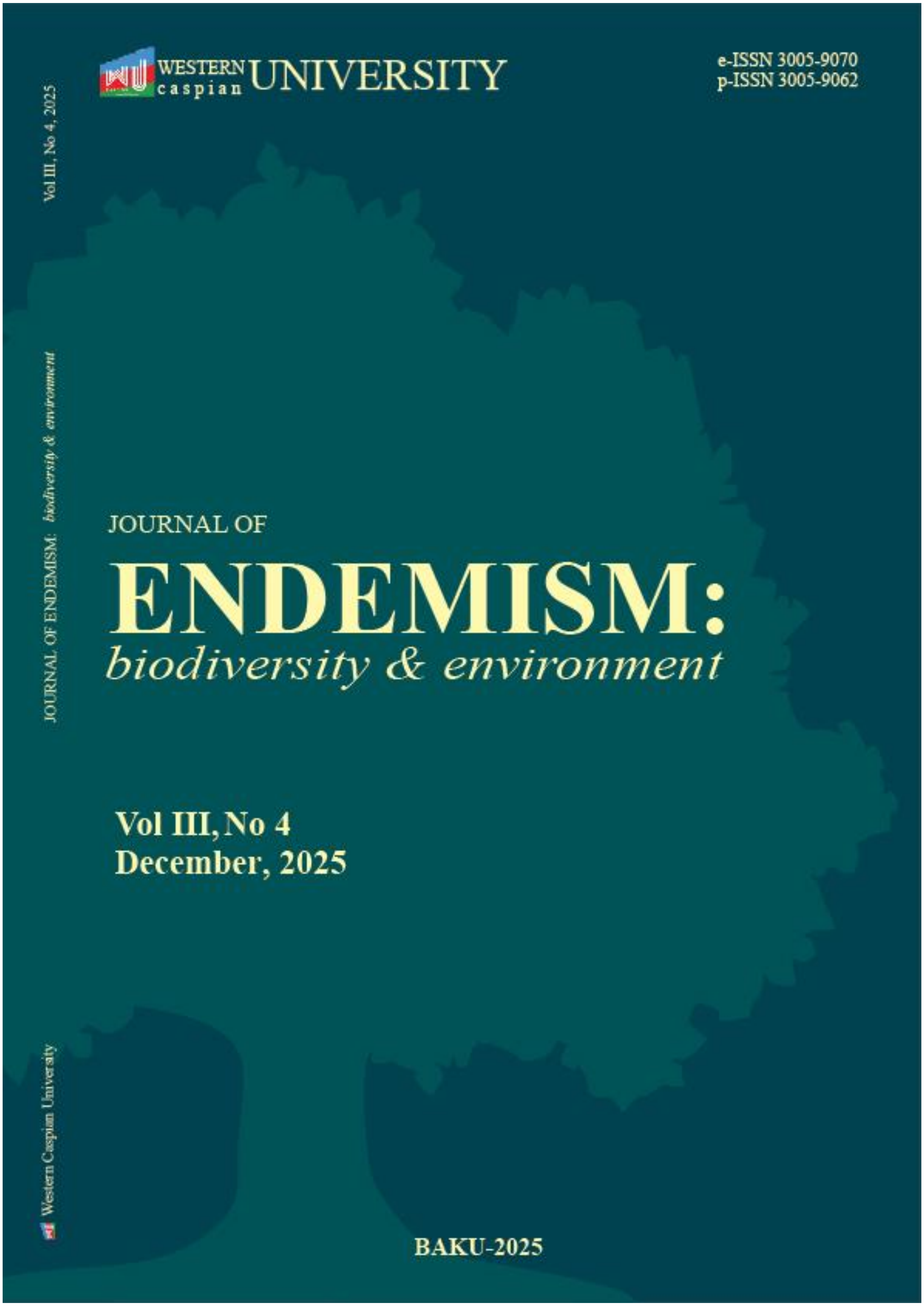

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GENETİCS OF CASPİAN SEA FİSH SPECİES

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Abstract: The Caspian Sea, the world's largest enclosed body of water, hosts a diverse and unique fish fauna, particularly the economically valuable sturgeons (e.g., *Huso huso*, *Acipenser gueldenstaedtii*), adapted to its unique brackish environment. Understanding the genetic composition of these fish is vital for studying their evolutionary adaptations and population dynamics.Genetic studies reveal features such as polyploidy in sturgeons, which contributes to high genetic variability, and osmoregulation genes which enable adaptation to fluctuating salinity. However, overfishing, pollution, and climate change are causing genetic erosion and population decline in these species.This research aims to assess the genetic diversity of key Caspian Sea fish species and to propose effective conservation and management strategies based on genetic findings. Utilizing molecular markers like mtDNA researchers can identify genetic bottlenecks and ensure the sustainability of the Caspian Sea's unique ichthyofauna.

Keywords: Caspian Sea, sturgeon (*Acipenseridae*), genetic diversity, conservation, polyploidy

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Introduction:

The Caspian Sea, the largest inland body of water on Earth, is a distinct and ecologically important ecosystem that supports a diverse range of fish species. Its semi-isolated nature and fluctuating salinity levels have facilitated the development of unique genetic adaptations in the fish populations. Understanding these genetic traits is essential for studying species diversity, the evolutionary processes, and the ecological stability of the region. Furthermore, many fish species in the Caspian Sea are of significant economic and cultural value, with sturgeons, renowned for their caviar production, being a prime example. Unfortunately, human activities such as overfishing, pollution, and habitat destruction pose serious threats to these species, underscoring the importance of genetic research for conservation efforts. By examining the genetic makeup of Caspian Sea fish, researchers can better understand their adaptability, population trends, and devise strategies for their sustainable management [12].

1. Caspian Sea Fish and Their Names:

The Caspian Sea, the largest enclosed inland body of water on the planet, is home to a wide range of fish species that have evolved in response to its unique and brackish waters. Its semi-isolated environment has fostered the adaptation of various fish species to the specific ecological conditions found in the region.

Spanning around 390,000 km² with a water volume of 78,700 km³ and a coastline of 7,000 km, the Caspian Sea plays a vital role in regional biodiversity, ecology, and fisheries [12]. Unlike typical seas, the Caspian Sea is a remnant of the ancient Paratethys Ocean, which became increasingly isolated due to tectonic activities. It is divided into three main areas:

The Northern Caspian, which is shallow and rich in nutrients; the Middle Caspian, which has moderate depths; and the Southern Caspian, which reaches depths exceeding 1,025 meters [4].

The Caspian Sea is home to a wide variety of fish species, many of which are either endemic or of considerable commercial value. With more than 155 fish species recorded, it serves as a crucial hub for both freshwater and marine-origin species [4]. Notably, sturgeons (Acipenseridae) are among the most important, as they have been heavily exploited for caviar production. Other significant species include herrings, gobies, and cyprinids, all of which play vital ecological and economic roles [1]. Despite the Caspian's rich biodiversity, its fish populations are under intense pressure from overfishing, habitat degradation, and pollution, highlighting the urgent need for conservation efforts.

According to a review of existing literature, the current ichthyofauna of Azerbaijan consists of 113 species and subspecies of cyclostomes and fish, distributed across 13 orders, 18 families, and 56 genera. Among the most commercially valuable fish species are the Russian and Kura sturgeons, as well as various other sturgeon species, asp, Caspian roach, common carp, shemaya, Caspian shad, and others, whose life cycles are intricately tied to freshwater ecosystems. These fish predominantly reside in and grow within the Caspian Sea, but they migrate to riverine habitats for spawning [11].

Some of the most notable fish species from the Caspian Sea include:

Beluga Sturgeon (Huso huso) – One of the largest freshwater fish in the world, renowned for its high-quality caviar production.

Russian Sturgeon (Acipenser gueldenstaedtii) – Another significant sturgeon species, highly prized for its roe.

Persian Sturgeon (Acipenser persicus) – Endemic to the Caspian Sea, playing a crucial role in the caviar industry.

Caspian Roach (Rutilus caspicus) – A common species found in both the freshwater and brackish areas of the sea.

Caspian Salmon (Salmo trutta caspius) – A subspecies of trout native to the Caspian region.

Caspian Kutum (Rutilus kutum) – A commercially valuable fish in local markets.

Northern Pike (Esox lucius) – A carnivorous fish found in the Caspian region.

Zander (Sander lucioperca) – A predatory fish widely distributed throughout the Caspian basin.

These species have evolved unique genetic traits that allow them to thrive in the Caspian Sea's variable salinity and temperature conditions [1], [12].

2. Structure of Caspian Sea Fish:

The structure of fish in the Caspian Sea varies according to their ecological roles and evolutionary adaptations. These fish can be classified based on their skeletal structure, body shape, and specific environmental adaptations.

Skeletal Structure: The majority of Caspian Sea fish possess either cartilaginous (e.g., sturgeons) or bony (e.g., roach, kutum) skeletal systems. Sturgeons, being ancient species, have partially cartilaginous skeletons, which provide flexibility that is beneficial in deep water environments [7].

Body Shape and Adaptations: For instance, the beluga sturgeon has a long, streamlined body that facilitates efficient navigation in deep waters. On the other hand, smaller species like the Caspian roach have a more compact body structure, suited to living in shallow, brackish waters [7].

Fins and Movement: Species like the Caspian salmon, which are fast swimmers, possess streamlined bodies and strong caudal fins that assist in long-distance migrations. In contrast, bottom-dwelling species like sturgeons have ventral mouths and barbels, specialized for detecting food along the sea floor [4].

Respiration and Circulatory System: Caspian Sea fish rely on their gills to extract oxygen from the water. Some species, such as sturgeons, have adapted to low-oxygen environments by developing efficient gill structures and unique hemoglobin variations, which enhance their ability to absorb oxygen.

The Caspian Sea is home to a diverse range of fish, each of which exhibits unique anatomical and morphological features. Below is a summary of some notable species and their specific structural adaptations [10].

1. Sturgeons (Family: Acipenseridae):

Russian Sturgeon (*Acipenser gueldenstaedtii*): Characterized by a cartilaginous endoskeleton and a series of bony scutes along the body, sturgeons have a heterocercal tail and an elongated snout equipped with barbels for detecting prey on the substrate [10].

Persian Sturgeon (*Acipenser persicus*): Similar in morphology to the Russian sturgeon, this species exhibits slight variations in scute patterns and snout length.

2. Caspian Shad (*Alosa caspia*):

This clupeid fish possesses a deep, laterally compressed body with long, thin gill rakers that are notably longer than the gill filaments. The species typically displays a black spot posterior to the gill opening, with occasional additional spots along the flank [6].

3.Caspian Salmon (*Salmo ciscaucasicus*):

Endemic to the Caspian Sea, the Caspian salmon can reach lengths up to 130 cm. It exhibits a streamlined body adapted for both lacustrine and anadromous lifestyles, with morphological forms varying between migratory and resident populations [14].

4. Gobies (Family: Gobiidae):

Round Goby (*Neogobius melanostomus*): This species exhibits alternative reproductive tactics, with males displaying a prominent mesorchial gland—a pheromone-releasing connective tissue structure attached to the testes, influencing reproductive behavior [9].

5. Caspian Lamprey (*Caspiomyzon wagneri*):

An endangered species, the Caspian lamprey exhibits at least two morphological forms with significant morphometric differentiation across rivers in the southern Caspian Sea basin. These variations are crucial for conservation strategies [5].

3. Genes Located in These Fish:

The genetic composition of Caspian Sea fish species has been extensively researched to understand their evolutionary adaptations, physiological functions, and conservation status. Sturgeons and other endemic fish species exhibit complex genetic structures that contribute to their unique biological characteristics.

Polyploidy in Sturgeons: Sturgeon species are known to exhibit polyploidy, a condition in which they have multiple sets of chromosomes. For example, the Beluga sturgeon (*Huso huso*) possesses between 270 and 290 chromosomes. This genetic trait contributes to their high genetic variability and adaptability to a wide range of environmental conditions. It is hypothesized that polyploidy enhances physiological resilience, growth potential, and reproductive flexibility.

Osmoregulation and Salinity Adaptation: Caspian Sea fish species carry genetic markers that regulate ion transport, a key process for osmoregulation in environments with varying salinity levels. Specific genes, such as those encoding Na+/K+-ATPase, aquaporins, and solute carrier proteins, play crucial roles in maintaining ionic balance, especially for anadromous species like the Caspian salmon (*Salmo trutta caspius*), which migrate between freshwater and marine environments.

Growth and Developmental Genes: The regulation of somatic growth in Caspian Sea fish is influenced by important hormonal genes, including those for growth hormone (GH) and insulin-like growth factor (IGF). These genes regulate metabolic processes, skeletal development, and reproductive maturity, particularly in commercially significant species like the Persian sturgeon (*Acipenser persicus*).

Reproductive and Caviar-Related Genetic Markers: The reproductive physiology of sturgeon species is controlled by the expression of zona pellucida (ZP) genes, which are essential for ovarian follicle development and egg formation. These genetic factors are crucial for caviar production, making them a primary focus in both aquaculture and genetic conservation efforts.

Disease Resistance and Immunogenetics: The immune response in Caspian Sea fish is largely mediated by genes within the major histocompatibility complex

(MHC), which encode proteins responsible for antigen presentation and immune recognition. Variability in MHC alleles has been linked to pathogen resistance, a critical factor for population sustainability and the viability of aquaculture.

Mitochondrial DNA and Conservation Genetics: Mitochondrial DNA (mtDNA) and microsatellite markers are widely used in genetic studies to assess the population structure, phylogenetic relationships, and genetic diversity of Caspian fish species. These molecular markers are vital for identifying genetic bottlenecks, hybridization events, and evolutionary paths, providing valuable insights for developing effective conservation strategies.

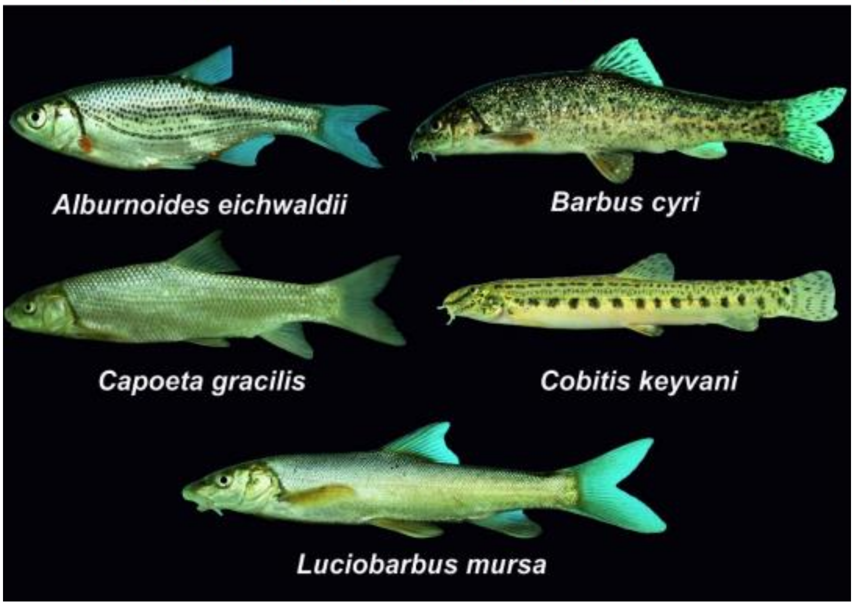
Biodiversity in fish species

Genetic research in marine biology is essential for understanding population dynamics, species adaptation, and developing effective conservation strategies. Modern genetic studies provide valuable insights into species differentiation, evolutionary history, and genetic diversity, which are crucial for managing fisheries and protecting endangered species. By analyzing DNA sequences, scientists can trace gene flow, detect hybridization, and evaluate the genetic health of populations.

Mitochondrial gene analysis involves studying the DNA in mitochondria, which is maternally inherited and used in genetic research due to its small size and high mutation rate. Mitochondrial DNA, particularly genes like 12S and 16S rRNA, is valuable for determining species' genetic relationships, evolutionary history, and species identification. These genes evolve faster than nuclear DNA, making them effective for differentiating closely related species and analyzing phylogenetic patterns. Mitochondrial DNA 16S rRNA gene analysis is a direct approach for differentiating marine animals, plants, and bacteria. mtDNA 12S and 16S rRNA genes have been widely used as molecular markers for categorizing mammals, birds, shrimp, and other species These genes show high variability compared to other markers, as the region is highly conserved Greig et al. (2005) used mtDNA 12S and 16S rRNA markers in North Atlantic Ocean sharks and found less sequence variability within species compared to between species, suggesting these markers are suitable for species identification. Due to the conserved nature of mitochondrial ribosomal genes, they are significant as genetic markers for closely related species. Therefore, the genetic relationships of selected marine fish species were studied and characterized using partial sequences of mtDNA 12S and 16S rRNA genes [8].

In the Caspian Sea**,** genetic research holds particular significance due to the sea's semi-enclosed and isolated nature, which limits genetic exchange with other marine systems. The use of molecular markers, mitochondrial DNA (mtDNA) analysis, and next-generation sequencing (NGS) has enabled researchers to study fish populations with greater accuracy, uncovering genetic bottlenecks caused by overfishing and habitat fragmentation (Esmaeili et al., 2014). Moreover, genetic research helps distinguish endemic species from invasive ones, providing critical information for fisheries management and conservation policy development [2].

The fish fauna of the Southern Caspian Sea Basin (SCSB) has been studied for over 200 years, yet new species continue to be discovered and renamed. This updated checklist, based on historical records and recent collections, lists 119 species across 63 genera, 18 families, and 16 orders. Of these, 19 species are exotic, belonging to seven families. The number of species surpasses previous checklists from 1988 (74 species, 42 genera) and 2010 (116 species, 61 genera). Fish taxa were categorized into four main groups, based on origin, ecoregion, and ecological factors such as saltwater tolerance and lifestyle. Two new species have been described since 2010, and some species' taxonomic statuses have been revised, with subspecies elevated to full species status. The region's high ichthyodiversity results from its ancient Paratethys origin, the closing of the Tethys Sea, glacial refugia, historical connections to fresh and marine waters, diverse species sources, varying latitudinal extent, and a mix of habitats, including fresh and brackish environments [3].



Iranian Journal of Ichthyology (September 2014), 1(3): 152-184

The Caspian Sea harbors one of the most genetically diverse fish populations globally. This diversity is attributed to its complex geological history, fluctuations in salinity, and varied ecological niches [12]. Major species, such as sturgeons (*Acipenser gueldenstaedtii*, *Acipenser stellatus*), herrings (Clupeidae), gobies (Gobiidae), and cyprinids (Cyprinidae), display distinct genetic lineages, reflecting their adaptation to diverse environmental conditions [1].

Historical events**,** such as glaciations, sea level changes, and tectonic shifts, have had a profound impact on the genetic diversity of Caspian fish species. These events have led to periods of isolation and reconnection of fish populations, resulting in the development of unique genetic adaptations [4]. Furthermore, the introduction of exotic species has influenced the genetic makeup, occasionally leading to hybridization and competition with native species.

Despite this genetic richness, many fish populations in the Caspian Sea have suffered significant genetic erosion due to human activities. Habitat fragmentation, overfishing, and pollution have led to a reduction in genetic variability, making species more susceptible to diseases and environmental changes [12]. Understanding these genetic patterns is critical for developing effective conservation and restoration programs.

The genetic diversity of Caspian fish species is under significant threat from anthropogenic factors. Overfishing, particularly of sturgeons for caviar, has sharply reduced wild populations, raising concerns about genetic bottlenecks and inbreeding [4]. Many species are now classified as endangered or critically endangered, with some populations nearing extinction.

Another major threat is pollution**,** primarily from oil extraction, industrial waste, and agricultural runoff. The Caspian Sea, surrounded by oil-rich nations, has been subjected to hydrocarbon pollution, which has been linked to genetic mutations and reproductive failures in fish populations [1]. Additionally, plastic pollution and heavy metal contamination contribute to genetic damage and reduced survival rates.

Climate change is further reshaping the genetic landscape of Caspian fish populations. Increasing temperatures, fluctuating water levels, and changes in salinity affect reproduction and migration patterns of fish species [12]. These environmental stressors, combined with habitat destruction, are accelerating the loss of genetic diversity, emphasizing the urgency of conservation efforts.

Despite significant progress in genetic research, many knowledge gaps remain concerning the genetic structure and adaptive mechanisms of Caspian fish species. While some studies have focused on phylogenetic relationships and population genetics, there is limited research on how genetic diversity impacts species resilience to environmental changes [4].

Furthermore, most genetic studies have focused on commercially valuable species like sturgeons, leaving many smaller, ecologically important fish species understudied [1]. Further research is required to understand the effects of invasive species on native fish genetics and how conservation strategies can be optimized using genomic data.

The primary objective of this study is to assess the genetic diversity of key fish species in the Caspian Sea, identify genetic markers of conservation concern, and propose management strategies based on genetic findings. By filling these research gaps, this study aims to contribute to sustainable fisheries, biodiversity conservation, and ecosystem resilience in the Caspian region [4].

Conclusion:

The genetic study of Caspian Sea fish species provides significant insights into their adaptation, evolution, and conservation. Understanding their genetic structure helps in the management of fish populations, particularly for commercially valuable species like sturgeons, which are threatened by overfishing and habitat degradation. Genetic research continues to play a crucial role in ensuring the sustainability of these unique aquatic species in the Caspian ecosystem [13].

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GENETIC POLYMORPHISM TNF- α GENE OF GUM DISEASE IN PATIENTS WITH DIABETS MELLITUS (TYPE2)

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Abstract: Approximately 400 million people worldwide suffer from diabetes, and this number will increase by about 50% by the year 2030. Gingivitis, is a gum disease of the teeth, which is part of the periodontium, supports the teeth. It is estimated that severe periodontal disease affects about 19% of the world's adult population and represents more than 1 billion cases worldwide. In the description WHO Oral Health Status Report (2022) poor oral hygiene and tobacco use are the most common factors for periodontal disease. There is evidence that there is an association between these two chronic conditions. Although studies have been conducted on the immune system and its components, mechanisms have not been fully understood. This article will discuss associations between diabetes and oral health, focusing on periodontal diseases, find relation genetic polymorphism in TNF-alpha gene.

Keywords*:* diabetes, gum disease, diabetus mellitus type 2, TNF-α gene, genetics of diabetes

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I. Introduction

Gingivitis is an inflammatory disease of the gum tissue, which is a component of the periodont that surrounds the tooth. Although the etiology includes the microflora of the oral cavity, changes in the body's metabolism and external environmental factors increase the risk of disease. We can see the most prominent effect of metabolic dysfunctions in the case of diabetes. Diabetes is a disease that is common against the background of hyperglycemia due to lack or lack of insulin hormone or inability to use it. In 1998, 4 types of forms were approved by the American Diabetes Asossation. Of these, although idiopathic and gestational diabetes are less common, type 1 and Type 2 have become a kind of epidemic [1]. It should also be noted that, in 1935 Hinsworth identified 2 types of diabetes, for almost 2000 years it has been identified as just 1 disease. Both common types of diabetes are characterized by a persistent increase in its glucose in the blood plasma, but type 1 diabetes (T1D) is an autoimmune disease that causes the complete loss of insulin-producing cells in the pancreatic islets, type 2 diabetes (T2D) occurs due to increased resistance to insulin circulating in target tissues (especially muscle, liver and fat) despite insulin secretion from the islets [2].

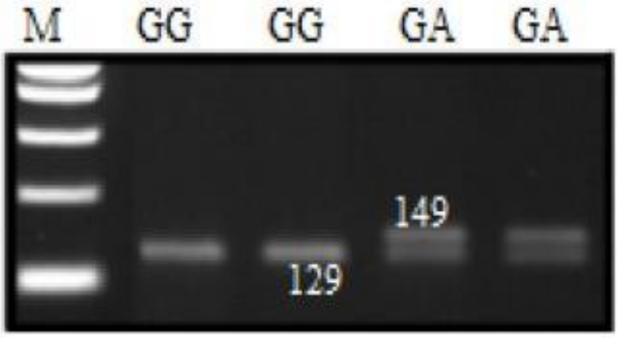
Etiopathogenesis of gingivitis

Quantitatively hundreds of thousands of bacteria colonize the oral cavity in lifetime [3]. The quantitative balance, which changes due to the existing status of the organism, does affect the soft tissues of the oral cavity including the gingiva. Mainly gram negative and gram positive bacteria are responsible for inflammation of the gum tissue. These bacteria secrete lipopolysaccharide endodoxins, stimulating magrophages that cause gingival destruction, synthesizing interleukin-1 beta (IL-1β), tumor necrosis factor-alpha (TNF-α), prostaglandin E2 (PGE2) [4]. Hyperglycemia in diabetes has been shown as an important risk factor for the manifestation of vascular complications. The five classic complications associated with T2D include retinopathy, neuropathy, nephropathy, cardiovascular complications (coronary arterial disease, stroke, and peripheral vascular disease), and chronic wound healing. Periodontal disease has recently been recognized as the *"sixth complication"* of type 2 diabetes [5] . As a manifestation of this complication, we can see accumulation non-enzymatic glycolysis products (AGE-advanced glycation end-products) and activation of sensitive receptors (RAGE – receptor advanced glycation end-products). These receptors are located on neutrophils and macrophages, which provide stimulation of phagocytic activity during inflammation. Under the influence of diabetes, proteins such as collagen, lipids, nucleic acids ,entering into non-enzymatic glycolysis and oxidation with aldose sugars, configuring irreversible molecular structure, which accelerates vascular wall permeability, immune response IL-1 and TNF-α hyperactivity, synthesis of IgA and IgG, leading to intensive disintegration of gums and surrounding tissues [6].

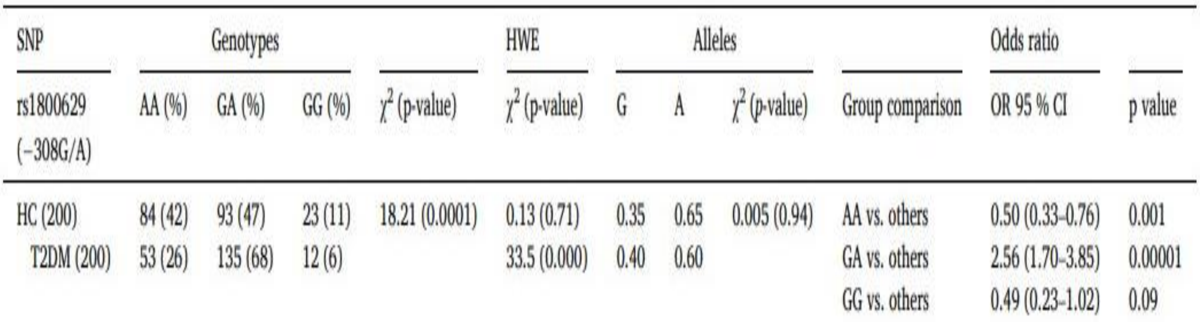
II. The role of TNF-α

TNF-α is mainly produced by macrophages. It is an effective immuno-inflammatory mediator and can promote bone resorption by activating the maturation of osteoclasts (bone-destroying cells). Stimulates the production of related cytokines, increases the adhesion expression of molecules, promotes the activation of neutrophils and T cells. It plays a key role in the pathogenesis of some serious chronic inflammatory and autoimmune diseases [7]. A Meta-analysis showed that TNF-alpha can be used as an additional criterion for a more accurate diagnosis of periodontal inflammation. Single nucleotide polymorphisms SNPs are the most common type of genetic variation in humans.. Studies have shown that single nucleotide polymorphisms, specifically the transition from G to A at position 308, increase TNF-a production fivefold in vitro [8]. Tumor necrosis factor alpha (TNF-α) is a proinflammatory cytokine that has an important role in the pathogenesis of a several diseases. The gene encoded by is located on the short arm of chromosome 6p21.3 (Figure 1), in the region of the main histocompatibility complex (MHC)Class III. Most TNF-α gene polymorphisms are located in its promoter region and are believed to affect the susceptibility

or severity of various human diseases. This review summarizes data on the relationship between the TNF-α gene and its receptor polymorphisms and the development of autoimmune diseases. Genetic changes in the promoter region can regulate TNF-α production, transcription, and affect susceptibility to inflammation-related diseases.



Some studies have investigated single nucleotide polymorphisms in the promoter region of the TNF gene, such as 238G/A, 308G/A, 857C/T, and 1031T/C in humans. *Although several studies have focused on the relationship between the TNF-α-308g/a polymorphism and T2DM, their results remain uncertain, leading to the need for further research.* It plays a central role in the development of T2DM, according to research by Feng, Y.Li, and others [9]. Swetha Chikoti, Umme Najiya and others was determined polymorphism of the TNF-alpha gene -308 G/A according to a study of 400 patients in the southern Indian population. As a result among 200 T2DM and 200 control patients, gender, age, sugar, cholestorol values were studied and statistical analysis was carried out. Genotyping was studied at these loci −238G/A; rs361525 and −308G/A; rs1800629. gel-agarose results of the rs1800629 locus GG / 129 n.c. GA / 149 n.c. (Figure 1) are monitored. Allele and genotype frequencies for all SNPs were calculated using the Chi-square criterion [χ2] to estimate intergroup significance. The risk of disease by genotype was determined by determining the odds ratio (OR) with a confidence interval (CI) of 95%, respectively (Figure 2). The G / A genotype increased more than 2 times (1.70-3.85) in relation to others [10].



SNP	Genotypes				HWE	Alleles				Odds ratio	
rs1800629 (−308G/A)	AA (%)	GA (%)	GG (%)	χ^2 (p-value)	χ^2 (p-value)	G	A	χ^2 (p-value)	Group comparison	OR 95 % CI	p value
HC (200)	84 (42)	93 (47)	23 (11)	18.21 (0.0001)	0.13 (0.71)	0.35	0.65	0.005 (0.94)	AA vs. others	0.50 (0.33-0.76)	0.001
T2DM (200)	53 (26)	135 (68)	12 (6)		33.5 (0.000)	0.40	0.60		GA vs. others	2.56 (1.70-3.85)	0.00001
									GG vs. others	0.49 (0.23-1.02)	0.09

It has been widely researched that Periodontal disease is one of the main causes of tooth loss in people with diabetes. Individually, many mechanisms have been proposed that explain the increased susceptibility to periodontal disease in patients with unchecked T2D, including changes in collagen metabolism and vascular wall. In addition, poorly controlled T2D patients show an excessive inflammatory reaction to the bacterial hazard of periodontitis. Such hypersensitive reactions lead to a delay in the regeneration of intra-oral tissues, the completeness of which is impaired against the background of increased inflammation, as well as to the degeneration of periodontal tissues [11]. A small percentage of non-autoimmune diabetes (5% or less) is caused by monogenic causes and is classified as juvenile or MODY(monogenic diabetes of the young) monogenic diabetes. These changes are caused by individual high penetrance genes, in which mutations in the nuclear factor-1a (HNF-1a) and Glucokinase (GCK) gene of hepatocytes are most common. These forms of diabetes are sometimes mistaken for T2D, but they are different diseases in terms of their clinical course. Decommunization is important, considering that the boundaries between polygenic and monogenic forms are not always clearly defined at the genetic level [12]. Poulami, Keheibamding and their colleagues found that single nucleotide polymorphism of this gene (TNF-afla) is found in the aggressive course of gum disease. So, as a result of research on 397 people, SNPs were detected. In this study, 40 people were identified as patients with aggressive periodontitis, 157 as patients with chronic periodontitis, and 200 as healthy controls. The study, conducted among both women and men of different age groups (Table 1), characterizes the population of the East-India region. Five SNPs of the promoter site of the TNF-alpha gene, (rs361525, rs1800629, rs1799724, rs1800630 and rs1799964) were genotyped by PCR sequences in patients with periodontitis and control group. The aim is to find out the relationship of polymorphisms of the TNF-alpha gene with both chronic and aggressive periodontal diseases in the Indian population and to analyze the combination and distribution of haplotypes in acute and chronic periodontitis in both populations of patients.

As a method, the current state of the oral cavity of individuals in this population including gingiva and bone melting was evaluated and indexed by evaluating gingival pockets on all teeth, (Table 2) and on the gene-238G/A (rs361525) polymorphism F-5` CAGTGGGGTCTGTGAATTCC3` R-5`TCCCTCTTAGCTGGTCCTCT3`,-308G/A(rs1800629) F-5` CAGTGGGGTCTGTGAATTCC3` ; R-5`GGGCGGGGAAAGAATCATTC3`, -857C/T (rs1799724) F-5` CTGCTTGTGTGTGTGTGTCT 3` R-5` CCGGAGACTCATAATGCTGGT3` -863C/a (rs1800630) and - 1031T/C (rs1799964) respectively F-5` GTGTGTGTCTGGGAGTGAGA3`; R-5` GCAGGCCTTCTTCTTCATTCT3`, F-5` GAGAGAAAGAAGTAGGCATGAGG3` R-5` TCTTAAACGTCCCCTGTATTCCA3` amplified by PCR method using primer sets.

Parameters	*AP*	*CP*	*Kontrol*	*AP vs Control (Pvalue)*	*CPvsControl (Pvalue)*
Age (year)	17-44	22-69	24-65		
Average	30,23± 6,81	41,59± 11,12	38,41± 9,48	0.0001	0.0038
Man(%)	60	65,33	47,5	0,1515	0,0016
Woman(%)	40	34,67	52,5	ref.	ref.

Table 1. Age, gender parameters of patients in the study (AP-agressive periodontitis, CP-chronic periodontitis, P<0,05)

Parameters	Aggressive periodontitis	Chronic periodontitis	Control
GP *(all teeth,ave. ±mm)*	6.01± 1.94	6.36 ±1.62	0.34 ±0.66
BR *(ave. ±mm)*	8.3±2.21	8.79±1.94	0.03±0.21
DI	2.83±1.08	2.95±0.81	0.05 ±0.2
GI	3.05 ±0.85	2.61±1.01	0.01±0.08

P value <0,05

Table 2. Gingiva rates in patients (GP-gingival pocket, BR-bone resorbtion, TP-tooth plaque index, Gİ-gingival index)

Amplified solutions were electrophoresized in 2-3% agarose gel. The PCR products were sequenced (by the Sanger method) by the Prism 3100 DNA Genetic Analyzer (biosystem, Carlsbad, CA, USA).

The difference between clinical parameters was assessed using a single - factor analysis-ANOVA. Age, gender, ethnicity, smoking, chewing tobacco, and the habit of drinking tea have been used as independent variables for their multiple analysis. All statistical analyses were performed with commercially available SPSS software (version 16.0, SPSS Inc., Chicago, Illinois, USA).

Genotypes – 238 G/A (rs361252) and – 308G/A in the AP population as well as polymorphisms-308G/A and-1031T/C (rs1799964) in the CP community are interrelated and are likely to be passed down from generation to generation. The genotype level of TNF-alpha-308 G/A (rs1800629) was significantly higher in patients with both AP and CP compared to healthy control groups [13]. Several studies have been conducted to assess the relationship between TNF-a promoter polymorphisms and periodontitis in different populations, but this is still a matter of controversial discussion [14,15]. There are several contradictions regarding the TNF-a gene as a candidate for genetic studies related to gingivitis and complications. There is reason to believe that the TNF-a gene plays an important role in the pathogenesis of periodontitis, since it is a powerful immunological mediator with anti-inflammatory properties [16].

III. Conculusion

Consequently, the TNF-alpha gene, which controls inflammatory processes and plays a leading role in the formation of immune response reactions, manifests itself with complications when exposed to polymorphism of the promoter region -308 G/A in both patients with gingivitis and patients diabetes mellitus with poor sugar control.

Abbreviation: T2DM - type2 diabetus mellitus, TNF -tumor necrosis factor, HWE - Hardy-Weinberg Equilibrium

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DESCRIPTION OF THE BIOLOGICAL CHARACTERISTICS OF LEMON (Citrus lemon L.)

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Abstract: Lemon (*Citrus limon* L.) is a valuable fruit known for its rich phytochemical composition and wide range of biological activities. Its fruit, peel, and seeds contain diverse bioactive compounds, including flavonoids (hesperidin, diosmin, eriocitrin), phenolic acids (ferulic, caffeic, sinapic), essential oils (D-limonene, β-pinene, γ-terpinene), vitamin C, carotenoids, and pectins. These constituents contribute to the fruit's potent antioxidant, antimicrobial, anti-inflammatory, and anticancer properties. Lemon extracts exhibit strong inhibitory effects against pathogenic microorganisms such as *Staphylococcus aureus*, *Escherichia coli*, and *Candida albicans*, acting as a natural antimicrobial agent. The antioxidant potential of lemon is attributed to its high flavonoid and phenolic content, which neutralizes free radicals and mitigates oxidative stress. Moreover, compounds like D-limonene and limonoids demonstrate anticancer potential by suppressing tumor growth and promoting apoptosis in malignant cells. Due to these multifaceted properties, lemon and its derivatives are extensively applied in the food industry as natural preservatives and in cosmetology as antioxidant, anti-inflammatory, and skin-brightening agents. An evaluation based on international descriptors further supports the significance of lemon as a functional fruit with considerable nutritional, medicinal, and industrial value.

Keywords: Lemon, biological characteristics, phytochemical composition, antioxidant, antimicrobial, pharmacological effect, food industry, cosmetology, hybrid lemons.

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Introduction:

The taxonomy and phylogeny of citrus are highly complex, controversial, and confusing. This is mainly due to the sexual compatibility between Citrus and related genera, the high frequency of bud mutations, and the long history of cultivation and wide distribution (Nicolosi et al., 2000). In addition, the level of variation among citrus species and their precise species status have not yet been fully determined. In the past, citrus taxonomy was primarily based on morphological and geographical characteristics, and numerous classification systems were developed. Among these, the systems proposed by Swingle & Reece (1967) and Tanaka (1977) are the most widely accepted.

Lemon (*Citrus limon*) is a plant species belonging to the Rutaceae family, naturally distributed in India, China, and South Asia. It has been used since ancient times for both medicinal purposes and as a food product. (Fig1.). Research on the origin of lemons suggests that they resulted from the hybridization of *Citrus medica* (citron) and *Citrus aurantium* (bitter orange). This unique genetic combination has endowed lemons with a rich phytochemical composition (Klimek-Szczykutowicz, M., Szopa, A., & Ekiert, H., 2020).

Fig.1. Lemon (***Citrus limon***)

The main components of lemons include vitamin C, flavonoids, phenolic compounds, pectin, and essential oils. These components provide various pharmacological properties. Studies show that the phytochemicals found in lemons exhibit strong antioxidant and anti-inflammatory effects, potentially preventing cardiovascular diseases, cancer, and certain metabolic disorders (Magalhães, D., Vilas-Boas, et al M., 2023). Additionally, the antibacterial and antifungal properties of lemons enable their use both as a natural preservative and as a food industry conservant. The bioactive compounds present in lemon peel and juice play a significant role in disease prevention and treatment.

Lemons are not only important in food and medicine but also play a crucial role in agriculture and environmental protection. Bioactive compounds derived from lemon waste are used in the production of environmentally friendly fertilizers and natural pesticides. Moreover, lemon oil serves as a natural antiseptic and is included in various cleaning products. Different lemon varieties vary in fruit size, color, acidity, and seed count (Salem Abdelmoaty, Mohammad Moneruzzaman Khandaker, et al., 2021).

This article provides a detailed analysis of the key biologically active compounds in lemons, their effects on the human body, and their industrial applications. It also explores the primary lemon varieties and their characteristics. The objective is to highlight the significance of lemons in health, industry, and environmental sectors while assessing their potential benefits more comprehensively (Rafiq, S., Kaul, R., Sofi, S. A. et al.,2018).

1. Phytochemical Composition of Lemon

Lemon (*Citrus limon* L.) is a rich source of biologically active phytochemicals that contribute to its nutritional, medicinal, and industrial importance. The fruit, peel, and seeds contain a wide spectrum of secondary metabolites, each playing a distinct physiological and pharmacological role. These compounds can be categorized into several main groups:

Flavonoid compounds (hesperidin, diosmin, eriocitrin): Flavonoids represent one of the most abundant classes of phytochemicals in lemon (Fig.2). They possess strong antioxidant and anti-inflammatory activities by scavenging reactive oxygen species (ROS) and reducing lipid peroxidation. These compounds also play a crucial role in vascular protection**,** improving capillary resistance and circulation. Moreover, hesperidin and eriocitrin are reported to modulate enzyme activity involved in detoxification and enhance the body's defense mechanisms against oxidative stress (Klimek-Szczykutowicz, M., Szopa, A., & Ekiert, H., 2020).

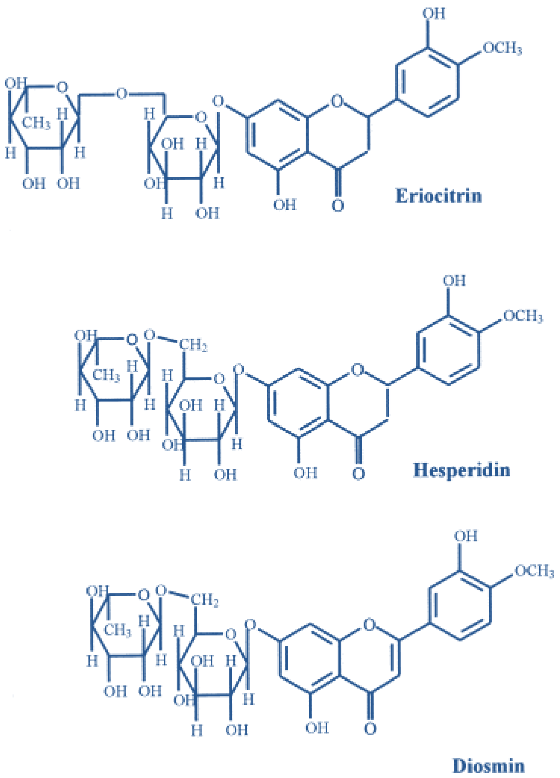

Figure. 2. Flavonoidd

Phenolic acids (ferulic, caffeic, sinapic): Phenolic acids are responsible for many of lemon's antioxidant and antimicrobial effects. They prevent oxidative damage to cellular lipids, proteins, and DNA, contributing to the reduction of inflammation and the risk of chronic diseases. Additionally, studies have shown that phenolic acids may inhibit cancer cell proliferation and induce apoptosis in tumor tissues. Their antimicrobial potential further enhances lemon's role as a natural preservative in food and pharmaceutical products (Magalhães, D., Vilas-Boas, et al M., 2023).

Essential oils (D-limonene, β-pinene, γ-terpinene): Lemon essential oils are complex mixtures of volatile compounds with broad-spectrum antimicrobial, antifungal, and antiviral properties. D-limonene, the major constituent, has been extensively studied for its antioxidant, anti-inflammatory, and chemopreventive effects. These oils can disrupt microbial cell membranes, leading to leakage of cellular contents and cell death. Additionally, their pleasant aroma makes them widely used in the food, perfume, and cosmetic industries (Hassan, S. M., Farman, M., Mughal, S. S. et al., 2020).

Vitamin C (ascorbic acid): Lemon is one of the best natural sources of vitamin C, a potent antioxidant that supports the immune system**,** enhances collagen synthesis**,** and maintains skin elasticity. It plays a protective role against cardiovascular diseases by promoting vasodilation and preventing oxidative modification of low-density lipoproteins (LDL). Furthermore, ascorbic acid improves the absorption of non-heme iron from plant-based foods, contributing to nutritional balance (Rafiq, S., Kaul, R., Sofi, S. A. et al.,2018).

Carotenoids and pectins: Carotenoids, including β-carotene and lutein, act as natural pigments and antioxidants that protect cells from oxidative damage. They also contribute to eye health and immune system regulation. Pectins, which are complex polysaccharides found in the lemon peel, exhibit prebiotic properties**,** supporting the growth of beneficial gut microbiota. They also help regulate blood glucose and cholesterol levels**,** improve digestion, and enhance detoxification processes by binding toxins in the gastrointestinal tract (IPGRI,1999).

In summary, the diverse phytochemical composition of lemon contributes to its multifunctional health-promoting effects**,** including antioxidant, antimicrobial, anti-inflammatory, and anticancer activities. These bioactive components make lemon an important natural source for pharmaceutical, nutraceutical, and food industry applications.

2. Antimicrobial Effect

Lemon extracts have been proven effective against pathogenic microorganisms such as *Staphylococcus aureus, Escherichia coli*, and *Candida albicans*. Essential oils degrade bacterial cell membranes, halting their activity. As a result, lemon acts as a natural antibiotic and helps prevent bacterial infections (Abbate, L., Mercati, F., et al, 2019).

3. Antioxidant Effect

The flavonoids and phenolic compounds in lemons reduce the formation of free radicals in the body, preventing oxidative stress. This effect decreases cell damage and slows down the aging process (Mabberley, D. J., 2004).

4. Anticancer Effect

D-limonene and flavonoid-containing compounds restrict the spread of tumor cells, activate apoptotic mechanisms, and help inhibit certain carcinogenic enzymes. Research suggests that limonoids found in lemon peel may prevent the development of some malignant tumor types (Rafiq, S., Kaul, R., Sofi, S. A. et al.,2018).

5. Applications in the Food Industry and Cosmetology

Lemon's natural preservative properties make it widely used in the food industry. Lemon extracts and essential oils function as preservatives by preventing the growth of bacteria and fungi. In cosmetics, lemon is utilized as a skin-brightening, antioxidant, and anti-inflammatory component (Hassan, S. M., Farman, M., Mughal, S. S. et al., 2020).

6. Evaluation of Lemon Based on International Descriptors

The following table presents the evaluation of lemon according to international descriptors (IPGRI 1999).

Table 1: Evaluation of Lemon Based on 12 Descriptors

Category	**Descriptor**	**Characteristics**
Botanical Characteristics	Type Weight Color Fruit form	Citrus lemon 80-200 gr Light yellow to dark yellow Round or elongated
Chemical Composition	Vitamin C amount Flavonoid content Essential oils	40-60mg/100mg Hesperidin, diosmin, eriocitrin D-limonen, γ-terpinen
Nutritional Value	Calories Pectin	29kcal/100mg 1-2%
Industrial Applications	Food Industry Cosmetology Pharmaceuticals	Natural preservative, aromatic additives Skincare and whitening agents Antiseptic, immune booster

7. Lemon Variety

Citrus fruits (including lemons) are mainly grown in the southern subtropical region of Azerbaijan — especially in the Lankaran District and Astara District. According to one source, lemons in Azerbaijan are cultivated from both introduced and local varieties.

Lemons are divided into two main groups: True lemons and hybrid lemons. Within both groups, there are various species with some significant characteristics as follows:

1. **True Lemons**

Eureka: This is one of the most popular lemon varieties and belongs to the non-hybrid lemon group. It is sensitive to cold climates. Known for its yellow rind and greenish-yellow pulp. (Fig.3)

Figure 3. Eureka

Lisbon: Compared to the Eureka variety, it is produced less but is more resistant to cold. It has yellow, rough-textured fruit, with light green-yellow pulp and very few seeds. (**Fig 4.**)

Figure 4. Lisbon

2. **Hybrid Lemons**

Meyer: This variety is a hybrid of lemon and mandarin orange. The fruit is orange-colored, and its acidity level is moderate. It is resistant to cold climates. **(Fig. 5.)**

Figure. 5. Meyer Lemon

Key Lime (Citrus aurantifolia): Widely grown in Malaysia, this lemon variety has small, green or lightyellow fruits. It is sensitive to cold climates, and its rind has antibacterial properties. **(Fig. 6.)**

Figure. 6. Lime (Citrus aurantifolia)

Calamansi Lime (*Citrus microcarpa*): Originating from China, this variety is widely spread in Malaysia. It has small, green fruits and mainly differs in its level of acidity. (**Fig. 7.**).

Figure. 7. Calamansi Lime (Citrus microcarpa)

Summary:

Lemon (Citrus limon) is a widely cultivated citrus fruit known for its rich phytochemical composition and extensive applications in the food, pharmaceutical, and cosmetic industries. It contains essential bioactive compounds such as flavonoids, phenolic acids, essential oils, vitamin C, and pectin, which contribute to its antioxidant, anti-inflammatory, antimicrobial, and anticancer properties (Abbate, L., Mercati, F., et al, 2019). Flavonoids and phenolic compounds in lemon play a crucial role in reducing oxidative stress and protecting cells from damage (Hassan, S. M., Farman, M., Mughal, S.S. et al., 2020). Its essential oils exhibit strong antibacterial and

antiviral properties, making them valuable in both food preservation and skincare formulations (IPGRI 1999). Additionally, lemon is recognized for its pharmacological benefits, including cardiovascular protection, immune system enhancement, and digestive health support Klimek-Szczykutowicz, M., Szopa, A., & Ekiert, H., 2020). In the food industry, lemon is utilized as a natural preservative due to its antimicrobial properties, which help extend shelf life and prevent spoilage (Mabberley, D. J., 2004). In cosmetics, lemon extracts contribute to skin brightening, elasticity improvement, and anti-aging effects (Magalhães, D., Vilas-Boas, et al M., 2023). Recent studies have also highlighted lemon's neuroprotective potential and its role in combating metabolic disorders (Rafiq, S., Kaul, R., Sofi, S. A. et al.,2018). This review comprehensively examines the biological properties of lemon, emphasizing its health benefits and industrial applications. Future research should focus on further exploring its bioactive compounds and their therapeutic potential through clinical studies.

Conclusion:

Lemon, being rich in biologically active compounds, makes a significant contribution to health and various industries. The flavonoids, phenolic acids, essential oils, and vitamins it contains stand out for their antioxidant, anti-inflammatory, antimicrobial, and anti-cancer properties. In the food industry, lemon extracts and essential oils are used as natural preservatives, which extend the shelf life of products (Magalhães, D., Vilas-Boas, et al M., 2023). In cosmetology, lemon is widely used for maintaining skin health, as well as for its whitening and anti-aging effects (Mabberley, D. J., 2004).

Additionally, lemon's pharmacological effects help maintain cardiovascular health, strengthen the immune system, and alleviate digestive problems (Rafiq, S., Kaul, R., Sofi, S. A. et al.,2018). Modern scientific research shows that the bioactive compounds in lemon may also positively impact the prevention of neurological diseases and metabolic syndromes (IPGRI 1999).

Future research should further explore the pharmacological effects of lemon's bioactive components and identify new applications for them. Specifically, more clinical studies are needed to assess the effectiveness of lemon-based preparations against various diseases and their use in medical practice.

In conclusion, lemon is an indispensable component in the food, pharmaceutical, and cosmetics industries and holds vast potential in preserving human health and serving as a natural remedy (Abbate, L., Mercati, F., et al, 2019).

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MOLECULAR VARIATION AND BIOTECHNOLOGICAL APPLICATIONS OF ALGAE

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Abstract: Food-significant algae (red, green, blue-green, and brown algae) are rich in vitamins, minerals, antioxidants, and other bioactive compounds, and they play an important role in both nutrition and medicine. In recent years, studies on molecular variation have allowed for a deeper understanding of the biological properties and beneficial components of algae by examining their genetic diversity. Through molecular approaches, the genetic variation of different species and populations can be identified, enabling the selection of more suitable and effective algae species for food and medical applications.

Keywords:Food-significant algae, molecular variation, genetic diversity, bioactive compounds, genetic markers, bioinformatics, food and medical applications.

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Introduction:

Algae are organisms with significant biotechnological potential in the fields of food, medicine, energy, and ecology. They possess diverse species and characteristics, and their biological diversity is extensively studied. Molecular variation is a key approach for studying the genetic diversity of algae and utilizing this diversity in biotechnological applications. These studies help improve our understanding of the biological properties of algae and allow for more efficient use of their beneficial traits.

Food-significant algae offer numerous beneficial components for the human body due to their rich composition. Depending on the species, algae are rich in various nutrients. They contain valuable substances such as proteins, vitamins, minerals, omega-3 fatty acids, antioxidants, amino acids, and dietary fiber. These compounds make algae an ideal choice as a nutritional supplement and for therapeutic purposes.

Algae, particularly microalgae, have high protein content. Algal species such as Spirulina and Chlorella contain between 60–70% protein. The proteins found in algae include all the essential amino acids required by the human body, making them a high-quality source of protein. With these properties, algae are considered an indispensable food source in vegetarian and vegan diets.

Algae are also rich in many essential vitamins. In particular, they contain B-group vitamins, vitamin A (beta-carotene), vitamin C, and vitamin E. The vitamin B12 content of algae is especially important, as B12 is typically found only in animal products, yet it naturally occurs in some algal species. This is especially beneficial for individuals who follow vegan or vegetarian diets.

Algae are also rich in minerals. They offer essential minerals such as potassium, calcium, magnesium, phosphorus, iron, and iodine. These minerals are crucial for human health, particularly for bone strength, immune system function, and the transport of oxygen in the blood. Algae, especially marine algae, contain high levels of iodine, which is essential for the proper functioning of the thyroid gland.

Algae are a valuable source of omega-3 fatty acids as well. These fatty acids, especially EPA (eicosapentaenoic acid) and DHA (docosahexaenoic acid), contribute to cardiovascular health, reduce inflammation, and support cognitive function. Marine algae are considered an irreplaceable plant-based source of omega-3 fatty acids (Guliyev, N., & Ismayilov, R, 2017)

Algae are also abundant in antioxidants. They contain compounds such as carotenoids and polyphenols, which help neutralize free radicals and prevent cellular damage. These antioxidants may slow the aging process and reduce the risk of chronic diseases such as cancer (Alizadeh, A., & Rzayev, I. (2018).

Lastly, algae are rich in dietary fiber. The fibers found in algae support digestive health, improve gut function, and help prevent constipation. They also aid in the elimination of toxins from the body, thereby promoting overall wellness.

Due to their nutrient-rich composition, food-significant algae are considered highly valuable for use as dietary supplements, health products, and functional foods. Their richness in diverse nutrients offers numerous health benefits and makes them an indispensable component of modern diets.

Molecular variation refers to changes that occur in an organism’s genetic material, including DNA, RNA, or proteins. Algae possess a high degree of genetic diversity due to their ability to thrive in various environmental conditions. Studies on molecular variation help identify these genetic differences and examine their biological effects. In order to explore the genetic diversity of algae, researchers utilize genetic markers, DNA barcoding, gene expression profiling, and other molecular biology techniques.

Such investigations enable a better understanding of the adaptation capabilities, biological activities, and ecological compatibility of different algal species within their respective ecosystems. Molecular variation studies are also critical for the conservation and sustainable development of algal genetic resources.

Algae have a wide range of biotechnological applications, particularly in food production, pharmaceuticals, cosmetics, bioenergy, and environmental protection. Understanding these applications on a molecular level is essential, as such research supports the selection of more beneficial and effective algal strains for industrial purposes.

Due to their richness in proteins, vitamins (especially B12), minerals, omega-3 fatty acids, and other nutrients, algae are extensively used in the food industry. Molecular variation studies allow for the identification of more nutritious and health-promoting algal species suitable for food production. For instance, algae such as Spirulina and Chlorella are widely used as dietary supplements due to their unique nutritional profiles, and exploring their genetic diversity can help enhance their productivity and quality. (Huseynova, M., & Mammadova, T., 2020)

Algae are used in the field of medicine, particularly as a source of bioactive compounds with anticancer, antibacterial, anti-inflammatory, and antiviral properties. Molecular variation facilitates the more efficient production of these potential pharmaceutical components. For example, some algal species produce substances that may contribute to the development of novel treatments for cancer. Genetic variation studies provide essential data for the genetic improvement and optimization of such species. (Huseynova, M., & Mammadova, T., 2020)

Algae also play an important role in the cosmetics industry, as they offer beneficial minerals, vitamins, and antioxidants for skin health. Products derived from algae are used to protect and rejuvenate the skin. Molecular variation research enables the identification of more effective and skin-compatible algal strains for cosmetic applications (Nasirov, A., & Veliyev, K., 2019). Algae can also be utilized in bioenergy production. It is possible to produce biodiesel and bioethanol from various algal species. Molecular variation aids in selecting species with enhanced energy production potential. Furthermore, algae absorb carbon dioxide from the atmosphere, helping to mitigate environmental pollution. Their genetic modification and adaptability allow for more efficient and scalable bioenergy processes.

Algae are also employed in environmental remediation and ecosystem restoration. They play a key role in water purification, prevention of soil degradation, and maintaining ecological balance. Molecular variation contributes to the identification of algae involved in these processes and supports the enhancement of their bioremediation capabilities (Rustamov, E., & Shukurova, Z., 2016).

Variation studies are essential for determining the genetic potential of algae and for using this potential more effectively in biotechnological applications. Algae are widely used in the food, pharmaceutical, cosmetic, bioenergy, and environmental sectors, and molecular variation accelerates the development of these fields. Genetic research facilitates the creation of more robust and beneficial algal strains, helping to shape the future of biotechnology (Rustamov, E., & Shukurova, Z., 2016).

Food-significant algae are also used for medical purposes. They are rich in vitamins, minerals, amino acids, and polysaccharides. However, the lack of comprehensive knowledge about their genetic diversity and biological properties limits their optimal use. Molecular variation research is a vital tool for overcoming these limitations (Ahmadov, F., & Safarov, M., 2021).

These algae have a wide range of applications in the food, pharmaceutical, and cosmetic industries. Their genetic diversity determines the variety of their metabolic and bioactive properties, which in turn broadens the scope of their practical uses. Studies on molecular variation are essential for understanding the evolution and adaptation of the biological and chemical characteristics of algae.

Main research. In recent years, advances in molecular biotechnology have opened new opportunities for investigating the genetic structure of algae. These studies reveal the presence of genetic variation across different algal populations and species, and how this variation correlates with their biological activity. Molecular markers, such as SSR (Simple Sequence Repeat), AFLP (Amplified Fragment Length Polymorphism), and RFLP (Restriction Fragment Length Polymorphism), are widely used to assess the genetic diversity of algae. Through these markers, genetic variation at the species and population levels is examined (Tahmazov, R., & Hasanov, N., 2015).

Bioinformatics tools are also used in the study of algal genetic diversity. These tools enhance the speed and accuracy of analyzing algal genetic data. As a result, researchers can identify the variety and quantity of bioactive compounds in algae, such as polyphenols, polysaccharides, fatty acids, vitamins, and minerals. These analyses also provide insight into how different algal species adapt to specific environmental conditions and ecosystems (Alizadeh, A., & Rzayev, I., 2018).

One of the most significant aspects of these studies is the ability to efficiently identify bioactive compounds associated with molecular diversity, and to select genetically superior algal strains. This enables improvements in the quality of algae used in food and medical industries, leading to the development of more targeted and effective products. For example, certain algae with high levels of antioxidants and vitamins can be used as nutritional supplements.

Genetic diversity demonstrates how algae adapt to diverse ecosystems and environmental conditions and how they develop specific beneficial traits. This makes it possible to select more effective and application-specific algal species, particularly for use in the food and pharmaceutical sectors. The use of genetic markers to analyze various species and populations of algae enhances their classification and suitability for specific purposes (Guliyev, N., & Ismayilov, R., 2017).

Environmental factors also influence the genetic structures and biochemical composition of algae. Conditions such as temperature, salinity, and light intensity can alter the production and content of bioactive compounds, which in turn determines how algae may be used in medical and food-related applications. Developments in biotechnology, especially in genetic engineering and selection methods, allow for the enhancement of desirable traits in algae and the cultivation of more suitable species.

Climate change also affects this process. Rising global temperatures and other environmental changes may influence the diversity of algae and their impact on ecosystems. Therefore, the conservation and sustainable use of algal genetic resources is of particular importance (Nasirov, A., & Veliyev, K., 2019)

In conclusion, the study of molecular variation in food-significant algae enables a deeper understanding of their biological characteristics and allows for more efficient use of these species in food and medical applications. Investigating the genetic diversity of algae and adapting them to environmental conditions will facilitate the selection of more productive and beneficial strains in the future. These studies are also crucial for ensuring food security, addressing health-related challenges, and promoting ecological sustainability

Results and Discussion:

Molecular variation studies of food-significant algae allow for a deeper understanding of their genetic structure and biological characteristics. Research in this field provides essential information for the more effective and targeted use of algae. By using molecular markers, scientists can identify both the genetic diversity and the range of bioactive compounds present in algal species, enabling more efficient selection for nutritional and medicinal purposes.

As a result, molecular variation studies expand the application of food-significant algae in biotechnology and pharmaceuticals. The outcomes of such studies pave the way for the development of healthier and more effective nutritional supplements and pharmaceutical products. Selecting algal strains with genetically superior traits is also important for ecological sustainability, as these strains are more adaptable to various ecosystems and can be cultivated in a more resilient and sustainable manner. A better understanding of the genetic diversity and bioactive potential of algae will help researchers discover new commercially valuable species in the future. These species will not only enhance the quality of food products, but also open new avenues in the biomedical and cosmetic industries. In conclusion, molecular variation research holds great potential both economically and ecologically.

Research on molecular variation and the biotechnological applications of algae enhances our understanding of the genetic potential of these organisms and promotes the efficient use of their beneficial properties. Algae are widely applied in the fields of nutrition, medicine, cosmetics, bioenergy, and environmental protection. By studying their genetic diversity through molecular variation, more productive, healthier, and effective strains can be selected. This approach accelerates the development of algal biotechnological applications, supports the creation of new bio-based products, and contributes to the advancement of existing technologies. Ultimately, molecular variation studies not only strengthen the ecological contributions of algae but also help unlock their full biotechnological potential.

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MORPHOBIOLOGY AND AQUACULTURE OF THE KUTUM (RUTILUS FRISII) DISTRIBUTED IN THE SOUTHERN REGION OF THE AZERBAIJANI SECTOR OF THE CASPIAN SEA

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Abstract: The kutum (Rutilus frisii kutum) is one of the economically important semi-anadromous fish species widely distributed in the southern and partly the central regions of the Caspian Sea.[1,12] The article investigates the morphometric and meristic indices, biological characteristics, distribution area, spawning behavior in rivers, ecological adaptation, and aquaculture potential of the kutum under Azerbaijani conditions. The study shows that the biometric parameters of the kutum directly depend on environmental factors - abiotic and biotic factors such as temperature, salinity, and food availability -as well as anthropogenic impacts including overfishing, degradation of spawning grounds, and water pollution.[1,9,11] Although the population density of the kutum along the southern Caspian coast has decreased compared to historical periods, it has been determined that the species possesses favorable biological characteristics for aquaculture cultivation.[2,3,14]

Keywords: Rutilus frisii, kutum, Caspian Sea, morphobiology, biometric parameters, aquaculture.

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İntroduction:

The kutum (*Rutilus frisii*) is one of the most valuable semi-anadromous fish species of the Caspian Sea and has been widely distributed along the Azerbaijani coast.[11,15] It is mainly observed at depths of 9–24 m along the western shores of the Middle and Southern Caspian, and during the spawning season it migrates into rivers to reproduce.[1,12] (Fig.1) For many years, this species was of significant commercial importance in the Caspian Sea, and in some years the total catch reached up to 7,000 tons.[11] However, due to anthropogenic impacts, river flow alterations, and pollution, its stocks have begun to decline.[9,14] Studying the morphology, biological characteristics, and aquaculture potential of the kutum is of special importance both for biodiversity conservation and for the development of artificial fish farming in Azerbaijan.[2,3,15]

The Caspian Sea, being the largest enclosed water body in the region, is characterized by sharp fluctuations in salinity and hydrological conditions. Salinity in the Southern Caspian ranges between 13–14‰, while water temperatures vary between +10 and +25 °C throughout the year. These parameters are among the major ecological factors influencing the distribution, feeding, and biological activity of the kutum.[10,14] The inflow of rivers such as the Kura, Lankaran, Samur, and others into the sea supports the semi-anadromous life cycle of the species.[11] Changes in river regimes (dams, reservoirs, diversion canals) are among the key factors directly affecting the natural reproduction of the population over the long term.[9,12]

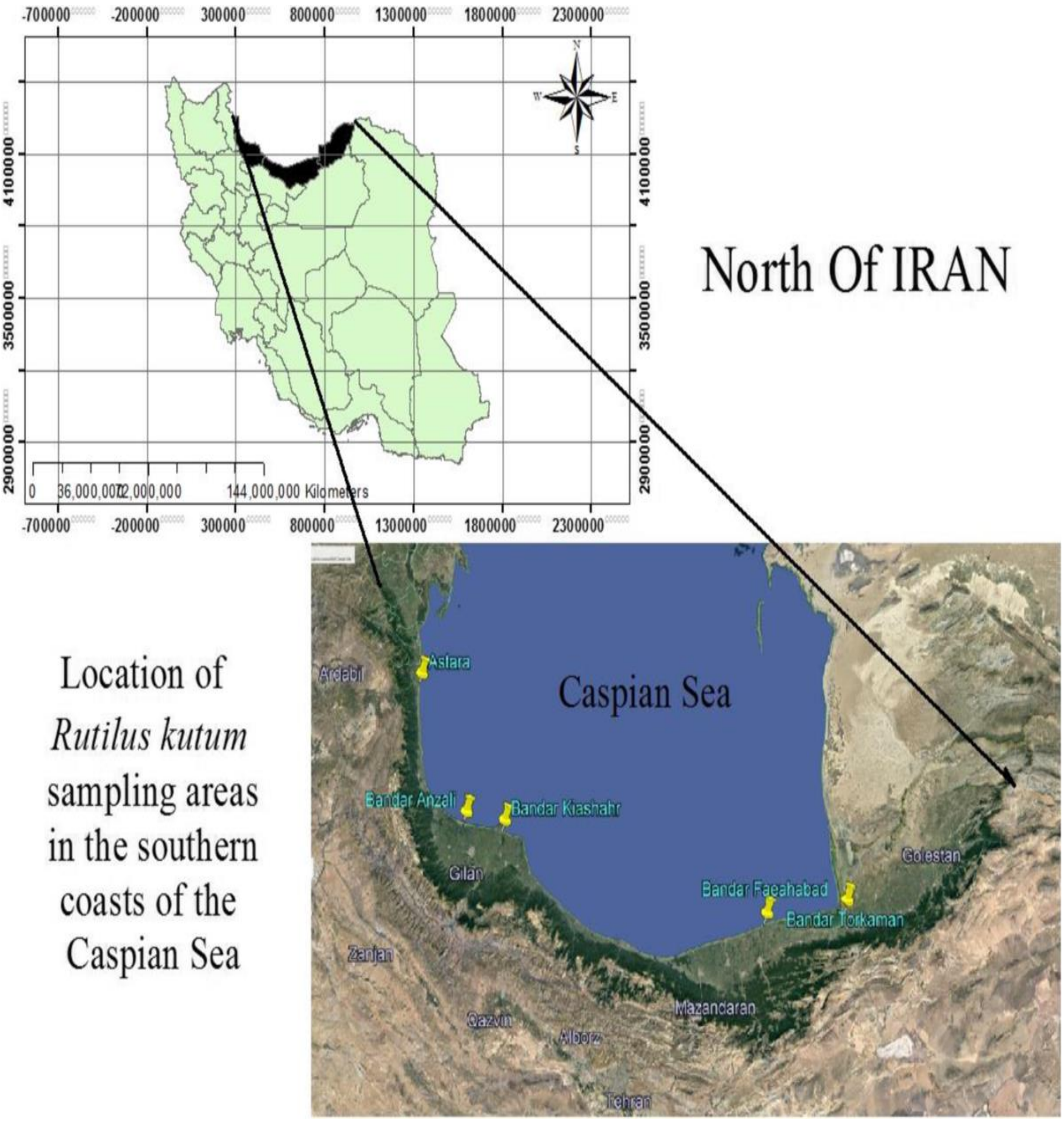

Fig.1 The distribution area of kutum

The general taxonomic position of species belonging to the family *Cyprinidae* is as follows:

Order: *Cypriniformes*
Family: *Cyprinidae*
Genus: *Rutilus*
Species: *Rutilus frisii* Nordmann, 1840
Subspecies: *Rutilus frisii kutum* (Caspian kutum)

The kutum is an endemic species distributed exclusively in the Caspian Sea. Its range stretches from the Terek River to the Gorgan Bay.[13] In Azerbaijan, it is most frequently found in the following areas:[15]

- Lankaran aquatory
- Gizilagaj Bay
- Kura–Araz delta
- Astara coastal zone

The taxonomic status of the kutum remains a subject of debate. Based on DNA markers, *Rutilus kutum* and *Rutilus frisii* inhabiting the Azov–Black Sea basin exhibit strong phylogenetic similarity.[13] Kutum is a large fish, and its scales are relatively smaller than those of the bream (*Abramis brama*). The caudal fin is well developed. The back is dark with a greenish tint; the sides are silvery and the belly is white. The dorsal fin and the upper lobe of the caudal fin are dark gray, while the pectoral, pelvic, anal fins and the lower lobe of the caudal fin are grayish in color.

During the reproductive period, sexual dimorphism becomes clearly pronounced. Large epithelial tubercles appear on the head and body of males, whereas females become noticeably deeper-bodied. As one of the endemic species of the Caspian Sea, kutum exhibits transitional or semi-anadromous behavior depending on environmental factors. There is no typical freshwater population of kutum in Azerbaijani waters. It is widely distributed in the Caspian Sea, particularly along the western coasts of the Middle and Southern Caspian.

During the spawning period, kutum migrates into rivers flowing into the Caspian Sea, large canals, and the Small Gizilagaj Bay. In males, nuptial tubercles (spawning rash) develop on the body during this period. Females are larger and fuller-bodied. Differences in the structure of the pelvic fins can also be observed. They reach sexual maturity at 3–4 years of age and can live up to 11 years. Fecundity ranges from approximately 26,000 to 270,000 eggs.[1] Spawning occurs from March to May. Kutum is a lithophilic species, meaning that it deposits its eggs at once on gravel–pebble substrates of rivers.[5,3] The eggs are adhesive and attach to stony-sandy riverbeds. After spawning, the broodstock returns to the sea. Many juveniles do not remain in rivers for long and drift back to the sea with the water flow.

Average biometric indicators of the Southern Caspian population:

- Total length: 32–45 cm (maximum 70 cm)
- Weight: 450–1100 g
- Body index: 3.5–4.2
- Lateral line scales: 48–54
- Gill rakers: 18–23 [12]

In some individuals, the elongated shape of the head and the laterally compressed body structure are clearly visible, which is associated with hydrodynamic adaptation.(Fig.3)

Fig. 2 The biological analysis of kutum

Biological characteristics:

Adult individuals mainly feed on mollusks and gastropods; however, small crustaceans also play a significant role in their diet. Juveniles primarily feed on cladocerans, cyclops, and diatom algae. Kutum meat is considered a high-quality commercial product, with individuals inhabiting the southern range exhibiting superior market characteristics. It has always been one of the commercially valuable species. Due to the degradation of some spawning habitats, artificial propagation has already been introduced, and the current stock level is satisfactory. Since the 1980s, larvae have been obtained and raised at the Gizilagaj fish reproduction plant in Liman settlement of Lankaran. Kutum was also introduced into the Mingachevir reservoir, where its maturation period accelerated. However, there is still insufficient evidence to conclude that its natural stock has significantly recovered. Kutum is considered one of the most promising species for aquaculture in Azerbaijan.[2,4]

Kutum has high adaptive capacity and can tolerate a wide range of salinity and temperature conditions. Positive traits for aquaculture include:

- High growth rate – reaching 250–350 g at 2 years of age
- High market value – fatty and high-quality flesh
- High fecundity

However, the species also presents several challenges for aquaculture.[9,11] Natural spawning depends heavily on river flow regimes. Reduced river discharge and dams hinder migration routes. Decreased genetic diversity poses risks in artificial breeding. Research shows that kutum in the southern Caspian region is of significant importance for biodiversity, fisheries, and aquaculture. Its morphobiological features confirm its high ecological adaptation potential.

Considering the decline in natural population size, propagation and cultivation of this species in aquaculture is an important measure for biodiversity conservation and food security.

During aquaculture cultivation, growth rate is moderate but can improve under proper feeding and optimal conditions. Kutum mainly feeds on zooplankton, phytoplankton, aquatic plants, and small aquatic organisms. Balanced diets and natural food availability are essential for healthy growth. This species releases a large number of eggs during artificial spawning, demonstrating excellent reproductive capacity—an important advantage for aquaculture.

Optimal aquaculture conditions require clean water, stable temperature, proper oxygenation, and balanced chemical composition. The species can grow in both freshwater and slightly brackish water, but the best growth is achieved in clean, well-oxygenated environments. Water temperature should range between 10–22°C, with an optimal level of 15–18°C, ensuring rapid growth. Dissolved oxygen must remain consistently high, as the species is highly sensitive to oxygen deficiency. Water pH should be 7.0–8.5.[8,4] Ammonia and nitrite levels must be zero because these compounds adversely affect fish health and growth performance. In the wild, kutum feeds on zooplankton and aquatic vegetation, whereas in aquaculture, a balanced feeding regimen is required.[2,4] High-protein fish feeds, small crustaceans, formulated pellets, and live foods (zooplankton, insects) are commonly used. Juveniles require light, high-protein feeds, while adults require more balanced diets.

For aquaculture reproduction, special conditions must be created. *Rutilus frisii* begins spawning mainly in spring. For breeding, broodstock aged 2–3 years are preferred. During spawning, fish are transferred to special areas where water flow is increased to protect the adhesive eggs. Incubation conditions depend on temperature and oxygen levels, and incubation lasts 7–15 days. Disease control is crucial: water quality and fish health must be monitored regularly. Antibacterial and antifungal treatments, regular water filtration, and maintaining microbiological balance are critical. Vaccination can also help prevent infections. The cultivation period varies depending on age, water conditions, and diet. Optimal market size for best flesh quality is 200–300 g.

Conclusion:

Rutilus frisii is a fish species with high aquaculture potential. Its cultivation and propagation represent a highly promising field. Under proper water conditions, feeding practices, and high-quality diets, kutum can achieve high productivity. Its production meets strong demand in both local and international markets, making it economically attractive for aquaculture. With proper management and optimal farming conditions, the species' economic value can increase in domestic and foreign markets.[14,15] Large-scale cultivation of kutum can significantly contribute to the development of the fisheries sector, food supply, and national economic growth.

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