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Zh.S. Baiguzhina[1,2], A.E. Hasenova[2], Sh.K. Yeleupayeva[3*], A.S. Dinmuhamedova[1], G.S. Alzhanova[2], R.I. Aizman[4], S.M. Bazarbayeva[5], S.R. Khamzina[6], A.Zh. Nusupova[5], Zh.Zh. Zhumagaliyeva[3]

[1] *L.N. Gumilyov Eurasian National University, Astana, Kazakhstan;*
[2] *Branch of the "National Center for Biotechnology" LLP, Stepnogorsk, Kazakhstan;*
[3] *Karaganda Buketov University, Karaganda, Kazakhstan;*
[4] *Novosibirsk State Pedagogical University, Novosibirsk, Russia;*
[5] *M. Kozybayev North-Kazakhstan State University, Petropavlovsk, Kazakhstan;*
[6] *Abay Myrzakhmetov Kokshetau University, Kokshetau, Kazakhstan*
**Corresponding author: karaganda_sh2007@mail.ru*

The importance of bacteria of the genus *Bifidobacterium* in intestinal microbiocenosis

Bifidobacteria are the most common microorganisms in the intestines of healthy breastfed children. The genus *Bifidobacterium* includes bacteria characterized by probiotic properties, such as the induction of immunomodulators, increasing the nutritional value of products due to the assimilation of substrates that are not broken down by the host, anticarcinogenic activity, synthesis of vitamins, production of antimicrobial drugs, which contribute to the promotion of health. Bifidobacteria demonstrate physiological and genetic characteristics including adhesion to the intestinal epithelium, as well as metabolism of glycans in the host body. Multitrophic interaction is formed based on various mechanisms of substrate recognition in the surrounding environment and the transmission of molecular and genetic information, which contributes to survival in the human gastrointestinal tract. Representatives of the *Bifidobacterium bifidum* species constitute a dominant taxon among bifidobacteria, demonstrating significant probiotic properties and extensive potential for the treatment and prevention of various diseases. Currently, a large number of *Bifidobacterium bifidum* species have been sequenced, which are of interest to medicine, biotechnology, and agriculture. Their genetic strategies for colonizing and persisting in the human intestine have been identified. Cross-interaction mechanisms of *Bifidobacterium bifidum* with the host and other microorganisms have been demonstrated using various structures. In this review, we discuss current knowledge about the biology of the genus *Bifidobacterium*, including the biological characteristics of *Bifidobacterium bifidum* species, which exhibit specific adaptations to the human intestine.

Keywords: bifidobacteria, *Bifidobacterium bifidum*, probiotics, human gut microbiota, microbiome, bifidobacterial metabolism, phylogeny, taxonomy.

Introduction

Bacteria of the genus *Bifidobacterium* are anaerobic, Gram-positive microorganisms belonging to the *Actinobacteria* phylum. They have a high G+C content and are common inhabitants of the gastrointestinal tracts of mammals, birds, and some ectothermic animals. The "intestinal microbiota" represents the collective population of microbes residing in the gastrointestinal tract, forming a highly complex microbial community, functions of which exert a significant influence on the physiological processes of the human body [1, 2].

Bifidobacteria were first isolated by Tissier. Members of the *Bifidobacteriaceae* family exhibit various cell shapes, including curved, short, and bifurcated Y-shaped forms. These cells lack capsules, do not form spores, and are non-motile and non-filamentous bacteria [3].

Currently, various ecological relationships have been identified between bacteria of the genus *Bifidobacterium* and their hosts, ranging from pathogenic *(Bifidobacterium scardovii)* to commensal *(Bifidobacterium dentium)* interactions and even those contributing to health promotion *(Bifidobacterium bifidum, Bifidobacterium breve)* [4–6]. Bifidobacteria are among the earliest and most important colonizers of the neonatal human gastrointestinal tract, exerting a broad influence on the early development of the host organism [7, 8]. Among the known health-promoting probiotic microorganisms, bifidobacteria represent one of the most dominant groups, and some species of bifidobacteria are frequently used as probiotic ingredients in various functional food products [9].

An analysis of publications from the last 10 years was conducted using databases such as PubMed, Web of Science, Scopus, and Elsevier. The following terms were employed: "bifidobacteria", "*Bifidobacterium bifidum"*, "probiotics", "human gut microbiota", "microbiome", "bifidobacterial metabolism", phylogeny", "taxonomy", "bifidobacterial genome", and "bifidobacterial glycome". Over 100 publications were examined, and for this review, 67 articles were selected, including randomized, blind, and unbiased studies.

The Bifidobacteriaceae family comprises nine genera: Bifidobacterium, Aeriscardovia, Alloscardovia, Bombiscardovia, Gardnerella, Neoscardovia, Parascardovia, Pseudoscardovia, and Scardovia, encompassing a total of 69 species [10].

Classification and phylogenetic studies of bifidobacteria until the end of the last century were based on the type of peptidoglycans, morphological and physiological properties, biochemical reactions, including carbohydrate fermentation patterns, enzyme activities, DNA G+C content, DNA-DNA hybridization, and 16S rRNA gene sequences [11]. A universal phylogenetic marker applicable to the entire *Bifidobacteriaceae* family has not yet been developed. *Glaeser et al.* argue that phylogeny based on the 16S rRNA gene sequence cannot provide sufficient resolution down to the species level. However, they suggest it should remain a fundamental approach in prokaryotic taxonomy as it reflects common prokaryotic relationships, enables the determination of the phylogenetic placement of both cultivated and uncultivated bacteria, generally provides initial genus assignments, and can reflect the overall phylogenetic diversity of the investigated bacteria. To achieve higher-resolution results in phylogenetic relationships between species within a genus or genera within a family, the authors propose considering a multilocus sequence analysis (MLSA) [12].

Killer et al. proposed a candidate gene for phylogenetic studies within the *Bifidobacteriaceae* family—the gene encoding cytidine triphosphate synthase, which catalyzes the ATP-dependent amination of uridine-5'-triphosphate to cytidine triphosphate, using L-glutamine or ammonia as a nitrogen source. Cytidine triphosphate synthase plays an essential role in RNA synthesis during transcription. It is ubiquitous in bacteria, homologous, exists as a single copy in the genome, undergoes stabilizing selection, is stable concerning rapid genetic modification, and is capable of constructing a reliable phylogenetic tree that maximally reflects the species evolution [13].

Current understanding of the complexity and diversity of bifidobacteria aims to utilize both 16S rRNA gene sequence analysis and sophisticated molecular methods for species and subspecies differentiation [14].

Jarocki et al. conducted an assessment of four molecular methods: ARDRA, RAPD-PCR, rep-PCR, and SDS-PAGE fingerprinting, widely used for the rapid differentiation of bifidobacteria down to the strain level. The results showed that BOX-PCR was the most suitable procedure for accurate identification of 21 strains of bifidobacteria compared to (GTG)5-PCR [15].

Jena et al. also noted the effectiveness of the BOX-PCR method, identifying the taxonomic status of 93 species of bifidobacteria isolated from various human and animal fecal samples [16].

Therefore, alternative molecular methods such as RAPD, MLSA, AFLP, ribotyping, PFGE, RFLP, and rep-PCR have been at the forefront of research for species identification within the *Bifidobacterium* genus. For example, the RAPD method characterized the following bifidobacteria: *Bifidobacterium bifidum, Bifidobacterium infantis, Bifidobacterium adolescentis, Bifidobacterium longum, Bifidobacterium animalis, Bifidobacterium breve* [62]. Some of these protocols are labor-intensive and time-consuming, especially when working with a large number of isolates [14, 15, 17].

Microbial interactions, either microbe-microbe and/or microbe-host, play a crucial role in the successful establishment and maintenance of microbial populations. They occur through the recognition of the environment and the transmission of molecular and genetic information, involving numerous mechanisms that lead to the formation of multitrophic interactions, aiding in survival and adaptation in the complex environment of the human gastrointestinal tract [18].

These mechanisms may include secondary metabolites, siderophores, quorum-sensing systems, biofilm formation, and cell transduction signal transmission. The ultimate unit of interaction is the gene expression of each organism in response to biotic or abiotic stimuli, responsible for the production of molecules involved in these relationships [19]. Microorganisms produce a wide variety of compounds known as secondary metabolites, which do not play a significant role in the growth, development, and reproduction of the producer organism. However, they represent biologically active compounds that can perform crucial functions such as protection, competition, signal transmission, and ecological interactions. Secondary metabolites and their functions have been studied through mass spectrometry and metabolomics [20, 21].

Siderophores are associated with competitive and cooperative interactions among microorganisms and may also play a role in signal transduction and antibiotic activity of microbes [22]. Many bacteria also em-

ploy intercellular communication, known as quorum sensing. It coordinates changes in microbial behavior based on population density. As a result of this system's response, it produces diffusible or secreted signals that vary significantly among different bacterial types. In some species, quorum sensing modulates virulence and is of significant importance for pathogenesis [23].

The formation of biofilms by various microorganisms occurs as a result of ecological stresses, such as insufficient nutrients, the action of antibiotics, pH, bile, and its induction by the quorum sensing system. *Kelly et al.* demonstrated that biofilm formation in *Bifidobacterium* bacteria is induced by high concentrations of bile, as well as individual bile salts, rather than due to acid or osmotic stress. An adaptive response to high bile concentrations was the formation of a biofilm, which included the production of exopolysaccharides, proteins, and the release of extracellular DNA, representing a crucial strategy to avoid the bactericidal effects of bile [24].

The interaction of bifidobacterial chaperones with human proteins suggests the modulating potential of bifidobacteria towards human proteins. It has been revealed that bifidobacterial proteins, capable of interacting with each other and with the host system, play a significant role and can be utilized as therapeutic targets for desired immunomodulation. In other words, probiotics can be used as therapeutic molecules to induce changes in the expression of these proteins, which can be employed to modify their cross-interaction with the human system within the context of prognostic, preventive, and personalized medicine [25].

Bifidobacteria exhibit a diverse range of hosts and demonstrate beneficial properties for their hosts. *Rodriguez et al.*'s study of 400 strains of bifidobacteria revealed that their diversity is highly adapted to specific hosts and the surrounding environment. Strains isolated from the same host showed phylogenetic relatedness, whereas strains from different sources exhibited differences in genome size, auxiliary gene composition, as well as specific features related to amino acid production and carbohydrate degradation [26].

The adaptation of bifidobacteria to hosts is reflected in the evolutionary history of the core genome, as well as in the composition of their auxiliary genes and specific gene sets. At the same time, within the genus, there is insufficient information regarding specialization in specific human habitats or developmental stages, which may be associated with limitations in sample selection or a higher degree of bacterial spread among humans than initially assumed. Thus, the assembly of bifidobacteria in their habitats is determined by a combination of ecological (host filtration) and evolutionary (host adaptation) forces [27].

In some studies, it is noted that the phylogeny of bifidobacteria differs from the phylogeny of hosts. This discrepancy may be associated with niche-specific evolution and the dietary carbohydrates of the hosts. *Satti et al.* investigated the evolutionary relationship between bifidobacteria and animal hosts based on the link between the host's diet and bacterial glycoside hydrolases (GH). Bifidobacterial strains were categorized into 5 groups based on their GH genes, determining differences in the host's diet. The study showed that species isolated from hosts with complex dietary habits had significantly more GH genes than species with simpler dietary patterns [28].

The genus *Bifidobacterium* contains one of the largest collections of representatives of the GH13, GH43, and GH51 families, indicating their ability to outcompete other microbiota for undigested plant-derived dietary fibers in the gut. Members of the GH13 (32.9 % of extracellular GH), GH43 (24 %), and GH51 (12 %) families are typical extracellular enzymes that can benefit the host in gaining access to dietary fibers. Bifidobacteria also have broad enzyme profiles, indicating a preference for mucin glycans, especially O-linked glycans, which may make a significant contribution to their adaptation to the host's lifestyle [29].

There have been several studies attempting comparative genomic analysis of the genus *Bifidobacterium* to explore evolutionarily conserved functional features. It was found that the core functions were associated with adaptation to specific environments or interactions with them. Some of the most common core functions included carbohydrate metabolism, cell wall biogenesis, amino acid biosynthesis, and transport, as well as nucleotide biosynthesis and transport [28, 30, 31].

Representatives of the genus *Bifidobacterium* demonstrate inter-species variations in the sizes of their genomes, reflecting differences in their metabolic capabilities [32].

In several studies, it has been shown that the genus *Bifidobacterium* contains between 400 to 500 core genes. The composition of auxiliary genes (approximately 6400 genes) has been linked to both the source of bacterial isolation and the phylogeny of bifidobacterial strains [26, 30, 31, 32].

The study of specific features, such as amino acid biosynthesis genes, revealed variations among different strains. For instance, strains isolated from bees showed the lowest diversity in amino acid biosynthesis genes, while strains isolated from other host categories carried from 86 to 90 genes. The search for carbohy-

drate-active enzymes showed that strains isolated from the oral cavity encoded the highest number of genes, whereas strains isolated from the adult intestine encoded the lowest number of genes [26].

Thus, the genomes of bifidobacteria also demonstrate adaptation to the host's environment through auxiliary genes and specific gene sets. *Sun et al.* identified that bifidobacteria isolated from bees, pigs, and humans share common unique gene sets. However, the correlation between auxiliary genes and isolation sources was weaker than the connection with phylogeny based on core genes for the entire genus [31]. Consequently, it is suggested that the specialization of bifidobacteria to host species is primarily determined by vertically inherited traits, while horizontal gene transfer of features captured through auxiliary gene composition plays a secondary role. Deb's study also showed that horizontal gene transfer, genome expansion, and reduction events lead to divergence in the metabolic functions of *Bifidobacterium* bacteria [33].

The primary approach providing both taxonomic assignments and information on functional capabilities is "metagenomics" ("metatranscriptomics"), used to determine which genes are present or expressed. Since such studies analyze sequences directly from the sample and do not require an intermediate amplification stage, they provide a relatively objective representation of the genomes present and reveal a set of functional genes that may play a specific role in the host's biology. Sequencing DNA from community samples is straightforward, and the homology of the sequenced genes with enzymes of known function is easily established using bioinformatics methods and constantly improving databases [34].

Lugli et al. also highlight the role of next-generation sequencing, which has provided access to the genome sequences of all currently known bacterial taxa, as well as publicly available databases allowing the comparison of genome sequences among microorganisms, providing information for genomic, phylogenomic, and evolutionary analyses. The authors suggest a phylogenomic approach to confirm new bacterial taxa within the genus Bifidobacterium [35].

The importance of microbial communities lies significantly in their metabolic capabilities, which can potentially be utilized by hosts to expand their ecological range. Examples of such capabilities include the digestion or detoxification of food components, the use of new energy sources, and the production of toxins that can affect the host or pathogenic organisms. Gut microbial interactions constitute a biological network that influences the growth of specific bacterial groups [36].

In vivo studies have identified correlational relationships between the 50 most dominant microbes, of which 38 bacterial genera were directly correlated with the growth of *Bifidobacterium* bacteria — 23 genera with positive correlation and 15 genera with negative correlation [37].

Fernandez-Julia et al. analyzed various types of β-glucans, which have beneficial effects such as reducing energy consumption and cholesterol levels, supporting the immune system, and serving as fermentable substrates for *Bacteroides* and bifidobacteria. The authors demonstrated syntrophic relationships between Bacteroides spp., specializing as primary degraders in the metabolism of complex carbohydrates, and *Bifidobacterium* spp. more often metabolize smaller glycans, particularly oligosaccharides, where they act as secondary degraders [38].

Beyond the probiotic properties of bifidobacteria, their niche adaptation is of great interest as these bacteria survive in the harsh conditions of the human gastrointestinal tract. Some species of bifidobacteria have demonstrated various strategies to overcome gastrointestinal stress, including the impact of digestive enzymes, acidic pH, defensins, and antimicrobial peptides. Most studied strains of *Bifidobacterium adolescentis* and all strains of *Bifidobacterium angulatum* lacked a set of active oxygen forms, explaining their high sensitivity to oxygen. Some presumed transcriptional regulators of stress responses differ among different species and strains, indicating various strategies for the transcriptional regulation of stress-related genes [39].

The genus *Bifidobacterium* consists of bacteria that naturally inhabit various ecological niches, including the gastrointestinal tract of humans and animals. Bifidobacteria are widely used as probiotics because they are associated with health benefits. The formation and persistence of *Bifidobacterium* strains in the intestine depend on the species and strain, natural history, genomic adaptation, metabolic interactions of bacteria with the microbiome, and the host's immune properties, all regulated by the diet. For commercial use, bifidobacterial strains are typically selected for fast growth, antibacterial activity, good adhesive properties, and the utilization of prebiotic substrates. Currently, they represent a significant interest in the development of biotechnology, medicine, and agriculture.

Bifidobacterium bifidum

Bifidobacterium bifidum is a species within the genus *Bifidobacterium* that is widely distributed in the human gut microbiome [40]. It is one of the earliest bacterial species to colonize the intestinal tract, and its

presence positively correlates with concentrations of aromatic lactic acids in the feces of breastfed infants [7]. *Stewart* also associates higher levels of *bifidobacteria* with breastfeeding, and the cessation of breastfeeding leads to a more rapid maturation of the gut microbiome [8]. *Bifidobacterium bifidum*, present in the intestines of infants, is transmitted from the mother through breast milk [41], and its predominance in the gastrointestinal tract of breastfed infants is due to its ability to release monosaccharides from breast milk oligosaccharides [42].

Bifidobacterium bifidum possesses powerful probiotic properties and has significant potential for the prevention and treatment of various human diseases. Currently, it is available as a functional food ingredient and can also be used for therapeutic purposes [43].

Genome and Glycobiome Features

In recent years, the GenBank database of the National Center for Biotechnology Information (NCBI) has accumulated over 100 sequenced genomes of *Bifidobacterium bifidum*, particularly those of interest to the probiotic industry. The deposited NCBI reference genome for Bifidobacterium bifidum is derived from the isolate PRL2010, obtained from infant feces and sequenced and published in 2010 [44]. The authors identified a prevalence of chromosomal loci in *Bifidobacterium bifidum* encoding specific enzymes responsible for mucin degradation. The genome size of *Bifidobacterium bifidum* BGN4, isolated from the feces of a breastfed infant, is approximately 2.2 Mb, comprising 1835 sequences [45]. *Ku et al.* assessed the biofunctionality of BGN4 through in vitro studies (anticancer and immunomodulatory effects), in vivo experiments (allergies and inflammatory bowel diseases), as well as clinical investigations (eczema, irritable bowel syndrome) [46]. *Zhurina et al.* annotated the genome sequence of *Bifidobacterium bifidum* S17, a strain firmly adhering to intestinal epithelial cells and exhibiting potent in vitro and in vivo anti-inflammatory activity [47]. *Gueimonde et al.* reported on the genome sequences of the strain *Bifidobacterium bifidum* LMG13195, capable of interacting with human immune cells and generating functional regulatory T-cells [48]. *Andryuschenko et al.* described the genome sequence project of the strain *Bifidobacterium bifidum* ICIS-310, isolated from the feces of a healthy 5-year-old child. The genome size was 2,219,632 base pairs (G+C content 62.4 %), with 1886 identified coding sequences, including 1718 proteins, 6 rRNA genes, and 52 tRNA genes [49]. *Morita et al.* deciphered the complete genome sequence of *Bifidobacterium bifidum* JCM 1255T, isolated from the feces of a breastfed infant [50].

Various strains of Bifidobacterium bifidum have undergone whole-genome sequencing, revealing specific genetic strategies that enable members of this species to attach to and persist in the human intestine. This is achieved through the synthesis of different types of pili [51, 52] or metabolic properties related to glycans obtained from the host [53].

Enzymes that degrade glycans initiate their action from the non-reducing end of the mucin glycan chain. When all glycans are removed, the protein core of mucin degrades, and the entire mucin polymer network dissolves. This contributes to the degradation of MUC2 mucin and mucus. When using glycans as an energy source, carbohydrate-active enzymes (glycoside hydrolases, sulfatases, and proteases) generate acetate and butyrate (short-chain fatty acids), which are absorbed and utilized by intestinal cells to recover some of the energy expended on the synthesis and secretion of MUC2 mucin [54].

The glycobiome of *Bifidobacterium bifidum* comprises over 3000 genes encoding carbohydrate-active enzymes, including glycosyl hydrolases (sialidases, fucosidosis, exo-β-N-acetylglucosaminidase, endo-β-N-acetylglucosaminidase, β-galactosidases, α-N-acetylglucosaminidase, α-N-acetylgalactosaminidase), glycosyltransferases, and carbohydrate esterases. However, research indicates that carbohydrate metabolism is constrained by a relatively small number of carbohydrates [42, 44].

The interaction between the mucosal layer and the intestinal microbiota develops in parallel during early postnatal life, contributing to the host's homeostasis. The mucosal layer serves as a framework and carbon source for gut microorganisms, while intestinal microorganisms influence the expression of mucin genes, glycosylation, and secretion. The integrity of the mucosal barrier is one of the first lines of defense for the gastrointestinal tract [54].

The interaction of Bifidobacterium bifidum with the host organism and other microorganisms

Commensal gut bacteria establish direct contact with the host using various structures such as pili, fimbriae, proteins, sialidase, human plasminogen receptor, enolase, capsule, etc. [44, 51, 52].

Turroni et al. demonstrated, using the example of *Bifidobacterium bifidum* PRL2010, that pili confer both adhesive properties to intestinal epithelial cells and in vivo immunomodulatory properties to this probiotic [55].

Andryuschenko et al. characterized strains of *Bifidobacterium bifidum* ICIS-504, which have a moderate number of sortase-dependent fimbrial determinants (4 genes with the LPxTG domain) and a small number of genes for two-component signal systems: 5 serine-threonine protein kinases, 8 histidine kinases, and 13 response regulators [56].

Ishikawa et al. identified multiple sortase-dependent proteins and pili in *Bifidobacterium bifidum* YIT 10347 (BF-1) that work collaboratively for adhesion. The "housekeeping" sortase is responsible for anchoring its substrates to the cell wall to ensure their biological function [52].

The interaction of certain strains of *Bifidobacterium bifidum* with the mucous membrane of the gastrointestinal tract is mediated through sialidases, which act as protein adhesins and process various carbohydrates, including oligosaccharides from breast milk. These carbohydrates are essential for the metabolism and growth stimulation of *Bifidobacteria*. Nishiyama et al. investigated the molecular mechanisms of nutrient uptake and adhesion of *Bifidobacterium bifidum* ATCC 15696, involving the exo-α-sialidase SiaBb2. It was found that the mutant strain exhibited reduced adhesion to human intestinal epithelial cells and pig mucin compared to the wild-type strain, highlighting the crucial role of sialidases as adhesins [57].

Other studies have demonstrated that *Bifidobacterium bifidum* PRL2010 targets host mucin glycans for nutrient assimilation. This catabolic process, conserved across different strains, is a significant factor in the colonization of *Bifidobacterium bifidum* [55].

Candela et al. demonstrated that *Bifidobacterium bifidum*, which binds plasminogen, utilizes the key glycolytic enzyme enolase as a surface receptor for human plasminogen [58]. α-enolase is expressed on the surface of various cell types, where it acts as a plasminogen receptor, concentrating plasmin's proteolytic activity on the cell surface. In addition to glycolysis, it possesses other cellular functions and subcellular localizations and is associated with several pathologies such as cancer, Alzheimer's disease, rheumatoid arthritis, and others [59].

Protective mechanisms of bifidobacteria on the intestinal epithelium were studied by *Kainulainen et al.*, showing that three proteins, SERPINB3, PKD1, and PAQR6, are involved in regulating cellular processes related to proliferation, differentiation, apoptosis, as well as inflammation and immunity. Blocking these proteins reduced the adhesion of *Bifidobacterium bifidum* [60].

The surface structure of bifidobacteria involved in the interaction with the host is the surface capsule (a layer of extracellular polysaccharides). It modulates the immune system, enhances bacterial resistance to adverse conditions in the intestine (bile and low pH), and can also serve as a substrate for the growth of other bacteria. Results showed that extracellular polysaccharides significantly increased the growth of lactobacilli and total anaerobic bacteria while inhibiting the growth of enterobacteria, enterococci, and *Bacteroides fragilis* [61].

Rodríguez et al.'s study showed that catalase-positive intestinal bacteria are capable of protecting neighboring catalase-negative bifidobacteria from oxidative stress, thereby providing a mechanism of cross-protection among intestinal bacteria that enhances the survival and colonization of bifidobacteria in the intestine [62].

Many strains of *Bifidobacterium bifidum* exhibit favorable effects, such as antibacterial properties against *Helicobacter pylori* [63], *Escherichia coli*, and *Cronobacter sakazakii* [42, 44]. The beneficial impact of *Bifidobacterium bifidum* also includes the restoration of damaged intestinal mucosa and the reduction of apoptosis in intestinal epithelial cells in a model of necrotizing enterocolitis in newborn rats [64], influence on intestinal barrier function and suppression of colitis [65], lowering cholesterol levels [6], reducing the risk of allergy development [66], protection against type 1 diabetes in early development [41], and improvement of cognitive functions when combined with *Lactobacillus plantarum* [67].

Numerous *in vitro* and *in vivo* studies have been conducted, and their results suggest that bifidobacteria when employed as probiotics, may fulfill crucial functions such as reinforcing the mucosal layer of the intestinal epithelium, shaping a balanced microbiota homeostasis, and contributing to immune system support. However, for bifidobacteria to execute these functions, they must survive the conditions of the human gastrointestinal tract, exhibiting viability in this organ system, i.e., demonstrating the capacity for colonization, competition, persistence in the human intestine, and impact on resident microbial communities. Consequently, further research and clinical trials involving *Bifidobacterium bifidum* are warranted.

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Ж.С. Байгужина, А.Е. Хасенова, Ш.К. Елеупаева, А.С. Динмухамедова, Г.С. Альжанова, Р.И. Айзман, С.М. Базарбаева, С.Р. Хамзина, А.Ж. Нусупова, Ж.Ж. Жумагалиева

Bifidobacterium туысына жататын бактериялардың ішек микробиоценозындағы маңызы

Бифидобактериялар — ана сүтімен тамақтанатын сау балалардың ең кең таралған ішек микроорганизмдері. *Bifidobacterium* туысы денсаулықты нығайтатын және пробиотикалық қасиеттерімен сипатталатын бактериялар, олар иммуномодуляторлардың индукциялау ретінде иесінің денесі ыдыратпайтын субстраттарды сіңіру арқылы тағамның тағамдық құндылығын арттырады, канцерогенге қарсы белсенді, витаминдер синтезін, микробқақарсы препараттарды өндіруде маңызды. Бифидобактериялар ішек эпителийінің адгезиясы, сонымен қатар иесінің ағзасындағы гликандар метаболизмін қамтитын физиологиялық және генетикалық ерекшеліктерге ие. Мультитрофты өзара әрекеттесу қоршаған ортаның субстраттарын танудың және адамның асқазан-ішек жолында өмір сүруге ықпал ететін молекулалық және генетикалық ақпаратты берудің әртүрлі механизмдері негізінде қалыптасады. *Bifidobacterium bifidum* түрінің өкілдері бифидобактериялар арасында басым болып келетін таксондардың бірі, оның пробиотикалық қасиеттері өте жоғары және әртүрлі ауруларды емдеу мен алдын алуда үлкен мүмкіндіктер береді. Қазіргі уақытта медицина, биотехнология және ауыл шаруашылығында қызығушылық тудыратын *Bifidobacterium bifidum* бактериясының көптеген түрлері секвенирленген. Олардың колонизациялануына және адамның ішегінде сақталуына мүмкіндік беретін генетикалық стратегиялары анықталды. *Bifidobacterium bifidum*-дің иесімен және басқа микроорганизмдермен өзара әрекеттесу механизмдері әртүрлі құрылымдарды қолдану арқылы көрсетілді. Мақалада біз *Bifidobacterium* тұқымдасының биологиясына қатысты заманауи деректерді, соның ішінде адамның ішегіне ерекше бейімделуді көрсететін *Bifidobacterium bifidum* түрінің биологиялық ерекшеліктерін талқыладық.

Кілт сөздер: бифидобактериялар, *Bifidobacterium bifidum*, пробиотиктер, адамның ішек микробиотасы, микробиом, бифидобактериялардың метаболизмі, филогения, таксономия.

Ж.С. Байгужина, А.Е. Хасенова, Ш.К. Елеупаева, А.С. Динмухамедова, Г.С. Альжанова, Р.И. Айзман, С.М. Базарбаева, С.Р. Хамзина, А.Ж. Нусупова, Ж.Ж. Жумагалиева

Значение бактерий рода *Bifidobacterium* в микробиоценозе кишечника

Бифидобактерии — наиболее распространенные микроорганизмы в кишечнике здоровых детей, находящихся на грудном вскармливании. К роду *Bifidobacterium* относятся бактерии, характеризующиеся пробиотическими свойствами, такими как индукция иммуномодуляторов; повышение пищевой ценности продуктов за счет усвоения субстратов, не расщепляемых хозяином; антиканцерогенная активность; синтез витаминов; производство противомикробных препаратов, которые способствуют укреплению здоровья. Бифидобактерии демонстрируют физиологические и генетические характеристики, включая адгезию к эпителию кишечника, а также метаболизм гликанов в организме хозяина. Мультитрофическое взаимодействие формируется на основе различных механизмов узнавания субстратов в окружающей среде и передачи молекулярно-генетической информации, что способствует выживанию в желудочно-кишечном тракте человека. Представители вида *Bifidobacterium bifidum* составляют доминирующий таксон среди бифидобактерий, демонстрируя значительные пробиотические свойства и обширный потенциал для лечения и профилактики различных заболеваний. В настоящее время секвенировано большое количество видов *Bifidobacterium bifidum*, представляющих интерес для медицины, биотехнологии и сельского хозяйства. Идентифицированы их генетические стратегии колонизации и персистирования в кишечнике человека. Механизмы перекрестного взаимодействия *Bifidobacterium bifidum* с хозяином и другими микроорганизмами были продемонстрированы с использованием различных структур. В этом обзоре мы обсуждаем современные знания о биологии рода *Bifidobacterium*, включая биологические характеристики видов *Bifidobacterium bifidum*, которые демонстрируют специфическую адаптацию к кишечнику человека.

Ключевые слова: бифидобактерии, *Bifidobacterium bifidum*, пробиотики, микробиота кишечника человека, микробиом, метаболизм бифидобактерий, филогения, таксономия.

Information about the authors

Baiguzhina Zhanar Sailauovna — 3rd-year PhD student, L.N. Gumilyov Eurasian National University, Astana, Kazakhstan; e-mail: janar_ktl@mail.ru;

Hasenova Akmaral Ertuganovna — Head of the Branch of the "National Center for Biotechnology" LLP, Stepnogorsk, Kazakhstan; e-mail: akmaral.hasenova@mail.ru;

Yeleupayeva Shynar Kaukerbekovna — Senior lecturer of the Department of Zoology, Karaganda Buketov University, Karaganda, Kazakhstan; e-mail: karaganda_sh2007@mail.ru;

Dinmuhamedova Aigul Salimzhanovna — Candidate of biological sciences, Acting Professor of the Department of General Biology and Genomics L.N. Gumilyov Eurasian National University, Astana, Kazakhstan; e-mail: a.s.d.14@yandex.ru;

Alzhanova Gulzhan Serzhanovna — Head of the Laboratory of Applied Biotechnology of the Branch of the "National Center of Biotechnology" LLP, Stepnogorsk, Kazakhstan; e-mail: karaganda_sh2007@mail.ru;

Aizman Roman Idelevich — Doctor of biological sciences, Professor, Head of the Department of Anatomy, Physiology and Life Safety, Novosibirsk State Pedagogical University, Novosibirsk, Russia; e-mail: aizman.roman@yandex.ru;

Bazarbayeva Saule Mukhametkalievna — PhD, Senior Lecturer of the Department of Biology, Manash Kozybayev North Kazakhstan State University, Petropavlovsk, Kazakhstan; e-mail: ssdarina12@mail.ru;

Khamzina Saltanat Rashidovna — PhD, Acting Associate Professor of the Department of Ecology, Life Safety and Environmental Protection, Abay Myrzakhmetov Kokshetau University, Kokshetau, Kazakhstan; e-mail: auez_salta@mail.ru;

Nusupova Aigerim Zhasulanovna — Master of Biology, Senior Lecturer at the Department of Biology, North Kazakhstan University named after Manash Kozybayev, Petropavlovsk, aigerim_nusupova@mail.ru;

Zhumagaliyeva Zharkyn — Ph.D. Associate Professor of the Department of Zoology, Karaganda Buketov University, Karaganda, Kazakhstan; e-mail: zharkyn.73@mail.ru.