

Biobanks as an important tool in modern translational oncology

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Abstract

The creation and use of biobanks is an actively growing field that plays an important role in the development of many branches of biotechnology and biomedicine, including oncology and translational medicine. In this review, based on the analysis of more than 80 Russian and foreign publications, we describe the current state of biobanking and its future perspectives. The diversity of biobanking and the problems arising from it, including the limits of applicability to different types of research, as well as the prospects for development are discussed. The role of biobanks in the study of malignant neoplasms, including rare/orphan diseases, and in the development of new diagnostic and therapeutic approaches, personalised medicine and pre-clinical screening studies, are highlighted.

Keywords: biobank, biobanking, biotechnology, malignant tumors, translational medicine, personalised medicine, drug development, oncology

Introduction

Currently, cancer is one of the major health threats worldwide. It is also detrimental for economy, leading to significant productivity losses (Barchuk, 2019). Thus, novel and more effective treatments and diagnostic approaches are urgently required. The creation and use of biobanks is an area of biotechnology that is actively developing in many countries and has applications in basic science, agriculture, environmental protection, and medicine, including translational oncology (Malsagova et al., 2020) — the branch of applied medicine which focuses on the translation of the knowledge and techniques/methods from basic research into new diagnostic, prevention and therapeutic approaches in clinical oncology. Many recent studies have demonstrated that biobanks can substantially underpin efforts of translational research and strengthen its capabilities, as will be discussed below. Economic benefits of biobanking in translational research have been estimated as significant (Rogers, Carolin, Vaught, and Compton, 2011). It is unsurprising that biobanks are gaining particular attention from oncologists, and our review adds to the wealth of the recent publications in this rapidly growing field (Kaprin, 2020; Kit, 2022; and others).

Definition, history and current status of biobanking, its legal and ethical aspects

The term biobank first appeared in 1996 (Loft and Poulsen, 1996), although organizational structures that are essentially prototypes of biobanks existed long before that, such as tissue and biopsy collections for pathomorphological and

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histological analysis in hospitals established as a part of standard medical practices. It is believed that in Russian Federation the first medical research biobank appeared in 1998 to study thyroid tumors (Roumiantsev and Mudunov, 2017). According to modern concepts, a biobank is a structure that includes collections of samples of biological materials (fluids, tissues, etc.), biological and/or medical images and associated data (for example, microscopy images, computed tomography data, etc) and related clinical, demographic, epidemiological and other information created for basic or clinical research, both ongoing and possible in the future (not yet planned). Thus, a biobank consists of two components: 1) collection of the biological material samples or/and biological images/other relevant biomedical data, as well as the infrastructure for storing them, and 2) a database, systematic information about the collection (Artene, 2013). Notably, in addition to the term biobank, other, synonymous terms, such as bioresource collections, bioresource centres, biological collections, biorepositories, etc., are also used in the current literature (Zinovieva, 2013; Kamenski, Sazonov, Fedyanin, and Sadovnichy, 2016); in Russian Federation unified glossary of biobanking, including definitions of the 161 key terms in both Russian and English, has been developed recently (Mikhailova, 2020).

International Standard ISO 20387 “Biobanking-General requirements for biobanking” formulated by the International Organization for Standardization (ISO) defines biobanking as “the process of collecting and storing, as well as some or all of the following activities: collection, preparation, storage, testing, analysis and distribution of characterized biological material, as well as relevant information and data”. In Russian Federation, biobanking is regulated by the first Russian biobanking standard GOST R ISO 20387 “Biotechnology. Biobanking. General requirements” (https://allgosts.ru/07/080/gost_r_iso_20387-2021), based on ISO 20387. Compliance with these requirements distinguishes biobanks from research collections of specimens. Aforementioned, biobanking requires compliance with legal regulations, which vary from country to country and in some aspects may not be fully regulated and fall into a so-called “legal gray zone” (comprehensively reviewed in Doludin et al., 2019; Nadelyaeva, 2020; Gorbunova, 2020; Boltanova and Imekova, 2021; Khokhlov et al., 2021). Thus, it’s important to know and take into account the difference in legal norms related to biobanks in different countries, especially at the stage of setting up a new biobank or merging several biobanks from different countries into consortium. Ethical aspects and guidelines of biobanking are also not fully defined (Ashcroft, 2019), which is perhaps one of the major drawbacks in biobanking now, yet to be addressed.

In Russian Federation, an important milestone in establishing a large-scale system of biobanks was the

creation, with the support of the Ministry of Health of the Russian Federation, of the “National Association of Biobanks and Biobanking Experts” (NASBio), which united the previously existing resources and expertise of several medical and research institutions, as well as commercial structures (Doludin et al., 2019; Anisimov, 2021). In particular, the association currently includes the Biobank of Sechenov University, Onko Bio Bank, Biobank of NMRC oncology, the Bank of biological samples of similarly treated cancer patients, and others (<http://nasbio.ru>; Soboleva, 2021). Notably, there are also biobanks that are not members of the NASBio association. The biobanks within this large system belong to several types of biobanks.

Types of biobanks

Historically, human biomaterial biobanks are subdivided into population biobanks (i.e., focusing on samples collected in certain populations) and nosological biobanks (i.e., focusing on certain diseases), but another classification is also possible, including subdivision into virtual biobanks, image biobanks, etc. (Coppola, 2019; Boltanova and Imekova, 2021). Nosological ones, in turn, can be subdivided into unspecialised biobanks (e.g., collections of biosamples from various human diseases) and specialized ones (e.g., collections of samples related to a particular type of malignant tumor). An example of the first type of biobanks created in the Russian Federation is the biobank of Sechenov University, and the second is a specialized biobank of human brain gliomas (Golbin, 2020). Also, biobanks can be classified as local, regional, state and international. Most of the currently existing large regional, state and international biobanks have been described in detail in the national literature (Reznik, Kuzmin, Skvortsov, and Reznik, 2016; Boltanova and Imekova, 2021). Many biobank resources are currently being pooled, for example the Global Biobank Metaanalysis Initiative (GBMI) brings together a network of 19 biobanks from 4 continents and includes samples from over 2.1 million donors (Zhou et al., 2022).

This review mainly focuses on biobanks of human biomaterial. At the same time, other bioresource collections, such as collections of microorganisms, plant-derived biosamples, collections of tissues and cells of laboratory animals also exist, and they are valuable tools for translational oncology. For example, producer strains from microbial collections can be used to produce substances that are used as drugs (Ferreira, Gaspar, and Mano, 2020). There are nosological animal biobanks, such as collections of malignant tumor tissues and their corresponding healthy cat and dog tissues (Walter et al., 2020). Biobanking of genetically modified laboratory animal tissues, such as cryopreservation of ovarian tissue (Agca and Agca, 2021), reduces the cost of maintaining a

colony of animals used in biomedical research. There are also collections of plants traditionally used in medicine or biologically active substances isolated from such plants. Their role in the development of new therapeutic approaches is obvious. In the Russian Federation, there are several bioresource collections belonging to the types of non-human bio-specimen collections described above.

Apart from the classification described above, human biomaterial biobanks can be classified based on the types of biobanked samples repertoire, for example biobanks of DNA, biobanks of blood and urine, and others.

Biobanked material repertoire

The most commonly biobanked samples in translational oncology are Formalin fixed paraffin embedded (FFPE) tissue samples, whole peripheral blood samples, urine, frozen biopsies of tumour and adjacent healthy tissues, O.C.T. compound-fixed samples, total DNA and RNA. However, biobanking of exosomes, organoids, circulating cell-free DNA, “liquid biopsy”, tumour-associated microbiome etc. is also developing (Mora, Álvarez-Cubela, and Oltra, 2015; Jacob, Ming, and Song, 2020; Velasquez, 2021; Kahana-Edwin, Cain, and Karpelowsky, 2021).

We suggest expanding the repertoire of material biobanked for the needs of translational oncology. For example, treated/modified tissues from laboratory animals are used in a number of translational oncology techniques, such as 3D culture systems based on decellularized extracellular matrix (dcECM) to assess the behaviour of patient tumor cells in response to various types of chemotherapy (Petersen et al., 2020). Since the peculiarities of dcECM preparation, such as decellularization method, age of animals, etc., affect the behaviour of tumor cells in such a model (Turner et al., 2012), standardization of methods of dcECM preparation and storage is necessary, and biobanks of dcECM of different animals can provide such an opportunity. This will also significantly reduce the costs associated with such studies, because from one animal a set of many tissues can be obtained and biobanked, which subsequently can be used by several teams of researchers, each using only a particular type of dcECM, while without biobanking services, the number of animals required for such studies increases manifold. Additionally, biobanks of materials obtained from animals make it possible to develop (often by trial and error, i.e., with significant consumption of biological material) new methods of sample storage and revitalization and their subsequent analysis, which can then be applied to human biological material, including rare tumor biopsy materials. This approach is optimal for both ethical and economic reasons.

Of particular interest are also biobanks of microbiota, including ones with samples obtained from cancer patients (Wirth et al., 2020; Ryan et al., 2021), which can be used to study the role of microbiome in cancer patho-

genesis and response to the therapy. We propose routine biobanking of microbiota for the needs of translational oncology, alongside the commonly collected types of biospecimens.

Such broad spectrum of biobanked specimens in contemporary biobanking requires particular attention to methods of sample collection and storage, methods which will allow to store the collection as long as possible and use its resources for as many types of analysis as possible.

Biobanked samples storage and sharing: methodology and approaches, challenges and limitations

An ideal scenario implies that biobanking involves long-term (decades, centuries) storage of samples. This makes it possible to conduct large-scale longitudinal studies apart from short-term projects. To prevent sample degradation during long-term storage in biobanks, the following methods are commonly used: cryogenic preservation (deep freezing, cryopreservation), chemical fixation, lyophilization, solidification (crystallization), etc. The choice of sample preparation and storage methods for biobanking should be determined primarily by their compatibility with the intended subsequent analysis methods, i.e., the so-called fit-for-purpose (FFP) approach should be applied. For example, the addition of EDTA to blood samples is recommended in the case of subsequent analysis by genomics methods, and heparin for metabolomics (Nasarabadi, Hogan, and Nelson, 2018), because the addition of heparin significantly hinders subsequent DNA analysis. The most common method for long-term preservation of tissue biopsy specimens as well as cell lines is deep freezing. Depending on the requirements for the quality of biological material after thawing and the need for its revitalization, different sample preparation methods, temperature regimes of freezing, storage, and thawing are recommended. As a rule, dimethyl sulfoxide (DMSO) is used as an agent preventing cell destruction by water crystals during freezing. However, the use of this approach is not ideal, so alternative methods of cell and tissue cryopreservation that do not use DMSO (Pogozhykh, 2020; Wang, 2022), allowing to reduce the amount of DMSO during cryopreservation (Tripathy, Singh, and Das, 2022), and methods minimizing the impact of cryopreservation on cells and reducing cellular stress associated with freezing-thawing (Baust, Snyder, Van Buskirk, and Baust, 2022) are developed and applied. Obviously, different cell sub-populations (in human tumor tissue or in microbiota community) may exhibit different sensitivity to preservation (Ryan et al., 2021), thus, during long-term storage and subsequent revitalization of tissues and cells, selective survival of only certain cell sub-populations, or clonal selec-

tion, may occur. Thus, the model will not be representative enough. Also, the very process of sample preservation (temperature, chemical, mechanical effects) can affect the phenotype of cells when they are revitalized, affect their transcriptome, metabolome, etc. For example, high doses of DMSO, which is used for cryopreservation of cells and tissues, affect their phenotype (Skorova et al., 2020). Thus, the comparison of tissue characteristics immediately before its placement into the biorepository and after long-term storage using different conservation approaches is of undoubted practical interest. For example, when selecting conditions for cryopreservation, revitalization and cultivation of primary cultures of glioblastoma, a comparative analysis showed that the use of CryoStor CS10 medium for cryopreservation (rather than 10% DMSO), enzymatic cleavage before freezing and 2D-culturing after thawing leads to successful cell revitalization. All this should be taken into account at the stage of experiment planning and when developing and choosing methods of preserving biosamples (Zaikina, 2021). Starting from the sample preparation step, it is important to consider and document pre-analytical parameters (e.g., duration and method of surgical resection of the tumor, transportation to the repository, etc.), as they can influence the result and interpretation of the subsequent analysis (Zhou, 2015; Bolck et al., 2019). It is recommended that these parameters be entered into the Sample Preanalytical Code (SPREC) (Lehmann et al., 2012). Guidelines have also been developed for preanalytical characterization of biosamples for research quality improvement (BRISQ) to be applied in any study that uses human biosamples (Moore et al., 2011).

The challenges of modern translational biomedicine require the combination of cytological and histological approaches with the methods of molecular biology and genetics, which, in turn, poses new challenges to the developers and compilers of bioresource collections. For example, highly specialized genetics-oriented collections contain specimens that are not suitable for cytological and histological analyses, as well as for revitalization and culturing. It is possible to obtain material for genetic analysis from some preparations for histological studies (for example, paraffin blocks), but this has limitations imposed by the original method of preservation. For example, formalin, which is often used for chemical fixation of samples, initiates DNA denaturation, formation of cross-links between adjacent DNA bases, between DNA and histones, DNA fragmentation, formation of single-strand breaks in DNA, etc. (Stiller et al., 2016). Tissue freezing in the optimal cutting temperature compound (O.C.T), one of the common methods of biosample storage, leads to signal suppression during mass spectrometry (MS), which, for example, limits the use of matrix-activated laser desorption/ionization for molecular mapping of tumor tissue and requires development of additional methodological

approaches (Truong et al., 2021). It is important to note that preserving the viability of cells and tissues placed in a biobank may be critical when building a collection for healthy tissue transplantation or for studying tumor behavior *ex vivo*, whereas it is not necessary for “omics” studies, which form different approaches to sample collection and storage with respect to their anticipated future research and use. The optimal approach is the one that, at the lowest cost of collecting and storing samples, provides the widest possible range of application of biobank materials. The creation of a multi-type biobank collection, which will combine samples obtained from a single donor for both genetic studies and cytological, histological and other studies, guarantees a comprehensive and in-depth analysis of the material. Preserving the viability of cells and tissues in a cryopreservation collection is one of the challenges researchers face, but the value of such bioresource collections justifies all the costs. Finally, in the case of cryopreservation of tissue samples for further cultivation, it is important not only to preserve the viability of all cell subpopulations within the tissue, but also to preserve the structure and composition of the extracellular matrix, tissue architecture and intercellular interactions, preventing clonal selection (Jacob, Ming, and Song, 2020). An even more difficult task is the biobanking of tissue-engineered complex 3D constructs, both devoid of a matrix and based on a synthetic or natural matrix, and there are currently many studies in this direction (Gryshkov et al., 2021; Arutyunyan, Elchaninov, Sukhikh, and Fatkhudinov, 2021; Wang et al., 2022). Herein, we will discuss biobanking of such complex systems, and their potential applications, in more detail.

Biobanks and “patient-like” tissue culture models, their applications in pre-clinical drug screening and personalized medicine

Biobanks are indispensable for creating collections of both primary tumor cell cultures and patient-like models, for example, 3D tumoroids, patient derived organoids, patient derived xenotransplants (PDX) (Pinto, 2021; Goncharova, Shevchenko, Dashkova, and Anisimov, 2021; Pernik et al., 2021; Foo et al., 2022). Based on the usage of the patient-like models, so-called “living biobanks” (also known as intravital biobanks) comprise viable tissues which retain key characteristics of the original tumor tissue in all its complexity and can be used for the analysis of the living tumor cell behaviour (Bolck et al., 2019; Perrone, and Zilbauer, 2021; Zaikina, 2021). For example, it has been shown that the response of biobanked organoids derived from tissues of patients with metastatic gastrointestinal cancer is similar to the tumor response to therapy, which emphasizes their value as a platform for pre-clinical screening and drug development (Vlachogiannis, 2018). Studies conducted on “living biobanks” of tumoroids created from biosamples

obtained from patients with colorectal cancer, BC and other types of malignancies have also demonstrated that tumoroids can be used as a test system to predict clinical response to chemotherapy (Danilova et al., 2021; Yao et al., 2022). A number of researchers question the feasibility of PDX in personalized medicine, particularly for selecting targeted therapy or monitoring tumor response to therapy, as PDX is relatively labour-intensive and time-consuming (Sachs et al., 2018), but PDX biobanks are created and successfully used (Abdirahman, 2020; Kiblitkaya, Shevchenko, Pandova, and Ardzha, 2021).

The tumor tissue microenvironment (TME), which includes extracellular matrix (ECM), plays an important role in the pathogenesis of malignancies and influences tumor cell behavior; therefore, translational oncologists should include ECM in complex tissue culture systems for the development of anticancer drugs and personalized therapy, as well as biomarkers from TME and ECM in diagnostic and prognostic panels (Petersen et al., 2020). Current technological capabilities allow for the integration of ECM into high-throughput screening platforms used in translational oncology (Ferreira, Gaspar, and Mano, 2020). This points to the need for ECM biobanking, both of laboratory animal ECM and of human ECM, including tumor-derived ECM.

Further, “living biobanks” of both 3D tumoroids and microbiota would be a more representative model of processes occurring *in vivo* (Flashner, Yan, and Nakagawa, 2021). Such biobanks, as far as we know, do not exist, while, aforementioned, the role of the microbiome in the etiology and pathogenesis of malignant neoplasms has been demonstrated in numerous works (Jain, 2021).

When creating “living biobanks”, the method of conditioned cell reprogramming (CR) is applicable in some cases, allowing to grow several million cells from a single biopsy of tumor tissue within a week, with preservation of the phenotype. CR also makes it possible to isolate and grow circulating tumor cells (CTCs) from urine (for bladder cancer) and blood (for prostate cancer). It has been shown that such cells can be used for drug screening and selection of personalized therapy (Palechor-Ceron et al., 2019; Cao, Chan, and Chow, 2022). Personalised therapy also heavily relies on the data from pharmacogenetics, studying the influence of human genetic characteristics on the susceptibility to drugs and biologically active substances (Malsagova et al., 2020), and biobanking has proven to be instrumental for cancer pharmacogenetics as well.

Biobanks and pharmacogenetics and personalised medicine

Recently, the emergence of large biobanks has significantly contributed to the progress in pharmacogenetics, including in translational oncology. For example, the resources of the UK Biobank (over 500,000 samples to date), allowed a study on a sample of 212,335 women (Marderstein et al., 2021).

The pharmacogenetics of breast cancer (BC) risk were studied, and it was found that corticosteroids are modulators of genetic BC risk, and that the rs62119267 polymorphism stratifies BC risk among women taking corticosteroids. This work also illustrates the importance of collecting as much detailed biosample information as possible in biobanking, as there was no information on the ER status (estrogen receptor status) of tumors for this sample, so dividing the sample into clinically different ER- and ER+ subgroups was not possible (McInnes and Altman, 2020). Pharmacogenetics in translational oncology studies both somatic and germinal nucleotide variants, so biobanking both blood samples to study germinal variants and tumor tissue samples to study somatic variants is important. Also, germinal variants detected from blood sample analysis can be associated with different cell phenotypes within the tumor, its mechanical, immune characteristics, etc., for example, carrying certain pathological variants in the *BRCA1* gene has been shown to be associated with changes in PD-1 and PD-L1 expression in ovarian cancer (Wieser et al., 2018), which suggests an effect on the response to therapy with immune checkpoint inhibitors (PD-1 or PD-L1 inhibitors). Therefore, even in the study of germinal nucleotide variants, biobanking and analysis of the tumor tissue using a wide range of methods (for example, to determine its PD-1 and PD-L1 expression status) is appropriate.

It is also important to consider both the genetic heterogeneity of tumor tissue and its evolution during therapy, such as the emergence and expansion of nucleotide variants associated with resistance to chemotherapy. Thus, it is of practical interest to collect and analyze series of samples at different stages of chemotherapy to study the mechanisms (including genetic mechanisms) of tumor resistance to therapy. An example of such study is the study of the evolution of glioblastoma multiforme during therapy (Kim et al., 2015). The same is true for radiotherapy. Biobanks with samples collected during radiotherapy to study the molecular mechanisms of individual susceptibility or resistance to radiotherapy exist (Ward et al., 2022), and in our opinion their network (as well as the network of biobanks with samples collected during the course of any other type of therapy, for example immunotherapy) should also broaden. Creation of broad networks of biobanks and merging single biobanks into consortium will also allow to answer the research questions and overcome research challenges which would not be possible otherwise, for example to address the challenges of the rare malignant neoplasms diagnostic and treatment.

Biobanking to study rare diseases

It has become apparent that biobanking is of particular value in case of studying rare, orphan diseases (Garcia, Downs, Russell, and Wang, 2018), i.e., according to Federal Law No. 323 “On the Fundamentals of Health Protec-

tion in the Russian Federation”, diseases that have an incidence of no more than 1 case per 10,000 people. Patients with such diseases may have an increased risk of iatrogeny associated with misdiagnosis, and, therefore, detection of a wide range of diagnostic biomarkers is particularly relevant. However, case-control studies to identify diagnostic biomarkers or evaluate the effectiveness of therapy are difficult for such diseases, since recruiting study participants at the local level takes a long time and becomes possible only by pooling the resources of many research teams. In addition, in comparison with diseases for which obtaining tissue samples is not particularly difficult and is a routine procedure, such as malignant tumors of the breast, the study of malignant neoplasms with localization that complicates their surgical resection and biopsy sampling, for example diffuse brain gliomas, for which tissue sampling *ante-mortem* is often impossible, is complicated. Previously, the few samples obtained from people with rare diseases were sometimes excluded from large biobank collections (Graham et al., 2015), due to the perceived unlikelihood that they could be used for further research. In contrast, biobanks focusing on rare diseases, such as rare malignancies, are now being actively established (www.rarecancerseurope.org; Kanakoglou et al., 2022). The creation of international biobank associations collecting such samples allows large-scale studies on relatively large samples of patients with such diseases, including malignant neoplasms with diffuse localization. In translational oncology, one example of this approach is the use of biobanks in the study of diffuse intrinsic pontine glioma (DIPG) in children, an extremely rare disease (Baugh et al., 2017) which remains one of the most severe diseases in pediatric oncology (Regentova et al., 2020). Thus, the study of more than one hundred of biobanked samples obtained from patients with DIPG in local hospitals (29 donors), in medical institutions throughout the country (19 donors), and from abroad (56 donors), allowed the screening of bioactive substances on a representative sample that reflected the genetic and phenotypic heterogeneity of tumor cells pro DIPG (Carvalho et al., 2020). As a result, biologically autologous substances with potential use for targeted therapy were identified, depending on the tumor subtype and spectrum of oncogenic mutations, for example, a synergistic effect of ALK2 kinase inhibitors and small molecule ONC201 was found in tumors with mutations in the *ACVR1* gene (Carvalho et al., 2020). Such a study would have been impossible to perform on a small sample of locally collected samples, given that DIPG is divided into several subtypes and the spectrum of oncogenic mutations in this disease is quite broad (Lapin, Tsoli, and Ziegler, 2017; Dufour et al., 2018). Also, such a study was only possible using a wide range of methods (3D cell cultures, genotyping, etc.) on a multi-type collection, and the samples in this study referred specifically to a multi-type biosphere collection containing 2D and 3D

(neurosphere) cultures, RNA-seq data, DNA sequencing, DNA methylation analysis, etc. Finally, such work became possible only with the introduction of standardised methods of collection, storage and cataloguing of samples in different biobanks, which allowed combining the resources of several biobanks to conduct large-scale studies. This once again emphasises the importance of following the requirements of international standard ISO 20387 and GOST R ISO 20387, as discussed earlier. The translational potential of biobanks in personalised medicine and targeted therapy is demonstrated by recent work in which biobanking of materials obtained from patients with various malignant brain tumors allowed to identify mutation carriers among patients by next generation sequencing (NGS), the presence of which made targeted therapy advisable (Darrigues et al., 2021). A medical image biobank, such as biobank of Magnetic Resonance Imaging (MRI) results, could provide additional opportunities for such a project. It has previously been shown that the presence of the K27M oncogenic mutation in DIPG tumor tissue can be inferred from computer analysis of MRI data, that is, noninvasively (Jung et al., 2019). Clearly, replacing invasive brain tissue biopsy or cerebrospinal fluid analysis with MRI data analysis in diagnosis and treatment significantly improves patient quality of life. Finally, given the difficulty of *ante-mortem* tissue sampling in a number of diseases, creating biobanks of tumor tissue collected *post-mortem* will greatly accelerate the search for new, more effective therapeutic approaches (Griffin et al., 2021).

It should be noted that cancer not only *per se* affects patients, but also results in long-term consequences of the disease; also, cancer therapy is associated with side effects and consequences of the therapy. Moreover, clinical oncology focuses not only on cancer treatment, but also on its prevention. All of this can be addressed with the help of biobanking.

Biobanking to study long-term consequences of the therapy and biomarker identification

Biobanks make it possible to study the molecular mechanisms of cancer complications and long-term consequences, which will allow the development of therapeutic approaches for their correction as well as palliative rehabilitation. In particular, biobanking is already being used in the study of cachexia in patients with pancreatic cancer (Vaes, 2020). Aforementioned, in translational oncology, in addition to developing new methods of diagnosis and therapy, biobanking is also being used to create new approaches to prevention. Thus, the association of certain food groups with lung cancer risk has been determined based on a study of 16588 samples from the UK Biobank (Wei et al., 2021), the same biobank resources were also used to evaluate the associations of vegetarian and non-vegetarian diets

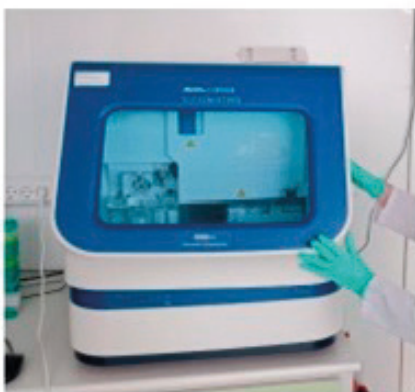
Biomedical image and associated data biobanking and analysis



Longitudinal studies
Rare disease studies
Consortia and sharing



Living organoid biobanks
Complex 3D tissue models
Predictive “patient avatars”



Genomics,
Transcriptomics,
Proteomics, Metabolomics
and other “Omics” studies



Disease modelling
Pre-clinical drug
screening
Personalized and
preventive medicine



IT-directed logistic
Big Data analysis
Artificial Intelligence applied
to biobanking

BIORESOURCE
COLLECTIONS

Fig. Biobanking features and capabilities making it a valuable tool in transnational oncology.

with risks of several types of cancer (Watling et al., 2022). Moreover, biobanking is helping to identify new biomarkers of disease, including noninvasive biomarkers (based on blood, saliva, buccal epithelium samples, etc.), for example the use of samples from the U-CAN biobank revealed elevated levels of myostatin in the blood of patients with chronic lymph leukemia (Larsson et al., 2020). The overall role of biobanks in biomarker research is described in several comprehensive reviews (Lommen, Odeh, de Theije, and Smits, 2020; Matzke and Watson, 2020).

Conclusion

The existence of a network of biobanks can greatly accelerate the introduction of personalised medicine based on individual molecular-genetic, diagnostic, therapeutic

and preventive approaches. Biobanks can also play an important role in the development of new and repositioning of known drugs and new therapeutic approaches, including the use of big data and artificial intelligence. In the future, as new technologies emerge, it will be possible to perform additional analyses on previously biobanked and already characterized samples. Overall, biobanking features and capabilities make it a valuable tool in transnational oncology (Fig.).

As for the future directions, one of the findings of our review is a gap in the spectrum of the commonly biobanked material. Here, we highlight the necessity to expand the spectrum of currently biobanked samples and, in addition to traditionally collected FFPE samples, O.C.T samples, whole peripheral blood samples, frozen biopsies of tumor and adjacent healthy tissue, DNA

and RNA, to include other specimens such as biological fluids, exosomes, ECM, dcECM, microbiota samples, samples collected at different stages of treatment, *post mortem* samples, various biomedical images, “live biobank” samples, and samples which can be used for any type of “omic”-analysis. Another finding of the current review is an urgent need for creation of biobanks of rare types of malignant neoplasms, which is particularly important for the number of reasons discussed above, and have been rather neglected until recently. We also advise to create and develop auxiliary biobanks of laboratory animal tissues for the needs of translational oncology, which remains an underdeveloped area in biobanking. Additionally, we point out a value of biobanks beyond cancer treatment and for its diagnostic and prevention. Finally, we emphasize the necessity to develop protocols and methods for sample preparation and storage of collections and accompanying information common for all biobanks, which will allow to pool biobanked resources into consortium (at any stage) and guarantee the high quality of the biobanked material.

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