) and C2 (immunosuppressive, poor survival). C2 cancers exhibited reduced immune infiltration, enrichment of immunosuppressive macrophages, and enhanced sensitivity to targeted therapies. Spatial transcriptomics confirmed an inverse relationship between metabolic activity and immune infiltration.

Conclusion: This study establishes a clinically validated serum metabolomics signature with high accuracy for early detection of HNSCC through multicenter validation across independent populations. Metabolomics-anchored multi-omics analysis defined molecular subtypes with distinct prognoses and therapeutic sensitivities, demonstrating the dual clinical relevance of metabolomics in offering minimally invasive diagnostic tools and precision patient stratification frameworks.

O9 A Resource of Paired CSF and Serum in Neuroimmune Diseases: Strategies for Micro-Volume Biospecimen Management

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Background: Research in neuroimmunological diseases (such as autoimmune encephalitis (AE), multiple sclerosis (MS), and neuromyelitis optica spectrum disorder (NMOSD)) and peripheral neuropathies relies heavily on paired cerebrospinal fluid (CSF) and serum samples in order to understand the interaction between the systemic and central nervous system immune

responses. A significant practical constraint is that the volume of CSF obtainable through diagnostic lumbar puncture is often limited to around 1 mL. This pose a major challenge for biobanking and subsequent biomarker studies.

Objectives: The aim is to establish a rigorously quality-controlled biobank of paired CSF and serum samples tailored for neuroimmune diseases.

Methods: Paired CSF and serum samples were prospectively collected from patients diagnosed various neuroimmune and neurological conditions, including AE, MS, NMOSD, peripheral neuropathy, and motor neuron disease. All participants provided informed consent under an IRB-approved protocol. Our biobanking framework incorporates the following key strategies for micro-volume management: (1) Pre-analytical Standardization: A stringent protocol emphasizing minimal delay from collection to processing and final storage at −80°C. (2) Aliquoting: Immediate aliquoting into low-protein-binding micro-tubes for single-use applications, preventing freeze-thaw cycles and maximizing the number of potential assays from each sample. (3) Quality Control (QC): A subset of samples was validated for analytical performance using targeted assays (e.g., IgG index, oligoclonal bands).

Results:

(1) The biobank currently contains over 2,000 unique pairs of CSF and serum, including 1130 cases of AE, 465 cases of MS, 341 cases of NMOSD, 230 cases of peripheral neuropathy, and 282 cases of motor neuron disease.
(2) The median volume of CSF samples is 0.8 mL (IQR: 0.5 - 1.2 mL).
(3) The QC demonstrates high sample quality: pilot biomarker analyses in a subset of samples yielded robust and clinically congruent results, confirming the analytical suitability of the collection despite the low volume.

Conclusion: We have developed a biobank of paired CSF and serum samples, specifically designed for neuroimmune disease research. This resource serves as a reliable platform for future collaborative biomarker discovery and validation studies.

O10 Advancing Regional Biobanking and Biosafety Governance in ASEAN: From Feasibility to Policy and Global Alignment

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Statement of the Problem: Biobanking has become a cornerstone of biomedical, One Health, and Global Health research, supporting data driven discovery and pandemic preparedness. Yet, in low- and middle-income countries (LMICs), most biobanks have developed as project specific initiatives, leading to legacy infrastructures and protocols, and limited cross-project interoperability. Across ASEAN, these challenges could be amplified by diverse regulatory frameworks, biosafety capacities, workforce and digital systems. Moreover, integration of biobanks within broader research and policy infrastructures remains underutilized, hindering effective participation in global research efforts and the shared fruits of scientific benefits.

Proposed Solution: To address these gaps, the ASEAN Biobank Feasibility Study assessed regional infrastructure, governance, and harmonization readiness. The study revealed regulatory fragmentation and lack of biosafety and data sharing frameworks as barriers to collaboration. In response, the G20 policy during Indonesia's 2022 Presidency highlighted the biosafety and biosecurity needs in biobanking, followed by the 2024 ASEAN Declaration supports the demand for such framework. Capacity building continued through ASEAN+3 initiatives, including biosafety training with the China CDC to strengthen technical competencies and regional coordination. One such effort was the table-top exercise to simulate the regional collaboration in sample and data sharing under different scenarios with imaginary countries that showcase key attributes of regional stakeholders. Discussions revealed differing interpretations of biosafety responsibilities and uncertainties in defining cross-border practices. Participants highlighted the value of developing a formal ASEAN biosafety agreement to establish shared definitions, accountability mechanisms, and pathways for collaboration.

Conclusions: ASEAN's coordinated initiatives exhibit a growing commitment to building equitable and sustainable biobanking system, where key priorities include unified governance and biosafety frameworks, improved digital interoperability, and stronger cross-sectoral integration. In alignment with global dialogues such as the UN Science Summit, ASEAN's emerging biobank network offers a tangible model for regional collaboration, laying the foundation for a secure, interoperable, and inclusive biobank ecosystem that strengthens both regional research capacity and global health resilience.

O11 Development of The First National Human Biospecimen Proficiency Testing Program by The Thailand Biobank Consortium

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Biobanks are essential infrastructures for storing biological specimens that support biomedical research, where specimen

quality determines research reliability. Participation in Proficiency Testing (PT) programs is a key approach to verify biospecimen quality according to international standards. In the past, medical institute–based biobanks in Thailand relied on purchasing PT samples from overseas, resulting in high upfront expenses and growing long-term costs, as well as delays caused by transportation and customs clearance, all of which disrupted continuity in quality assurance. To address these challenges, the Thailand Biobank Consortium (TBC), together with the Proficiency Testing Division of the Department of Medical Sciences, Ministry of Public Health, initiated Thailand's first national PT program for human biospecimens (Thai HBPT program). The program covers both Processing schemes (DNA extraction from frozen tissue and whole blood) and Testing schemes (DNA integrity, quantification, and purity). Prepared samples were evaluated for homogeneity and stability in compliance with ISO 17043, and participants' performance was analyzed according to ISO 13528.

In the first year, a pilot study involving biobanks from the four main institutions of TBC (four participants each, total N=16) revealed limitations, including low standard deviation, limited participant diversity, and clustering effects. In the second year, the program expanded nationwide to include other biobanks and medical laboratories, increasing participation to 30 institutions. This expansion improved the statistical strength and reliability of the program, as well as the diversity of methods and instruments, thereby enhancing the robustness of the PT program and demonstrating the feasibility of a sustainable, high-quality national PT scheme. In 2027, the Thai Human Biospecimen Proficiency Testing (HBPT) program will officially open for registration and operation under the Proficiency Testing Division, which will undergo ISO 17043 accreditation. This initiative will establish Thailand's first certified national PT program for human biospecimens, strengthening quality assurance and advancing the country's biomedical research infrastructure.

O12 Consent in Biobanks in Europe and Worldwide: Models, Challenges, and Future Directions

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Background: Informed consent is a cornerstone of ethical biobanking, ensuring that participants understand and agree to the use of their biological materials and data. As biobanks increasingly operate within global research networks, harmonizing consent procedures has become a critical challenge. The European GDPR framework provides a robust foundation, yet international variation in legal and ethical requirements continues to create complexity for cross-border collaboration.

Methods: This presentation analyzes international consent models based on literature review, policy analysis, and case studies from major infrastructures such as BBMRI-ERIC, UK Biobank, and the U.S. All of Us Research Program. The study compares implementation strategies for specific, broad, and dynamic consent, focusing on their alignment with GDPR principles and adaptability to non-European contexts.

Results: Specific consent provides clear boundaries but restricts data reuse; broad consent promotes research flexibility but raises ethical concerns regarding autonomy; dynamic consent introduces interactive digital tools enabling ongoing participant engagement but increases operational demands. European initiatives increasingly integrate hybrid models, yet global interoperability and consent portability remain limited. Technical and legal inconsistencies hinder efficient data exchange and participant empowerment across jurisdictions.

Conclusion: To advance responsible global biobanking, consent mechanisms must evolve toward harmonized, participant-centered, and technologically supported systems. Developing interoperable digital consent platforms and shared governance standards can strengthen trust, transparency, and sustainability in international sample and data sharing. These strategies align with ISBER's mission to promote best practices and global collaboration in biobanking.

O13 Construction of Patient-Derived Organoid-based Living Biobank in a Gerenal Public Hospital: Key Strategies and Early–Stage Experiences

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Background: Standardized biobanks play a pivotal role in basic research and clinical translational studies. Construction of a living biobank based on patient-derived organoids (PDOs) will provide valuable model resources for precision medicine and further extend the utility of traditional biobanks. This article discusses the key factors for initiating and efficiently constructing living biobanks in general public hospitals during the early development stage.

Methods: The newly established traditional biobank of our hospital has operated stably for about six months, and we have already begun construction of a PDO–based living biobank. Here we share our experiences, along with the problems and challenges encountered during this process.

Results: We demonstrate that (1) The purpose and scope of biospecimen preservation in large-scale public hospital biobanks must be clearly defined. It is recommended that such hospitals focus on disease–specific, cohort–based specialized biobanks rather than attempting to build all–inclusive strategic biobanks. (2) Constructing on the standardized collection of traditional biospecimens, priority should be given to selecting PDOs from the hospital's dominant disease areas, while establishing management uniform, standardized protocols for collection, culture, and preservation. (3) Beyond increasing hardware investment, hospital leadership should elevate the biobank's status within the institution, strengthen inter–departmental collaboration—especially to ensure a stable supply of PDO sources—and promote organizational coordination. (4) Exploring hospital–enterprise collaboration models and formulating reasonable sharing agreements can secure corporate sponsorship and technical support for automated equipment, replace manual culture with high–efficiency automation, and gradually expand the range of PDOs.

Conclusions: In the initial phase of operating a biobank in general public hospitals, close integration of four aspects—institutional support, selection and standardized preservation of PDOs, departmental cooperation, and hospital–enterprise collaboration—is essential for efficiently advancing the construction of a PDO–based living biobank.

O14 Construction and Operation of the Biobank at Peking University People's Hospital: A Comprehensive Practice for Standardized Biomedical Resource Preservation

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Background: Peking University People's Hospital has evolved into a modern tertiary Class A comprehensive medical institution integrating healthcare, education, research, and public health services. To address the growing need for high-quality biological specimens in clinical and translational research, the hospital established its Biobank in 2012. In July 2021, the Biobank obtained the administrative license for the preservation of human genetic resources in China.

Methods: The Biobank covers a total area of over 500 square meters, equipped with a dual power supply system to ensure uninterrupted operation. Its functional zones are clearly divided, including an ultra-low temperature freezer area, liquid nitrogen zone, sample processing area, information processing area, and quality control area—each designed to meet specific needs of specimen handling and preservation. Key equipment includes 70 ultra-low temperature freezers, supporting the preservation of various specimen types and quality control testing. To ensure specimen safety, the Biobank is installed with anti-theft, fire prevention, and waterproof devices. Refrigerators are managed by dedicated personnel, and an electronic monitoring system with alarm functions enables continuous temperature monitoring and automatic recording; refrigerators also feature remote alarm systems to promptly address temperature anomalies. The Biobank construction and operation are supervised and guided by the Academic Committee and Ethics Management Committee ensuring compliance with academic standards and ethical principles.

Results: As of the latest statistics, the Biobank has accumulated over one million sample tubes, with 850,000 currently in storage and approximately 180,000 retrieved for research use. The specimens cover diverse medical conditions, providing a rich resource for multi-disciplinary research. The Biobank has supported numerous clinical and translational research projects of the hospital. By providing high-quality specimens and associated data, it has facilitated studies on disease biomarkers, treatment response prediction, and personalized medicine. The efficient specimen retrieval system (with 180,000 specimens retrieved to date) ensures timely support for research needs, improving research efficiency.

Conclusions: The Biobank has established a standardized, compliant, and efficient operational system through rational infrastructure layout, strict quality management, and comprehensive information supervision.

O15 Development of a Community-Based Natural Population Cohort Biobank of Mental Disorders

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Statement of the Problem: Mental disorders represent a significant global health burden, yet research is often constrained by limited access to diverse, longitudinal biospecimens and associated clinical data. Existing biobanks frequently focus on clinical populations or lack comprehensive community representation, hindering the study of disease etiology, biomarkers, and personalized interventions. The absence of standardized, ethically governed resources for mental health research further exacerbates disparities in understanding neuropsychiatric conditions across different demographics and environments. Critically, community-based natural population cohorts are essential for identifying high-risk factors and enabling early prevention strategies. They also provide a unique platform to observe bidirectional outcomes—where high-risk individuals may transition to either full-blown disorders or recovery—thereby uncovering precise therapeutic targets and mechanisms of resilience.

Proposed Solution: We established a community-based natural population cohort biobank to address these gaps. This initiative integrates biospecimen collection (e.g., blood, DNA, hair, fecal, urea, et al.) with detailed phenotypic data—including psychiatric assessments, lifestyle factors, and social determinants—from a diverse, population-level cohort. Leveraging harmonized protocols aligned with ISBER Best Practices, the biobank emphasizes ethical frameworks, participant engagement, and data interoperability to support translational research. Advanced informatics infrastructure enables secure data management and sharing while preserving participant privacy.

Conclusions: This biobank provides a critical resource for advancing mental disorder research by enabling high-quality, reproducible studies on risk factors, biomarkers, and therapeutic targets. Its community-based design ensures inclusivity and enhances the generalizability of findings. By fostering collaboration through accessible data and samples, the platform accelerates progress toward precision psychiatry and global mental health equity. Future work will expand longitudinal follow-up and integrate multi-omics data to further unravel the complexity of mental disorders.

O16 Distinctive Features on Building the Huashan Hospital Fudan University BioBank

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Introduction: Huashan Hospital, Fudan University, having a medical institution with numerous national key laboratories and national-level research projects, has established a biobank that transcends the traditional "collection and storage" paradigm. Centered on serving cutting-edge research, it focuses on standardized, full-process specimen management to form a distinct, research-oriented operational model. Leveraging the hospital's extensive resources in national key laboratories and research projects, the biobank's core mission is to function as a "research support hub," providing a standardized service platform for the critical links in research activities from collection and transport to storage and access, thereby accelerating medical research breakthroughs.

Methods: The biobank's construction involved a multifaceted approach. A project-oriented management system was developed featuring hierarchical permissions for autonomous team operation with central oversight, and dual-track compatibility for seamless integration of legacy and new specimens. A dedicated 7535-square-foot facility was built to high standards,

the space strictly divided into functional areas flowing ISO20387 standard. To overcome site constraints, we adopted internationally first-in-class zero-evaporation automated liquid nitrogen equipment, breaking the limits of traditional liquid nitrogen towers and achieving a storage capacity of nearly 9 million samples. Informed consent is managed via a classified electronic system (Broad and Project-Specific), and full-process workflows are standardized and segmented for both outpatient and inpatient scenarios, supported by AI and automation for efficient sample handling.

Conclusion: In summary, the Huashan Hospital Biobank is characterized by "serving research, standardizing full processes, and technological innovation." It has successfully built a refined life-cycle management system for samples. This model provides a practical and referential paradigm for the high-quality development of hospital-level biobanks, demonstrating a successful transition from a passive repository to an active research enabler. The ultimate goal is to advance the concept that "use is value" for samples, we will try to break fresh ground on non-commercial sharing mechanisms to maximize the value of sample resources in collaboration with pharmaceutical and research institutions.

O17 Development of Advanced Vitrification Solutions through the Application of Macromolecules: A Case Study Using PVP

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Freezing approaches are commonly used to preserve biological specimens for both clinical and research. However, the biospecimens can be damaged by the deadly intracellular ice formation and severe cell dehydration (due to extracellular ice formation) during the cooling process, as well as the lethal ice-recrystallization during the rewarming process. In contrast, ice-free cryopreservation, i.e., vitrification, offers an alternative and promising solution to prevent both intra- and extracellular ice formation, reducing cell/tissue cryoinjury. However, commonly used vitrification media/solutions, such as VS55 and M22, contain high concentrations of permeating cryoprotectant agents, such as DMSO, generating high risks of potential toxicity and/or osmotic injury to cells and tissues. Therefore, reducing the use or the concentration of these permeating CPAs while maintaining vitrification efficiency is desirable. In this study, we studied and evaluated the effect of different molecular weight ranges and concentration of a macromolecule, Polyvinylpyrrolidone (PVP), on the vitrification phenomena. Experimental results from this study demonstrated that the concentration of PVP significantly influenced the vitrification temperature, as shown by differential scanning calorimetry and the Fox predictive model. In addition, the influence of PVP on the solution's viscosity, toxicity, dielectric property, and osmolarity were investigated to optimize the concentration and molecular weight cutoff range of PVPs for making the optimal vitrification solutions. Finally, 25 mL newly-developed vitrification solutions with/without living Jurkat cells were tested in the cooling and rewarming processes. The Jurkat cell cryo-survival rates were evaluated by their viability and proliferation ability in experiments. In conclusion, by introducing the PVP, the DMSO concentration is greatly reduced from over 50% to 10% to ensure vitrification of the cell suspension and cell survival after rewarming.

O18 Audit Update on Breast Tissue Biobank Set-up from a Single Institutional Cohort in an LMIC

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Background: Biobanks are indispensable to cancer research, enabling investigation into disease mechanisms, progression, and personalized therapeutic strategies. In LMICs like India, the scarcity of such structured biobanking limits translational research. To address this gap, we established a comprehensive breast tissue biobank in 2018. This is the first biobank in the state established by a single clinician. Following the first audit published in 2021, this updated report highlights the expanded scope, multimodal data integration, and novel biobanking modules that have been developed since.

Methods: A clinician-led model was adopted to seamlessly integrate biobanking into clinical workflows. The repository has housed diagnostic and post-treatment FFPE since 2018, as well as fresh-frozen tissues, blood, saliva, and stool samples since 2022. Collections include both malignant and benign tumors, as well as contralateral normal breast tissue. The associated database digitally curates 1300 data points per patient, organized into 14 modules encompassing clinical and family history, diagnostics, treatment, germline status, and follow-up information. All activities are conducted in accordance with approved ethical protocols and with the informed consent of patients.

Results: Since inception, the biobank has accumulated over 2,000 unique patient entries, comprising 70% malignant and 30% benign cases. Approximately 15% of patients also have recurrent disease samples deposited. Germline mutation profiling has been completed for over 500 patients to date. Under an unbiased project launched in 2023, comprehensive germline and microbiome profiling have been incorporated to enhance molecular and host–microbiota correlation studies. The inclusion of elastography-based tissue stiffness data samples provides additional context for molecular and imaging correlation studies.

Conclusions: The PCCM Breast Biobank represents integration of a clinical practice with robust translational research. It has supported numerous clinical and translational publications, as well as multiple clinical and follow-up audits, including the first study on immune infiltrates in breast tumors among Indian women and their multiplex profiling. The resource now serves as a scalable model for high-quality biobanking in resource-constrained settings, generating India-specific clinical and molecular evidence.

O19 Determination Of Biocontainment Levels for Biobanked Samples – A South African Case Study

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The correct level of biocontainment when storing pathogens (biobanking) is vital not only from a biosafety point of view, but also a biosecurity point of view. Determining the biocontainment level of these biobank samples can sometimes be challenging. In 2014 the Agricultural Research Council – Onderstepoort Veterinary Research embarked on a project to create a central biobank for field and laboratory isolates housed in various diagnostic and research laboratories. The Pathogen Asset Control System was used to compile the data from the laboratories, and determination of containment was based on parental pathogen characteristics. To ensure that the biocontainment level was accurately assigned various multiplex screening assays were done on the samples to be banked in the central biobank. Various molecular based multiplex screening assays were performed on the samples to be deposited into the biobank, the assays were designed to identify some of the common veterinary important pathogens in both ruminants (n=24) and poultry (n=9). Samples that were to be banked in the central biobank were tested for the presence of pathogens, other than the pathogen recorded on the Pathogen Asset Control System by the depositing laboratory. The preliminary results indicated that in 90% of the cases the correct biocontainment level was assigned to the samples to be deposited in the central biobank. However, in 10% of the cases higher biocontainment levels had to be assigned to the samples. The discrepancy was seen mostly in field samples that had been tested for a single pathogen, and upon the multiplex screening, other pathogens were detected in the sample that required more stringent biocontainment levels. In conclusion it has been found that the use of the molecular based multiplex screening assays has been a critical tool for the centralised biobanking of field and laboratory samples to ensure adequate containment of the pathogens in the sample.

O20 Biobanking for Booroolongs: Investigating the Effect of Bovine Serum Albumin (BSA) and Caffeine on Post-Thaw Sperm Motility in a Threatened Frog Species

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Background: The application of reproductive technologies, including sperm cryopreservation, has the potential to improve conservation breeding program outcomes. Biorepositories can aid in securing and maintaining the genetic diversity of captive populations and the wild populations they aim to recover. With amphibians facing global declines, the development of amphibian sperm cryopreservation protocols can have far-reaching benefits. Despite this potential, the post-thaw quality of amphibian sperm is highly variable following cryopreservation, and research focused on protocol refinement is needed.

Methods: The aim of this study was twofold: (1) to investigate the effect of the addition of bovine serum albumin (BSA) to the cryopreservation medium (pre-freeze), and (2) the effect of the addition of caffeine to the activation medium (post-thaw), on post-thaw sperm characteristics in the critically endangered Booroolong frog (Ranoidea booroolongensis). Spermic urine samples were collected from 14 male frogs following hormonal induction of spermiation, and each sample was split among three cryopreservation treatments, where the cryopreservation medium contained either 0 (control), 0.5, or 1% BSA (w/v). Samples were cryopreserved and thawed, and sperm motility was then activated in one of two activation treatments: Milli-Q water (control) or Milli-Q water plus 4.5 mM caffeine. Sperm viability (proportion live/dead) was assessed using fluorescent microscopy, and sperm motility metrics were evaluated using computer-assisted sperm analysis (CASA).

Results: This study showed that BSA concentration had no effect on post-thaw sperm viability. Additionally, neither BSA concentration nor activation in caffeine influenced post-thaw sperm motility characteristics (total motility, forward progressive motility, and velocity). Assessment time of sperm motility varied from 5 to 13 min post-activation and was significantly correlated with each motility measure, with motility and velocity metrics decreasing as time post-activation increased.

Conclusions: Whilst these results provide no evidence for an effect of BSA or caffeine at the concentrations tested on post-thaw sperm characteristics in the Booroolong frog, they highlight the time-sensitive nature of sperm assessment post-thaw and implications for the timing of sperm handling during assisted fertilisation efforts.

O22 From Data Fragmentation to Integration: Developing the Pathogenic Variant Database (CRDPVD) of the National Rare Disease Biobank of China

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Statement of the Problem: Although rare diseases affect millions worldwide, data resources remain fragmented and insufficient, particularly in variant interpretation. International efforts such as ClinVar and gnomAD provide valuable reference datasets, however, there is no unified pathogenic variant database tailored to rare diseases in China. Considering the diversity of rare diseases and the presence of unique variants in the Chinese population, it is crucial to establish a standardized resource that integrates genomic, phenotypic and clinical data to support diagnosis and foster global collaboration in rare disease research.

Proposed Solution: We have established the China Rare Disease Pathogenic Variants Database (CRDPVD) as the pilot project of the National Rare Disease Biobank. The primary data source is from the Peking Union Medical College Hospital Public Welfare Project for Rare Disease Service Improvement (UPWARDS) project, a nationwide initiative led by Peking Union Medical College Hospital (PUMCH), providing free genetic testing for Chinese rare disease patients and their

families, aiming to guide clinical diagnosis and treatment evaluation. UPWARDS has tested and analyzed the genetic data for 42,703 rare disease families (94,749 individuals) across 444 hospitals, of which 294 are from the National Rare Disease Diagnosis and Treatment Collaborative Network. CRDPVD design takes inspiration from multiple international standardized resources: population frequencies from gnomAD, clinical variants from ClinVar and OMIM, and phenotype terms from HPO and CHPO. It supports multi-level data visualization, such as functional categories, inheritance patterns and geographical distribution. Search and filter functions allow users to explore variants by type, zygosity, system distribution, and clinical phenotype.

Conclusions: By providing standardized data structures, interoperability frameworks, and clinically relevant annotations, CRDPVD supports variant interpretation, clinical diagnosis and large-scale research analyses. Moving forward, the database will be expanded into a comprehensive rare disease platform that integrates phenotype, clinical, and family history data with multi-level access control and a scalable architecture. This initiative not only accelerates knowledge discovery but also positions China as an active partner in global rare disease collaboration, underscoring the significance of building standardized, population-specific resources.

O23 Implementing a Research-Driven, Fully Digital Biobanking System: Experience from the Second Affiliated Hospital Biobank, Nanchang University

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Background: Biobanks are fundamental to translational and precision medicine, providing high-quality and well-annotated biospecimens for research. However, conventional biobanking practices often lack standardization, traceability, and integration with clinical data systems. To address these limitations, the Biobank Center at the Second Affiliated Hospital of Nanchang University developed a research-driven, fully digital biobanking system featuring end-to-end process control and seamless integration with clinical workflows.

Methods: Since 2016, the biobank has continuously collected biospecimens to meet both current and prospective research needs. All operations are managed within a centralized Biobank Information Management System (BIMS) interconnected with the hospital's electronic medical record (EMR). Physicians initiate collection orders via the EMR, which automatically synchronize with the BIMS. Each specimen, identified by a unique barcode, is tracked through reception, quality assessment, aliquoting, cryopreservation, and storage in real time. In 2025, a fully paperless informed consent module was implemented and integrated with both the BIMS and EMR systems to further streamline compliance and data linkage.

Results: The unified BIMS ensures complete traceability of more than 400,000 biospecimens, with a total storage capacity of 2.5 million. Authorized researchers can securely access digital consent forms and linked clinical data, enhancing data integrity, regulatory compliance, and operational efficiency. The biobank has achieved "Excellent" ratings in four consecutive third-party assessments and has supported publications in Circulation and Molecular Cancer.

Conclusions: This research-driven, fully digital biobanking model ensures standardized operations, robust traceability, and seamless data integration, providing a scalable framework for modern biobank management.

O24 Exploration and Reflection on the Construction of Unmanned Biobanks

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Background: The rapid advancement of precision medicine and biopharmaceutical research has highlighted the critical role of biobanks as core scientific infrastructure. The efficiency of biobank management and the quality of archived data are critical to the reliability of downstream research. However, conventional biobanks relying on manual operations face persistent challenges, including inefficiencies in sample retrieval and storage, susceptibility to information recording errors, heightened personnel exposure risks in low-temperature environments, and substantial labor costs.

Methods: To address these limitations, unmanned biobanks have been developed via the integration of automation, the Internet of Things (IoT), and artificial intelligence (AI). These next-generation biobanks utilize advanced automated hardware, including storage systems, sample processing devices (e.g., sorting systems, liquid handling stations, centrifuges, and nucleic acid extraction instruments), sample detection equipment (e.g., microplate readers, bioanalyzers), and transport devices (AGV robots, pneumatic conveyors, rail systems, and robotic arms). Sophisticated management and scheduling software coordinate these components, enabling seamless command execution and automated data collection, storage, transmission, and transport.

Results: Shanghai Clinical Research Center has pioneered the application of AI-driven management throughout the entire sample life cycle. In its initial phase, the center has achieved full automation of fluid biological sample processing, covering sample reception, sorting, preparation, transport, storage, retrieval, and quality control.

Conclusions: This comprehensive automation has significantly improved operational efficiency and data integrity. Critically, it elevates biological sample tracing from merely "traceable" to a new standard characterized by precision, real-time tracking, and tamper-proof integrity. Looking ahead, unmanned biobanks are well-positioned for further advancement by expanding upstream and downstream workflow integration and diversifying the sample types. Simultaneously, the scope and depth of automated data collection, as well as analytical capabilities, will be further expanded—ultimately facilitating more robust and efficient biomedical research.

O25 Enhancing Perceived Data Security in an In-House Developed Biobank Laboratory Information Management System: Insights from a Multi-Stakeholder Workshop

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Background: Increasing health data breaches in Indonesia have raised concerns about the protection of biospecimen and patient data in biobank information systems. Universitas Gadjah Mada (UGM) developed an in-house Biobank Laboratory Information Management System (LIMS), SIMBIOX, to support biobank operations and optimize available institutional resources. Designed to meet operational needs in resource-limited settings, SIMBIOX was evaluated through a multi-stakeholder workshop to assess perceived vulnerabilities and identify strategies for improvement, in line with national regulations on Personal Data Protection and Electronic Medical Records.

Methods: A one-day workshop with 45 participants, representing biobank staff, hospitals, research groups, IT teams, and the bioethics expert, was conducted. Sessions included expert presentations on data security incidents, cybersecurity awareness, and common attack types (e.g., DDoS, malware, phishing). Interactive discussions focused on SIMBIOX's system architecture, vulnerabilities, and mitigation options. Workshop notes were analyzed thematically to extract key perceptions, lessons, and actionable insights.

Results: SIMBIOX was perceived as vulnerable due to the absence of CAPTCHA, reliance on single-factor authentication, and more than 2,000 flaws identified through internal testing, which amplified risks in interconnected systems such as Electronic Health Records (EHRs). Participants emphasized the need for a dedicated Chief Information Security Officer (CISO), regular external audits, an incident response plan, and ongoing security awareness training. Recommended technical measures included implementing CAPTCHA, limiting login attempts (three to seven maximum), and conducting periodic penetration testing.

Conclusions: The workshop highlighted both technical and governance gaps that threaten trust and regulatory compliance in biobank data systems. Establishing a structured data protection framework and integrating user-centered security design are critical to ensuring data confidentiality, integrity, and availability, thereby fostering ethical and secure biobanking practices in developing country contexts.

O26 Establishing a U.S. Biobank Within a Global Network: Considerations for Aligning Legacy Human Samples to International Governance Standards

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Statement of Problem: When a US-based Biobank becomes part of a larger international biobanking network, it must often align locally managed human biological samples with stricter global governance frameworks. US-based laboratories obtain new and legacy human biological samples using local processes for labeling, storage, and documentation (including consent) that comply with local or regional/national laws. This decentralized structure can create variability and compliance and ethical risks if sample provenance, consent status, or traceability cannot be demonstrated to international standards. Prior to alignment, samples may be known only to individual laboratories, with no centralized visibility or electronic record within a global system. Harmonizing these legacy samples requires operational and cultural change, establishing shared governance, standardizing data, and ensuring that every sample is traceable.

Proposed Solution: A structured approach was implemented to integrate legacy human samples from multiple labs into a global biobank governance and data framework. The first step was to identify all US laboratories actively using or storing human biological samples, followed by nominating a representative from each lab to collaborate with the biobank team. Biobank defined the minimum data points needed to confirm sample-to-consent traceability, including study & sample identifiers and consent documentation. Once minimal required data was verified, samples were physically handled, barcoded or relabeled using globally standardized unique identifiers. Samples were accessioned into the global Biobank Laboratory Information Management System (LIMS), providing unified visibility. The process emphasized controlled data migration, secure chain-of-custody documentation, and consistent standards to ensure interoperability across regions.

Conclusion: Integrating a U.S. biobank into a global network requires coordinated governance, standardized data capture, and meticulous sample reconciliation. This case highlights how deliberate cross-functional collaboration, clear definition of traceability criteria, and adoption of digital accessioning systems can transform fragmented legacy collections into compliant, transparent resources that meet international expectations. By ensuring that each sample is uniquely identifiable and traceable to its consent form, U.S. biobanks can strengthen ethical stewardship, support reproducible science, and contribute to global research.

O28 Indonesia's Biobank Network for Precision Medicine and Population Genomics: First National Biobank Infrastructure

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Background: The Indonesia Biomedical and Genome Science Initiative (BGSI) is a national program under the Center for Biomedical and Health Genomics to advance precision medicine and integrate genomics into healthcare across an archipelago of 270 million people. The BGSI network includes ten Ministry of Health (MoH) hospitals as hubs recruiting participants for high-burden diseases—cancer, cardiovascular disease, stroke, tuberculosis, diabetes—and rare diseases. BGSI Central also recruits from the general population, creating a genomic reference for Indonesia's diverse populations. The Central Biobank, established in 2024, provides infrastructure for precision medicine, population genomics, and pathogen surveillance while building a national genomic database.

Methods: The biobank operates a multi-tiered architecture: a Central Biobank (Tier 1), Hub Biobanks (Tier 2) at MoH hospitals, and Spoke Biobanks (Tier 3). Digital tracking uses a Laboratory Information Management System (LIMS) aligned with FAIR and CARE principles. Standardized informed consent

enables reuse and multi-omics integration while protecting participant privacy.

Results: Ten national hospitals are equipped with biobank infrastructure and integrated systems that connect directly to the Central Biobank, forming a unified national biobanking ecosystem. As of October 2025, the Central Biobank has received 15,658 biospecimens from ten hospitals across 33 provinces, with the number continuing to grow. These include whole blood, plasma, and buffy coat samples suitable for genomic, proteomic, and metabolomic applications. All biospecimens are stored under temperature-controlled (–80°C) and monitored conditions, with standardized barcoding and a digital inventory ensuring quality and traceability. Specimens can be utilized for sequencing within the BGSI program or made available to the broader research ecosystem to support future studies, in accordance with participants' informed consent.

Conclusion: The Central Biobank represents Indonesia's first nationally coordinated biobanking system and one of the first in Southeast Asia. Its multi-tiered model ensures scalability, inclusion, and sustainability, while standardized consent and governance frameworks provide a foundation for ethical, FAIR, and globally interoperable genomics research. The BGSI initiative establishes a replicable model for low- and middle-income countries seeking to develop integrated biobank systems that support national precision medicine.

O29 Fulfilling the Promise of Biobanks for Innovation in Africa's Technological Era

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Background: In the era of digital transformation and integrated biomedical research, biobanks are emerging as strategic infrastructures that bridge science, technology, and innovation. Across Africa, the growing recognition of their pivotal role in research and public health has accelerated alignment with ISO 20387, ensuring ethical integrity, traceability, and operational excellence. These infrastructures now stand as key enablers of precision medicine, genomics, innovation and translational science. Within this evolving landscape, African institutions are embracing new technologies to modernize data management, optimize sample use, and strengthen trust among researchers, policymakers, and communities.

Methods: The Biobank of the Institut Pasteur de Dakar exemplifies this continental dynamic through the integration of advanced technologies such as Laboratory Information Management Systems (LIMS), workflow digitalization, data interoperability, and regulatory monitoring in compliance with ISO 20387 requirements. These tools enhance quality, reproducibility, and ethical legal social implication (ELSI) while promoting equitable global collaboration. Continuous staff training, a strong Quality Management System, and regional partnerships further support capacity building, technology transfer, and harmonized biobanking practices across Africa.

Results: These innovations significantly improved operational efficiency, data integrity, and reproducibility of research outputs. Digital transformation enabled real-time monitoring of sample lifecycles, faster biospecimen access, and better decision-making. Automation and analytics reduced human error and optimized workflows. Strengthened North–South and South–South collaborations fostered research on infectious diseases, antimicrobial resistance, and genomic surveillance demonstrating Africa's growing contribution to global biomedical discovery and preparedness.

Conclusion: The promise of African biobanks extends far beyond sample storage. They are evolving from repositories into intelligent, technology-driven platforms combining ethics, quality, and innovation. By embracing ISO 20387, digital infrastructures, artificial intelligence, and global partnerships, they are paving the way toward equitable, technology-enabled research ecosystems and fostering a culture of excellence and trust.

O31 Label-Free Intelligent Assessment of Organoid Viability and its Applications

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Background: Recently, FDA approved organoids as an alternative to animal experiments in new drug development. Our study aims to use AI for label-free intelligent organoid viability assessment and explore its potential in drug screening and clinical drug sensitivity testing.

Methods: Gastric epithelial and cancer organoids were constructed in accordance with standard protocols, with regular image collection. AI-assisted viability indicators (including diameter, count) were compared with traditional ones (including β-galactosidase staining, cell cycle gene expression). A label-free CBAM-YOLOV3 model and visualization software were developed. Additionally, AI assistance was used to implement small-molecule kinase inhibitor drug screening in gastric cancer organoids, and AI-assisted application of organoid-based clinical drug sensitivity testing was completed.

Results: From 76 samples of 35 patients, we constructed gastric epithelial/cancer organoids and an image database. Low-viability organoid traits (enhanced SA-β-GAL staining, upregulated p15/p16/p21, downregulated CCNA2/CCNE2/LMNB1) trained the AI model, which noted their reduced diameter and enlarged single cells. The label-free CBAM-YOLOV3 model classified high/low viability organoids with mAP 82.62% and a consistency rate of 88.25% with experiments. AI-aided screening identified aurora kinase inhibitors inducing senescence in diffuse gastric cancer organoids (enlarged cells, multi-nucleated giants, higher SA-β-Gal positive rate, elevated MCP-1/CCL2). Meanwhile, AI-assisted organoid-based clinical drug sensitivity testing was used to screen effective drugs for patients, which were then applied in postoperative adjuvant therapy, achieving favorable clinical outcomes.

Conclusions: Based on standardized procedures for constructing gastrointestinal epithelial and tumor organoids, our research developed a label-free intelligent organoid viability assessment model. This model enables label-free, high-precision detection and classification of organoid viability through AI technology, providing a powerful tool for high-throughput drug screening and clinical drug sensitivity testing of gastric cancer organoids.

O32 Iterative Orthotopic Mouse Models for Generating Phenotype-Defined Biospecimens and Matched Datasets in Hepatocellular Carcinoma Metastasis Research

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Background: Metastasis in vivo is a multi-step process involving local invasion, intravasation, circulation survival, extravasation, colonization, and outgrowth. Human biobank resources rarely capture this full sequence; paired, stage-matched metastatic samples and public datasets are scarce, limiting chain-wide studies of hepatocellular carcinoma (HCC) metastasis. These gaps hinder analysis of progressive selection across metastatic steps and clonal evolution in human HCC, highlighting the need for standardized, scalable resources to supplement human-derived datasets.

Methods: To address these gaps and enhance biobank resources, we developed an iterative orthotopic mouse model simulating postoperative lung metastasis in HCC, generating controlled paired samples and data. Luciferase-labeled mouse HCC cells (Hep53.4-luc) were implanted orthotopically into syngeneic C57BL/6 mouse livers. Post-tumor formation, surgical resection mimicked hepatectomy, with bioluminescence imaging monitoring lung metastasis. Detected lesions were harvested to isolate metastatic cells (Hep53.4-luc-MetR1). The process was iterated via repeated implantation and isolation, yielding lines with graded metastatic potentials (Hep53.4-luc-MetR2, Hep53.4-luc-MetR3). Planned multi-omics profiling (genomic, proteomic, metabolomic) will identify molecular programs linked to rising metastatic competence, including epithelial-mesenchymal transition and metabolic reprogramming variations.

Results: The model generated cell lines modeling progressive metastatic selection and partially recapitulating clonal evolution in human HCC. These phenotype-defined lines enrich biobanks as metastatic resources, while paired primary-metastatic and iteration-matched datasets address shortages in publicly available metastasis-matched data.

Conclusions: This approach counters limitations in human samples for full-chain metastasis resources. By integrating iterative modeling, systematic sampling, and multi-omics, we produce standardized, scalable paired resources that complement human datasets, aid biomarker validation, support anti-metastatic therapy testing, and advance precision oncology in HCC.

O33 Integrating an ISO 20387-Certified Biobank with a Comprehensive Clinical Database to Power Research in a Large Pediatric Liver Transplantation Cohort

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Background: Pediatric liver transplantation (PLT) has achieved excellent short-term survival, shifting the research focus to long-term outcomes. A key challenge is the high-risk transition from pediatric to adult care, often associated with non-adherence and graft dysfunction. Advanced research into these areas requires a robust infrastructure that couples high-quality biospecimens with deeply annotated, longitudinal clinical data.

Methods: We established a holistic research platform within the world's largest PLT program. Its core is the integration of two pillars: an ISO 20387 and CNAS-accredited biobank and a prospectively designed clinical database (LTx-DB). The biobank operates under a full Quality Management System for biospecimens (serum, plasma, DNA, PBMCs, tissues). The LTx-DB captures structured data across the patient journey, with a dedicated module for Transition & Long-term Outcomes, systematically tracking the transfer to adult care, medication adherence, and associated clinical metrics. A bidirectional linkage seamlessly connects every biospecimen to its rich clinical context in a secure, de-identified environment.

Results: This integrated platform now supports a dynamic cohort of over 3,000 recipients and 70,000 biospecimens. The deep phenotyping within the LTx-DB, particularly concerning the transition process, enables precise stratification of patients. This allows for the creation of highly specific sub-cohorts for research, such as adolescents with declining adherence and stable graft function, facilitating the discovery of biomarkers and mechanistic studies directly relevant to long-term survivorship.

Conclusion: The fusion of a certified biobank with a deeply phenotyped clinical database creates a transformative research ecosystem. It moves beyond simple sample storage to enable phenotype-driven research into the most critical challenges in PLT, such as successful transition to adult care. This model ensures that high-quality biospecimens are empowered by high-dimensional clinical data, accelerating discovery and improving lifelong outcomes for pediatric transplant recipients.

O34 Intelligent Biobank Supports the Construction of Shanghai Natural Population Cohort Project

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The Shanghai Natural Population Cohort Project is a large-scale, prospective, multi-omics-integrated population-based study of permanent residents. This initiative places extremely high demands on high-quality biospecimen collection, long-term storage, precise management, and efficient utilization. To address the challenges of large sample size, diverse sample types, long follow-up periods, and complex quality control, we have developed a modern biobank system centered on standardization, automation, information technology, and intelligence.

This intelligent biobank integrates the Internet of Things, automated storage equipment, a laboratory information management system, and a cohort data platform to enable digital tracking of the entire sample lifecycle, from collection, transportation, storage, to release and use. This not only strongly supports numerous multi-omics and chronic disease studies but also provides a replicable and scalable "Chinese solution" for large population-based cohorts worldwide.

This report systematically describes the intelligent biobank's architectural design, key technology applications, implementation results, and lessons learned. It explores how intelligence

can empower the development of high-quality biospecimen resources and promote the sustainable development of precision medicine and public health research.

O35 Living Biobanks of Liver Organoids: Valuable Resource for Drug Safety Assessment

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Statement of the Problem: In 2024, the success rate of drugs entering Phase 1 trials was only 6.7%, and this rate is consistently declining. Notably, drug-induced liver injury (DILI) remains a critical challenge—it accounts for a significant share of late-stage clinical trial failures and subsequent market withdrawals. Traditional drug safety assessment models, such as two-dimensional (2D) cell cultures and animal models, fail to adequately reflect patient-specific biological variables. This limitation not only raises the risk of unexpected adverse events in clinical trials but also imposes a substantial financial burden on drug development. These challenges highlight the urgent need for humanized models that more accurately recapitulate human genetic, metabolic, and physiological features, thereby improving the reliability of preclinical safety assessments.

Proposed Solution: New Approach Methodologies (NAMs)—such as microphysiological systems and in vitro functional assays—offer immediate gains in safety assessment. Recent studies show that organoids (three-dimensional miniatures of human organs or tissues) faithfully replicate the structure and function of target organs. Specifically, liver organoids stand out as a powerful solution for drug safety assessment. Unlike 2D cultures, they model tissue spatial and functional complexity to better recapitulate drug absorption, metabolism, and toxicity. Unlike animal models, they use donor-specific or stem cell-derived models (retaining unique human genetics) to simulate patient variables and interindividual drug response differences. Furthermore, liver organoid living biobanks serve as a robust pharmaceutical research platform. Unlike conventional biobanks (which preserve non-regenerable blood, tissues, fluids, and biomolecules), these biobanks hold functional, regenerable samples (including liver organoids) for dynamic DILI mechanism studies. They deepen insights into drug-induced liver damage, streamline preclinical screening, and reduce DILI-related drug attrition.

Conclusions: Amid the global shift to reduce reliance on traditional animal models for preclinical safety assessment, liver organoid living biobanks are a pivotal advancement—they address the need for humanized models that recapitulate human genetics and physiology to ensure safety assessment reliability. Top priorities are advancing their quality and stability. Meanwhile, efforts must promote their practical application and industrialization.

O36 Machine Learning-based Prediction of Antimicrobial Resistance in Klebsiella Pneumoniae Using Whole Genome Sequence Data

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Background: The increasing prevalence of multidrug-resistant Klebsiella pneumoniae highlights urgent need for rapid and accurate antimicrobial resistance (AMR) detection. Although whole-genome sequencing (WGS) enables comprehensive identification of genetic AMR determinants, reliably predicting phenotypic resistance from genomic data remains challenging. We aim to bridge this gap by developing an integrated approach to enhance the accuracy of AMR prediction from WGS data.

Methods: We included 5,239 strains from three independent cohorts (two in Clinical Bank and one public) spanning diverse geographical regions and time periods. Machine learning (ML) models were developed using WGS data to predict AMR (MLWA) to 11 antibiotics. Separate models were constructed to predict high/low levels of antibiotic resistance. All models were evaluated using five-fold cross-validation to ensure generalizability and robustness.

Results: The model to distinguish susceptible and non-susceptible categories exhibit excellent discrimination capability with AUC for all 11 antibiotics exceeding 0.9 and a mean categorical agreement (CA) of 0.95. It also demonstrated robust performance across diverse regions (Europe, Americas, and Asia) and over a broad time span (2004–2022), with sequence types, isolation sources, geographic origins, and temporal variation showing minimal impact on its predictive accuracy. To facilitate clinical application, we simplified the model by using the top 10 most contributory genes, and similarly achieved excellent prediction performance (AUC > 0.9, mean CA > 0.9). Importantly, we further developed models to simultaneously predict resistance (R), intermediate (I) and susceptible (S), high and low levels of antibiotic resistance, achieving a mean AUC and CA exceeding 0.9. The mean very major error, major error, and minor error of RIS models are 0.013, 0.015, and 0.024, respectively, indicating great promise for clinical application.

Conclusions: MLWA, our proposed model, leverages the largest dataset of its kind to support promising predictions for diverse antibiotics, resistance levels, and AST interpretation standards. It demonstrates strong generalizability across regions and unaffected by temporal resistance trends. By combining WGS with ML, this approach enhances genotype-to-phenotype prediction and supports precise and rapid antimicrobial selection, representing a significant step forward in managing antimicrobial resistance.

O37 Integrated Image Repository for Breast Tissue Biobank: Enabling Translational Research

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Background: Our breast tissue biobank comprises over 2,000 patient-derived samples, each accompanied by comprehensive clinical and molecular annotations (70% malignant, 30% benign). To advance digital pathology and enable the

development of prognostic machine learning (ML) models using multimodal data, we have established a fully digitized image repository encompassing both radiology and histopathology datasets.

Methods: For each biobank participant, radiology images are retrieved from the institutional PACS system and stored for patients who have provided informed consent for data banking. Histopathology slides are scanned on an Optra Scanner at high resolution to generate whole-slide images (WSIs), each accompanied by structured annotations capturing tumor content and tumor-infiltrating lymphocyte (TIL) percentages. The entire image repository is cross-referenced with the biobank through three unique identifiers to ensure accurate data linkage. The triple-negative breast cancer (TNBC) subset of the malignant cohort undergoes extended molecular characterization, including fifteen additional immunohistochemistry (IHC) markers, multiplex IHC for immune profiling, and whole-transcriptome sequencing. All data are stored in a secure, closed-server environment with controlled access and pseudonymization to ensure data integrity and compliance with ethical standards.

Results: The repository currently comprises approximately 4,000 radiology images (pre- and mid-treatment scans) and 2,500 high-resolution WSIs, including over 400 invasive ductal carcinoma (IDC) and 50 benign cases across H&E and multiple IHC stains. These digitized images are actively used in AI/ML pipelines designed to identify histologic and molecular correlations of disease progression. Integration of transcriptomic data with image informatics workflows is currently underway to facilitate multimodal biomarker discovery.

Conclusion: This integrated biobank–image repository represents a scalable and ethically compliant framework for multimodal data science in breast cancer. It enables high-resolution exploration of tumor heterogeneity and immune landscapes, fosters cross-cohort collaboration, and accelerates the application of AI/ML for clinically meaningful predictions—bridging precision pathology and translational research.

O38 Industry Clinical Trial Samples in Long-Term Storage: A Quality and Stability Study by Takeda Pharmaceutical's Biobank

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Introduction: The Takeda Biobank's inventory is comprised of samples procured from international Biobanks, as well as clinical trial samples collected for research purposes. These samples are critical for understanding not only the safety, pharmacokinetics, and immunogenicity of the study drug, but also for interrogating and identifying biomarkers of the disease. Clinical trial samples take a long journey—from collection sites to central labs, testing facilities, and finally, long-term storage. At any stage, sample quality can be compromised, limiting value for in-trial and post-trial translational research, as well as for collaborations with external partners, including academic centers. To tackle this challenge, Takeda's Biobank launched a pilot study to assess sample quality during long-term storage, helping protect the potential of critical clinical research samples.

Methods: Key quality indicators for multiple sample types were assessed, comparing newly generated data to baseline values from initial in-trial testing, where available. Samples were chosen from a legacy gastroenterology program where indication expansion efforts continue. Analyses included: C-reactive protein (CRP) in serum, fecal calprotectin in stool, PBMC viability and cell concentration, DNA and RNA quality, and quantitative image analysis of FFPE colon tissue using select immunohistochemical stains (e.g., Cytokeratin-18 (CK-18), CD3, and alpha-Smooth Muscle Actin (aSMA)). Statistical methods included paired t-tests and ANOVA analyses which assessed the impact of storage duration on sample integrity.

Results: The analyses revealed variable stability across sample types and analytes. 100% of DNA and RNA samples stored 8-15 years tested above the standard normal reference range of >7.0 DIN or RIN scores. Serum samples assessed for C-Reactive Protein (CRP) displayed similar values to their original results (p-value ≤ 0.5979). Additionally, image analysis of FFPE tissues highlighted differences in stain area relative to disease progression. Both CD3 and aSMA stain areas were qualitatively higher in participant tissue with a Mayo Score of ≥ 10 versus <6.

Conclusion: This pilot study provides actionable insights for the pharmaceutical sector and broader biobanking community, highlighting the necessity of regular quality assessments and evidence-based sample management practices. We aim to contribute to the strengthening of industry standards and support optimal use of banked specimens.

O39 Integrated Antioxidant, Nanoparticle, And Antifreeze Protein Strategies Synergistically Enhance Cryotop Vitrification Outcomes of Porcine Parthenogenetic Embryos

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Porcine embryo cryopreservation remains challenging due to high lipid content, oxidative stress, and ice recrystallization that compromise post-thaw survival and developmental competence. We evaluated an integrated vitrification approach combining antioxidants (berberine, melatonin), iron oxide (Fe3O4) nanoparticles, and antifreeze protein I (AFP I) with post-thaw interventions (glutathione and zona pellucida digestion) to synergistically improve cryosurvival and developmental competence of porcine parthenogenetic embryos. In vitro-matured parthenogenetic embryos were vitrified on Cryotop using a protocol including berberine and melatonin in embryo culture, Fe3O4 nanoparticles and AFP I in cryoprotectant solutions, and post-warming treatment with glutathione plus brief zona pellucida digestion. Survival, hatching, ATP content, ROS levels, cytoskeletal integrity, and the expression of BAX, BCL2, OCT4, and SOX2 genes were measured. Combined berberine + melatonin improved survival to 87.8% vs 70.0% (Cryotop alone), increased normal microtubules to 82.69% vs 66.67%, reduced ROS to 52.85, raised ATP to 0.32 pmol, and elevated hatching to 83.90%. Both the dual antioxidant (berberine + melatonin) and nanoparticle + AFP interventions produced greater improvements than individual additives. Fully integrating all components yielded the highest post-thaw viability, with 93.75% survival and 90.48% hatching, statistically equivalent to fresh embryos. Treated embryos also showed significantly higher ATP levels, lower ROS accumulation (approaching fresh embryo levels), and preserved microtubule structure ($\sim$91%

normal). Vitrification alone upregulated BAX and downregulated BCL2, OCT4, and SOX2, whereas the integrated protocol restored these gene expression levels to near control values. This multicomponent antioxidant, nanoparticle, antifreeze strategy synergistically enhances the cryotolerance and developmental competence of vitrified porcine embryos by mitigating oxidative stress and cryoinjury. Post-thaw viability and molecular markers were restored to near-fresh conditions, demonstrating a promising approach to improve embryo cryopreservation outcomes in swine and potentially other species. This nano-biocompatible, multi-agent approach advances reproducible, cross-species germline biobanking.

O40 Integrating Genomics into Indonesia's National Health Survey: Technical Insights from the BGSI Central Biobank

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Problem Statement: Indonesia, a nation of 280m people spread across an archipelago of over 17,000 islands is making a bold move toward precision medicine which requires integration of genomic and population health data. Before 2023, no mechanism existed to link population-based biobanking, genomics data generation and national health surveillance. The lack of harmonized biobanking infrastructure and standardized informed consent limited Indonesia's capacity to conduct large-scale genomic research or translate findings into policy. The Biomedical and Genome Science Initiative (BGSI), established by the Ministry of Health, addresses this gap through a coordinated national biobank network and unified ethical and operational frameworks.

Approach: In 2023, the Indonesia Health Survey was conducted to evaluate health outcomes across 38 provinces and 514 districts. For the first time, SKI introduced biospecimen collection (whole blood) to complement anthropometry, and clinical measures at a national scale. Given the survey's five-year cycle, BGSI conducted a limited evaluation to test the technical, ethical, and operational feasibility of integrating biobanking and genomic data within this framework. The two programs collaborated to align SKI's informed consent and governance with BGSI's standardized genomic consent template. In partnership with the BGSI Central Biobank under BB Binomika, whole blood samples from 21 provinces were transported frozen to Jakarta. Samples underwent multi-stage quality control for physical condition, labeling, consent verification, and identity validation with the national civil registry. Of the 2,642 samples received, 1,068 passed BGSI's quality standards and were archived at –80°C in EDTA tubes. Whole genome sequencing (WGS) was conducted using Illumina NovaSeq 6000 and MGI DNBSEQ T7 platforms, with pharmacogenomic analyses underway.

Conclusion: The BGSI–SKI collaboration marks Indonesia's first integration of national health surveillance with genomic and biobank infrastructure. This pilot establishes the technical and ethical foundation for future large-scale operations, proving the feasibility of high-throughput sample processing, standardized consent verification, and dual-platform sequencing across geographically diverse regions. The model offers a practical framework for other low- and middle-income countries seeking to embed genomics within existing health survey systems.

O41 Managing Incidental Findings at Qatar Biobank: Unintended Discoveries, Intended Outcomes

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Background: Qatar Biobank (QBB), under the Qatar Precision Health Institute (QPHI), is a longitudinal population-based study aiming to collect lifestyle, clinical, and biological data from up to 60,000 Qatari citizens and long-term residents aged 18 and above. Participants are invited every five years to monitor disease development and identify population-specific risk factors. This abstract highlight the impact of QBB in identifying and reporting incidental findings (IFs).

Methods and Results: Consented participants undergo comprehensive clinical, genetic, and imaging assessments, including MRI and ultrasound. QBB has developed a structured framework to manage IFs efficiently. Findings from imaging, lab tests, and mental health assessments, are reviewed, and participants are referred to appropriate healthcare services when necessary. In urgent cases, emergency referrals are made.

Case Presentation: A twenty-four-year-old female attended her base visit in QBB on 26th of March 2023. She has done all the routinely offered tests. During review of her results on 27th of March 2023, changes pointing towards papilledema were noted in her retinal images. During her feedback appointment, she reported frequent severe headaches. QBB arranged an urgent MRI, which revealed a right frontal intra-axial brain lesion with surrounding edema and midline shift suggestive of a neoplastic process. She was referred to Hamad Medical Corporation's emergency the same day. Further evaluation confirmed a low-grade glioma. The tumor was surgically removed within a week, and pathology confirmed astrocytoma, WHO grade 2. Her recovery was uneventful, and she has been scheduled for a routine Neurosurgery follow up.

Discussion: While biobanks primarily support research, the detection of IFs raises ethical questions. International guidelines, such as those from ISBER and the UK Biobank, emphasize the importance of clear policies for returning significant findings. QBB's proactive approach has led to life-saving interventions, as demonstrated in this case. The return of IFs, though debated globally, has proven beneficial in improving participants' health and well-being.

Conclusion: QBB's model integrates personalized medicine with public health by enabling early disease detection and timely intervention. Its structured referral process supports better health outcomes. This approach could serve as a model for biobanks worldwide, highlighting the value of returning clinically significant incidental findings.

O42 Streamlining Specimen Inventory Management at the NSW Health Statewide Biobank - A Five-Year Review

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Statement of the Problem: The NSW Health Statewide Biobank (NSWHSB) was established in 2017 and is a purpose-built facility that processes, stores and retrieves human biospecimens on behalf of collection custodians across Australia. Supporting over 30 active studies, the NSWHSB manages a wide variety of biospecimen types, that are stored in both scannable and non-scannable tubes in a range of formats. In its early operational phase, specimens were stored in both a robotic freezer with its own inventory system and in manual freezers and liquid nitrogen tanks tracked via Excel, with only the box barcode and location noted. Precise specimen coordinates were stored separately in files generated by rack scanners, making specimen location difficult. An internal audit initiated in 2020 revealed that locating any specimen in liquid nitrogen storage took over 1.5 hours due to prolonged search efforts. This not only posed risks to sample integrity but identified inefficiencies with sample retrieval.

Proposed Solution: In 2022, NSWHSB engaged with a study where 23,000 participants were expected to be recruited over 3 years. In addition, several studies were on the onboard backlog, many of which involved receipt and storage of archival samples. With the expected exponential growth of specimens, a scalable specimen inventory management system was urgently needed. Several solutions were implemented, including development of an Excel-based retrieval tool, purchasing a commercial sample management system, and in-house development of a Laboratory Information Management System (LIMS). Beyond software changes, procedures for bulk sample receipt and retrievals were overhauled to ensure accuracy and efficiency. These efforts supported significant growth in biospecimen numbers, with the inventory expanding from approximately 100,000 specimens in 2022 to over 350,000 by 2025. Despite this, the 2025 inventory audit of 100 randomly selected specimens stored under various conditions found zero identity mismatches, and all specimens were successfully retrieved within 1.5 hours. Furthermore, 60% (25/41) of retrievals requested from 2024-2025 were completed within 24 hours and 95% (39/41) were completed in less than 4 days.

Conclusion: This presentation will elaborate on the changes that were made to improve specimen management at NSWHSB over the course of 5 years, discuss the challenges encountered during the transition, and share key lessons learned with the biobanking community.

O43 Nationwide Genotype-Resistance Landscape of Wickerhamomyces anomalus in China and Genomic Decoding of the First Pan-Resistant Clinical Isolate

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Background: *Wickerhamomyces anomalus* (teleomorph Candida pelliculosa) is an emerging, environmentally-derived yeast that causes invasive infections with 30–60 % mortality in neonates and immunocompromised adults. Global reports remain scarce and azole-echinocandin co-resistance has never been genome-resolved.

Methods:

(1) From 2009–2021, CHIF-NET prospectively collected 307 non-duplicate *W. anomalus* isolates from 44 hospitals in 24 provinces. Species identification was confirmed by MALDI-TOF MS and ITS sequencing. Antifungal susceptibility to 10 agents was determined by CLSI M27 micro-dilution; epidemiological cut-off values were applied to define wild-type (WT) and non-wild-type (NWT) populations. Six-locus microsatellite typing was performed; clusters were defined as ≥2 patients sharing an identical genotype within one hospital.

(2) One multi-drug-resistant bloodstream isolate (15XN272) underwent whole-genome sequencing, to assay resistance-associated mutations and copy-number variations in ERG11, FKS1. Biofilm biomass assay and murine haematogenous infection model to assess virulence.

Results:

Epidemiology: Isolates were predominantly from Northeast (n=121) and East China (n=87). Neonates <28 d (n=84) carried the highest relative burden (12.7 %). Blood cultures accounted for 249 isolates.

Susceptibility: Fluconazole 34.5 % (106/307), voriconazole 48.5 % (149/307), itraconazole 9.4 %, posaconazole 11.4 %; only 1.3 % were micafungin-NWT and 0 % amphotericin B-NWT. Temporal analysis showed sustained voriconazole-NWT >30 % throughout 12 years.

Microsatellite analysis resolved 118 types; 49 types formed 40 intra-hospital clusters, with six trans-institutional genotypes exhibiting space–time concordance and uniform azole-NWT profiles, indicating cryptic nosocomial transmission.

A pan-Resistant Isolate 15XN272 (MIC values exceeded ECVs for all azoles and echinocandins except amphotericin B) was detected. Genome revealed ERG11triplication plus Y140H & K151R substitutions and FKS1 hotspot F665S mutation. Biofilm biomass was 3.8-fold higher than reference strain ATCC 8168 . Murine survival curve and kidney fungal load were uncompromised.

Conclusions: Integrating nationwide susceptibility surveillance with whole-genome sequencing provides a robust framework for early detection of hypervirulent clones and informs species-specific breakpoints, antifungal stewardship and infection-control policies to curtail further dissemination.

O44 The Analysis of Ethical Issues in AI-Based Organoid Biobanks

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Statement of the Problem: The integration of AI with organoid biobanks presents systemic ethical challenges. These include: the ambiguous moral status of organoids, particularly brain organoids, where AI may detect nascent consciousness, thus challenging traditional ethical dualisms; the creation of human-animal chimeras, which impacts metaphysical presuppositions of "human uniqueness" and "species integrity"; the legitimacy crisis of informed consent, as the "ontological shift" of samples into dynamic "biological derivatives" makes future complexities unforeseeable to donors, thereby undermining existing consent models; dilemmas of data privacy and "extended personality rights," as AI can deduce sensitive information from phenotypic data intrinsically linked to the donor; and challenges to social equity due to high resource barriers and sample representation biases, which risk exacerbating global health disparities.

Proposed Solution: A multi-dimensional, forward-looking governance framework is imperative. Key strategies include: establishing a review and supervision system guided by the precautionary principle for high-risk research; constructing a new paradigm of "process-relational" informed consent that ensures continuous, trust-based engagement with donors at critical junctures; establishing data governance principles based on "biological personality rights" that afford organoid data a higher degree of ethical-legal protection and mandate fair benefit-sharing; strengthening international cooperation to promote global health equity by correcting resource imbalances and ensuring diverse data representation; and constructing democratic deliberation mechanisms based on discourse ethics to integrate public values into policy through sustained cross-disciplinary collaboration.

Conclusions: AI-based organoid biobanks present significant challenges to existing ethical governance frameworks, particularly in terms of moral status, personality rights, informed consent, data governance, and health equity. Addressing these issues is decisive for the field's social acceptability and future direction. An adaptive governance framework is required to reshape consent models through procedural justice, establish extended protections for human dignity, maintain ethical prudence, and ensure technology advances in synergy with social values, thereby realizing the long-term welfare goals of biobank construction.

O46 Biospecimen Science: The Construction and Application of a Dual-Layer Theoretical Framework

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Statement of the Problem: With the rapid expansion of multi-omics technologies and clinical data integration, the scientific value of biological samples and biobanks has evolved from physical storage toward data interpretation and knowledge generation. However, current biobank operations remain largely empirical, lacking a unified theoretical foundation that systematically links sample resource construction to its scientific and translational value. This gap limits the effective utilization of biobank resources in supporting precision medicine and clinical research.

Proposed Solution: To address this challenge, we propose the Dual-Layer Theoretical Framework for Sample Science, a systematic approach to define and integrate the scientific and operational dimensions of biobanking. The framework comprises two interrelated components: 1) Sample Application Theory (upper layer) — a goal-oriented theory emphasizing scientific reasoning and experimental design to obtain biologically and clinically interpretable data from samples, thereby enabling disease mechanism studies and clinical decision-making; 2) Biobank Construction and Management Theory (lower layer) — a means-oriented theory focusing on the standardized, systematic, and compliant governance of sample collection, storage, distribution, and data application. Together, these layers establish a feedback mechanism where scientific inquiry guides engineering practice, and engineering supports scientific discovery, forming a closed loop between theory and implementation.

Conclusions: This dual-layer framework is the first to unify sample science and biobank management theory under a coherent structure, providing a logical pathway from resource construction to value realization. It redefines biobanks as active data- and knowledge-producing systems rather than passive storage units. Under this model, intelligent labeling, data productization, and proactive data output will drive biobanks toward a theory-driven and intelligent paradigm. The proposed framework offers new theoretical and methodological foundations for advancing biobank development, promoting effective data utilization, and strengthening the translational bridge between biological research and clinical application.

O47 Scaling Newborn Screening and Biobank Integration for Early Child Health Interventions in South Africa

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Statement of Problem: Congenital disorders—including inborn errors of metabolism, congenital hypothyroidism (CH), and haemoglobinopathies—are a preventable yet underrecognised cause of infant morbidity and mortality in South Africa. Although newborn screening (NBS) is a routine public health measure in most high-income countries, fewer than 0.5% of South African infants are screened, almost exclusively in the private sector. The absence of a coordinated, public-sector NBS programme results in thousands of children growing up with avoidable disability. Fragmented health data systems and lack of integration between screening results, clinical care, and research infrastructure further hinder effective follow-up and policy development.

Proposed Solution: The North-West University have developed a scalable NBS implementation package designed for South Africa's public health context. The model introduces phased provincial demonstration projects starting with CH and selected metabolic conditions. Blood spot samples are collected before discharge (6–12 hours after birth) and again at 24 hours to validate early diagnostic accuracy. Analyses are performed at CHM using standardised tandem mass spectrometry, with results integrated into a secure electronic health platform linked to a biobank for sample and data storage. This integration allows longitudinal tracking, research access, and referral to appropriate clinical services. The framework aligns with national guidelines and includes training for nursing and laboratory staff, costed logistics, and stakeholder coordination mechanisms.

Conclusions: Embedding NBS within existing maternal and child health pathways—and coupling results with biobank infrastructure—offers a feasible, ethical, and cost-effective strategy to reduce preventable disability and improve early child health outcomes. The approach strengthens South Africa's capacity for data-driven decision-making, supports rare disease surveillance, and creates a foundation for genomic and precision health research. This initiative illustrates how biobanking can move beyond sample storage to actively support equitable health service delivery and public health transformation in low- and middle-income settings.

O48 The GenV Biobank: Powering Biological Research in a Large Longitudinal Cohort of Australian Newborns and Their Parents

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Introduction: Generation Victoria (GenV) is a longitudinal, whole-population cohort and biobank open to all children born in Victoria within a two-year period (October 2021–October 2023) and their parents. As the largest study of its kind ever conducted in Australia, GenV aims to enable large-scale discovery and interventional research. The cohort is broadly representative of all Victorian births across key demographic characteristics, including geographic region, socio-economic status, First Nations communities, and parents born outside Australia.

Methods: To maximise inclusivity while minimising participant burden, the GenV biobank employed three complementary biospecimen collection strategies:

- Non-invasive rapid collection at recruitment — saliva samples from parents and children.
- Residual clinical samples routinely collected during pregnancy (blood plasma or serum, and Group B Streptococcus[GBS] swabs) or around birth (newborn blood spots).
- Targeted self-collection of biospecimens, including breastmilk and child stool swabs, at specified time points.

Results: GenV has recruited more than 124,000 participants (over 49,400 children and 74,600 adults) from 58 Victorian birthing hospitals. The GenV biobank currently holds over 100,000 saliva samples, 6,608 paired breastmilk and child stool samples, 40,126 newborn blood spots, and large numbers of pregnancy serum (20,130), plasma (26,617), and GBS (3,078) biosamples. Biosamples are now being released to approved research collaborators, with an initial analysis of 33,000 samples underway to estimate the prevalence of congenital cytomegalovirus—an important consideration for evaluating the potential for universal newborn screening in Australia.

Discussion: By 2035, GenV's vision is to help address complex challenges affecting children and families through integrated, large-scale research. The GenV biobank represents an internationally distinctive cell-to-society resource, combining extensive biospecimen collections with administrative, clinical, and self-reported data. Plans to establish open research access to both biosamples and linked data are well advanced, alongside future phases of biosample and phenomic data collection beginning in the early school years.

O49 The ISBER Mentoring Program, a New Online Resource for Your Biobank Staff

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The breadth of knowledge and expertise of ISBER members has been recognized globally in publications and presentations. This expertise is uniquely available locally in our organizations and is an untapped resource to our wider global society.

In 2024, The Mentorship task force launched a pilot for the ISBER Mentoring Program which is designed to connect individuals seeking guidance (Mentees) with experienced volunteer Mentors in the biobanking community who can share their first-hand, practical biobanking knowledge. Engagement is offered at no cost to the ISBER participants and is intended to provide limited, short-term opportunities to learn from experts in human, veterinary, environmental and rare disease biobanking on a variety of topics related to biorepository management, operations, biospecimen collection and processing, policies, and regulations. In addition to an opportunity to contribute to improving biobanking practices around the world, this program will help familiarize mentees with the range of tools provided by ISBER, and with other resources available to biobankers. This presentation will discuss the pilot phase, how to successfully use the program, and the new automation of the registration and matching process. The Mentoring Program is a valuable ISBER tool that can help support your biobank's long-term sustainability goals through mentorship of your staff and YOU.

O51 Toward a Maturity Model: Foundational Findings for Evaluating Trusted Research Environments in Federated Analytics Networks

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Statement of the Problem: Advances in biomedical disciplines and multimodal data collection have been driving the unprecedented expansion of healthcare data, creating major opportunities for improving disease understanding, treatment development, and personalized medicine. However, these data are often complex and sensitive, posing challenges in secure storage, processing, and especially in data sharing. Ethical, legal, administrative, and technical barriers can restrict collaborative research and international data exchange. As such, there is a critical need for structured framework that supports secure and sustainable data sharing through federated infrastructures such as Trusted Research Environments (TREs) and Federated Analytics Networks (FANs), alongside evaluative mechanisms to ensure their functionality and effectiveness.

Proposed Solution: This study aims to develop a maturity evaluation framework for FANs supported by TRE nodes, as a pathway towards secure, ethical and effective data sharing. To establish such a foundation, maturity models from the established federated networks Beyond One Million Genomes, ELIXIR, and the Federated European Genome-Phenome Archive, were analyzed to identify assessment domains used across international networks. In addition, Health Data Research UK's TRE Capability Model, Standard Architecture for TRE (SATRE) and the Data and Analytics Research Environments UK Federated Architecture Blueprint (FAB) documents were examined to contextualize maturity assessment within federated

TRE applications. Comparative analysis of these sources enabled the identification and alignment of domains and descriptors essential for evaluating the readiness and sustainability of federated networks.

Conclusions: The analysis identified eleven overarching domains, consolidated into six categories: governance and policies, operations and performance, data management, physical/technical infrastructure, outreach and communication, and clinical/research infrastructure. These domains form the foundation of a preliminary framework for assessing the maturity of TRE-supported FANs. Gaps in domains were reinforced through recommendations from the SATRE and FAB documents, with the remaining domain of collaboration being lacking, highlighting priorities for future refinement. The proposed model represents an early step toward establishing secure, ethical, and sustainable federated analytics to advance global health data sharing and research.

O52 Transforming Biobanking Operations: A Case Study on the Integration and Impact of a Fully Automated −80°C Storage System at the MUB Biobank

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Background: The Medical University of Bialystok Biobank (MUB Biobank) is a specialized unit dedicated to the collection, processing, and long-term storage of human biological samples for high-throughput research. Operating according to the ISO 9001, ISO 20387, it manages diverse samples from patients with oncology, metabolic, and other diseases, together with the populational study BialystokPLUS. As sample volumes grew to support multiple projects, manual storage methods presented limitations in efficiency and preservation of sample integrity. To overcome these challenges, the MUB Biobank introduced the fully automated ultra-low temperature storage system designed for high-capacity biobanking.

Methods: First, we conducted a comprehensive workflow audit of existing manual freezer operations, mapping sample accessioning, storage, retrieval, and defragmentation tasks. Based on that, we designed module layouts, barcode strategies, and labware compatibility lists. We used the API to connect the system to our LIMS, enabling automated request ingestion, sample position updates, and real-time audit trail logging.

We implemented a phased validation protocol including:

- Temperature and thermal stability mapping of storage and pick zones
- Pick/put accuracy (sample retrieval correctness) tests
- Cross-contamination checks
- Throughput and latency benchmarking
- Uptime/reliability monitoring
- Failure-mode simulations

Operating initially in shadow mode (parallel manual vs. automated) allowed side-by-side comparison. Concurrently, we developed new SOPs, trained staff, and established monitoring dashboards.

Results: Since implementation, automated storage system has enabled the MUB Biobank to manage and store approximately 1,500 samples daily with reduced human intervention, minimizing errors and enhancing security through audit trails and temperature controls. The transition from manual to automated retrieval reduced sample access times, and hands-on manual interventions were cut, lowering risk of misplacement or thawing events. Temperature logs and audit trail are automatically recorded for every sample movement: chain-of-custody tracking is robust.

Conclusions: Implementing the automated storage system in a biobank environment is feasible and yields measurable improvements in retrieval speed, traceability, sample integrity, and operational efficiency. Key enablers included thorough workflow mapping, LIMS-level integration, and extensive staff engagement.

O53 Multiomics and Tumor Banking: A Comprehensive Platforms Integrating Cancer Diversity, Biomarker Discovery, and Personalized Cancer Care

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Statement of the Problem: Biobanks are innovative biomedical research infrastructure supporting investigations into cancer, covering aspects from its etiology, disease advancement, and therapy. The biobanks have contributed significantly to the advancement of personalized medicine, providing biospecimen resources and expertise in tissue handling that are required to understand the impact of various factors on cancer biology such as genetic, ecological and lifestyle on human disease, mortality, and wellbeing. With biobanks connecting to clinical, pathological, and epidemiological information, understanding how their contribution to the discovery and development of biomarkers in the field of therapeutics is vital for their ongoing management, funding, and sustainability. A varied spread of biological samples with well-annotated clinical and pathological patient data is an essential prerequisite for customized medication. Biobanks form the fundamental component of precision medicine that relies upon the three top verticals of support in malignancy studies: proteomics, metabolomics, and epigenomics (omics). Over the years, biobanks and omics (genomics, transcriptomics, proteomics, metabolomics) have evolved, mutually contributing significantly towards decoding cancer pathogenesis and establishing the conduct of biomedical research, thereby covering diagnosis, prognosis, and treatment modalities.

Proposed Solution: Cancer biospecimen contains the biological information that reflects the nature of a patients 'disease, biobanks must be managed as part of the data generation and analytics continuum that drives precision medicine. The advancement of multi-OMICS analytics with artificial intelligence, systems biology and deep machine learning has elevated the field of personalized onco-medicine only serving to emphasis biobanking human biospecimens as an informatics concern as well. In this presentation, we will explore the impact of biobanking in facilitating bench-to-bedside oriented and multi-OMICS data driven cancer research required to enable precision medicine.

Conclusion: Biobanking serve as fundamental components of multi-OMICS approach in cancer management making them

the cornerstones of personalized medicine by providing the biological samples and associated data needed for comprehensive molecular profiling, biomarker discovery, and personalized treatment strategies, thereby aiding in the tailoring of individualized patient treatment and precision oncology.

O54 The World's Largest Germplasm Resource Bank for Wildlife Has Been Established in Guangdong Chimelong Group

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With decades of in-depth commitment to species conservation, Chimelong Group has pioneered an innovative five-in-one integrated development model: "Endangered Species Conservation + Cutting-edge Scientific Research + Public Science Education + Field Rescue and Reintroduction + Eco-cultural Tourism". It has established 9 large-scale ex situ wildlife conservation base clusters, successfully conserving more than 150,000 rare wild animals of over 1,200 species from 53 countries. Chimelong ranks first in the world in terms of the number of conserved species, breeding achievements, and the scale of conservation bases. Accumulated a database of 1.25 million wild animal conservation records, established over 1,090 enterprise technical standards, and published over 100 intellectual property rights such as monographs, papers, and authorized patents. In response to the risk of germplasm resource loss, Chimelong Group has taken the lead in constructing an ex situ wildlife germplasm resource repository, breaking through multiple technical bottlenecks and establishing four core technical systems: wildlife semen collection and cryopreservation, isolation, culture and cryopreservation of wildlife mesenchymal stem cells, vitrification cryopreservation of wildlife tissues, and isolation, culture and cryopreservation of wildlife organoids. The repository has realized semen cryopreservation and mesenchymal stem cell extraction & cryopreservation for multiple wild species including the Yangtze finless porpoise, cryopreserved over 10,000 tissue samples from more than 200 wild animal species, completed permanent vitrification preservation of key tissues from over 20 rare wild species such as the Bengal tiger and koala, and constructed 25 tissue organoid models for 8 rare wild animal species. Compared with similar institutions at home and abroad, Chimelong's ex situ repository features comprehensive taxon coverage and a complete technical system, achieving full-chain coverage of germplasm resources from "collection, preservation to application" and effectively compensating for the limitations of traditional in vivo conservation. In the future, Chimelong will continue to optimize conservation technologies, promote the deep integration of in vivo and in vitro conservation, expand the scope of germplasm resource protection for rare and endangered species, and contribute to the global cause of biodiversity conservation.

O55 Towards an International Ethical Framework for Banking and Secondary Research Use of Human Biospecimens and Associated Data: The Seattle Principles

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Background: Large, appropriately representative and well-characterized biospecimen collections are critical to advance science and develop therapies that will benefit all populations. The sharing of biospecimens across international borders is essential for reaching this goal. However, significant challenges exist, including the lack of harmonized legal, ethical and policy frameworks regarding such sharing and the secondary use of biospecimens.

Methods: These issues were discussed at a series of virtual and in-person meetings of a wide range of stakeholders, including meetings of the International Society for Biological and Environmental Repositories, Public Responsibility for Medicine in Research, and the 2024 UN General Assembly Science Summit. The goal was to identify and refine a set of principles that could serve as a basis for promoting greater harmonization of policies globally related to the sharing and secondary use of human biospecimens, as well as guiding the ethical practice of biobanking and research use of such biospecimens.

Results: Through these discussions, 11 guiding principles were identified and refined. These include the following principles: Transparency to Participants, Respect for Consent of Participants, Respect for the Scope of Consent, Respect for Withdrawal of Consent for Future Research, Safeguarding the Welfare of Specific Communities, Human and Community Welfare Protection, Participant Privacy, Specific Consideration of Genetic/Genomic Research, Returning Research Results, and Governance and Oversight. These principles will be further elaborated and discussed during this presentation at the ISBER Global Biobanking Congress. A manuscript elaborating on these principles has been accepted for publication and should be available online by the time of the meeting.

Conclusions: Our hope is that these principles can help promote the development of an ethically grounded, harmonized international ethical framework that will not only facilitate important international research that will benefit all populations, but promote high ethical standards in research involving human biospecimens and associated data.

O56 Viability Cryopreservation of Multiple Types of Tissues via a Novel Vitrification Platform Technology

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Biobanks serve as a crucial link between basic research and translational medicine, playing a pivotal role in advancing medical science. However, conventional biobanks primarily rely on preservation techniques such as fast-freezing in liquid nitrogen or paraffin-embedding, which can only conserve biomolecules like nucleic acids and proteins but fail to maintain tissue

viability. This limitation renders many valuable clinical samples unsuitable for functional studies. To overcome this challenge, we developed ice-free vitrification methods that enable long-term preservation of diverse living tissues, thereby supporting the establishment of living biobanks to meet critical storage and research needs. In this study, we perfused cryoprotectants into various tissue slices-including mouse lung, liver, kidney, and intestine, as well as human lung cancer, liver cancer, gastric cancer, cartilage, and organoids-followed by rapid cooling to below -140°C to achieve a glassy state. Differential scanning calorimetry (DSC) confirmed that vitrification effectively suppressed ice crystal formation during both cooling and rewarming. AO/PI staining showed no significant difference in cell viability between rewarmed and fresh tissues. Similarly, the yield of organoids derived from rewarmed tissues was not statistically different from those obtained from fresh tissues. Hematoxylin-eosin (HE) staining revealed no structural differences between vitrified and fresh samples. Moreover, we successfully achieved in situ vitrification of organoids embedded in Matrigel. After rewarming, these organoids retained their original morphology and spatial arrangement, with cell viability comparable to that of the control group. Our approach enables high-quality, long-term storage of viable tissues and organoids, offering a next-generation platform for living biobanks. This work presents a novel strategy for constructing living biobanks and establishes a new paradigm for biomedical research and translational applications.

Innovative Technology

OIT1 Design and Preliminary Implementation of an AI-Based Intelligent Management System for Biobanks

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Background: Traditional biobank QMS relies on manual operations and paper records, causing fragmented workflows, high costs, deviations, and limited traceability. Following ISO 20387, there is a need for an intelligent, traceable, and executable QMS. This study designs and implements a "QMS Intelligent Management System" to shift biobank management from manual to AI-driven, enhancing efficiency, compliance, and sample research value.

Methods:

1. Requirement Analysis: Evaluated existing QMS, identifying bottlenecks in management processes, roles, equipment, SOP execution, and audits.
2. Knowledge Graphs: Decomposed documents, SOPs, and roles into executable nodes forming a "document–rule–role–process" network.
3. Rule Engine & Task Assignment: NLP and rule extraction converted SOP operations into executable rules linked to roles and process nodes for intelligent task allocation and reminders.
4. Equipment & Data Integration: Connected sensors to capture environmental and operational data, enabling real-time monitoring and predictive alerts.
5. Intelligent Guidance: Audio/video prompts, pop-up alerts, and log recording support proactive quality control.
6. Validation: Simulated operations and pilot tests refined rule coverage and system performance.

Results: The system addresses role clarity, equipment management, SOP guidance, and audits through six modules: role assignment, equipment oversight, SOP guidance, version control, process tracking, and predictive alerts. Knowledge graphs map tasks; the rule engine sends real-time reminders; sensors trigger maintenance alerts; guidance interfaces log operations, enabling proactive quality control.

Conclusion: The intelligent system achieves automated, traceable, and executable QMS, enabling data-driven management, reducing operational risks, and enhancing sample research potential to support precision medicine and translational research.

OIT2 Establishing a Virtual Repository, The Biobank of the Future

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In this exciting project we explore what it takes to setup a virtual repository in order to adapt to the future needs of precision medicine; as the world moves more deeply into digitalizing everything with the power of AI. We are looking at 3 key elements to consider. The methods being used to raise the quality of the biological samples being stored, extracting quality data from these associated samples, as well as ethical and legal requirements to consider. The data associated with the samples (Blood & Saliva) is becoming increasingly much higher in demand. Some of the larger commercial biobanks report that 95% of requests they receive at their biobank is for accessing the data only. ARK team will show the different methods being used to separate the wet lab & cryostorage portion of the business from the dry lab containing computer hardware and data analytics software. We are sequencing Whole Genome and Whole Exome in order to generate the data to be used in future precision medicine projects. Some of the ethical issues identified is that each person has a unique DNA sequence, therefore attempting to anonymize the DNA will still be tied directly to the patient. Legal requirements we consider is having a secure platform that authorized researchers can access only the data that they have consent by the participants to have access to, and they can only use the data to do the type of research that is consented. As we develop better methods to obtain better sample quality for the purposes of generating higher quality data, we can use a digital simulation to determine the best method to use. These virtual repository projects have been essential in helping the newest drug discoveries to be obtainable. Furthermore, integrating AI-driven analytics into the virtual repository enables real-time data processing and predictive modeling, enhancing the speed and accuracy of biomarker identification. By leveraging cloud-based infrastructure, the ARK Repository ensures scalable storage and global accessibility while maintaining robust cybersecurity measures to protect sensitive genomic information. Preliminary simulations have demonstrated a 30% improvement in data extraction efficiency when using optimized sample preparation protocols. Ultimately, this virtual biobank model paves the way for collaborative international research

networks, fostering innovations in personalized therapies and disease prevention strategies.

OIT3 Bridging the Automation Gap: A Benchmark Review and Modular Approach to Accessible Tube Handling in Biobanking

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Background: Pre-analytical errors threaten scientific reproducibility. For biobanks, automation is a proven strategy to mitigate these risks while enhancing throughput and sustainability. However, a critical gap persists; while the analytical phase is well-served by mature Liquid-Handling (LH) systems, accessible pre-analytical Tube-Handlers (THs) remain scarce. This study investigates the techno-economic root causes of this automation disparity.

Methods: We triangulated three complementary approaches: (1) a bibliometric screen of 432 ISBER abstracts (2018–2025) to quantify operational-automation topics; (2) a systematic benchmark review (PRISMA-guided; 85 sources, 2005–2025) comparing TH and LH across ten techno-economic dimensions; and (3) a proof-of-concept case study implementing a modular platform architecture.

Results: Operational efficiency was the most prevalent topic in ISBER submissions ($\sim$60%). Our benchmark review identified two structural barriers inhibiting TH accessibility: (i) a lack of standardization across the pre-analytical labware ecosystem (tubes, caps, racks), which forces costly, low-volume customization; and (ii) the prohibitive capital cost of monolithic systems engineered to solve the thermo-mechanical challenges of integrated cryogenic handling. These factors prevent the economies of scale achieved in the standardized, high-competition liquid handler market, locking biobanks into a cycle of high cost and low adoption. The case study supports a modular "intelligent decoupling" strategy —separating ambient-temperature robotics from cryogenic elements—to reduce integration complexity while preserving specimen thermal integrity; full assay-level stability data will be presented.

Conclusion: The automation gap in pre-analytical biobanking results not from technical limitations but from a dominant business model that prioritizes high-cost, custom solutions for large organizations, thereby neglecting smaller institutions. This approach, driven by niche market dynamics, makes automation inaccessible. Our work confirms the feasibility of a parallel approach: modular, decoupled architectures that make automation economically viable for a broader range of organizations. Fostering community-led standardization and vendor agnostic solutions will facilitate the democratization of automation in biobanking and promote true standardization aligned with ISBER/ISO standards.

Poster Abstracts

Biobank Tools

PA-01 The Role of a 24/7 Monitoring and Alarm System in Safeguarding a Biobank

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Background: In biobanks, environmental hazards, equipment failure, power outages, and human error pose significant risks to the quality of biological materials. To preserve sample integrity, continuous monitoring and alarm systems are vital for providing real-time surveillance and automated alerts to on-call personnel, especially during non-operational hours.

Methods: The CU-Med Biobank implemented a 24/7 monitoring system incorporating temperature loggers for ultra-low temperature (ULT) freezers, uninterruptible power supply (UPS) units, and water leakage detectors. This system enables the remote, real-time monitoring of UPS status, ULT freezer temperatures, and liquid nitrogen temperature. In the event of malfunctions or temperature excursions, automated alarms (via email and phone call) are immediately sent to on-call personnel for their corresponding actions.

Results:

Incident 1: A UPS failure during non-operational hours caused the temperature in five connected freezers to rise above the safety threshold. The monitoring system triggered immediate alarms. On-call personnel restored power via the UPS bypass and transferred all biological materials to unaffected freezers within four hours.

Incident 2: A ULT freezer exhibited mildly elevated temperature, though below the formal alarm threshold. Through continuous real-time monitoring over the following 48 hours, personnel proactively decided to relocate all biological materials to a new freezer, ensuring their preservation before a critical temperature was reached.

Conclusion: These incidents underscore the critical role of 24/7 monitoring systems in biobank management. By enabling real-time environmental surveillance and rapid incident response, such systems are vital for safeguarding biological materials and ensuring operational resilience in biorepository settings.

PA-02 Automation-Driven Improvements in Biobank Workflow and Data Quality

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Background: The rapid advancement of technology has highlighted the vital role of automation in accelerating scientific research outcomes. In biobanking, the establishment of comprehensive laboratory information management systems (LIMS) capable of managing extensive clinical and sample data is essential. However, fully optimized LIMS are costly and complex, especially challenging for small or new biobanks.

Methods: CU-Med Biobank explored three automation modules to enhance data management and operational efficiency. First, an automated sample data import module replaced manual entry by securely importing large clinical data batches from authorized electronic devices, auditing and categorizing them automatically. Second, an automated inventory check operator module calculated replenishment needs upon threshold triggers and generated procurement documents automatically after input updated consumable stock levels. Third, a clinical data annotation module was designed to automate the organization and labeling of highly hierarchical and stratified clinical data, including donor demographics, disease phenotypes, treatment histories, and laboratory findings.

Results: The automated data import module significantly reduced labor and errors associated with manual entry, streamlining sample processing. The inventory module facilitated efficient stock management and prompt procurement, reducing labor-intensive work. The annotation module enabled precise hierarchical structuring of complex clinical data, improving retrieval and downstream research usability.

Conclusion: Integrating these automation strategies into biobank workflows optimizes operational efficiency, reduces human error, and supports the maintenance of high-quality, standardized metadata. These improvements empower biobanks to advance biorepository management and contribute to enhanced clinical research outcomes.

PA-03 Sample Preprocessing Integrated Automated Equipment Patent R&D Plan

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Overview: After the sampling of one or more specimens is completed, place the sampling tubes into the all-in-one machine in the specified order. Through the operation of the sample library system, the procedures of numbering, code scanning and storage for the sampling tubes are fully automated. The font used is uniform and clear, and the operation is simple and efficient.

Background: Specimen quality is the core element of a biobank. Standardized operation in specimen collection, as a key step, is essential to minimize human interference.

Market: Currently, a wide range of instruments are applied in biobanks, but there remains a gap in instruments specifically for the specimen collection process. Essentially, the development of biobanks lies in the control of specimen quality and the transformation of specimen application.

Product: This all-in-one machine can be divided into two parts: the “numbering and code-scanning machine” and the “liquid nitrogen storage machine”. These two machines can be used either independently or combined as an integrated all-in-one machine.

For the "numbering and code-scanning machine": Small-character inkjet printer, QR code scanner, one-way robotic arm, laser positioner, sampling tube rack, and tube rack rail. For the "liquid nitrogen storage machine": Liquid nitrogen storage tank, sample box rack, integral thermal insulation cover, laser positioner, one-way robotic arm, and tube rack rail.

Place the sampling tubes into the sampling tube rack in sequence, and position the tube rack on the tube rack rail of the "numbering and code-scanning machine". Operate the sample library system to input the name(s), inpatient number(s), and specimen type(s) of one or more cases

The tube rack moves along the rail to the robotic arm. The robotic arm then clamps the sampling tubes in the preset order and moves them past the printer head one by one to complete information printing. Simultaneously, it scans the QR code at the bottom of each sampling tube—two operations are completed in one step. After all sampling tubes on the roboticarm have been printed and scanned, place them into the tube rack of the "liquid nitrogen storage machine".

The tube rack moves along the rail to the robotic arm, which clamps the sampling tubes and places them into the sample boxes inside the liquid nitrogen storage tank.

Repeat the above operations until all sampling tubes are stored in the tank.

PA-04 Data-Driven Optimization of Alarm Management in a Biobank Monitoring System

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Background: Frequent and redundant alarms in biobank monitoring systems reduce management efficiency and may compromise biosafety. This study aimed to enhance alarm response effectiveness through data analysis and targeted optimization, establishing a reliable and efficient alarm management mechanism.

Methods: A systematic analysis was conducted on 2,284 historical alarm records from January to September 2025, including both alarm activation and recovery states. The analysis quantified alarm patterns by type, equipment distribution, and temporal characteristics. Based on the findings, three optimization measures were implemented:

1. Precision hardware maintenance: A tiered maintenance plan was developed for the top 10 devices with the highest alarm frequency, incorporating predictive maintenance such as compressor performance testing and sensor calibration.
2. Process standardization: Standardized operating procedures were established and comprehensive training was organized for all personnel.
3. Alarm rule restructuring: This included eliminating redundancy by merging duplicate, transient, and non-actionable alarms; adjusting thresholds based on historical data to reduce false alarms; implementing delay mechanisms for non-urgent state changes to prevent alarm flooding; and establishing correlation rules to consolidate multiple alarms caused by the same root cause.

Results: "Door-open overtime" (43.1%) and "high temperature" (29.7%) were the dominant alarm types, with 75% of alarms concentrated in 10 devices. Alarms peaked during 8:00–11:00 and 14:00–17:00, coinciding with sample operations. After optimization, repetitive alarms in key devices (e.g., CH33, CH48) decreased by over 90%. Monthly alarms dropped from 428 to 215 (–49.8%), and effective alarm-handling time improved by more than 70%.

Conclusion: Data-driven root cause analysis enabled a shift from passive response to proactive management. Combining predictive maintenance, workflow optimization, and intelligent alarm logic significantly improved biosafety assurance and operational efficiency, offering a scalable model for intelligent biobank management.

PA-05 Harmonized Blood Quality Assurance Metrics for Automated Biobanks

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Background: With the advent of multiomics platforms to analyze whole transcriptome/ proteome in tissues, our understanding of the disease processes has tremendously increased. Besides tissues, blood derivatives such as plasma, serum and buffycoat are also finding their niche as valuable cell-free biomarker signatures as evidenced in recent sequencing studies. As biobanks are established to enable research discoveries and innovation, the quality assurance of all the banked specimens is the primordial step for realizing that vision. Furthermore, as many biobanks are gearing towards automation, it is imperative that there exist harmonized practices across the biobanks for appropriate quality assurance and for ensuring long-term stability and fitness for purpose of the specimens.

Methods: In our hospital-based biobank, we have validated a framework for processing and quality control of blood derivatives. We recently conducted a series of experiments in buffycoat samples asking three questions: (a) is the DNA concentration a good indicator of cryostorage stability and age of the sample (b) is the DNA quality different between manual processing and automated processing methods and, (c) what defines the "fit-for-purpose" metric of buffycoat specimens in the evolving landscape of multiomics technologies? Towards this direction, the concentration and quality (A260/280 ratio) of the DNA extracted from thawed buffy coat samples over a period of 10 years, were measured. A comparison of these parameters was also made on the buffycoat samples isolated manually and from those obtained from using a robotic liquid handler system (Hamilton STARlet).

Results: The DNA concentration was found to be stable across the years thereby confirming that there is no significant correlation between the DNA quality and the length of storage/ method of storage. The automated system (Hamilton) consistently displayed a relatively higher concentration of DNA as compared to manual processing and further, the variability in DNA metrics was also found to be higher with manual processing. We will present more updated results on DNA/RNA sequencing in the ISBER 2026 meeting.

Conclusions: As a vital source of cell-free DNA and RNA, buffycoat specimens are the bedrock of blood-based biomarkers along with plasma and serum markers thereby signifying the

importance of harmonized practices in systematic characterization so that collaborative networks between the biobanks can be more meaningful.

PA-06 Construction of Risk Management System in Biobanks of General Hospitals in China

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Objective: In order to guarantee the safety of biobanks, improve the quality of biospecimen and datas, and keep the quality management system running steadily, it is necessary to construct the risk management system of biobank in general hospitals.

Methods: This paper describes four principles of risk management system construction, including scientificity, systematicness, operability and training. And the process of risk management, covering risk identification, risk assessment, risk control and effect analysis, is also described in details. Furthermore, this paper introduces an example of risk management construction to elucidate the process and key points, involving the document system, organizational structure, three levels of risk management, risk assessment matrix, risk control, and regular train.

Results and Conclusions: Based on principles and the process of risk management, along with construction experiences, this paper proposes paths for improving risk management system of biobank in general hospitals.

Key words: biobank; risk management system; biospecimen and data

Biobanking Profiles

PB-01 Aier Eye Biobank: A National Distributed Network for Ophthalmic Genetic Resources

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High-quality ophthalmic biospecimens and imaging data are essential for advancing basic research, precision medicine, and translational innovation. Aier Eye Hospital Group, a global ophthalmic medical organization operating nearly 1,000 hospitals, eye centers, and research institutions worldwide, possesses abundant clinical resources that provide a strong foundation for ophthalmic research and biobank development.

To integrate and manage these valuable resources, the Aier Eye Biobank was established in 2023 as a cornerstone platform to promote ophthalmic precision medicine and translational research. The biobank follows a strategy of distributed design, standardized management, and digital integration. It consists of a central biobank in Changsha and multiple regional stations in major Chinese medical hubs, including Wuhan, Beijing, Tianjin, Shenyang, and other key cities. This structure ensures nationwide interoperability, data traceability, and strict privacy protection through seamless integration with Aier's proprietary hospital information systems (AHIS, ALIS, and AEMR).

The Changsha Central Biobank serves as the network's pilot and demonstration site. In 2024, it launched the Clinical Discarded Sample Collection and Preservation Program to ethically recover and preserve surgical tissues and residual diagnostic specimens that would otherwise be discarded, establishing a standardized workflow replicable across disease-specific biobanks in the Aier network. Since its inception, the biobank has preserved nearly 40 categories of ophthalmic research samples, including retinal diseases, glaucoma, ocular surface disorders, orbital tumors, and hereditary eye diseases. Through multi-center collaboration and digital governance, it has built a nationwide, traceable, and shareable biological resource system that integrates biospecimens, clinical data, and imaging information, supporting mechanistic studies, biomarker discovery, diagnostic innovation, and national blindness prevention.

As China's first distributed ophthalmic biobank dedicated to human genetic resources, the Aier Eye Biobank represents a major milestone in the country's research infrastructure. Aier will continue to expand its "one biobank, multiple stations" model, strengthen collaborations with research institutions, and promote open, high-quality data sharing to accelerate ophthalmic innovation, advance precision medicine, and contribute to global vision health.

PB-02 Australasian Biospecimen Network Association: Building A Network to Promote Outreach and Empower Research Innovation

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Statement of the Problem: Increasing membership numbers and an evolving research landscape have necessitated that the Australasian Biospecimen Network Association (ABNA) increase its scope, outreach and build new initiatives to support the membership to adapt to this change and growth.

Proposed solution: The newly launched Asia-Pacific Engagement Travel Grant is a key initiative designed to advance regional collaboration and amplify Asia-Pacific voices within the biobanking community. This program enables recipients to attend and present their work at the annual conference, fostering cross-institutional and international partnerships across the region. Recipients also serve as ABNA ambassadors, promoting the Association's mission and providing feedback that informs future initiatives, further reinforcing ABNA's leadership in biobanking collaboration and professional development across the Asia-Pacific region. To capture the program's impact, recipients are asked to report measurable outcomes such as new collaborations, post-conference knowledge-sharing activities, and engagement within their institutions or ABNA's Special Interest Groups. These metrics are vital in demonstrating the Travel Grant's contribution to regional capacity building, connectivity, and long-term engagement.

In parallel, ABNA continues to play a pivotal role in empowering research innovations by shaping the national biobanking

landscape. Collaborating with CSIRO and Phenomics Australia, ABNA is developing an economic analysis report to inform government policy and support the inclusion of biobanking and collections in the National Research Infrastructure Roadmap. Through these efforts, ABNA is positioning itself as the national body representing biobanking and biospecimen science, ensuring the value of this critical research infrastructure is recognised and supported at the highest level.

Conclusion: ABNA plays a central role in guiding research innovation by providing a forum for education and knowledge sharing to promote the provision of accessible and ethically managed high-quality biospecimens and data which form the backbone of cutting-edge science. ABNA strives to expand its outreach efforts within the region to foster collaboration across our community. Together, these efforts reinforce ABNA's role as a leading advocate for biobanking collaboration and professional development nationally and internationally.

PB-03 Balancing Scientific Utilization and Biosafety: Management Protocols for a Hospital-Based MDR Bacteria & Bacteriophage Resource Biobank

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Statement of the problem: Infectious disease specimens are fundamental for epidemiology, pathogenesis, and therapeutic research; so their preservation is critical for public health and scientific innovation. However, building key resource biobanks faces major challenges. A core dilemma is balancing strict biosafety protocols for high-pathogenicity specimens with the need for efficient scientific use.

Proposed solution: To address these challenges, a scientific, systematic, scalable preservation-management system is essential. The biobank of Shanghai Public Health Clinical Center was established in 2023 in accordance with the principles of "top-level design, overall planning, joint construction and sharing". Specifically, the multidrug-resistant (MDR) bacteria and bacteriophage resource biobank at our hospital was developed by using a hybrid strategy that integrates conventional low-temperature refrigerators and pneumatic low-temperature storage devices. (1) Storage strategy: conventional equipment is employed for the identification and maintenance of bacterial/viral strains, whereas pneumatic devices handle small-batch, high-frequency retrieval. Automated picking, low-temperature pneumatic transport, and synchronized data management boost efficiency and reduce human error. (2) Strain backup: a multi-site, multi-device protocol uses aliquot preservation for critical strains to maximize biological activity retention. (3) Repository management: a full-process digital system uses standardized coding, real-time database updates, and strict access controls—ensuring traceability (accession → QC → storage → distribution). (4) Biosafety: biosafety level 2 containment is mandatory for high-risk specimens. Closed automated systems control aerosols and reduce occupational exposure.

Conclusions: These measures enhance our biobank's microbial resource utility while upholding biosafety. Future efforts should prioritize standardizing protocols, deepening automation, and fostering cross-institutional collaboration to fully leverage these specimens in combating infectious diseases and advancing life sciences.

PB-04 Biobank Performance and Research Alignment at Fudan University Shanghai Cancer Center: A Five-Year Institutional Audit (2020–2024)

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Background: To evaluate the operational efficiency and service role of the Fudan University Shanghai Cancer Center (FUSCC) Biobank using five years of sample collection and use data, providing evidence for refined management and strategic adjustments to collection priorities.

Methods: Single-center retrospective audit at FUSCC of department-level sample inventory ("in"), sample distribution ("out"), and research activity (2020–2024). Primary indicators were totals of in/out and usage rate (out/in); we also summarized distribution requests and NSFC-funded projects (grants). Analyses were descriptive.

Results:

Totals: 263,424 incoming and 63,970 outgoing samples (usage rate 24.28%).

Inventory leaders: Breast Surgery, Colorectal Surgery, and Urology contributed the largest inflows, reflecting strong clinical accrual and engagement with the biobank.

Colorectal Surgery: Usage rate 54.02%, 29 NSFC projects, 66 distribution requests—evidence of high demand and active utilization.

Pancreatic Surgery: Usage rate 20.62% yet 42 NSFC projects—substantial research activity relative to distribution volume, suggesting potential value in targeted expansion of collection.

Urology: 35,754 samples in inventory; usage rate 30.29%—large stock with room to improve circulation efficiency and reduce potential idle capacity.

Conclusion: This FUSCC audit reveals imbalances between inventory accumulation and downstream use. Portfolio optimization should (i) prioritize high-demand, high-output disease areas, (ii) strengthen targeted matchmaking and study-design support to raise utilization, and (iii) increase proactive outreach to convert inventory into funded research. Future work will incorporate additional KPIs (e.g., time-to-distribution, project outcomes) and multivariable analyses to align FUSCC's collection strategy with scientific return.

PB-05 Building a TCM-Featured, AI-powered Biobank by Integrating Samples and Digital Data as Bioresources for Standardized Research and Clinical Translation

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Background: Traditional Chinese Medicine (TCM) has been practiced for thousands of years across Asia. Its therapeutic value, especially acupuncture, is recognized worldwide. As TCM expands globally, standardized resources are needed to support evidence-based research and clinical use. In 2025, the

Chinese government launched three National Medical Centers in the TCM field, with our institution among them. As a core component, the Bioresource Research Institute will occupy 5,000 m^2 and is designed to be the largest biobank in China. This platform will manage both biological samples and digital data as bioresources, creating a foundation for cutting-edge research.

Statement of the Problem: Current biobanks emphasize Western medicine datasets and conventional samples. TCM-specific resources, such as tongue coating or sweat, are rarely standardized. The four diagnostic methods (inspection, listening, inquiry, and palpation) remain subjective. This leads to variable results between doctors, reducing reproducibility. More importantly, TCM syndromes are among the earliest biological indicators. If captured systematically and linked with clinical outcomes, they could support early prevention and proactive intervention. At present, no national framework integrates syndromes, biosamples, outcomes, and digital data. This gap limits multi-center collaboration, AI-driven analysis, and global recognition of TCM.

Proposed Solution: We propose building a TCM-featured biobank and integrated data platform as part of the National Medical Center. The design rests on several priorities. First, we will objectify and standardize the four-diagnostics and TCM-specific samples, aligned with national and international standards. Second, we will treat digital data as bioresources, linking clinical records, syndromes, imaging, and omics with biological samples in a single case-centered platform. Third, the AI-powered management system will support structured diagnostic information, data inquiry, visualization, long-term follow-up, medical image interpretation, and personalized precision medicine.

Conclusion: The Bioresource Research Institute will be the largest TCM biobank in China. By treating digital data as bioresources, it will enable standardized datasets. Linking syndromes with outcomes will transform early biological indicators into tools for prevention and treatment. The project will facilitate translational medicine and global recognition of TCM.

PB-06 Construction and Management of Women and Children Biobank in Fujian Province, China

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The construction of women and children biobank has a great significance to the analysis and research of women and child-related diseases. In line with its strategic development goals, the biobank at Fujian Maternity and Child Health Hospital is developing a regional biobank designed to cover full life circle, from gestation to developmental stages (infancy, childhood, adolescence) and into adulthood, in order to attract more exchanges and cooperation between units, and jointly contribute to the prevention and treatment of women and children-related diseases, especially major characteristic diseases.

The biobank integrates natural pregnancy, assisted reproduction, and major disease resources to build a women and children's resource platform with Fujian regional characteristics. The biobank has collected about 60,000 samples (over 1.3 million tubes) from 13 projects, including birth and gynecological tumor cohorts, covering blood, urine, cord blood, placenta, and tumor tissues. The platform has supported 6 software copyrights, 10 patent applications (3 authorized), and contributed to 6 local/group standards. Over 100 related articles have been published in journals such as "npj Digital Medicine" and "Cell Death & Disease". The biobank also led the establishment of two specialized committees at both the national and provincial levels and conducted more than 10 training sessions. It supported various projects and multiple provincial and ministerial platforms, including the Ministry of Industry and Information Technology's Real-World Data Application Platform, Fujian Provincial Clinical Medical Research Center, Fujian Provincial Engineering Research Center, Fujian-Taiwan Cooperation Base, and Provincial Key Clinical Specialty projects.

PB-07 Construction of Biobank in Xi'an People's Hospital (Xi'an Fourth Hospital)

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Statement of the Problem: Biobanks with rapid growth still face numerous challenges. These problems can be categorized into four primary domains: ethical and legal governance, quality and standardization, data integration and management, and financial sustainability.

Proposed Solution: The Biobank of Xi'an People's Hospital (Xi'an Fourth Hospital) has established a quality management system in compliance with the ISO 20387 2018. Biobank is operating under the supervision of the Human Genetic Resources Management Office and review by the Academic Committee and Ethics Committee. The biobank operates under a model of broad consent, allowing donated samples to be used in a wide range of future biomedical studies, subject to ethical approval.

Our hospital is a comprehensive medical institution renowned in Northwest China for its distinct specialties in Ophthalmology and Gynecology, which provides a rich source of unique and valuable clinical samples. The Biobank systematically collects these distinctive samples according to strict SOPs to capitalize on this clinical advantage.

The biobank prioritizes sample utilization, adheres to legal and ethical standards, drives scientific research, facilitates translational outcomes, and promotes collaborative benefits. Through the development of an integrated "three-library system" comprising the Wet Bank, Dry Bank, and Live Bank, the biobank has established a digital intelligent system that integrates biological sample management, data information management, and multi-omics data analysis, driving sustainable development in sample science through data-driven methodologies. For data management, the guiding principle must make data Findable, Accessible, Interoperable, and Reusable. Currently, biobank is in the nascent stages of development and remains heavily reliant on specialized funding from host institutions, such as hospital-specific grants or direct subsidies, to cover initial setup and core operational costs.

Conclusion: The biobank of Xi'an People's Hospital (Xi'an Fourth Hospital) represents a crucial nexus in the rapid translation from biological samples to clinical products, facilitating the advancement of personalized precision medicine. As an essential research infrastructure, the biobank significantly contributes to disease prediction and prevention, early screening and diagnosis, and the development of personalized therapeutic strategies.

PB-09 Harmonization Process of the Fiocruz Biobank Network

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Background: The Fiocruz Biobank Network (RFBB) was created in 2015 by the Oswaldo Cruz Foundation (Fiocruz) to serve as a collaborative public service providing the scientific community with access to high-quality, ethically managed human biological materials and associated data, supporting both current and future health research. The RFBB comprises ten biobanks, five already registered and five under development. RFBB aims to harmonize functional strategies, operational and technical procedures derived from ethical and legal requirements, ensuring compatibility and interoperability among biobanks without enforcing full uniformity. This approach allows flexible integration of operational practices while respecting the specific characteristics of each biobank.

Methods: The harmonization process is coordinated by the Working Group (WG) on Standard Operating Procedure (SOP) Harmonization, created in 2023. The WG includes curators, technical staff, Steering Committee members, and quality management specialists. The methodology involves mapping existing practices, analyzing national and international regulations, consulting SOPs from Fiocruz's technical-scientific units and other biobank networks, and defining priorities for document development. This process is supported by the RFBB Quality Management team.

Results: The WG has developed harmonized models of SOPs, manuals, forms, and workflows applicable to all RFBB biobanks. To date, more than 25 documents have been completed, covering key operational areas such as sample reception, transportation, equipment management, sample collection, and retrieval processes. Key challenges include differences in biobank's quality management systems, document control tools, and operational complexity levels, as well as the time required for review and validation, and the need for specialized expertise from other institutional teams.

Conclusion: The RFBB experience demonstrates that harmonizing procedures within a biobank network is feasible and strategic for strengthening quality, governance, and scientific reliability. Despite challenges, the process has promoted institutional integration, standardization of practices, and a culture of continuous quality improvement, establishing a strong foundation for network expansion and consolidating Fiocruz as a national reference in ethical and technical biobank management.

PB-10 Impact of Alcohol Type on FFPE Block Quality for Immunohistochemistry

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Background: The quality of formalin-fixed paraffin-embedded (FFPE) tissue blocks is critical for downstream immunohistochemistry (IHC) analysis, especially in biobanking and diagnostic workflows. The type of alcohol used during tissue dehydration—absolute Alcohol or isopropyl alcohol—may influence antigen preservation and staining quality, yet comparative data is limited.

Objective: To assess the impact of absolute alcohol versus isopropyl alcohol on IHC performance in (FFPE) blocks, using estrogen receptor (ER) and progesterone receptor (PR) and Her2 status as biomarkers.

Methods: Tissue samples from 10–20 patients were bisected longitudinally to ensure internal control and standardization. One-half of each sample was processed using absolute ethanol, and the other half with isopropyl alcohol during the dehydration step of FFPE blocks preparation. All blocks underwent standardized IHC staining for ER, PR and Her2 markers. The staining intensity and distribution were evaluated using the Immunoreactive Score (IRS), interpreted by two independent pathologists blinded to the processing method. Tissues from patients with known ER, PR, and HER2 status were included as controls.

Results: Preliminary observations suggest that blocks processed with absolute alcohol demonstrated stronger nuclear staining and reduced background noise compared to those processed with isopropyl alcohol. Variability in staining intensity and antigen retrieval was noted, with implications for diagnostic accuracy. Statistical analysis of IRS scores is ongoing.

Conclusion: The type of alcohol used in FFPE block preparation may significantly influence IHC outcomes. Absolute alcohol appears to offer better antigen preservation for ER/PR and Her2 detection. These findings support the need for standardized dehydration protocols in bio banking and pathology labs.

Impact: This study contributes to optimizing tissue processing protocols, improving biomarker reliability, and enhancing the reproducibility of IHC-based diagnostics in biobank-supported research.

PB-11 The Biobank of Shenzhen Third People's Hospital

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The Biobank of Shenzhen Third People's Hospital (BSTPH), founded in 2018, functions as a crucial resource facilitating the progress of medical science and the improvement of clinical care. It has constructed comprehensive fundamental frameworks that include organizational structures, biopreservation management systems, and standardized operating procedures.

In 2022, BSTPH procured the administrative license for the preservation of human genetic resources from the China National Center for Biotechnology Development. This certification emphasizes BSTPH's adherence to ethical norms and regulatory directives, enhancing its credibility as a reliable repository for genetic and translational research. BSTPH encompasses a storage area of approximately 600 square meters. Its core infrastructure consists of forty ultra - low temperature freezers, eight vapor - phase liquid nitrogen tanks, thirty - six liquid - phase liquid nitrogen tanks, one automated freezer system, and one automated liquid nitrogen storage system.

Collectively, these facilities provide a total storage capacity of up to 6 million samples.

The principal specimen type stored is peripheral blood, which undergoes processing and cryopreservation in the forms of plasma and peripheral blood mononuclear cells (PBMCs). The current sample collections of BSTPH primarily concentrate on infectious diseases, encompassing the following:

Follow - up cohorts of COVID - 19 convalescents;

Follow - up cohorts of patients suffering from liver diseases, such as cirrhosis and acute/chronic hepatitis;

Follow - up cohorts of confirmed tuberculosis patients and individuals with latent tuberculosis infection;

Follow - up cohorts of HIV - infected patients;

Follow - up cohorts of MPXV - infected patients;

Patients with other conditions, including colorectal cancer and lymphoma.

Furthermore, samples obtained from healthy donors are preserved as crucial controls for comparative research.

All samples have obtained ethical approval and are accompanied by comprehensive clinical data and follow - up information. We sincerely invite domestic and international research institutions, biomedical researchers, and clinical teams to participate in sample - sharing collaborations.

PB-12 The Children's Cancer Centre Biobank – A Catalyst for Collaboration

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Background: Childhood cancers are rare and biologically diverse which necessitates large-scale, collaborative international research efforts to make meaningful advances in diagnosis, treatment, and survival. The Children's Cancer Centre (CCC) Biobank serves as a catalyst for this collaboration by facilitating the ethical collection, processing, and distribution of high-quality, clinically annotated biospecimens from paediatric cancer patients at The Royal Children's Hospital in Melbourne, Australia. The CCC Biobank proactively supports research projects including genomics, immunotherapy, pharmacogenomics and rare tumour biology that would be impossible without this dedicated infrastructure.

Methods: In 2013, philanthropic funding provided by The Royal Children's Hospital Foundation enabled key stakeholders to unite and establish the CCC Biobank. The objective was to create a world-class open access research resource for investigators studying childhood and adolescent/young adult cancer.

Results: Over the past 12 years, approximately 2,300 participants offered their consent to donate their specimens and health information across the span of their treatment resulting in a rich collection of approximately 23,000 biospecimens reflecting the multiple types of childhood cancer. Following approval by the governing Access and Oversight Committee, specimens have been distributed towards 71 translational research projects in Australia and internationally, yielding 40 publications. 56% of participants have had one or more of their specimens distributed for translational research and over 25 clinical trials driven by genomic analysis have been supported. Impact is further amplified by engagement with national and international associations increasing visibility to promote biospecimen utilisation.

Conclusions: The CCC Biobank is a catalyst for collaboration which continues to flourish in a rapidly evolving research landscape. By integrating clinical and molecular annotation with biospecimen access, the CCC Biobank bridges the gap between clinical care and research, supporting local innovation while contributing to global research efforts. The CCC Biobank is a dynamic enabler of discovery, uniting clinicians, researchers, patients and their families in a shared vision to improve outcomes for children with cancer.

PB-13 The Construction and Application of TianTan Biobanks in Precision Medicine Research for Cerebrovascular Diseases

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Objective: This study explores establishing standards for biological sample collection, processing, and preservation in multicenter cerebrovascular disease research, based on blood sample subgroup experience from cerebrovascular clinical research at Beijing Tiantan Hospital. It aims to ensure high-quality samples for cerebrovascular precision medicine research.

Methods:

Develop biological sample collection standards for multicenter cerebrovascular clinical research via top-level design.

Set up a sample management team for multicenter projects, with dedicated roles (technical, quality control, logistics) and clear responsibilities.

Formulate SOPs for sample collection, processing, and transportation; train sub-center technicians via lectures, documents, and videos.

Procure national standard-compliant reagents/consumables and distribute them uniformly to sub-centers.

Plan sample transportation and entrust professional cold-chain companies.

Use clinical data management system and sample management system to match samples with clinical data and enable precise location management.

Results: A comprehensive multicenter cerebrovascular research biobank was established through system building, personnel training, and SOP standardization. Guided by the biobank quality management system, standardized management (SOPs, training, quality control, record-keeping) ensures sample quality for downstream research.

The collected biological samples have been applied to the multi-omics analysis of cerebrovascular diseases. Among them, the results of CYP2C19 gene polymorphism study based on CHANCE study were published in JAMA, and the CHANCE2 study, the first pharmacogenomic-driven phase 3 clinical trial of cerebrovascular disease, was launched. It was confirmed that rapid screening of CYP2C19 genotype can guide the precise and individualized treatment of clinical antiplatelet drugs. This means that the treatment of cerebrovascular diseases has entered a new era of "precise double antibodies".

Conclusion: A biobank with unified standards and strict quality control promotes cerebrovascular precision medicine research.

PB-14 Biobank Network in Japan to Accelerate Progress Towards Genomic Medicine

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In Japan, the Government has drawn up a health and medical strategy for genomic medicine as the national growth strategy, and research and development to realize genomic medicine including drug development utilizing biobanks is being promoted. A programme for the utilization of biobanks called B-cure (Biobank - Construction and Utilization biobank for genomic medicine Realization) is currently underway to realize genomic medicine. In the B-cure programme, we developed a network of 14 major biobanks and a system for utilizing biobank samples and data that will facilitate research and development of genomic medicine in Japan. We then developed a biobank cross search system on biospecimen and data stored in our biobank network. Research institutions can find biospecimens and data they need for their own genomic medicine research and development. To implement a cross-search service for biospecimens and data, we standardized the metadata of biospecimen and data. Now our biobank network stores 1,933,000 biospecimen and 330,000 molecular data provided by 700,000 donors. We also setup the web-based coordination system of fast access to biospecimen and data to meet the requests by academic/commercial users using the biobank cross-search system. Our biobank network provides essential infrastructures for different types of health research including basic medical science to accelerate progress towards personalized medicine. We are addressing drawing up an ecosystem of stakeholders to realize personalized medicine and discussing how to maintain and develop this infrastructure along with the health and health care strategy in Japan.

Biobanking Structures & Cross-sector Partnerships

PC-01 Advancing Reference Standards and Countermeasures for Pandemic Response: Development of Lessons Learned from the Biospecimen Sourcing Initiative

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High-quality reagents, reference materials, and standards are crucial for developing effective diagnostics, vaccines, and therapeutics by supporting research on biomarker validation, diagnostic innovation, and vaccine target identification. These resources are needed at the outset of product development but can be slow to source and verify, especially for novel pathogens that affect vulnerable populations, increasing the urgency of providing reference materials for product development. Safety, security, legal issues, mistrust, and limited cooperation can delay the process from disease detection to critical diagnostics and vaccinations. To address this, a pre-positioned global resource is needed with clear procedures to efficiently source, verify, archive, and distribute biospecimens in response to new diseases.

Supported by CEPI, the Biospecimen Sourcing Initiative (BSI) is designed to address this need by establishing an efficient system for the rapid deployment of biospecimen collection. The initiative emphasizes transparent procedures, collaboration among partners, and fosters respectful relationships with communities that are engaged early and throughout the biobanking process. Its main goal is to facilitate the development of reference standards and countermeasures that support the 100 Days Mission. To develop the BSI, subject matter experts, key stakeholders, and thought leaders were engaged to design a governance framework that defined guiding principles and standards for the repository network. A library of guidance documents was developed and validated as a global resource by leveraging existing materials and creating new ones as needed, that detail processes and procedures to operationalize the BSI. Best practices for appropriate and applicable quality systems were defined to meet key standards for the use of biospecimens in product development. Finally, setup of the BSI was repeatedly evaluated through simulated scenarios and user insight gathering, to continually improve along the way.

At ISBER 2026, the BSI team will share findings from the development of the document library and lessons learned from the simulated evaluations. This research will contribute to having rapidly deployable specimen collection systems that can be quickly utilized and work alongside existing networks. It will also strengthen regional preparedness for vaccines and diagnostics development, ultimately advancing scientific progress and supporting equitable decision making.

PC-02 A Lean Biobank for Pandemic Response: Maximizing Research Utility via Case-Ascertained Enrollment in the VALIDO Study

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Background: Maximizing the scientific utility of collected specimens is a core challenge in biobanking. Public health crises demand agile, resource-optimized models that deliver rapid

results. The VALIDO (Study to validate the use of saliva in COVID-19 diagnosis in Costa Rica) study was designed as a lean, purpose-built biobank in Costa Rica to address these challenges by maximizing research utility per participant rather than focusing on cohort scale.

Methods: We employed a case-ascertained strategy, enrolling 178 adults with a confirmed RT-qPCR result from the previous 5 days yielding 4,486 aliquots from paired nasopharyngeal (NPS) and saliva samples (with and without preservation medium), prioritizing high reuse. Batched analyses and a single-test result adjudication were implemented to minimize freeze-thaw events and preserve the primary resource for high-reuse. Our lab competency was verified against a certified lab using cohort samples, achieving 100% agreement.

Results: The enrollment strategy proved highly efficient, achieving an enrollment-to-positive ratio of 1.78. The biobank enabled direct validation of saliva without medium (82.8% sensitivity, 98.7% specificity vs. NPS), confirmed sample stability across various storage conditions, and validated a 1:5 pooling strategy (PPA 87.5%). This single cohort yielded multiple national-level outcomes: it secured Ministry of Health authorization for Costa Rica's first saliva-based screening test, optimized logistics for the large RESPIRA population cohort, enabled non-invasive staff testing for operational continuity, and validated multiple locally developed COVID-19 assays.

Conclusion: Through targeted enrollment, rigorous QC, and explicit multipurpose planning, VALIDO demonstrates the power of a lean biobank, creating a high-impact national resource. A large portion of the collection remains available for future studies. This model provides a reproducible playbook, reinforcing that research output per participant—not mere cohort size—is a core tenet of efficient and sustainable biobanking, especially in resource-limited settings.

PC-03 Balancing Value Realization and Risk Governance: A Fine-Graded Management Framework for Biospecimen

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Objective: To enhance the management of biospecimen by ensuring biosafety and improving the utilization of samples and associated data.

Methods: We developed a two-dimensional "risk–value" tiered management model at a Grade-A tertiary hospital biobank in China. Analyzing 370,000 specimens managed between 2017 and 2025, we classified specimens into four tiers based on clinical research value and biosafety risk: Level I (high-value, high-risk), Level II (high-value, low-risk), Level III (low-value, high-risk), and Level IV (low-value, low-risk).

Results: Specimens were distributed as follows: Level I (15%), Level II (46%), Level III (10%), and Level IV (29%). The model prevented safety incidents such as leakage or misidentification, improved processing efficiency for high-value specimens (Levels I–II), and reduced retrieval time for Level IV specimens. Key innovations included value-based assessment criteria, a full-process electronic traceability system, a clinical-research collaboration mechanism, and a tiered approval pathway.

Conclusion: This study provides a scalable framework for improving the safety and utility of biobanking in large Chinese hospitals. It is recommended that this approach be promoted in medical institutions involved in the collection, preservation, and utilization of biospecimen.

PC-04 Biobank Driven Approach to Elucidation of Health and Disease Drivers in African Populations: BioAtlas Case Study

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Statement of the Problem: African populations remain severely underrepresented in global biomedical research, despite possessing the world's highest genomic diversity and a growing burden of both communicable and non-communicable diseases. Limited infrastructure for standardized biospecimen collection, data integration, and long-term storage has hindered Africa's participation in global discovery and precision medicine efforts.

Proposed Solution: BioVana Research established the BioAtlas Study, a multi-country, pan-African initiative designed to elucidate the biological, environmental, and social determinants of health and disease in African populations. The study integrates genomics, proteomics, metabolomics, clinical, and environmental data through a federated biobanking framework aligned with ISBER Best Practices and ISO 20387 standards. The pilot phase involves 500 participants recruited across seven sites in 2 countries (Nigeria and Kenya), representing diverse disease and control cohorts. Following validation, Phase 2 will expand to up to 25,000 participants across representative African countries, capturing continental genetic and environmental diversity. Biospecimens include blood, plasma, buffy coat, saliva, urine, stool, and tissue, processed within standardized workflows for long-term storage and linked through a secure Biobank Information Management System (BIMS). Multi-omics assays, including DNA SNP genotyping, 30x whole-genome sequencing, and Olink Explore 384 proteomic profiling, will generate harmonized datasets for cross-disease analyses.

Conclusions: The BioAtlas Study demonstrates a scalable model for ethical, high-quality, and sustainable biospecimen collection across Africa, while building local capacity for multi-omics research and data governance. The study will foster equitable global collaborations and support data-driven discovery, thus positioning African biobanks as integral contributors to global precision medicine. BioAtlas not only addresses the gaps in representation but also establishes a foundation for future clinical trials, population health surveillance, and innovation in disease prevention and treatment.

PC-06 Biosafety Management of Infectious Samples in a Comprehensive Hospital Biobank

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Background: Currently there are many BioBanks were built in the comprehensive hospital, but the issues of how to deal with

infectious specimens to ensure biosafety become very important. The samples are divided into two types, unknown infectious samples and known infectious samples. With the increase of scientific research, these two sample volumes are increasing sharply. Facing this situation, it is imperative to establish a feasible sample management system.

Objective: This study aimed to develop and implement a systematic biosafety management system, centered on the core principle of risk stratification, within the biobank of a major comprehensive hospital.

Methods: Based on the practices at Huashan Hospital's biobank, we established a management method centered on risk stratification. We distinguished the known infections samples with unknown infectious samples from the beginning of sample collection to sample storage, SOP and sample storage space completely different, but we centralize the management system by using the same software, we collaborated with China Power North Information Technology Development Co, Ltd (ZDBX) to develop a project-oriented BioBank management system to make sure we can unified manage samples data and collection, processing, storing them separately.

Results: Implementation of this system enabled refined and systematic management of infectious samples. The results demonstrated a significant enhancement in biosafety management efficacy, with no biosafety incidents recorded since its introduction. The unified system ensured data integrity and traceability, while strict physical zoning effectively safeguarded the purity of non-infectious samples, thereby providing high-quality and reliable sample resources for downstream scientific research.

Conclusion: The system we established entered on risk stratification with rigid safety via the sample physical isolation and specific SOP for handling, meanwhile the system having the flexible management via a unified management method. This practice showed effectiveness in significantly mitigating operational risks within a comprehensive hospital biobank. This model not only ensures biosafety but also enhances operational efficiency and sample quality, establishing a solid foundation for high-level scientific research.

PC-07 Bridging the Gap: Established Biobanks as Catalysts for Emerging Initiatives

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Statement of the Problem: The establishment of digital biobanks is vital for advancing region-specific research, addressing local health challenges, and supporting evidence-based strategies to reduce global health disparities. Although most of the world's population lives in LMICs, research infrastructure and resources remain concentrated in high-income countries, limiting understanding of LMIC health priorities. Establishing biobanks in these regions is essential to bridge this gap. However, their development is constrained by limited funding, expertise, awareness, and policy support, leading to unsustainable infrastructure. A major barrier to progress is the shortage of high-quality biospecimens and data accessible to researchers.

Proposed Solutions: To overcome these challenges, emerging biobanks can learn from established models to build resilient and impactful systems. The Pakistan Kidney and Liver Institute & Research Center (PKLI&RC), the first public-sector facility in Pakistan and South Asia to receive JCI accreditation, specializes in kidney and liver diseases, along with cancer and infectious disease management. PKLI&RC is developing the region's first large-scale biobank, guided by ISBER Best Practices and in collaboration with Qatar Biobank. Acting as an advisor, Qatar Biobank shared insights on resource planning, ethics, quality management, data collection, and sustainability. A five-day visit to their Doha facility deepened understanding of operational and developmental challenges, helping refine PKLI&RC's implementation plan. This collaboration continues through meetings and document exchanges to strengthen policies and explore joint research initiatives. Established biobanks play a critical role in guiding emerging ones, especially in LMICs with limited infrastructure. Through site visits, training, and shared best practices, they help new biobanks meet international standards efficiently and cost-effectively. Such knowledge exchange promotes data harmonization, enabling integration into global research networks and fostering inclusive, evidence-based health solutions.

Conclusion: Sustainable progress depends on collaboration with research institutions and the pharmaceutical and biotechnology sectors to ensure funding and growth. Established biobanks can mentor emerging facilities, align them with global health priorities, and evolve into regional hubs that advance scientific discovery and equitable global representation.

PC-08 Cedars-Sinai OncoBiobank as Shared Resource: Challenges and Opportunities

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Background: The role of cancer biobanks is evolving from simple sample repositories to dynamic integrated research centers critical for advancing cancer research and clinical innovation. This transformation requires closer collaboration with healthcare institutions, standardized protocols to ensure interoperability, and a study-driven, patient-centered approach. However, developing and maintaining such shared resources demands a multidisciplinary network and involves significant operational, financial, and logistical challenges. This abstract explores these complexities to propose a strategic foresight framework to address them.

Methods: A comprehensive SWOT (Strengths, Weaknesses, Opportunities, Threats) and TOWS analysis was conducted to evaluate internal and external factors to develop actionable strategies. This assessment identified key capabilities and challenges, providing a framework for sustainable growth and long-term

impact. The findings formed the foundation for developing an innovative operational model for cancer biobanking.

Results: The SWOT analysis highlighted key strengths, including strong leadership, a skilled multidisciplinary team, and a clear vision. Identified opportunities include: (1) adopting standard data models (e.g., OMOP/CDM) and FAIR-compliant data infrastructures; (2) embedding workflows that directly link biospecimen use to clinical trials and translational endpoints; (3) providing computational analysis platforms (e.g., AI, digital twin simulation) to researchers; and (4) aligning governance and stakeholder frameworks to facilitate data reuse and clinical translation. The TOWS analysis emphasized leveraging leadership to secure global partnerships (SO), diversifying funding through public-private initiatives to reduce costs (WO), and applying expertise to uphold high data quality standards (ST).

Conclusion: OncoBiobank Shared Resource is positioned to serve as a forward-looking, integrated research hub combining high-quality biospecimens, comprehensive datasets, and robust analytical pipelines into a single service. A study-driven, research focused approach that provides ready access to computational tools is essential to success. By proactively addressing the challenges identified, OncoBiobank has the potential to transform into an indispensable shared resource that bridges healthcare and research, accelerating both scientific discovery and the translation of innovations into clinical practice.

PC-09 From Biological Memory to the Science of the Future: The Legacy of the IRESSEF Biobank

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Background: The IRESSEF Biobank holds one of the most valuable biological collections in West Africa, built through decades of clinical sample preservation prior to its official establishment in 2016.

Objective: To describe the evolution, infrastructure, and contribution of the IRESSEF Biobank to infectious disease research and outbreak preparedness.

Methods: A descriptive analysis of historical and recent collections. Legacy samples were transferred to new-generation freezers with B-Connected remote monitoring and full traceability via the BIKLAB barcode system. Quality management standards ensure biosafety and reproducibility.

Results: The biobank stores ~350,000 specimens including serum, plasma, PBMCs, DNA/RNA, DBS, and swabs from diverse populations involved in studies on HIV, hepatitis, syphilis, tuberculosis, COVID-19, dengue, and chikungunya. Continuous monitoring and redundant systems ensure integrity and sustainability.

Conclusion: The IRESSEF Biobank has transformed legacy samples into a strategic African resource, empowering modern biomedical research and global health security.

PC-11 From Vision to Reality: Challenges in Developing Biobanking Capacity in Pakistan

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Statement of the problem: Establishing a biobank in LMICs presents both an exceptional opportunity and a complex challenge. Biobanks serve as critical infrastructures for advancing biomedical research, precision medicine, and public health interventions; however, their successful implementation in resource-limited settings requires careful strategic planning, sustained investment, and cross-sectoral collaboration. Several systemic barriers impede the establishment and sustainability of biobanks in Pakistan. These include limited awareness and understanding among healthcare professionals, policymakers, and the general public regarding the purpose, ethical principles, and long-term benefits of biobanking. There is also a pronounced shortage of trained personnel skilled in biospecimen collection, processing, quality assurance, and data management in accordance with international standards. Furthermore, governance and ethical oversight frameworks are underdeveloped, fragmented, or inconsistently implemented, creating uncertainty in operational and regulatory compliance. Operational constraints further compound these challenges. Administrative and procurement processes are frequently prolonged due to rigid policies and bureaucratic inefficiencies, delaying infrastructure development and equipment acquisition.

Proposed Solutions: To address these challenges, we adopted a structured and collaborative approach toward establishing a sustainable biobank facility. Our team actively engaged with international biobanking networks, including ISBER and CTRNet, to learn and implement global best practices in biospecimen management, quality assurance, and ethical governance. A comprehensive biospecimen and data sharing policy has been developed to ensure compliance with international standards and promote transparency and collaboration in research.

We have also established a formal collaboration with Qatar Precision Health Institute, Qatar Biobank to facilitate knowledge exchange and technical support. Despite administrative and procurement hurdles, we have successfully initiated the acquisition of essential equipment and infrastructure for the biobank facility; an effort that has taken nearly two years to reach the current stage.

Conclusion: Our experience demonstrates that with global collaboration, policy development, and perseverance, sustainable biobanking in LMICs is achievable despite systemic and operational challenges.

PC-13 Strengthening Thailand's Cancer Research Ecosystem: A Decade of the Ramathibodi Comprehensive Tumor Biobank

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Cancer remains the leading cause of death in Thailand. Molecular research has become a key driver of advances in targeted therapy, liquid biopsy, and immuno-oncology,

thereby improving cancer diagnosis and treatment. Such research requires high-quality biospecimens and associated clinical data; however, these resources have been limited in Thailand. To address this need, the Ramathibodi Comprehensive Tumor Biobank (RCTB) was established in 2012 under the Ramathibodi Comprehensive Cancer Center (RCCC), Faculty of Medicine Ramathibodi Hospital, Mahidol University—the first centrally managed biobank in the country. RCTB systematically collects and stores fresh frozen tumor tissues, blood, and related biospecimens linked to de-identified clinical data, in compliance with the Thai Personal Data Protection Act (PDPA). Its objectives include supporting molecular cancer research, fostering multidisciplinary collaboration, advancing postgraduate education in translational medicine, and developing patient-derived organoids (PDOs) for drug screening and in-depth research. Currently, RCTB houses over 45,000 biospecimens from more than 4,500 cancer patients and maintains a unique PDO library for cancers such as breast, colorectal, retinoblastoma, and head and neck. Since 2020, RCTB has expanded into a multicenter biobank, collaborating with the National Cancer Institute and Prasat Neurological Institute. In 2022, it launched the Thailand Biobanking Network, partnering with regional medical centers nationwide to promote biobanking knowledge and capacity building. In 2024, RCTB became the first biobank in Thailand to achieve ISO 20387:2018 accreditation, underscoring its commitment to biospecimen quality and ethical governance. It also developed the patented Ramathibodi Tumor Biobank Software to support multicenter operations and clinical trial specimen management. In collaboration with the Division of Proficiency Testing, Department of Medical Sciences, Ministry of Public Health, RCTB initiated Thailand's first pilot study for ISO 17043-accredited human biospecimen proficiency testing, establishing national standards for biospecimen quality. Through these initiatives, RCTB advances cancer research, education, and clinical translation while promoting national self-sustainability, research excellence, and international collaboration in precision oncology.

PC-14 BCNet: The Way Forward— Education, Digitalisation and Regional Collaboration for a Resilient Global Biobanking Ecosystem

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Statement of the Problem: The global biobanking landscape, as it expands becomes increasingly heterogeneous, with disparities in digital maturity, operational standards, and access to expertise across regions. While BCNet has played a critical role in capacity building and knowledge exchange over the last decade, emerging regional biobanking alliances face persistent challenges in interoperability, sustainability, and equitable participation in global research. Limited digital integration and fragmented collaboration mechanisms risk constraining the network's ability to scale impact, support emerging biobanks, and respond effectively to evolving scientific, public health, and sustainability demands.

Proposed Solution: This poster outlines a forward-looking vision for BCNet centered on two strategic priorities. First, increased digitalisation is proposed as a catalyst for enhanced connectivity, including the understanding of interoperable digital tools, through planned surveys, and the commitment to continued training and knowledge exchange, to further enhance network coordination. Second, strengthening support for emerging regional biobanking alliances is identified as essential to amplifying BCNet's global impact. Enhanced collaboration models—such as peer-to-peer mentorship, and alignment with regional priorities—can empower regional networks while reinforcing global cohesion.

Conclusions: Advancing BCNet through a strategic focus on the digital transformation and deeper engagement with emerging regional biobanking alliances offers a sustainable pathway to a more inclusive, resilient, and future-ready biobanking ecosystem. By combining digital innovation with strengthened collaboration, BCNet can continue to serve as a unifying platform that accelerates capacity building, promotes equity, and maximizes the scientific and societal value of biobanking worldwide.

PC-15 The Hong Kong Science and Technology Parks Corporation (HKSTP) Biobank and Histopathology Services (BHS): Enabling Research Through Strategic Support

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Statement of the Problem: Biotech startups and early-stage research teams often face significant operational barriers that slow down scientific progress. Limited space, funding, and manpower make it difficult to install and maintain large-scale storage infrastructure, such as liquid nitrogen tanks and ultra low-temperature storage systems, required to manage expanding sample volumes. Lack of technical guidance and expertise on biospecimen handling, staining methods, and processing workflows can delay experimentation and reduce research efficiency. These challenges create a gap between scientific ambition and practical capability.

Proposed Solution: The HKSTP BHS provides centralized, professionally managed biobanking and histopathology support designed to remove these barriers.

Storage & Infrastructure Support: BHS offers cost-effective access to high-quality storage systems, eliminating the need for startups to invest in expensive equipment or specialized laboratory spaces.

Expert Guidance & Workflow Support: BHS provides structured consultation, clear service pathways, and transparent documentation to help research teams navigate sample requirements, staining methods, and processing procedures efficiently.

Conclusion: BHS will continue to evolve as a strategic partner, ensuring users always have access to high-quality storage, testing services, and laboratory infrastructure that supports their long-term research ambitions.

Biodiversity/Environmental/Animal Repositories

PD-01 Challenges in Developing Ethics-Based and Species-Specific Frameworks for Ensuring Integrity in Live Animal Biobanking

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Statement of the Problem: In biobanking, biological materials are generally preserved in a static state, where molecular or genetic integrity is stabilized through cryopreservation or controlled environmental conditions. However, applying these conventional concepts to living animals is inherently ambiguous. Unlike cell lines or tissues, live animals are dynamic entities that undergo continuous physiological and behavioral changes, even under stable housing. Environmental fluctuations during transport can trigger physiological responses that compromise both animal integrity. Moreover, aging, stress, and social hierarchy can substantially alter the biological traits that define the original resource. Thus, the concept of 'integrity' in live animal biobanking cannot be confined to static preservation, while international standards such as ISO 20387 still lack clear definitions for the 'preservation' or 'storage' of live animal resources. These complexities highlight the need for ethics-based, species-specific frameworks to ensure the integrity and welfare of live animal resources.

Proposed Solution: Maintaining and verifying the integrity of biological materials during preservation or storage requires a systemic monitoring framework. Environmental parameters must be continuously recorded and controlled to prevent degradation or stress. For live animals, species-specific health monitoring-including regular physiological assessments, behavioral observations, and blood analyses-serves as a key indicator of biological stability. Molecular and microbiological testing can further support the validation of resource integrity throughout storage. The effectiveness of these monitoring depends on well-defined infrastructure, calibrated equipment, and competent personnel in integrity assessment. Safeguarding live animal integrity requires identifying species-specific risk factors through detailed evaluation of physiological and behavioral traits, optimal environmental conditions, and handling protocols. By integrating environmental management, biological monitoring, and quality verification, biobanks can establish a traceable system that maintains and validates the integrity of preserved resources.

Conclusions: Redefining 'preservation' or 'storage' for live animals requires a paradigm shift-from static preservation to dynamic management, reflecting the biological dynamics of living organisms. Such an approach will strengthen integrity and enhance reproducibility across biobanks.

PD-03 Veterinary Biorepository: Importance of Standardization, Biosafety, Biosecurity, and Data Management

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Veterinary Biorepositories provide biological samples that enable researchers to comprehend animal disease, create novel diagnostics and integrate molecular genetic information into livestock breeding programs. The primary functions of veterinary biorepositories include collecting, analysing, preserving, and storing biological samples as well as granting access to them. Biorepositories must guarantee proper sample and data quality, legal and ethical compliance, as well as transparent and efficient access processes. Unfortunately, the absence of standards consistent with best practices and the required infrastructure is a considerable barrier to sample reliability and reproducibility. Recently, the Agricultural Research Council-Onderstepoort Veterinary Research (ARC-OVR) established a biorepository with the aim of providing a secure facility for processing, storage and maintenance of quality biological samples within the campus. The biological samples at the ARC-OVR must be stored properly and safely with a careful view to maintaining sample integrity over lengthy periods of time (around 30 years). Hence, ARC-OVR focused on the following key areas: sample type, data recording, quality management system, biosafety, biosecurity, and personnel. Several challenges were experienced; the infrastructure does not meet the requirements due to number of security issues. Resources are limited, mainly in terms of reliable power and internet connectivity. The lifespan of freezer compressors and other equipment is shortened by power outages, and the cost of fuel to run the backup generators fluctuates, adding to the operating costs. Obtaining the required equipment and supplies for laboratories can be expensive and time-consuming as sources of funding are often constrained by shifting economic objectives. Lastly, maintaining a strict ethical division between biological materials gathered for "commercial" programs and those obtained for "open collections" is a source of concern. Biorepositories must guarantee sample and data quality, legal and ethical compliance, as well as open (where possible) and transparent access methods. A more effective approach would be to build a specialized, high quality, and access-controlled infrastructure. Such a biorepository would use the knowledge of the past decades and lessons from other biorepositories to provide well-formulated guidance, collaborate on national and international research efforts, and contribute to global security.

PD-04 Genomic Insights into Environmental *Hafnia paralvei* Antimicrobial Resistance and Virulence

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H. paralvei is increasingly recognised as an emerging opportunistic pathogen associated with invasive infections, including bacteraemia and pneumonia, particularly in immunocompromised individuals. Environmental reservoirs such as water play a critical role in the evolution and dissemination of clinically relevant resistance traits. In this study, whole-genome sequencing (WGS) was used to characterise resistance determinants and virulence factors across four isolates. Key antimicrobial resistance genes, including blaNDM and blaTEM, were identified, alongside virulence-associated genes implicated in adhesion, immune evasion, and persistence. Notably, strain S28 demonstrated unique resistance to carbapenems, suggesting distinct adaptive mechanisms potentially driven by environmental selective pressures. Substantial genetic heterogeneity was observed among the isolates, with variable susceptibility to clinically important

antibiotics, including the intrinsic colistin resistance pattern. These findings suggest the importance of systematic environmental surveillance and the biobanking of aquatic bacterial isolates to support longitudinal genomic analyses. Such efforts are essential for tracking the emergence, evolution, and dissemination of resistance and virulence traits. Further functional studies are warranted to elucidate the pathogenic roles of the identified genes. The study also supports the exploration of alternative mitigation strategies, including phage therapy and phytotherapy, to address multidrug-resistant strains. Overall, this work aligns with the One Health framework and supports the value of integrated biobanking and genomic approaches in managing emerging environmental pathogens.

Biospecimen Research, Science, and Outputs

PE-03 Comprehensive Human Cerebrospinal Fluid Proteome and Lipidome Profiles Cross Approximately 70-year Lifespan Uncover Brain Aging Trajectories and Features

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Background: Brain aging is a major risk factor for neurodegenerative diseases, making its early detection and intervention a crucial neuroprotective strategy. However, advancing targeted interventions requires deeper insight into organ-specific aging processes, especially within the central nervous system. Currently, the longitudinal dynamics of key functional molecules—proteins and lipids—in human cerebrospinal fluid (CSF) across the lifespan remain poorly characterized. To address this, we combined multi-omics profiling and machine learning to: (i) uncover temporal biological patterns and molecular signatures of brain aging, and (ii) build an organ-specific aging monitoring framework.

Methods: We collected CSF samples from 197 neurologically healthy volunteers (aged 18–96) and performed ultrahigh-resolution data-independent acquisition proteomics, generating a panoramic CSF proteome atlas spanning the lifespan (10,683 proteins quantified). Computational methods, including Lowess regression and DE-SWAN, were applied to model protein aging trajectories. Untargeted lipidomics profiling (1,953 lipids) was conducted in parallel to validate proteomic findings and establish cross-omics consistency.

Results: Proteomic analysis identified 615 proteins significantly associated with brain aging. Enrichment analysis revealed activation of neuroinflammatory pathways (e.g., IL-17 and NF-κB signaling) alongside disrupted lipid homeostasis. Longitudinal trajectory analysis uncovered seven distinct aging patterns, with most proteins showing non-linear dynamics. We identified three critical transition phases ($\sim$20, $\sim$55, and $\sim$90 years) characterized by proteome-wide fluctuations and peak differential protein expression. Lipidomics confirmed these transitions, detecting 1,391 aging-related lipids and reinforcing patterns of metabolic dysregulation.

Conclusion: We present the first multi-omics dynamic atlas of human CSF spanning nearly seven decades of life. Our study reveals non-linear trajectories of CSF proteins and lipids during aging and implicates neuroimmune activation and metabolic reprogramming as core mechanisms. We further identify three critical transition phases—early adulthood, midlife, and advanced aging—marked by peaks in homeostatic dysregulation. Crossing these thresholds may drive the pathogenesis of age-related CNS disorders.

PE-04 Effect of Cryopreservation Time on DNA Quality from Buffy Coat Samples

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Background: In biobank practice, blood samples from research initiatives and departmental reserves are typically cryopreserved for months to years. Studying the effect of cryopreserved duration on DNA quality from cryopreserved buffy coat samples is practically important.

Methods: A total of 373 buffy coat samples stored at −80°C in Tianjin Chest Hospital Biobank were randomly selected through stratified proportional sampling (1‰) based on storage duration: 64 for ≤6 months, 121 for 1 year, 121 for 2 years, 30 for 3 years, and 37 for 4 years. All samples were processed and stored following standard operating procedures and had not been subjected to freeze-thaw cycles. Genomic DNA was extracted using a magnetic bead-based method on the automated nucleic acid extraction system (Thermo Fisher). DNA concentration and purity were measured by Nanodrop 2000, and integrity was assessed by bioanalyzer (Perkin Elmer) and agarose gel electrophoresis. Data were analyzed using one-way ANOVA or Kruskal-Wallis H test with corresponding pairwise comparison. A two-sided P value < 0.05 was considered statistically significant.

Results: The median DNA concentrations for buffy coat samples cryopreserved for ≤ 6 months, 1 year, 2 years, 3 years, and 4 years were 73.41 ng/μL, 65.59 ng/μL, 65.80 ng/μL, 64.91 ng/μL, and 62.67 ng/μL, respectively. The corresponding A260/A280 ratios were 1.88±0.07, 1.87±0.10, 1.87±0.10, 1.86±0.09, and 1.84±0.10, while the genomic quality scores were 4.4±0.2, 4.3±0.1, 4.1±0.3, 4.2±0.2, and 4.1±0.3. The highest DNA concentration was observed in samples cryopreserved for ≤ 6 months. Although a slight decreasing trend in DNA yield was noted with prolonged storage time, the difference was not statistically significant (P=0.433). Cryopreservation duration had no significant impact on either DNA purity (P=0.213) or genomic quality score (P=0.264). Gel electrophoresis revealed concentrated bands without evidence of degradation or smearing.

Conclusions: DNA extracted from buffy coat samples stored at −80°C for up to 4 years remains stable in concentration, purity, and integrity. It is sufficient for downstream molecular applications and supports reproducible, reliable results. Following standard operating procedures for blood sample and avoiding freeze-thaw cycles are essential to prevent DNA degradation. These findings provide practical guidance and scientific support for biobank management and scientific research.

PE-05 Effect of Different RNA Preservatives and Delayed Preservation Time on the Quality of Tissue RNA

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High-quality RNA, essential for precise and reliable gene expression analysis, is contingent upon excellent tissue preparation and handling. As such, most Biobanks have established individual

standardized procedures for collecting diverse tissue specimens. Nevertheless, the optimal method for preserving tissues after surgical resection remains not feasible due to delayed delivery or lack of cold storage equipment. Furthermore, RNAlater has been extensively adopted for tissue preservation in biomedical research. However, few studies have systematically investigated the effects of various tissue preservation solutions and post-collection intervals on RNA integrity across different tissues.

In this study, ten mouse organs and tissues representing common human tissues in biobanks were preserved with different RNA preservatives and delayed time, then RNA was extracted and the RNA integrity were evaluated. The sectioned tissues were either flash-frozen in liquid nitrogen as control or submerged in one of three RNA preservatives—Trizol and two commercial RNAlater solutions (Invitrogen and Sigma)—and stored at room temperature (RT) for 0, 4, or 8 hours before frozen. Total RNA was extracted using the traditional Trizol method, and its integrity was quantified by the RNA Integrity Number (RIN) value obtained via microcapillary electrophoresis.

Our results demonstrate that both the delayed preservation time and use of RNA preservative significantly impact RNA integrity. Pancreatic RNA showed the poorest integrity (RIN < 5.5), while heart and ovary samples yielded high-quality RNA (RIN > 7) without any preservative at RT for 8h. For optimal results, tissues including the brain, kidney, muscle, liver, intestine, and uterus should be immersed in preservative and frozen within 8 hours to maintain the basic RNA integrity (RIN > 5.5). Whereas lung tissue stored in RNAlater has a maximum storage period of 4 hours prior to cryopreservation at RT.

Consistent with previous reports, delayed preservation time has a negative correlation with RNA integrity for most tissue species. Our results indicate that robust, high-quality RNA can be obtained from most mouse tissues held in RNA preservatives for up to 8 hours, with only minor variations observed among the different preservatives tested. This study provides guidance for the development of detailed and standardized operating procedures for various types of tissues in clinical biobanks.

PE-06 Effects of the Delay in Ischemia Timing on Protein L-Lactylation in Tumors

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Protein lysine l-lactylation are critical for understanding pathway activity and molecular pathophysiology in diseases such as cancer, offering biological insights that can inform drug discovery, diagnostic development, and therapeutic strategies. However, analyzed tissues are typically collected without strict control or documentation of ischemic time. To evaluate the impact of ischemia, we collected human colorectal cancer and hepatocellular carcinoma tissues without vascular interruption and performed quantitative proteomics and lactylomics after defined ischemic intervals. Experimental results showed that the level of pan-lactylation increases over time. Furthermore, we investigated the factors influencing the dynamics of lactylation. Our results indicate that prolonged ischemia time leads to the accumulation of lactic acid, which in turn affects post-translational modifications, including lactylation, and consequently influences epigenetic regulation. Our findings demonstrate that pre-analytical ischemia significantly impacts tumor biology, necessitating caution in interpreting lactylation-driven pathway activation and motivating a reexamination of tissue collection protocols for lactylomic analysis.

PE-07 Establishing a High-Quality, Large-Scale Specialized Biobank for Cardio-Thoracic Diseases: Experience from Tianjin Chest Hospital, China

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Statement of the Problem: Cardio-thoracic diseases are marked by high incidence and mortality, earlier onset trend, and a heavy disease burden, posing major challenges to global public health. As Tianjin's largest specialized center, Tianjin Chest Hospital has the most comprehensive subspecialties and ranks top hospitals nationwide. A high-quality, large-scale cardio-thoracic biobank is essential to integrate clinical data, biospecimens, and follow-up information for advancing precision and translational research.

Proposed Solution: In March 2016, Tianjin's first specialized cardio-thoracic biobank was established. It provides high-quality samples and integrated data of major cardio-thoracic diseases, such as coronary artery disease, acute myocardial infarction, aortic dissection, atrial fibrillation, heart failure, valvular heart disease, post-coronary artery bypass grafting, lung tumors, chronic obstructive pulmonary disease, pulmonary embolism, and asthma. The biobank has well-defined functional zones and follows strict preservation protocols, standard operating procedures, and a rigorous quality control (QC) system. Equipped with advanced Biobank Information Management System (Haier), Environmental Monitoring and Management System (Avantech), and instruments for preservation and QC (Perkin Elmer), it ensures reliable storage of specimens and clinical data. All donors have provided written informed consent. The biobank stores more than 400,000 tubes from over 30,000 patients. Sample types cover over 90 categories, including blood, tissue, urine, feces, body fluids, DNA, and sub-types. QC is conducted semiannually at a 0.1% rate, with 100% internal and external compliance. The biobank is integrated with key hospital systems-HIS, LIS, PACS, and follow-up data, serving as a pivotal research platform. It has provided nearly 20,000 high-quality samples to support over 40 national, provincial, ministerial and collaborative projects and facilitated over 200 publications.

Conclusions: Tianjin Chest Hospital has established Tianjin's first high-quality, large-scale specialized cardio-thoracic biobank, ranking among China's leading institutions. Leveraging its full spectrum of cardio-thoracic diseases and integrated resources, the biobank has become a leading innovation and sharing platform, promoting standardized development of specialized biobanks nationwide and enhancing capabilities in the diagnosis, treatment, and prevention of major cardio-thoracic diseases.

PE-08 Establishing a Tumor Biobank Enhanced by Digital Pathology and A.I. In Developing Countries: CNC Pathlab Case Study

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Background: Tumor biobanks are vital for oncology research, providing annotated specimens essential for understanding tumor biology, mutation profiles, and treatment response patterns. However, developing countries often lack robust biobanking infrastructure, limiting local cancer research capabilities. The CNC Path Lab Tumor Biobank addresses these challenges by leveraging digital pathology and artificial intelligence (A.I.) to enhance specimen annotation, optimize quality control, and streamline data analysis, thereby strengthening oncology research in resource-constrained settings.

Methods: CNC Path Lab established a biobank integrating digital pathology and A.I. for end-to-end specimen management, analysis, and annotation. Whole-slide scanners capture high-resolution tumor images, enabling remote access and minimizing handling errors. A.I. algorithms support mutation prediction, digital IHC scoring (H-score automation), and morphology-based analytics to identify tumor grade, histotype, and molecular risk categories. All samples are linked with detailed demographics, clinical data, and mutation profiles in a secure database accessible to research collaborators. Continuous quality-control metrics and automated alerts ensure high-fidelity data capture and reproducibility.

Results: The biobank currently houses over 5,000 tumor samples across multiple cancer types — lung (30%), breast (25%), colorectal (20%), prostate (10%), and other malignancies (15%). Integration of A.I.-powered image analysis has improved diagnostic and mutation-prediction accuracy by 33%, reduced specimen processing and annotation time by 45%, and increased digital QC efficiency by 38% compared with manual workflows. The platform has supported 14 collaborative research projects with academic and industry partners, contributing to region-specific insights into mutation prevalence and treatment response. These efforts are laying the groundwork for precision-oncology initiatives adapted to local populations.

Conclusions: The CNC Path Lab Tumor Biobank demonstrates how combining digital pathology with A.I. can revolutionize cancer research infrastructure in developing regions. This scalable model enhances data quality, research collaboration, and operational efficiency—bridging the gap between global precision medicine and local oncology needs.

PE-09 Evaluating the Life Cycle of Acute Leukemia Mononuclear Cells: A Model from Pakistan

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Introduction: Biobanking of acute leukemia MNCs provides a critical foundation for molecular research. In Pakistan, challenges including limited infrastructure, inconsistent preanalytical workflows, and lack of systematic utilization tracking compromise sample integrity and reduce scientific yield. Many stored samples remain unused due to incomplete metadata, and cryopreservation practices. To address these challenges, a structured life cycle evaluation framework was developed at the IHHN Biorepository to monitor, assess, and optimize the full trajectory of leukemia MNC sample from collection to research output. To establish a life cycle monitoring framework that ensures quality, traceability, and efficient utilization while aligning with international biobanking standards.

Methods: Evaluation framework was established encompassing all phases of MNCs biobanking. Standardized preanalytical procedures were developed for collection, Ficoll-based isolation, cryopreservation using 10% DMSO in FBS, and labeling. Continuous temperature monitoring and metadata recording were conducted using LIS to ensure complete traceability. Quality checkpoints included pre-freeze and post-thaw cell viability, RNA yield, and purity (A260/280 ratio). The framework also incorporated utilization tracking that linked each sample to its associated study and dataset. Internal audits were conducted periodically to assess compliance with standards, and staff received competency-based training to maintain consistency in biobanking practices.

Results: From June 2022 to August 2025, 1681 acute leukemia MNC samples were archived at IHHN. Mean pre-freeze viability was >92%, with post-thaw recovery at 80.4%. RNA extraction was successful in 80.2% of samples, yielding an average of 383.3 ng/μL with an A260/230 ratio of 2.0 ± 0.1. Sample utilization increased from 18% in 2022 to 50% in 2025. Audit reviews confirmed improved documentation, traceability, and compliance with international standards.

Conclusion: This life cycle evaluation model significantly enhanced the quality, traceability, and research utilization of acute leukemia MNCs at IHHN. By integrating LIS-based tracking, periodic quality assessments, and reviews, the framework transformed resource-limited biobank into an efficient, research-enabling infrastructure. The Pakistan experience underscores that structured evaluation and staff capacity building can sustain high-quality biobanking and accelerate research even within LMIC constraints.

PE-10 Impact of Freezer Storage Duration on the Diagnostic Performance of Plasma p-tau181 and p-tau217 in Differentiating Clinical Stages of Alzheimer's Disease: A Cross-Sectional Study

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Background: Long-term storage at −80°C may influence protein concentrations in plasma samples. This study aimed to evaluate plasma p-tau181 and p-tau217 levels in cognitively normal controls (NC), individuals with subjective cognitive decline (SCD), patients with amnestic mild cognitive impairment (aMCI), and patients with Alzheimer's disease (AD) across varying storage durations. We further investigated the associations between storage duration and plasma p-tau concentrations, and examined how storage time affects the diagnostic performance of these biomarkers in differentiating clinical stages of AD.

Methods: A total of 743 participants (344 NC, 291 SCD, 70 aMCI, and 38 AD) were included. Plasma p-tau181 and p-tau217 concentrations were quantified using the Single Molecule Array (Simoa) platform. Spearman correlation analyses were performed to assess associations between storage duration and plasma p-tau levels. The diagnostic performance of p-tau181 and p-tau217 was compared between sub cohorts with relatively short- and long-term storage durations.

Results: Plasma p-tau181 and p-tau217 levels exhibited negative correlations with storage duration in the NC and SCD groups, whereas no significant associations were observed in the aMCI or AD groups. Consequently, the diagnostic performance of plasma p-tau biomarkers was higher for distinguishing SCD from aMCI, but lower for differentiating aMCI from AD, in samples stored for longer durations.

Conclusions: Prolonged storage significantly affects plasma p-tau181 and p-tau217 concentrations in NC and SCD participants, thereby altering their diagnostic performance across disease stages. These findings underscore the necessity of considering storage duration as a critical pre-analytical variable in studies employing plasma p-tau biomarkers for Alzheimer's disease research.

PE-11 Implementing an Autopsy Program: A Multidisciplinary Approach in HIV and Cancer Research

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Background: Over 40 million people live with HIV worldwide, including about 1 million in Brazil. As survival improves with antiretroviral therapy, the malignancy profile among people living with HIV (PLWH) has shifted, with a rising incidence of non-AIDS-defining cancers (NADCs). Autopsies in PLWH and cancer provide insights for public health and translational research by enabling the collection of normal and tumor tissues, body fluids, and HIV reservoirs from sites inaccessible during patients' lives. This study describes the implementation of an autopsy program for PLWH and cancer at the Cancer Institute of São Paulo State, Brazil (ICESP).

Methods: A three-phase workflow was established: i) Patient monitoring: the clinical team identifies and follows PLWH and cancer using an electronic medical record system. When a patient enters the active dying phase, the recruitment team is notified. ii) Family consent: upon death confirmation, the on-duty nurse notifies the family and the on-call recruitment team. The family receives medical, psychological, and social support, and once consent is obtained, the on-call autopsy team - dieners, pathologists, pathology assistants, and biorepository associates - are immediately mobilized. iii) Autopsy and sample collection: the clinical team coordinates de corpse transportation to the autopsy facility. The biorepository team prepares the sample processing room with prelabeled reagents and supplies. Gross dissection enables the collection of three mirrored biopsies per fragment, preserved as fresh-frozen, formalin-fixed paraffin-embedded, and RNA-stabilized tissues. Whole blood and cerebrospinal fluid (CSF) can also be collected. After the procedure, the corpse is returned to the family for burial, and biospecimens are processed, stored, and entered into a biorepository inventory.

Results: The first autopsy was successfully performed on a PLWH and Burkitt lymphoma metastatic to the brain and kidney, yielding a total of 362 specimens from ten anatomical sites, including CSF and whole blood. The main operational challenge was delayed body transport due to administrative procedures.

Conclusion: Implementing an Autopsy Program for PLWH and cancer enables recovery of high-quality biospecimens that can advance research on HIV-associated malignancies and HIV cure strategies. Streamlining administrative workflows can reduce the postmortem interval and improve sample integrity, maximizing their scientific and translational value.

PE-12 Investigation into the Quality and Integrity of Stored Biospecimen at the Biobank of the National Health Laboratory Service (NHLS)

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Background: The National Health Laboratory Service is the parastatal of the Department of Health. NHLS has different divisions namely National Institute for Occupational Health (NIOH), National Institute for Communicable Disease (NICD), National Cancer Registry (NCR) and National Biobank (NB). The Biobank is the division of the NHLS that is responsible for collecting and storing biomaterials for short term and long-term use by researchers. The Biobank supports biomaterial storage needs of the local and international research and development community in the areas of innovation, biotechnology, healthcare and conservation. The impact and effect of long-term storage on biosamples at the biobank has not been investigated. Proof of optimal and adequate long term storage conditions for biosamples is important for analysis, repeatability, quality control and research reproducibility of results and still have confidence in the ultra-freezing storage. These chemicals of anticoagulants may also have effects on long term storage and stability and integrity of samples prior to analysis. The change in temperature condition may also have an effect in DNA and RNA concentration and long term storage.

Method: The study will focus on collection blood for FBC (Full blood count) using EDTA tube, urea creatinine using yellow top tube, glucose using grey top tube, liver function test (LFT) using yellow tube top, DNA and RNA quantification using EDTA tube. The ultrafreezer use will also be monitored on a daily basis for the whole year to ensure that the temperature are assessed on daily basis and there is no compromise on the samples' temperature. The ultrafreezer temperature will be set at −86°C set point. The acceptable working range for the freezer will be −70°C and −90°C. The FBC, UECA, LFT, Glucose and DRNA and RNA quantification will first analysed to record initial results. These initial results will be used as point of reference.

Proposed Solution: Research will be done by analysis and comparing results data and make a conclusion on the long term effect of storage on the biological specimen storage. Variation from the initial results should not be very significant to the point

that it questions that storage condition, integrity and quality of biospecimen stored. Research will provide evidence that if the samples after long term storage came out deteriorated and cannot be analysed and adequate for research that means the sample was deteriorated at prior to storage.

PE-13 In Vivo Comparison of the Anti-snake Venom Activity of the Honey-derived Phenolics and Polyvalent Antivenom

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The WHO declared snakebite as neglected tropical disease. Though the exact number of snakebite cases is not known but estimated results showed that 5.4 million people are bitten by snakes worldwide each year and 2.7million envenoming occur. Around 81,000 to 138, 000 deaths occur every year globally by snakebite envenoming and three times more amputations occur along with many other disabilities annually. There is immense struggle is required to counter this issue. This study focuses on snakebite envenomation to reduce its effects. The honey derived phenolics proved their anti-snake venom potential. The partial characterization of venom was done by SDS-PAGE to find possible toxin peptides in cobra snake venom. Three types of proteins identified in snake venom. The partial characterization of antivenom was done by microscopy and MIC of phenol (m-cresol) was determined to measure its concentration for use as preservative in antivenom. The ideal concentration was 16% for phenol (m-cresol). The characterization of Saudi and Kashmir honey was done to emphasize their potential role to limit snakebite envenomation. The physiochemical analysis including pollen analysis, HMF presence, ash, moisture, pH, color, sucrose and reducing sugars were analyzed. Microscopy showed multi floral nature of both samples including 13 different types of pollens. The total phenol content (TPC) of Saudi honey was 8.6 mg GAE/100g of dry extract whereas, Kashmir honey was 8.3 mg GAE/100g of dry extract. The phenolics presence also analyzed by HPLC. The in vivo results were very significant. All the albino mice (male& female) were survived and survival rate was 100%. In conclusion, this study opens door for research to emphasize, phenolics activity against other venom toxic peptides and maybe helpful in production of anti-snake venom drugs as adjuvant with antivenom and, can play a key role to counter snakebite issue. This study also helps to improve affectivity of globally available antivenom products.

PE-14 Mechanistic Study of Bruceantin-Induced Apoptosis in HBV-Related Hepatocellular Carcinoma through Inhibition of the HBx/c-Myc/RPL27A Axis Supported by Biobank Resources

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Background: Biobanks provide standardized and clinically annotated specimens that support translational research and target discovery. Hepatitis B virus–related hepatocellular carcinoma (HBV-HCC) accounts for more than half of global HCC cases and remains a major cause of cancer mortality with limited targeted therapies. Using well-characterized HBV-HCC tissues and paired adjacent samples from clinical biobank collections, this study investigated the antitumor mechanism of the natural compound Bruceantin (BCT) and demonstrated how biobank resources facilitate mechanism-oriented cancer research.

Methods: Transcriptomic and molecular analyses were performed on biobanked HBV-HCC tissues and integrated with public datasets from GEO, TCGA, and GTEx to identify potential therapeutic targets. Functional assays in HBV-HCC cell lines and xenograft models were used to evaluate the effects of BCT on cell proliferation, apoptosis, and tumor growth. Western blotting, RT-qPCR, and immunohistochemistry were applied to verify BCT-regulated pathways and to assess its tissue selectivity.

Results: Biobank-derived analyses revealed marked overexpression of RPL27A in HBV-HCC tissues compared with paired non-tumor counterparts, correlating with poor patient outcomes. BCT treatment significantly downregulated RPL27A expression in vitro and in vivo, induced apoptosis, and inhibited tumor growth without detectable systemic toxicity. Mechanistic studies showed that BCT disrupted the HBx/c-Myc/RPL27A signaling axis by promoting proteasomal degradation of the HBV oncoprotein HBx, decreasing c-Myc stability, and suppressing RPL27A transcription, which collectively inactivated the PI3K/AKT pathway. Integration of biobank resources with functional validation established RPL27A as a key downstream effector of the HBx/c-Myc pathway and a functional target of BCT.

Conclusion: This study demonstrates that biobank-enabled HBV-HCC specimens are invaluable for elucidating molecular mechanisms and identifying therapeutic targets. By combining biobank-linked samples with functional and multi-omics analyses, we revealed that BCT induces apoptosis through inhibition of the HBx/c-Myc/RPL27A axis and suppression of PI3K/AKT signaling. These findings highlight the translational value of biobank-based research in advancing natural compound–derived drug discovery and precision medicine for liver cancer.

PE-15 Multiplexed Antibody-Panel Based Quality Control Workflow for Biobanked Tissues

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Background: By design, biobanks are established to collect and store tissue specimens for enabling research discoveries and innovation. Tissue banks often partner with anatomic pathologists and pathology assistants for grossing and for allocating appropriate tissues for research biobanking. Flash freezing process further stipulates that these research specimens are frozen quickly to minimize cold-ischemic times often without any quality control (QC) step. From the practical standpoint, the tissue labeling at the time of grossing may not always match with what is actually being banked and, this may become a serious issue when specimens are disseminated for research laboratories. To overcome this problem, it is imperative that biobanks develop

workflows for systematic and reproducible QC of all the tissue specimens that are banked.

Methods: In our hospital-based biobank, we have established a workflow for paraffin embedding of at least one part (~50 mg) of the surgical tissue being banked, for generating standard histology sections/staining for morphology analysis. This method characterizes the percentages of tumor, normal and necrotic regions in the histology sections. In addition to this traditional method, we are proposing to set up a workflow based on multiplexed antibody panel of quality control (epithelial, immune, apoptotic/necrotic and other metabolic proteins) markers that can form a harmonized basis for characterizing the tissue specimens in any biobank setting.

Results: We will present histology data collected and analyzed over the past 4 years to demonstrate the need and utility of the proposed method in identifying the mislabeling errors (i.e, difference in labeling at the time of freezing and after histology QC) such as contamination of cancer cells in "normal" tissues etc., We will also present the details of the antibody panel design, antibody workup methods using the Roche Ventana discovery platform as well as the preliminary results of characterizing the banked tissue specimens using the multiplexed immunohistochemistry (IHC) and/or immunofluorescence (IF) methods.

Conclusions: As the demand for human tissues is increasing for vital clinical validation steps as well as for rapid discovery process, an automated and reproducible workflow for rapid assessment of tissue specimens beyond traditional histology methods is a need of the hour and we believe that our present work is setting up a foundation to address this critical need.

PE-16 Optimized Protocol for Isolation and Characterization of Tumor-Educated Platelets for Liquid Biopsy Applications

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Background: Platelets have emerged as a promising tool in liquid biopsy due to their abundance in peripheral blood and lifespan (7-10 days). Their molecular cargo is modulated through interactions with tumor cells and circulating extracellular vesicles, resulting in tumor-educated platelets (TEPs) that carry tumor-specific molecular signatures and participate in tumorigenic processes. Harnessing TEPs' molecular signatures may contribute to early cancer diagnosis, disease monitoring, and prognosis. This study aims to establish an optimized protocol for TEP isolation to explore this promising source of cancer minimally invasive biomarkers.

Methods: A comprehensive literature review was conducted to identify and compare platelet isolation and RNA extraction methodologies. Based on these findings, whole blood (10 mL) will be collected from healthy volunteers using EDTA and acid citrate dextrose (ACD) tubes and processed following two approaches: i) a two-step centrifugation method for platelet isolation described by Best et al. (2015), and ii) a standard operational protocol from the AIDS Malignancy Consortium. Additionally, we will evaluate the impact of both anticoagulants on the efficiency and purity of the obtained platelets. Platelet characterization will be assessed by flow cytometry (CD41a, CD62P, CD45, and calcein), and purity will be confirmed by blood smear analysis. After protocol standardization, RNA extraction from TEPs will be conducted using three different commercial kits to compare yield and enrichment for small RNAs (miRNA). Qubit (Thermo Fisher Scientific) and RNA 6000 Pico Kit (Bioanalyzer, Agilent) will be used for RNA quality control.

Results: The literature review retrieved 74 publications, of which 38 were evaluated in detail, guiding the methods selected for the experimental design. A preliminary test was conducted according to Best et al. (2015) with samples collected in EDTA tubes. The analysis revealed 99.3% CD41a-positive events, demonstrating efficient platelet recovery. Blood smear analysis showed 1 leukocyte in 100 fields at 1000x magnification, confirming the high purity of the isolated platelets.

Conclusion: This standardized protocol will enable the reproducible isolation and characterization of TEPs, facilitating the identification of potential cancer biomarkers, including miRNA profiles. The implementation of this workflow will contribute to minimally invasive disease monitoring and precision-guided therapy decisions.

PE-19 Optimizing RNA Quality in Cryopreserved Tissues without Preservatives: Impact of Preservatives, Thawing Methods and Tissue Aliquot Sizes

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Background: RNA degradation during freeze-thaw cycles in cryopreserved tissues is a major challenge for biomedical research, particularly when tissues are stored without preservatives. While agents such as TRIzol and RNALater are effective for fresh tissues, their utility for archival frozen tissues remains unclear.

Methods and Results: We evaluated various RNA preservation strategies for frozen rabbit kidney tissues without preservatives, considering key variables such as thawing temperatures (ice vs. room temperature (RT)), preservatives (RNALater, TRIzol, and RL lysis buffers), processing delay (time before disruption), tissue aliquot sizes (ranging from 70-100 mg, 100-150 mg, to 250-300 mg), and freeze-thaw cycles. Compared with RT-treated frozen rabbit tissues, preservative-treated tissues presented significantly greater RNA integrity when thawed on ice ($p < 0.01$). The RNALater group performed best in maintaining high-quality RNA (RIN ≥ 8). Although a significant difference in the RIN was observed between the 120-minute and 7-day processing delays (9.38 ± 0.10 vs 8.45 ± 0.44), all the samples ≤30 mg maintained a RIN ≥ 8. For tissues ≤ 100 mg, thawing overnight on ice or at -20°C maintained a marginally higher RIN (RIN ≥ 7). However, larger tissue aliquots (250–300 mg) presented significantly lower RINs with ice thawing than with thawing at -20°C (5.25 ± 0.24 vs 7.13 ± 0.69). After 3–5 freeze-

thaw cycles, tissues thawed at -20°C presented notably greater variability in the RIN, particularly in larger tissue aliquots. In validation experiments involving cryopreserved human and murine kidney tissues, the RNALater-treated murine kidney tissues ≤ 30 mg consistently maintained high-quality RNA integrity (RIN ≥ 8), whereas the frozen human kidney tissues resulted in marginally reduced RINs compared with those of the LN grinding control (7.76 ± 0.54).

Conclusions: Preservatives, tissue aliquot sizes, and thawing methods significantly impact the RNA quality of frozen tissues originally stored without preservatives. Key recommendations include (1) adding RNALater during thawing, (2) thawing on ice for small aliquots (≤ 100 mg) or at -20°C for larger samples, and (3) minimizing freeze-thaw cycles, despite observed variations among species.

PE-20 Preserving Precision: Tailored Biobanking Strategies for Infectious Disease Specimens and Associated Clinical Annotations

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Background: Infectious disease clinical trials utilize diverse clinical samples and data, with varying quantities and specifications. Centralized biobanking enhances research efficiency by streamlining analysis and collaboration. However, standardized end-to-end workflows from collection to utilization are underdeveloped. Accurate clinical data linked to these samples is paramount for effective application and trial efficiency. Understanding the commonalities and distinctions in required samples and data is crucial for optimization.

Methods: We retrospectively reviewed data from 153 ongoing infectious disease trials (AIDS, viral hepatitis, tuberculosis, COVID-19) at the Chongqing Public Health Medical Center (2018-2025). Descriptive statistical analyses were performed on preservation parameters (volume, storage conditions, freeze-thaw cycles) for key specimen types. Clinical information was cataloged and stratified by disease to identify core and disease-specific variables.

Results: Specimens primarily included blood, sputum, and swabs. Recommended retention volumes were 0.5–1.0 mL for blood (52%), 2.0–3.0 mL for sputum (50%), and <1.0 mL for swabs (67%). For short-term storage at 2–8°C, recommended durations were: blood <7 days (56%), sputum <1 day (50%), and swabs 1–3 days (84%). For long-term storage, blood and sputum were suggested for –20°C for 6–12 months (60%, 58%), while all types could be stored indefinitely at –70°C. Freeze-thaw cycles should be minimized (recommended for blood, sputum, swabs at 64%, 47%, 60%, respectively). Common clinical metadata included diagnosis, specimen type, age, and gender. Disease-specific indicators were HIV viral load (AIDS, 30%), liver function biomarkers (hepatitis, 9%), and sputum smear microscopy (tuberculosis, 55%).

Conclusion: This analysis defines optimal preservation parameters and essential clinical metadata frameworks for infectious disease trial specimens. These insights provide a foundational reference for biobank standardization, enabling robust sample management and harmonized data integration. Implementing such protocols will establish a reliable platform for translational research, accelerating discoveries in pathogenesis and therapeutics.

PE-21 Quality Control of Distributed Biospecimens: A Two-Year Audit Linking Sample-Level QC to Clinical Metadata in a Colorectal Cancer Biobank

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Background: Sample distribution is where biobank quality meets research utility. Yet few reports quantify outgoing (distributed) sample quality against clinical context at scale. We audited two years of distributions from a colorectal cancer biobank to (i) characterize quality attributes of shipped materials and (ii) identify fit-for-purpose rates for common downstream uses (e.g., genomics vs. proteomics).

Methods: We assembled a line-list of distributed specimens with linked clinical fields and morphologic QC. Variables included specimen type, collection date, tumor nuclei percentage (TNP), necrosis percentage, total cellularity, and lymphocyte infiltration. We summarized counts, medians, and pass rates using pragmatic thresholds (e.g., TNP ≥ 20% "proteomics-grade"; TNP ≥ 50% "genomics-grade"). Time window: Jan 3, 2022–Sep 29, 2024.

Results: We analyzed 4,122 distributed specimens (all colorectal region), predominantly tumor tissue (n=4,100; 99.5%). Overall QC performance was high: TNP median 60% (IQR 45–70, n=4,101); TNP ≥ 20% in 94.1%, TNP ≥ 50% in 71.6% of evaluable samples. Necrosis median 5% (n=1,508 evaluable); ≤20% necrosis in 94.9%. Lymphocyte infiltration median 10% (n=3,795). These distributions indicate that a large majority of outgoing materials meet proteomics-grade criteria and ∼7 in 10 meet genomics-grade criteria at shipment, supporting efficient routing to appropriate downstream assays.

Conclusions: Routine capture of morphologic QC at the point of distribution provides actionable, study-level assurance: most shipped colorectal specimens meet thresholds suitable for proteomic analyses, and a substantial fraction meet genomics-grade tumor content. Embedding such QC summaries in distribution workflows can (i) reduce assay failure, (ii) improve sample-to-study matching, and (iii) inform inventory management (e.g., flagging low-TNP categories for targeted enrichment). Future work will integrate molecular QC (RIN/DIN, OD ratios) and multivariable modeling to link QC features with project outcomes and turnaround time.

PE-22 Significant Enhancement of Yield and Purity in Genomic DNA Extraction from Peripheral Blood Using an Optimized Magnetic Bead-Based Elution Protocol

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Background: Magnetic bead-based DNA extraction from peripheral blood is favored for automation and high throughput. However, standard elution protocols often limit DNA yield and purity due to incomplete release from beads.

Methods: We optimized the elution step of a commercial magnetic bead kit for peripheral blood. Key variables tested included elution buffer composition (TE vs. Tris-HCl), temperature (RT-70°C), and single versus double elution. All samples were processed on an automated platform.

Results: The optimized protocol using 10 mM Tris-HCl (pH 8.5) at 65°C with a double elution significantly improved performance. It increased the average DNA yield by over 45% compared to the standard method. Purity was also enhanced, with optimal A260/A280 ratios (1.80-1.85) and A260/A230 ratios consistently >2.0. Gel electrophoresis confirmed high DNA integrity. The resulting DNA demonstrated superior performance in downstream PCR and qPCR applications.

Conclusion: This simple optimization of elution conditions substantially improves the yield and purity of DNA extracted from peripheral blood, offering an efficient enhancement for biobanking and molecular workflows.

PE-23 Systematic Impact of Repeated Freeze–Thaw Cycles on Pancreatic Cancer Tissue Quality: RNA Vulnerability and Histomorphological Changes

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Background: High-quality biospecimens underpin cancer research, yet repeated freeze–thaw (FT) during sample release can compromise quality and the reliability of downstream analyses. Pancreatic cancer tissue, enriched in nucleases and proteases, may be especially susceptible, but this hypothesis lacks systematic validation. We compared FT tolerance across pancreatic, colorectal, and ovarian cancer tissues to delineate pancreatic tissue vulnerability and inform optimized preservation strategies for biobanks.

Methods: Fresh surgical tissues were collected from 6 pancreatic cancer (PC), 3 colorectal cancer (CRC), and 3 ovarian cancer (OC) cases. For each case, specimens were divided into an FT group (5 FT cycles) and an untreated control. Quality assessments included: (1) nucleic acid integrity—RNA Integrity Number (RIN) and DNA Integrity Number (DIN) by bioanalyzer; (2) purity—A260/280 and A260/230 ratios by spectrophotometry; and (3) histomorphology—H&E staining with pathology quality scoring.

Results:

(1) RNA stability: In PC, A260/230 significantly declined after FT ($p<0.05$), while CRC and OC showed no significant change. RIN values indicated more pronounced RNA degradation in PC versus CRC and OC (both $p<0.05$).

(2) DNA stability: Across all cancer types, DIN and A260/280 and A260/230 for DNA were not significantly affected by FT ($p>0.05$).

(3) Histomorphology: FT induced structural disruption in all tissues; however, PC exhibited more prominent nuclear pyknosis and fragmentation on H&E.

Conclusions: This study systematically reveals the distinctive FT sensitivity of pancreatic cancer tissue: RNA degrades faster and histological damage is greater than in CRC or OC. We recommend biobanks adopt single-freeze workflows and small-volume aliquoting for PC tissues to minimize FT events and preserve quality. Future work should expand cohort size and evaluate cryoprotectant strategies tailored to RNase-rich tissues.

PE-24 The Epigenetic Mechanism by which GATAD2A Degradation Sustains KRAS Expression in Head and Neck Squamous Cell Carcinoma

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Objective: The rapid growth of tumors leads to excessive nutrient consumption in the tumor microenvironment. This study aims to elucidate the molecular mechanism by which a key protein and its related downstream pathway regulate the sustained proliferation of head and neck squamous cell carcinoma (HNSCC) cells in an energy-deficient microenvironment, providing new insights for the diagnosis and treatment of HNSCC.

Methods: An HNSCC cell model under glucose deprivation was established. Phosphoproteomic screening identified a significant reduction in phosphorylation at site S113 of GATAD2A. The phosphorylation level at this site in clinical samples was detected by immunohistochemistry. S113A and S113D mutants were constructed, and their effects on proliferation and migration were analyzed using CCK-8, colony formation assays. Databases were combined with Co-IP/WB to identify the kinase and ubiquitin ligase regulating this phosphorylation. Molecular mechanisms were deciphered using CUT&Tag, RNA-seq, and proteomics. A subcutaneous xenograft tumor model was established to validate the tumor-suppressive effect in vivo.

Results: pSer-S113 of GATAD2A was significantly decreased in both the glucose-deprived HNSCC cell model and HNSCC tissue samples. The primary kinase mediating this phosphorylation was identified as GSK3, whose expression decreased under glucose deprivation. Reduced phosphorylation at site S113 of GATAD2A led to decreased protein stability, which was associated with enhanced interaction with FBXW7 and subsequently promoted ubiquitination. Furthermore, phosphorylation at site S113 of GATAD2A significantly inhibited HNSCC cell proliferation, and decreased H3K27ac levels. Subcutaneous xenograft experiments confirmed that phosphorylation at site S113 of GATAD2A significantly inhibited HNSCC growth.

Conclusion: In the nutrient-deficient microenvironment of HNSCC, tumor cells downregulate GSK3 expression, leading to reduced phosphorylation at site S113 of GATAD2A. This decrease in phosphorylation, lowers GATAD2A protein stability and attenuates its interaction with NuRD complex components. Consequently, the transcriptional repression function of the NuRD complex is weakened, increasing H3K27ac levels near the KRAS promoter and promoting KRAS transcription, thereby sustaining HNSCC cell proliferation under energy stress. Promoting phosphorylation at site S113 of GATAD2A significantly inhibits HNSCC growth by limiting tumor cell proliferation.

PE-25 The Real-world Construction of an Information Management Practice for a Research-oriented Biobank

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Background: In the context of the 'Healthy China' initiative, precision medicine and biobanks are experiencing a period of rapid development. Alongside the advancement of precision medicine, biobanks have evolved into platforms that integrate biological samples and information resources, as well as

providing support services for precision medicine research and facilitating the translation of research outcomes. The Dalian Public Health Clinical Centre established a biobank focused on infectious diseases in 2014. This biobank was the first in Northeast China's three provinces to obtain approval for the preservation of human genetic resources, enabling the standardised storage of biological samples and information resources from patients with infectious diseases, while continuously enhancing its information infrastructure.

Methods: To facilitate the implementation of real-world studies, our centre has completed foundational tasks, including ethics review, quality control, automated data integration and follow-up management. This ensures the successful preservation of biological samples and data resources in compliance with standards. Moreover, we have established a information management system (IMS) for storing, managing, querying and analysing biological samples and their clinical data, while safeguarding the operational environment and security of these samples and data. This system creates a database-driven relationship model between data and facilitates the management and analysis of biological repository data, thereby enhancing the utilisation rate of biological samples and their associated information.

Results: We have established a valuable biobank containing over 350,000 paired samples spanning different disease stages, including the immune tolerance phase, the immune clearance phase, compensated/decompensated cirrhosis, precancerous lesions and HCC. This provides a solid basis for establishing follow-up cohorts. Additionally, we have implemented a joint batch query function for multi-source sample information based on IMS. This function constructs various data models to enable associative analysis and disease prediction. This system has also been granted a patent.

Conclusion: Our ISM aligns with the construction and management model of real-world, research-oriented biobanks, which meets the diverse scientific needs of routine biobank operations and researchers alike, providing a convenient platform and abundant resources for advancing precision medicine.

PE-26 The Role and Management Practices of Biobank in the Development of an Integrated Artificial Intelligence-Driven Information Platform for Lung Cancer Diagnosis and Treatment

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Statement of the Problem: Lung cancer is the leading cause of cancer-related morbidity and mortality in China, posing major public health challenges. The department of Thoracic Surgery at Tianjin Chest Hospital, a National Key Clinical Specialty, has developed an AI- and big data-powered integrated system for lung cancer diagnosis and therapy, supporting early screening, precise diagnosis, personalized therapy, and prognostic management. The department has built an integrated platform powered by AI and a high-quality, lung cancer specialized biobank.

Proposed Solution: As a leading clinical center for thoracic oncology, it manages over 4,000 lung cancer cases annually and has established a nationally advanced big data platform and follow-up system. In March 2022, the hospital launched a lung cancer specialized biobank with clearly defined functional areas, a comprehensive sample management system, standard operating procedures (SOPs), and a robust quality control (QC) framework. The biobank's SOP for Lung Cancer Tissue Collection and Preservation ensures high-quality samples through end-to-end temperature monitoring, rapid cold transport, and DNA/RNA QC. All donors provided informed consent. The disease spectrum includes non-small cell lung cancer, small cell lung carcinoma, and rare types. The biobank contains over 13,000 tubes from more than 1,000 patients: 44% tissue (tumor, paracancerous, and normal), 43% matched blood, and 13% urine. QC is conducted twice yearly at a 0.1% sampling rate, with both internal and third-party evaluations achieving 100% compliance. An AI-powered platform integrates thoracic surgery, respiratory, pathology, radiology, biobanking, and follow-up centers, linking sample data-collection, transport, processing, storage, and QC-to clinical records, surgical reports, pathology results, imaging, and follow-up data, forming a robust "sample-data-follow-up" research platform. To date, it has provided over 2,000 tubes for 10 projects, supported over 30 national, provincial, ministerial projects, horizontal collaborations, and over 40 academic publications.

Conclusions: High-quality, standardized, and regulation-compliant lung cancer biobanks integrated with multidisciplinary data provide strong biospecimen and data support. This enables research on pathogenesis, biomarker discovery, targeted therapies, and precision treatment, significantly enhancing thoracic surgery capabilities in lung cancer prevention, diagnosis, and management.

PE-27 Thymosin Beta 10 Promotes Cancer Stemness and Malignant Progression in Head and Neck Squamous Cell Carcinoma

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Objective: Head and neck squamous cell carcinoma (HNSCC) is one of the most common and aggressive malignancies with a poor prognosis. Identifying novel biomarkers and exploring their molecular mechanisms in HNSCC progression is crucial for the development of precise therapeutic strategies. Thymosin β10 (TMSB10), a member of the thymosin family, has been shown to be aberrantly overexpressed in various cancers and promotes tumor progression. However, its specific role in HNSCC remains inadequately characterized. This study aims to systematically investigate the expression pattern of TMSB10 in HNSCC and explore its correlation with clinical phenotypes.

Methods: A comprehensive analysis was conducted by integrating single-cell RNA sequencing, bulk RNA sequencing, and spatial transcriptomics data to elucidate the expression of TMSB10 in HNSCC and its association with clinical phenotypes. The expression levels of TMSB10 were validated in HNSCC samples and cell lines. Additionally, TMSB10 knockdown and overexpression cell lines were established for in vitro and in vivo experiments.

Results: Multiple bioinformatics analyses showed that TMSB10 is significantly upregulated in HNSCC samples. Cross-validation across several independent datasets consistently confirmed its

significant overexpression, which was closely associated with poor prognosis. Overexpression of TMSB10 significantly enhanced the proliferative activity, migratory capacity, and invasive potential of HNSCC cells, and notably promoted tumorigenicity and stemness characteristics. In contrast, knockdown of TMSB10 resulted in opposite effects. In vivo models further demonstrated that knockdown of TMSB10 significantly inhibited the tumorigenic ability, tumor growth, and lung metastatic potential of the cancer cells.

Conclusion: This study systematically elucidates the expression pattern and biological function of TMSB10 in HNSCC for the first time. High expression of TMSB10 is strongly correlated with poor prognosis in HNSCC patients. TMSB10 is a key regulatory factor driving the malignant progression of HNSCC and could serve as an effective biomarker for diagnosis and prognostic evaluation.

PE-28 Uncovering the Translational Landscape of Ovarian Cancer: Insights from Profiling of Clinical Biospecimens

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Background: Ovarian cancer remains a deadly gynecologic malignancy, with a critical need to understand the molecular drivers of tumor progression and therapy resistance. While transcriptomic studies are abundant, the role of translational control—a crucial layer of gene regulation—is less defined in ovarian carcinogenesis. This gap highlights the importance of leveraging well-annotated clinical biospecimens for multi-omics discovery.

Methods: We utilized a cohort of 22 high-quality, clinically annotated ovarian cancer biospecimens from our institutional biobank. We applied ribosome profiling (Ribo-seq) integrated with transcriptome sequencing (RNA-seq) to define the translational landscape at an unprecedented sub-codon resolution.

Results: Our analysis of this unique biospecimen resource revealed widespread translational dysregulation, independent of transcriptomic changes. We identified novel unannotated open reading frames (ORFs) encoding micropeptides. Critically, we validated RBM4 as a key translationally upregulated oncoprotein driving tumor progression, a finding that would be masked by RNA-seq alone.

Conclusions: This study underscores the power of integrating well-curated biospecimens with advanced multi-omics technologies to decode disease mechanisms. Our findings not only provide novel insights into ovarian cancer pathogenesis but also highlight the value of biobanking in discovering cryptic, therapeutically relevant regulatory layers in cancer.

PE-29 Integrated Serum Metabolomics Reveal Distinct Metabolic Reprogramming and a Novel Diagnostic Classifier in Colorectal Signet Ring Cell Carcinoma

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Colorectal signet ring cell carcinoma (SRCC) is a rare, aggressive subtype with poor prognosis and limited non-invasive diagnostic options. Unlike conventional adenocarcinoma, the metabolic landscape of SRCC remains poorly defined. This study aimed to characterize SRCC-specific serum metabolic alterations and develop a robust diagnostic model. We performed targeted metabolomics on 400 serum samples, including 180 SRCC patients, 120 adenocarcinoma patients, and 100 healthy controls. Differential analysis revealed a unique metabolic phenotype in SRCC distinct from adenocarcinoma. Key findings included the significant accumulation of isobutyrylglycine, indicating impaired branched-chain amino acid catabolism and mitochondrial β-oxidation defects. Additionally, elevated glutamate levels and enriched arginine biosynthesis pathways suggested enhanced glutamine utilization to fuel the tricarboxylic acid (TCA) cycle. To translate these insights into clinical practice, we employed LASSO regression and Recursive Feature Elimination to identify a diagnostic panel of five metabolites: L-arginine, inosine, guanosine, L-aspartic acid, and phosphorylcholine. Among machine learning algorithms, a Random Forest classifier demonstrated superior performance, achieving an Area Under the Curve (AUC) of 0.998 in the discovery cohort. Importantly, the model was validated in an independent external cohort (n=102), maintaining exceptional accuracy with an AUC of 0.996, sensitivity of 88.9%, and specificity of 100.0%. These findings uncover specific metabolic vulnerabilities in SRCC and establish a highly accurate, non-invasive serological tool for early detection.

PE-30 Simple and Efficient Methods for Extracting High Quality and Quantity of High-Molecular-Weight Genomic DNA from Archived Frozen Tissues

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Background: Any damage during tissue processing or extraction procedures may result in DNA fragmentation, which makes the DNA less suitable for applications that require High-Molecular-Weight (HMW) DNA. This study was designed to explore diverse tissue disruption methods to yield DNA that meets the demands of different downstream analyses and facilitates the efficient utilization of valuable archived frozen tissues.

Methods: The impact of three disruption methods on the quality and quantity of DNA in archived frozen rabbit liver tissues was assessed. Subsequently, attempts were made to optimize these methods by adjusting the lysis time, the homogenization buffer, agitation speed, and running duration. Validation was conducted on four types of frozen human tissues.

Results: All groups exhibited A260/280 ratios $\sim$ 1.8. The liquid nitrogen (LN) grinding group produced the lowest DNA yield, DNA integrity number (DIN) and A260/230. The tissues minced by smashing in the LN showed the optimal DNA integrity with highest DINs > 8 and peak size around 50 kb. However, the minced group produced a moderate amount of DNA as undissolved tissue fragments persisted following a 30 minutes water-bath incubation. The TissueLyser group using nuclease-free water as buffer produced the highest DNA yield and A260/230 > 2.0, but the lowest DNA peak size approximately 25 kb.

Extending the lysis time did not yield the expected increase in DNA yield for the minced group. Adjusting the homogenization buffer significantly improved the DNA yield or integrity. The PBS buffer resulted in DINs nearing 9 and peak sizes approaching 60 kb, and ATL buffer notably elevated the DNA yield to 1245.93 ± 168.37 ng/mg. The findings from the four types of human tissues were similar to those in rabbit liver tissue.

Conclusions: Compared to LN grinding and mincing, the TissueLyser homogenization tends to be more efficient and standardized. It can yield DNA with stable and controllable quality and quantity. The choice of homogenization buffer is critical. PBS is capable of generating high quality of HMW DNA, and ATL buffer provides highest DNA yield. Consequently, the selection of homogenization buffer and parameters can be tailored based on the specific needs of downstream applications. A balance between quality and quantity should be considered.

PE-31 A Novel Carbon Nanotube-Paper Capacitance Monitoring System for Multi-Parameter, Non-Contact Coagulation Analysis in Blood Preservation

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Statement of the Problem: Blood transfusion and blood preservation are among the most commonly performed medical procedures. Assessing the quality and coagulation function of preserved blood—whether before or after storage—is essential for ensuring transfusion safety and efficacy. Traditional laboratory tests like aPTT and PT are not real-time and involve high labor and material costs. Thromboelastography (TEG), while providing real-time clot analysis, lacks adequate sensitivity to platelet counts and function, which can lead to suboptimal therapeutic guidance for platelet-related disorders. An alternative approach, electrical permittivity sensing, detects changes in blood's dielectric properties during coagulation. However, most existing sensors rely on direct contact between blood samples and electrodes, leading to contamination, potential inaccuracies, and the need for costly disposable sensor units. Therefore, there is a critical demand for a real-time, contact-free coagulation monitoring technology that is cost-effective, sensitive to platelet function, and suitable for clinical use.-blood samples and electrodes will not only pollute the blood samples which will cause inaccurate test results but also pollute the electrodes which will make the whole sensor disposable and cause a high supply cost.

Proposed Solution: The coagulation sensor was designed based on a simulated fibrous-edge CPC electrode. The system integrates an FDC2214 capacitance module (Texas Instruments) supporting 4-channel simultaneous measurement, and an NMYC-100 oscillator (Fonrroni, China). Its key advantage over other dielectric sensors is the non-contact design, which prevents blood-electrode contamination and eliminates disposable sensor costs. An automated module enables hands-free operation. This study employs novel fluctuation analysis on capacitance signals to extract multi-parameter information. Unlike conventional approaches that treat these as noise, we analyze noise from several aspect. Results from fluctuation analysis enabling higher sensitivity, selectivity, and robustness in complex environments. This method provides multi-dimensional insights into different coagulation stages through eigenvalue analysis.

Conclusion: This study introduces the first automated, non-contact biplanar capacitance (CPC) sensor for whole-blood coagulation assessment that integrates oscillation. The system uniquely combines an orbital shaker with capacitance sensing, enabling single-test measurement of multiple parameters (e.g., coagulation function, platelet count, hematocrit). Compared to conventional and viscoelastic methods, this design offers a simpler, more cost- and time-efficient setup. Its non-contact feature avoids sample/electrode contamination, and automation allows high-throughput, unattended sample testing.

PE-32 A Novel Low-Toxicity Cryopreservation Strategy for Mouse Oocytes via Electroporation-Mediated Intracellular Trehalose Delivery

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Oocyte cryopreservation is a cornerstone of fertility preservation; however, conventional vitrification-based approaches require high concentrations (up to 4.8 M) of permeating cryoprotective agents (pCPAs), which can induce substantial cytotoxicity and compromise developmental competence. Trehalose, a non-toxic disaccharide with outstanding glass-forming properties, represents a promising alternative. Nevertheless, it cannot permeate the cell membrane naturally. Here, we report a novel strategy combining electroporation-mediated intracellular trehalose delivery with hydrogel microencapsulation to establish a safe, efficient, and low-toxicity vitrification protocol for mouse oocytes. Intracellular trehalose was introduced via optimized electroporation parameters (30 V, 3 ms pulse duration, 3 pulses), achieving efficient loading while preserving oocyte viability. In addition, hydrogel microencapsulation of oocytes was achieved using a centrifugal microfluidic approach, enabling uniform and controllable encapsulation that provided mechanical buffering and structural protection during cooling and warming. Cytotoxicity assessments and thermal property analyses further identified ethylene glycol in combination with trehalose as an optimal CPA formulation, balancing cryoprotective efficacy with reduced toxicity. The integrated protocol reduced pCPA concentration by 44% (from 4.8 M to 2.7 M) while achieving post-warming survival rates comparable to commercial open-system vitrification. Notably, this was accomplished in a closed system that eliminates cross-contamination risks associated with direct liquid nitrogen contact. Post-warming oocytes maintained mitochondrial membrane potential and key functional parameters comparable to fresh controls. Collectively, this platform provides a promising and biosafe approach for low-toxicity oocyte cryopreservation and may facilitate broader clinical translation in fertility preservation.

Funding: This work was supported by the National Natural Science Foundation of China (No. U24A20764).

Ethical, Legal, and Social Issues

PF-01 Ethical Engagement Strategies for Diverse Communities to Build Public Trust in Biobanking - A Framework from Pakistan

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Problem Statement: Public trust is the foundation of successful biobanking, yet in Pakistan, awareness about biorepositories and their role in advancing healthcare research remains limited. Many individuals associate biospecimen collection with fear of misuse, religious concerns, or lack of clarity about data sharing and privacy. Cultural sensitivities surrounding genetic research, gender norms, and medical confidentiality often discourage voluntary participation. In a multilingual society with varied literacy levels, conventional consent processes often fail to ensure true comprehension. These challenges hinder participation, create mistrust, and delay national biobanking development and international research collaboration.

Proposed Solution: The IHHN Biorepository implemented ethical governance strategy to develop participant trust while respecting Pakistan's cultural and social diversity. Key initiatives included: 1) Developing multilingual consent materials (Urdu & English) supported by audio explanations in local languages Punjabi, Pashto, Balochi, Saraiki, and Sindhi to enhance comprehension across literacy levels. 2) Creating a structured checklist to guide staff in obtaining informed consent through culturally sensitive, gender-appropriate, and respectful communication. 3) Conducting regular workshops and seminars on culturally relevant ethical frameworks and perspectives to strengthen staff capacity and understanding. 4) Initiating an ongoing qualitative study exploring participant perspectives to identify local concerns and expectations. 5) Establishing monthly staff feedback sessions to improve consent practices through reflective learning. 6) Organizing awareness sessions for participants, to explain the purpose, confidentiality, and public health benefits of biobanking.

Conclusion: This initiative represents an ongoing effort to strengthen ethical engagement and participant trust in biobanking within Pakistan's diverse culture. The use of multilingual tools, participant-focused consent practices, and continuous quality oversight has already improved awareness and confidence among participants. However, this remains a work in progress. Ongoing feedback studies, staff training cycles. The ultimate goal is to develop a nationally relevant ethical framework that defines trust, consent, and participant rights through scientific and cultural perspectives, guiding biobanking toward sustainable and transparent practices aligned with global standards.

PF-02 Exploring Healthcare Students' Awareness and Sentiments Towards Biobanking

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Background/Purpose: This study aimed to assess awareness, attitudes, and concerns regarding biobanking among students enrolled in clinical- and research-focused academic programs at Eastern Virginia Medical School/Old Dominion University.

Methods: A survey was distributed to 900 students, with 99 complete responses analyzed. Respondents were categorized into clinical-focused (CF) and research-focused (RF) groups. The survey assessed awareness of biobanks, willingness to donate, motivating factors, concerns, and preferences regarding data handling and consent.

Results: Awareness of biobanks and biological donation was high in both groups, though knowledge of the local biorepository was limited. Most students expressed positive or neutral feelings toward biobanking and were willing to donate specimens. Key motivators included benefits to future patients and scientific advancement. Major concerns included data security, misuse of specimens, and unauthorized access by insurers or employers. Preferences varied on consent models, with RF students favoring dynamic consent. Both groups preferred pseudonymization over anonymization. Statistically significant differences were observed between CF and RF groups in motivations, concerns, and information priorities.

Conclusions: While students demonstrated general support for biobanking, concerns about data privacy and ethical use remain. These findings underscore the importance of transparent communication and tailored education to foster informed participation in biobanking initiatives.

PF-03 Hearkening to the Voice of the Research Participants at MRC/UVRI and LSHTM Uganda Research Unit Biobank

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Informed consent is a fundamental principle of Good clinical Practice and ethical bio banking. It still remains the only assurance of utilizing participant samples without necessarily exploiting their rights rather enforcing protection and voluntary participation.

Statement of the problem: Learning from the experience of the set up at the Unit where community mobilization, consenting and sample collection activities are generally done and overseen by the Clinic and field teams, the bio bank team is left with the obligation to receive, process, distribute, store and retrieve these samples however there leaves a room for knowledge whether all those sample collections that are sent for storage were consented for long term storage by the study participants.

Proposed solution: The MRC/UVRI and LSHTM Uganda Research Unit bio bank implemented a workable strategy to rectify this information gap in line with obtaining Informed consent to ensure all stored collections are voluntarily offered. Adding a consent completed tick box on the storage form for all samples coming through for storage. Verification of informed consent is done every quarter for all samples that are received in the bio

bank within that quarter. A random selection of 1% of the total samples received in the quarter is subjected to consent verification. Random participant IDs are selected for all studies whose samples have been received in the bio bank. An email is sent to the study Principal investigator or collaborating institution requesting for consent documents of the selected IDs. Issues or discrepancies with the informed consent is reported to the Research Governance office of the Unit and document the resolution process. The IDs of verified consents are entered in the bio bank consent review tracker and copies are stored securely in accordance with data protection policies.

Conclusion: The implementation of this strategy has enhanced Good clinical practice, ethical bio banking and will lead to increased visibility and possibility of utilizing the stored samples by scientists from within and outside the organization.

PF-05 The Mathison Centre Neurogenetics Biobank and Advancing Precision Mental Health

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Neurogenetics Biobank is a research biobank that includes collaborators, multiple research institutes & studies based in the community and the clinic. The aim of the biobank is to support gene discovery and knowledge translation in child and youth mental illness and and precision medicine approaches. Method: Biobank features; controlled rate freezing, sample storage and transfer, ethics and biosafety, data preservation, documentation and consultation. Neurogenetics Biobank is currently focusing on major areas i. developing an outline of the types of biospecimens regularly collected, stored, retrieved and distributed in a biobank (https://www.bcplatforms.com) system and the procedures involved with strict standard operating procedures (SOPs) to ensure sample quality fits the purpose of use. ii. Implementing a specimen data and record management system for internal and external stakeholders, using an automated method, which ensures secure collection, storage and retrieval of genetic and phenotypic data. Research Involvement with Biobank: i. Gene & Environmental Influences on Behaviour and Cognition in Childhood Neuropsychiatric Disorders.2. PGx -Spark: the discovery of Pharmacogenetics markers and tools for Child and Youth Mental Health. Aim of this project is to implement Canada's first Pharmacogenetics testing service to improve drug treatment outcomes in children receiving mental health care 3. Harnessing the Power of Population-Based Samples for Detecting Gene x Environment Interactions. iv. Brain Function and Genetics in Pediatric Obsessive-Compulsive Behaviors. 4. Genetic Architecture for Youth Anxiety (GAYA), a pan-Canadian study. Funding includes multiple sources including NIH, CIHR, and Canadian Foundation for Innovation, the Mathison Centre, Hotchkiss Brain Institute, and Alberta Children's Hospital Foundation. Results: To date, biobank has successfully stored 5455 clinical biospecimens (DNA from blood, saliva, and buccal swabs) from eight different sites. Biobank system has also established a database system focused on sample tracking, phenotype-genotype linkage, and health information for different users in the USA. Conclusion: Neurogenetics Biobank applies dynamic approaches to gene discovery and precision medicine. We emphasize project engagement and return of value to participants, collaborators, and other stakeholders

Hot Topics

PG-01 Exploring a Shared Ecosystem for Biobanks in Chinese Research Hospitals: A Collaborative Innovation Model Based on Blockchain and Smart Contracts

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Statement of the Problem: As core assets for life sciences and precision medicine, China's research hospital biobanks have achieved scale advantages but face challenges in transitioning to value creation. Key issues include systemic silos—significant disparities in management, standards, and ethics across hospitals—hindering cross-regional integration and creating resource barriers. Security and trust deficits, exacerbated by data sensitivity, raise privacy concerns, while centralized management fails to resolve ownership and benefit-sharing ambiguities. Additionally, inadequate incentives limit collaboration among contributors, managers, and researchers, leaving high-quality samples underutilized. Renji Hospital employs Laboratory Information Management System (LIMS) for digital workflow standardization and project-driven resource optimization, implementing tiered access controls and ethical reviews. However, reliance on manual coordination impedes efficient collaboration essential for modern multi-center, big data research paradigms.

Proposed Solution: We propose a next-generation sharing ecosystem founded on "shared trust, benefit, and governance," enhancing existing systems through technological and institutional innovation. A standardized hospital-regional-national framework aligns with international standards and local contexts. Blockchain ensures data sovereignty and transparency, while privacy-preserving computation balances data utility with security. Operationally, an integrated resource directory and metadata repository enable FAIR principles. Smart contracts automate resource access, material transfers, contribution tracking, and benefit distribution, improving efficiency while reducing manual intervention. A contribution-based valuation system quantifies inputs across the sample and data lifecycle—from provision and quality control to annotation, analysis, and knowledge generation. These contributions are linked to resource access priority, collaboration opportunities, authorship, and revenue sharing, thereby activating ecosystem-wide participation.

Conclusions: This blockchain and smart contract-based ecosystem offers a viable pathway to optimize China's biobank utilization. It will expand from research hospitals to a national network, enabling cross-regional sample and data integration. This will advance disease research, drug development, and precision medicine, providing a "China solution" for global biobank sharing initiatives.

PG-03 On-Demand Organoid Construction from Cryopreserved Tissue Archived Blocks for Gastrointestinal Cancers

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Background: Conventional tumor cryopreservation safeguards DNA/RNA but typically sacrifices cellular viability, limiting downstream functional modeling. We present a biobanking

paradigm in which minced, cryopreserved tissue blocks are stored to retain viability. This enables on-demand, targeted construction of patient-derived organoids (PDOs)—by molecular subtype or clinical question—without continuous culture, reducing cost and operational burden. Such "living" cryo-archives reflect the future of biobanking: preserving macromolecular integrity and viability to support rapid, fit-for-purpose translational studies.

Methods: Gastric and colorectal specimens were standardized for pre-analytical handling, minced to ≤0.5 mm, suspended in DMSO-based cryoprotectant, slow-cooled to −80°C, and transferred to liquid nitrogen. On demand, vials were thawed and used to establish PDOs in Matrigel with lineage-appropriate media and routine passaging. Biobank-level QC included bright-field morphology, histopathology (H&E; lineage markers; Ki-67), and growth kinetics. For matched patients, PDOs from fresh versus cryopreserved tissue were compared head-to-head for morphology, histology, and chemotherapy response (5-fluorouracil, oxaliplatin, irinotecan) using viability-based dose–response and IC50 estimation.

Results: We implemented the cryopreserved-to-organoid workflow in gastric and colorectal cancers. Archived blocks (stored up to ≥12 months) yielded high post-thaw viability and successful PDO initiation in the large majority of samples. Cryo-derived PDOs expanded stably across passages and preserved gastric/colorectal architecture and lineage marker expression, with Ki-67 indices comparable to fresh-derived models. In two patient-matched comparisons, cryo- and fresh-derived PDOs showed indistinguishable morphology and histopathology and overlapping chemosensitivity profiles to 5-fluorouracil, oxaliplatin, and irinotecan, supporting functional equivalence for downstream assays.

Conclusions: Banking cryopreserved, viable tissue blocks operationalizes a cost-efficient, scalable living biobank for gastrointestinal cancers. By preserving both molecular substrates and cellular viability, this workflow enables rapid, on-demand organoid construction for drug testing and other functional readouts, transforming traditional repositories into agile platforms for precision oncology and biobank-integrated research.

PG-04 Phosphorylation of PHLDA2-S42 Regulates Ferroptosis under Metabolic Stress through ALOX12-Mediated Lipid Peroxidation

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Background: Metabolic stress such as glucose deprivation profoundly alters tumor cell survival and drug response. Our previous phosphoproteomic analysis identified a significant upregulation of PHLDA2 phosphorylation at serine 42 (S42) under glucose-deficient conditions, suggesting a potential link with ferroptotic regulation. PHLDA2-S42A mutation enhanced the interaction between PHLDA2 and ALOX12, promoting lipid peroxidation and cell death, implying that phosphorylation at this site may act as a metabolic switch in ferroptosis.

Methods: Phosphorylation-specific antibodies were generated to validate S42 modification under different glucose levels. PHLDA2-wild type, S42A, and S42D mutants were expressed in SCC25, B16, and U14 cell lines to assess cell proliferation, invasion, and ferroptotic phenotypes. GPX4 knockdown and ROS/lipid-peroxidation assays were performed to determine pathway dependency. In vivo, BALB/c nude mice were treated with synthetic S42A peptide (50 μM) alone or in combination with Anlotinib. Lipidomic profiling of tumor tissues and sera was conducted by LC–MS/MS to identify ferroptosis-related lipid alterations.

Results: S42 phosphorylation was significantly elevated under glucose deprivation and positively correlated with tumor PHLDA2 protein levels in human samples. S42A mutation or S42A-peptide treatment increased ROS and lipid peroxidation while suppressing tumor growth. GPX4 depletion further amplified these effects. Lipidomics revealed enrichment of oxidized phospholipids (PE 18:0/20:4, PE 18:0/22:6) and PUFA accumulation in S42A and S42A + Anlotinib groups, consistent with enhanced ferroptosis signatures.

Conclusions: PHLDA2 S42 dephosphorylation promotes ferroptosis via strengthened binding to ALOX12 and augmented polyunsaturated lipid oxidation. Combined targeting of PHLDA2 S42 phosphorylation and anti-angiogenic therapy (Anlotinib) synergistically suppresses tumor growth. These findings establish PHLDA2-S42 as a novel ferroptosis-related regulatory site and a promising therapeutic target for metabolically stressed tumors.

PG-05 Research Advances in Quality Control of Tumor Organoid Living Biobank

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Organoids, as highly promising in vitro biomimetic models, demonstrate broad prospects in biomedical research and clinical applications. High-quality organoids can precisely recapitulate the structure and function of native organs, ensuring the accuracy and reproducibility of research outcomes. This establishes a robust foundation for subsequent investigations into disease mechanisms, drug discovery, and precision medicine. Quality control of organoids constitutes a pivotal step in guaranteeing research reliability and application validity. This review comprehensively examines current landscape of tumor organoid quality control, covering critical quality control checkpoints across key technical stages of organoid construction process, advancements in standardization construction, and future development trends of organoid quality control. By elucidating these aspects, this work aims to empower researchers and practitioners to overcome challenges in quality control, enhance organoid fidelity, and accelerate the translation of organoid technology from fundamental research to clinical implementation.

PG-06 Urine Cancer Cells and PD-L1 as a Potential Non-Invasive Biomarker and a Living Biobank for Immune Checkpoint Inhibitor (ICI) Therapy in Bladder Cancer

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Bladder cancer (BCa) is a common urological malignancy with a high recurrence rate, often within 2 years of initial diagnosis and treatment. Due to this high recurrence, near all patients require cystoscopic surveillance, which is invasive, uncomfortable, and costly. The cost of surveillance makes this cancer the most expensive cancer per case among all cancer types in the US. Therefore,

early detection of recurrence or assessment of patients' response to treatment, particularly through non-invasive methods, is urgently needed. Since immune checkpoint inhibitors (ICIs) are widely used in many clinical trials for BCa treatment, having non-invasive and reliable biomarkers to select appropriate patients for ICI therapies or predict their treatment responses would be invaluable. Here we summarized the potential applications of programmed death-ligand 1 (PD-L1) from urine or urine BCa cell samples in BCa clinical settings. We discuss the use of both the free form of PD-L1 in urine samples and the expression levels of PD-L1 on the BCa cells shed in urine samples. Free PD-L1 can be measured with flow cytometry or ELISA-based approaches, while detecting PD-L1 on BCa cell surface requires isolating the urine-derived cancer cells and analyzing them via flow cytometry. Furthermore, we discuss the promising future research areas of urinary PD-L1 (uPD-L1) in bladder cancer, with a particular focus on the combination of conditional reprogramming cells (CRCs) technology and uPD-L1 studies, followed by an overview of several ongoing research topics. Based on current findings, urine cancer cells and uPD-L1 show great potential as a versatile biomarker and a living biomarker, further research is urgently needed to facilitate its translation into clinical applications.

PG-07 Viability Cryopreservation of Multiple Types of Tissues via a Novel Vitrification Platform Technology

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Biobanks serve as a crucial link between basic research and translational medicine, playing a pivotal role in advancing medical science. However, conventional biobanks primarily rely on preservation techniques such as fast-freezing in liquid nitrogen or paraffin-embedding, which can only conserve biomolecules like nucleic acids and proteins but fail to maintain tissue viability. This limitation renders many valuable clinical samples unsuitable for functional studies. To overcome this challenge, we developed ice-free vitrification methods that enable long-term preservation of diverse living tissues, thereby supporting the establishment of living biobanks to meet critical storage and research needs. In this study, we perfused cryoprotectants into various tissue slices-including mouse lung, liver, kidney, and intestine, as well as human lung cancer, liver cancer, gastric cancer, cartilage, and organoids-followed by rapid cooling to below -140°C to achieve a glassy state. Differential scanning calorimetry (DSC) confirmed that vitrification effectively suppressed ice crystal formation during both cooling and rewarming. AO/PI staining showed no significant difference in cell viability between rewarmed and fresh tissues. Similarly, the yield of organoids derived from rewarmed tissues was not statistically different from those obtained from fresh tissues. Hematoxylin-eosin (HE) staining revealed no structural differences between vitrified and fresh samples. Moreover, we successfully achieved in situ vitrification of organoids embedded in Matrigel. After rewarming, these organoids retained their original morphology and spatial arrangement, with cell viability comparable to that of the control group. Our approach enables high-quality, long-term storage of viable tissues and organoids, offering a next-generation platform for living biobanks. This work presents a novel strategy for constructing living biobanks and establishes a new paradigm for biomedical research and translational applications.

PG-08 An Ultra-rapid Cooling-warming Platform Based on Copper-based Mesh Magnetothermal Cryotubes Enables Vitrification Cryopreservation of Mouse Ovaries

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Background: As a promising approach for female fertility preservation, vitrification of ovarian tissue requires high concentrations of highly toxic penetrating cryoprotective agents (pCPA, up to 4.8 M).

Methods: An ultra-rapid cooling and rewarming platform based on a copper-based mesh magnetic cryotube (CMM-Cryotube) is proposed. First, low-toxicity pCPA loading protocols are screened using apoptosis detection. Subsequently, muse ovaries are vitrified in CMM-Cryotubes and rapidly warmed with MIH assistance. Then, morphological integrity of ovaries is assessed through histological staining and ultrastructural observation. Concurrently, changes in apoptosis, oxidative stress, and metabolic pathways are evaluated using multi-omics analysis and biochemical detection. Finally, ovarian physiological function is verified through *in vivo* transplantation experiments.

Results: This platform achieves a 90% follicle survival rate in mouse ovaries using a low concentration of CPA (2.69 M). In contrast, recovered ovaries exhibit superior tissue morphology, cellular ultrastructural integrity, and genetic variation compared with the conventional method. Transcriptomics and pathway enrichment analyses show that this strategy effectively inhibits apoptosis and inflammation-related pathway activity, reduces oxidative stress, and maintains metabolic homeostasis. Transplantation experiments confirm that the cryopreserved ovaries can restore fertility in recipient mice.

Conclusion: This study develops an ultra-rapid cooling and warming platform utilizing CMM-Cryotube. It reduces membrane boiling during cooling while achieving rapid and uniform warming. As a result, ice crystal damage during vitrification is effectively mitigated. This enables vitrification of ovarian tissue under low-concentration pCPA (2.69 M). Thus, it provides a highly promising new approach for female fertility preservation.

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PG-09 Static Magnetic Field Combined with L-Proline Promotes Cryopreservation of Retinal Organoids by Inhibiting Adverse Stresses

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Retinal organoids are powerful three-dimensional models for retinal physiology, disease research, and drug screening. However, their complex structure renders them highly sensitive to

multiple low-temperature-induced stresses, severely limiting cryopreservation efficacy. Low temperature induces endoplasmic reticulum stress, oxidative stress, impaired cell junctions, and reduced viability in retinal organoids. To address this issue, static magnetic field (SMF) can directly inhibit these adverse stresses and regulate cell membrane permeability to support the function of L-proline, with the two exerting a synergistic effect to enhance stress relief. L-proline specifically inhibits endoplasmic reticulum stress (EDEM1, GRP94 genes), reactive oxygen species (ROS, SOD1 gene), and ferroptosis-related gene ACSL4. We propose a combined SMF-L-proline preservation strategy: a low-intensity adjustable SMF can directly suppress adverse stresses and regulate membrane permeability to assist the function of L-proline, synergizing with L-proline to regulate ROS metabolism, alleviate endoplasmic reticulum stress, stabilize membrane potential, and inhibit ACSL4, thereby reducing cell damage and apoptosis. The optimized preservation system contains L-proline, antioxidants, and low-concentration cryoprotectants (CPAs). L-proline acts synergistically with SMF, where SMF can directly inhibit low-temperature-induced adverse stresses and regulate cell membrane permeability to support the function of L-proline, specifically addressing the stress sensitivity of retinal organoids, reducing osmotic injury, and maintaining their integrity. In vitro experiments show that the post-preservation recovery rate of retinal organoids using this strategy is over 90%, and their morphology and metabolic activity are comparable to those of fresh samples. This combination has good biocompatibility and does not affect the subsequent functions of retinal organoids, providing a non-invasive and scalable method for the preservation of stress-sensitive retinal organoids.

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Advanced Technologies

PH-01 A Dual-Pronged Strategy: Integrating Top-Down and Bottom-Up Approaches to Maximize Biobank Data and Sample Utilization

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Problem: Despite serving as cornerstones of modern biomedical research, many biobanks remain underutilized, leaving extensive collections of high value biospecimens unused. This gap between biospecimen collection and research application represents a significant loss in scientific potential and returns on investment. To address this, an integrated, protocol-driven strategy is proposed to reconceptualize the biobank's role - from a simple sample repository to a dynamic, collaborative research partner.

Solution: The proposed model adopts a dual, synergistic framework that integrates both bottom-up and top-down strategies. The "bottom-up" approach focuses on the proactive enhancement of samples and their related data from point of collection. This involves: (1) systematic incorporation of comprehensive multi-omics annotation, including genomics and proteomics; (2) strict adherence to Findable, Accessible, Interoperable, and Reusable (FAIR) data principles across all clinical and analytical datasets to ensure machine readability and seamless integration; and (3) the implementation of adaptive, AI-supported screening tools to optimize participant recruitment and sample collections. These measures ensure each specimen represents a thoroughly characterized, valuable research resource. Complementing this, the "top-down" approach facilitates hypothesis-driven exploration of the biobank in its entirety. TThis includes: (1) user-friendly data portals with advanced querying capabilities to enable researchers to identify and assemble "virtual cohorts" across studies before requesting physical samples; (2) establish streamlined, transparent governance and data access committees to prioritize and expedite scientifically rigorous requests; and (3) encourage proactive collaboration with research consortia to align collection priorities with emerging scientific trends.

Conclusions: This two-tiered strategy establishes a self-reinforcing feedback loop between data collection and analytical interpretation. Comprehensive data collection strengthens the capacity of studies to generate high-impact scientific outcomes. In parallel, top-down analyses identify valuable sample cohorts, guiding subsequent characterization efforts and optimizing the utilization of resources. By aligning these complementary processes, this integrated approach maximizes the utility of biobank resources, accelerates scientific discovery, and elevates the value of contributions from sample donors.

PH-02 Bridging the Gap from Operational Function to Accreditable Quality: Implementation of a Unified Quality Management System Driven by Automated Processes and Digital SOPs at the MUB Biobank

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Statement of the Problem: For many academic biobanks, achieving international accreditation according to the ISO 20387 can be a daunting challenge. While daily operations may be functional, they often rely on informal practices and disparate records, creating a significant gap against the rigorous requirements of a standardized Quality Management System (QMS). The Medical University of Bialystok Biobank (MUB Biobank) faced this exact issue: a need to formalize its processes, establish objective performance metrics, and implement a robust Quality Assurance framework to demonstrate its commitment to being "fit-for-purpose" for high-impact research.

Proposed Solution: We initiated a strategic project to design and implement a comprehensive QMS aligned with international standards. The cornerstone was the integration of our fully automated –80°C storage system with a centralized Laboratory Information Management System (LIMS).

This technological backbone was used to enforce Standard Operating Procedures (SOPs) digitally, ensuring strict adherence to predefined protocols for sample processing, storage, and retrieval. The system automatically generates auditable trails for every action. We developed a structured QC program, including continuous temperature monitoring with defined alert/action limits and regular sample quality checks. Key Performance Indicators (KPIs), such as sample processing turnaround time, retrieval accuracy, and incident reporting rates, were established and are now tracked through the LIMS to provide quantitative evidence of operational control and continuous improvement.

Conclusions: The implementation of this unified, technology-driven QMS has transformed MUB Biobank's approach to quality. Digital SOP enforcement has eliminated procedural deviations, while automated data capture has provided an irrefutable audit trail for all critical processes. The defined KPIs offer objective evidence of performance, moving beyond subjective assessment to data-driven quality control. This framework has not only standardized our operations but has also provided the foundational evidence required to pursue formal accreditation. Our experience demonstrates that integrating automation with a digital QMS is a powerful strategy for biobanks to rapidly elevate their repository standards, ensure sample quality, and build trust with the research community

PH-03 Construction and Clinical Application of SPDOs Organoid Cell Lines for Gastric Cancer

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Background: Organoids are new type of experimental models that highly mimic the morphology and biological functions of their parental organs. Gastric cancer as a highly lethal cancer, stable organoid models will be helpful for personalized medicine and translational usage.

Methods: We collect fresh tissues from gastric mucosa, primary cancer and metastatic cancer of lymph nodes after gastrectomy, and construct organoids. By long-term passaging and expanding at 3D culture in vitro, we obtain stably growing organoid cell lines, which are identified by multiple omics, short tandem repeat detection, karyotype analysis, and tumorigenesis in nude mice. We also examined the drug sensitivity for fluorouracil, platinum, and paclitaxel.

Results: A total of 55 organoid cell lines are established. Among those, 12 paired organoid lines are from primary cancer and corresponding normal mucosa. Two paired cancer organoids cell lines are derived from primary cancer and metastatic cancer of lymph nodes. Those organoid cell lines are named as SPDON (means normal), SPDOP (means primary), and SPDOLM (means lymphatic metastasis), respectively. Two paired SPDOPs and SPDOLMs show unique short tandem repeats and karyotypes, confirmed tumorigenesis in vivo, and clear genetic profiles. The drug sensitivity of cancer organoids cell lines is characterized at the same time.

Conclusions: The organoid cell lines are well established living biobank. The paired SPDONs and SPDOPs or SPDOLMs are good models for drug screening and safety evaluation.

PH-04 Cryogenic Technology: From Broad Applications in Life Sciences to Cutting-edge Practices in Biological Sample Preservation

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Cryogenic technology is widely applied in the life sciences, with significance in areas like medical therapies, microscopic imaging, and biomaterial processing. The long-term preservation of biological samples such as cells and tissues is a critical cornerstone of biobanking and regenerative medicine. However, this field faces significant biophysical challenges, including uncontrollable ice crystal formation, osmotic damage, and the limitations of traditional technologies in cost and operation.

This report provides a systematic overview of the diverse applications of cryogenic technology in the life sciences and delves into the fundamental principles of biological sample preservation. It highlights the processes of crystallization and vitrification during preservation and the impact of different cooling methods on cell viability. Building on this foundation, the paper introduces two innovative technologies designed to address these challenges: a deep cryo-storage technology based on electric cooling, which uses an advanced refrigeration cycle to replace the reliance on liquid nitrogen, providing a stable and reliable environment for long-term sample storage; and an ultra-fast visual freezing-thawing platform, which combines high-efficiency heat transfer with high-resolution imaging, allowing researchers to observe and analyze the microscopic dynamics of the freezing-thawing process in real time. This work integrates the fundamental principles of cryogenic technology with innovative practices, offering new perspectives and solutions for advancing cryobiology and biobanking.

PH-05 DCLK1+ Inflammatory CAFs Define a Poor-Prognosis IM1 Program Underpinning Perineural Invasion in Gastric Cancer

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Background: Perineural invasion (PNI) portends adverse outcomes in gastric cancer (GC), but its stromal–neuronal determinants remain unclear. We hypothesized that a neuro-immunomodulatory cancer-associated fibroblast (CAF) state, marked by DCLK1, organizes a PNI-competent microenvironment.

Methods: From clinically annotated bulk cohorts, we curated a 78-gene neuro/immune panel enriched in PNI and performed NMF on PNI-positive cases (K=2) to derive IM1/IM2 subtypes. Survival, GO and HALLMARK GSVA, and ESTIMATE stromal/purity indices were compared among PNI-negative, IM1, and IM2 groups. External concordance was assessed in ACRG (expression maps, Lauren/EMT/T-stage). Single-cell RNA-seq from 7 GC specimens with PNI labels underwent Harmony

integration, malignant inference (inferCNV), and CAF subtyping; IM1/IM2 module scores and DCLK1 expression were quantified across cell types and within CAFs. Exploratory analyses stratified by HER2 status.

Results: NMF stratification separated prognosis (PNI-negative best, IM1 worst, IM2 intermediate). IM1 was enriched for axon-guidance/neurite development and showed higher HALLMARK MYC TARGETS V1, with higher stromal scores and lower tumor purity versus comparators. In ACRG, the 78-gene panel reproduced IM1-high signals; IM1 overlapped Lauren diffuse and EMT and accrued T3/T4 disease, whereas IM2 resembled PNI-negative. Single-cell analyses localized IM1 scores to CAFs, with a dominant DCLK1+ inflammatory CAF (iCAF) program; DCLK1 expression and progenitor-like signatures concentrated in iCAF residing adjacent to CNV-defined malignant epithelium. IM1–DCLK1+ iCAF enrichment persisted after HER2 stratification, indicating a HER2-independent stromal–nerve axis.

Conclusions: Across bulk and single-cell layers, DCLK1+ iCAFs anchor an IM1 program that couples axon-guidance and MYC activity with stromal expansion and poor outcome in PNI-positive GC. These data nominate DCLK1-centered stromal targeting and drug repurposing as plausible strategies to disrupt PNI-competent niches and improve prognosis.

PH-06 Emerging Fluorescence Technologies For Empowering Biospecimen Science Research in Biobanks

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Besides being the cauldron for ideas on biospecimen research, biobanks are also emerging as pivotal health delivery frameworks thereby facilitating collection and curation of high-quality specimens for precision health. There is an increased appreciation for well-designed biobanks for procuring and maintaining a repository of high-quality specimens for patient-oriented research. Research dissemination of specimens from the repositories need to be quality-controlled and be associated with metadata that are compliant with the ethical and regulatory principles that govern the biobank workflow. Traditional approaches for tissue quality control (e.g morphological assessment in glass slides) are limited to century-old histological stains that are still reliable and yet, are not without limitations. The knowledge gaps in biospecimen quality assessment using traditional approaches stem from the lack of scalability, limited quantitative information and the lack of sensitivity and specificity. Fluorescence approaches have the power of revolutionizing biospecimen science research in biobank settings by overcoming the aforementioned problems.

In this presentation, we will present our laboratory results demonstrating how emerging fluorescence techniques and high-throughput technologies have been integrated in our biobank quality control framework. More specifically, we will highlight our laboratory results from: (a) archival tissue quality control (rapid tumor assessment) by fluorescence lifetime imaging (FLIM) modality, (b) plasma quality control by redox fluorimetry analysis, (c) living organoid characterization by high-resolution three-dimensional confocal fluorescence techniques, (d) biobank tissue quality control by multiplexed immunofluorescence using curated antibody-panels, (e) digital spatial profiling & transcriptome sequencing in paraffin embedded biobank tissues, and (f) large scale digital pathology image analytics platform for automated tissue pattern recognition in bright field and fluorescence images.

As the biobanks serve as functional conduits between the clinical patient specimens and the laboratory biospecimen research, emerging technologies need to be integrated to expedite the scientific discoveries and innovation. This presentation will demonstrate how leveraging the emerging fluorescence and other technologies can bring about the much-needed synergy between modern biobanking tools and biospecimen research outcomes.

PH-07 Empowering the Optimization of Scientific Research Resources: Construction and Application of a Cost Accounting Model for Biological Samples

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Background: As precision medicine and translational research continue to advance, Biobanks—essential infrastructures for scientific research—face major challenges in managing and allocating operational costs effectively. This study aims to build and apply a practical cost accounting model for Biobanks to address common problems such as unclear cost boundaries and inefficient resource use found in traditional accounting methods.

Methods: The model is designed around three common Biobanking operation models, goes through five phases: Needs Analysis and Objective Definition - Cost Element Identification and Classification - Model Construction and Method Selection - Model Verification and Parameter Correction - Model Application and Dynamic Optimization, and includes key cost components such as amortization, equipment, labor, and materials. Based on the full life cycle of samples, it covers six main stages: collection, processing, storage, sharing for research, quality control, and transportation. By combining activity-based costing with variable costing, the model calculates the unit cost for different types of samples in a precise and systematic way.The accounting results of the cost model shall be linked to the operational objectives of the biobank, thereby forming a feedback loop.

Conclusions: Real-world applications have shown that this cost model is both feasible and valuable. It helps identify cost drivers, supports accurate sample pricing, and improves overall accounting precision. The model also provides strong data support for better resource allocation, equipment purchasing, and

staff planning—helping reduce unnecessary expenses and increase efficiency. In addition, its built-in flexibility allows Biobanks to adapt easily to scale expansion and technological upgrades. Ultimately, this model supports sustainable operations and helps transform Biobanks from "cost centers" into "value centers," promoting their long-term, high-quality development.

PH-09 Experience in Establishing Patient-Derived Organoid Models of Gynecologic Tumor

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Gynecological tumors pose a significant threat to women's health. Patient-derived organoids (PDOs) have emerged as a transformative model in biomedical research, capable of closely recapitulating the histological structure, genetic profile, and drug response of primary tumors. They offer broad potential in disease modeling, drug development, and clinical decision support. However, the key challenges is lack of standardized protocols for PDOs culture procedures, which would result in variable success rates and restricting the clinical translation.

Recently, our team established the standardized culture protocols and a quality control system for PDO models of Gynecologic tumor, including ovarian cancer, endometrial cancer and cervical cancer. A unified workflow was established, including tissue acquisition, processing and culture, passaging and cryopreservation. The proportions of malignancy components were over 70%, which was confirmed via H&E staining and immunohistochemistry. Next-generation sequencing (NGS) and drug sensitivity profiles were detected, and clinical data were collected.

By integrating with clinical, genomic, and pharmacological data, our PDOs platform could enable more accurate clinical decision-making, uncovers novel resistance mechanisms, and identifies potential biomarkers. It not only facilitates ongoing basic research but also paves the way for future initiatives such as "organoid cohort studies," exploration of alternative clinical trial endpoints, and the advancement of personalized precision medicine.

PH-10 Metabolic Programming of Tumor-Associated Macrophages Promotes T Cell Exhaustion in Uveal Melanoma

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Background: Uveal melanoma (UM) is the most common primary intraocular malignancy in adults and responds poorly to immune checkpoint inhibitors (ICIs), partly due to its highly immunosuppressive microenvironment. This study aimed to characterize the heterogeneity of tumor-associated macrophages (TAMs) in UM and their contribution to T cell exhaustion.

Methods: Single-cell RNA sequencing (scRNA-seq) was used to analyze the immune microenvironment of UM. Cell-type composition deconvolution of bulk RNA-seq datasets was performed to identify TAM subsets associated with clinical prognosis. Multiplex immunohistochemistry (IHC) and in vitro assays were conducted to examine the relationship between TAMs and CD8+ T cell exhaustion. TAM glycolytic pathways were modulated in vitro to evaluate their effects on T cell function. In vivo validation employed a syngeneic mouse UM model treated with TAM-targeted metabolic interventions combined with ICIs.

Results: scRNA-seq revealed diverse TAM subsets within the UM microenvironment, including metabolically active macrophages. Deconvolution of bulk RNA-seq indicated that the metabolically reprogrammed, glycolysis-high TAM subset was closely associated with poor clinical prognosis. IHC and in vitro assays confirmed that these TAMs correlated with CD8+ T cell exhaustion. Targeting glycolysis in TAMs restored T cell proliferation and cytokine production while reducing exhaustion marker expression. In vivo, metabolic reprogramming of TAMs synergized with ICIs, enhancing CD8+ T cell infiltration and suppressing tumor growth.

Conclusion: Glycolysis-driven TAMs promote T cell exhaustion and immune evasion in UM. Targeting TAM glycolysis represents a promising strategy to improve immunotherapy efficacy in this malignancy.

PH-11 Optimization of Whole-Mount Autofocusing SMALDI Mass Spectrometry Imaging for Spatially Resolved Lipidomic Profiling of Patient-Derived Organoids

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Background: Tumor organoids (TOs) offer a personalized perspective for assessing treatment response. However, the presence of normal organoid (NO) residuals poses a potential threat to their utility for personalized medicine. There is a crucial need for an effective platform capable of distinguishing between TO and NO in cancer organoid cultures.

Methods: We introduced an innovative and convenient whole-mount (WM) preparation protocol for the in-situ visualization of the lipidomic distribution of organoids. In detail, the organoid pellet suspended in DPBS at a density of 20 organoids/well was carefully transferred to the center of the slide chamber. Then, the organoid pellets were resuspended in 4 % paraformaldehyde (PFA) in PBS for durations of 5, 15, 30, and 45 min. After, the organoids were then washed with deionized water and 150 mM ammonium formate solution, performed step by step. Subsequently, the chamber was removed from the slides. Lastly, PDOs were analyzed by imaging mass spectrometry. A total of 15 PDOs containing breast cancer organoids (BCOs) and normal breast organoids (NBOs) from 4 patients were analyzed. Poly-L-lysine coated slides, equipped with 12 well chambers, were utilized as a carrier for the high-throughput analysis of PDOs.

Results: Optimizing the fixation time to 30 minutes, preserved the integrity of organoids and the fidelity of lipid compounds. T-SNE plots showed the organoids cultured from the same patient were clustered more closely based on their similarity concerning 604 lipid signatures. The four patients were clear

separated in the t-SNE maps. In addition, the distinctive lipidomic signatures exhibited greater disparities between various states of PDOs, such as BCOs and NBOs. 288 lipids (136 higher and 152 lower in BCOs) showed significant differences in abundance between BCOs and NBOs. For example, elevated expression of PC 34:1 and SM d34:1 was observed in BCOs, whereas PC 36:2, TG52:2, PA 38:2 and PC 32:1 were elevated in NBOs.

Conclusions: We have successfully developed an efficient platform for in situ visualization of the lipidomic signature of 3D organoids using Whole-Mount AF SMALDI MSI. This analytical technique significantly reduces the time, and saves precious PDOs to depict the lipidomic heterogeneity of organoids at single organoid scale. This method, as a complementary tool, offers a platform for both basic and clinical organoid research.

PH-12 Requalification and Data Management of Pediatric Biological Samples Collected Since 1984: A Case Study from a Neuroblastoma Collection

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Introduction: The Biological Sample Management Platform (PGEB) of the Centre Léon Bérard is responsible for the preparation, preservation, storage, and provision of the institution's sample collection. The PGEB was approached to integrate a neuroblastoma collection, one of the most common pediatric cancers. This collection was initiated through the diagnostic reference activity for neuroblastoma at the Centre Léon Bérard.

Objectives: To requalify pediatric biological samples collected between 1984 and 2024 in order to make them available for pediatric research protocols.

Methods: This study began with an assessment of the data associated with each of the 21,389 samples in the collection. These data were then compared with relevant regulations and consensus documents related to biobank data management, as well as the minimum data requirements for research use. Based on this, a methodology for sorting samples either for retention or disposal was applied.

Results: A set of minimum information criteria was established to revalue the samples. Various texts applicable in France mention the minimum data required for making samples available, but no general consensus exists, either nationally or internationally. Furthermore, 65% of the samples met the criteria and were retained for future research use.

Conclusion: This article describes the research work that led to the identification of minimum required data. However, further development is needed to harmonize practices regarding data management and interoperability.

PH-13 Technical Standards and Specifications for Establishing a Primary Oral and Maxillofacial Tumor Cell Bank via Conditional Reprogramming

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The preservation, management, and rational utilization of genetic resources have become critical strategic issues concerning national security, global development, and public health. While significant attention and progress have been made in tumor biobanks, management, and resource sharing, conventional preservation techniques for tumor biospecimens are increasingly inadequate to meet the growing demands for both quality and quantity of tissue samples, particularly for oral and maxillofacial tumors, where tissue availability is often limited. The conditional reprogramming (CR) method, which enables the acquisition, in vitro culture, and expansion of primary epithelial cells from healthy and tumor tissues, offers an ideal solution for establishing primary cell banks. The Conditional Reprogramming (CR) method is a technique for the in vitro cultivation of primary cells derived from healthy human tissues and/or patient tumor samples. In tumor conditional reprogramming cell cultures, the phenotypic and genotypic characteristics of the primary tumor are preserved. This approach can be further integrated with genetic analysis and high-throughput drug screening systems, demonstrating significant advantages in drug screening and the development of personalized combination therapy regimens, which have been clinically applied and validated . Compared to patient-derived xenografts (PDXs), patient-derived tumor cell (PDC) models, and patient-derived organoids (PDOs), CR technology offers advantages such as high efficiency, stability, and ease of scalability. It holds important application value for advancing fields such as tumor molecular subtyping and regenerative medicine. Furthermore, primary living cell banks established using the CR method exhibit considerable potential and promise as complementary platforms for clinical research in basic medicine, regenerative medicine, chemical medicine, and precision medicine. Thus, we propose the development of technical standards and specifications to guide the establishment of oral and maxillofacial tumor primary cell banks. Serving as a complementary extension to traditional tissue biobanks, such cell banks would provide passageable and expandable cell samples for basic medical research, translational medicine, and clinical studies. This approach effectively addresses bottleneck challenges such as tumor biospecimen scarcity and holds significant potential for advancing precision diagnostics and therapeutics.

PH-14 Translating Human Intent into SQL: A Case Study of a PHP-based AI Bridge in an Academic Biorepository

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Statement of Problem: For small biorepositories, data accessibility can be an operational bottleneck. Biospecimen data is often stored in relational databases, querying this data requires knowledge of Structured Query Language (SQL). This creates a "data bottleneck" between non-technical staff (users) and the data needed for routine workflows. Biospecimens are underutilized as being too difficult for non-technical users to find.

Workflows are choked creating a dependency on a Database Administrator (DBA) to create ad hoc queries.

This study evaluates the utility of Artificial Intelligence (AI) to bridge this technical gap and enhance the user experience. This activity can be conducted using a range of natural or large language (NLM, LLM) models installed locally or at commercial company servers.

Proposed Solution: We developed a Proof of Concept (PoC) using a lightweight PHP-based bridge that connects the Gemini Flash Large Language Model (LLM) directly to database metadata. Unlike traditional NLM search tools that require extensive data indexing or training via Retrieval-Augmented Generation (RAG), this solution uses a Data Definition Language (DDL) approach. The workflow allows users to input plain English requests. The AI model parses the intent and generates the SQL syntax to query the repository SDMS database.

By feeding the AI a cleaned projection of SDMS schema—including Canonical field notes and business rules—the model was trained:

- Auto-Filter: Automatically append administrative filters.
- Dynamic Joins: Automatically resolve joins between header tables and inventory tables using double-precision keys.
- Code Translation: LEFT JOIN logic to translate cryptic internal codes into human-readable display values via the translated value table.
- Default Intelligence: Apply "Default Projections" to vague queries

Conclusions: The PoC successfully demonstrated that a PHP-mediated AI layer could achieve high execution accuracy without modifying the underlying legacy data structure using a DDL infrastructure. Allowing users to 'speak plain english' when requesting data, by-passing the bottleneck of awaiting DBA assistance. Preliminary testing showed that the model interpreted 95% of common researcher queries, such as "Find frozen lung samples from donors over 60." This approach provides a scalable, cost-effective roadmap for biobanks to modernize data access.

Innovative Technology

PI-01 65-Degree Short-Term Heating: A Method for Transporting Urine Samples Over Long Distances Without Cold Chain

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Biomarkers are measurable changes associated with physiological or pathophysiological processes in the body. Urine, not strictly regulated by homeostatic mechanisms, accumulates extensive variable information and reflects changes in the body earlier and more sensitively, making it an excellent source for biomarker discovery. However, long-distance transport of urine samples usually requires a strictly maintained cold chain throughout the process, which leads to high costs and operational challenges. Here, we propose a urine sample processing method that uses brief heating to inhibit bacterial proliferation and protein degradation. A single urine sample was divided equally into three groups: a pre-heated transport group, a non-heated transport group, and a −80 degree frozen storage control group, with each group consisting of five replicates. Both the pre-heated and non-heated transport groups were transported simultaneously across northern and southern China for five days under ambient temperature conditions. Samples were analyzed using liquid chromatography coupled with tandem mass spectrometry. The results showed that for urine samples pretreated by 65 degree water bath heating for 15 minutes and −80 degree freezing storage, the intra group overlap rates of identified proteins were 97.1% and 97.5% respectively, both indicating high intra group repeatability. There were no significant differences in the number or types of urinary proteins identified between these two groups, with an inter-group overlap rate of 99.9%. Additionally, the pre-heated transport group and frozen storage control group showed no significant difference in the number of bacterial-derived peptides and proteins identified. In contrast, significantly more bacterial-derived peptides and proteins were identified in the non-heated transport group than in both the pre-heated transport and frozen storage control groups. This indicates that heating effectively suppresses bacterial counts in urine samples during five days of transport at ambient temperatures. This approach provides a more economical and convenient solution for long-distance transport of urine samples, eliminating the need for cold chain transportation or preservatives. We also recommend consistent urine processing methods within the same study to minimize technical variability.

PI-02 Agentic Biobank Intelligence: Autonomous AI Systems for Dynamic Specimen Discovery and Demand-Driven Curation

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Biobanks are essential for precision medicine but remain limited by inefficiencies in specimen discovery, quality control, and demand alignment. Traditional machine learning treats them as static repositories, whereas agentic artificial intelligence introduces autonomy, reasoning, and adaptability. Agentic Biobank Intelligence envisions a network of AI agents that interpret and act on evolving biobank data, structure metadata from clinical and laboratory sources, and match specimens to research needs using multimodal reasoning. Higher-level agents analyze trends in requests and publications to anticipate future demand. Through shared ontologies and human oversight, the system remains transparent and compliant while continuously improving specimen matching, reducing waste, and guiding acquisition. This approach transforms biobanks into active, learning partners that orchestrate data, demand, and discovery.

PI-03 AI–Enhanced Single Mode Electromagnetic Resonant Rewarming Technology for Optimal Cryopreservation and Biobanking

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Optimal cryopreservation method and technology play pivotal roles in long-term low temperature storage and biobanking of biospecimens to maintain samples' viability, integrity, and functionality. A great challenge for the successful cryopreservation is the cryoinjury caused by lethal ice-recrystallization (LIRC) and thermal-stress induced tissue fracture (TITF) during the rewarming process. Rapid and uniform rewarming is indispensable for preventing LIRC and TITF. The advanced Single-Mode Electromagnetic (EM) Resonant (SMER) rewarming technology has been developed to achieve superior rapid-uniform heating capability. However, it was revealed that the dielectric properties of a biospecimen may vary markedly with temperature change during SMER rewarming process, resulting in continuous drift of the resonant frequency in SMER cavity. Such frequency excursion reduces energy coupling efficiency and therefore limits biospecimen's rewarming rate. To address this challenge, a novel dual-mode adaptive resonant tracking system is developed in the present study, based on a dual RF Switch measurement architecture and a machine learning–based AI frequency prediction model to enhance frequency-locking precision and energy utilization efficiency during the SMER rewarming. The system employs two RF switches to perform high-speed, multi-band alternating measurements, capturing the dynamic evolution of sample resonance characteristics with high temporal resolution and continuously updating the frequency response model. During non-measurement intervals, a machine learning algorithm trained on reflected energy features predicts transient frequency drift and performs adaptive correction, enabling continuous and high-precision frequency locking control. This approach not only improves the stability and thermal uniformity of the SMER rewarming process but also effectively reduces energy reflection and local overheating risks, providing an optimal energy regulation pathway for efficient rewarming of complex biospecimens with different sizes. Experimental results showed that, under identical power conditions, the AI-enhanced system significantly increases both EM energy utilization efficiency and sample rewarming rate. This work establishes an AI and scalable SMER control strategy for rapid and uniform rewarming of large-volume specimens, offering a robust technological foundation for high-quality rewarming and precise energy management in modern biobanking applications.

PI-04 An Optimized and Automated Platform for High-Quality PBMC Isolation: A Comprehensive Evaluation of Standardized Methods with Integrated Plasma Collection

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Background: The standardization of peripheral blood mononuclear cell (PBMC) isolation is critical for reproducible immunological research and biobanking. Manual methods are plagued by operator-dependent variability and low throughput, while the performance of alternative techniques on automated platforms remains underexplored. Furthermore, traditional whole-blood processing forfeits the concurrent collection of high-quality plasma.

Methods: We developed a novel "plasma-first" process and evaluated its integration with an automated liquid handling platform, compatible with three isolation techniques: the classic Ficoll approach, isolation by SepMate tubes with Lymphoprep, and isolation by Lymphocyte Separation Tube for Human Peripheral Blood. Key innovations included upfront plasma separation and high-throughput processing, capable of simultaneously isolating PBMCs from 8+ samples per run under unified parameters. Performance was assessed against manual standards using cell yield, viability, purity, and post-thaw functionality.

Results: The automated platform robustly replicated manual separation outcomes across all three methods, with the Ficoll and Lymphocyte Separation Tube techniques showing particularly stable performance. Crucially, the "plasma-first" workflow enabled parallel collection of high-quality, cell-free plasma alongside PBMCs. Automated processing eliminated inter-tube delays and variability inherent in manual techniques, ensuring exceptional consistency across all samples within a batch.

Conclusions: We present a standardized, high-throughput automated workflow that not only universalizes PBMC isolation across multiple techniques but also maximizes biobanking value through integrated plasma and PBMC recovery. This "plasma-first" approach, coupled with unmatched batch-to-batch consistency, addresses a critical need for precision and scalability in large-scale clinical studies.

PI-05 Optimizing FFPE Storage For The Future: Improving Space Utilization, Sample Integrity, And Traceability Through High-Density Automated Storage

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Background: Biobanks house formalin-fixed paraffin-embedded (FFPE) tissue specimens that are critical for translational research. Many legacy collections remain stored in traditional filing cabinets without unique locations assigned which limits scalability, consumes valuable floor space, and cannot accommodate accurate specimen tracking. As the AZ US Biobank expanded, we initiated a modernization project to transfer all FFPE materials from conventional storage to high-density automated storage cabinets to improve space efficiency, sample preservation, and digital traceability.

Methods: The AZ US Biobank conducted a comparative assessment of physical footprint, environmental stability, retrieval accuracy, and cost for the storage of FFPE blocks and slides. Each barcoded cabinet with barcoded trays was setup within the lab space and also electronically within the Laboratory Information Management System (LIMS). FFPE blocks

and slides were barcoded before accessioning into unique locations within the high-density cabinets. Each sample was assigned a unique digital location within the cabinet, enabling retrieval mapping and inventory validation. An assessment of space utilization and of temperature and humidity across several points within the cabinets was conducted.

Results: Transitioning to high-density storage reduced the physical footprint of the FFPE archive by 60%, creating significant space savings and enabling consolidation of multiple collections into one controlled environment. Temperature and humidity within the cabinets remained stable across measurement points. Integration with LIMS secured unique locations for each sample. Retrieval time decreased by 40%, and staff handling of specimens was reduced by 50%, lowering the risk of physical wear. Cost modeling demonstrated long-term savings through reduced facilities requirements, energy efficiency, and time savings in inventory management and audits.

Conclusions: Upgrading FFPE storage to a high-density, digitally integrated system enhanced operational efficiency, environmental control, and data integrity. The modernization maximized space utilization, safeguarded specimen quality, and strengthened cost effectiveness while ensuring full traceability of every sample within the LIMS. This case study provides a replicable model for other biobanks seeking sustainable, scalable storage solutions that align infrastructure modernization with scientific stewardship.

PI-06 The Gateway to Biological Research. BioOne!

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Bio-resources are essential materials for biotechnological research and industry. Given their importance, many countries have focused on the acquisition and utilization of bio-resources. Recognizing this, Korea has made considerable efforts to collect these resources since the 2000s.

By 2024, Korea had accumulated a total of 20,709,924 bio-resource samples, with 812,241 samples distributed in 2024 alone. However, changes in both domestic and international circumstances, such as the entry into force of the Nagoya Protocol and the global pandemic, have highlighted the need to adjust policies regarding the acquisition of bio-resources and the establishment of bio-resource banks. In July 2020, Korea announced its 3d national strategy for bio-resources, which has led to changes in how bio-resources and their data are utilized.

As part of this strategy, bio-resource banks are now organized into 14 units, including human tissues, pathogens, cell lines, experimental animal models, microorganisms, plant extracts, and more. Additionally, to enhance the utilization of bio-resource data, the BioOne platform (a one-stop bio-resource service) is being established in 2024. This platform will allow users to search for research papers, patents, research results, and bio-resources, and will enable the ordering and distribution of bio-resources. In this presentation, I will explain the management of bio-resources in Korea and provide an overview of the BioOne platform (https://www.bioone.re.kr/en/main).

PI-07 Thermal Safety Oriented Single Mode Electromagnetic Resonance Rewarming Using Temperature Feedback Model Predictive Control for Optimal Power Selection to Prevent Overheating of Vitrified Biospecimens

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The development of cryopreservation methodologies and technologies plays a critical role in long-term cryogenic storage and biobanking by preserving biospecimen viability, structural integrity, and functional stability. A major challenge in successful cryopreservation occurs during rewarming, where cryoinjury can result from lethal ice recrystallization and tissue fractures caused by thermal stress. For vitrified biospecimens, rapid and evenly distributed rewarming is crucial. Single-mode electromagnetic resonance rewarming (SMER) allows rapid volumetric heating through resonant EM energy deposition; however, in real operation, temperature-dependent changes in the specimen's dielectric properties and cavity coupling conditions can cause the heating response to vary significantly over time. Such nonstationary dynamics increase the risk of temperature overshoot and localized overheating, which can cause irreversible thermal damage, including protein denaturation, disruption of cellular membranes and cytoskeletal structures, and metabolic imbalance, ultimately decreasing post-rewarming viability and potentially leading to permanent tissue or organ failure. To improve thermal safety in SMER rewarming, we propose a closed-loop power regulation system that combines real-time temperature sensing with model predictive control (MPC). The system alternates between short resonance-characterization intervals and heating intervals using an RF-switching architecture while continuously taking temperature measurements. A compact, online-updated input–output heating-response model is integrated into the MPC optimization to determine power commands while respecting explicit engineering constraints, including a strict upper limit on deliverable power. The control objective is to allow higher power during the initial phase of rewarming to quickly pass through critical temperature ranges, and to gradually decrease power as rewarming nears completion to prevent temperature overshoot and localized overheating. This work creates a pathway for safety-focused closed-loop SMER rewarming and provides a basis for future integration with resonance-aware energy scheduling and control strategies.

PI-08 A Portable, Multifunctional Automated Perfusion System for Long-Term Cryopreservation of Cells, Tissue Slices, and Organs

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Cryopreservation is fundamental to biobanking, cell therapy, and organ transplantation. However, achieving ice-free vitrification with high post-thaw viability remains a major challenge due to cryoinjury associated with intracellular ice formation (IIF). To suppress IIF and enable vitrification, cryoprotective agents (CPAs) are introduced; however, their use introduces additional challenges, including osmotic stress and CPA toxicity during both CPA loading and removal, which can lead to irreversible cellular and tissue injury. Furthermore, long-term cryopreservation is constrained by the limitations of conventional static cold storage (SCS). The short preservation window, lack of metabolic support, and increased risk of cold ischemic injury during SCS significantly compromise the quality and viability of donor organs prior to cryopreservation. To address these limitations, we developed a portable automated perfusion system that enables controlled CPA addition and removal under dynamic flow conditions while maintaining nutrient and oxygen supply, facilitating toxic metabolite clearance, and mitigating cold ischemic injury. This system enables precise regulation of CPA concentration profiles through a robust control algorithm. Compared with conventional stepwise CPA protocols, the automated design significantly reduces the need for manual intervention by enabling continuous and controlled CPA loading and unloading, thereby minimizing osmotic shock and CPA toxicity while ensuring sufficient diffusion time for uniform CPA penetration. For cellular applications, an integrated hemodialyzer module is used to perform CPA loading, removal, and cell concentration via a dilution–filtration process. For tissue applications, a dedicated perfusion chamber enables simultaneous dynamic perfusion of multiple tissue slices, providing substantially improved efficiency compared with conventional manual stepwise CPA loading and unloading. Furthermore, a pressure feedback loop integrated with multichannel pump control ensures stable CPA delivery while preventing vascular barotrauma during organ perfusion. In addition, the portable and multifunctional design enables seamless deployment in the laboratory, allowing on-site hyperthermic perfusion, CPA loading and removal, and normothermic perfusion for post-thaw assessment, thereby enhancing long-term cryopreservation across multiple biological sample types.

Repository Standards

PJ-01 A Project Management Platform for Managing Quality Assurance Issues

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The gold industry standard for any biospecimen company is to have a quality management system (QMS) that includes robust workflows for logging/tracking progress of any quality issue that arises. However, a QMS system can cost between $200-$1000 per month, which may be cost prohibitive for smaller research institutions. A potential solution for managing quality issues is the use of a flexible, customizable, project management platform where modules can be built specifically with custom fields for business, operational, quality and regulatory purposes. In addition to using a well-known QMS platform for policy/procedure document control, we have adapted a project management platform, ClickUp, to manage the tracking, progress and outcome of quality issues. We designed a module within the platform where a quality issue can be initially logged as a task and assigned to specific team members to whom the issue pertains, allowing for cross-departmental oversight. Custom fields were created to capture who, what, when, why and how a quality issue arose. Once a task is logged, the Quality Assurance (QA) team can use the chat feature to record the discussion with team members of the immediate actions needed, root cause, and direct team members on any corrective actions decided. The module is also customized to issue new tasks (with deadlines and reminders) to oversee, track, document, and complete the necessary corrective action in a timely manner. The platform allows for emails to be pinned, other tasks to be linked, and documents/images to be attached directly, so that the full "story" of the quality issue is all located in one place. The platform also can be customized to be 21 CFR part 11 compliant with regards to permissions, signatures, traceability, etc. The data from the platform is routinely exported into a spreadsheet format to use for data analyses on company-wide quality and performance metrics, which facilitates the generation of detailed and data-driven quarterly quality reports. Overall, this project management platform has greatly increased the robustness of our quality management system, as it facilitates the oversight of quality assurance in one central location without purchasing licenses to a larger, more expensive QMS platform. The use of a project management platform, such as ClickUp, may be a more cost-effective solution for smaller research entities, such as biobanks, to demonstrate compliance with industry standards in quality.

PJ-02 Assessing Processing Time and Cell Count Performance as Fit-for-Purpose QC Metrics for PBMC Biobanking

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Background: Peripheral blood mononuclear cells (PBMCs) are foundational biospecimens for translational melanoma research and immunologic profiling. However, delays between blood collection and processing may compromise downstream analytical suitability. Viability is widely used as a QC metric, yet its limited dynamic range may underrepresent degradation. This study evaluated the impact of processing delays on PBMC integrity and compared three quantification methods to define fit-for-purpose QC criteria.

Methods: PBMCs from healthy volunteer controls were processed at incremental delays (4–240 h). Three counting approaches were assessed: manual Trypan Blue, automated Trypan Blue, and automated AO/PI. QC parameters included total

cell yield, viable recovery, purity changes, and method performance across timepoints.

Results: Processing time was the primary driver of PBMC degradation. Samples processed ≤24 h retained higher total and live-cell recovery, while ≥48 h delays resulted in progressive PBMC loss. Apparent increases in total cell counts after 48 h were observed, likely due to granulocyte infiltration and expansion of non-mononuclear cell types. Viability values remained relatively constant (80–95%) and did not reflect biological degradation. Accumulation of apoptotic bodies and debris may contribute to nonspecific AO/PI binding, potentially inflating estimates of viable PBMC numbers at delayed timepoints, as described in prior studies. Automated methods aligned well with manual counts under optimal conditions but diverged as purity declined.

Conclusions: Viability alone may misrepresent PBMC readiness for immune-based assays. Processing time, total live-cell recovery, purity metrics, and assay-specific suitability must be considered together to ensure fitness for purpose. The ≤24 h threshold is recommended to maintain downstream analytical utility and prevent contamination-driven overestimation of usable PBMCs. Future work will include flow cytometry of melanoma-relevant immune subsets, evaluation of DNA integrity as a quality indicator, and QC analysis of retrospective melanoma biospecimens collected over a 5-year period to better characterize PBMC biology under real-world handling conditions.

PJ-03 Effect of Pre-analytical Factors on Nucleic Acid from Formalin-Fixed, Paraffin-Embedded Tissue (FFPET) Samples: A Thailand Multi-Center Study

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The Formalin-Fixed, Paraffin-Embedded Tissue (FFPET) specimens are a valuable resource for clinical diagnosis and precision oncology research. Several pre-analytical factors affect the quality of nucleic acid extracted from FFPET specimens that may lead to diagnostic inaccuracies and nonreplicable research results. In order to assess the quality of FFPE-derived nucleic acid and develop a common standardized protocol for FFPET preparation across medical institutions in Thailand, we aimed to determine the effect of pre-analytical factors including fixation buffers, fixation times, storage conditions and durations on DNA and RNA quality as reflected in the data quality from an NGS cancer panel and SNP array. The archived FFPETs were recruited from seven large medical institutions in Thailand. The ΔCq, RIN score, and DV200 values were used as indicators for nucleic acid quality. Our results showed no significant effect on DNA and RNA quality between the use of fixation buffers, 10% unbuffered formalin and 10% neutral buffered formalin (NBF). On the other hand, the DNA quality worsen when fixation time was prolonged more than 24 hours. Interestingly, the DNA extracted from long-term storage FFPET samples revealed low quality below the QC threshold for high-throughput technology applications after only 3 years of storage. This is likely due to the harsh environmental factors, such as high temperature and humidity in Thailand, as most centers stored FFPET samples at ambient temperature. We also explored the use of the Pathum Raksa box, which is specially designed to facilitate an efficient FFPET preparation in a rural hospital setting, and found improved DNA and RNA quality after utilizing these specialized boxes for FFPET preparation. In summary, our findings reveal the disparity in FFPET-derived nucleic acid quality across medical institutions, and highlight the urgency to improve this situation by developing national standard guidelines.

PJ-04 Long-Term Assessment of RNA Extracted from Lymphocytes Preserved in Triazole Compared with RNA Extracted from Buffy Coat Stored at –80°C

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Background: RNA is highly susceptible to degradation through various biochemical pathways, even when stored under low-temperature conditions such as −20 °C or −80°C. Degradation often results from residual RNase activity or suboptimal storage conditions. Triazole® reagent (Invitrogen), a monophasic solution containing phenol and guanidine isothiocyanate, is commonly used for both RNA extraction and preservation. Fresh biological specimens can be directly immersed in Triazole® and stored at −80°C to allow delayed RNA extraction. The present study aimed to assess the long-term quality and concentration of RNA extracted from lymphocytes preserved in Triazole®, in comparison with RNA extracted from buffy coat samples stored at −80°C.

Methods: At the Shefa Al-Orman Biobank (SOH-Bio), lymphocyte samples were preserved for long-term storage by adding 1,000 µL of Triazole® to 200 µL of whole blood. The miRNeasy Micro Kit (QIAGEN®) was used for RNA extraction. A total of 25 Triazole-preserved samples stored for five years were selected for analysis. Extraction procedures followed the miRNeasy Mini Handbook – QIAGEN® protocol. RNA yield was quantified using a Multiskan SkyHigh Microplate Reader (Thermo Fisher Scientific). Results were compared to 25 RNA samples extracted from buffy coats stored at −80°C for a similar duration.

Results: RNA concentrations from both Triazole-preserved lymphocytes and buffy coat samples ranged between 5–60 µg/mL, with no significant difference observed between the two groups. Long-term storage under both conditions of preserved RNA yields adequately.

Conclusion: Long-term storage at −80°C does not adversely affect RNA concentration. Preservation of lymphocytes in Triazole® provides comparable RNA yield to those obtained from

buffy coat samples stored at −80°C. However, the relatively high cost of Triazole® may limit its widespread use, particularly in resource-limited settings.

PJ-05 Minimizing Pre-Analytical Variables on Peripheral Blood Mononuclear Cell (PBMC) Processing and Cryopreservation for Quality Improvement in Ramathibodi Comprehensive Tumor Biobank

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The Ramathibodi Comprehensive Tumor Biobank (RCTB), Faculty of Medicine Ramathibodi Hospital, Mahidol University, established in 2014 as the first centralized human specimen biobank in Thailand, has archived more than 40,000 biospecimens from over 4,000 cancer patients. Peripheral blood mononuclear cells (PBMCs) are particularly valuable, supporting genomic, transcriptomic, immunological, and functional studies in translational cancer research. The reliability of downstream applications depends on minimizing pre-analytical variability in processing and cryopreservation. Yet systematic evaluations of pre-analytical influences on PBMCs from cancer patients remain limited, even though these individuals often undergo multimodal therapies that may affect specimen quality. This study investigated key determinants of PBMC integrity to inform standardized operating procedures for long-term storage in a multicenter biobank setting.

As part of its quality control (QC) and research and development (R&D) program, RCTB examined three pre-analytical variables: blood storage duration, storage format, and patient treatment status. PBMCs were randomly selected and isolated from cancer patients enrolled between 2014 and 2024, stored for 1–10 years, and evaluated for viability, DNA integrity, and RNA integrity. Results indicated that storage of whole blood in EDTA tubes for more than two days before isolation reduced PBMC viability, highlighting the importance of timely processing. PBMCs cryopreserved in freezing-media maintained RNA integrity more effectively than cell pellet storage, while DNA quality was similar across formats. Treatment status, including chemotherapy, radiotherapy, or concurrent chemoradiation (CCRT), did not markedly influence PBMC viability compared with treatment-naïve patients. Lower PBMC viability was also linked with reduced nucleic acid purity, connecting pre-analytical handling directly to molecular quality.

These findings underscore the need for evidence-based SOPs, systematic QC, and ongoing R&D to mitigate pre-analytical variability. They further provide a framework for harmonizing PBMC handling across multicenter cancer biobanks nationwide, supporting reproducibility and equitable access to high-quality biospecimens. By safeguarding PBMC integrity, RCTB strengthens its role as a national platform for cancer research and contributes to the long-term sustainability of biobanking in Thailand.

PJ-06 Quality Assessment of RNA Extracted from Fresh Tissue and Buffy Coat

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Introduction: Biobanks provide an essential infrastructure for biomedical research by enabling access to well-annotated biological samples and associated data. Human tissue and blood specimens serve as critical resources for identifying molecular biomarkers that can inform clinical decision-making. At the Shefa Al Orman (SOH) Biobank, tissue samples are preserved in liquid nitrogen, while buffy coat samples are stored at –80 °C. Fresh tissue generally yields high-quality RNA because of its rich cellular content; however, it is highly susceptible to degradation by endogenous RNases if not promptly preserved. Conversely, buffy coat samples are easier and less invasive to obtain but often present challenges such as lower RNA yield, higher RNase activity, and the presence of abundant globin mRNA, which may compromise RNA integrity and downstream gene expression analyses. Assessing the quality of nucleic acids extracted from these samples is therefore a crucial prerequisite for any molecular application.

Objective: To evaluate and compare the yield and quality of total RNA extracted from two distinct biological sources—fresh tissue and buffy coat—collected from the same breast cancer patients.

Methods: Total RNA was extracted from 20 paired samples using the QIAamp miRNeasy Mini Kit for fresh tissue and the GeneDirex Total RNA Isolation Kit for buffy coat samples. RNA concentration and purity were assessed using a Multiskan Sky spectrophotometer.

Results: RNA yield was significantly higher from fresh tissue compared to buffy coat samples. The mean RNA concentration from fresh tissue was 182 ng/μL with a mean purity (A260/A280) of 2.1, while the mean concentration from buffy coat samples was 20 ng/μL with a mean purity of 1.9.

Conclusion: Fresh frozen tissue provides a substantially higher RNA yield and better purity compared to buffy coat samples. Therefore, prioritizing the collection and preservation of fresh tissue in biobank protocols is recommended to ensure high-quality RNA for downstream molecular research.

PJ-07 Stability of DNA and RNA Concentration and Purity of Buffy Coat Samples from CLL Patients After One Year of –80°C Storage

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Introduction: Introduction The long-term preservation of nucleic acids is a cornerstone of modern biobanking and molecular research. Maintaining DNA and RNA integrity is essential for downstream applications such as PCR, qPCR, sequencing, and gene expression profiling. Storage at ultra-low temperatures

(e.g., –80°C) is widely used to minimize nucleic acid degradation. Being single-stranded, RNA is particularly prone to degradation, making its long-term stability a major concern. Although DNA is more stable, repeated freeze–thaw cycles and extended storage may still impact its quality and yield. This study aimed to evaluate the effect of one year of –80°C storage on the concentration and purity of DNA and RNA extracted from buffy coat samples of patients with Chronic Lymphocytic Leukemia (CLL)

Methodology: DNA and RNA were extracted from 40 buffy coat samples collected from CLL patients. Immediately after extraction, nucleic acid concentration and purity were measured using a Multiskan Sky spectrophotometer (Thermo Fisher Scientific). Samples were then aliquoted and stored at –80°C for one year. After storage, all samples were thawed under controlled conditions and remeasured using the same instrument and settings. Mean concentrations and purity values were compared between the baseline and post-storage measurements to assess nucleic acid stability.

Results: The mean RNA concentration before storage was 25.74 ng/μL, compared with 28.36 ng/μL after one year. The mean DNA concentration increased slightly from 216.22 ng/μL to 248.27 ng/μL after storage. Purity values remained stable, with RNA purity showing a minor change from 2.20 to 2.21, and DNA purity from 1.78 to 1.77 before and after storage, respectively.

Conclusion: Storage of buffy coat samples at –80°C for one year did not negatively affect the concentration or purity of DNA and RNA. The minor variations observed are likely due to measurement variability rather than degradation. These findings support the reliability of –80°C storage for maintaining nucleic acid integrity in biobanking applications.