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The abstracts that follow demonstrate the broad range of timely issues addressed in the contributed oral and poster presentations at ISBER's 2017 Annual Meeting & Exhibits.

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Conclusion: DNA is cold-resistant for long-term cryopreservation. If the frozen period is more than 5 years, RNA molecules appeared to have serious degradation. At the same, the degradation of proteins with higher molecular weight appeared too.

BRS-22 Flow Cytometry Characterization of Patient Bone Marrow Samples

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Background: Eastern Maine Medical Center (EMMC) Cancer Care/Cancer Care of Maine recognized the need, opportunity, and challenge to contribute to basic and translational research by developing a biobank of well-annotated human specimens. The EMMC BioBank is based within a clinical oncology practice and has expertise in patient consent, clinical practice integration, and prospective collection and processing of solid and liquid specimens, especially from hematologic malignancies.

Methods: We have designed a characterization schema using flow cytometry for banked bone marrow specimens. The schema includes four flow cytometry panels that can appropriately characterize subpopulations of B-cells, T-cells, and myeloid and stem cells in the sample as well as measure viability and apoptosis. This characterization will allow our researchers to choose the best samples needed for a particular research project.

Results: To date we have completed this characterization schema on 18 bone marrow samples, primarily from B-cell leukemias and lymphomas. We have collected bone marrow from patients with chronic lymphocytic leukemia (5), diffuse large B-cell lymphoma (3), Hodgkin's lymphoma (3), acute lymphoblastic leukemia (2), follicular lymphoma (2), and two patients with anemia. Four flow cytometry antibody panels were designed to determine relative percentages of relevant leukocyte subpopulations. Flow cytometry panels and the subpopulations identified include: 1) B-Cells; (transitional, memory, plasmablasts, plasma cells), 2) T-Cells; (T effector, T Helper, terminal effector, transitional memory, effector memory, central memory, naïve, memory stem cells, senescent, and natural killer cells), 3) myeloid and stem cells (granulocytes, monocytes, CD34+, CD117+, CD133+, and erythrocytes), 4) viability and apoptosis (annexin V, 7AAD and Hoechst 33342 for cell cycle analysis).

Conclusions: We believe that this flow cytometry characterization can be a great asset when evaluating banked samples for research investigations. We also have begun to assess the practicality of flow cytometry on dissociated solid tumors. This added information allows researchers to determine which samples are best for their research based on their complete phenotypic characterization.

BRS-23

BRS-24

BRS-25 The Molecular Classification of Oral Cancer Based on Bio-Tissue and Bio-Information Bank

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Oral cancer (OC) is one of the most common cancers that badly affects the health and living quality of people. The surgical therapy for OC is limited by its operational area. Because of its unique anatomy and primary achievements from genetic studies, OC is an ideal model for carrying out molecular classification strategy. The tumorigenesis and development of OC is a continuous and multi-process event. Integration of description of tumorigenesis regulatory network and searching for their vital junction and regulatory factors are the most effective strategy for conducting precise medicine.

To date, the molecular study of OC is conducted in parallel by national and international researchers. We still lack a multi-level molecular standard to overwhelming by evaluating the process of OC development. The purpose of this study is mainly based on the OC tissue bank and bio-information data, to investigate the proteomics and genomics classification of OC development; the complex regulatory network and vital molecular event that drive the cancer development, diagnosis and treatment; the idea molecular targets for tumorigenesis, molecular prediction, and prevention.

We have used high throughput screening technology to describe the OC develop processing systemic and multi-divisionally. We have also developed original multi-study integration analysis technologies to draw the molecular regulator network of OC. Based on the innovative bio-informatics analysis models, many driver genes during oral oncogenesis have been obtained. The filtration and verification of gene targets and molecular markers for OC prevention and treatment have being carried out. The new system for OC molecular diagnosis and individual treatment will be built. Some diagnosis and treatment molecular markers have being evaluated using big-size clinical OC samples. This study will illustrate the molecular process of different stages of OC and help to develop the molecular classification technologies.

The study is supported by National Program on Key Research Project of China (NO. 2016YFC0902700).

BRS-26 Best Practices vs. Traditional Practices of Procedures and Technology for Preserving Viability and Functionality of T-Cells at Both −80°C and −190°C

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Statement of Problem: The quality of procedures and products used for preparing, transporting, and storage of cells at both −80°C and −190°C temperatures have a direct impact on post-thaw viability and functionality. Sub-standard preparation, handling, storage, and products may subject cells to improper cryoprotectant exposure, poorly controlled shipping and storage conditions and temperatures.

The objective of this study is to compare two methods of preparing, transporting and storing live T-cells at both −80°C and −190°C to demonstrate best practices to achieve the highest post-thaw viability.

Methods: Jurkat cells, a human T-cell line from ATCC, were cultured, analyzed for viability (membrane dye exclusion) and functionality (alamarBlue metabolic indicator), and prepared for storage preservation via identical protocols. Half were prepared with CryoStor CS5® (BioLife Solutions) containing 5% w/v dimethyl sulfoxide (DMSO) and was frozen to −80°C using an isopropyl alcohol freezing device. The frozen cells were shipped using an evo® −80°C Smart Shipper to Brooks Life Science Systems.

The other half were prepared with a traditional home-brew cryoprotective media consisting of 95% fetal bovine serum and 5% w/v DMSO and frozen to −80°C using an isopropyl alcohol freezing device and shipped using a conventional Expanded Polystyrene dry ice shipping container to Brooks.

Upon arrival, all cryovials containing Jurkat cells were handled identically and stored in either a −80°C ultra-low-temperature freezer or the −190°C BioStore III Cryo system.

After frozen storage of one year, the cryovials were packed and shipped back to BioLife in the same containers and using the same methods as employed previously. Both groups were thawed and analyzed for viability and functionality immediately post-thaw and at 24- and 48-hr post-thaw using the identical pre-freeze assays.

Results: Thawed cell results were compared to each other and to the pre-freeze baseline. The cells prepared with CryoStor and shipped with evo showed higher viability and higher functional recovery. The procedures and products used for preparing, transporting and shipping were also compared.

Conclusion: The outcome of this study recommends evidence based best practices for preservation, procedures, and products to ensure consistency and control of the cold chain and to maximize post-thaw cell viability and functionality.

freezing can result in a decrease in DNA yield but with little effect on purity. The aim of this study was therefore to investigate the effect of ultra-low −80°C temperature storage over time on the yield and purity of DNA extracted from biobanked whole blood samples.

Methods: 20 samples of whole blood in biobank −80c storage were selected for DNA extraction. Samples had been collected in EDTA blood collection tubes prior to freezing and were stratified according to disease type (5 each from colorectal, breast, gynaecology and prostate) and year of collection (5 each from years 2012–2016). DNA was extracted from the whole blood using a Maxwell Kit on the automated Maxwell extractor. Nanodrop technology and QuBit were used to assess the yield and purity of the extracted DNA.

Results: High yields of DNA were obtained from all 20 whole blood samples (nanodrop range 118.8–361.2 ng/μl; QuBit range (48.5–429 ng/μl). All samples had a 260/280 ratio of ~1.8 which is generally accepted as 'pure' for DNA.

Conclusions: Ultra-low −80c temperature storage over time did not have an impact on the quality and yield of DNA extracted from whole blood in this cohort of samples.

BRS-28 CPTAC Phase III, Continuation of the Proteogenomic Analysis of Cancers

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The Clinical Proteomics Tumor Analysis Consortium (CPTAC) is a National Cancer Institute initiative that seeks to uncover the molecular basis of cancer using a proteogenomic approach to study prospective cancer biospecimens. Leidos Biomed provides an infrastructure for supporting the collection of high-quality biospecimens and data, in addition to project and subcontract management for the program. CPTAC applies the understanding of the molecular basis of cancer to identify biomarker candidates. Phase II of CPTAC, completed in 2016, collected over 500 cases from breast, colon, and ovarian patients. Since early 2016, CPTAC Phase III has been collecting and will analyze 200 cases of each of ten additional cancers. The cancers include glioblastoma, pancreatic ductal carcinoma, lung adenocarcinoma, lung squamous cell carcinoma, sarcoma, head and neck squamous cell carcinoma, uterine corpus endometrial carcinoma, clear cell renal cell carcinoma, and acute myeloid leukemia. The goal is to collect 200 qualified cases of as many of these tumor types as possible.

This project is funded by NCI Contract No. HHSN261200800001E.

The study entails collection and pathology evaluation of tissue specimens, high-quality clinical data, and images from clinical sites around the world. A biorepository receives, evaluates and processes the biospecimens, sending nucleic acids to a sequencing center and tissues to proteomics groups. Data are combined and analyzed by translational centers. Genomic data are made available to the research community through the NCI Genomic Data Commons. Proteomic data are made available through the Data Coordinating Center. We report here on progress in collection of tissues and clinical data, and progress through biorepository, proteomics and genomics, and analysis centers.