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U. Sarsenbayeva[1,2,3]*, A. Almasbekova[1,2,3], K. Sharipov[2,3], S. Taipakova[1], M. Saparbayev[1]
[1]al-Farabi Kazakh National University,
050040, Republic of Kazakhstan, Almaty, 71 Al-Farabi Avenue
[2]M. Aitkozhin Institute of Molecular Biology and Biochemistry,
050012, Republic of Kazakhstan, Almaty, Dosmukhamedova 86
[3]S. Asfendiyarov Kazakh National Medical University,
050000, Republic of Kazakhstan, Almaty, Tole bi 94
*e-mail: ulansarsenbayeva@gmail.com

THE ROLE OF DNA GLYCOSYLASES IN MAINTAINING GENOME STABILITY

Abstract: *Genome stability is fundamental to cell viability, the evolutionary stability of organisms, and the preservation of their functional integrity. Endogenous damage, particularly the oxidative modification of nitrogenous bases resulting from cellular metabolism, is one of the main factors disrupting DNA structure. To prevent the accumulation of mutations, cells utilize a base excision repair (BER) system in which DNA glycosylases play a pivotal role. These enzymes recognize and remove damaged or mismatched bases, thereby initiating a cascade of repair reactions.*

Adenine DNA glycosylases belonging to the MutY/MUTYH family are unique in that they do not directly remove damaged bases, but rather correct replication errors arising from oxidative damage to guanine. In bacteria, this function is performed by the MutY enzyme, whereas in eukaryotes it is performed by its homologue, MUTYH. These enzymes prevent G:C → T:A transition mutations from becoming fixed, thereby significantly reducing the level of spontaneous mutagenesis.

This review discusses the role of DNA glycosylases in maintaining genomic stability, focusing on the molecular mechanisms of adenine DNA glycosylase function, their place in the BER system, evolutionary conservation, and their significance in biotechnology, molecular genetics, and applied research.

Key words: *DNA glycosylase, 8-oxoguanine, DNA repair, base excision repair.*

Introduction

Maintaining genomic stability is essential for preserving cell viability and the integrity of genetic information. In aerobic organisms, DNA is constantly exposed to damaging endogenous factors, including reactive oxygen species, byproducts of cellular metabolism, and spontaneous chemical reactions [1, 2]. Consequently, continuous nitrogenous base modifications occur in the genome, despite the absence of gross DNA structural damage. These modifications have a pronounced mutagenic potential [3]. The base excision repair (BER) system effectively eliminates such damage, with DNA glycosylases playing a central role [4].

DNA glycosylases are a class of enzymes that recognize damaged or abnormal bases in the DNA double helix. They hydrolytically cleave the N-glycosidic bond between the nitrogenous base and deoxyribose, forming an apurine or apyrimidine site – a universal intermediate product of BER [5]. The direction and effectiveness of the entire repair process are determined at the stage of DNA glycosylase action, since each enzyme has a strictly defined substrate specificity [6].

Modern research reveals that DNA glycosylases are not only «repair» enzymes, but also act as sensors that can detect even slight distortions in the DNA structure. This is achieved through a process known as base flipping, where the enzyme temporarily removes a potentially damaged base from the double helix to the active site for chemical identification [5, 7]. This strategy enables even damage that does not result in significant changes to DNA conformation to be recognized. Thus, DNA glycosylases act as the main «decision makers» who determine which modifications of endogenous bases will be transferred, restored, or transformed into mutations [8].

Among the many DNA glycosylases, which are enzymes that protect the genome from the effects of oxidative stress, some occupy a special place. Oxidative damage to guanine, resulting in the formation of 8-oxo-7,8-dihydroguanine (8-oxoG), is considered one of the most common and

biologically significant types of endogenous DNA damage [9]. The ability of 8-oxoG to form a stable pair is associated with its mutagenic potential, not only with cytosine but also with adenine. This leads to the fixation of G:C → T:A transitions during replication [10].

Cells have a specialised system for preventing oxidative-induced mutagenesis, which is key to preventing such mutations. This system involves MutY/MUTYH family adenine DNA glycosylases [10]. Most glycosylases directly remove damaged bases, but these enzymes are different. They recognise and remove unmodified adenine that has been mistakenly incorporated opposite 8-oxoG. Therefore, adenine DNA glycosylases perform the unique function of post-replicative DNA quality control, eliminating potential mutations before they are incorporated into the genome [11, 12].

Prokaryotes have a MutY enzyme that performs this function as part of the GO system. In eukaryotes, its functional homolog is MUTYH [10]. Despite differences in genome and chromatin organization, these enzymes show a high degree of structural and functional conservation, underscoring their importance in maintaining genomic stability. The human MUTYH gene is expressed both in the nucleus and in the mitochondria, where it protects the genomes of these compartments from errors that occur during oxidative replication [13]. In addition, experimental studies show that MUTYH can function as a molecular switch linking oxidative DNA damage with programmed cell death, thereby contributing to tumor suppression under conditions of severe oxidative stress. [14].

Adenine DNA glycosylases function closely with other components of the BER system, including AP endonuclease APE1, DNA polymerase β, and DNA ligase. The coordinated action of these enzymes ensures the highly accurate replacement of mispaired adenine and the restoration of the original nucleotide sequence. The accumulation of mutations, increased sensitivity of cells to oxidative stress, and increased genomic instability are all caused by disruption of this interaction [3, 13, 15, 16].

DNA glycosylases, and adenine DNA glycosylases in particular, are key elements in the molecular mechanisms that protect the genome. Their function extends beyond merely «repairing» DNA damage, encompassing the active prevention of mutations, coordination with replication and transcription, and adaptation of cells to oxidative stress. Understanding these processes is of fundamental importance for both fundamental molecular biology and biotechnological and biomedical applications. However, repair errors can also lead to mutations and contribute to genomic instability [1, 2, 13].

Despite the growing body of literature on base excision repair (BER) and DNA glycosylases, several key questions remain unresolved and warrant detailed consideration in this review. Firstly, the regulatory hierarchy that governs glycosylase activity in vivo, particularly under conditions of concurrent oxidative and alkylating stress, is not well understood. Secondly, the extent to which glycosylase functional redundancy is truly compensatory rather than merely partial is a subject of active debate. Single knockouts often exhibit mild phenotypes, whereas double knockouts lead to synergistic genomic instability, suggesting that redundancy masks rather than eliminates vulnerability [1, 17]. Thirdly, the role of post-translational modifications (phosphorylation, acetylation, and SUMOylation) in regulating the substrate specificity of glycosylases and their interactions with the replicative apparatus is not well characterised.

The purpose of this review is to summarize current data on DNA glycosylases and critically evaluate the prevailing patterns of fiber organization in vivo. We argue that the traditional linear view of BER, largely based on biochemical analyses of exposed DNA, does not take into account the context of chromatin, the dynamics associated with replication and transcription, or the competition between enzymes in common lesions [18]. We also emphasize that the apparent excess of glycosylases may mask the fragility of the basic repair network, especially under combined oxidative and alkylating stress. Finally, we will discuss why simple knockout phenotypes do not always accurately reflect the true biological role of these enzymes [19].

DNA glycosylases are key initiators of base excision repair

Base excision repair (BER) is a fundamental mechanism for maintaining genomic stability, ensuring the elimination of minor chemical modifications of the nitrogenous bases of DNA. Unlike bulk damage, changes such as alkylation, oxidation, and deamination of bases, as a rule, do not cause significant distortion of the double helix, but they have a high mutagenic potential. Their accumulation poses a serious threat to the integrity of the genome, especially in actively dividing and metabolically active cells [12, 13].

It is estimated that several thousand base damages occur daily in mammalian cells due to the action of reactive oxygen species, endogenous methylating agents, and spontaneous chemical reactions such as hydrolytic deamination [13]. These lesions need to be repaired quickly and specifically before replication, as their fixation leads to the accumulation of point mutations and the formation of genomic instability [15].

The BER process is initiated by DNA glycosylases, enzymes that recognize and cleave the N-glycosidic bond between a damaged base and deoxyribose. These enzymes can do this because they recognize abnormal bases in intact DNA double helices. This stage is crucial to the entire repair process, as it is at the level of DNA glycosylases that the substrate is selected and further repair is directed [16].

Despite the extreme variety of chemical damage to bases, about eleven DNA glycosylases have been identified in the mammalian genome. Collectively, these enzymes recognise most endogenous damage. These enzymes are divided into several structural superfamilies, which reflect both their evolutionary origin and their catalytic features. These include uracil DNA glycosylases (UNG, SMUG1 and TDG); glycosylases of the helix-hairpin-helix (HhH) family (OGG1, MUTYH, NTH1, and MBD4); 3-methylpurine DNA glycosylase (MPG); and NEIL family enzymes, which are structurally related to bacterial endonuclease VIII (Table 1) [5].

Table 1 – Human DNA glycosylases involved in excisional base repair (BER)

DNA glycosylase	The structural family	The main substrates	Functional role in BER	Key references
UNG	Uracil-DNA glycosylase	U:G, U:A	Uracil removal prevents C→T transitions	[4, 5]
SMUG1	Uracil-DNA glycosylase	Uracil, 5-hydroxyuracil	Repair of uracil and oxidized pyrimidines	[4, 15]
TDG	Uracil-DNA glycosylase	T:G, 5-fC, 5-caC	BER and active DNA demethylation, epigenetic regulation	[4, 7]
OGG1	HhH-glycosylase	8-oxoG:C	Removal of 8-oxoguanine: prevention of G→T transversions	[9, 13]
MUTYH	HhH-glycosylase	A:8-oxoG	Adenine removal from erroneous pairs, anti-mutation protection	[10, 11]
NTH1 (NTHL1)	HhH-glycosylase	Thymine-glycol, 5-hydroxycytosine	Elimination of replication-blocking damages	[5, 13]
MBD4	HhH-glycosylase	T:G в CpG (after deamination of 5-mC)	Repair of deaminated methylated cytosines	[4, 17]
MPG (AAG)	Helix-2Turn-Helix Glycosylases	3-meA, 7-meG, εA, εC	Repair of alkylated and exocyclic bases	[5, 18]
NEIL1	NEIL (Endo VIII-like)	Oxidized purines and pyrimidines	Repair in replication forks	[12, 14]
NEIL2	NEIL (Endo VIII-like)	Oxidized pyrimidines	Transcriptionally-related BER	[14, 17]
NEIL3	NEIL (Endo VIII-like)	8-oxoG and other oxidized bases in ssDNA	Repair in proliferating cells	[7, 12]

The BER system's functionality is characterized by the partial redundancy of its DNA glycosylases. Several enzymes can recognize similar types of damage, which increases the reliability of repair under conditions of expression fluctuations or local changes in the chromatin structure. Mice with one of these enzymes removed have been used as an experimental model. This has shown that the loss of a single enzyme rarely leads to death. However, it is often accompanied by an increase in the number of mutations and an increase in sensitivity to genotoxic stress [20, 21, 22]. These observations indicate that the classical picture of BER is oversimplified. BER is not a uniformly robust and fully redundant network. This oversimplification does not fully explain tissue-specific phenotypes observed in vivo.

The effects of DNA damage on living things depend on the chemical nature of the damage and the structure and catalytic properties of the corresponding DNA glycosylases. Replication can be effectively blocked by some damages, such as thymine glycol, and these are quickly eliminated

by specialized enzymes (NTH1). Other modifications do not affect the movement of replicative and transcription complexes, but they become toxic during the formation of stable DNA-glycosylase complexes. These complexes create a physical obstacle for DNA polymerases [17, 18].

The BER system is further complicated by the ability of a number of DNA glycosylases to function in various structural contexts of DNA, including single-stranded regions, loop structures, replication forks and DNA-RNA hybrids. This is especially important for maintaining the integrity of actively transcribed regions of the genome and preventing conflicts between the processes of repair, transcription, and replication. Taken together, these data confirm a model. This model shows that the BER result is determined not only by substrate specificity. It is also determined by the chromatin context. And the phase of the cell cycle. And the dynamic redistribution of individual glycosylases between different DNA structures.

TDG is unique among DNA glycosylases because its function extends beyond the scope of damage repair. TDG is involved in the active demethylation of DNA by removing oxidised 5-methylcytosine derivatives, and it plays a critical role in the epigenetic regulation of development. Genetic studies have shown that TDG deficiency leads to fetal mortality, highlighting the unique importance of this enzyme for cellular homeostasis [4, 7]. This example illustrates in a broader sense that many DNA glycosylases act not only as repair factors, but also as regulators of gene expression and chromatin status, reinforcing the idea of BER as an integrated regulatory network rather than as a purely economic pathway [23].

Collectively, DNA glycosylases represent the first and most specific level of genome protection, determining the effectiveness of BER and the prevention of mutations. When there is oxidative stress, glycosylases are particularly important. These are enzymes that repair oxidised bases. Two of the most important are OGG1 and MUTYH. Together, they form the basis of the 8-oxoguanine-induced mutation prevention system [9-11, 17].

One critical point often overlooked in reviews of linear base excision repair (BER) is the paradox of functional redundancy: if multiple glycosylases can process overlapping substrate spectra, why does the loss of a single enzyme, such as OGG1 or NEIL1, lead to significant phenotypic effects in certain tissues? One possible explanation is that redundancy depends on the context: while enzymes that share substrates function in various in vitro conditions, they operate in different in vivo chromatin media, cell cycle phases or transcriptional contexts [17, 18]. For instance, NEIL1 is primarily active at replication forks, whereas NEIL2 is primarily associated with transcription, indicating a division of labour that is not apparent in vitro. An alternative, more provocative interpretation, proposed by Dianov and Hubscher, is that the apparent reliability of BER conceals a «fragile system» that is susceptible to failure when several stress factors coincide [21]. Taken together, these views challenge the idea of a fully functionally redundant repair network and are crucial for understanding why heterozygous glycosylase mutations can affect the risk of cancer and other disease phenotypes [24].

Mechanisms of DNA repair containing 8-oxoguanine

Oxidative DNA damage is considered to be one of the main causes of endogenous mutagenesis in eukaryotic cells. In conditions of normal metabolism, the body constantly produces reactive oxygen species (ROS), but exposure to external factors can significantly increase their levels. Among the numerous products of nitrogenous base oxidation, 7,8-dihydro-8-oxoguanine (8-oxoG) occupies a special place, which is considered the most widespread and biologically significant modification of guanine. The increased sensitivity of guanine to oxidation is explained by its lower redox potential compared to other bases, which makes it a primary target for ROS [25, 26].

An important feature of 8-oxoG is that it does not significantly deform the DNA double helix and usually does not directly block replication or transcription (Figure 1). This distinguishes it from other oxidized bases, which effectively block polymerases. However, the biological hazard of 8-oxoG is determined by its high premutagenic potential. Due to its structural properties, 8-oxoG can take at least two conformations: in one it combines with cytosine, and in the other with adenine. Consequently, during replication, polymerases may mistakenly include adenine, the opposite of 8-oxoG. This, in turn, leads to the fixation of G:C → T:A transversions, one of the most common types of mutations caused by oxidative damage to the genome. [8, 9, 26].

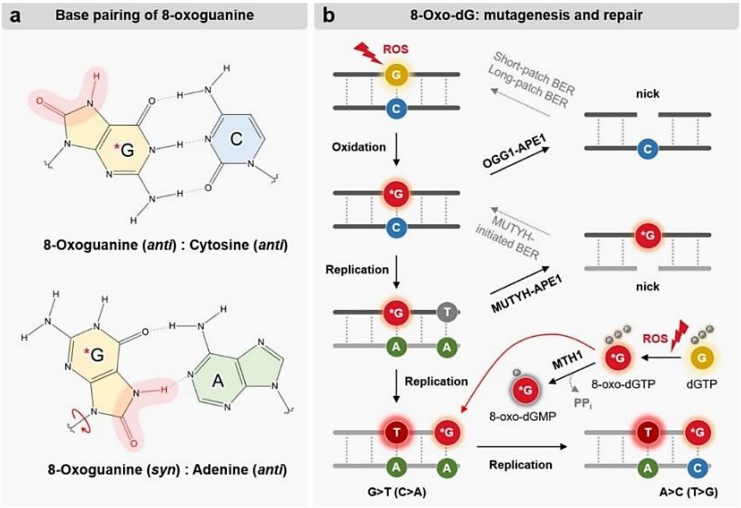

Figure 1 – Schematic representation of 8-oxoguanine mating preferences in anti- and syn conformations (left) and an overview of the GO DNA repair system (right) [19]

The GO-repair system is a specialized and extremely conservative repair mechanism that has been developed to stop the accumulation of such mutations in cells. This system offers multilevel control over the occurrence and biological effects of 8-oxoG and is found in organisms across all domains of life. Three enzymes, OGG1, MUTYH, and MTH1 (NUDT1), each of which functions at a different level of DNA and nucleotide metabolism, are essential parts of the GO system in human cells [27, 28].

A DNA glycosylase called OGG1 (8-oxoguanine DNA glycosylase 1) can identify and eliminate 8-oxoG when it is paired with cytosine. The classical excisional base repair (BER) pathway is started when OGG1 binds to the damaged base pair. After the N-glycoside bond is hydrolyzed, an apurin/apyrimidine (AP) site is created. This site is then further cleaved by APE1 endonuclease, and DNA polymerase β and DNA ligase help restore DNA integrity.

Nevertheless, when 8-oxoG has already paired with adenine, OGG1's efficacy is greatly diminished. Adenine DNA glycosylase MUTYH is crucial in stopping mutation fixation in such circumstances. In contrast to OGG1, MUTYH specifically identifies mismatch 8-oxoG.:A and catalyzes the excision of adenine instead of removing the oxidized guanine itself. This seemingly paradoxical process prevents a transient mating error from becoming a stable mutation and sets up OGG1's reaction, which eliminates 8-oxoG that has already been paired with cytosine.

MUTYH's molecular mechanism of action involves hydrolyzing the N-glycosidic bond, recognizing a damaged base pair, and extruding adenine from the DNA double helix via the base-flipping mechanism. According to structural research, MUTYH is a member of the HhH glycosylase family and has a [4Fe-4S] cluster, which is crucial for preserving the protein's conformational stability and accurately identifying the substrate. Furthermore, the catalytic activity of the enzyme and the efficiency of repair have been demonstrated to be impacted by the binding of metal ions [25, 26, 27].

The third part of the GO system is MTH1 (NUDT1). This enzyme works not on DNA itself, but on the pool of free nucleotides. MTH1 breaks down 8-oxo-dGTP into its monophosphate form. This prevents the oxidized nucleotide from being added to DNA during replication. As a result, this enzyme reduces the chance of 8-oxoG formation before any damage occurs in the genome [29].

The functional importance of the coordinated operation of the GO-repair system components is substantiated by genetic research findings. In mice lacking OGG1 or MUTYH, an increase in the frequency of G:C → T:A transversions is noted; however, the most pronounced mutational phenotype, along with heightened spontaneous tumorigenesis, is observed in double OGG1/MUTYH knockout models [30]. These findings underscore the functional complementarity of the enzymes and the essential role of the GO system in preserving genomic stability.

Therefore, repairing DNA that contains 8-oxoguanine is a multi-step, tightly coordinated process that involves controlling the nucleotide pool, removing damaged bases, and fixing replication mistakes. MUTYH adenine-DNA glycosylase plays a crucial role in preserving genomic stability and

shielding cells from oxidative stress-related carcinogenesis by blocking the fixing of redox-induced mutations [28, 29, 31].

Although the above mechanistic picture of 8-oxoG recovery is well-founded, it reveals several inconsistencies that require recognition upon careful analysis. Firstly, the division of labour between OGG1 and MUTYH – OGG1 removes 8-oxoG in combination with cytosine and MUTYH removes adenine in combination with 8-oxoG – is conceptually elegant. Whereas some authors propose that MUTYH and OGG1 act in a strictly ordered succession, single-molecule and biochemical studies suggest that their competition for 8-oxoG-containing substrates can lead to transient trapping of lesions and even increased mutagenesis if one enzyme is over- or under-expressed. However, the temporal and spatial coordination of these actions in vivo is much less clear than is suggested by simplified biochemical models. Recent single-molecule studies show that competition between OGG1 and MUTYH for access to damage during the S phase can increase the likelihood of erroneous processing rather than ensuring strictly ordered recovery. [29].

Secondly, although the role of MTH1 (NUDT1) in the GO system is intuitively understandable from a mechanical point of view, it remains controversial. Pharmacological inhibition of MTH1 was initially proposed as an anti-tumour strategy, but contradictory results in different tumour models cast doubt on its universal applicability [28].

These contradictions demonstrate that, despite decades of biochemical research, the GO system is not as well understood as is often imagined. They also emphasise the importance of studying the reduction of 8-oxoG under physiologically significant oxidative conditions and in chromatin-native contexts.

The role of MUTYH in maintaining genomic stability and biotechnological aspects

MUTYH plays a crucial role in maintaining genomic stability and biotechnological aspects. After removing 8-oxoguanine with OGG1, adenine DNA glycosylase MUTYH corrects mismatches A:8-oxoG that occur after DNA replication [9-11]. MUTYH removes adenine from the faulty pair, creating an AP site that is then processed by classical BER enzymes such as APE1, DNA polymerase β, and DNA ligase. This process hinders the fixation of G:C → T:A transversions, ensuring genomic stability [19, 20].

Structural investigations have indicated that the presence of a [4Fe-4S] cluster and a HhH domain, which stabilize the enzyme and direct adenine extrusion from the double helix, ensures MUTYH identification accuracy [32]. The cooperation of MUTYH and OGG1 allows for several error correction opportunities: if 8-oxoG is originally paired with cytosine, OGG1 removes the damaged base, and if adenine is wrongly introduced, MUTYH prevents the mutation from fixing [10, 25, 33]. However, the elegant functional separation often depicted in schematic models does not fully reflect the complexity of their interactions in vivo. In the cellular context, OGG1 and MUTYH may compete for access to 8-oxoG-containing lesions, particularly in replicating chromatin, where DNA accessibility is subject to dynamic regulation. Their relative activity is likely influenced by the cell cycle phase, local chromatin structure and the assembly of replication-associated protein complexes. These factors collectively determine lesion accessibility and the outcomes of their processing.

The functional significance of MUTYH has been confirmed by genetic modelling. Mice with a double knockout of OGG1 and MUTYH exhibit a pronounced mutator phenotype and spontaneous tumour formation. In contrast, a MUTYH-only knockout results in a more moderate increase in the frequency of G → T transversions. Furthermore, MUTYH interacts with replication-associated proteins, such as PCNA and the 9-1-1 complex. These proteins facilitate the recruitment of base excision repair (BER) factors to replication forks and coordinate repair with DNA synthesis [10, 31]. Together, these findings imply that the 8-oxoG repair network exhibits buffering capabilities, yet is not entirely redundant. Consequently, impairments in the activity of individual enzymes or the efficiency of their recruitment can alter the equilibrium between precise repair and mutagenic processing.

From a translational point of view, particular interest is also held for MUTYH because germline mutations in this gene underlie MUTYH-associated polyposis and colorectal cancer risk is increased, whereas the impact of monoallelic variants remains controversial. Furthermore, given that MUTYH and other BER components process intermediates generated by base editors, it is probable that their activity exerts a significant influence on the efficiency and fidelity of CRISPR-based genome

editing. This suggests that the controlled modulation of MUTYH could become a tool for optimising editing outcomes in the future.

DNA glycosylase disorders: clinical and biotechnological implications

DNA glycosylases are the primary initiators of base excision repair (BER). They detect and eliminate a wide variety of DNA base lesions. Malfunction of these enzymes can lead to the accumulation of lesions, increased genomic instability, and the development of numerous diseases. What is particularly important to note is that defects in individual glycosylases are linked to specific biological phenotypes. This indicates that, even within BER, there is functional overlap which is incomplete and highly dependent on the cellular context.

UNG and SMUG1 remove uracil as part of the spontaneous cytosine deamination pathway. UNG deficiency causes more C→T transitions in the genome, indicating an inability to fix uracil-containing mispairs. It also leads to decreased immune system functions, such as somatic hypermutation of B cells. Such abnormalities are linked to an elevated risk of cancer and immunodeficiency phenotypes. SMUG1 partially compensates for UNG loss, but a twofold defect causes uracil buildup and increased mutational load, highlighting the necessity of the BER system's redundancy [5].

TDG (thymine DNA glycosylase) removes T:G proteins and oxidized derivatives of methylated cytosine (5-fC and 5-caC), making it vital for both damage repair and epigenetic remodeling. Mutations or TDG deficiency in animal models cause embryonic death, developmental abnormalities, and oxidative stress reactions, demonstrating its vital role in gene development and regulation [34, 35].

MUTYH eliminates adenine that was accidentally implanted opposite 8-oxoG after replication to ensure quality control. MUTYH genetic variations enhance the risk of colorectal cancer and cause MUTYH-associated adenomatous polyposis (MAP), indicating a loss of BER antimutation defense. These conditions are especially important in the diagnosis of genetic predispositions and in biological cancer research.

Oxidized pyrimidines and other oxidized bases are eliminated by NTHL1 and NEIL1-3, which are members of the HhH/Nei glycosylases family. Hereditary NTHL1 syndrome, which is characterized by a higher risk of colorectal and other cancers, is linked to NTHL1 mutations. Impaired NTHL1 expression can result in genomic instability and replication stress, which has been linked to carcinogenesis in many human and animal models and studies. The study also demonstrates that an imbalance in NTHL1 levels (both deficit and overexpression) might lead to genomic instability and cellular transformation, highlighting the importance of precise regulatory control over BER components [18-21].

Both single-stranded DNA structures and actively transcribed areas are shielded by NEIL glycosylases. For instance, NEIL1 is involved in the removal of oxidized bases in replication forks, and its lack may lead to the build-up of untreated damage, which is linked to greater susceptibility to oxidative stress and neurodegenerative phenotypes. Research indicates that inflammatory and infectious processes (e.g., in tissue infected with H. pylori) lower NEIL2 expression, which leads to the buildup of DNA damage and carcinogenesis. These examples show that disease symptoms are due not only to damage that has not been repaired, but also to the way in which a glycosylase usually copies or writes itself [36].

BER and particular DNA glycosylase disorders can present with a range of clinical symptoms:

Oncology. Defects in MUTYH, NTHL1, MBD4, and OGG1 raise the risk of both sporadic and inherited tumor disorders, such as leukemia, colorectal cancer, and other neoplasms. For instance, germline variations of MBD4 are linked to a higher risk of polyposis and acute myeloid leukemia; however, systematic studies of unselected patient cohorts indicate that the contribution of heterozygous variants is heterogeneous and not yet fully defined.

Immune regulation. A lack of UNG increases the likelihood of immunodeficiency, lymphomas, and somatic hypermutation diseases.

Epigenetic diseases. TDG abnormalities can impact the control of gene expression throughout development and differentiation by impairing active demethylation.

Neurodegenerative and aging-related syndromes. The pathophysiology of the central nervous system, including accelerated aging and the advancement of neurodegeneration, is intimately linked to the buildup of oxidized bases and compromised BER. According to review data,

BER deficiency is linked to a variety of illnesses, including inflammatory diseases and age-related ailments (Table 2) [37].

Table 2 – DNA glycosylase disorder: clinical and biotechnological consequences

DNA Glycosylase	Major damage/ substrates	Clinical consequences	Biotechnological consequences
UNG	Uracil (C→U)	Immunodeficiency, increased risk of lymphomas, disorders of somatic hypermutation of B cells	Increased mutation load in cell lines
SMUG1	Uracil, 5-hydroxyuracil	Partial compensation of UNG deficiency, with double deficiency, and accumulation of mutations	Potential genome instability in cultures
TDG	T:G, 5-fC, 5-caC	Fetal mortality (mouse models), epigenetic regulation disorder, and oncogenic potential	Violation of the accuracy of epigenetic models, increased risk of errors in DNA editing
OGG1	8-oxoG:C	Increased spontaneous mutations, carcinogenesis in the intestine and lungs	Decreased fidelity of replication and editing, accumulation of 8-oxoG in cell lines
MUTYH	A:8-oxoG	Familial adenomatous polyposis (MAP), increased risk of colorectal cancer	Increased frequency of G:C → T:A tranversions in cultures, decreased CRISPR accuracy
NTH1 (NTHL1)	Thymine-glycol, 5-hydroxycytosine	Hereditary NTHL1 syndrome, increased risk of colorectal and other cancers	Genomic instability in cellular models, replication stress
MBD4	T:G в CpG (after deamination of 5-mC)	Increased risk of leukemia and tumors, CpG mutations	Violation of the accuracy of epigenetic models and induced mutations
MPG (AAG)	3-meA, 7-meG, εA, εC	Hypersensitivity to alkylating agents, carcinogenesis by chemical exposure	Reducing the effectiveness of controlled alkylating mutagenesis
NEIL1	Oxidized purines and pyrimidines	Metabolic syndrome, hypersensitivity to oxidative stress, tumor transformation	Accumulation of oxidized bases in cell lines, reduced replication stability
NEIL2	Oxidized pyrimidines	Damage to actively transcribed genes, increased risk of mutations and cytotoxicity	Violation of fidelity of transcriptionally-related BER, risk of editing errors
NEIL3	8-oxoG and other oxidized bases in ssDNA	Repair in proliferating cells; deficiency may increase the risk of tumor transformation	Impaired stabilization of replication forks, accumulation of damage in rapidly dividing cells

In biotechnological practice, genome stability and replication fidelity are extremely important

1. Editing genomes. BER violations increase the likelihood of errors and spontaneous mutations during base editing or CRISPR/Cas editing, which lowers the precision of genetic manipulations and makes it more difficult to understand the outcomes.

2. Cell line stability. In iPSC models, embryonic cells, and industrial lines, deficiencies in BER components can result in unanticipated phenotypes and increase the diversity of cell cultures.

3. Controlled mutagenesis. In some areas of biotechnology, the temporary change in BER activity can be used to increase the mutation rate during directed enzyme evolution or the optimization of biocatalysts. At the same time, the likelihood of off-target mutations and unintended genomic instability can also be increased by disruption of BER function. This necessitates the careful control of experimental conditions and adherence to biosafety measures.

Understanding the molecular mechanisms of BER and the activities of each DNA glycosylase enables us to develop techniques for increasing genetic stability and lowering the risk of mutations in biotechnological and therapeutic applications. This is critical for both the development of therapeutic approaches to addressing BER faults and the dependability of genomic technologies.

The clinical and technological data in general back up the main idea of this review. DNA glycosylases form a context-dependent and only partially redundant network, whose perturbation can either promote disease or, in specific settings, be harnessed to modulate genome stability in a controlled way.

Conclusion

The data presented in this review suggest that DNA glycosylases are part of a complex genome defense mechanism that involves much more than simply removing damaged bases. At the same time, a number of aspects of their *in vivo* biology remain poorly understood and require further investigation. The accumulated data indicate that base excision repair (BER) is not a simple, linear, and fully redundant cascade; it is much more accurate to view it as a context-dependent network. The behavior of this network is determined by the organization of chromatin, the dynamics of replication and transcription, as well as the competition between individual glycosylases for access to damaged areas [16].

The main limitation of current models is that they are largely based on biochemical analyses using «naked» DNA, whereas in eukaryotic cells, DNA is tightly packed into nucleosomes. Cryo-EM and structural studies show that enzymes such as OGG1 and NEIL1 interact with lesions in nucleosomal DNA via conformational mechanisms distinct from those observed in solution, suggesting that in vitro kinetics do not fully reflect the dynamics of repair within the cell [18-21]. The recently described «triage» behavior of hNEIL1, which can direct damaged bases either to catalytic removal or to a transitional unproductive state, depending on the dynamics of local interaction, illustrates how damage recognition can be regulated by chromatin.

The clinical significance of heterozygous variants of glycosylase genes also remains unclear. Although biallelic mutations in MUTYH and NTHL1 are unambiguously associated with hereditary cancer syndromes, the risk associated with monoallelic variants is a matter of debate. Epidemiological studies have yielded contradictory results, and functional studies have not revealed a stable haploinsufficient phenotype. Solving this problem will require large-scale population genomic studies combined with careful functional stratification of individual variants.

In addition to canonical repair, glycosylases can perform additional regulatory functions. Thus, TDG is a key component of active DNA demethylation, and OGG1 is considered as a potential transcriptional coactivator due to interaction with NF-kB, although this issue remains a subject of discussion. Similarly, it is hypothesized that 8-oxoG can function as a context-dependent epigenetic label, but this concept requires rigorous testing in in vivo models [25-28].

In the context of genomic engineering, BER affects both the efficiency and accuracy of genome editing. Base editors (ABE/CBE) generate repair intermediates, which are subsequently processed by UNG, TDG, and other BER-associated proteins, thereby influencing the results of editing and the range of possible modifications. Thus, modulation of individual glycosylases can provide a strategy for improving the accuracy and controllability of base editing, although the consequences of such approaches in vivo remain poorly understood [18-21].

References

1. Jackson S.P. DNA-damage response signaling and cancer / S.P. Jackson, J. Bartek // Nature Reviews Molecular Cell Biology. – 2019. – Vol. 20, № 4. – P. 197-214. https://doi.org/10.1038/s41580-019-0135-3.

2. Hoeijmakers J.H.J. DNA damage, aging, and cancer / J.H.J. Hoeijmakers // New England Journal of Medicine. – 2016. – Vol. 377, № 7. – P. 640-649. https://doi.org/10.1056/NEJMra1604219.

3. Markkanen E. Not breathing is not an option: How to deal with oxidative DNA damage / E. Markkanen // DNA Repair. – 2017. – Vol. 59. – P. 82-105. https://doi.org/10.1016/j.dnarep.2017.09.002.

4. Sousa M.M.L. DNA glycosylases in genome maintenance and biotechnology / M.M.L. Sousa, H.E. Krokan, G. Slupphaug // Biotechnology Advances. – 2020. – Vol. 42. – 107579. https://doi.org/10.1016/j.biotechadv.2020.107579.

5. Krokan H.E. Base excision repair / H.E. Krokan, M. Bjørås // Cold Spring Harbor Perspectives in Biology. – 2013 (concept updated in recent reviews 2017–2021).

6. Krokan H.E. BER coordination and protein interactions / H.E. Krokan, A.B. Robertson // DNA Repair. – 2017. – Vol. 56. – P. 1-12. https://doi.org/10.1016/j.dnarep.2017.04.002.

7. DNA repair and transcriptional regulation / S. Amente et al // Trends in Genetics. – 2019. – Vol. 35, № 9. – P. 669-682. https://doi.org/10.1016/j.tig.2019.06.002.
8. Lirussi L. DNA Glycosylases Define the Outcome of Endogenous Base Modifications / L. Lirussi, H.L. Nilsen // International Journal of Molecular Sciences. – 2023. – Vol. 24, № 12. – Art. 10307. – https://doi.org/10.3390/ijms241210307.
9. Boiteux S. Repair of 8-oxoG lesions in DNA / S. Boiteux, F. Coste, B. Castaing // Free Radical Biology and Medicine. – 2017. – Vol. 107. – P. 1-12. https://doi.org/10.1016/j.freeradbiomed.2017.01.008.
10. Banda D.M. Repair of 8-oxoG:A mismatches by MUTYH / D.M. Banda, C.R.R. Rocha, C.F.M. Menck // Free Radical Biology and Medicine. – 2017. – Vol. 107. – P. 26-35. https://doi.org/10.1016/j.freeradbiomed.2017.01.008.
11. Oka S. MUTYH, cancer, and genome instability / S. Oka, J. Leon, D. Tsuchimoto // Mutation Research. – 2021. – Vol. 808. – 108423. https://doi.org/10.1016/j.mrrev.2021.108423.
12. van Loon B. An 8-oxoG perspective on mitochondrial genome instability / B. van Loon, U. Hübscher // DNA Repair. – 2019. – Vol. 75. – P. 52-60. https://doi.org/10.1016/j.dnarep.2019.02.006.
13. Mullins E.A. Toxicity and repair of oxidative DNA damage / E.A. Mullins, R. Shi, B.F. Eichman // Cellular and Molecular Life Sciences. – 2017. – Vol. 74, № 18. – P. 3367-3387. https://doi.org/10.1007/s00018-017-2478-8.
14. Oka S. DNA glycosylase encoded by MUTYH functions as a molecular switch for programmed cell death under oxidative stress to suppress tumorigenesis / S. Oka, Y. Nakabeppu // Cancer Science. – 2011. – Vol. 102, № 4. – P. 677-682. https://doi.org/10.1111/j.1349-7006.2011.01869.x.
15. Van Loon B. An 8-oxoG perspective on mitochondrial genome instability / B. van Loon, U. Hübscher // DNA Repair. – 2019. – Vol. 75. – P. 52-60. https://doi.org/10.1016/j.dnarep.2019.02.006.
16. Recent advances in the structural mechanisms of DNA glycosylases / S.C. Brooks et al // Biochimica et Biophysica Acta – Proteins and Proteomics. – 2013. – Vol. 1834. – P. 247-271.
17. Human POLβ gene mutation induces a mutator phenotype in mammalian cells / K.A. Donigan et al // Proceedings of the National Academy of Sciences USA. – 2016. – Vol. 113. – P. E2951-E2959. https://doi.org/10.1073/pnas.1520466113.
18. Focus on DNA Glycosylases – A Set of Tightly Regulated Enzymes with a High Potential as Anticancer Drug Targets / F. Hans et al // International Journal of Molecular Sciences. – 2020. – Vol. 21, № 23. – Art. 9226. https://doi.org/10.3390/ijms21239226.
19. Emerging Roles of DNA Glycosylases and the Base Excision Repair Pathway / E.A. Mullins et al // Trends in Biochemical Sciences. – 2019. – Vol. 44, № 9. – P. 765-781. https://doi.org/10.1016/j.tibs.2019.04.006.
20. Sobol R.W. Mammalian DNA base excision repair: Mechanisms and regulation / R.W. Sobol, S.H. Wilson // Progress in Molecular Biology and Translational Science. – 2020. – Vol. 168. – P. 1-35. https://doi.org/10.1016/bs.pmbts.2019.12.003.
21. Dianov G.L. Mammalian base excision repair: The forgotten archangel / G.L. Dianov, U. Hübscher // Nucleic Acids Research. – 2013. – Vol. 41, № 6. – P. 3483-3490. https://doi.org/10.1093/nar/gkt076 stress.
22. Sykora P. Base excision repair in the mammalian brain: Implication for age-related neurodegeneration / P. Sykora, D.M. Wilson, V.A. Bohr // Mechanisms of Ageing and Development. – 2018. – Vol. 174. – P. 19-27. https://doi.org/10.1016/j.mad.2017.11.001.
23. DNA glycosylases provide antiviral defence in prokaryotes / A.A. Hossain et al // Nature. – 2024. – Vol. 629. – P. 410-416.
24. Single molecule analysis indicates stimulation of MUTYH by UV-DDB through enzyme turnover / S. Jang et al // Nucleic Acids Research. – 2021. – Vol. 49, № 14. – P. 8177-8188. https://doi.org/10.1093/nar/gkab591.
25. 8-Oxoguanine: from oxidative damage to epigenetic and epitranscriptional modification / J.Y. Hahm et al // Experimental & Molecular Medicine. – 2022. – Vol. 54. – P. 1626-1642. https://doi.org/10.1038/s12276-022-00801-x.
26. Dynamics of 8-Oxoguanine in DNA: Decisive Effects of Base Pairing and Nucleotide Context / S.S. Ovcherenko et al // Journal of the American Chemical Society. – 2023. – Vol. 145, № 10. – P. 5201-5213. https://doi.org/10.1021/jacs.3c00421.
27. 8-Oxoguanine DNA Glycosylase1 conceals oxidized guanine in nucleoprotein-associated RNA of respiratory syncytial virus / L. Pan et al // PLoS Pathogens. – 2024. – Vol. 20, № 10. – Article e1012616. https://doi.org/10.1371/journal.ppat.1012616.

28. De Rosa M. Roles for the 8-Oxoguanine DNA Repair System in Protecting Telomeres From Oxidative Stress / M. De Rosa, S.A. Johnson, P.L. Opresko // Frontiers in Cell and Developmental Biology. – 2021. – Vol. 9. – Article 758402. https://doi.org/10.3389/fcell.2021.758402.
29. Cellular Repair of Synthetic Analogs of Oxidative DNA Damage Reveals a Key Structure–Activity Relationship of the Cancer-Associated MUTYH DNA Repair Glycosylase / S.G. Conlon et al // ACS Central Science. – 2024. – Vol. 10, № 2. – P. 291-301. https://doi.org/10.1021/acscentsci.3c00784.
30. OGG1 and MUTYH repair activities promote telomeric 8-oxoguanine induced senescence in human fibroblasts / M. De Rosa et al // Nature Communications. – 2025. – Vol. 16. – Article 893. https://doi.org/10.1038/s41467-025-00345-2.
31. Structure of the mammalian adenine DNA glycosylase MUTYH: insights into the base excision repair pathway and cancer / T. Nakamura et al // Nucleic Acids Research. – 2021. – Vol. 49, № 12. – P. 7154-7163. https://doi.org/10.1093/nar/gkab492.
32. Energetic preference of 8-oxoG eversion pathways in a DNA glycosylase / C. Bergonzo et al // Journal of the American Chemical Society. – 2011. – Vol. 133, № 37. – P. 14504-14506. https://doi.org/10.1021/ja205142d.
33. Cellular repair of synthetic analogs of oxidative DNA damage reveals a key structure–activity relationship of the cancer-associated MUTYH DNA repair glycosylase / S.G. Conlon et al // ACS Central Science. – 2024. – Vol. 10, № 2. – P. 291-301. https://doi.org/10.1021/acscentsci.3c00784.
34. Embryonic lethal phenotype reveals a function of TDG in maintaining epigenetic stability / S. Cortellino et al // Nature. – 2011. – Vol. 470, № 7334. – P. 419-423. https://doi.org/10.1038/nature09672.
35. Dalton S.R. DNA demethylation by TDG / S.R. Dalton, A. Bellacosa // Epigenomics. – 2012. – Vol. 4, № 4. – P. 459-467. https://doi.org/10.2217/epi.12.36.
36. Helicobacter pylori infection downregulates the DNA glycosylase NEIL2, resulting in increased genome damage and inflammation in gastric epithelial cells / I.M. Sayed et al // Journal of Biological Chemistry. – 2020. – Vol. 295, № 32. – P. 11082-11098. https://doi.org/10.1074/jbc.RA120.013933.
37. Novel roles of DNA glycosylases in neurodegenerative diseases and aging / V. Tiwari et al // Neural Regeneration Research. – 2025. – Vol. 21, № 5. – P. 1991-1992. https://doi.org/10.4103/NRR.NRR-D-24-01588.
38. DNA repair glycosylase hNEIL1 triages damaged bases via competing interaction modes / Liu Menghao et al // Nature Communications. – 2021. – Vol. 12. – Article 4108. https://doi.org/10.1038/s41467-021-24431-y.

У. Сарсенбаева[1,2,3]*, А. Алмасбекова[1,2,3], К. Шарипов[2,3], С. Тайпақова[1], М. Сапарбаев[1]
[1]әл-Фараби атындағы Қазақ Ұлттық университеті,
050040, Алматы, Қазақстан Республикасы; әл-Фараби даңғылы 71
[2]М. Айтхожин атындағы Молекулалық биология және биохимия институты,
050012, Алматы, Қазақстан Республикасы, Досмухамедов к-сі 86
[3]С.Ж. Асфендияров атындағы Қазақ ұлттық медицина университеті,
050000, Алматы, Қазақстан Республикасы, Төлеби к-сі 94
*e-mail: ulansarsenbayeva@gmail.com

ГЕНОМ ТҰРАҚТЫЛЫҒЫН САҚТАУДАҒЫ ДНҚ-ГЛИКОЗИЛАЗАЛАРДЫҢ РӨЛІ

Геном тұрақтылығы жасушалардың тіршілікке қабілеттілігінің, организмдердің эволюциялық тұрақтылығының және олардың функционалдық тұтастығын сақтаудың негізі болып табылады. Эндогенді зақымданулар, әсіресе жасушалық метаболизм нәтижесінде пайда болатын азотты негіздердің тотығу арқылы модификациялануы, ДНҚ құрылымын бұзатын негізгі факторлардың бірі болып саналады. Мутациялардың жиналуын болдырмау үшін жасушалар негіздерді кесіп алып тастау арқылы жүретін репарация жүйесін (BER) қолданады, мұнда ДНҚ-гликозилазалар шешуші рөл атқарады. Бұл ферменттер зақымданған немесе қате жұптасқан негіздерді танып, оларды алып тастау арқылы репарация реакцияларының каскадын бастайды.

MutY/MUTYH тұқымдасына жататын адениндік ДНҚ-гликозилазалар зақымданған негіздерді тікелей алып тастамай, гуаниннің тотығу зақымдануы нәтижесінде туындайтын репликациялық қателерді түзетуімен ерекшеленеді. Бактерияларда бұл қызметті MutY ферменті атқарса, эукариоттарда оның гомологы – MUTYH орындайды. Бұл ферменттер G:C → T:A типті транзициялық мутациялардың бекітілуінің алдын алып, спонтанды мутагенез деңгейін едәуір төмендетеді.

Осы шолуда геном тұрақтылығын сақтаудағы ДНҚ-гликозилазалардың рөлі қарастырылып, адениндік ДНҚ-гликозилазаның молекулалық механизмдері, оның BER жүйесіндегі орны, эволюциялық консервативтілігі, сондай-ақ биотехнология, молекулалық генетика және қолданбалы зерттеулердегі маңызы талданады.

Түйін сөздер: *ДНҚ-гликозилаза, 8-оксогуанин, ДНҚ репарациясы, негіздерді кесіп алып тастау арқылы репарация (BER).*

У. Сарсенбаева[1,2,3]*, А. Алмасбекова[1,2,3], К. Шарипов[2,3], С. Тайпақова[1], М. Сапарбаев[1]
[1]Казахский Национальный университет имени аль-Фараби,
050040, Алматы, Республика Казахстан; проспект аль-Фараби 71
[2]Институт молекулярной биологии и биохимии им. М. Айтхожина,
050012, Алматы, Республика Казахстан; ул. Досмухамедова 86
[3]Казахский Национальный Медицинский университет имени С.Д. Асфендиярова,
050000, Алматы, Республика Казахстан, ул. Толеби 94
*e-mail: ulansarsenbayeva@gmail.com

РОЛЬ ДНК-ГЛИКОЗИЛАЗ В ПОДДЕРЖАНИИ СТАБИЛЬНОСТИ ГЕНОМА

Стабильность генома имеет основополагающее значение для жизнеспособности клеток, эволюционной стабильности организмов и сохранения их функциональной целостности. Эндогенные повреждения, в частности окислительная модификация азотистых оснований, возникающая в результате клеточного метаболизма, являются одним из основных факторов, нарушающих структуру ДНК. Чтобы предотвратить накопление мутаций, клетки используют систему репарации эксцизией оснований (BER), в которой ДНК-гликозилазы играют ключевую роль. Эти ферменты распознают и удаляют поврежденные или несоответствующие основания, тем самым инициируя каскад реакций репарации.

Аденин ДНК-гликозилазы, принадлежащие к семейству MutY/MUTYH, уникальны тем, что они не удаляют поврежденные основания напрямую, а скорее исправляют ошибки репликации, возникающие в результате окислительного повреждения гуанина. У бактерий эту функцию выполняет фермент MutY, тогда как у эукариот – его гомолог MUTYH. Эти ферменты предотвращают закрепление мутаций перехода G:C → T:A, тем самым значительно снижая уровень спонтанного мутагенеза.

В данном обзоре обсуждается роль ДНК-гликозилаз в поддержании геномной стабильности, особое внимание уделяется молекулярным механизмам функционирования аденин-ДНК-гликозилаз, их месту в системе BER, эволюционной консервативности, а также их значению в биотехнологии, молекулярной генетике и прикладных исследованиях.

Ключевые слова: *ДНК-гликозилаза, 8-оксогуанин, репарация ДНК, репарация с эксцизией оснований.*

Information about the authors

Ulan Sarsenbayeva* – PhD student, Faculty of Biology and Biotechnology, Al-Farabi Kazakh National University, Almaty, Kazakhstan; e-mail: ulansarsenbayeva@gmail.com. ORCID: https://orcid.org/0009-0003-9292-0153.

Adina Almasbekova – PhD student, Faculty of Biology and Biotechnology, Al-Farabi Kazakh National University, Almaty, Kazakhstan; e-mail: almasbekovaadina94@gmail.com. ORCID: https://orcid.org/0009-0005-9957-1747.

Kamalidin Sharipov – Doctor of Biological Sciences, Professor and Director of the Institute of Molecular Biology and Biochemistry named after M. Aitkhozhin, Almaty, Kazakhstan; e-mail: sharipov.k@kaznmu.kz, ORCID: https://orcid.org/0000-0001-5946-5521.

Sabira Taipakova – PhD, Associate Professor of the Department of Molecular Biology and Genetics, Al-Farabi Kazakh National University, Almaty, the Republic of Kazakhstan; e-mail: sabira.taipakova@gmail.com. ORCID: https://orcid.org/0000-0001-9499-1682.

Murat Saparbayev – candidate biological sciences, professor of the Department of Molecular Biology and Genetics, Al-Farabi Kazakh National University, Almaty, the Republic of Kazakhstan; e-mail: murat.saparbaev@gustaveroussy.fr. ORCID: https://orcid.org/0000-0002-4630-1074.

Авторлар туралы мәліметтер

Улан Базарбаевна Сарсенбаева* – әл-Фараби атындағы Қазақ ұлттық университетінің «Биология және биотехнология» факультетінің докторанты, Алматы қ., Қазақстан Республикасы; e-mail: ulansarsenbayeva@gmail.com. ORCID: https://orcid.org/0009-0003-9292-0153.

Адина Әшірханқызы Алмасбекова – әл-Фараби атындағы қазақ ұлттық университетінің «Биология және биотехнология» факультетінің докторанты, Алматы қ., Қазақстан Республикасы; e-mail: almasbekovaadina94@gmail.com. ORCID: https://orcid.org/0009-0005-9957-1747.

Камалидин Орынбаевич Шарипов – Биология ғылымдарының докторы, профессор, М. Айтхожин атындағы «Молекулалық биология және биохимия» институтының директоры, Алматы қ., Қазақстан Республикасы; e-mail: sharipov.k@kaznmu.kz. ORCID: https://orcid.org/0000-0001-5946-5521.

Сабира Мықтыбекқызы Тайпақова – PhD, әл-Фараби атындағы Қазақ ұлттық университетінің «Молекулалық биология және генетика» кафедрасының қауымдастырылған профессоры, Қазақстан Республикасы; e-mail: sabira.taipakova@gmail.com. ORCID: https://orcid.org/0000-0001-9499-1682.

Мурат Калиевич Сапарбаев – биология ғылымдарының кандидаты, әл-Фараби атындағы Қазақ ұлттық университетінің «Молекулалық биология және генетика» кафедрасының профессоры, Алматы қ., Қазақстан Республикасы; e-mail: murat.saparbaev@gustaveroussy.fr. ORCID: https://orcid.org/0000-0002-4630-1074.

Сведения об авторах

Улан Базарбаевна Сарсенбаева* – докторант факультета «Биологии и биотехнологии», Казахский национальный университет им. аль-Фараби, Алматы, Казахстан; e-mail: ulansarsenbayeva@gmail.com. ORCID: https://orcid.org/0009-0003-9292-0153.

Адина Әшірханқызы Алмасбекова – докторант факультета «Биологии и биотехнологии», Казахский национальный университет им. Аль-Фараби, Алматы, Казахстан; e-mail: almasbekovaadina94@gmail.com. ORCID: https://orcid.org/0009-0005-9957-1747.

Камалидин Орынбаевич Шарипов – Доктор биологических наук, профессор, директор института «Молекулярной биологии и биохимии им. М. Айтхожина», Алматы, Казахстан; e-mail: sharipov.k@kaznmu.kz. ORCID: https://orcid.org/0000-0001-5946-5521.

Сабира Мықтыбекқызы Тайпақова – PhD, ассоциированный профессор кафедры «Молекулярной биологии и генетики», Казахский национальный университет им. аль-Фараби, Алматы, Республика Казахстан; e-mail: sabira.taipakova@gmail.com. ORCID: https://orcid.org/0000-0001-9499-1682.

Мурат Калиевич Сапарбаев – кандидат биологических наук, профессор кафедры молекулярной биологии и генетики, Казахский национальный университет им. аль-Фараби, Алматы, Республика Казахстан; e-mail: murat.saparbaev@gustaveroussy.fr. ORCID: https://orcid.org/0000-0002-4630-1074.

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M.K. Kurmanahynova, Sh.A. Abzhanova*, G.N. Zhaksylykova, A.U. Baibekova, N.K. Akhmetova
Almaty Technological University,
050012, Republic of Kazakhstan, Almaty, Tole bi street, 100
*e-mail: sholpan-ab@mail.ru

EVALUATION OF MICROBIOLOGICAL SAFETY, QUALITY, AND ORGANOLEPTIC PROPERTIES OF BROILER CHICKEN MEAT WITH INCLUSION OF GRAPE SEED MEAL IN THE DIET

Annotation: *The study aimed to evaluate the microbiological safety, quality, and organoleptic properties of broiler chicken meat when grape seed meal was included in the diet. The research was conducted on two groups of broilers: a control group fed a standard balanced diet, and an experimental group whose diet was supplemented with grape seed meal as a source of natural polyphenolic compounds and antioxidants. Microbiological analysis of whole carcasses and livers, collected on the day of slaughter after cooling, showed lower microbial counts in the experimental group. The total count of mesophilic aerobic and facultative*