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REFERENCE-GRADE GENOMES AS A TOOL FOR CONSERVING
KAZAKHSTAN'S NATIONAL PRIDE SPECIES:
THE CASES OF THE CASPIAN SEAL AND GREIG'S TULIP

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Abstract

This article presents the potential of third-generation sequencing (TGS) technologies to support biodiversity conservation efforts in Kazakhstan. We focus on two emblematic species – *Pusa caspica* (Caspian seal) and *Tulipa greigii* – that are both under conservation threat and lack comprehensive genomic resources. This mini-review highlights the transformative role of third-generation sequencing (TGS) in biodiversity conservation, using Kazakhstan as a case study. We do not aim to systematically compare sequencing technologies or exhaustively catalog all available genomic data. Rather, we discuss how high quality gapless reference genomes produced using TGS platforms such as PacBio HiFi and Oxford Nanopore represent an effective tool for species conservation efforts providing valuable information for the assessment of population genomic health, and for the identification of genes linked to adaptation and disease resistance. Finally, we suggest expanding this approach to include additional species of national importance, such as the saiga antelope, the Tazy and Tobet dogs, and the pink flamingo, as part of a national genomic biodiversity initiative.

Keywords: conservation genomics, Caspian seal, *Tulipa greigii*, third-generation sequencing, platinum-standard reference genome, Kazakhstan biodiversity.

ҚАЗАҚСТАННЫҢ ҰЛТТЫҚ МАҚТАНЫШТАРЫ БОЛЫП ТАБЫЛАТЫН
ТҮРЛЕРДІ САҚТАУДАҒЫ РЕФЕРЕНСТІК ДЕҢГЕЙДЕГІ ГЕНОМДАРДЫҢ
МАҢЫЗЫ: КАСПИЙ ИТБАЛЫҒЫ МЕН ГРЕЙГ ҚЫЗҒАЛДАҒЫ
МЫСАЛЫНДА

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Аңдатпа

Бұл мақалада Қазақстандағы биоәртүрлілікті сақтау жөніндегі күш-жігерді қолдау үшін үшінші буын секвенирлеу (TGS) технологияларының әлеуеті берілген. Біз екі эмблемалық түрге – *Pusa caspica* (каспий итбалығы) және *Tulipa greigii* - қорғалу қаупі төніп тұрған және жан-жақты геномдық ресурстары

жок түрлерге назар аударамыз. Бұл шағын шолу Қазақстанды мысал ретінде пайдалана отырып, биоалуантүрлілікті сақтаудағы үшінші ұрпақ секвенциясының (TGS) трансформациялық рөлін көрсетеді. Біз секвенирлеу технологияларын жүйелі түрде салыстыруды немесе барлық қолжетімді геномдық деректерді толық каталогтауды мақсат етпейміз. Біз PacBio HiFi және Oxford Nanopore сияқты TGS платформалары арқылы өндірілген жоғары сапалы саңылаусыз анықтамалық геномдардың популяцияның геномдық денсаулығын бағалау және бейімделу мен ауруға төзімділікпен байланысты гендерді анықтау үшін құнды ақпарат беретін түрлерді сақтау жұмыстарының тиімді құралы болып табылатынын талқылаймыз. Соңында, біз ұлттық геномдық биоәртүрлілік бастамасының бөлігі ретінде акбөкен, Тазы және Төбет иттері және қызғылт қоқиқаз сияқты ұлттық маңызы бар қосымша түрлерді қосу үшін осы тәсілді кеңейтуді ұсынамыз.

Кілт сөздер: консервациялық геномика, каспий итбалығы, *Tulipa greigii*, үшінші буын секвенирлеу, референстік геном, Қазақстан биоалуантүрлілігі.

ЗНАЧЕНИЕ ЭТАЛОННЫХ ГЕНОМОВ ДЛЯ СОХРАНЕНИЯ ВИДОВ – НАЦИОНАЛЬНЫХ СИМВОЛОВ КАЗАХСТАНА: НА ПРИМЕРЕ КАСПИЙСКОГО ТЮЛЕНЯ И ТЮЛЬПАНА ГРЕЙГА

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Аннотация

В этой статье представлен потенциал технологий секвенирования третьего поколения (TGS) для поддержки усилий по сохранению биоразнообразия в Казахстане. Мы фокусируемся на двух знаковых видах - *Pusa caspica* (каспийский тюлень) и *Tulipa greigii*, которые оба находятся под угрозой сохранения и не имеют комплексных геномных ресурсов. В этом мини-обзоре подчеркивается преобразующая роль секвенирования третьего поколения (TGS) в сохранении биоразнообразия, используя Казахстан в качестве примера. Мы не ставим своей целью систематическое сравнение технологий секвенирования или исчерпывающую каталогизацию всех доступных геномных данных. Вместо этого мы обсуждаем, как высококачественные референтные геномы без пробелов, полученные с использованием платформ TGS, таких как PacBio HiFi и Oxford Nanopore, представляют собой эффективный инструмент для усилий по сохранению видов, предоставляя ценную информацию для оценки геномного здоровья популяции и для идентификации генов, связанных с адаптацией и устойчивостью к болезням. Наконец, мы предлагаем расширить этот подход, включив в него дополнительные виды национального значения, такие как сайгак, собаки тазы и тобет, а также розовый фламинго, в рамках национальной инициативы по геномному биоразнообразию.

Ключевые слова: геномика охраны природы, каспийский тюлень, *Tulipa greigii*, секвенирование третьего поколения, эталонный геном, биоразнообразие Казахстана.

1. Introduction

As we are facing increased environmental challenges due to climate change and man-made impact on habitats, preserving biodiversity is becoming increasingly important, in particular, to ensure the survival of rare and endemic species. For Kazakhstan, biodiversity conservation is key as the country possesses several unique species and some of these unique endemics are highlight linked to national pride, culture and heritage. For example, species such as the critically endangered Caspian seal (*Pusa caspica*), the Kazakh Tazy dog, and wild tulips like *Tulipa greigii* stand as living symbols of the country's natural identity. Protecting these

emblematic species for future generations should leverage informed, long-term conservation strategies, and modern genomic technologies now offer unprecedented tools to support these efforts.

First, it is important to highlight that the aim of this review is to synthesize emerging applications of third-generation sequencing (TGS) in biodiversity conservation, with an emphasis on its underused potential in Kazakhstan. Through the lens of two emblematic species, we highlight how access to platinum-standard reference genomes can reshape conservation strategies. This review does not intend to present a meta-analysis of genomic data across all Kazakh species but to advocate for strategic genomics integration in national conservation planning.

High-quality genomic data, particularly generated through long-read third-generation sequencing (TGS), can reveal key insights of the genetic diversity and health, population structure, and vulnerabilities of endangered species (Theissinger et al., 2023). Global initiatives such as the Earth BioGenome Project have demonstrated how creating comprehensive genomic resources can directly support conservation at national and regional levels (Lewin et al., 2022, Huddart et al., 2022, Hogg et al., 2022). Similarly, the Native Genome Project in Saudi Arabia initiated by Professor Rod Wing at King Abdullah University of Science and Technology (KAUST) underscores the value of building high-quality genome assemblies to guide biodiversity preservation efforts encompassing the unique species of the country including the Taif rose (*Rosa × damascena*), miswak tree (*Salvadora persica*) and the gyrfalcon (*Falco rusticolus*), emblematic of the Saudi cultural landscape (N. Mohammed, personal communication, 2023; Zuccolo et al., 2023).

A recent practical example comes from the development of a gapless genome for Hong Kong's iconic orchid tree (*Bauhinia × blakeana*), which clarified its hybrid origin and provided a vital tool for targeted conservation (Mu et al., 2025). For Kazakhstan, developing similarly high-quality genomic resources for species such as the Caspian seal and *Tulipa greigii* could become a cornerstone of national conservation strategies.

The importance of such efforts is recognized at the highest state level. As President Kassym-Jomart Tokayev recently emphasized: “Нашего пристального внимания требуют каспийские тюлени, розовые фламинго и другие уникальные животные, которыми одарила нас сама природа, но которые сейчас находятся в опасности из-за деструктивной, разрушительной деятельности людей. Считаю необходимым создать Фонд охраны биологического разнообразия. Как Глава государства готов лично возглавить данную общественную организацию, чтобы подчеркнуть особую важность этой большой работы.” This commitment highlights not only the urgency of protecting biodiversity but also the unique responsibility Kazakhstan holds in preserving its natural heritage. In parallel, the successful inclusion of the Tazy dog into the international registry as a recognized Kazakh breed reflects the growing global recognition of Kazakhstan's unique biological and cultural assets.

By leveraging cutting-edge genomic tools, including capabilities available at the Arizona Genomics Institute (AGI) and King Abdullah University of Science and Technology (KAUST), Kazakhstan can enhance biodiversity conservation for current and future generations. With the goal of achieving these ambitions aim of preserving the unique endemic species, we have launched at Kozybayev University's Center of Agrocompetence an initiative called “Genomics of National Treasures”.

2. The Role of Third-Generation Sequencing for Biodiversity Conservation

2.1 Overview and Benefits of TGS for biodiversity conservation

Third-generation sequencing (TGS) technologies, such as PacBio HiFi and Oxford Nanopore, represent a major leap forward in our ability to generate complete, high-quality genomes. Unlike short-read sequencing platforms, which often produce fragmented assemblies with gaps in repetitive or complex regions, TGS delivers long, contiguous reads that allow for the reconstruction of near-complete, phased genomes (Marx et al., 2023). For biodiversity conservation, this technological advancement is particularly critical. Many endangered or poorly studied species require high-quality reference genomes to enable meaningful genetic analyses, yet until recently, the majority of available genomes have been partial or draft-quality (Formenti et al., 2022).

Long-read sequencing brings several decisive advantages for conservation efforts. First, it captures structural variation—including gene duplications, inversions, and transposable element insertional polymorphisms—that is often invisible to short-read methods. These structural features play a key role in shaping adaptation, evolutionary resilience, and disease resistance, traits that are essential for the survival of threatened species (Formenti et al., 2022). Second, TGS enables the reconstruction of accurate demographic histories and fine-scale population structures, providing deep insights into population health, past bottlenecks, and connectivity across fragmented habitats - the examples of the studies that leverage TGS for these purposes include genomic population studies in sailfish *Istiophorus platypterus* (Ferrette et al., 2023) and *Sogatella furcifera*, a destructive agricultural pest that threatens rice production in China and Southeast Asian countries (Cui et al., 2023).

An emerging standard in conservation genomics is the creation of gapless or near-gapless reference genomes, which serve as foundational tools for future monitoring and management. A recent example comes from Hong Kong's iconic orchid tree (*Bauhinia* × *blakeana*), where third-generation sequencing allowed researchers to assemble a complete genome and confirm its hybrid origins (Mu et al., 2025). Such a resource not only deepened scientific understanding but also provided critical information to guide conservation strategies. Kazakhstan could similarly prioritize the development of high-quality, reference-grade genomes for its national symbols, beginning with the Caspian seal (*Pusa caspica*) and *Tulipa greigii*.

It is important to highlight the current state of genomic resources available for *Tulipa greigii* and the Caspian seal. For *T. greigii*, no complete nuclear genome has been published to date, to the best of the authors' knowledge. Only plastid and chloroplast genomes have been sequenced so far (Almerikova et al., 2024; Tussipkan et al., 2024), leaving major gaps in our ability to study nuclear variation, structural rearrangements, or adaptive evolution. In the case of the Caspian seal, a draft genome assembly based on Illumina short-read sequencing was released in early 2025, spanning 2.36 Gbp and distributed across more than 442,000 scaffolds (Gomes-dos-Santos et al., 2025). However, short-read platforms often fall short in assembling complex or repetitive regions, which leads to highly fragmented genomes and limits their usefulness for conservation genomics. In contrast, third-generation sequencing technologies such as PacBio HiFi and Oxford Nanopore can generate long, high-fidelity reads capable of producing *gapless*, chromosome-scale assemblies. These approaches also enable haplotype phasing, essential for capturing inbreeding signals, structural variants, and subtle population differences. For rare or endangered species with structurally complex genomes or small, isolated populations, these high-quality assemblies serve as a foundational resource for effective conservation planning.

For rapidly declining populations such as the Caspian seal, access to a gapless reference genome would offer immediate and practical benefits. High-resolution genomic data could be used to assess genetic diversity (e.g. extreme variations in lifespan in the rockfish species from 11 to 200 years have been linked to 137 longevity-associated genes with the help of long-read sequencing as outlined by Kolora et al., 2021), detect signs of inbreeding depression (e.g. a recent study in the flightless parrot *kākāpō*, endemic to New Zealand by Dussex et al., 2021), monitor changes in effective population size, and identify potential genetic vulnerabilities that could compromise recovery efforts. As highlighted by recent conservation frameworks, early intervention based on genetic health studies is crucial to prevent irreversible losses in endangered species (Formenti et al., 2022; Lewin et al., 2022).

At a broader level, investment into TGS for national biodiversity would align Kazakhstan with major international efforts such as the Earth BioGenome Project (Lewin et al., 2022), which aims to generate reference genomes for all known eukaryotic species. It would also follow the model set by the Native Genome Project in Saudi Arabia, demonstrating Kazakhstan's commitment to protecting and studying its unique natural heritage using the most advanced scientific tools available (N. Mohammed, personal communication, 2023).

Thus, the strategic application of third-generation sequencing is not only a scientific imperative but also a necessary foundation for building a robust, forward-looking conservation framework. By establishing high-quality genomic resources for emblematic species, Kazakhstan can ensure that biodiversity conservation efforts are informed, effective, and lasting.

2.2 Case Study 1: Application to Greig's tulip (*Tulipa greigii*)

Tulipa greigii Regel is one of Kazakhstan's most emblematic wild species, recognized not only for its striking patterned foliage and vivid red blooms, but also for its deep cultural and geographic connection to the country, particularly the Southern region. In fact, the Aksu-Jabagly nature reserve's emblem (the oldest natural reserve in Central Asia located in Southern Kazakhstan) is fashioned after the image of the Greig's tulip. Native to Tian Shan mountains, this species has long symbolized Kazakhstan's identity as the homeland of wild tulips. Today, however, *T. greigii* is increasingly threatened by habitat degradation, overgrazing, and illegal bulb collection, with wild populations already in decline and listed in the national Red Book.

Despite its significance, *T. greigii* remains genetically poorly characterized, limiting both our understanding of its evolutionary history and our ability to design effective conservation strategies. While some recent efforts have employed molecular markers such as EST-SSRs to assess genetic diversity across populations (Almerekova et al., 2024), the absence of a high-quality reference genome continues to limit comprehensive population studies, restrict phylogenetic resolution, comparative analysis, and targeted restoration planning. Key traits such as adaptation to arid environments, flowering timing, and pathogen resistance cannot be studied at the genome level without a complete and annotated assembly.

Our effort to generate a reference-grade genome for *Tulipa greigii* will address this gap directly. A gapless assembly will allow us to identify genes linked to ecological adaptation, analyze historical population dynamics, and understand the species' placement within the broader tulip phylogeny. It will also serve as a foundational resource for *in situ* and *ex situ* conservation strategies.

2.3 Case Study 2: Application to Caspian Seal (*Pusa caspica*)

The Caspian seal (*Pusa caspica*) is the sole marine mammal endemic to the Caspian Sea and holds significant ecological and cultural value in the region. Historically numbering over a million, the population has experienced a dramatic decline exceeding 70%, primarily due to

climate change, habitat degradation, disease outbreaks, industrial pollution, and unsustainable hunting practices (Goodman and Dmitrieva, 2016). The species is currently classified as "Endangered" on the IUCN Red List and is included in Kazakhstan's national Red Book.

The lack of a high-quality reference genome has impeded comprehensive studies on the genetic health, population structure, and adaptive potential of *P. caspica*. Critical questions regarding inbreeding levels, gene flow, and disease susceptibility remain difficult to address without a robust genomic framework. Recognizing this gap, a collaborative initiative between the Central Asian Institute for Environmental Research (CAIER) and King Abdullah University of Science and Technology (KAUST) is underway to develop a chromosome-scale genome assembly for the Caspian seal (Asian Ecology, 2025).

This reference genome will serve multiple conservation objectives. First, it will form the first step for the accurate assessment of genetic diversity and inbreeding depression, which is essential for understanding reproductive viability and long-term survival. Second, it will support the identification of immune-related genes and help assess the species' vulnerability to pathogens. Canine distemper virus (CDV), phocine herpesvirus, and influenza A have all been detected in Caspian seal populations, and past outbreaks have caused significant mortality events (Karamendin et al., 2024; Namroodi et al., 2018; Gadzhiev et al., 2024). Third, the sequencing efforts starting with the high-quality reference genome will allow researchers to track shifts in effective population size over time and reconstruct the species' demographic history.

Comparative genomic analysis with other pinnipeds, such as the Baikal seal (*Pusa sibirica*), will also provide insights into the evolutionary adaptations of *P. caspica*—a species uniquely adapted to a large, enclosed inland sea. Moreover, high-resolution genomic data will help clarify the seal's capacity for adaptation under environmental stress, supporting predictive models under changing climatic and ecological conditions.

Recent research has also highlighted the wide range of pathogens circulating in the Caspian seal population. A viral metagenomic survey identified sequences from Circoviridae, Parvoviridae, Herpesviridae, and Orthomyxoviridae, pointing to a complex and potentially unstable virological landscape (Karamendin et al., 2024). Other studies confirmed exposure to *Leptospira interrogans* and *Toxoplasma gondii*, raising concerns about environmental contamination and zoonotic risks (Namroodi et al., 2018).

The Caspian seal's conservation is further challenged by persistent pollution from oil and gas infrastructure, shipping, and runoff, as well as bycatch from illegal fishing practices—all of which erode already fragile habitats (Gulden, NIBIO, 2023). In this context, a reference genome is not just a scientific milestone—it is an urgently needed tool for building long-term, evidence-based conservation strategies.

By generating the first high-quality genome for *P. caspica*, this project lays the groundwork for genomic surveillance, disease risk monitoring, and adaptive management. As Kazakhstan builds its own biodiversity genome archive, the Caspian seal genome will stand as both a scientific resource and a national commitment to the region's most threatened species.

3. Toward a National Biodiversity Genome Initiative: Conclusions and Future Directions

Kazakhstan is home to several emblematic species that carry ecological, evolutionary, and cultural significance. Among them, the Caspian seal (*Pusa caspica*) and *Tulipa greigii* represent two distinct taxa currently facing significant conservation threats. Until recently, conservation efforts for these species have been constrained by the lack of high-resolution genomic data. This limitation has hindered the development of evidence-based management

strategies, particularly those requiring precise information about population structure, genetic diversity, and adaptive capacity.

The application of third-generation sequencing technologies to generate reference-quality genomes for these species offers an opportunity to close this gap. For *P. caspica*, a high-quality genome will facilitate the detection of inbreeding, reconstruct historical demography, and enable the identification of immune-related genes relevant to disease monitoring. For *T. greigii*, genomic resources will support the study of local adaptation, guide *in situ* and *ex situ* conservation strategies, and provide a reference for other Central Asian wild tulips. In both cases, the availability of complete, annotated genomes will allow for the integration of molecular tools into long-term conservation planning, including genetic monitoring and assisted gene flow if required.

Looking ahead, it is essential to expand genomic efforts beyond these initial species. Other national pride taxa such as the saiga antelope (*Saiga tatarica*), the Tazy and Tobet hunting dog breeds, and the pink flamingo (*Phoenicopterus roseus*) would benefit from similar genomic characterization. These species are exposed to different anthropogenic pressures, ranging from habitat fragmentation and climate vulnerability to hybridization and disease risk. The development of a national biodiversity genomics initiative, with high-quality genome assemblies as its foundation, would strengthen Kazakhstan's capacity to lead in the application of genomics to conservation science.

The tools now exist to transition from fragmented data to comprehensive, species-specific genomic resources. Leveraging these capabilities in a coordinated framework will be critical for preserving Kazakhstan's biodiversity and ensuring that future conservation decisions are informed by the best available molecular evidence.

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