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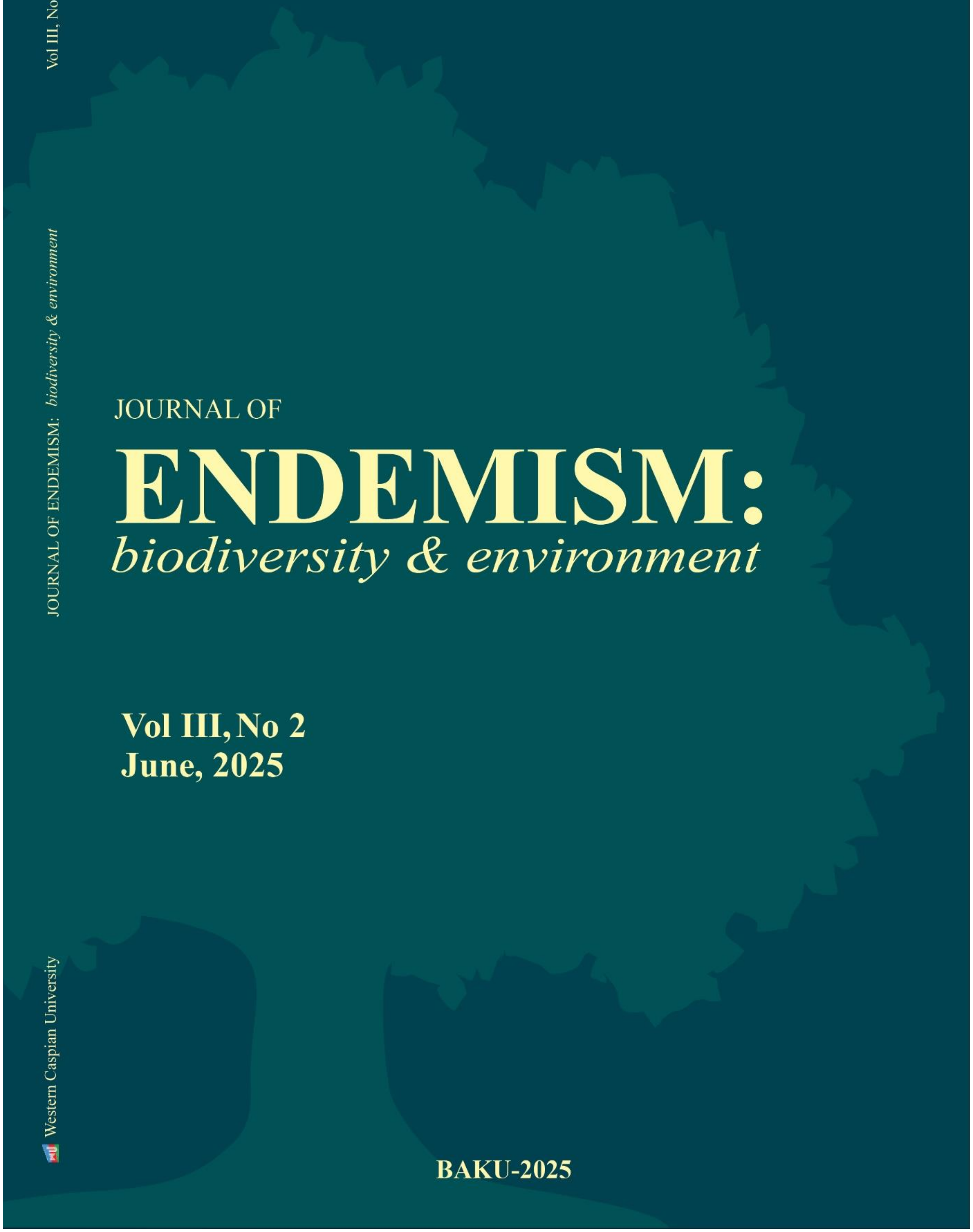

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RESULTS OF THE RESEARCH ON LEGAL, PSYCHOLOGİCAL, AND SOCİAL ISSUES ENCOUNTERED BY VETERANS OF THE 44-DAY WAR

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Abstract: The Second Karabakh War, which occurred in the autumn of 2020 and became known in history as the “44-Day Patriotic War,” marked a significant turning point in the modern history of Azerbaijan. Although the country restored its territorial integrity as a result of the conflict, thousands of veterans who participated in the military operations were left with lasting physical and psychological scars. In the post-war period, the medical, psychological, and social problems faced by veterans, as well as the legal violations committed against them, have become a serious subject of contemporary research. Despite important steps taken by the state toward the rehabilitation, social protection, and legal safeguarding of veterans, there are still numerous cases where these individuals are deprived of adequate medical assistance, excluded from social support systems, and subjected to violations of their rights. Investigating and publicizing such cases is crucial both for improving the living conditions of veterans and for contributing to the improvement of relevant legislation. Another factor that increases the urgency of this issue is the impact of veterans’ psychological well-being on society and their limited social integration. A systematic, evidence-based analysis of the health problems and legal violations experienced by veterans of the 44-day war is of great scientific and social importance. The present article reflects the findings of a comprehensive study aimed at improving the quality of life of veterans and facilitating their integration into society.

Keywords: post-war veterans, mental health challenges, social reintegration, legal rights violations, psychosocial issues, armed conflict consequences

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Introduction:

Wars are an inevitable reality of the modern era. When disputes in international relations cannot be resolved through diplomacy, the use of armed force between at least two parties to impose a solution is defined as war [21,22]. For soldiers returning from war, reintegrating into society can often be an extremely difficult process. After living under constant threat during war, many veterans struggle to reconnect with the slow, predictable pace of civilian life. Veterans often feel distant from their loved ones and struggle to express emotions, leading to a sense of being disconnected from those around them. Many veterans hesitate to talk about their time at war because they feel most people wouldn’t truly understand what it was like. Combat experience tends to deeply influence a person’s thoughts, emotions, and overall outlook on life. Many veterans feel fundamentally different from others—like people from “another world.” They come to believe that they have lived through something that most cannot understand, which gradually leads them into deeper isolation. This, in turn, can result in depression, loss of motivation, and a sense of hopelessness. The psychological state of war participants and the health, adaptation, and other problems they face have long been topics of public discussion. War veterans, especially those who have experienced serious psychological and physical trauma in combat, often face difficulties in adapting to social and legal frameworks [4,8,10,19].

After the war, many veterans struggle with pain that doesn't go away — both in their bodies and in their minds. For a lot of veterans, war leaves behind more than memories — it leaves them with pain, scars, damaged spines, and limbs they no longer have. War can leave lasting scars — lost limbs, broken bones, serious wounds, and damage to key organs are just a few of the injuries many veterans face. Many veterans say they still deal with constant body aches and physical discomfort long after returning from war. Conditions like arthritis or heart disease often show up much later, reminding us how deeply trauma can affect the body over time. Long after the war, many veterans still deal with the hidden effects of toxic exposure — whether from smoke, chemicals, or tobacco. Veterans facing these issues often find it difficult to stay employed, take care of themselves, or stick to a stable routine. For many veterans, regaining a sense of normal life depends on whether they can get proper medical care and support like prosthetics and rehabilitation [1,3,6,14,16,20].

War is an extraordinary event that affects not only the physical condition of individuals but also causes profound psychological trauma. The fear, death, loss, constant sense of danger, and witnessing the death of comrades on the battlefield significantly disrupt an individual's psychological balance. Consequently, mental health disorders are widely prevalent among veterans returning from war, often resulting in long-term or even lifelong consequences. Contemporary psychology and trauma research emphasize that war conditions function as acute and persistent stress factors that deeply affect the human psyche. Among war veterans, the most commonly observed psychological disorders include post-traumatic stress disorder (PTSD), depression, anxiety disorders, emotional instability, suicidal tendencies, social isolation, and substance or alcohol dependence [12,17,20]. Studies show that the psychological responses triggered by traumatic experiences negatively affect not only the individual's emotional well-being but also their family relationships, professional life, and ability to socially reintegrate. In some cases, psychological injuries among veterans result in more severe and longer-lasting consequences than physical wounds. Psychological trauma and emotional disturbances are widespread among veterans [5,7,9,11,15]. In particular, symptoms such as PTSD, depression, panic attacks, social isolation, and aggressive behavior are frequently reported [10,12,17,18]. According to statistics from the Ministry of Health of the Republic of Azerbaijan (2022), approximately 32% of veterans have been diagnosed with PTSD [2]. These problems are also widely recognized at the international level. According to the World Health Organization (WHO), 25–30% of individuals in the post-war period require psychosocial support [13,18].

Considering the aforementioned points, the topic of the present article is highly relevant and represents one of the most extensively studied scientific directions of the current era.

Research object. The object of the present article is the analysis of health problems and legal violations experienced by veterans of the 44-Day War. For this purpose, individual research was carried out on a voluntary basis among individuals who participated in the 44-Day Patriotic War in 2020 and were granted veteran status following the military operations. The study focuses on the physical and psychological health issues faced by these individuals in the post-war period, the availability of rehabilitation services, challenges related to social reintegration, and cases of violations of their rights guaranteed by the Constitution and other legislative acts.

Research Methodology. In accordance with the purpose of the study, both theoretical and empirical research methods were employed in this scientific work. The combination of various academic approaches and data collection techniques ensured the objectivity and scientific validity of the research.

1. Analytical Method

To thoroughly examine the health-related and legal issues faced by war veterans, existing legal documents, state programs, normative acts, international conventions, as well as medical and psychological research materials were reviewed and subjected to comparative analysis.

2. Sociological Survey Method

Surveys were conducted among veterans to collect empirical data. The aim of the surveys was to assess the veterans' health conditions, access to rehabilitation, level of social protection, and instances of rights violations. Both open- and close-ended questions were used in the surveys.

3. Statistical Analysis

The empirical data obtained were organized and analyzed using SPSS and Excel software. Statistical outcomes were evaluated primarily through percentages, averages, and correlation analysis.

4. Comparative Legal Analysis

The legislation of Azerbaijan was compared with international legal instruments to determine the extent to which veterans' rights are protected and to identify existing gaps in this area.

5. Document Analysis Method

Reports, statistical data, legal acts, and other official documents published by the Ministry of Labor and Social Protection, the Ministry of Defense, the Ministry of Health, and various NGOs were analyzed.

Results and Discussion.

Within the framework of this study, surveys and interviews were conducted with 30 individuals who participated in the 44-Day Patriotic War and currently hold official "veteran" status. The surveys were carried out in a semi-structured format, incorporating both open-ended and close-ended questions.

The summarized results are presented below:

1. *Demographic Indicators*

The participants were all male and ranged in age from 23 to 38. Of them, 60% were single, and 40% were married. The distribution of their educational background was as follows (Figure 1):

- 10% – higher education,
- 50% – vocational (secondary specialized) education,
- 40% – secondary (general) education.

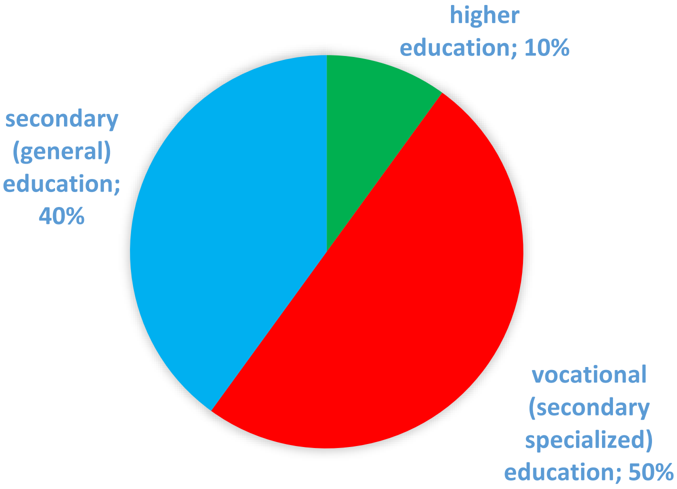

Figure 1. Distribution of Veterans by Educational Level (in %).

2. *Combat Experience*

All participants stated that they were engaged in combat operations during the September–November 2020 period. Of them, 70% had combat experience in the directions of Jabrayil, Fuzuli, and Shusha, while 30% reported serving in the areas of Aghdam, Zangilan, and other regions.

3. *Disability and Health Status*

A total of 80% of participants reported sustaining physical injuries during the war. Among them:

- 3 individuals were granted second-degree disability status,
- 5 individuals received third-

degree disability status.

The remaining participants stated that they were unable to obtain official disability status, mainly due to documentation issues and bureaucratic obstacles.

4. *Psychological Condition and Rehabilitation*

Among the 30 participants (Figure 2):

- 21 individuals (70%) reported experiencing post-traumatic stress, insomnia, and anxiety disorders
- 14 individuals mentioned receiving psychological support but emphasized that it was short-term and ineffective.

9 individuals stated that they had not received any psychological assistance.

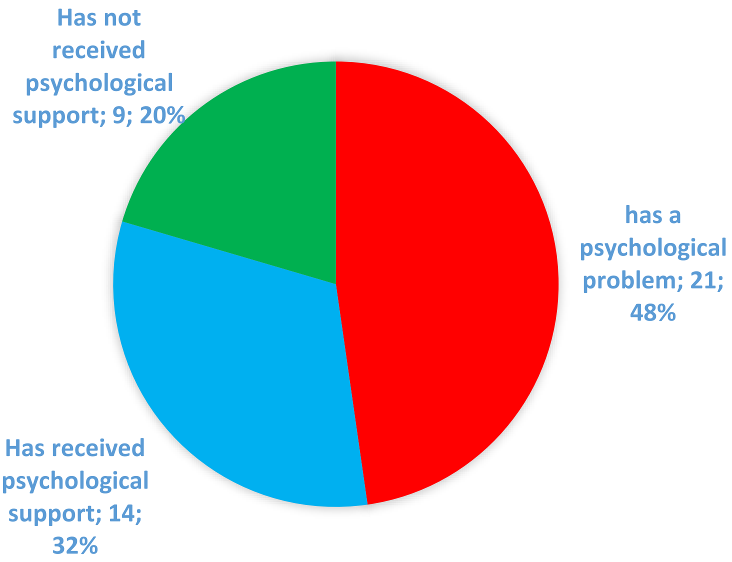

Figure 2. Psychological Condition and Access to Psychological Support among Veterans.

60% of those who applied to rehabilitation centers reported that they were not fully satisfied with the services provided.

5. *State Institutions and Social Support*

Among the participants, 14 individuals reported having officially received “veteran” status. The remaining 16 stated that they were unable to obtain this status, citing documentation issues as the primary reason.

Regarding the use of social assistance allocated for veterans (Figure 3):

- 30% of participants reported fully utilizing the available support,
- 25% benefited partially,
- 45% stated they had not been able to benefit it at all

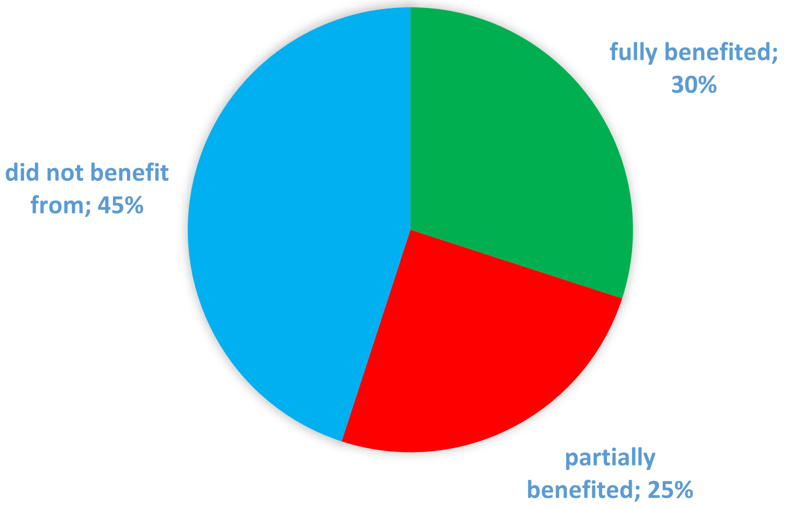

Figure 3. Utilization of Social Assistance among Veterans (in %).

Furthermore, 60% of participants indicated they experienced difficulties communicating with state institutions.

6. Legal Rights and Attitudes

Only 30% of participants stated that their rights had not been violated.

40% reported experiencing violations of their rights,

30% indicated being subjected to unfair treatment (Figure 4).

The main areas of dissatisfaction included:

- Challenges in obtaining veteran status
- Barriers to accessing social assistance and services
- Delays in medical documentation

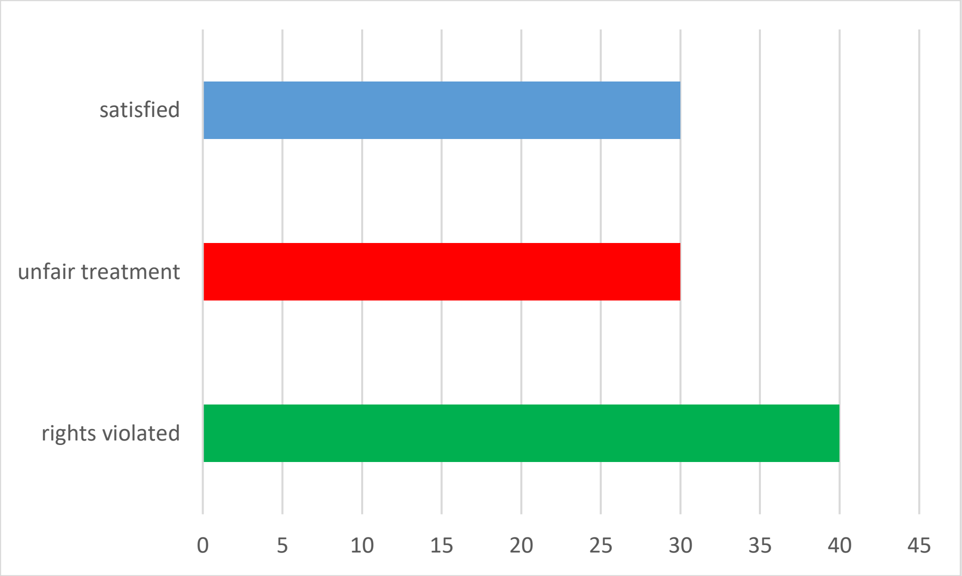

Figure 4. Percentage of Veterans Experiencing Legal Violations.

7. Employment and Education

- 70% of participants reported difficulties in finding employment,
- 30% stated that they were currently unemployed.
- 8 participants mentioned facing challenges in pursuing education, citing psychological and financial difficulties as the main reasons (Figure 5).

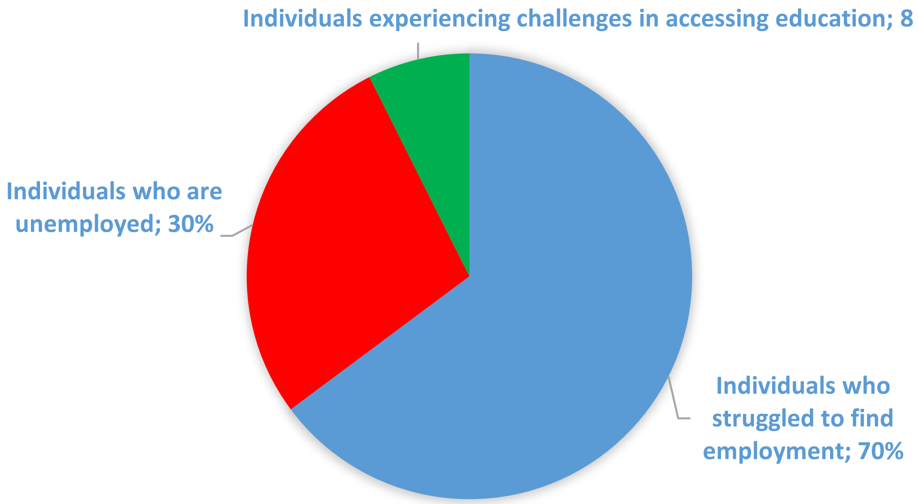

Figure 5. Challenges Faced by Veterans in Employment and Education (in %).

8. Societal and Media Attitudes

60% of participants believed that society treats veterans with respect. However, 40% felt that the media and the public do not pay sufficient attention to the real problems faced by veterans.

9. Perceptions of the War

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- 16 participants stated that they voluntarily enlisted in the war,
- Of these, 3 individuals expressed partial regret about this decision, primarily due to the difficulties encountered afterwards.
- 14 participants were conscripted (Figure6)

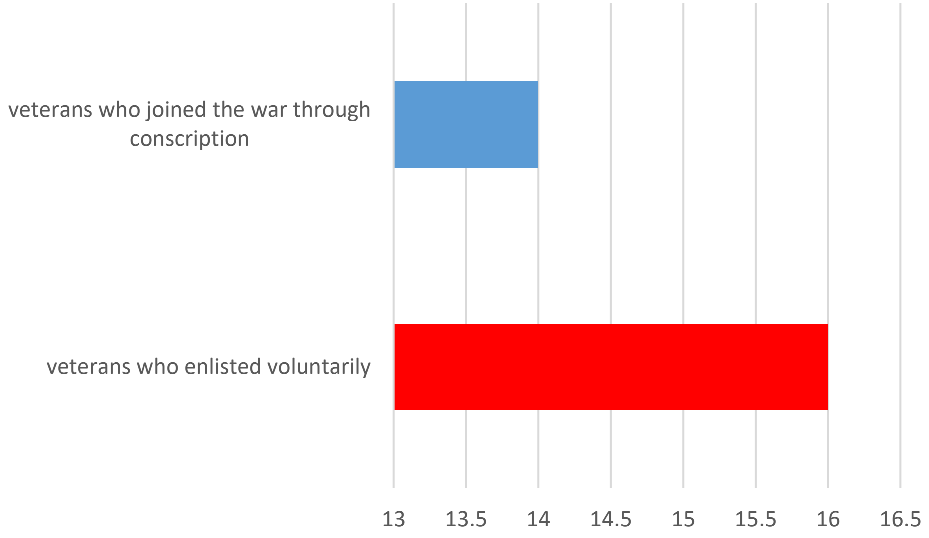

Figure 6. Reasons for Veterans' Participation in the War.

10. Recommendations and Expectations

In the final question of the study, all participants provided various suggestions related to the protection of veterans' health and legal rights. The most frequently repeated recommendations were as follows:

- Expansion of psychological support and rehabilitation services
- Simplification of procedures for obtaining veteran status
- Improved accessibility to medical and legal assistance
- Enhanced support for veterans in the labor market
- Increased activity and transparency in the work of social workers

The discussion of the results revealed several important insights. In this section, the empirical findings are interpreted within relevant scientific and social contexts. The study highlights significant trends and challenges concerning the psychological, social, and legal conditions of veterans who participated in the 44-Day Patriotic War..

1. Psychological Well-being and Rehabilitation Services

It was found that the majority of participants (70%) exhibited psychological symptoms such as post-traumatic stress disorder (PTSD), anxiety, insomnia, and emotional distress. This finding aligns with international research, where similar post-war psychological disorders have been observed in 50–80% of veterans in countries like the United States, Germany, and others [7,8,18,20].

Although some veterans reported receiving psychological support, most noted that such support was neither systematic nor long-term. This points to inadequacies in the organization of psychosocial rehabilitation services in the country. Psychological recovery should not be limited to clinical assistance but must also be seen as a broader process involving the social environment and family support.

2. Health and Disability Issues

Many participants stated that they had suffered various physical injuries as a result of the war, and some were granted official disability status. However, others faced significant obstacles in obtaining disability recognition, often due to documentation issues, medical examination delays, or administrative negligence. These findings suggest the need for serious reforms in the state's medical and legal service provision to veterans. Participants frequently mentioned inadequate healthcare and the negative impact of long-term health problems on their daily lives.

3. Social Protection and Relations with State Institutions

A significant portion of the participants (approximately 60%) reported difficulties in communication with state agencies and noted limited or no access to social benefits and allowances. Some also faced challenges in obtaining official veteran status. These issues point to a need for increased transparency and efficiency in state institutions working with this social group.

4. Societal and Media Attitudes

According to participants, society's general attitude toward veterans is positive; however, they noted that this support is not adequately reflected in media coverage or public discourse. Veterans expressed that their daily struggles are often misunderstood or overlooked by the wider public, and in some cases, they face indifference.

5. Employment and Educational Opportunities

Several participants indicated that they were unable to find employment after the war, while others experienced physical or psychological challenges in their current jobs. The reintegration process was particularly difficult for those with disabilities. This highlights that state and private sector mechanisms for supporting veteran employment remain underdeveloped and insufficiently responsive.

6. Legal Issues and Fair Treatment

Many participants reported that their legal rights had been violated or that they had encountered unfair treatment. The most commonly cited issues included:

- Delays in obtaining veteran status
- Delays or denial of social benefits
- Inaccuracies and complications

in medical documentation

These findings underline the need for improvements in the legal framework to strengthen the protection of veterans' rights.

Conclusion:

1. The conducted research demonstrated that individuals who participated in the 44-Day Patriotic War—veterans—face multifaceted and deeply rooted problems in the post-war period. These challenges are not limited to medical and psychological dimensions but also manifest in social, legal, and institutional contexts. The findings reaffirm that the rehabilitation of veterans requires a comprehensive and multidisciplinary approach.

2. The severe traumas inflicted by the war—particularly battlefield losses, physical injuries, and emotional shocks—have led to significant disruptions in veterans' health. Many continue to live with persistent physical and psychological pain. The loss of limbs, restricted mobility, and chronic pain negatively affect their daily functioning. Additionally, psychological conditions such as post-traumatic stress disorder (PTSD), depression, anxiety disorders, and emotional numbness further complicate their reintegration into society.

3. Although there have been some improvements in rehabilitation and medical

and a lack of adequate legal protection. Tendencies toward unlawful behavior can often be attributed to exclusion from rehabilitation, psychological distress, and the absence of social support.

6. This research has proven that issues related to veterans' social protection, healthcare needs, and legal rights cannot be addressed through fragmented reforms alone—they require a comprehensive and strategic approach. The state's social policy, healthcare and legal systems, as well as civil society and non-governmental organizations, must act in coordinated collaboration. Policy toward veterans must not be short-term or symbolic but should be based on long-term, sustainable support, ensuring not only survival but also a life of dignity.

References:

services, disparities in access, delays in medical oversight, and instances of negligence remain prevalent among veterans. Psychological support, in particular, requires focused attention, as some veterans are either reluctant to seek help or express distrust in the existing system. This leads to worsening of trauma, intra-family tensions, and social isolation.

4. The difficulties veterans face do not remain confined to individual experiences—their families are also significantly affected. Psychological strain in family relationships, economic hardship, and concerns about future security draw family members into the veterans' struggle. Existing mechanisms for labor market integration, social adaptation, and legal protection often appear formalistic and fail to address the real needs of veterans.

5. Legal violations are not solely the result of institutional inefficiency or inactivity, but are also linked to societal stereotypes and stigmatization directed at veterans. In some cases, veterans face discrimination, social withdrawal,

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STURGEONS IN THE CASPIAN SEA AND THEIR CONSERVATION MEASURES

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Abstract: The Caspian Sea, which hosts a wide variety of sturgeon species, has experienced a significant decline in sturgeon populations due to pollution, overfishing, and habitat destruction. These factors have led to a drastic reduction in their numbers. There are three sturgeon species that are crucial for maintaining ecological balance: Beluga (Huso huso), Russian sturgeon (Acipenser gueldenstaedtii), and Starry sturgeon (Acipenser stellatus). In particular, pollution continues to drive these species toward extinction, resulting in a significant decline in their populations. Research findings indicate that several factors hinder the survival of sturgeons. These factors negatively impact the ability of sturgeon species to sustain their populations. Unsustainable fishing practices, the construction of dams, and industrial development have led to the abandonment of spawning grounds, while pollution further disrupts the ecosystem. Conservation strategies, such as fisheries management and habitat restoration projects, are currently key topics of discussion. Sturgeons are the primary research focus of this study. The research suggests that further investigation and collaboration with international organizations are necessary to ensure the sustainable and protective management of sturgeon species in the Caspian Sea.

Keywords: Caspian Sea, sturgeons, conservation measures, pollution, fish species

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Introduction

There is evidence that sturgeons living in the Caspian Sea have historically played a significant role in both the region's economy and its biological system. To ensure the preservation of the region's biodiversity, it is crucial to investigate the existence of these ancient fish, which have been present in the area for over two hundred million years. Over the past few decades, the number of these fish has significantly decreased due to various anthropogenic impacts, including pollution, overfishing, and habitat degradation [4]. This decline has occurred as a result of a combination of factors—the result of several different conditions coming together simultaneously. These threats have affected sturgeons, including species such as Beluga (*Huso huso*), Russian sturgeon (*Acipenser gueldenstaedtii*), and Stellate sturgeon (*Acipenser stellatus*), with a significant portion of these species now facing the threat of extinction within the next few decades [1].

Figure 1. Sturgeon Fish Species

Source [6]

One of the most important factors contributing to the decline of sturgeons is the high demand for sturgeon caviar production. This demand has led to a decrease in their numbers. Another key factor causing the decline of sturgeons is overfishing. It is possible that the construction of dams, as well as the pollution of freshwater rivers and the spawning grounds where sturgeons deposit their caviar, has disrupted the typical migration patterns of these fish, which in turn adversely affects their viability. There are many other factors contributing to this problem. Pollution of the Caspian Sea as a result of industrial and agricultural activities has further complicated the resolution of these issues. This is because pollution affects not only the health of sturgeons but also their habitat [2].

In response to these concerns, a range of conservation measures have been developed. Some of these initiatives include the restriction of fishing, habitat restoration, and the establishment of programs for the artificial breeding of fish. Considering that these methods have limited impact, participating in even more coordinated international cooperation to ensure the survival of these species is of vital importance. Unfortunately, despite all these efforts, the effectiveness of these measures remains quite limited.

Caspian Sea and Sturgeon Species

The sturgeon species in the Caspian Sea have been significantly influenced by various natural and anthropogenic factors. Throughout human history, the Caspian Sea has served as a habitat for numerous different sturgeon species. The implementation of industrial fishing and the growing demand for caviar that began in the 19th century led to the depletion of these species due to unsustainable fishing practices. This occurred in the 19th century and was the primary cause of the decline of sturgeon populations.

Fishing practices—including large-scale fishing and illegal poaching—have had a significant impact on sturgeons, especially in light of the sharp increase in caviar demand. The normal reproductive cycles of sturgeons have been disrupted, leading to the degradation of their spawning grounds as a result of the damming of rivers flowing into the Caspian Sea. Sturgeons are among the species encountered in the Caspian Sea. It has been determined by the International Union for Conservation of Nature (IUCN) that the Beluga sturgeon is in a critically endangered state. This is one of the many sturgeon species in the Caspian Sea facing the threat of extinction [1].

Furthermore, the construction of dams, pollution, and changes in weather conditions are also among the factors that pose specific threats to sturgeons. All of these factors have contributed to an increase in these risks. Dams hinder sturgeons from reaching their spawning grounds in freshwater rivers, resulting in an inability to achieve their normal migration. It is crucial for their reproductive success that they reach these spawning areas; however, dams obstruct this process. Additionally, the water quality in the Caspian Sea has deteriorated due to pollution from industrial, agricultural, and municipal sources, creating an even more dangerous situation regarding the ability of sturgeons to persist.

Various Strategies for the Conservation of Sturgeon Species in the Caspian Sea

Sturgeon species are currently in

decline, and various conservation measures are being implemented to counteract this trend. Fishing restrictions, artificial breeding programs, habitat restoration, and international cooperation are examples of these efforts.

Table 1. Self-Sufficiency Level in Azerbaijan, Percentage

	2020	**2021**	**2022**	**2023**
All Types of Meat and Meat Products	84,5	86,4	86,0	85,3
Fish and Fish Products	81,7	78,2	76,7	75,4

Source: [5]

According to the conclusion, the levels of self-sufficiency in meat, fish, and products derived from these sources in Azerbaijan between 2020 and 2023 have been substantiated withvariousexamples.

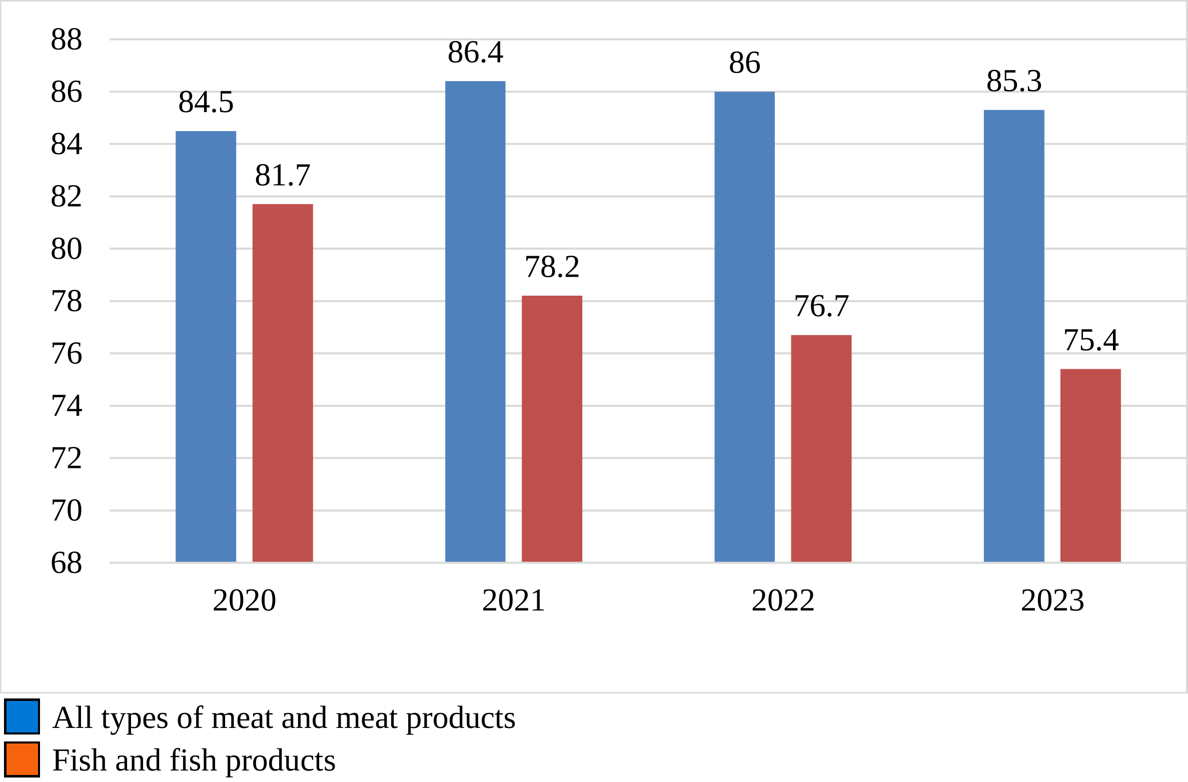

Figure 1. Graphical Representation of Self-Sufficiency Level in Azerbaijan, Percentage
Source: [5] based on

Based on Graph 1, it can be observed that the self-sufficiency level for meat and meat products increased from 84.5% in 2020 to 86.4% in 2021, followed by a slight decline to 86.0% in 2022 and 85.3% in 2023. In contrast, the self-sufficiency percentage for fish and fish products has shown a continuous decline, decreasing from 81.7% in 2020 to 75.4% in 2023.

Overall, while Azerbaijan has managed to maintain a high level of self-sufficiency in meat production, the declining trend in fish and fish products raises concerns. To reverse this trend and enhance food security in the sector, issues such as overfishing, investments in aquaculture, and improved fisheries management must be addressed.

To combat overfishing and reduce illegal fishing activities, countries surrounding the Caspian Sea have imposed fishing restrictions. The objective of these restrictions is to curb excessive fishing practices. Strict fishing quotas, seasonal fishing bans, and regulations controlling the sale of caviar are part of efforts to prevent the overexploitation of the caviar sector. However, enforcement remains a challenge, particularly in regions where illegal poaching practices are still widespread [2].

Several countries have initiated efforts to restore critical habitats necessary for sturgeon spawning. These ecosystems are essential for the survival of sturgeon species. A key goal of these initiatives is to replenish the Caspian Sea with natural nutrients that support sturgeon spawning grounds. One of the most crucial aspects of these conservation efforts has been the implementation of programs aimed at restoring wetland areas and modifying or removing dams to facilitate migratory fish passage. To facilitate these habitat restoration operations, the United Nations Environment Programme (UNEP) has established a regional framework under the Tehran Convention [2].

The implementation of artificial breeding and rearing programs is another conservation strategy for sturgeon species. These projects aim to provide a controlled environment for sturgeon reproduction and, after successful juvenile development, release them back into the wild. Although this approach has shown some success, it is not a long-term standalone solution. It must be complemented by environmental improvements and strengthened fishing regulations [3].

Ultimately, global coordination is essential for the success of conservation initiatives. Given that the Caspian Sea spans international borders and sturgeon species migrate across different regions, cross-border cooperation is crucial. The Tehran Convention, a regional environmental agreement, has proposed a structured approach to the conservation of Caspian Sea ecosystems, including the protection of sturgeon species, which are an integral part of these ecosystems. Additionally, the Caspian Environment Programme (CEP) aims to minimize pollution levels in the Caspian Sea and ensure the sustainable management of its natural resources.

Conclusion:

Despite the significant decline in sturgeon populations in the Caspian Sea, addressing this issue requires a comprehensive conservation strategy that integrates multiple approaches. While efforts have been made to mitigate these challenges, much remains to be done. Sturgeon species face serious threats due to pollution, habitat degradation, and overfishing, all of which jeopardize their survival.

To ensure the future of these ecologically and culturally valuable species, international cooperation, stricter fisheries regulations, habitat restoration, and breeding programs will be essential. In recent years, artificial breeding initiatives have become increasingly important in conservation efforts. If collaboration and investment in conservation programs continue, there is reason for optimism that sturgeon populations can be safeguarded, and their aquatic environment in the Caspian Sea can be improved.

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BIOLOGICAL CHARACTERISTICS OF THE MULBERRY SILKWORM (BOMBYX MORI) AND ITS IMPORTANCE IN SILK PRODUCTION

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Abstract: Bombyx mori L., 1758 (Lepidoptera: Bombycidae), is the mainstay of the silk industry and is economically highly significant. It depends on humans to complete its life cycle and has a short lifespan. Among its genes, there are many that show high homology with genes causing human diseases. At the same time, its low breeding and maintenance costs, along with minimal ethical issues and the availability of its complete genome sequence, make it a potential candidate as an alternative invertebrate model organism for life science research. In recent decades, Bombyx mori L. has been successfully used as an alternative invertebrate model organism in various scientific fields. These applications include modeling human diseases, environmental monitoring, epigenetic studies, as well as testing and discovering microbial drugs.

Keywords: pupa, cocoon, fibroin, silkworm

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Introduction:

The Lepidoptera order includes butterflies, skippers, and moths. These insects perform various functions in ecosystems, serving as food sources for agricultural pests, birds, bats, and other insects, and acting as nocturnal pollinators (Dar and Camal, 2021a, 2021b). Bombyx mori Linnaeus 1758, known as the silkworm, is famous for silk production and forms the foundation of the silk industry. Generally, while other lepidopteran species are polyphagous, the silkworm is a monophagous species. Its food source is exclusively the leaves of the mulberry tree, which is the only food it consumes during its larval stage.

After mating, the adult female silkworm lays eggs, which hatch into small, black, and hairy larvae. These larvae go through four molts, resulting in five different instar stages. The larvae of the fifth instar stage spin a silk cocoon, and a mature individual emerges, searches for a mate, and reproduces. After mating, the female silkworm lays eggs. When the silkworm eggs are laid, they are creamy white in color, and if they are fertile, they turn black.

History:

China, known as the "cradle of silk," has made significant progress since 1949, demonstrating incredible development in the silk industry over the last five decades and becoming the world's largest silk producer. In recent years, the silk farming of mulberry silkworms has become a key factor in ensuring sustainable employment in agriculture and strengthening economic development. The achievements in this field have been made possible through effective government policies, targeted and intensive research and development activities, and the precise implementation of these measures.

Silk farming has a 5000-year history in China. The first written information about the characteristics of silkworms in captivity was recorded in 1637 by Song Yinxing in his book Tian Gong Kai Wu. Improving the productivity of silk farming has always been considered a crucial factor, with the selection, breeding, and maintenance of better-quality silkworm species being carried out both consciously and unconsciously for a long time. However, the systematic collection and study of silkworm breeds began only in the 19th century.

The development of silk farming in Azerbaijan is based on ancient history and rich traditions. The widespread cultivation of this industry, especially in the North-Western region, particularly in Sheki, is not coincidental. Over the centuries, silk farming traditions have been preserved and developed here, playing an important role in the lives of the local population. The recognition of Sheki as a silk farming center and the widespread application of this industry in agriculture has also been confirmed by archaeological research. In the past, silk farming in Sheki (Nukha) was carried out by entrepreneurs in individual factories and workshops and developed on a limited scale. However, over time, the reputation of this valuable product – Sheki silk – spread not only within the country but also abroad, resulting in a significant increase in demand. Sheki has been one of the main silk farming centers in Azerbaijan and the entire region, a fact even reflected in the city's coat of arms. Sheki silk has always been highly valued in world markets, maintaining its reputation. The silkworms and silk threads produced here have always been considered precious. Over time, alongside the development of silk farming, a specialized class that mastered the technology and production methods of this industry has also formed.

Azerbaijan's historical location on the "Silk Road" has contributed to the formation and development of this industry, especially in Sheki. This factor also helped expand trade and economic relations with other countries. Archaeological findings prove that silk farming was already practiced during the ancient Caucasian Albania period in the temple lands. In 1985, during research in the Kudurlu village area of Sheki, valuable metal earrings resembling silkworms and a kauri-shaped cut piece were found in mound number 7.

For the first time in the field of silk farming, adaptive selection methods were applied with the aim of creating ecologically resilient hybrid lines of the mulberry silkworm. This approach not only enhanced the silkworms' ability to adapt to various ecological conditions but also enabled improvements in their biological, technological, and productivity traits. During the adaptive selection process, the most resilient and high-yielding individuals from silkworm populations were selected through natural and artificial selection methods.

As a result, the hybrid lines obtained through the application of the adaptive selection method demonstrated high adaptation capabilities, were able to develop optimally under various ecological conditions, and created a more favorable genetic foundation for silk production. This approach has opened new perspectives for the future sustainable and efficient development of silk farming.

Life Cycle of the Silkworm:

The life cycle of the silkworm begins with the female silkworm laying eggs. From the eggs, caterpillars or larvae emerge. The silkworms feed on mulberry leaves and go through the pupa stage. During the pupa stage, the silkworm attaches itself to its surroundings with a thread. Then, by waving its head, it spins a protein-based fiber into silk. Several caterpillars create a protective layer around the pupa, which is known as a cocoon. The silk thread (fiber) is obtained from the silkworm's cocoon.

The egg is the initial stage of the silkworm's life cycle. The female moth lays a single egg, about the size of a complex dot, in the summer or early autumn. The eggs remain stationary until spring, when the warmth triggers their hatching. The Bombyx mori egg is very small and has a hard structure; it is the size of a pinhead and resembles a poppy seed. The egg's shell provides protection to the developing embryo, covering it. When first laid, the egg is pale yellow in color. Within a few days, the fertile egg cell turns a bluish-gray color.

The larval stage is the vegetative phase where growth occurs. The Bombyx mori larva, commonly known as the silkworm, is a specific host of the mulberry tree. During its growth, the larva can molt four times. The stages between molts are called instars. When the silkworm hatches from the egg, it is about 1/8 inch in size and very hairy.

The new silkworms emerging from the cocoon feed exclusively on soft mulberry leaves, but as they grow, they can also eat tougher mulberry leaves. The larval stage lasts about 27 days, during which the silkworm goes through 5 instar stages.

During the pupa stage, the silkworm spins a protective cocoon. The size of the cocoon is compared to a cotton ball, and its color changes; the cocoon is spun from continuous silk threads, about 1.5 meters (approximately one mile) long. This cocoon serves as protection for the pupa. The cocoon is primarily white, but depending on the silkworm's genetics, it can also turn creamy or yellow. After the final molt inside, the cocoon transforms into a brown, chitin-covered pupa structure.

During the pupa stage, metamorphic changes occur, resulting in the silkworm transforming into a moth. If the silkworms are allowed to pass through the cocoon and mature, the silk cannot be used for commercial purposes. Therefore, after the cocoon is produced, the silkworms are killed, and the insects are immersed in boiling water to dissolve the cocoon's adhesive. The silk is then unwound and spread out over a distance of one mile to transform into thread (Figure 1).

The cocoon is the stage during which silk threads are spun around the larva to form a protective structure, serving to protect it from predators. The larva remains inside the cocoon as it transitions into the pupa stage. The color of the cocoon varies depending on the silkworm's diet, ranging from white to golden yellow. After the second larval stage is completed and the pupa turns brown, molting occurs inside the cocoon. During this period, the pupa transforms into an adult moth over approximately 2-3 weeks.

Figure 1. The pupal stage of the mulberry silkworm

The adult stage completes the life cycle of Bombyx mori. This stage is the reproductive period during which the adults mate, and females lay eggs. Moths are incapable of flying and cannot consume food as they lack functional mouthparts (Figure 2).

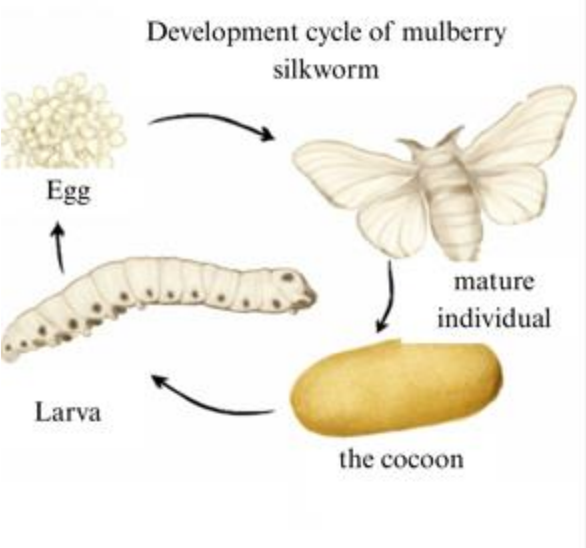

Figure 2. Development cycle of the mulberry silkworm

Feeding of the Mulberry Silkworm:

The mulberry silkworm is a delicate creature that requires great attention and care, but in return, it yields high productivity. Therefore, to achieve maximum output from the silkworms, the care and management provided to them must be of a high standard.

The most important factors that affect the growth, development, and high-quality cocoon production of the mulberry silkworm are as follows:

- Quality of the feed
- Quantity of the feed
- Feeding technique

From the moment the silkworm hatches, it begins searching for food, and with its weak mandibles, it finely cuts and consumes the leaves

Figure 3. Nutrition in the early years

Figure 4. Nutrition of an adult worm

A silkworm can consume an amount of leaves equivalent to its body weight in a single day. When provided with sufficient food, the

larvae develop rapidly and accumulate a large amount of fat in their bodies. This fat reserve allows them to survive without food during the pupa, moth, and egg (grana) stages.

Mulberry leaves are the only food of the mulberry silkworm. In the early days of the first instar, the larvae feed only on the soft parts of the leaves; (Figure 3) as they grow, they feed on the entire leaf, except for the veins. (Figure 4) As the larvae approach their final instar, they may even consume the petiole of the leaf and, in some cases, the mulberry tree itself.

Mature larvae rapidly and voraciously consume the leaves. Using their strong mandibles, they create oval-shaped notches on the leaves and slice them thinly. The larvae cut the leaves when they lower their heads, but cannot cut when they raise their heads.

Silk threads are distinguished by their durability, strength, and smooth texture. (Figure 5) While spinning the cocoon, the silkworm protects itself from environmental influences, and during this process, it takes on a special shape. Once the cocoon is completed, the silkworm exits this protective structure and transforms into a moth

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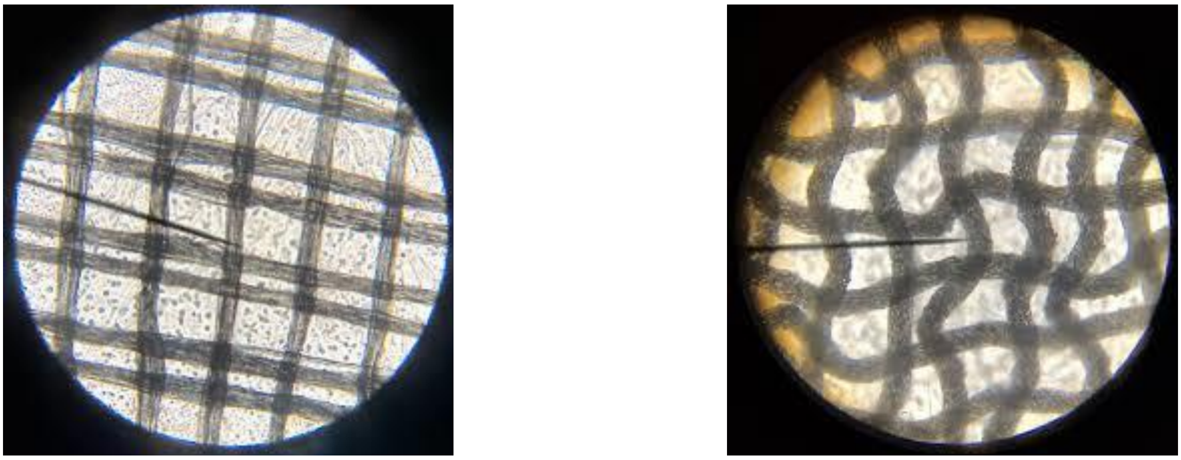

Figure 5. Appearance of silk threads under a microscope

Silk is a naturally occurring material composed of two biomacromolecules, fibroin and sericin, and is used as a high-quality textile material. In recent times, silk has been reported to have good blood compatibility [1], [2], cytocompatibility, to cause low levels of inflammation in the body, and to be biologically biodegradable. Due to these properties, silk has been studied for various applications in the biomedical field, including the production of artificial ear drums, membranes for controlled bone regeneration, bone substitute materials [10], scaffolds for tissue engineering, burn dressings, and the creation of nerve and irritation models.

Unlike synthetic polymers, silk polymers (fibroin and sericin) are naturally produced by the silkworm. Therefore, the structural characteristics and properties of silk polymers are determined during production by the silkworm. Some limitations of silk have posed obstacles to its use in biomedical fields. For example, the molecular weight (MW) of silk fibroin (SF) decreases during degumming [11] and dissolution processes. As a result, various efforts have been made to minimize the molecular degradation of SF during these processes, as the molecular weight of natural silk is determined by nature and cannot be increased. Therefore, the methods applied to produce less degraded SF play a crucial role in improving its mechanical properties.

The primary sequence of silk protein consists of hydrophobic domains made up of short side-chain amino acids, which contribute to its crystalline β-sheet structures. These structures enable the tight packing of anti-parallel chains through hydrogen bonding, ensuring that silk fibers have high mechanical strength and tensile resistance. The predominance of hydrophobic domains enhances the water resistance of silk, thereby ensuring its biological stability.

Additionally, the presence of smaller hydrophilic domains in silk fibroin interacts with the hydrophobic regions, regulating the proper assembly of the protein. This balance between hydrophilic and hydrophobic domains enhances the strength and elasticity of silk fibers, making it an ideal material for various biomedical and industrial applications. [4] These unique properties of silk make it highly suitable for use in fields ranging from the textile industry to medicine and biotechnology. Silk derived from silkworms, particularly the Bombyx mori species, and orb-weaving spiders, such as *Nephila clavipes*, have been extensively studied to understand their processing mechanisms and to explore the potential applications of these proteins as biomaterials. These silks, both natural fibers and promising materials in biomaterials engineering and nanotechnology, have attracted significant attention.

Silks produced by silkworms and orb-weaving spiders possess a range of unique characteristics. Among these features, high ecological stability, biocompatibility with living organisms, and controlled proteolytic biodegradation are of particular importance. Through proteolytic biodegradation, silk fibers gradually break down and integrate into the organism's natural metabolic pathways, making them an ideal material for medical implants and regenerative tissue engineering. [4]

Furthermore, these silks exhibit morphological flexibility and can be easily modified to create different shapes and structures. The functional groups of amino acids in silk proteins allow for specific chemical modifications, which enable the immobilization of growth factors, i.e., biomolecules that promote cell proliferation and tissue regeneration, stabilizing them on the surface of silk fibers.

In addition to all these characteristics, silk fibers possess impressive mechanical durability. Silk produced by spider silk and silkworms exhibits high tensile strength and elasticity, making them suitable for use in various fields where strong, lightweight, and durable materials are needed. [2] Therefore, silk biomaterials offer vast potential in numerous areas such as biomedicine, biotechnology, drug delivery systems, wound dressings, and tissue engineering (Table 1).

Table 1. Mechanical Properties of Biodegradable Polymer Materials

Biomaterial Source	**Modulus (GPa)**	**UTS (MPa)**	**Tensile Strain at Break (%)**
B. mori silk (with sericin)	5-12	500	19
B. mori silk (without sericin)	15-18	610-690	4-16
B. mori silk	10	740	20
N. clavipes silk	11-15	875-972	17-18
Collagen	0.0018-0.046	0.9-7.4	24-68
Crosslinked collagen	0.4-0.8	47-72	12-16
Polylactic acid	1.2-3.0	28-50	2-6

B. mori Silk Fibroin Structure:

When examining the amino acid composition of B. mori silk fibroin, it is primarily composed of glycine (Gli) (43%), alanine (Ala) (30%), and serine (Ser) (12%) (Figure 6). In heavy-chain silk fibers, there are 12 domains that form crystalline regions, and these domains intersect with non-repetitive primary sequences, leading to the formation of less organized areas within the fibers. The crystalline regions are primarily composed of Gly-X repeats, where X amino acids are represented by alanine (Ala), serine (Ser), threonine (Thr), and valine (Val). The crystalline regions typically consist of approximately 381 amino acid residues, although this number varies across different domains. For instance, the seventh domain contains 596 residues, while the twelfth domain has as few as 36 residues. This variation influences the structural and mechanical [1] properties of silk fibers.

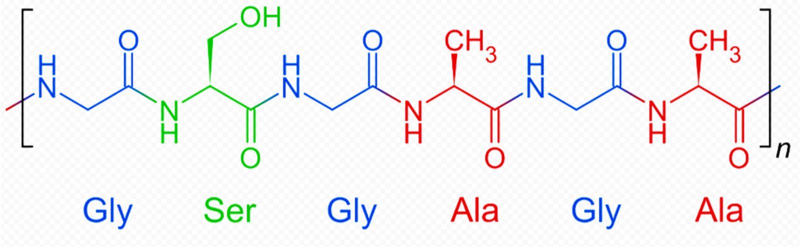

Figure 6. B. mori silk fibroin structure

Each crystalline domain is composed of smaller subdomains of hexapeptides. These subdomains include motifs such as GAGAGS, GAGAGY, GAGAGA, or GAGYGA, where G stands for glycine, A for alanine, S for serine, and Y for tyrosine. These sequences play a crucial role in the formation of the crystalline regions of silk fibers and determine their characteristics, such as strength and elasticity. [3]

Additionally, these subdomains are typically completed by tetrapeptides like GAAS or GAGS. These tetrapeptides regulate the assembly and organization of silk proteins, creating transition zones between crystalline and amorphous regions. As a result, the structural properties of silk fibers are optimized, facilitating their use in various biomaterial and industrial applications.

The biodiversity of local silkworm breeds and hybrids (*Bombyx mori* L.) in Azerbaijan was assessed for the first time using RAPD (Random Amplified Polymorphic DNA) molecular markers. In total, four RAPD primers (BGN 04, BGY 06, BGA 02, and BGW 02) and four ISSR primers (UBC 807, UBC 857, UBC 813, and UBC 827) were employed in the study. The RAPD primers generated 32 distinct bands, with fragment sizes ranging between 200 and 1200 base pairs. The number of amplicons produced per primer varied from 6 to 11, with an average polymorphism rate of 81% [13].

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LONGEVITY IN THE CAUCASIAN POPULATION

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Abstract: The Caucasian population, which lives in the mountainous regions of the Caucasus, is known for its exceptional longevity, which is attributed to a combination of genetic, environmental and lifestyle factors. This article will examine and analyze longevity and the factors affecting it, the statistical analysis of the lifespan of people in the Caucasian peoples, as well as the regions and countries of the region of the Caucasus. The issue of the concept of longevity is now becoming more and more important due to the influence of other factors. Thus, despite the fact that people's lifespans have increased with the development of modern technologies, the widespread use of these technologies in the food industry has caused certain problems by affecting genetics and shortening people's lives.

Keywords: Caucasian peoples, genetic features, longevity, Caucasus region

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İntroduction:

When discussing longevity in the population of the Caucasus, it is necessary to first provide information about the location and characteristics of the Caucasus on the map. The Caucasus is a geographical region located in both Asia and Europe. The eastern border of the Caucasus is the Caspian Sea, while its western border is the Black Sea. The northern physical-geographical boundary of the Caucasus is the Kuma-Manych Depression (which includes the northern borders of the Krasnodar and Stavropol regions and Dagestan) and, sometimes, Kalmykia is conditionally considered part of the Caucasus. Considering that a large part of the North Caucasus is historically and ethnographically closer to the Russian steppes and the Lower Volga region, the northern border of the Caucasus can be traced along the Kuban River and the ridges of Kuma, Malka, and Terek. Thus, the southern part of Krasnodar region, Adygea, Karachay-Cherkessia, Kabardino-Balkaria, North Ossetia, Ingushetia, Chechnya, and a large part of Dagestan are included in this area. The southern borders are politically formed by the boundaries with Azerbaijan, Armenia, and Georgia, as well as with Iran and Turkey. Azerbaijan is a Caucasus country (7). The population of the Caucasus is 30.2 million people: 55% of the population lives in the South Caucasus, and 45% in the North Caucasus. The ethnic composition of the Caucasus population is the most complex in the region. Currently, more than 50 different peoples live in the territory of the Caucasus. Relatively, the Lesser Caucasus region includes four states: Azerbaijan, Georgia, Armenia, and the southern part of the Russian Federation. Most of the peoples of the Caucasus belong to four language families: 1) North Caucasian ethnic group; 2) Kartvelian; 3) Indo-European; 4) Altaic (7,8).

According to the Indo-European language family, Slavs and Armenians belong to this group, while Georgians belong to the Kartvelian family. They live south of the Caucasus Mountains. The Turkic language group in the Caucasus includes Azerbaijanis, Karachays, Balkars, Kumyks, Nogais, and Turkmens. Azerbaijanis mainly live in the Republic of Azerbaijan and make up 90% of the population. Currently, a large number of Armenians live in Georgia and the North Caucasus (7,8).

Figure 1. Map of the Caucasus. (https://az.wikipedia.org/wiki/Qafqaz).

South of the Greater Caucasus, along the coast of the Black Sea, lies the alluvial Kolkheti plain, the site of ancient Colchis. South of the Caspian mountain range, between the Greater and Lesser Caucasus ranges, the Shirak steppe sharply descends into the Kura-Aras plain. In the center of this large depression, the Kura River receives its main right tributary, the Aras River. To the northeast, the Gobustan hills separate the Absheron Peninsula from the Kura-Aras plain. The Lankaran plain stretches to the south between the Caspian Sea and the Talysh Mountains, which reach heights of over 2,400 meters.

The Caucasus is divided into two main regions: The North Caucasus, which covers the southern part of Russia, and the South Caucasus, which includes Georgia, Armenia, and Azerbaijan. The region's rugged mountains and isolated valleys have contributed to its cultural and linguistic diversity. The Caucasus serves as a natural corridor between Europe, Asia, and the Middle East, leading over time to interaction and mixing among various peoples and traditions.

The Caucasus is mainly known as a land of longevity. In fact, the phenomenon of longevity has been identified in many of the peoples living here, and during the Soviet era, most research on the physiology of aging was conducted in this region. Along with longevity, high health indicators have also attracted attention (Karamova N.Y., 2025). Even before modern medical treatments emerged, it was known that a healthy lifestyle improved quality of life and extended life expectancy. Through epidemiological models that assess the impact of different lifestyle factors on quality of life and expected lifespan, the contribution of a healthy lifestyle can soon be quantified, which can enable important steps to strengthen the health of the population. Besides a healthy lifestyle, it is known that a number of other factors influence longevity. The total exposure to various xenobiotics and stress factors accumulated over an individual's lifetime in living and working environments is known as the exposome, which affects both quality of life and longevity. The exposome can currently be linked not only to clinical outcomes but also to biomarkers of exposure that help in the prevention and management of diseases and aid in mechanistically understanding how the human body interacts with environmental factors. Additionally, biomarkers of exposure help quantitatively determine an individual's susceptibility to damage from environmental stressors. Longevity is the result of a complex interaction between healthy genes and the environment, where the environment modulates gene expression through epigenetic effects. The interplay between the genome and gene expression modulation also plays an important role in longevity. The study of populations spanning many centuries has helped identify genes related to life expectancy, and polymorphisms of such genes can be used to determine susceptibility and resistance to diseases. Polymorphic variations in important genes interacting with the environment can significantly influence the risk of developing a specific disease. High consumption of alcohol, drugs, and tobacco are among lifestyle factors known to have toxic effects on the body and to substantially increase health risks.

Longevity and Factors Affecting It:

Longevity, or the length of an individual's life, is a complex phenomenon influenced by the interaction of genetic, environmental, lifestyle, and social factors. Understanding the determinants of longevity is crucial not only for extending lifespan but also for improving quality of life during aging (Christensen, K., Johnson, T. E., & Vaupel, J. W., 2006).

Genetics plays a key role in determining longevity. Studies conducted on centenarians and long-lived families have revealed that certain genetic variants are associated with enhanced cellular repair, efficient metabolic pathways, and resistance to age-related diseases such as cancer, cardiovascular diseases, and neurodegenerative disorders. For example, genes like SIRT1, FOXO3, and APOE, which are involved in antioxidant activity and regulation of inflammation, have been linked to lifespan extension. These genes slow down the cellular aging process and increase the body’s resistance to stress factors. The ability of cells to renew themselves, prevention of DNA damage, and effective metabolism are considered key biological mechanisms related to longevity. Telomeres also play an important role in this process. Telomeres are structures located at the ends of chromosomes that prevent the loss of genetic information during cell division. The enzyme telomerase maintains telomere length, and longer telomeres allow cells to remain functional for a longer period. Among the peoples of the Caucasus, especially in long-lived individuals, telomere length has been observed to be greater compared to other regions. Similar genetic characteristics have been noted repeatedly among members of long-lived families. This fact indicates that hereditary factors play a significant role in healthy aging. While genetic factors determine the potential for longevity, their interaction with other factors ultimately shapes actual lifespan. In other words, genetic advantages alone are not sufficient for a person to live a long and healthy life. Longevity is closely linked not only to hereditary factors but also to lifestyle. Healthy nutrition, physical activity, effective stress management, and timely medical prevention create conditions for the full realization of genetic potential. Studies conducted in areas inhabited by long-lived people prove that proper nutrition and an active lifestyle are among the main factors that enhance the influence of genetic factors.

The environment significantly affects longevity through factors such as air quality and pollution. Individuals living in certain mountainous regions, where environmental pollution is low, tend to have fewer respiratory and cardiovascular diseases, which contributes to a longer lifespan. Additionally, access to medical care and preventive measures against environmental hazards play an important role in reducing risks related to environmental factors (Chung, W. H., Dao, R. L., et al., 2010).

Lifestyle is perhaps the most modifiable element of longevity. Key aspects include: diet; water resources; physical activity; sleep; and stress.

Modern science and technology also play a crucial role in increasing longevity. Medical achievements such as vaccinations, early disease detection, and innovative treatment methods have significantly increased life expectancy in the past century. Emerging fields like genomics and biotechnology, including gene therapy and personalized medicine, hold promise for identifying interventions that promote longevity (Salvioli, S., Olivieri, F., Marchegiani, F., Cardelli, M., et al., 2006).

Longevity Zones of the Caucasus:

The Caucasus region, located between the Black Sea and the Caspian Sea, is famous for its stunning landscapes, cultural diversity, and fascinating history. One of the lesser-known but intriguing aspects of this area is its designation as a center of longevity. The areas known as the "longevity zones" of the Caucasus have attracted attention from both researchers and the public due to the remarkable life expectancy of their inhabitants. Primarily located in the mountainous regions of Georgia, Azerbaijan, and Armenia, these zones provide insights into factors that contribute to extended life expectancy. The mountainous terrain of the Caucasus creates favorable conditions for longevity. Together with clean air and pure water sources, the high altitudes create an environment that supports health. The region's mineral-rich waters, often praised for their therapeutic properties, contribute to the health of the local population. Additionally, the mild climate and abundance of unpolluted natural surroundings reduce bodily stress and improve overall well-being. At the same time, the social and cultural characteristics of the region play an important role in longevity. Strong social ties based on family values, intergenerational unity, and high respect for the elderly enhance psychological well-being, leading to longer and healthier lives. Traditional lifestyles, consumption of natural and minimally processed foods, and daily activities rich in physical exercise are also key factors contributing to longevity(https://www.britannica.com/topic/Caucasian-languages).

Additionally, the optimism and acceptance of life observed in much of the region's population, along with minimal stress levels, can slow down the biological aging process of the body. Research investigating the genetic basis of longevity among local residents shows that this trait also stems from hereditary factors. Thus, the longevity zones of the Caucasus represent a rare example of the integration of natural, social, and genetic factors.

Traditional nutrition plays an important role in the longevity of the inhabitants of these areas. The diet, mainly consisting of organic, locally sourced foods, includes whole grains, fresh vegetables, fruits, nuts, and dairy products. Fermented foods rich in probiotics, such as yogurt and kefir, also hold significant importance. The predominance of agriculture in the region greatly contributes to the health and longevity of the people of the Caucasus. Daily activities like farming, animal husbandry, and household chores help individuals remain physically active well into old age. Moderate physical activity combined with this constant engagement supports cardiovascular health, muscle strength, and overall resistance to age-related diseases. Importantly, this lifestyle is not intense but consistent, allowing individuals to maintain energy and vitality over decades. While lifestyle and environment are significant, genetic factors also contribute to the longevity of the peoples of the Caucasus. Studies have shown that some populations in the region possess genetic traits associated with resistance to age-related diseases. Additionally, natural therapies complement modern medical treatments, providing a dual approach through the use of natural health remedies.

The longevity zones of the Caucasus offer valuable insights for modern society, serving as a model for achieving better health and longevity through an active lifestyle and strong social connections. As researchers continue to study these areas, they are uncovering ideas that may help combat the increasing prevalence of chronic diseases and improve quality of life on a global scale.

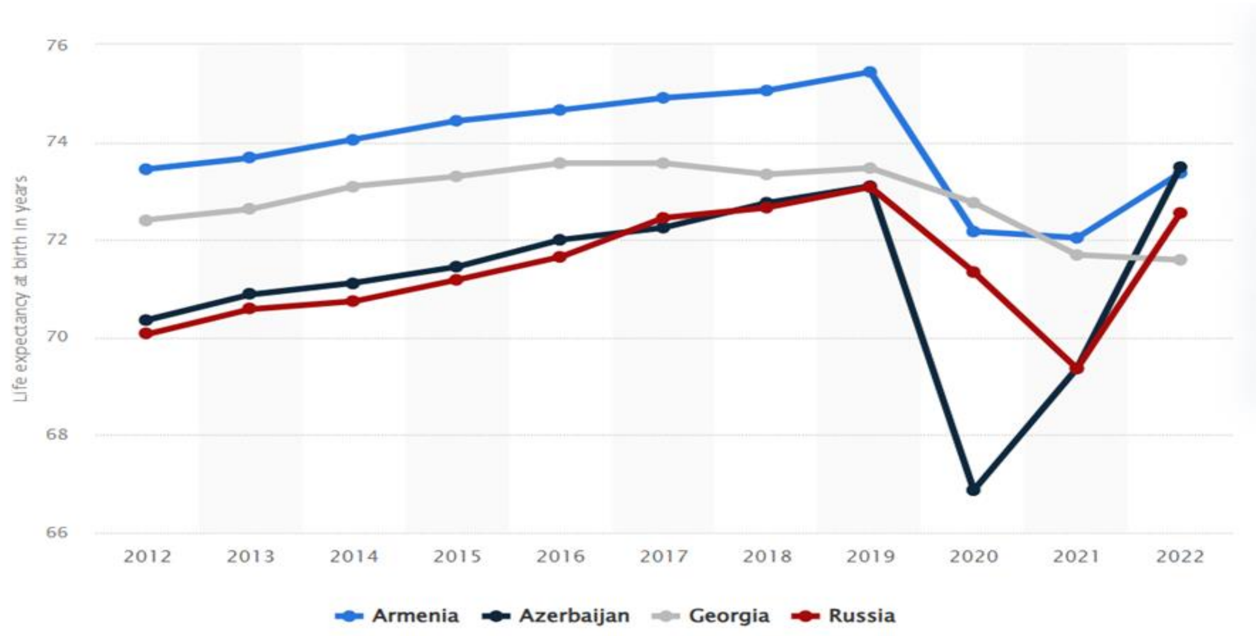

Figure 2. Caucasus countries: Life expectancy at birth from 2012 to 2022 (https://www.statista.com/statistics/980505/life-expectancy-at-birth-in-the-caucasus-countries).

Figure 2 shows the life expectancy at birth for individuals born in the Caucasus region of Asia between 2012 and 2022. Observations and statistical analyses conducted during these years indicate that life expectancy in this area has been higher compared to other regions. This fact further confirms that geographical and ecological factors are directly linked to human health and longevity. Various sources note that the majority of long-lived individuals primarily reside in mountainous and foothill zones. The favorable ecological environment in these areas and the close contact of people with nature positively influence their quality of life.

The overall life expectancy index in the Caucasus region is at a high level. For example, in Dagestan, there are more than 70 long-lived individuals per 100,000 people, whereas this figure is only 6 per 100,000 in the United States. Experiments conducted in our country have also shown that long-lived individuals mainly reside in mountainous and foothill areas. These studies revealed that long-lived people living in these regions have a satisfactory health status and physiological functioning. Their physiological functions remain stable and balanced. The aging process in these individuals progresses relatively slowly, and their adaptability is higher (9).

Conclusion:

Longevity is the result of a complex interaction between genetics, environment, lifestyle, and socio-economic factors. While genetic predisposition lays the foundation for lifespan potential, environmental influences—such as air quality and exposure to pollutants—play a significant role in shaping health outcomes. Lifestyle choices, including diet, physical activity, sleep, and stress management, are among the most modifiable factors and offer the greatest opportunities for intervention to improve both lifespan and quality of life. Advances in medical technology, such as genomic research and exposure biomarkers, further enhance our ability to prevent disease and extend healthy life years.

The Caucasus region exemplifies the impact of environmental and lifestyle factors on longevity. The area's clean air and nutrient-rich food sources contribute to longer lifespans. The region's diverse flora, climate, and soil composition, along with its capacity to support various populations, make it a rich resource for studying human health and aging. The Caucasus is truly a land of longevity, and uncovering the health secrets of its long-lived populations remains a highly relevant scientific endeavor.

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GENETIC CHARACTERISTICS OF OLIVE (OLEA EUROPAEA) AND THEIR IMPORTANCE IN BREEDING PROCEDURES

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Abstract: Olive (Olea europaea L.) is one of the oldest cultivated plants with significant genetic diversity. Studying its genetic characteristics is essential for advancing breeding programs, improving productivity, and developing disease-resistant varieties. Recent progress in genomics and molecular biology has provided a deeper understanding of olive's genetic structure. Techniques such as Simple Sequence Repeats (SSR) and Single Nucleotide Polymorphisms (SNPs) are widely used to investigate genetic variation and optimize breeding strategies. These technologies also play a crucial role in preserving genetic resources and restoring valuable cultivars. This article provides a comprehensive overview of the genetic structure of olives, the use of molecular tools in breeding, and the implications of biotechnological advancements for the future of olive cultivation.

Keywords*:* Olive (Olea europaea), genetic diversity, molecular markers, breeding, SNP and SSR markers, genetic studies

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Introduction:

The olive tree (*Olea europaea L.*) is a highly significant and ancient species, predominantly found in the Mediterranean basin, though its cultivation has spread across temperate regions globally. As one of the oldest cultivated plants, the olive has been a central part of human civilization for thousands of years, offering vital resources for food, medicine, and cosmetics. The fruit, rich in beneficial compounds such as monounsaturated fatty acids, antioxidants, and vitamins, has made olive oil an essential dietary staple, especially in the Mediterranean diet. Moreover, olive oil is widely used in the pharmaceutical and cosmetic industries due to its anti-inflammatory, antimicrobial, and moisturizing properties.

The olive tree is particularly known for its resilience and longevity, with some trees living for centuries, adapting to a wide range of climatic conditions. This adaptability has allowed the olive to flourish in diverse environments, from arid regions to temperate climates, and it thrives in well-drained soils with Mediterranean-type climates, characterized by hot, dry summers and mild, wet winters. However, despite its resilience, olives face various challenges, including pests, diseases, and changing environmental conditions, making the study of their genetic diversity and improvement through breeding even more critical.

Advancements in the fields of genomics and biotechnology have revolutionized the way we study the genetic structure of plants, including the olive tree. The ability to delve into the molecular level of olives has enhanced our understanding of their genetic makeup and provided a powerful tool for their improvement (Baldoni et al., 2019). The use of molecular markers, especially Simple Sequence Repeats (SSR) and Single Nucleotide Polymorphisms (SNP), has enabled scientists to identify genetic differences between various olive varieties (Muzzalupo et al., 2014; Kaya et al., 2013). These markers are pivotal in optimizing breeding programs, enhancing genetic diversity, and developing varieties that are more resistant to diseases, pests, and environmental stresses.

Molecular research methods have become indispensable tools in modern breeding programs, providing precise and reliable methods to track desirable traits such as disease resistance, fruit quality, and yield. For example, SSR markers, due to their high degree of polymorphism and reliability, are commonly used to assess genetic variation within olive populations and identify genetic relationships between different cultivars. On the other hand, SNP markers offer a more refined approach, enabling fine-scale genetic mapping and marker-assisted selection for improving traits related to yield and quality.

Moreover, modern biotechnology and genomics not only play a crucial role in enhancing breeding efficiency but are also central to the preservation of the olive's genetic diversity. As climate change and human activities continue to pose threats to biodiversity, genetic resources are at risk of being lost. The application of genomic tools, such as high-throughput sequencing and bioinformatics, allows for the preservation of the olive's genetic pool by identifying and cataloging valuable genetic traits that can be used in future breeding efforts. In this way, biotechnology also serves as a safeguard for the olive tree's future resilience.

Additionally, the study of the genetic diversity of olives provides critical insights into their evolutionary history and origins. Through molecular studies, researchers have uncovered new evidence regarding the domestication of olives, tracing their origins back to ancient civilizations and offering a clearer picture of their spread and evolution across regions. Understanding the genetic makeup of olives helps clarify their domestication process, providing a framework for identifying and conserving ancient cultivars that hold unique genetic traits.

Overall, the high genetic polymorphism in *Olea europaea* is key to its ability to adapt to a wide range of climatic conditions and soil types. This genetic flexibility not only supports the cultivation of olives in various parts of the world but also allows for the development of new varieties tailored to meet the changing demands of the global market. The vast genetic pool of olives is a resource that continues to fuel innovations in breeding and offers tremendous potential for future improvements.

This paper delves into the genetic diversity of olives, examining the various molecular techniques used to study and enhance their genetic features. It also discusses the significance of these innovations in the context of olive breeding and how modern genomic tools are shaping the future of olive cultivation. Furthermore, it highlights the importance of maintaining genetic diversity in olive trees as an integral part of ensuring their sustainability and resilience in an ever-changing world.

The olive tree (Olea europaea L.) is primarily found in the Mediterranean basin and is one of the most ancient cultivated plants. Its fruits and oil are important in food, medicine, and cosmetics. The tree is known for its longevity and adaptability to various ecological conditions. However, studying its genetic diversity and improving it through breeding are vital to enhance yield and resistance to diseases and pests.

Advancements in genomics and biotechnology have enabled deeper investigations into the genetic features of olives. Modern molecular marker techniques, especially SSR and SNP markers, are extensively used to detect genetic differences among olive varieties and to optimize breeding programs. These tools are also significant in preserving the genetic pool and restoring genetic resources. Understanding olive's genetic makeup also helps clarify its origins and evolutionary history. High genetic polymorphism in Olea europaea facilitates adaptation to diverse climates and soils.

This paper explores the genetic diversity of olives, molecular research methods, and their importance in breeding. Additionally, it discusses how recent genomic and biotechnological innovations are shaping olive breeding processes.

Genetic Structure and Polymorphism

The olive tree (*Olea europaea L.*) is a diploid plant with a chromosome number of 2n = 46, which provides a fundamental framework for its genetic structure. Research has consistently shown that olives possess a high level of genetic diversity, a trait that is essential for their adaptability to various environmental conditions. This genetic variation arises from several key factors, each contributing to the overall polymorphism observed in olive populations.

Geographical Distribution and Environmental Factors: The genetic structure of *Olea europaea* is heavily influenced by the tree's wide geographical distribution. Olive cultivation spans across the Mediterranean basin, as well as parts of Asia, Africa, and the Americas. The variations in climate, including temperature, precipitation, and soil type, play a significant role in shaping the genetic diversity within and among olive populations. For example, olives cultivated in coastal regions may show genetic adaptations to salt tolerance, while those grown in more arid, inland areas exhibit traits that enhance drought resistance (Besnard et al., 2008).

Reproductive Methods: Olives reproduce through both vegetative (asexual) and generative (sexual) methods, and these processes significantly contribute to genetic diversity. Vegetative reproduction, through cuttings, is commonly used in commercial olive orchards, leading to the clonal propagation of specific cultivars. While this method helps maintain desirable traits, it can reduce genetic variability within a given orchard. In contrast, sexual reproduction through seed formation introduces new genetic combinations, fostering a broader range of genetic diversity. FThis dual mode of reproduction enables the olive tree to maintain both stability in its desirable traits and the ability to adapt to changing environments.

Genetic Impact of Wild Relatives: Another significant source of genetic variation in olives comes from wild relatives, especially *Olea europaea* subsp. *sylvestris* (wild olive). These wild populations are considered an essential genetic resource for the cultivation of domestic olives, as they contribute valuable traits such as pest resistance, drought tolerance, and enhanced resilience to environmental stress (Besnard et al., 2008). Crossbreeding between cultivated olives and wild olives can introduce new alleles into cultivated populations, improving the genetic base and ensuring greater adaptability to climate change and other ecological pressures.

This rich genetic diversity plays a crucial role in the olive tree's ability to adapt to diverse environmental stresses, including salinity, drought, extreme temperatures, and pest infestations. The unique combination of traits within local cultivars, shaped by centuries of human selection, regional climate conditions, and environmental pressures, has resulted in a wide array of olive varieties with specialized characteristics. These local varieties not only represent the cultural heritage of different Mediterranean regions but also provide valuable genetic resources that are essential for future breeding programs.

The use of molecular marker techniques, particularly Simple Sequence Repeats (SSR) and Single Nucleotide Polymorphisms (SNP), has greatly advanced the study of olive genetic diversity. SSR markers, known for their high level of polymorphism, allow researchers to distinguish between different cultivars and wild populations by detecting variations in specific regions of the genome. (Muzzalupo et al., 2014). These markers are particularly useful for studying genetic relationships, population structure, and the level of genetic differentiation within olive species. They can also identify genetic bottlenecks or inbreeding within specific populations, which is essential for maintaining genetic health in breeding programs.

On the other hand, SNP markers offer even more precise insights into genetic variation (Kaya et al., 2013; Kaya et al., 2021).By examining individual base-pair changes, SNP markers enable the detection of subtle genetic differences that can be crucial for trait selection in breeding. These markers are particularly valuable in fine-scale mapping of traits like disease resistance, fruit quality, and yield improvement. As SNP-based technology advances, it is increasingly used in marker-assisted selection, speeding up the breeding process and allowing for more targeted improvements in olive cultivars.

Molecular marker techniques are not

only fundamental for understanding the genetic structure of olives but also play an essential role in conservation efforts. By assessing the genetic diversity of wild olive populations and local cultivars, scientists can prioritize conservation strategies to preserve rare or endangered varieties. Furthermore, these tools aid in the restoration of genetic resources, ensuring that valuable traits are not lost in the face of environmental challenges or human-induced changes.

In summary, the genetic structure and polymorphism of *Olea europaea* are shaped by a combination of factors, including geographical distribution, reproductive methods, and genetic contributions from wild relatives. The high genetic variability within olive populations is a key factor in the tree's ability to thrive across diverse ecological conditions. Molecular markers, such as SSR and SNP, are indispensable tools for studying this genetic diversity, allowing researchers to uncover hidden genetic resources and optimize breeding programs for enhanced yield, resilience, and sustainability.

Molecular Markers and Genomic Studies:

The application of molecular tools has enhanced the understanding of olive's genetic diversity. SSR and SNP markers help in identifying the origin and genetic relationships of different cultivars (Muzzalupo et al., 2014; Kaya et al., 2013). Studies show that the genetic structure of olive has been shaped by selective breeding and human intervention (Besnard et al., 2008).

Genomic studies have identified genes that influence stress resistance and productivity. For instance, Ole e1 and Ole e10 genes are associated with allergenicity and oil content (Hernández et al., 2020). These findings contribute to developing improved olive varieties. Further, transcriptome analysis has highlighted gene expression profiles related to lipid biosynthesis, fruit development, and flowering time regulation.

Advanced tools like whole genome sequencing (WGS), genotyping-by-sequencing (GBS), and RNA sequencing have expanded our ability to identify quantitative trait loci (QTLs) linked to economically valuable traits. These discoveries support the development of marker-assisted selection (MAS) strategies (Baldoni et al., 2019; Kaya et al., 2021).

Genetic Diversity and Breeding:

Olive cultivars from regions such as Azerbaijan, Turkey, Spain, and Italy have been subject to different breeding histories and show varying levels of polymorphism. Studies have shown that cultivars from Eastern Mediterranean regions tend to retain more ancestral genetic traits, while. Western populations have undergone more intense artificial selection (Duran Sevin Teoman., Aghayeva Saltanat., 2022).

The main goals in breeding include:

- Enhancing resistance to pests and diseases
- Increasing drought and salinity tolerance
- Optimizing fruit size, oil content, and quality
- Improving growth and reproduction characteristics

Modern technologies like genome editing, especially CRISPR/Cas9, allow for more precise and effective breeding. CRISPR/Cas9 has already been demonstrated to target specific genes such as FAD2, which is associated with fatty acid desaturation, opening possibilities for enhanced oil composition (Kaya et al., 2021).

Somatic embryogenesis, tissue culture, and double haploid technologies are also being explored for clonal propagation and rapid development of homozygous lines. These techniques are essential in accelerating the breeding cycle and developing genetically uniform lines.

Conservation of Genetic Resources:

Conservation of olive genetic resources is vital to maintain biodiversity and ensure food security. Ex situ collections, such as field genebanks and cryopreservation of shoot tips and embryos, are crucial for preserving rare and endemic varieties (Baldoni et al., 2019).

In situ conservation through traditional agroecosystems also plays a key role. Many small-scale farmers maintain landraces with unique traits that are often adapted to local environmental conditions and cultural practices. Preserving this traditional knowledge alongsidegenetic material is essential for holistic conservation.

International collaborations, such as the Olive Germplasm Bank of Córdoba (Spain), contribute to the global efforts of characterization, documentation, and sustainable use of olive genetic diversity (Besnard et al., 2008).

Biotechnological Innovations in Olive Improvement:

The integration of biotechnology in olive breeding has opened new avenues for sustainable agriculture. Technologies such as genetic transformation using Agrobacterium tumefaciens, RNA interference (RNAi), and gene silencing have been investigated to improve traits like oil stability, pathogen resistance, and abiotic stress tolerance (Baldoni et al., 2019; Kaya et al., 2021).

Nanotechnology is an emerging area in plant biotechnology with potential applications in olive cultivation. Nanofertilizers and nanopesticides are being studied to reduce chemical usage and environmental impact while enhancing nutrient uptake and plant protection.

Bioinformatics and machine learning tools are increasingly used to analyze large genomic datasets, predict gene functions, and model phenotypic responses. These computational approaches can guide precision breeding and decision-making in cultivar selection (Zulfiqar Saman et al., 2025).

Conclusion

The genetic characterization of *Olea europaea* plays a crucial role in preserving biodiversity, enhancing breeding programs, and ensuring sustainable cultivation practices. Advances in molecular genetics-especially the use of SSR and SNP markers-have significantly deepened our understanding of the olive's genetic diversity and evolutionary history (Muzzalupo et al., 2014; Kaya et al., 2013). The identification of genes responsible for key agronomic traits, such as oil composition, stress resistance, and adaptability, has opened new avenues for targeted breeding and conservation efforts (Hernández et al., 2020; Baldoni et al., 2019).

Moreover, the integration of modern biotechnological approaches, including whole genome sequencing, genotyping-by-sequencing, and CRISPR/Cas9 genome editing, offers unprecedented precision in developing superior olive cultivars (Kaya et al., 2021; Baldoni et al., 2019). These technologies facilitate the selection and enhancement of desirable traits without compromising genetic diversity-an essential requirement for the long-term sustainability of olive cultivation.

The conservation of wild and local olive populations remains a strategic priority. These gene pools are indispensable for maintaining genetic resilience and for adapting to the challenges posed by climate change, pests, and diseases (Besnard et al., 2008; Duran Sevin Teoman., Aghayeva Saltanat, 2022). Thus, integrating classical breeding methods with molecular and genomic tools will accelerate the development of high-yielding, resilient, and high-quality olive varieties.

Future research should focus on:

- Completing high-resolution genome sequencing for a broader range of cultivars (Baldoni et al., 2019),
- Applying genome editing tools (e.g., CRISPR) in practical breeding (Kaya et al., 2021),
- Expanding germplasm collections and encouraging international collaboration for conservation (Besnard et al., 2008).

Ultimately, a multidisciplinary approach-combining genetics, biotechnology, and ecological conservation-will ensure the effective utilization and preservation of olive genetic resources for future generations.

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