ABSTRACTS

NORDIC Biobank Conference

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Abstracts - oral presentations

Symposium 1

Combining registries with biobank samples, September 7, 2022, 11:00 - 12:30

The Northern Sweden Health and Disease Study – Prospective blood samples and data from >140 000 individuals in Västerbotten county

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Abstract
An aim of the Northern Sweden health and Disease Study (NSHDS) is to support frontline research, in particular on diagnostic tools for clinical use, as well as early markers of disease. Furthermore, basic research regarding risk factors as well as pathogenic pathways are promoted. The previously collected NSHDS blood samples and associated health data in combination with blood and pathologic tissues collected after disease onset enable good research.

NSHDS is an umbrella term for a prospective biobank with related survey data. The sample collection consists of three subcohorts, Västerbotten Intervention Programme (VIP), Mammography Screening Project (MA) and the northern Sweden MONICA (Monitoring of Trends and Determinants in Cardiovascular Disease) Study. It is estimated that about 60 % of Västerbottens inhabitants aged over 40 years have had a health survey and donated a blood sample for research within these cohorts. The blood samples are stored at Biobanken Norr, Region Västerbotten.

The prospective blood samples and related survey data can be linked to national registers for disease outcomes. Thus, the NSHDS cohort has the potential to be used to identify risk markers, biomarkers and lifestyle factors predictable for several common diseases.

As a current example of use of NSHDS, an impressive cohort of individuals diagnosed with severe Covid-19 with preclinical data and samples can be created through register linkage. Such a cohort can be of great benefit to identify risk individuals vulnerable for future infection threats.

For more information, visit our homepages (https://www.umu.se/en/biobank-research-unit/, https://www.regionvasterbotten.se/forskning/stod-till-forskning/biobanken-norr) or contact us by email.

THL Biobank's Availability Service utilizes register data for focused responses on researchers' feasibility studies

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Background
THL Biobank, a country-wide biobank, hosts significant national research collections. The Biobank Act allows linkage of biobank data to the national health and welfare registers. THL Biobank operates in the Finnish Institute of Health and Welfare (THL), which also maintains the national Care Register for Health Care (HILMO). THL Biobank may utilize the diagnostic data compiled and stored in HILMO for feasibility study purposes.

Methods
Researchers have the right to enquire the availability of samples and data required for their planned biobank research. Diagnostic information is often needed to meet the inclusion or exclusion criteria, in addition to the baseline, lifestyle and omics data available through biobank. As part of the IT infrastructure, in 2020 THL Biobank has developed an internal database, the Availability Service, that contains information from a selection of ~2 000 ICD10 codes from all biobank sample donors. By the end of 2021 the Availability Service will be extended to cover all ICD10 diagnoses used in Finland.

Results
THL Biobank can provide extensive and reliable answers to researchers' feasibility queries by utilizing the diagnoses in the Availability Service. To access the health registers' data (including also e.g. medications, causes of death) in an actual biobank study, a separate permission is needed from competent authorities, usually from Findata, the Finnish Health and Social Data Permit Authority.

Conclusions
Multiple projects combining extensive register data and the research data stored in THL Biobank have been carried out, and many more are being planned. Once the applications to THL Biobank and Findata are prepared consistently, the processes to grant accesses can be parallel, thus resulting to fluent data extraction and linkage. THL Biobank is constantly developing practices in good collaboration with Findata to secure the researchers smooth access to the data required for high-quality research.

Symposium 2a Sample quality, September 7, 2022, 14:00 - 15:30

Structural and molecular quality of Tissue samples after 10 years storage under different protocols based on -80°C and liquid nitrogen

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Background
Molecular analyses are the backbone in precision medicine. RNA sequencing, alone or in combination with omic-analyses are crucial for new therapeutic strategies. Biobanks store tissue samples to promote translational research for precision medicine. However, the optimal storage conditions are a matter of debate especially with view to the storage temperature. We compared parallel samples from the same tumour, stored at -80°C and in the vapour phase of liquid nitrogen (LN2).

Methods
Breast cancer samples from 16 patients were analysed. From each tumour, we took biobank specimens in parallel for storage in -80°C and in LN2. All specimens were processed according the same SOP's and were stored at the same day in the two different storage facilities located in the same biobank. Each pair of samples was stored for at least 10 years and then analysed by use of DIN and RIN analyses, histological tissue-sections with haematoxylin & Eosin staining (HE) and transmission electron microscopy (TEM).

Results
RNA isolated from breast cancer samples showed significantly higher RIN-values after 10 years of storage in LN2 compared to storage at -80°C. In contrast, no significant difference was found regarding the DIN-values. Histological changes of the nuclei namely eosinophilic inclusions and relevant tissue artefacts were obvious in the samples stored at -80°C. TEM analyses revealed a significant loss of cell-cell-contacts and defects in cell- and organelle membranes after storage in -80°C.

Conclusion
Our findings demonstrate that the vapour phase of liquid nitrogen represent the preferable storage condition for breast cancer tissue samples with view to RNA-quality, and for its use in downstream analyses. Furthermore, our findings give insights for degenerative tissue effects after long-term storage in -80°C, whereas cell-cell contacts and cell membranes are highly preserved after 10 years of storage in LN2.

NMR as a general tool for assessing serum/plasma sample quality: identify sampling tube, sample integrity and other preanalytical characteristics

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Nuclear Magnetic Resonance (NMR) spectroscopy is the de facto golden standard for small molecule structural characterization and is also widely employed in the metabolomics field. The inherent quantitative properties of NMR, the minimal sample preparation and non-existing direct sample–instrument contact, allow non-destructive quantification of metabolites in complex biofluids with exquisite reproducibility. As such, NMR acts as a facile and sensitive quality control method for biobank samples. Matrix type and integrity (e.g. presence of known contaminants) can be directly assessed from the raw NMR spectrum. Detailed analysis of spectra allows the assessment of preanalytical (mis)handling. Here, we present results from an EDTA-plasma mishandling study on 28 participants (total of 951 samples) where the effects of temperature, incubation time and ambient light/dark were varied before centrifugation and freezing and assessed with ^{1}H NMR. Orthogonal Partial Least Squares Discriminant Analysis (OPLS-DA) grouping on participants was employed in models, rather than time to centrifugation, temperature, and light status which instinctively would be the first choice. The taken multivariate approach leaves all 'aging' effects in the orthogonal space, allowing assessment also of other potential aging processes in future studies apart from the variables chosen here. In preanalytical low temperature samples, a distinct, reversible and to our knowledge previously uncharacterized process is observed, in addition to the well known changes in glucose/lactate and ornithine metabolism upon incubation at ambient and elevated temperatures. In fact, even subtle differences between ambient light and dark incubation can be detected. Our results support previously published work that ^{1}H NMR is an excellent tool not only for metabolomics projects per se but also for quality assessment of human serum/plasma. A routine procedure could easily be established for spot-checks of biobank collections, historical or current.

Symposium 2b Legal and ethical perspectives, September 7, 2022, 14:00 - 15:30

Secondary research use of personal medical data: Patient attitudes towards data donation

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Background
The SARS-CoV-2 pandemic has highlighted the need for comprehensive access to patient data for medical research. Such secondary data use is a prerequisite for translation and personalisation in medicine, and for public health. Balancing scientific interest and a demand for individual autonomy, privacy and social justice is a great challenge for patient-based medical research.

Methods
We conducted two questionnaire-based surveys among North-German outpatients (n=650) to assess their attitude towards data donation for medical research, implemented as an opt-out process (i.e. legal permission of data use unless actively denied).

Results
We observed great acceptance of data donation (75.0%) mainly due to the conviction that every citizen has a duty to contribute to medical research (>80% of those approving data donation). Patients distinguished sharply between research inside and outside the EU, and the willingness to allow data use by commercial research was low (companies located outside EU: 7.1%, in Germany: 29.1%). The most popular measure to counteract such reservations was regulation by law (61.4%), stipulating that data are not sold (84.6%). A majority requested independent control of data use (46.8%) and data protection (41.5%).

Discussion
Considerations got under way of a legal basis of data donation in Germany. Previous studies suggested acceptance of data donation, but had not differentiated the legal and organizational concept in detail yet. We identified reasons for reservations about commercial research with donated data and corresponding counteracting measures, useful designing a data donation process. Most frequent concerns were insufficient data protection by commercial users and an objection of their profit-making through the use of the data, explaining the demand for a legal ban on commercializing the data.

Data donation for medical research, implemented as a legal entitlement with easy-to-exercise opt-out, is supported by German patients and therefore warrants further consideration for a transposition into national law.

Experience from information letter sent to 301.363 patients with a sample in The Copenhagen Hospital Biobank.

PhD Janna Nissen[1], PhD Lise Wegner Thørner[1], PhD Margit Larsen[1], MD PhD Ole Birger Vesterager Pedersen[2], MD PhD Henrik Ullum[3], Professor Sisse Rye Ostrowski[1], Laboratory Manager Erik Sørensen[1]
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Background
Since 2009, leftovermaterial from blood samples used for RBC-type and screen testing of patients in the Capital Region of Denmark, has been stored in The Copenhagen Hospital Biobank (CHB), with the purpose of being used for research in health and disease.
The storage of samples is not consented, but patients are informed, that leftover blood- or tissue samples may be stored in biobanks for future research. Furthermore, patients are informed about the general opt-out possibility of having their samples excluded from research use through the National Register on Tissue Application ("Vævsanvendelsesregistret").
To increase awareness of the biobank, information letters were sent to all patients with a sample in CHB or included in CHB related research, who were alive 1. November 2020.

Methods
Two types of information letters were sent: One letter to patients with a sample in CHB and one letter to patients whose sample in CHB had already been used in a research-project.
The information letter was sent as a postal- or digital letter. In order to handle inquiries from patients, a call-centre was established, and our website was updated.

Results
In November 2020, the information letters were sent to 301.363 patients.
A total of 1.916 patients responded by phone or email. Of these:

- 28% wanted their sample and data destroyed
- 18% were in general dissatisfied for not being directly informed earlier
- 27% had in-depth questions
- 21% gave positive feedback
- 6 % wanted to enquire about their blood type

Moreover, 1.043 patients registered in the "Vævsanvendelsesregistret".

Discussion/Conclusions
Only 0.5% of contacted patients opted-out of CHB. This emphasizes that Danish patients in general support and are willing to take part in research.
The information letters did not give rise to negative publicity.
From now on all newly included patients receives an information letter.

Symposium 3a Next generation biobanking, September 7, 2022, 16:00 - 17:30

Next Generation Biobanking: The Future of Personalized Medicine

Stephan C[1] [1]KAIROS - an IQVIA business

Biobanks provide a large number of biological samples that come from a wide variety of patients with diseases in various stages. While they have always played an important role in medical research, their value is being realized with the increasing focus on personalized medicine. If these samples are analyzed and the patient's data is linked to them (anamnesis, therapy, laboratory and outcomes) conclusions can be drawn about the effectiveness of therapies or new interventions can be found.

The methods required to take what some view as service providers and freezer farms managed with Excel sheets to next generation biobanking, is about data quality and creating a system and processes that focus on the patient.

Not only is sample quality critical to their success, but quality data against those samples help eliminate the cycle of garbage in, garbage out. This process must be seamless though, to ensure quality documentation of samples and paired clinical data. The biobank system needs to include interfaces to devices and medical data systems to create one quality data pool. This allows the biobank to be an integral part of a comprehensive research data integration platform for personalized medicine.

These components result in initiatives like SepsisDataNet, the project combines multidisciplinary institutions to analyze the samples collected along with clinical data, evaluates the resulting Big Data findings, and translates them into personalized treatments. The success of this project prompted the creation of CovidDataNet to support personalized treatments of COVID-19 based on the combination of sample and intensive care data.

Modern biobanks - including the technical requirements - contribute significantly to personalized medicine through the sustainable collection and analysis of biological samples. Quality samples and data play an important role on the way to this goal, especially when it comes to integrating AI-processes to improve medical "decision support" treatment.

Delivery of Federated Trusted Research Environments for collaborative, secure analysis of distributed clinico-genomic data

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With 90+ population genomics projects now operating around the world, biobanks are facing a unique challenge. To understand genetic variants and facilitate treatments and cures for diseases, biobanks must provide easy access to and utilisation of disparate big data to pharmaceutical and research organisations. At the same time, patient data security is of utmost importance. Researchers working with biobank cohorts struggle to combine disparate datasets to perform meaningful analyses, with regulations around sensitive patient data transfers exacerbating the problem. Until now, potential solutions have been ineffective. Federated analysis, or bring-analysis-to-data, is the future of big data analysis in the realm of biobanks. A federated approach enables different entities to access data for distributed analysis without physically sharing it, thereby providing an ideal foundation for an increasingly fragmented and distributed global genomics community. Genomics England (GEL) partnered with Lifebit to deliver its federated Research Environment (RE), GEL CloudOS, which allows researchers to seamlessly access, navigate, analyse and collaborate over GEL's 100,000 Genomes Project cohort and the newly added COVID-19 cohort (35,000 whole genomes). Deployed directly in GEL's own cloud, participant data remains within GEL's secure environment, assuring 'Fort Knox-grade' data security. GEL's new federated architecture enables researchers to query the GEL cohort all while leaving data at its source, link and combine in-house data, introduce cutting-edge analytical tools of their choice and collaborate within segregated and secure workspaces. By adopting federation, GEL is poised to significantly improve the odds of major scientific breakthroughs in the near future, bring opportunities for commercialisation in underfunded research as well as collaboration across large-scale biomedical cohorts globally.

Symposium 3b Biobank sustainability, September 7, 2022, 16:00 - 17:30

It's Imperative to be Intuitive – How to lower the threshold for access to samples

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Background
It's Imperative to be Intuitive (Lätt att göra rätt) is a strategic umbrella project initiated by Biobank Sweden in 2020. The purpose of the initiative is to improve Biobank Sweden's processes and services for the benefit of biobank research, thus making it easier – i.e. more intuitive – for researchers to store and gain access to samples and sample data. The project addresses multiple areas of the infrastructure, including operational, regulatory and communication processes, and an extensive list of subsequent activities.

Methods
The project was coordinated by nationally appointed project managers and the scope unilaterally sanctioned by all organizational entities within Biobank Sweden, including regulatory and operational services, and academic and industrial research. In general, the project activities covered the ambition to generate easier application processes and better educated users and were prioritized according to viability and estimated effect.

Results
Through national coordination and involvement It's Imperative to be Intuitive resulted in a number of improvements for both external researchers and administrative functions within Biobank Sweden, such as: amended and enhanced interactive e-education, a web based guide for researchers, a national model for administrative turnaround time, harmonized work instructions for advisory services, standardization of fluid based sample information, improved document layout, cost calculation templates, and a re-modeled internal web and information structure.
In addition, the project has spawned dedicated efforts for further improvements now pursued as long-term standalone initiatives.

Discussion/Conclusion
It's Imperative to be Intuitive introduced an adaptive model to ensure continuous progress and increased efficiency for the national Swedish biobanking infrastructure.

THL Biobank provides endless possibilities in health-related research

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Background
The Finnish Institute for Health and Welfare (THL) has systematically surveyed the health and wellbeing of Finns since the 1960's. Subsequently, THL established THL Biobank in 2014 as an infrastructure to host these population cohorts along with other nationally significant sample collections, such as cohorts focusing on cardiovascular diseases, diabetes and severe mental illnesses. Currently, THL Biobank hosts samples and sample-related health and lifestyle data from ~220 000 individuals. Biobanking enables use of legacy and new collections with broad consent for secondary research use, and linkage to national registers.

Methods
Data on demographics, lifestyle and health status were collected through questionnaires/interviews, clinical data and samples were collected during clinical visits. DNA samples and derived genomic data are available for almost all cohorts. Most serum and plasma samples have been collected in a standardized way and have already been converted to biomolecular data, while still securing the sample availability for future research purposes. Additionally, processed samples i.e. RNA and cells are available.

Results
THL Biobank offers high-quality samples, well-documented lifestyle and health-related information and versatile data derived from the samples originating from the research collaborations and biobank projects. Biobank's database contains over 35M phenotypes. In addition to basic biomarkers, such as lipids, imputed GWAS data of ~120 000 sample donors, and for some donors, WGS (5000) and WES (18 000) data is also available for more deeper genetic analyses. Moreover, detailed serum NMR measurements of ~45 000 donors and new gut microbiome sequence data from 7000 donors are available.

Discussion
By hosting the extensive amount of data both from the samples and the sample donors, THL Biobank is truly a next generation biobank enabling wide-range opportunities for researchers. Possibility to link national register data to the biobank samples and data enables longitudinal follow-up and opens even more opportunities for research.

Symposium 4a The role of Nordic biobanks in pandemics, September 8, 2022, 09:00 - 10:30

HUNT COVID - a prospective population study for pandemic surveillance

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Background
The Health Survey in Trøndelag (HUNT), was established as a prospective, longitudinal, population study in central Norway, so far conducted in four waves (HUNT1-4, 1984-2019), with 250 000 unique participants. HUNT 4 (55 000 participants) was completed in 2019, just before the pandemic and lock-down reached Norway. HUNT databank and HUNT biobank (European Biobank of the year 2013) holds comprehensive health data, clinical data, genetic profiles and other omics data from all HUNT4-participants, of whom 34 000 also participated in HUNT3 (2006-2008).

Aim
To study the effects of national control measures, lock-down, SARS-CoV2-infections and long Covid symptoms, all HUNT4-particpants are invited to a HUNT COVID follow-up over a 21-month period with blood sampling and collection of questionnaire data.

Methods
Participants are examined at field stations established in each municipality. Biological material is transported daily to HUNT biobank at 4°C. SST and EDTA primary tubes are fractionated to serum, buffy coat and plasma aliquots and stored at –80oC within 18-32 hours after collection.
SARS-CoV2 antibodies against both spike protein and nucleocapsid are analyzed for mapping of SARS-CoV2-infections and vaccination response. A panel of other viruses is also included.

Results
The study commenced on September 1st, 2021. During the first 10 weeks, 3936 individuals (58% female) have attended the study (60% of invited). Age distribution in the figure.
Antibody response will be reported back to each participant. We plan the first data freeze early 2022 and preliminary results will be presented during the Nordic Biobank Conference in March 2022.

Discussion/Conclusions:
On short notice, a population cohort and biobank have been transformed into an invaluable clinical research platform for contingency studies of a new and life-threatening disease where valid prospective, population-based research is pivotal. This ad hoc endeavor is fully dependent on the necessary in-house capacity, flexibility, and highly skilled personnel.

National coordination of biobanking related to covid-19

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Background
Covid research is needed to increase the understanding of how the disease may be managed and prevented. In order to get a good foundation for increased knowledge for healthcare, method development and research, it is important to collect and store various sample types with representative geographical distribution.
The purpose of this activity was to nationally coordinate biobanking of covid-19 related samples.

Methods
Biobank Sweden has been allocated SEK 10 million from the Swedish Research Council to finance covid-19 biobanking within Sweden's healthcare regions. A national working group within Biobank Sweden has performed an inventory as well as a plan to distribute the funds with the aim to include all 21 regions and to include different sample types.

Results
The allocation of the grant was divided into two stages. During the first stage, approximately SEK 4.7 million was distributed among 17 of the 21 healthcare regions. Thus, the regions were reimbursed for approximately 30.000 biobanked samples. Covid-19 sample collections can be found via the COVID-19 Data Portal (https://biobanks.covid19dataportal.se/), developed in collaboration between Biobank Sweden and SciLifeLab.

Discussion/conclusion
Despite the heavy workload in clinical practice due to the pandemic, it is important to secure samples for healthcare and to enable research. The allocation of the second part is planned to be implemented Q4 2021.

Symposium 4b Good examples of biobank research, September 8, 2022, 09:00 - 10:30

Improving biobank collection usability by computational HLA and KIR typing methods

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Background
Highly developed genotyping techniques and computational methods enable a cost-effective and rapid way to screen and analyze large cohorts based on DNA variation. The aim of this project is to produce HLA and KIR data for Finnish blood donor biobank samples by imputation, a computational method for predicting gene variants.

Methods
SNP genotyping of biobank samples was originally performed on a customized ThermoFisher Axiom array as a part of the FinnGen initiative. The produced genotypes were returned to the Blood Service Biobank. Clinical grade HLA and KIR typing results were acquired either from FRC Blood Service HLA laboratory or by Histogenetics LLC by sequencing based typing. Imputation reference panels were designed to include the most common HLA and KIR variants in the population. Alleles of 7 classical HLA genes were imputed by HIBAG v1.14.0 (Ritari et al. 2019). KIR gene content comprising the 12 non-framework genes was predicted by the random forest algorithm. R v3.4.4 and v4.0.4 were used for data analysis and scripts (Ritari et al. 2021, submitted).

Results
The overall imputation accuracy was dependent on the gene and varied between 0.95-0.98 or 0.96-1.00 for HLA and KIR, respectively. Computational HLA-A, -B, -C, -DRB1, -DQA1, -DQB1 and -DPB1 types have been produced for more than 20 000 Finnish Blood Service Biobank donors, and KIR gene content for the same biobank samples will be produced in the near future.

Conclusions
The HLA and KIR immunogenetic loci are crucial players of the immune system. Therefore, HLA/KIR typed biobank donor samples may be beneficial especially for immunobiological research. Inferring HLA alleles and KIR gene content for biobank collection improves the quality, performance and services of The Finnish Red Cross Blood Service Biobank.

Large Scale Investigation of Biomarkers using MesoScale Discovery Platform

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Background
Biomarkers are cornerstones in scientific research revealing both biological mechanisms and diagnostic, prognostic, and predictive information. The study of biomarkers has expanded greatly as technology has advanced. Not only does the simultaneous measurement of multiple analytes in a single sample allow for more complex studies, the automatization and increased speed of sample handling also makes larger studies feasible. It is however important to establish an analytical study plan with proper validation and quality control of the underlying data of the applied assays.

Methods
The MesoScale Discovery (MSD) platform was applied to measure 54 biomarkers in a large study cohort (N>10,000) using seven different MSD V-PLEX panels: Proinflammatory Panel 1, Cytokine Panel 1 and 2, Chemokine Panel 1, Angiogenesis Panel 1, TH17 Panel 1, and Vascular Injury Panel 2 (Meso Scale Diagnostics, Maryland, US).

The implemented analytical study plan included semi-automation of methods on robotics and various critical milestones, the first one being an initial feasibility study of 10% of the samples assessing the performance of the MSD analyses and establishment of acceptance criteria and quality control.

Results
We established a semi-automated platform for the MSD analyses. Based on the feasibility study, acceptance criteria were defined for each biomarker (on calculated concentrations):

- Mean acceptance criteria of calibration curve: 80-120%
- CV of calibration curve: ≤20%
- Internal calibrator for quality control: within ± 3*SD mean concentration

Importantly, we demonstrated acceptable long-term stability of samples with freezing times within 10 years at -200C.

Discussion/Conclusions
The implementation of an analytical study plan should be considered in relation to the study objective. One of the challenges in a multiplex assay setup is decision making about the final assay conditions and acceptance criteria for standardizing. Also, the GMP manufacturing of the multiplex assay, which must meet rigorous testing criteria, can be very complex.

Symposium 5a Infrastructure, September 8, 2022, 11:00 - 12:30

The Swedish Childhood Tumor Biobank -A national sample-collection and genomic characterization initiative of pediatric solid tumors for research purpose

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Background
In Sweden 340 children are diagnosed with cancer each year. Today more than 85% of the patients will survive, even so, cancer is one of the major medical causes of childhood death. The survivors often suffer from sequelae due to the treatment. Therefore, deeper biological knowledge regarding these malignancies is essential for improved survival and quality of life for affected children. The aim of The Swedish Childhood Tumor Biobank (Barntumörbanken, BTB) is to increase the understanding of pediatric solid tumors by providing biological samples and molecular genetic/genomic data for research.

Methods
BTB has a multidisciplinary nation-wide collaboration with the six university hospitals that treat and operate pediatric cancer patients. Fresh frozen tumors and blood samples are collected. BTB registers, prepares and stores the biobank samples as well as performs whole genome sequencing (WGS), whole transcriptome sequencing (WTS) and methylation array (MA) profiling. BTB also develops bioinformatic pipelines with the Science for Life Laboratory.

Results
1700 cases are now registered in BTB and 20 000 samples collected. More than 600 cases have been genomically characterized and 450 cases will be analyzed during 2022. BTB is also coordinating the “GMS Barncancer” study and responsible for storing WGS, WTS and MA-data from this national clinical implementation project; 300 pediatric cancer cases for 2021-2022. BTB samples and generated data have been distributed to several research projects after formal application processes. BTB is moreover assisting different clinical studies with sample logistics and data analysis/interpretation.

Discussion/Conclusions
BTB systematically collects biological specimens and informed consent from more than 90% of the Swedish pediatric patients with solid tumors, and produce high quality data. The continuous usage of the samples and the genomic data in approved research projects will contribute to increased knowledge and likely have a positive impact on the future clinical care of children with cancer.

Data management and design in Biobank-merging

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Background
Merging many smaller biobanks into a few physical storage locations with central data storage has many advantages: energy efficiency, storage space economy, dependable freezer backup and surveillance, cheaper hardware due to larger contracts, easier data- and sample-access and easier region wide inventory.

While yielding the above advantages, merging also presents several data related challenges, ranging from subtle differences in sample numbering systems in large, well-organized biobanks - over GDPR-related issues - to smaller biobanks where most of the location data and metadata is in someone's head.

Even with all these differences, the conceptual data model of a biobank remains:
"Observed/measured data" <- Sample core data -> Sample location data

Methods
"Observed/measured data" can typically be divided as: demographic, health, person, lab-results and *omics-data, i.e. "the interesting stuff". We have found it necessary to de-couple this from the central data storage model, due to heterogeneity, sensitivity and ownership issues. We focus on Sample core data -> Sample location data.

This simplification makes the design of a central sample storage data model simpler, but also makes a harmonized sample ID crucial, since this remains the key to the "Observed/measured data" which is stored de-centrally.

Results
We present our experiences from the establishment of a centralized long-term storage facility for material from a 100+ biobanks in the Copenhagen Capital Region, comprising several million specimens.
Key concepts are central data model, foreign keys, minimal data storage, strict demands on the submitted data, labelling harmonization, re-findability, re-deliverability, non-location specific labelling, storage unit mobility and strict rules for customer storage unit labelling.

Discussion
The "Perfect Solution": making new aliquots, re-labelling and storing all the "Observed/measured data" together with the sample location data was never an option, so the merging of biobanks in "The Real World" is an iterative process that requires pragmatism and exformation.

Symposium 5b Patient engagement and return of genomic data, September 8, 2022, 11:00 - 12:30

Collaborating with Patients and Next of Kin: Towards a Culture of Equal Partnership

Clareborn A, Biobank Sweden, Eskil Degsell, Svenska Hjärntumörföreningen, Kristina Kannisto, ATMP 2030
Margareta Haag, Nätverket mot cancer, Mikaela Friedman, Genomic Medicine Sweden (GMS)
Sara Riggare, Forum Spetspatient, Stephanie Juran, Riksförbundet Sällsynta diagnoser

Background
The organizations ATMP Sweden, Biobank Sweden and Genomic Medicine Sweden have all identified a need for innovative Patient and Public Involvement (PPI), including building a collaborative structure with patient and next of kin representatives.

Methods
In order for collaboration within such a structure to be successful, a thorough needs analysis and situation assessment are necessary starting points. A core team of representatives from the three organizations together with patient and next of kin representatives have been conducting a pilot study with the objective of defining and building flexible frameworks for successful collaboration. The team has been working with case studies in order to apply tentative models of collaboration on current challenges faced by ATMP Sweden, Biobank Sweden and Genomic Medicine Sweden in terms of patient and next of kin partnering. We have also conducted a selective literature review.

Results
The ongoing literature review and case study approach have clearly characterized trust as a major challenge, as well as the dissemination and application of successful initiatives in other contexts. A final hurdle has to do with misconceptions regarding the usefulness and impact of patient collaboration.

Discussion/Conclusions
It is a common occurrence that patient- and next of kin representatives are called in at the last minute in order for a formal box to be checked in a study, a workshop or at a conference. But asking for a final stage greenlight, or symbolically inviting individuals to quietly participate are not viable strategies for sustainable, long-term collaboration. True partnering requires frameworks supporting far-reaching changes in terms of culture, as well as tools for measuring outcomes and managing feedback. Even at this stage, the ongoing pilot study has clearly shown that the value of truly equal partnerships, rather than just superficial engagement with patient- and next of kin representatives, is considerable.

Viking Genes: Return of actionable genetic research results to Scottish cohort participants

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Background
The Viking Genes research study is completing the recruitment of 8,000 participants with ancestry from the Northern Isles of Scotland. All volunteers have two or more grandparents from Orkney or Shetland and nearly half have joined online in the past two years (www.ed.ac.uk/viking). The distinct gene pools we have measured in these isolated populations mean that different approaches to genomic medicine are required.

Methods
Eligible people can take part in Viking Genes from anywhere in the world, with DNA extracted from their saliva samples after postage to the University of Edinburgh. To date over half of the volunteer DNAs have been exome-sequenced, with the remainder of the data due soon. We have also generated a rich phenotype dataset, including electronic health record linkage and multi-omics phenotypes, on our initial clinic-based volunteers. We have permissions in place for return of results (RoR) for selected “actionable” genetic variants, working closely with NHS Scotland.

Results
The potential impacts of RoR are evidenced by our pilot work with Long QT Syndrome in Shetland and Hereditary Breast and Ovarian Cancer in Orkney. The return of medically actionable genetic results to Viking Genes participants living in the UK is optional. This respects their individual wishes on feedback of research results. To date, 97.8% of nearly 4,000 consented participants have agreed to have actionable results returned.

Discussion/Conclusions
We are developing an exemplar approach to the delivery of genomic medicine in these outlier populations by first understanding the landscape of pathogenic variation, then translating this into evidence for screening programmes for drifted variants. There will be direct benefit to the ~100 research subjects we estimate will have actionable findings. By offering RoR we are recognising the accountability of genomics researchers towards participants, and the need for transparency through engagement and involvement of our Viking Genes volunteers.

Symposium 6a Digitalization, September 8, 2022, 13:30 - 15:00

National Biobank Register (NBR) - the regions' common IT system with data about samples kept in biobanks.

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[1]Biobank Sweden

Background
NBR is the IT system of the regions with data about biobank samples. The purpose of NBR is to make samples and data searchable, and to make it easier to meet the demands of the Biobanks in Medical Care Act regarding safe and functional traceability of samples and consent management. In 2020, all regions came together and decided to develop NBR according to a new form of collaboration linked to Biobank Sweden's work. Biobank Sweden IT was created ¬and is regulated by a Municipal Collaboration Agreement and a Personal Data Processor Agreement.

Method
Development started in January 2021 and will continue indefinitely.
There is a steering group responsible for prioritizing the development. Stakeholders, product owner and developers have collaborated closely to break down the work into sub-goals and specific activities. New features are released regularly.

Results
NBR was launched in September 2021 and consisted of basic functions for the daily administrative work of biobanks and had a basic structure to enable structural migration of data into the system. In the autumn of 2021, the migration of sample data from the regions' Laboratory Information Systems, and the development of a search functionality, will be starting.
Simultaneously, the development to simplify the administrative work for the biobanks, and to make it easier to be legally compliant, proceeds.

Discussion/conclusion
Samples, with associated data, are a foundation for medical research and method development. NBR shall enable samples to be found and to be combined with data. As a result, samples and data can much easier be used in various medical research projects, leading to Sweden being better equipped for future health challenges. The system will also make it easier to find samples for healthcare reasons – especially if a patient has been cared for in several regions.

Development and implementation of electronic informed consent for cancer research

Mrs Nina Krüger[1], MD.Prof. Karine Sargsyan[2]
[1]Oslo University Hospital, Division of Cancer Medicine, Norway, [2]Medical University of Graz, International Biobanking and Education, Austria

Cancer research in general is largely dependent of access to biobank samples, and access to large scale biobank collections is of crucial importance for the development and implementation of precision cancer medicine.

The informed consent is the fundament of all research activities, including the collection of biological samples for cancer research. It is therefore of crucial importance that there is a system in place so that each patient that is diagnosed with cancer is given the opportunity to participate in cancer research, and that the informed consent is retrieved in a systematic and trustworthy manner. Cancer patients represent a large and heterogeneous group, differing in sex, age and physical condition, and cancer research is equally dependent on all of them to participate.

Although we are using electronic solutions in many aspects of our daily life, using such systems to involve people in medical research is still a rather unexplored field. This abstract will explore and map benefits achievable with an electronic informed consent solution for cancer research.

To understand the total impact, a literature review with focus on stakeholders perspective, design and implementation efforts and experience have been carried out. A survey on the use of electronic informed consent solutions in cancer biobanks internationally has been conducted. In addition the process of designing and implementing an electronic informed consent solution for cancer research is described in detail.

It has been found several issues related to the design and implementation of an electronic informed consent solution. These issues run in the ethical, technical and security related dimension. Comprehensive work with design, implementation and hospital logistics are demanded for a successful implementation, and thereby the realization of the achievable benefits of an electronic informed consent solution.

Symposium 6b Innovative technologies, September 8, 2022, 13:30 - 15:00

Evaluation of DNA damage in biosamples

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Background
DNA is an important constituent of biosamples and it is frequently analyzed using complex procedures in molecular genetics. DNA damage either in vivo or in vitro, as part of purification or storage, can affect efficiency and quality of DNA analysis. This needs to be further studied.

Methods
The Northern Lights Assay (NLA) in microgels can detect various types of DNA damage in cells and cell-free samples including single-stranded breaks, double-stranded breaks, intrastrand and interstrand DNA crosslinks (ICL), single-stranded DNA and bulky lesions in DNA. DNA is isolated with gentle methods before analysis. We tested samples isolated from whole blood, plasma, saliva, urine sediment and cell-free urine taken from healthy subjects and patients with various diseases. We also studied FFPE samples.

Results
We tested NLA on DNA isolated from various body fluids. cfDNA samples from each body fluid showed DNA damage patterns that were variable between healthy individuals, but distinctive for each type of fluid. cfDNA from plasma had variable apoptosis patterns in different healthy individuals. cfDNA in salvia had very variable but extensive damage, and single-stranded breaks where very prominent. cfDNA in cell-free urine showed predominantly a necrosis pattern. Blood cell DNA had minimal DNA damage in healthy individuals, but DNA from urinary sediment cells had a combination of apoptosis and necrosis pattern. FFPE samples contained single-stranded DNA, intrastrand and interstrand crosslinks and relatively little undamaged double-stranded DNA. Chip-Seq DNA had variable amount of crosslinks. In both cases the amount of DNA damage correlated inversely with indicators of NGS performance.

Discussion/Conclusions
DNA in body fluids and FFPE samples contained substantial but variable damage that can affect analysis.

Proximity extension assay in combination with Next-Generation Sequencing for high-throughput proteome-wide analysis in large population health and biobank studies

PhD Cindy Lawley[1], Lotta Wik[2], Niklas Nordberg[2], John Broberg[3], Johan Björkesten[4], Erika Assarsson[4], Sara Henriksson[2], PhD Ida Grundberg[5], Christina Westerberg[2], Elin Liljeroth[2], Adam Falck[2], Martin Lundberg[4], Anna Lejon[6], Sara Sadi[6], Yan Chen[7], Anders Mälarstig[7]
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Understanding the dynamics of the human proteome is crucial for identifying biomarkers to be used as measurable indicators for disease severity and progression, patient stratification, and drug development. The Proximity Extension Assay (PEA) is a technology that translates protein information into actionable insights across large samples sizes in both healthy and disease samples. The high-throughput nature of the assay is enabled by linking protein-specific antibodies to DNA-encoded tags that can be read out on a next generation sequencer. Here we have combined the unique PEA technology with automated sample preparation and high-throughput sequencing readout for parallel measurement of ~3,000 proteins for up to 384 samples at a time, generating over 1 million data points per run. Characterizing the proteome alongside genetic and clinical data enables a pQTL framework to not only validate known clinical targets and identify new clinical targets but to also suggest repurposing opportunities of clinical candidates for new indications. Join us to hear how proteomics is impacting large population health studies like the UK Biobank, SCALLOP and TOPMed to advance precision and personalized medicine.

Abstracts – poster presentations

P01

Realizing the concept of incidental finding reports: A case study into a Finnish biobank tumor cohort

MD Erik Vahtola[1], Merja Perälä[2], Lila Kallio[2], Erika Alanne[3], Petr Martinek[4], Sebastian Bender[5], Renate Schulze-Rath[5], Wei Zhang[6], Jihong Zong[6], **Arndt Schmitz[5]**
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Background Novel anti-cancer drugs target specific genetic aberrations found in a patient's tumor sample. Biobank research may reveal incidental findings i.e. genetic aberrations from donor samples which are outside the scope of the primary research question. These findings may have clinical relevance for treatment decisions. NGS is a multiplex technique making it more likely that incidental findings are made. Returning genetic results to the donor is subject to consent and governed by applicable local law.
Methods Auria Biobank is located at the Turku University Hospital in Finland. Research use of retrospective tumor samples were covered by the Finnish biobanking Act. Donor consents and approvals received from the biobank steering committee. We tested 351 samples across solid tumors with NGS using the TruSight Tumor 170 assay for somatic aberrations in DNA and RNA. The results were analyzed for aberrations with relevance to drugs approved for use in Finland, namely fusions of NTRK, ALK, RET or ROS1 and mutations in KRAS, NRAS, BRAF or EGFR.
Results A total of 42 such incidental findings were identified across tumor types. Reports including histology, blinded IDs and information on specific genetic aberration were sent to the biobank. Auria re-identified donors and after receiving their consent, cases were evaluated by the hospital Molecular Tumor Board. Treating physicians were encouraged to consider validating the results, adding the data into the EHR and discussing the options with the donor.
Discussion/Conclusions Biobank research of retrospective tumor samples yield new clinically relevant data on the prevalence of genetic aberrations across tumor types. We provide a case study of "from bedside to bench and back" where biobank research results might benefit the health of sample donors. Returning genetic data to the biobank and including the new genetic information to patients' EHR may influence present or future treatment decisions.

P02

Practical Methods in Reducing Biobank Footprint

Ms Ida Gidlöf[1], Ms Karin Gedda[1], **Mr Cameron McPheat[1]**, Ms Gabriela Baeza[1], Ms Malin Möller[1], Ms Josefin Aleke[1]
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Background

Environmental protection is a key focus area in AstraZeneca's global sustainability strategy, with such commitments as Ambition Zero Carbon – to have zero operational carbon emissions by 2025 and be carbon-negative across the entire value chain by 2030.

Biobanking can have a significant energy footprint by way of the equipment necessary for operations, notably Ultra Low Temperature (ULT) freezers.

Methods

AstraZeneca's Gothenburg Biobank has approached this problem from multiple angles. One key aspect is consolidation of available storage space. Since Q3 2018, we have reformatted our long-term storage of incoming samples to a higher density system (e.g. 9x9 to 10x10), and updated the racking system to allow for greater utilization of the internal space of each freezer.
In combination with this, we have procured modern, compressor-free ULT freezers, which are more energy efficient and provide a greater internal volume to floor space ratio.
To reduce our waste footprint, we reuse boxes from incoming shipments for applications outside the scope of long-term storage (e.g. checking samples out for analysis), and have a LIMS that allows for a completely digital audit trail of samples, including request and approvals – removing the need for paper printouts.

Results

More than 700 000 samples have been reformatted over the past 3 years, including a concerted effort to consolidate our largest collections of samples. The combined effect of reformatting changes equates to 11 fewer ULT freezers required to store these samples.
The AstraZeneca Gothenburg Biobank was awarded the My Green Lab Gold Certification (Oct 2020) for our efforts in sustainability.

Discussion

Next steps: we are currently investigating the feasibility in raising our long-term storage temperature to -70°C; including testing to determine actual energy savings in practice, and impact on freezer issues, such as response time to breakdown.

P03

Increasing the efficacy in sample handling with the HBS Request Picking-Tool

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Background

Biobanking of Human Biological samples (HBS) collected in clinical trials is essential for the discovery of new medicines and personalized healthcare. All HBS stored in the AstraZeneca Biobanks are tracked in a Laboratory Information Management system (LIMS) named AstraZeneca Biobank Application (ABBA), to ensure full traceability of the samples, from registration to disposal. However, preparing sample requests and cherry-picking samples stored in the system has been very time consuming and includes a lot of manual work.

Method

To generate a more efficient workflow, the AZ Biobank in Gothenburg developed a tool that simplifies the picking of samples by communicating with the database directly to collect positional information and display that data as a visual map. The tool has further been updated to enable picking for two requests simultaneously.

Result/Discussion

This visual tool enables quicker identification of the samples, therefore many hours have been saved and, more importantly, reduced the time that samples are handled outside of cold storage.

P04

AZ Gothenburg Biobank working strategies during Covid-19

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Background

In the start of the global pandemic, the AstraZeneca Gothenburg site was forced to change the way of working to ensure a safe work environment. The Gothenburg biobank stayed on site throughout the pandemic whilst all non-lab based staff started to work from home. Therefore, the biobank was able to maintain a good flow of incoming and outcoming samples, and more importantly, support scientists with their projects.

Method

To meet the criteria of a safe workplace, the group was divided in two groups, only prioritized studies were allowed to ship samples to the Biobank and mandatory usage of face masks were implemented on site. The Biobank team was also involved and supporting the PCR assessment on

site, to keep the lab based colleagues safe and to reduce the spreading of Covid-19 in the workspace.

Result/Discussion

With the safety measures described above, the biobank team has ensured that deliveries have been maintained in line with agreed timelines.

P05

Stability study: Long-term storage of serum; three different -80 °C storage environments

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In biobanks, biological specimens are often stored on long-term basis prior to retrieval and analysis. Storage conditions play a key role in sample degradation, therefore an optimization of these conditions is needed to maintain the quality of the biological material.

At the Biobank of the Norwegian Institute of Public Health (NIPH) serum is stored at -80 °C. The samples are stored in a) an automated store (Hamilton), b) chest freezers that are rarely opened and c) chest freezers that are opened regularly. The purpose of this study is to assess the effects on the levels of several components in serum during long-term storage in these three different -80 °C storage environments.

In January 2018 blood samples were collected from 32 adults, and serum from each donor was divided in multiple aliquots. One aliquot from each participant was analyzed at the collection day (timepoint zero). The rest of the aliquots were stored at -80 °C with 1/3 from each participant in an automated store, 1/3 in the upper parts of a chest freezer that is rarely opened and 1/3 in the upper parts of a chest freezer that is opened on a daily basis.

To assess any changes in analyte levels, the serum will be analyzed for 15 different components after 0 months (fresh), 6 months, 12 months, 2, 3 ½, 5, 7 and 10 years. At each time point from 6 months and forward, one aliquot from each of the three storage environments will be analyzed.

Analysis results from the 15 serum components will be presented after up to 3 ½ years of storage will be presented.

P06

Coordinating sample withdrawals from nationally collected sample collections within Biobank Sweden

Background

Many biomedical studies rely on existing or newly collected human samples. In Sweden, national sample collections are often collected through regional hospital-integrated biobanking and stored in local biobanks. In recent years, a growing number of projects has started using national sample collections, which has brought to attention issues in the current nationwide withdrawal process. There are differences in administrative and operative processes, for example, forms, storage formats, laboratory systems, and IT setups, between the nodes. These differences make nationwide withdrawals resource intensive and time-consuming for both researchers and biobanks alike.

The overall goal of the infrastructure Biobank Sweden is to enable nationwide collaboration between local biobanks to increase the competitiveness of Swedish research and development and drive the development of health care. The aim of this project is to support that goal by identifying and implementing strategies that enable coordinated and more resource effecient nationwide withdrawals from national sample collections.

Methods

The withdrawal processes at each of the seven Biobank Sweden nodes were mapped and compared. Differences and similarities were explored, and potential bottlenecks were identified. Next, the project group identified solutions and suggested new processes to form a national withdrawal strategy.

Results

The main elements of the strategy are using an existing nationwide network of regional coordinators (operational and regulatory), formation of a national workgroup, creating clearer communication channels for researchers, and creating supporting documents, including checklists, instructions, and process maps. The strategy also includes several measures to strengthen the collaboration between the operational and the regulatory bodies during the sample withdrawal process.

P07

Healthcare integrated biobanking (SIB) via mobile SIB equipment

Background

Healthcare-integrated biobanking (SIB) is a system for collecting and saving samples for research using the infrastructure available at a healthcare laboratory. Sampling is ordered and performed within the framework of a hospital sampling facility, the samples are handled in the laboratory in a standardized way, with high quality and continuity.
In Örebro County Council, we have introduced and set up a study with the help of a mobile SIB equipment, where trained laboratory staff can perform aliquoting and freezing on site, for later transportation of frozen samples to final storage in a biobank. Thus, the same sample quality can be achieved with the advantage that sampling can be performed at a health center nearer the sample donors.

Method

A device for manual pipetting of samples was set up at the primary health center's laboratory. The study nurse on site orders sampling of the study participant, the laboratory staff performs sampling, centrifugation and aliquotation of the samples in the biobank plate, 225 uL serum / plasma in a maximum of 8 aliquots. The computer program, AliBi, then forwards data about the plate and the location of the samples to LIMS. The sample plate is frozen in the on-site freezer for temporary storage. At least every 14 days, frozen plates are sent to the central laboratory for long term storage in the biobank.

Results

Samples for research are handled within 4 hours after sampling, even though the sampling physically takes place outside the central laboratory.

Discussion

High quality and continuity of samples taken for research purposes can be maintained, even when study participants are included and sampled far from the central laboratory and biobank. A prerequisite is mobile equipment, data connection between the primary health center and the central laboratory and trained staff on site.

P08

Working towards the ISO 20387:2018 standard: Validation of processing methods – experiences from EDTA-plasma

Ms Liv Paltiel[1], Hanne Bragmo[1], Miia Marika Taipale[1], Pietro Grassi[1], Camilla Lysa Fredlund[1], PhD Kishan Kumar Chudasama[1]
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Background

The biobank of the Norwegian Institute of Public Health (NIPH) has decided to work towards the ISO 20387:2018 standard. Chapter 7 of the standard focuses on the processing of the biological material and associated data. The paragraphs of 7.9 consist of requirements regarding validation and verification of methods to ensure that the biological material is fit for the intended purpose.

One of the sub-classes of biological material processed and stored in the NIPH biobank, is EDTA-plasma. Processing of plasma includes centrifugation, separation of plasma from blood, aliquoting plasma, and subsequently long-term storage. The validation carried out in our Biobank focused on the pureness of plasma after separation from blood, and if different aliquots are homogenous.

Method

For separation of plasma from blood, we set the requirement of presence of platelets and cells to a maximum number of 10 000 and 1 000 per mL, respectively. To investigate the difference between the aliquots after distribution and retrieval, a maximum of 5 % difference in creatinine concentration were decided.
All samples were collected and processed according to the SOPs of the biobank, and then analyzed for the presence of cells and platelets and for creatinine concentrations.

Results

Results showed that samples had an unsatisfying separation of plasma from blood and that the concentration of the aliquots was higher than 5%.
For retrieval of plasma, the requirements were met with a maximum difference of 1,6 % between aliquots which were retrieved.

Discussion/conclusion

The NIPH biobank continue to work towards validating our processing methods for plasma.

Validation of processing methods is a valuable contribution when working towards reproducible results and biological material which is fit for the intended purpose. It is recommended also for the biobanks not planning to work towards the ISO 20387:2018 Biobanking standard.

P09

Adaption to new regulation of clinical trials regarding biobank application – keep Sweden as an attractive country for clinical trials

PhD Hanna Schierbeck[1], Camilla Hildesjö[2], Elin Stenfeldt[3,4], Jenny Björkström[4], PhD Sonja Eaker Fält[1]

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Background

The process of clinical trials in EU will undergo a major change when the new Clinical Trials Regulation (Regulation (EU) No 536/2014) applies on 31 January 2022 in order to increase safety and transparency of the trial and facilitate the application process. The clinical trials will be harmonised across EU via a Clinical Trials Information System (CTIS). For Sweden, the assessment will be performed jointly by the Medical Products Agency (Läkemedelsverket, LV) and the Ethical Review Authority (Etikprövningsmyndigheten, EPM) and then consolidated by LV.

Access to biological samples is critical in most clinical trials and it may not start in Sweden until the biobank agreement is approved. Thus, the aim of this project is to evaluate an effective process of handling the biobank application in parallel with the clinical trial application to avoid a delayed study start.

Methods

In collaboration with LV and EPM, Regional Biobank Centres (RBC) in Sweden have established and tested new collaboration structures and processes. RBC have also prepared a new internal process including forms for biobank application in order to facilitate for both sponsor and RBC.

Results

A new process for assessment of biobank application in parallel with the application of clinical trial has been presented. A selected RBC will perform the assessment and, if applicable, specialised pathologists will assess the reasonableness of requested amount of existing tissue samples in relation to aim and analyses in the protocol. After the clinical trial approval, the biobank application will be ready for approval.

Discussion/Conclusions

It is of utmost importance that the consequences and the need of a new process is properly evaluated before the new regulation applies, to ensure the aim. An important conclusion is that the biobank application must be included in the process for Sweden to be an attractive country for clinical trials.

P010

Normal variability of biomarkers – examined in a "variability biobank"

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Background

For most biomarkers there is limited information about normal within-individual (day-to-day or within-day) and between-individual variability. For urine there may be diurnal variability making it important to fix the time of day for sampling. Our aim was to examine normal variability.

Methods

We established a "variability biobank" of blood (plasma, erythrocytes, and whole blood) and urine (six fixed times: first morning, 9:30, 12:00, 14:30, 17:30, 22:00, and 24h excretion) samples from 60 healthy non-smoking participants aged 21-64 years (29 men, 31 women). Blood and urine samples were collected twice, about one week apart. Aliquots are stored frozen (-80°C). Height, weight, and estimated glomerular filtration rate, urinary flow rate, creatinine, and specific gravity are available for each urine sample.

Results

Up to now we can report 1) ICCs (Intra class correlation: between-individual variability/total variability) for 24h excretions of 22 elements were high (0.75–0.90) for Cd, Co, Hg, Pb, Sn, Se, V, Zn; moderate (0.35–0.75) for As, Br, Cu, Fe, Li, Mn, Mo, Ni, P, S, U, W; and low for Cr and Sb (<0.35). 2) ICCs for urinary creatinine showed ICC=0.64 for 24h excretion, 0.48 for overnight samples, and 0.23 for all spot samples. 3) For Pb excretion ICCs were 0.81 for 24h, 0.71 for overnight urine, and 0.57 (men) and 0.41 (women) for all spot samples.

Conclusions

Although 24h excretion is the gold standard for urinary biomonitoring, day-to-day variability is high for some elements. The ICC for urinary creatinine depends on time of day and is affected by urinary flow rate. Lead in urine has a diurnal variability. The biobank (> 20 000 aliquots) is open for researchers to examine normal variability of their favorite biomarker(s). It is suitable for analysis of diurnal variation in urine (12 samples/ subject) but could also be used for blood biomarkers.

P011

The history of Biobank West – development of a healthcare integrated research infrastructure

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Background

Sahlgrenska Biobank, the regional biobank for Västra Götaland was founded in 2010. The first research study using the biobank's sample services started in 2012. In 2017, Regulatory Biobank Centre West merged with Sahlgrenska Biobank forming a strong customer-oriented biobank with a near teamwork between regulatory and operative services. The organisation, a close collaboration between Region Västra Götaland and Gothenburg University, has since developed further and in 2018 changed name to Biobank West. Biobank West is also a part of Biobank Sweden. Here, we give an overview of Biobank West's advancement over a decade.

Methods

A biobanking service was initiated to meet the needs of the large Swedish national cohort study SCAPIS. Since then, a growing number of research groups have discovered the convenience and reproducibility of the biobank's sample collection services. We have over time grown in collaboration with the diverse field of research studies.

Results

A demand from our customers has been to collect biobank samples under standardised conditions, to improve quality and make test results reproducible and comparable. Biobank West consequently operates according to a quality management system and offers regionally healthcare integrated biobanking. In collaboration with Biobank Sweden there is an infrastructure for collecting biobank samples in national studies. We are also part of Biobank Sweden projects facilitating national studies' sample withdrawals, quality management systems and sample quality. Other biobanking services are DNA extraction, cell isolation and reformatting of sample volume.

Discussion/Conclusions

Biobank West is in constant development and now offer comprehensive services for sample collection, handling, secure storage, traceability, and sample withdrawals. Future plans are expanded services for regional collection of samples, improved databases, and quality assessment of samples with unknown pre-analytic handling. All to have a complete service for biobanking and to make biobanking as easy as possible.

P012

The Biobank Sweden network of sample collections in the BBMRI-ERIC Directory: where we are at and future visions

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Background

Sweden, similarly to other Nordic countries, has a strong tradition of building and studying prospective cohorts with associated sample collections in biobanks. Combining analysis of such cohorts with for example health registries is a gold mine for medical research. Ensuring visibility and searchability of sample collections is, however, critical for increasing their use in future research.

Methods

Biobank Sweden, the Swedish node of BBMRI-ERIC, has provided support to Swedish sample collections and biobanks to become listed in the BBMRI-ERIC Directory – the world's largest biobank catalogue. In this poster we summarise which sample collections are included under the Biobank Sweden network of the directory, as well as some points for future action and discussion.

Results

To date, there are 24 sample collections in 8 different biobanks around Sweden that are included in the Biobank Sweden network in the BBMRI-ERIC Directory. Some of the population-based sample collections started already in the 1970's and 1980's. In more recent years, newer cohorts with sample collections have for example focused on follow-up of cardiovascular risk factors, or prognosis and treatment effects in people diagnosed with cancer. A third of the collections are in the size range of 100.000-1.000.000 samples, and another third are in the range of 10.000-100.000 samples.

Discussion/Conclusions

Biobank Sweden should contribute to continued development of this tool, for example, by ensuring that the information in the directory is kept up to date. In addition, we would like to better understand the benefits of the directory, for example, by enquiring if Swedish samples collections perceive that being listed in the directory has resulted in increased visibility and therefore increased opportunities to participate in European research projects.

P013

Example of recalling biobank donors to a new study: In vivo metabolic study to investigate nonalcoholic fatty liver disease (NAFLD)

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Introduction

Nonalcoholic fatty liver disease (NAFLD) is a growing health burden in the world. PNPLA3variant I148M is known to be a genetic risk factor for NAFLD, which is not associated with insulin resistance. Recent studies have also shown this gene variant to be protective against cardiovascular disease. However, metabolic consequences caused by the variant have been unclear, and there were no studies addressing the function of the PNPLA3-I148M in humans in vivo. Researchers of University of Helsinki and Helsinki University Hospital wanted to carry out a clinical in vivo study on the metabolic consequences of genetic variants of PNPLA3 associated with nonalcoholic liver disease.

Methods

Participants were selected among the donors of THL Biobank based on the genetic data, alcohol consumption, BMI and age. Biobank approached the selected donors and asked the donors permission to give their contact details and genetic information (PNPLA3 variant) to the clinical research group. About 50% of the recontacted biobank donors were willing to provide their details through biobank and were interested in hearing more about the new study. Clinical research group then contacted the donors, who gave a separate consent for their participation in the new study.

Results

Processing of labelled fatty acids in participants with different genetic variants of PNPLA3 gene could be compared in the accurate clinical setting (Luukkonen et al, Human PNPLA3-I148M variant increases hepatic retention of polyunsaturated fatty acids.JCI Insight. 4(16): e127902, 2019).

Conclusions

Selection of the pre-characterized donors via THL Biobank was possible due to large amount of stored biobank data consisting of genomic (GWAS, WES and WGS) and other omics data, laboratory measurements, physical examination data, life-style information etc. Above all, the general positive attitude of Finnish biobank donors towards the research enabled a new study.

P014

Functional transcriptomics in 17 year-old blood samples? Yes, we can!

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Background

Analysis of blood RNA transcription profiles is hindered by ex vivo gene expression changes, and degradation and loss of RNA. In 2003, the NOWAC Post-genome Cohort chose the PAXgene Blood RNA Tubes for a nation-wide blood sampling. The PAXgene Blood RNA Tube stabilizes and preserves RNA in blood specimens for 11 years. Could the 17 year old NOWAC blood samples still be used for research?

Methods

We analyzed 198 blood specimens collected from a random sample of Norwegian women, at local doctor's offices. Specimens were shipped by mail at ambient temperature, and frozen at -80^{o}C until RNA isolation with PAXgene Blood RNA Kit on QIAcube, followed by analysis of quantity, purity, integrity and suitability for RT-PCR.

Results

RNA extraction from all specimens yielded sufficient amounts of pure, highly intact RNA, suitable for downstream assays without any inhibition. 99% of the samples showed gDNA contamination of ≤1% w/w after additional DNA digestion and RNA clean-up for selected samples. RNA yield was 5.7+/-3.2 µg/2.5ml blood on average (+/- 1SD). 21 blood specimens did not produce a visible pellet after blood tube centrifugation, although sample processing turned out successful.

Discussion and conclusion

The de-centralized NOWAC sample collection procedure is likely to have introduced variability in RNA yield, due to lack of standardization as one of the important pre-analytical steps. Samples with lower RNA yield trended towards higher gDNA contamination. We conclude that the PAXgene Blood RNA System provides high quality RNA from blood samples stored for 17 years.

P015

Long-term stability of urine samples at HUNT biobank

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Background

Most studies recommend measurement of urine albumin in fresh samples to avoid analytical problems, since prolonged frozen storage of urine samples at -20 ºC show degeneration of albumin. Loss of albumin after freezing depends not only on freezing temperature, but also on detection method. However, storage at -80 ºC seems to prevent albumin loss. The aim of this study is to examine the stability of urine albumin.

Methods

In the Trøndelag Health Study (HUNT), a panel of urine-samples was established in 2018 and includes the inflammation biomarker albumin. The study is based on urine samples stored at -80°C. Factors assumed to influence stability are several, where time and numbers of freeze/thaw cycles were considered. The study includes one 900 µl sample and several 150 µl samples from 111 individuals. The 900 µl sample was for studying effects of freeze/thaw cycles and the 150 µl samples for general long-term storage effects. The analytical instrument used was Alinity, and urine albumin was determined by a turbidimetric method. Albuminuria was calculated as albumin/creatinine ratio (ACR), and measurements were performed approximately once every year. Mean effects over time have been analysed by correlation analyses and visualized by scatter-plots.

Results

The results after three years, investigating both storage time and number or freeze/thaw cycles, shows an excellent correlation. Pearsons's correlation coefficient was 1,00 ($p<0,0001$) when comparing the first and second, second and third and first and third urine ACR from the 900 µl sample and from the 150 µl samples. The figure shows the scatter-plot comparing the first and third urine-ACR.

Discussion/Conclusions

The results from the study show an excellent stability of urine albumin after three years frozen samples at -80 ºC, analyzing both the freeze/thaw cycles and the long-term storage effects. The study will continue in the future.

P016

Biobank West - a platform facilitating research infrastructure to make biobanking easy

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Background

Biobank West is a collaboration between Region Västra Götaland and Gothenburg University, which offers cost-based biobanking service for human biological samples. Biobank West operates according to a health care integrated process and provides services for local, regional and national sample collection. Our customers span from small research groups to large multi-centre research initiatives and clinical trials.

In Gothenburg, we have three laboratories:
* At Sahlgrenska hospital, we offer sample reception and biobanking services in collaboration with the Clinical chemistry department.
* At Östra hospital, we have our own lab for sample reception and biobanking services.
* At Biobank West´s laboratory at Guldhedsgatan, we provide additional biobanking services such as DNA extraction, cell isolation and reformatting of sample volumes.

Methods

When contacted by a new research study, one of our study coordinators in collaboration with the study, sets up a standardized biobanking process according to a quality assurance system. For example, our services include handling samples of whole blood, plasma, serum, PBMC, urine, faeces, tissue, and DNA. Samples are handled according to the agreed process providing high quality and sample traceability. Our processes include robotic aliquoting and secured storage in alarm monitored freezers. Later, when a study is ready for sample analysis, we start the process of samples withdrawal from the biobank.

Results

Today, we provide biobanking services for a total of 85 sample collections/clinical studies. In addition, we handle withdrawals of 40.000 aliquots each year. Altogether, we store more than 1 630 000 samples.

Discussion/Conclusions

Providing standardized healthcare integrated research infrastructure, Biobank West can help advance clinical research quality. We are continuously striving to develop our service to make biobanking easy and improve sample quality. We are also continuously building new processes to facilitate research.

P017

Update of ISBER Biobank Assessment Tool (BAT) Based on ISBER Best Practices 4th and Addendum on LN2 Based Cryogenic Storage

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Background
The International Society for Biological and Environmental Repositories (ISBER) Biobank Assessment Tool (BAT) is a questionnaire aimed to help biobanks to evaluate how well they comply to the ISBER Best Practices (BP). It was first made available in 2011, since then ISBER has published the 4:th edition of its BP and an addendum on Liquid Nitrogen-based cryogenic storage. In addition, the international biobanking standard-ISO 20387:2018 has been published. The BAT was in well need of an update.

Methods
The BAT was updated in accordance to the latest ISBER BP by removing questions that no longer corresponded to neither the latest edition of the BP nor the addendum, and replace these with new questions that did correspond. In addition, a new data model was developed to ease interpretation and comparison of the data over time, while ensuring security, reliability, and usability of the data.

Results
The BAT questionnaire provides the user with an overall score of compliance to the ISBER BP. Each question has a risk-balanced assessment score attached to them. The score is based on an algorithm that attributes a different grade to each answer, depending on the severity of the risk associated with the subject of the question, the frequency of occurrence of the risk, and the ease of detection of the situation. After completion, a report will help the biorepository to evaluate how well it conforms to the ISBER BP, where applicable, references to the ISO20387 will be included in the report.

Conclusions
The updated BAT will help biobanks to assess their compliance to the latest ISBER BP, and on a higher level also the ISO20387 biobanking standard. The BAT can be used repeatedly, which allows follow up every year, giving it a natural place in any QMS where implementation and follow-up of quantitative indicators are required.

P018

Qualification in Biorepository Science (QBRS) Examination developed by ISBER and ASCP BOC Enhances Biobank Sustainability

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Background
Modern biobanking is a complex activity that requires well-trained and skilled repository staff essential for assuring high-quality research specimens. The International Society for Biological and Environmental Repositories (ISBER) and the American Society for Clinical Pathology Board of Certification (ASCP BOC), an organization providing excellence in global medical laboratory professional certification, have developed a shared qualification examination through which individuals may earn an international biorepository qualification credential, the Qualification in Biorepository Science (QBRS).

Methods
The QBRS Workgroup (WG) was established as a standing committee of the ASCP BOC. The WG's task was to develop, review and update the qualification examination itself, develop the examination content guidelines, eligibility requirements, and candidate professional experience documentation forms. All QBRS credentials awarded will be time-limited and must be revalidated every three years with documentation of continuing education or other educational activities as defined by ASCP BOC. ISBER and ASCP BOC responsibilities have been established and will be reviewed periodically.

Results
The QBRS credential program application process became available for applicants in January 2020. Since April 2020, an international cohort of applicants have applied for and taken the exam. As of September 30, 2021, there have been 30 successful applicants attaining the QBRS, 24 from USA, 2 from Hong Kong, 1 from UK, 1 from Saudi Arabia, 1 from UAE and 1 from Nigeria.

Conclusion
ISBER has joined forces with ASCP BOC to develop a QBRS credential program. ASCP BOC is an experienced, well-recognized organization for certifying professional competency among individuals worldwide, while ISBER WG participants provide content knowledge and biobanking expertise. This agreement has allowed ISBER to fully participate in development of a global QBRS credential program, requirements of which are essential for the future of standardized and sustainable quality biobanking.

More information is available at www.isber.org/qualification.

P019

IT infrastructure for improving data protection in biobank data management – use-case THL Biobank

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Background

THL Biobank is established within the Finnish Institute of Health and Welfare (THL), and one of its main functions is to host nationally significant sample collections and ensure their biobank research use. Biobank data derived from samples and obtained from the donors is sensitive data containing health information. Therefore, THL Biobank has been developing its IT infrastructure to support biobank data management while securing the privacy of sample donors.

Methods

When being under a governmental research organization, the expectations towards good quality performance and efficient processes are high. Therefore, THL Biobank has employed a variety of IT tools to facilitate data processing as well as to document and track every step of in biobank data-related processes from researchers' applications to data harmonization, data release and result management. Also, data protection is an integral part of biobank's IT infrastructure and data management processes.

Results

The most important applications in THL Biobank's IT infrastructure are (1) REMS2, developed by CSC, for managing resource access inquiries; (2) PRIMS for managing biobank research project information and sample and data transfers; (3) SamWise for sample information handling including LIMS functionalities; (4) PhenoWeb for phenotype data management and data extraction tools; (5) THL Biobank's Availability Service for querying diagnosis information from Care Register for Health Care; and to link all these databases (5) CORE for sample donor consent and code registry information management.

Discussion

The aim of building IT infrastructure for data processing is to provide the best quality of samples and data to researchers applying to use THL Biobank resources. The most important aspects are to take the best possible care of the research collections stored in THL Biobank and to integrate data protection aspects in all the data management solutions.

Conclusion

ISBER has joined forces with ASCP BOC to develop a QBRS credential program. ASCP BOC is an experienced, well-recognized organization for certifying professional competency among individuals worldwide, while ISBER WG participants provide content knowledge and biobanking expertise. This agreement has allowed ISBER to fully participate in development of a global QBRS credential program, requirements of which are essential for the future of standardized and sustainable quality biobanking.

More information is available at www.isber.org/qualification.

P020

Biobank Sweden – A Continuously Evolving National Infrastructure for Biobanking

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Background
Sweden has a complex biobank landscape with over 160 million samples, mainly collected for healthcare purposes at hospitals, but often used in ethically approved research in academia and the industry. Hospitals, academia and industry have long lived in symbiosis and the next step was evolving into a collaboration platform.

Methods
The national biobank infrastructure Biobank Sweden was founded in 2017 as a joint initiative by Swedish healthcare and universities with a medical faculty, as well as industrial partners and patient organisations. During the initial phase we have refined our organisation and collaboration with the overall goal to build a sustainable biobank infrastructure that is nationally accessible and cost-effective, while securing access to high quality samples.

Results
We work on national harmonisation of several aspects of biobanking. A major project on creating a database for healthcare samples, the National Biobank Registry, is underway, and data is also gathered on the sample collection level. Support in sample handling and logistics is offered to researchers when starting new sample collections using the harmonised process of hospital-integrated biobanking now implemented in 31 hospitals, ensuring high and comparable sample quality. Sample utilisation is enhanced through national projects on streamlined processes. The regulatory support functions ensure that samples are utilised in accordance with national legislation, and e-learning is also provided to make it easier for researchers to educate themselves. An increasing focus has been on activities regarding ethico-legal issues, quality management as well as patient engagement, and how to allow these aspects to permeate all of Biobank Sweden's projects and activities.

Discussion/Conclusions
The infrastructure is maturing, and we continuously pick up new ideas, for example through an active utilisation of the research representatives within our organisation, continually evolving our agenda but maintaining the goal of supporting medical research and clinical trials.

P021

The long-term stability study of serum samples stored at HUNT biobank – an update

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Background

Biobanks are involved in storage and processing of biosamples for future studies. Biomarkers within the samples may serve as surrogate clinical endpoints, indicate disease progression, and allow clinical outcome predictions. Little knowledge exists concerning long-term stability and effects of pre-analytical conditions on biomarkers in the stored, often heterogenous samples. The aim of this study is therefore to assess this in serum samples stored at HUNT Biobank.

Methods

Two long-term stability studies of serum samples were initiated in 2012 (Panel 1) and 2014 (Panel 2). Panel 1 includes the markers ALAT, ALP, triglycerides, and phosphate. Panel 2 includes albumin, calcium, CK-NAC, magnesium, potassium, sodium and total protein. Serum samples were collected in SST tubes and stored at -80°C in polypropylene matrix tubes. Factors such as time and numbers of freeze/thaw cycles were considered. The studies each includes one 900 µl sample and several 150 µl samples from 17 individuals in Panel 1, and 59 individuals in Panel 2. The 900 µl samples were for studying effects of freeze/thaw cycles and the 150 µl samples for long-term storage effects.

The analytical instruments were ABX Pentra 400, Architect and Alinity ci. Measurements were performed 3 times the first year, twice the second year and then once a year. Mean effects over time were analysed by ANOVA Repeated Measures.

Results

Results from 2018 suggested freeze/thaw cycles to affect the level of potassium, sodium and CK-NAK content within the samples. Over the last two years additional measurements of all the biomarkers have been performed.

Discussion/Conclusion

An update on the effect of storage time and number or freeze/thaw cycles on all the biomarkers will be presented.

P022

THE BIOBANK AND ITS IMPORTANCE IN HEMATOONCOLOGY

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Background

Biobank at the University Hospital Ostrava was founded in 2012 and specializes in the collection and archiving of samples from patients with hematooncological diagnoses. Over the years, Biobank has been involved in a large number of projects and grants at the national and international levels.

Methods

The collected biological material is processed according to standard operating procedures, which ensures the high quality of samples. Blood is used primarily to obtain plasma, serum, and DNA. Different cell types are further separated from the bone marrow according to the specific diagnosis. All samples are frozen and stored in monitored conditions. In the case of specific projects, the collection and transport of fresh samples are also provided.

Results

At the end of 2020, a total of 49,968 samples from 2,750 patients were archived at Biobank. Biobank has also been actively involved in more than 25 projects at the national and international levels out of which the cooperation with the Spanish laboratory Vivia Biotech dealing with treatment personalization and participation in the international project "iMMunocell" which focuses on research into the progression of smoldering multiple myeloma were the most significant. Biobank has provided samples to several grants and functions as a central laboratory for clinical studies. Biobank is also closely cooperating with the Blood Cancer Research Group on various projects such as MRD monitoring in patients with multiple myeloma. More than 4,000 samples were released from the biobank for these projects.

Conclusions

Biobank has become an important part of the research activities not only at the Clinic of Hematooncology, but also provides rare patient samples to other laboratories in the world.

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P023

Harmonization of PSHP oncology dataset into the OMOP Common Data Model

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Harmonization of PSHP oncology dataset into the OMOP Common Data Model

Hospitals use different data systems for storing patient data, and the information is coded using various national or local coding systems and local languages. Observational Medical Outcomes Partnership (OMOP) is a common data model (CDM) that has been designed to enable research on clinical data. The OMOP CDM has a limited set of standardized tables for storing various real-world data, and it uses standardized concepts instead of local codes. The OMOP CDM makes clinical data more accessible to researchers, and makes it possible to carry out federated analyses across hospitals and countries.

We piloted the conversion of clinical data from the Pirkanmaa Hospital District (PSHP) into OMOP. This pilot project was carried out with a stable, pseudonymized dataset of 114,697 patients with an ICD10 diagnosis of C* or D*. The dataset consists of structured data retrieved from the PSHP data systems, and it contains basic demographic data, visits and inpatient stays, medication, procedures, laboratory measurements and pathology results. National and local codes in the source data were mapped into OMOP standard concepts, and we built the OMOP database on Microsoft SQL Server.

We were able to map 87-99 % of the rows in the source dataset into OMOP, with the exception of pathology (61 %). We shared vocabulary mapping efforts, especially diagnoses, procedure codes and laboratory measurement codes, with other university hospitals. We found that collaboration with other university hospitals and the Finngen project helped to ensure the quality of the OMOP database.

In the future, we will build an OMOP database with data from the whole PSHP datalake, with visits and other data for more than 700,000 patients.

P024

An integrated quality control and sample identification system

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The last two decades have witnessed the development of and increasing dependence on biorepositories for advancing basic, translational and clinical sciences. However, with the rising number of samples deposited in biobanks come challenges including sample misidentification due to labeling errors or contamination and the introduction of poor-quality samples.

While many means of externally tracking samples exist (for example, by labeling the tube, rack or plate in which the sample is conserved), an ideal system would allow you to assess the identity and quality of the genetic biomaterial (for example, DNA) inside the tube. Such a system provides a proactive workflow that drastically reduces the number of samples making it to analysis or redistribution. Molecular sample identification (DNA fingerprinting) is such a system. With DNA fingerprinting, panels of DNA markers are analyzed for each sample, generating a unique fingerprint that is an indelible, nontransferable identifier.

The Advanta Sample ID solution is a high-throughput, automated solution for molecular sample identification. It can simultaneously perform molecular fingerprinting, quality assessment and integrity confirmation of every sample with minimum hands-on time and maximum reproducibility.

P025

BUILDING A NEW GENOTYPE BASED BIOBANKING PIPELINE WITH FINNGEN

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Background

The Finnish Red Cross Blood Service Biobank has participated the FinnGen project by providing DNA samples from over 40 000 healthy blood donors who have given an informed biobanking consent. The FinnGen study has identified over 100 disease associating gene variants enriched in Finnish population. To gain insight in clinical, functional and metabolic consequences of the Finnish enriched variants we established a pipeline for collecting new sample types from 2500 genotyped blood donors.

Methods

Blood Service Biobank is now collecting plasma and serum samples and live frozen PBMCs from blood donors in Helsinki area. Blood plasma is separated from EDTA-whole blood, aliquoted and frozen at -80^{o}C under four hours from donation.. Buffy Coat fraction of the donated blood is used for isolation of PBMCs the day after blood donation. Live PBMCs are frozen in liquid nitrogen for later use. Based on the genome data new sample types can be requested from blood donors with a specific genotype of interest.

Results

The genotype analysis of the collected first 1000 samples revealed a good catchment rate of the Finnish enriched variants in Helsinki region. The analysis of genotyped blood donor pool in the Biobank demonstrated that all genotypes could be found in the donor pool as heterozygotes, many even in hundreds. The cryopreserved PBMCs showed a good viability and responsiveness after thawing. All plasma samples collected were processed and frozen under 4 hours.

Conclusions

Our newly established biobanking pipeline demonstrates capacity to collect high quality genotype-based biobank samples. The plasma and live cryopreserved PBMC biobank samples are suitable for multiomics analyses and complex immunophenotyping. Expanding our new biobanking pipeline outside Helsinki area and harnessing the genome data for biobanking will significantly increase the potential to collect genotyped samples with high quality.

P026

Liquid biopsy: automating the processing of STRECK tubes for improved precision medicine.

Liquid biopsy has emerged as a powerful tool to elucidate dynamic genomic, transcriptomic, and epigenomic tumor profiling in real-time. One of the considerable challenges of the liquid biopsy is the handling of the glass STRECK tube from which plasma cell-free DNA (cfDNA) can be isolated. STRECK tubes have an elevated risk of breaking and present significant automation challenges including shattering, which generally excludes them from healthcare workflows and limits their use on automated platforms. The KI Biobank partnered with the Prostate Biomarkers study, an international, phase 3 trial in men with prostate cancer to extract patient cfDNA. The process initially started off as a complex manual procedure. As sample numbers increased, the risk of manual error increased. We implemented an automated pathway to improve sample security without increasing sample loss due to automation tube shattering.

Methods

cfDNA extraction requires the sample to be centrifuged twice. As STRECK tubes could not be used on our automated tube sorters, we needed to find a way of centrifuging the samples without breaking the tubes and subsequently accurately measuring the volume of plasma before use on our liquid handling platforms.

Results

After upgrading our centrifuges to process glass tubes, sample loss rates dropped dramatically to <0.5%. We also successfully implemented an on platform workflow to accurately measure sample volume using our Tecan Tube Inspection Unit (TIU) instead of our regular automated tube sorters. The result was an automation based workflow compatible with STRECK tubes.

Conclusion

The KI Biobank, is the first biobank in Sweden to successfully automate the processing of STRECK tubes from clinical environments. The move to automated processing has improved sample traceability and process standardization. KI Biobank should be considered as the first choice partner for precision medicine research or clinical trials wanting to isolate cfDNA.

P027

Metabolic biomarkers in long-term stored serum samples from the Janus Serum Bank Cohort in Norway

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Background
Metabolomics is increasingly in use in research to investigate the aetiology, prognosis, and outcomes of disease or provide more detailed information on normal human biochemistry. Metabolites detected in long-term stored serum can give a snapshot of the donor's genotypic and phenotypic expression levels at the time of donation and may reveal metabolic changes that are difficult to detect on a genetic level. Metabolic patterns have the potential as early biomarkers of disease.

The purpose of this study was to investigate if long-term stored samples from biorepositories, such as the Janus Serum Bank, are of high enough quality to use for large-scale metabolomics studies.

Material and Methods
The samples were from healthy donors, including both genders, aged 40 years and non-fasting. The selection covers different sample collection periods, pre-analytical treatments, and gender in 3 groups. Group 1 samples were collected in 10-mL tubes containing 5 mg sodium iodoacetate, group 2 were collected without additives and group 3 were collected in gel vials. After coagulation at room temperature and centrifugation, the samples were shipped cold (+1°C–10°C) to a central facility and frozen within days, depending on transportation route and analyses performed.

300 serum samples collected from the early seventies and onwards were analysed using nuclear magnetic resonance (NMR), on a panel of ~ 200 biomarkers specific for blood derived samples. Results were compared to measurements made at the time of blood draw.

Results
Overall success rate of biomarker quantification was good. However, some biomarker distributions differed from general population cohorts, which might be caused by sample degradation, multiple freeze-thaw cycles, long storage time and/or elevated storage temperatures. These biomarkers were tagged in the result report.

Discussion/Conclusion
Long-term stored serum is suitable for metabolic biomarker studies. However, caution should be taken for tagged metabolites.

P028

Pathology Core Facility Karolinska, PCFK (Tissue Biobank)

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Pathology Core Facility Karolinska (PCFK) provides the possibility for prospective and retrospective tissue biobanking in combination with both sample and data handling at different hospitals in Stockholm Region by using the infrastructure of PCFK at local and national level. At the PCFK we offer both operational support and study design services for research and clinical trials, moving from setting up advanced methods and procedures in pathophysiology, to collect and analyze data.

PCFK provides the possibility for research within e.g., the ex vivo field based on different tissue types (organotypic models) and primary single cell cultures (PSCC).

PCFK has exclusive responsibility for tissue biobanking at the Department of Pathology and Cancer Diagnostics at Karolinska University Hospital, supported by the infrastructure at four hospitals in the Stockholm area. PCFK is the hub for tissue biobank and research support services in different research areas with easily accessible tissue biobank services at the national and international levels with various laboratory analysis and services in pathology, in addition to cellular and tissue research (Fig 1).

Figure 1PCFK's services and facilities for research

PCFK has plans to develop and implement competence supply strategies for employees within the core facility, to increase awareness about the importance of core facilities for research and development within the advanced health care systems. Furthermore, we aim to consolidate synergic activities between Region Stockholm and KI Core Facilities to attract experts and skilled

employees to develop more innovative methods for personalized medicine and drug development based on the importance of tissue biobanking. The core facility is accredited by Organization of European cancer Institute, OECI and hence a part of Karolinska's accreditation as a Comprehensive Cancer Center (CCC).