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## Perspectives and directions of biobanking in case of rare types of cancer

E.V. Petersen<sup>1</sup>, D.A. Chudakova<sup>1</sup>, A.A. Shiryayev<sup>1,2</sup>, A.M. Khrushchova<sup>3</sup>,  
E.Y. Shabalina<sup>1</sup>, A.A.S. Shaker<sup>1</sup>, T.A. Chernov<sup>1</sup>, P.A. Karalkin<sup>1,2</sup>, I.V. Reshetov<sup>1,2</sup>

<sup>1</sup>Moscow Institute of Physics and Technology, Moscow, Russia

<sup>2</sup>I.M. Sechenov First Moscow State Medical University, Moscow, Russia

<sup>3</sup>A.N. Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences, Moscow, Russia

Contacts: Petersen Elena Vladimirovna – e-mail: Petersen.ev@mipt.ru

## Перспективы и направления биобанкирования при редких видах рака

Е.В. Петерсен<sup>1</sup>, Д.А. Чудакова<sup>1</sup>, А.А. Ширяев<sup>1,2</sup>, А.М. Хрущова<sup>3</sup>, Е.Ю. Шабалина<sup>1</sup>,  
А.А.С. Шакер<sup>1</sup>, Т.А. Чернов<sup>1</sup>, П.А. Каралкин<sup>1,2</sup>, И.В. Решетов<sup>1,2</sup>

<sup>1</sup>Московский физико-технический институт, Москва, Россия

<sup>2</sup>Первый Московский государственный медицинский университет имени И.М. Сеченова, Москва, Россия

<sup>3</sup>Институт проблем экологии и эволюции имени А. Н. Северцова, Москва, Россия

Контакты: Петерсен Елена Владимировна – e-mail: Petersen.ev@mipt.ru

## 罕见癌症病例中生物银行的前景和方向

E.V. Petersen<sup>1</sup>, D.A. Chudakova<sup>1</sup>, A.A. Shiryayev<sup>1,2</sup>, A.M. Khrushchova<sup>3</sup>,  
E.Y. Shabalina<sup>1</sup>, A.A.S. Shaker<sup>1</sup>, T.A. Chernov<sup>1</sup>, P.A. Karalkin<sup>1,2</sup>, I.V. Reshetov<sup>1,2</sup>

<sup>1</sup>Moscow Institute of Physics and Technology, Moscow, Russia

<sup>2</sup>I.M. Sechenov First Moscow State Medical University, Moscow, Russia

<sup>3</sup>A.N. Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences, Moscow, Russia

Contacts: Petersen Elena – e-mail: Petersen.ev@mipt.ru

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Biobanking is an actively developing area of biotechnology and biomedicine. Briefly, Biobank is a comprehensively characterised biological material collected and stored by standardized methods and accompanied by detailed corresponding information, potentially available to many users. Modern biobanks are instrumental for development of new diagnostic and therapeutic approaches, drug development, personalized medicine and many aspects of pre-clinical research. In part, this is because biobanks are not only «places of sample storage», but also places for conducting research using collections of biomedical materials and all associated data, as well as teaching/learning hubs providing methodology training and guidance with experiment design to biobank's clients (and here we emphasize the importance of the human resources component of biobanks – researchers and their unique expertise in biobanking, as an integral part of biobank). Biobanking makes possible to perform various “omics” studies, such as genomics, epigenomics, transcriptomics, proteomics, lipidomics, metabolomics, microbiomics and other “omics” data, and combine them with data obtained on complex 3D tissue culture models, ex-vivo cultures, “patient-like” organoids and “avatars”, data obtained from medical image biobanks, radiology biobanks, and others. Such studies can be longitudinal, recruit participants from several geographical regions and of different ethnicity, involve big data analysis using artificial intelligence, include both ante mortem and post mortem samples, samples collected at different time points of chemo- and/or radio-therapy, et cetera.

This review briefly describes the current state of biobanking and discusses the role of biobanks in the study of malignant neoplasms, with particular focus on the rare or poorly differentiated types of cancer (RPDC) and cancers of unknown primary (CUP). Unlike well-described types of cancer with known primary, there are cases of CUP when the primary sites of the appearance of cancer cells are not known, of them up to 25 percent are poorly differentiated, which significantly complicates histological typing of the tumor and selection of adequate therapy. Historically, poorly differentiated cancers have been excluded from many biospecimen collections. Rare cancers are malignant neoplasms with very low incidence, but despite low incidence they account to approximately 25 percent of all diagnosed cancers. There is a plethora of rare cancer types among Head and Neck cancers (HNC). In case of rare cancers, paucity of samples and sample-associated data, as well as slow accrual of the samples (so called “sample bottlenecks”) create significant drawbacks for translational oncologists. As a result, there are still significant inequalities in healthcare in case of RPDC/CUPs compared to common cancers, such as diagnosis uncertainty, limited therapies, drawbacks in the identification of novel therapeutic targets, and finally difficulties

in conducting pre-clinical research and clinical trials, resulting in a survival gap between common cancers and RPDCs. Therefore, addressing these challenges is of utmost importance. Noteworthy, although rare subgroups of common cancers are not classified as rare cancers, patients belonging to such subgroups might face challenges similar to those affected by the rare cancers. Creating Rare and Poorly Differentiated Cancer Biobanks (RPDCB) and merging single biobanks into big consortia, as well as long-term sample collection in RPDCB, creates unique opportunity to use biobanking to study such diseases and can significantly facilitate research on their etiology and pathogenesis, drug development and therapy development, including personalized, targeted, and per-emptive therapies. In conclusion, there is an unmet need for creation of RPDCBs which should be addressed.

**Key words:** biobank, biobanking, head and neck cancer, malignant tumors, translational medicine, personalized medicine, oncology, extracellular matrix, 3D cell culture models

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Биобанкирование – это активно развивающаяся область биотехнологии и биомедицины. Вкратце, биобанк – это всесторонне охарактеризованный биологический материал, собранный и сохраненный стандартизированными методами и сопровождаемый подробной соответствующей информацией, потенциально доступной многим пользователям. Современные биобанки играют важную роль в разработке новых диагностических и терапевтических подходов, разработке лекарственных препаратов, персонализированной медицине и многих аспектах доклинических исследований. Отчасти это объясняется тем, что биобанки – это не только “места хранения образцов”, но и места для проведения исследований с использованием коллекций биомедицинских материалов и всех связанных с ними данных, а также центры преподавания/обучения, предоставляющие клиентам биобанка методическую подготовку и руководство по разработке экспериментов (и здесь мы подчеркиваем важность кадрового компонента биобанков – исследователей и их уникального опыта в области биобанкирования, как неотъемлемой части биобанка). Биобанкирование позволяет проводить различные “омические” исследования, такие как геномика, эпигеномика, транскриптомика, протеомика, липидомика, метаболомика, микробиомика и другие “омические” данные, и объединять их с данными, полученными на сложных 3D моделях культур тканей, культурах ex-vivo, “пациентоподобных” органоидах и “аватарах”, данных, полученных из биобанков медицинских изображений, радиологических биобанков и др. Такие исследования могут быть продолжительными по времени, набирать участников из нескольких географических регионов и разной этнической принадлежности, включать анализ больших данных с использованием искусственного интеллекта, включать как прижизненные, так и посмертные образцы, образцы, собранные в разные временные точки химио- и/или радиотерапии, и т.д.

В данном обзоре кратко описывается современное состояние биобанков и обсуждается роль биобанков в изучении злокачественных новообразований, особое внимание уделяется редким или плохо дифференцированным типам рака (РПДР) и раку с неизвестным первичным очагом (РНПО). В отличие от хорошо описанных типов рака с известной первичностью, при РНПО встречаются случаи, когда первичные очаги появления раковых клеток неизвестны, из них до 25 процентов являются низкодифференцированными, что значительно затрудняет гистологическую типизацию опухоли и подбор адекватной терапии. Исторически сложилось так, что плохо дифференцированные раковые опухоли исключались из многих коллекций биобанков. Редкие виды рака – это злокачественные новообразования с очень низкой частотой встречаемости, но, несмотря на низкую частоту, они составляют около 25 процентов от всех диагностированных видов рака. Среди рака головы и шеи (РГШ) существует множество редких видов рака. В случае редких видов рака нехватка образцов и данных, связанных с образцами, а также медленное накопление образцов (так называемые “узкие места”) создают значительные трудности для трансляционных онкологов. В результате в здравоохранении все еще существуют значительные неравенства в случае РПДР/РНПО по сравнению с обычными раками, такие как неопределенность диагноза, ограниченность методов лечения, недостатки в определении новых терапевтических мишеней, и, наконец, трудности в проведении доклинических исследо-

ваний и клинических испытаний, что приводит к разнице в выживаемости между обычными раками и РПДР. Поэтому решение этих проблем имеет первостепенное значение. Примечательно, что хотя редкие подгруппы распространенных видов рака не классифицируются как редкие раки, пациенты, принадлежащие к таким подгруппам, могут сталкиваться с проблемами, аналогичными тем, которые возникают при редких видах рака. Создание биобанков редких и плохо дифференцированных раков (РПДРБ) и объединение отдельных биобанков в крупные консорциумы, а также долгосрочный сбор образцов в РПДРБ создает уникальную возможность использования биобанков для изучения таких заболеваний и может значительно облегчить исследования их этиологии и патогенеза, разработку лекарств и терапии, включая персонализированные, целевые и упреждающие методы лечения. В заключение следует отметить, что существует неудовлетворенная потребность в создании РПДРБ, которую необходимо удовлетворить.

Ключевые слова: биобанк, биобанкирование, рак головы и шеи, злокачественные опухоли, трансляционная медицина, персонализированная медицина, онкология, внеклеточный матрикс, 3D модели клеточных культур

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Авторы несут ответственность за оригинальность представленных данных и возможность публикации иллюстративного материала – таблиц, рисунков, фотографий пациентов.

Биобанк является биотехнологической и биомедицинской областью. Проще говоря, биобанк – это стандартизированный метод сбора и хранения биоматериала с полными характеристиками, и с подробными данными, которые могут использоваться многими пользователями. Современный биобанк способствует разработке новых методов диагностики и лечения, разработке лекарств, персонализированной медицине и клиническим исследованиям. Причины этого в том, что биобанк – это не только «место хранения образцов», но и место, где биоматериалы и все связанные с ними данные собираются для исследований, а также для обучения и консультирования клиентов биобанка. Мы подчеркиваем важность роли персонала биобанка – исследователей и их уникальных знаний, как части биобанка. Биобанк может использоваться для различных «омиксных» исследований, таких как геномика, транскриптомика, протеомика, липидомика, метаболомика, микробиомика и другие «омиксные» данные, и их интеграция с 3D-моделями клеточных культур, культивированием «органоидов» и «органоидов», от биомедицинских биобанков, данных биомедицинских биобанков, и других. Эти исследования могут быть продольными, с участием нескольких географических регионов и этнических групп, с использованием искусственного интеллекта для анализа больших данных, включая данные до и после операции, в химии и/или радиационной терапии в различные моменты времени, и т.д.

В этом обзоре описаны биобанки, и обсуждается их роль в исследовании рака, с особым вниманием к редким или низкодифференцированным ракам (RPDC) и неизвестным первичным ракам (CUP). В отличие от описанных ранее типов, когда опухоли возникают в определенных частях тела, в CUP опухоли возникают в различных частях тела, что усложняет диагностику и выбор лечения. Исторически, низкодифференцированные раки исключались из большинства биобанков. Редкие раки – это опухоли с очень низкой частотой, но они составляют около 25% всех диагностированных раков. Редкие раки (HNC) имеют несколько редких типов. В редких раках, недостаток данных об образцах и связанных с ними данных, а также медленное накопление (так называемый «бутылочное горло») создает серьезные проблемы. Поэтому, по сравнению с распространенными раками, RPDC/CUP имеют проблемы с доступом к лечению, например, с диагностической неопределенностью, ограниченными методами лечения, отсутствием новых мишеней для лечения, а также с трудностями проведения клинических исследований и испытаний, что приводит к разрыву выживаемости между распространенными раками и RPDC. Поэтому, преодоление этих проблем имеет решающее значение. Важно отметить, что редкие раки, которые ранее считались редкими раками, но относятся к редким ракам, могут столкнуться с проблемами, похожими на редкие раки. Создание редких и низкодифференцированных раковых биобанков (RPDCB), объединение отдельных биобанков в крупные консорциумы, а также долгосрочный сбор образцов в RPDCB, для использования биобанков в исследовании этих заболеваний, может способствовать пониманию причин и механизмов заболевания, разработке лекарств и лечению, включая персонализированное, таргетное, и профилактическое лечение. В целом, создание RPDCB требует дальнейшего развития, и его необходимо решить.

Ключевые слова: биобанк, биобанкирование, рак головы и шеи, злокачественные опухоли, трансляционная медицина, персонализированная медицина, онкология, внеклеточный матрикс, 3D модели клеточных культур

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## Introduction

Over the course of the last couple of decades, biobanks have become one of the crucial tools in biomedical research, including translational oncology. In the modern sense of the term, a biobank is a structure that includes collections of samples of biological materials (such as tissues, biological fluids, and others), medical and biological images (for example, MRI, PET scan, microscopy images), other relevant data, as well as a descriptive database corresponding to the samples. Descriptive database can be of a clinical and sociology-demographic nature, include information about methods of collecting, processing and storing of the samples, their geographical origin, and any other relevant information. Biobanks comply with the standard ISO 20387 and, in Russian Federation, GOST R ISO 20387-2021. Such standardization of biobanking allows merging data and results from multiple independent interdisciplinary studies as well as creating biobanks consortia. All of this distinguishes biobanks from conventional scientific and/or medical collections, increases precision of the studies based on their resources, makes biobanks a valuable tool for development of new therapies, diagnostic and prognostic markers, as well as novel methodological approaches in translational medicine. Biobanks are also instrumental for optimization of the standard practical tasks in medicine (organ and tissue transplantation, reproduction medicine) [1]. The ideal scenario for biobanking assumes that its collections will be utilized to solve a wide range of interdisciplinary problems using many different technologies, by independent teams of researchers with different scientific aims and expertise, during long time period.

According to the standard ISO 20387 developed by the International Organization for Standardization (ISO), biobanking is “the process of collecting and storing, as well as some or all of the following: collection, preparation, storage, testing, analysis and dissemination of biological material, as well as related information and data”. It is also expected that biobanks strictly adhere to all relevant legal and ethical standards [2].

Biobanks in medical research are traditionally divided into populational and nosological ones, and the latter are sub-divided into non-specialised or general biobanks (for example, biobanks of any types of malignant tumors) and specialized ones (for example, collections of a certain types of rare cancer). By the size and localisation, biobanks are classified into local, regional, state, international biobanks, as well as global networks of biobanks [3]. Biobanks already have proven to be instrumental to study common cancers.

As mentioned above, biobanks include not only biological samples and related information, but also so-called “material and technical base” (equipment, software, facilities, etc) necessary to replenish, maintain, and characterize the collection. Appropriately qualified personnel with experience and expertise in this particular area is also a key component of a biobank [4]. Thus, standardisation should be extended not only to the methods of collecting, validating and storing biosamples, but also to all other relevant standard operating procedures in biobanking, including collecting and storing related information, as well as to procedures of the personnel training [5].

There are several excellent reviews about problems and achievements of contemporary biobanking published already ((6-9), and others), thus to avoid redundancy in our review we will focus solely on the most recent milestones in the biobanking of HNC or RPDC/CUPs, and also propose and discuss possible

methodological approaches and practical applications of biobanking not outlined elsewhere in details.

## Cancer biobanks consortia

Aforementioned, as a result of the combining several biobanks into a single consortium it becomes possible to reach a new level of translational research, including interdisciplinary research in translational medicine and translational oncology. Biobank consortia exist worldwide, in a number of countries, for example the International Head and Neck Cancer Epidemiology consortium (<https://medicine.utah.edu/dfpm/inhance>). In Russian Federation, such a consortium is the National Association of Biobanks and Biobanking Specialists (NASbio) [6]. Hitherto, the association comprises several biobanks, including biobanks solely focusing on aspects and needs of translational oncology (<http://nasbio.ru/>), but there are also other biobanks that are not members of the NASbio association, and biobanks not related to oncology. There are no RPDCB consortia established in Russian Federation yet.

## Methodological approaches and repertoire of biobanked material

Historically, biobanks collected predominantly DNA, blood, frozen tumour tissue samples (diagnostic biopsies, autopsy samples, excess tissue from surgery, etc), and formalin-fixed paraffin-embedded (FFPE) blocks. Recent advances in “omics” studies (transcriptomics, genomics, proteomics, metabolomics, epigenomics, microbiomics, etc), development of 3D tissue culture systems, as well as big-data bioinformatic analysis tools and approaches revolutionized biobanking and led to significant advance in its capabilities, at the same time expanding the methodological approaches to biobanking and repertoire of material to be biobanked.

One of the most accurate *in vitro* models of solid tumor behavior are three-dimensional (3D) multicellular models, especially the scaffold-based systems including elements of the tumor tissue environment, such as the extracellular matrix (ECM) [10, 11]. There are notable differences between 2D and 3D cell culture models of HNC in terms of sensitivity to drugs and other tumor characteristics [12]. A valuable tool for creating 3D cell systems is decellularized ECM (dECM) prepared from animal tissues, production of which, for a number of reasons, including ethical ones, is a more feasible task than obtaining materials from humans. Currently, such 3D HNC models utilizing dECM derived from animal tissues are being developed [13]. Hence, for example when studying tumour pathogenesis and predicting the response of tumour cells to therapy (personalized therapy), it's possible to roughly evaluate the behavior of tumor cells in a 3D model consisting of HNC cells obtained from patient and extracellular decellularized matrix of animals obtained from a biobank (taking into account differences in the ECM from the healthy and malignant tissue micro-environment and also obvious differences between the species). Biobanking of animal tissue for the needs of applied medicine is cost-efficient. Firstly, it allows to use all tissues from the same animal by several research teams, minimizing the total cost of the studies. Secondly, the teams that apply to the biobank for usage of animal tissues do not have to have expertise in working with animals or have an animal facility in their research center. Finally, biobanking of animal tissues will also allow to develop and optimize methods and

approaches to cryopreservation and revitalization of human tissues for the needs of translational oncology. It's important to note that components of patient's tumor micro-environment (TME) itself, including ECM, are promising targets for therapy [14], thus human TME specimens should also be biobanked if feasible.

Currently, in the field of HNC study, rapidly grows the usage of so-called "living biobanks" of the patient-derived 3D tumor cell culture models [15]. Patient-derived xenograft and organoid platforms are instrumental to study the tumour microenvironment in HNC and for co-clinical precision therapy guiding, as outlined in the recent comprehensive review [16]. Organoid cultures provide a suitable model for clonality studies and precision therapeutics [17]. They also can be used for preclinical research of HNC, as demonstrated [18], and recapitulate genomic/transcriptomic characteristic of the patient tissue, for example EGFR expression levels [19].

As for transcriptomics, it is of particular interest to study transcriptome of individual cells (single-cell RNA sequencing, scRNA-seq), since tumors are represented by cells of different types with different patterns of gene expression. Such patterns can not be evaluated when analyzing the bulk RNA transcriptome, and as a result we do not understand the role of particular subpopulations of cells in cancer development, or their role in response to the treatment. Comparative transcriptomics of individual cells in different subpopulations, including the data obtained at different stages during the therapy, as gene expression pattern is not static, could provide valuable data that cannot be otherwise obtained when analyzing the bulk transcriptome. For example, cell-type-specific gene expression signatures of the stromal, cancer, and TME cells in HNC have been characterized recently by scRNAseq using collection of solid tissues and corresponding peripheral blood from HNC patients, which allowed to predict therapeutically targetable checkpoint receptor-ligand interactions [20].

### **Biobanks to study tumour genetic heterogeneity**

Intra-tumour genetic heterogeneity is a well-known clinical challenge, including in HNC [21]. Cells with a different spectrum of oncogenic mutations may be present within the same tumor tissue, partially as a result of a tumor genomic instability. Moreover, during the therapy tumors constantly "evolve" and may acquire new mutations that, subsequently, increases resistance to therapy. Thus, within the framework of approaches known as personalized therapy and pharmacogenetics (selection of medication based on the patient's genotype), it is necessary to assess the genetic heterogeneity of the tumor during the course of treatment, in search for 'targetable genomic alterations' (alterations resulting in a target against which a medication exists), for example RAS or EGFR mutations in HNC (reviewed in [22]). This can become possible with the aid of biobanking of multiple biopsies during the treatment to monitor response to the therapy, and adjust/change it accordingly. Additional screening for nucleotide variants that are not associated with the oncogenesis per se, but may affect pharmacokinetics during the chemotherapy is important to select the optimal treatment dose and regimen. It is also worth assessing the genetic and phenotypic heterogeneity of tumor cells before and after cryopreservation for biobanking, that is, to check how cryopreservation and subsequent revitalization change the cellular composition of the tumor and particular sub-

populations within the tumor. It is important to select the optimal method of cryopreservation and revitalization to preserve the native heterogeneity of the sample, which makes it a representative model of the in vivo tumour. When taking and genotyping a biopsy from one part of the tumor, there is a high probability that the full spectre of oncogenic mutations of the neoplasm may not be detected, therefore, along with a tumour tissue biopsy, other clinically informative samples for genotyping should be biobanked, for example, cerebrospinal fluid, whole blood, saliva, urine, etc, allowing for detection of cell-free circulating DNA derived from the tumor cells [23, 24]. Here we emphasize that the genotype profiles of many rare HNC types remain unknown [25] and need to be characterised.

Promising approach in personalized medicine is a comprehensive genetic screening, for example whole genome sequencing not only of the DNA from tumor cells, but from immune cells in the tumor microenvironment, and cells from other tissues of the same patient, which might be targets of metastasis. Such genetic screening allows to identify new genes and nucleotide variants involved in the cancer pathogenesis and response to the therapy.

### **Pre-emptive medicine and pre-diagnostic material biobanking**

Additionally, biobanking can provide a unique opportunity for detection of the cancer-associated viruses in pre-diagnostic samples (such as papillomavirus 16 associated with a subset of head and neck squamous cell carcinomas), and search for avoidable causes of cancer. For example, genotyping of the samples from UK biobank was used to assess the causal effect of cholesterol lowering on risk of HNC [26], another study based on UK Biobank's resources and focused on preventable causes of HNC investigated an association between alcohol consumption and the likelihood of developing HNC [27], and circulating tumor human papillomavirus DNA was detected in biobanked samples before HNC diagnosis [28].

Moreover, biobanking provides an opportunity to discover novel therapeutic targets and develop risk prediction models. For example, analysis of the HNC biopsy samples and corresponding healthy tissue samples provided by two national biobanks integrated into the National Biobanks Network in Spain, allowed to identify novel predictive marker and therapeutic target, glycosphingolipid globotriaosylceramide [28]. Studies based on materials from one of the world's largest biobanks, the UK Biobank, allowed to create a model of the risk for developing HNC [29].

### **Microbiota biobanking for translational oncology**

Undoubtedly, it is expedient to include samples of human microbiome (microbiota) in the nosological biobank collections. Biobanking of the patient's microbiota will further provide an opportunity to build in vitro models of the relationship between the microbiota and the development of malignant neoplasms. There is an association between the microbiome of the oral cavity, pharynx, throat and the HNC [30–32]. Moreover, in oral squamous cell carcinoma an association of oral microbiome with lymph node metastasis was found recently [33]. Taking microbiome samples from the oral cavity is a simple, non-invasive process, which makes it especially attractive for biobanking and creates new avenues for diagnostics and therapy based on the microbiome.

## Biobanking for longitudinal studies

In addition, the resources of biobanks can be used to predict the long-term consequences of the disease, side effects from treatment, as well as to compare the course of the disease and treatment depending on various common comorbidities, such as diabetes, cardiovascular diseases, etc. In light of the recent COVID-19 pandemic, it's plausible to propose that biobank resources may be used to optimise the therapy approaches for the HNC patients affected by COVID-19.

The modern classification of neoplasms is often based mainly on the pathomorphology and immunohistochemistry data. Therefore, using biobanks for the accumulation of a large amount of novel data from "omics" studies, longitudinal studies, including samples from different geographical locations and ethnic groups, can help to revisit the classification of tumors, thus increasing diagnostics accuracy and therapy efficiency. As mentioned, biobanking can allow to find novel diagnostic and prognostic biomarkers based on analysis on biobanked 'omics' data. For example, recent longitudinal study of the patient's plasma proteome demonstrated that these data can be used to detect HNC [34].

## Post-mortem biobanking

For many types of HNC, surgical resection of tumors is not possible due to the peculiarities of the localization of the tumor, including in the case of a diffuse nature of localization or aggressive metastasis. In such case, post-mortem biobank collections of the tissue can be an alternative option to collect study material. However, the creation of post-mortem banks is a difficult task for a number of ethical and technical reasons.

## Biobanking to study rare cancers

Based on all above mentioned, it is undoubtedly clear that biobanking represents an unparalleled opportunity to study rare, orphan diseases. According to Federal Law No. 323-ФЗ of the Russian Federation "On the Basics of Protecting the Health of Citizens in the Russian Federation", orphan (rare) diseases are diseases that have an incidence of no more than 10 cases per 100000 people. Rare diseases are "individually rare, but collectively common" [35], or "although rare in isolation, are not rare in aggregate", collectively affecting up to 7% of the whole population [36]. However, due to the rare occurrence of such diseases, and therefore lack of the deep knowledge of their etiology, pathogenesis and clinical manifestation, patients with orphan diseases are at risk of misdiagnosis. For this category of patients, the identification of novel diagnostic and prognostic biomarkers, as well as best therapeutic approaches, is urgently needed, whereas insufficient amount of biological material from such patients, and small study cohorts, makes it challenging to perform corresponding clinical and pre-clinical studies. Thus, the use of biobanks allowing to collect a sufficient amount of biomaterial from such patients is almost the only way to address these challenges. Such approach has proven successful in case of several types of rare cancers, such as cholangiocarcinoma [37] or some rare childhood cancers [38]. Patients with rare HNC, for example salivary gland cancer (SGC) [39], might benefit from biobanking too. Indeed, in a recent study, the pooling of the resources from three different biobanks allowed to collect sufficient material to study rare type of HNC [40]. It is important to note that patient with common type of the cancer may

also have a rare condition of a different nature, affecting the course of the disease. In this case, the resources of the biobank will make it possible to assess the impact of such rare disease on the course of the oncopathology.

Overall, in light of the current advances in biobanking and associated technologies/methodological approaches, we envision the key role of the biobanks as a platform to study not only common, but also rare types of cancer – the unmet need in contemporary translational oncology.

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#### Information about the authors:

Petersen Elena Vladimirovna — M.D., Ph.D, Biologist, Moscow Institute of Physics and Technology. Address: 9 Institute Lane, Dolgoprudny, Moscow Region, Russia, 141701 E-mail: Petersen.ev@mipt.ru. ORCID: <http://orcid.org/0000-0002-8150-7553>

Chudakova Daria Aleksandrovna — Ph.D, Biologist, Moscow Institute of Physics and Technology. Address: 9 Institute Lane, Dolgoprudny, Moscow Region, Russia, 141701 E-mail: chudakova.da@mipt.ru. ORCID: <http://orcid.org/0000-0002-9354-6824>

Shiryayev Artyom Anatolievich — M.D., Ph.D., Surgeon doctor, I.M. Sechenov First Moscow State Medical University. Address: Moscow, Russia, 8 Trubetskaya St., bld. 2, 119991 E-mail: artemdok@mail.ru. ORCID: <http://orcid.org/0000-0001-9421-420X>

Khrushchova Anastassia Mikhailovna — Ph.D., Biologist, A.N. Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences. Address: 33 Leninsky Prospekt, Moscow, 119071 E-mail: cricetus@yandex.ru. ORCID: <https://orcid.org/0000-0002-3956-8395>

Shabalina Evgeniya Yurievna — M.Sc, Biologist, Moscow Institute of Physics and Technology. Address: 9 Institute Lane, Dolgoprudny, Moscow Region, Russia, 141701 E-mail: evgenyashb@mail.ru. ORCID: <http://orcid.org/0000-0002-8184-7363>

Shaker Abanoub Ashraf Saleh — B.Sc, Biologist, Moscow Institute of Physics and Technology. Address: 9 Institute Lane, Dolgoprudny, Moscow Region, Russia, 141701 E-mail: Shaker.a@phystech.edu. ORCID: <http://orcid.org/0000-0002-3025-6504>

Chernov Timur Alexandrovich — Ph.D., Biologist, Moscow Institute of Physics and Technology. Address: 9 Institute Lane, Dolgoprudny, Moscow Region,

Russia, 141701 E-mail: chtimur@yandex.ru. ORCID: <https://orcid.org/0000-0002-7784-7045>

Karalkin Pavel Anatolievich – M.D., Ph.D., Biochemist, Moscow Institute of Physics and Technology. Address: 9 Institute Lane, Dolgoprudny, Moscow Region, Russia, 141701 E-mail: pkaralkin@gmail.com. ORCID: <http://orcid.org/0000-0002-2838-0776>

Reshetov Igor Vladimirovich – M.D., D.Sc., Oncologist, I.M. Sechenov First Moscow State Medical University. Address: 119991, Moscow, Russia, 8 Trubetskaya St., bld. 2 E-mail: reshetoviv@mail.ru. ORCID: <http://orcid.org/0000-0002-3888-8004>

#### Информация об авторах:

Петерсен Елена Владимировна – к.м.н., биолог, Московский физико-технический институт. Адрес: 141701, Россия, Московская область, Долгопрудный, Институтский переулок, 9. E-mail: Petersen.ev@mipt.ru. ORCID: <http://orcid.org/0000-0002-8150-7553>

Чудакова Дарья Александровна – к.б.н., биолог, Московский физико-технический институт. Адрес: 141701, Россия, Московская область, Долгопрудный, Институтский переулок, 9. E-mail: chudakova.da@mipt.ru. ORCID: <http://orcid.org/0000-0002-9354-6824>

Ширяев Артем Анатольевич – к.м.н., врач-хирург, Первый Московский государственный медицинский университет имени И.М. Сеченова. Адрес: Москва, Россия, ул. Трубецкая, д. 8, стр. 2, 119991. E-mail: artemdoc@mail.ru. ORCID: <http://orcid.org/0000-0001-9421-420X>

Хрущова Анастасия Михайловна – к.б.н., биолог, Институт проблем экологии и эволюции имени А.Н. Северцова Российской академии наук. Адрес: 119071, Москва, Ленинский проспект, 33. E-mail: cricetus@yandex.ru. ORCID: <https://orcid.org/0000-0002-3956-8395>

Шабалина Евгения Юрьевна – магистр биологических наук, биолог, Московский физико-технический институт. Адрес: 141701, Россия, Московская область, Долгопрудный, Институтский переулок, дом 9. E-mail: evgenyashb@mail.ru. ORCID: <http://orcid.org/0000-0002-8184-7363>

Шакер Абануб Ашраф Салех – бакалавр биологических наук, биолог, Московский физико-технический институт. Адрес: 141701, Россия, Московская область, Долгопрудный, Институтский переулок, 9. E-mail: Shaker.a@phystech.edu. ORCID: <http://orcid.org/0000-0002-3025-6504>

Чернов Тимур Александрович – к.б.н., биолог, Московский физико-технический институт. Адрес: 141701, Россия, Московская область, Долгопрудный, Институтский переулок, 9. E-mail: chtimur@yandex.ru. ORCID: <https://orcid.org/0000-0002-7784-7045>

Каралкин Павел Анатольевич – к.м.н., биохимик, Московский физико-технический институт. Адрес: 141701, Россия, Московская область, Долгопрудный, Институтский переулок, 9. E-mail: pkaralkin@gmail.com. ORCID: <http://orcid.org/0000-0002-2838-0776>

Решетов Игорь Владимирович – д.м.н., онколог, Первый Московский государственный медицинский университет имени И.М. Сеченова. Адрес: 119991, Москва, Россия, ул. Трубецкая, д. 8, стр. 2. E-mail: reshetoviv@mail.ru. ORCID: <http://orcid.org/0000-0002-3888-8004>