

Age-related changes in intestinal microflora in elderly women

Bibigul Orunbaeva*

PhD in Biological Sciences
Osh International Medical University
723500, 428 Alymbek Datka Str., Osh, Kyrgyz Republic
Osh State University
723500, 331 Alymbek Datka Str., Osh, Kyrgyz Republic
<https://orcid.org/0000-0003-1922-6512>

Ainagul Zhumabaeva

Lecturer
Osh State University
723500, 331 Alymbek Datka Str., Osh, Kyrgyz Republic
<https://orcid.org/0009-0005-3922-6562>

Jazgul Abdyrakhmanova

Lecturer
Osh State University
723500, 331 Alymbek Datka Str., Osh, Kyrgyz Republic
<https://orcid.org/0000-0001-8706-6675>

Zamirbek Arynov

PhD in Medical Sciences, Associate Professor
Osh International Medical University
723500, 428 Alymbek Datka Str., Osh, Kyrgyz Republic
Osh State University
723500, 331 Alymbek Datka Str., Osh, Kyrgyz Republic
<https://orcid.org/0000-0003-4115-6223>

Aisalkyn Atamkulova

Lecturer
Osh State University
723500, 331 Alymbek Datka Str., Osh, Kyrgyz Republic
<https://orcid.org/0009-0008-3065-6074>

Abstract. The ageing process is accompanied by profound changes in the body's functional systems, including the digestive and microbiological spheres. Processes occurring in the intestinal microflora are of particular importance, as it plays a key role in maintaining homeostasis and immunological stability. The aim of this study was to investigate the characteristics of intestinal microbiological systems in elderly and senile women in the context of age-related changes in metabolic processes and a decrease in the body's resistance. The study was conducted using traditional bacteriological methods of intestinal microflora analysis, including the isolation, quantitative assessment and identification of microorganisms on selective and differential diagnostic culture media in strict compliance with sanitary, hygienic and ethical standards. The analysis showed that women of geriatric age experience pronounced changes in the composition of the intestinal microbiota, characterized by a decrease in the number of representatives of the normal obligate flora and an increase in the proportion of conditionally pathogenic microorganisms, as well as yeast-like fungi of the genus *Candida*. Most of the subjects examined showed signs of grade I-II dysbiotic disorders, indicating a decrease in intestinal colonisation resistance. In a number of cases, the increase in the content of *Candida* fungi exceeded the reference values, indicating a tendency towards candidal transformation of the microbiocenosis. The changes identified reflect a disturbance in microbial homeostasis caused by the combined effects of age-related physiological and metabolic factors, as well as dietary characteristics. The results confirm that the intestinal microflora is a sensitive indicator

Suggested Citation:

Orunbaeva B, Zhumabaeva A, Abdyrakhmanova J, Arynov Z, Atamkulova A. Age-related changes in intestinal microflora in elderly women. J Hum Biol Clin Med, 2026;2(1):40–8.

*Corresponding author



Copyright © The Author(s). This is an open access article distributed under the terms of the Creative Commons Attribution License 4.0 (<https://creativecommons.org/licenses/by/4.0/>)

of the body's ageing processes and can be considered an important biomarker of age-related transformations and the general health status of elderly and senile women

Keywords: intestinal microbiota; putrefactive bacteria; *Candida*; dysbiosis; gerontology; Uzgen district

INTRODUCTION

Age-related changes in the intestinal microflora are currently considered one of the key factors affecting the health of elderly and senile people. Microbial imbalance is associated with decreased immune resistance, metabolic disorders, and an increased risk of developing chronic non-infectious diseases. This problem is particularly significant for postmenopausal women, who experience pronounced hormonal and physiological changes that have an additional impact on the state of microbial homeostasis in the intestine. In the context of global population ageing, the study of age-related changes in the microbiota is of not only medical but also social importance, as it is directly related to the quality of life of older people.

Current research shows that with age, there is a decrease in the diversity of the intestinal microbiota and a reduction in the number of obligate symbiotic microorganisms, primarily bifidobacteria and lactobacilli, with a simultaneous increase in the proportion of conditionally pathogenic and putrefactive flora. The works of R. Ira *et al.* [1] showed that individuals over 65 years of age experience a marked decrease in obligate representatives of the normobiota, accompanied by an increase in enterobacteria and fungi of the genus *Candida*. Similar data were presented by T.S. Ghosh *et al.* [2], who associated age-related changes in the microbiota with digestive disorders, decreased enzymatic activity, and the peculiarities of the eating habits of older people.

A number of studies emphasise the particular vulnerability of the female body during the postmenopausal period. According to M. Yang *et al.* [3], hormonal changes in women are accompanied by significant shifts in the composition of the intestinal microflora, including a decrease in the number of obligate bacteria and an increase in the fungal component of the microbiocenosis. Y. Zhang *et al.* [4] further demonstrated that age-related alterations in the microbiota are microbiota-dependent in nature and exert a significant influence on the processes of systemic inflammation, immunological ageing, and metabolic regulation. The authors conducted a comprehensive analysis of the relationship between the intestinal microbiota and ageing processes, demonstrating that older individuals exhibited an increase in representatives of the phyla *Proteobacteria* and *Bacteroidetes*, accompanied by a simultaneous reduction in *Firmicutes*. The authors established that a decline in the relative abundance of the families Lachnospiraceae, Bacteroidaceae, and Faecalibacterium was characteristic of age-related changes in the microbiome. Of particular significance was the finding of a reduction in the population of beneficial microorganisms,

including *Bifidobacterium*, concurrent with an increase in opportunistic anaerobes. The study concluded that the intestinal microbiota may be regarded as a sensitive indicator of ageing processes.

In parallel, the study by E. Ragonnaud & A. Biragyn [5] focused on the role of the gut microbiota as a key controller of healthy ageing. The authors found that in older people, the composition of intestinal commensals changed with the accumulation of potentially pro-inflammatory commensals and a decrease in beneficial microbes, especially representatives of the phylum Verrucomicrobia, in particular *Akkermansia muciniphila*. *A. muciniphila* was shown to play a critical role in maintaining the integrity of the intestinal barrier and preventing the leakage of bacterial products, which could lead to systemic inflammation. The study emphasised that a reduction in microbial diversity and the loss of beneficial commensals contributed to intestinal permeability and the subsequent development of inflammation, which facilitated the development of age-related diseases. Authors F. Zhang *et al.* [6] noted that multiple factors influenced the composition of the microbiome, including age, gender, diet, comorbidities, and drug therapy. The study emphasised that the intestinal mycobiome was a key factor in both physiological processes (e.g., immune system training) and pathological conditions, including inflammatory bowel disease and metabolic syndromes. Particular attention was paid to the role of *C. albicans* as a major component of the microbiome, although its function in the gastrointestinal tract remained poorly understood.

The study by L. Deng *et al.* [7] investigated age-related changes in the gut microbiota in elderly people and centenarians. The authors showed that older individuals experience shifts in the composition of their microflora, while centenarians maintain a more favourable microbiotic profile with an increased content of beneficial bacteria (*Akkermansia*, *Bifidobacterium*). It was also found that changes in the microbiota are associated with the physical condition of older people, including indicators of muscle strength. The study confirms the importance of the intestinal microflora as a key factor in healthy ageing.

X. Ai *et al.* [8] conducted a cross-sectional study of 100 healthy older people (≥ 60 years). Metagenomic analysis showed that both the taxonomic composition of the microbiota and its functional potential changed with age, and the differences between age groups persisted even when possible confounders were taken into account. The study is important in that it demonstrates age-associated shifts in the microbiota specifically in relatively

healthy elderly people, which makes it convenient for comparison with studies of dysbiotic changes. Y. Wang *et al.* [9] showed that age-related changes in the gut microbiota differ between healthy and pathological ageing and may be associated with a decrease in the body's resistance and the development of chronic diseases.

Thus, analysis of the current literature indicates the high significance of the problem of age-related changes in the intestinal microflora and, at the same time, points to significant gaps in knowledge related to regional characteristics of the formation of the microbiocenosis in elderly and senile women. The lack of data on the state of the intestinal microflora in the female population of the Uzgen district of the Kyrgyz Republic determines the scientific novelty and practical significance of this study. At the same time, despite a significant number of publications devoted to age-related changes in the intestinal microflora, most studies have been conducted in large cities and industrially developed regions. Data on the state of the microbiota in the elderly population of rural areas, especially in Central Asian countries, remain extremely limited.

The aim of this study was to investigate the characteristics of intestinal microbiological systems in elderly and senile women living in the Uzgen district in the context of age-related changes in homeostasis and metabolic processes.

MATERIALS AND METHODS

This study was cross-sectional and descriptive in nature and was conducted in 2024 in the southern part of the Kyrgyz Republic, in the Uzgen district of the Osh region, in the rural district of Kurshab. The study included elderly and senile women permanently residing in the study region. In accordance with the international classification of the World Health Organisation (WHO) [10], women aged 60 to 80 years were included. The sample was formed on the basis of voluntary participation. The inclusion criteria were female gender, age 60 years and older, permanent residence in the Uzgen district, and absence of acute infectious diseases at the time of the examination. Exclusion criteria were taking antibacterial drugs within three months prior to the study, the presence of acute diseases of the gastrointestinal tract, oncological diseases, as well as refusal to sign an informed consent form. Bacteriological research was conducted at the bacteriological laboratory of the Institute for Medical and Biological Research at Osh State University (Osh, Kyrgyz Republic).

A sample size of 34 individuals was considered sufficient for a descriptive microbiological study aimed at identifying the main trends in age-related changes in the intestinal microflora in a limited regional population. The data obtained were considered preliminary and allowed for the identification of characteristic shifts in the microbiocenosis. The study material consisted of faecal samples collected from the women in the morning in volumes of 5-10 g in compliance with

sanitary and hygienic requirements. The biological material was placed in sterile containers designed for microbiological research and delivered to the laboratory no later than 1.5-2 hours after collection at a temperature of +2...+8°C. Prior to analysis, the samples were stored at a temperature of +4°C. Standardised conditions for the collection, transport and storage of material minimised distortions in the microbiological picture. Bacteriological research was conducted at the bacteriological laboratory of the Institute for Medical and Biological Research. For analysis, approximately 1 g of faecal samples were suspended in 9-10 ml of isotonic sodium chloride solution (0.9%), after which the resulting suspension was kept at room temperature for 10-15 minutes to allow large particles to settle. The supernatant was used for sowing on selective and differential diagnostic culture media. The study focused on the main representatives of obligate intestinal microflora (*Escherichia coli*, bifidobacteria, lactobacilli), as well as opportunistic microorganisms and fungi of the genus *Candida*, as the most sensitive markers of dysbiotic changes in older age. The microflora was quantitatively assessed by counting CFU/g. Normal values were taken to be those corresponding to the reference ranges accepted in clinical microbiology: for bifidobacteria and lactobacilli – not less than 10^7 CFU/g, for fungi of the genus *Candida* – not more than 10^3 - 10^4 CFU/g.

Microorganisms were identified based on morphological, tinctorial, cultural, and biochemical characteristics in accordance with Order of the Ministry of Health of the Kyrgyz Republic No. 421 [11] and Order of the Ministry of Health of the Kyrgyz Republic No. 104 [12]. The degree of dysbiotic intestinal disorders was determined by the deviation of quantitative microflora indicators from reference values and classified as dysbiosis of I-II degree in accordance with current methodological recommendations. Statistical data processing was performed using Microsoft Excel. Frequency analysis was applied with the calculation of relative indicators (in percent) and average values. Differences were considered statistically significant at $p < 0.05$. The study was conducted in compliance with the ethical principles of the Declaration of Helsinki [13]. The study protocol was approved by the local ethics committee of Osh State University (protocol No. 1 dated 15 January 2024). Written informed consent to participate in the study was obtained from all participants.

RESULTS AND DISCUSSION

As a result of bacteriological examination of intestinal contents in elderly and senile women ($n = 34$) living in the Uzgen district of the Osh region, significant changes in the quantitative and qualitative composition of the intestinal microflora were established. Quantitative indicators of the main representatives of obligate and conditionally pathogenic microbiota are presented in Table 1.

Table 1. Quantitative indicators of intestinal microflora in elderly and senile women (n = 34)

Microorganisms	Reference values, CFU/g	Actual values, CFU/g	Frequency of deviations, %
<i>Bifidobacterium spp.</i>	$\geq 10^7$	$10^5 - 10^6$	82
<i>Lactobacillus spp.</i>	$\geq 10^7$	$10^5 - 10^6$	79
<i>Escherichia coli</i> (typical forms)	$10^6 - 10^8$	$10^4 - 10^5$	68
Conditionally pathogenic enterobacteria	$\leq 10^4$	$10^5 - 10^6$	61
Fungi of the genus <i>Candida</i>	$\leq 10^3 - 10^4$	$\geq 10^4$	68

Source: developed by the authors

Analysis of the data presented in Table 1 showed that most of the elderly and senile women examined had pronounced dysbiotic changes in their intestinal microflora. The most significant deviations were noted in obligate representatives of the normobiota. A decrease in the quantitative content of *Bifidobacterium spp.* and *Lactobacillus spp.* below the reference values was detected in more than 75% of the examined patients, which indicates a violation of the colonisation resistance of the intestine. At the same time, a significant proportion of patients showed an increase in the number of opportunistic microorganisms and yeast-like fungi of the genus *Candida*. Exceeding the permissible threshold values for *Candida* content was detected in 68% of women, which indicates the formation of a candidal component of dysbiosis. The combination of changes identified corresponds to grade I-II dysbiotic disorders and reflects the characteristic age-related shifts in the intestinal microbiocenosis in women in the gerontological group.

Analysis of the data obtained showed that all women examined (100%) had signs of grade I-II dysbiotic disorders of the intestinal microflora. The most pronounced changes were related to a decrease in the number of obligate representatives of the normobiota. Thus, a decrease in the content of *Bifidobacterium spp.* below the reference values ($\geq 10^7$ CFU/g) was recorded in 82% of those examined, and a decrease in the number of *Lactobacillus spp.* was recorded in 79% of women. A similar trend was observed for typical forms of *Escherichia coli*, whose concentration was below the physiological range ($10^6 - 10^8$ CFU/g) in 68% of patients. Simultaneously with the deficiency of obligate microflora, a significant proportion of the women examined showed an increase in opportunistic microorganisms. An increase in the number of opportunistic enterobacteria above the acceptable level ($\leq 10^4$ CFU/g) was detected in 61% of women. Of particular note is the high frequency of detection of fungi of the genus *Candida*. Exceeding the threshold values for *Candida* content (more than 10^4 CFU/g) was recorded in 23 patients, which accounted for 68% of the total number of those examined.

Thus, elderly and senile women were found to have a combination of obligate microflora deficiency and excessive growth of conditionally pathogenic microorganisms, including fungal components, which indicates a decrease in intestinal colonisation resistance and the formation of persistent dysbiotic changes. The results of the study are of practical importance and allow us to identify the main

directions for the prevention of dysbiotic disorders in elderly and senile women. The identified decrease in obligate microflora and the growth of conditionally pathogenic microorganisms, including fungi of the genus *Candida*, indicate the need to correct dietary factors, in particular, the formation of a rational and balanced diet with sufficient content of dietary fibre and fermented milk products while limiting easily digestible carbohydrates. It is essential to comply with sanitary and hygienic standards, control the quality of drinking water and food, and maintain a healthy lifestyle, including adequate sleep, moderate physical activity, and social involvement of elderly women. Given the high frequency of dysbiotic changes, it seems advisable to use probiotic and prebiotic agents aimed at restoring the normal intestinal flora, as well as conducting periodic microbiological monitoring for early detection and correction of microbial imbalances.

Age-related changes in the intestinal microbiota are considered an important biological mechanism reflecting the processes of ageing and a decrease in the body's adaptive capabilities. In old age, microbial homeostasis undergoes a restructuring, accompanied by a decrease in the number of obligate symbiotic microorganisms and an increase in conditionally pathogenic flora. The results obtained confirm this pattern, since in the study group of elderly and senile women, there was a marked decrease in the main representatives of the normobiota, including bifidobacteria and lactobacilli, as well as an increase in the proportion of conditionally pathogenic microorganisms and fungi of the genus *Candida*.

The fundamental role of the intestinal microbiota in maintaining the physiological balance of the body is described in detail in the review by F. Sommer & F. Bäckhed [14], where the microbiota is presented as a key regulator of the host's immune, metabolic and barrier functions. The authors emphasise that intestinal microbial communities are involved in the formation of immunological resistance and protection against colonisation by pathogens. Consequently, the decrease in the number of obligate bacteria identified in the current study can be considered one of the factors weakening the colonisation resistance of the intestine in elderly women. An additional significance of age-related changes in the microbiota lies in their impact on the systemic state of the body and quality of life. The work of M. Valles-Colomer *et al.* [15] showed that the intestinal microbiota has neuroactive potential and may be associated with psycho-emotional state and overall

well-being. These data suggest that dysbiotic changes characteristic of old age may go beyond local disorders of the gastrointestinal tract and have a broader impact on health, including a decrease in quality of life and increased vulnerability to chronic diseases.

Contemporary research pays particular attention to microbial diversity as an indicator of the stability of the intestinal ecosystem. In a large population metagenome study, A. Zhernakova *et al.* [16] identified markers that determine the variability and diversity of the human microbiome. The authors note that a decrease in microbial diversity is associated with adverse changes in the composition of the intestinal microflora. In the context of the current study, the identified decrease in the number of obligate bacteria and the growth of opportunistic microorganisms may reflect a similar trend towards a decrease in microbiological stability characteristic of the ageing process. Thus, the results of the study are consistent with current ideas that old age is accompanied by a disturbance in microbial balance, a decrease in the protective potential of the normobiota, and an increase in the proportion of conditionally pathogenic flora. These changes can be considered an important biomarker of age-associated transformations in the body and require further study, taking into account regional and alimentary factors.

Age-related changes in the intestinal microbiota are one of the key characteristics of ageing and are accompanied by a disruption in the stability of the microbial community. In old age, there is a decrease in the number of obligate symbiotic bacteria and an increase in conditionally pathogenic flora, which contributes to the formation of dysbiotic conditions. The results confirm this trend, as the examined women of elderly and senile age groups showed a decrease in the content of the main representatives of the normobiota, as well as an increase in the proportion of conditionally pathogenic microorganisms and fungi of the genus *Candida*. Modern ideas about the composition of healthy intestinal microbiota emphasise that it is not a fixed system, but a dynamic ecosystem that changes under the influence of age, nutrition, environmental conditions, and concomitant diseases. A review by E. Rinninella *et al.* [17] shows that with age, there is a restructuring of the microbial balance, accompanied by a decrease in microbial diversity and a reduction in the population of beneficial bacteria, which increases the body's susceptibility to dysbiotic disorders. These findings are consistent with the results of the current study, where most elderly women had a deficiency of bifidobacteria and lactobacilli, reflecting a decrease in the protective potential of the intestinal microbiocenosis.

An additional significance of age-related changes in microflora lies in their close connection with metabolic processes. The work of K.Y. Hur & M.-S. Lee [18] emphasised that the intestinal microbiota plays an important role in regulating metabolism, affecting energy balance, inflammatory reactions and the development of

metabolic disorders. Given that old age is often accompanied by chronic diseases and changes in metabolic processes, the identified dysbiotic changes can be considered as one of the factors contributing to a decrease in the physiological stability of the body and the formation of age-associated pathologies. Of particular interest is the study by C. Xu *et al.* [19] on the progression of age-related changes in the intestinal microbiota. The authors showed that ageing is accompanied by sequential shifts in the composition of microbial communities, including a decrease in the proportion of obligate symbionts and an increase in opportunistic microorganisms. These data confirm that the dysbiotic disorders identified in the current study correspond to the general patterns of microbiological transformations during ageing.

One of the most significant aspects of intestinal microbiota ageing is the change in its stability and individual variability. A classic study by M.J. Claesson *et al.* [20] showed that the microbiota of older people is highly variable and less stable over time compared to younger groups. The authors emphasise that age-related microbiological shifts are accompanied by a decrease in beneficial bacteria and an increase in susceptibility to dysbiosis. These data are consistent with the deficiency of obligate flora in most of the women examined in the current study. A summary of the relationship between the microbiota and ageing processes was presented in a review by P.W. O'Toole & I.B. Jeffery [21], which emphasised that the gut microbiome is one of the key factors influencing immunological ageing and the development of age-associated diseases. The authors consider the microbiota to be an important biomarker of ageing, and dysbiotic changes to be a potential mechanism for reducing the body's resistance in old age. This confirms the relevance of the identified disturbances in microbial balance in women of older age groups.

The phenomenon of chronic low-intensity inflammation, known as inflammageing, is particularly important in older age. A review by P.C. Calder *et al.* [22] showed that age-related inflammation is closely linked to changes in the microbiota and can be exacerbated by unfavourable dietary factors. The authors emphasise the role of nutrition as one of the key modifiable factors affecting the microbial balance and inflammatory background of the body. Consequently, the identified dysbiotic changes may be associated not only with physiological ageing, but also with the nutritional and metabolic status of the women examined. In addition, the intestinal microbiota is considered an important regulator of metabolic health. The work of Y. Fan & O. Pedersen [23] emphasised that disturbances in the microbial composition of the intestine are associated with the development of metabolic diseases and systemic inflammation. Given that old age is often accompanied by metabolic disorders, dysbiosis can be considered an additional risk factor for the deterioration of overall health. Current data emphasise that the menopausal transition

is accompanied by a restructuring of microbial niches and a change in the interaction between the microbiota and the immune system. A review by M.R. Nieto *et al.* [24] showed that a decrease in oestrogen levels in postmenopausal women affects microbial diversity and contributes to the formation of dysbiotic conditions. The authors note that hormonal changes can lead to a decrease in the population of beneficial symbiotic bacteria and an increase in the proportion of opportunistic microorganisms, which increases the vulnerability of older women to inflammatory and metabolic disorders.

The results obtained in the study indicate a high prevalence of dysbiotic disorders of the intestinal microflora in elderly and senile women, which determines the need to develop and implement comprehensive preventive and corrective measures. Given the identified decrease in the number of obligate representatives of the normobiota and the growth of conditionally pathogenic microflora, including fungal microflora, special attention should be paid to the correction of alimentary factors. The diet of elderly and senile women should be balanced and meet the physiological needs of the body, with sufficient dietary fibre, fermented milk products and a restriction on easily digestible carbohydrates, which contribute to the excessive growth of conditionally pathogenic microorganisms. An important aspect of dysbiosis prevention is compliance with sanitary and hygienic standards, including regular personal and household hygiene, and monitoring the quality of drinking water and food. Given the age-related characteristics and reduced adaptive capabilities of the body, the formation of favourable lifestyle conditions plays a significant role, including adequate sleep, moderate physical activity, maintaining optimal temperature and psychological comfort, as well as social involvement of elderly women.

Given the high frequency of dysbiotic changes detected, it seems advisable to use probiotic and prebiotic agents aimed at restoring the normal composition of the intestinal microflora and increasing the body's non-specific resistance. These agents should be used taking into account individual characteristics and under the supervision of specialists. For the timely detection and correction of microbial imbalances, periodic microbiological monitoring of the intestinal flora in elderly and senile women is recommended. This approach will allow for early diagnosis of dysbiotic changes, assessment of the effectiveness of preventive measures, and reduction of the risk of age-related complications.

CONCLUSIONS

The study provided empirical data characterising the state of the intestinal microflora in elderly and

senile women living in the Uzgen district of the Osh region. The results indicate the presence of pronounced age-associated changes in the microbiological profile of intestinal contents, manifested by disturbances in the quantitative and qualitative composition of the microflora. It was found that all the women examined showed signs of grade I-II dysbiotic intestinal disorders, indicating the systemic nature of changes in the microbiocenosis in the geriatric population. The most pronounced shifts were related to a decrease in the number of obligate representatives of the normobiota, primarily *Bifidobacterium* spp. *Lactobacillus* spp. and typical forms of *Escherichia coli*. The deficiency of these microorganisms was accompanied by an increase in the proportion of conditionally pathogenic flora, which indicates a decrease in the colonisation resistance of the intestine in elderly and senile women.

Of particular importance are the results reflecting the growth of fungi of the genus *Candida*, the concentration of which exceeded the reference values in a significant proportion of the subjects examined. The presence of a candidal component in the structure of the microbiocenosis indicates the formation of stable dysbiotic conditions and can be considered as one of the markers of microbial homeostasis disruption in old age. The combination of the identified changes confirms that the intestinal microflora in women of the gerontological group is characterised by a decrease in protective potential and increased vulnerability to dysbiotic processes. The results obtained emphasise the need for early detection of dysbiotic changes in elderly women for the purpose of timely preventive correction. In the future, it is advisable to conduct extended studies with an increase in the number of subjects, the inclusion of control groups, and the use of molecular genetic methods of microbiota analysis, which will allow for a deeper understanding of the mechanisms of age-related changes in the intestinal microflora and increase the evidential value of the data obtained. Another promising area of research is the study of the influence of alimentary and regional factors on the formation of the microbial profile of the intestine in the geriatric population.

ACKNOWLEDGEMENTS

None.

FUNDING

None.

CONFLICT OF INTEREST

None.

REFERENCES

- [1] Ira R, Adwani J, Krishnan AO, Subramanian G, Yadav S, Shukla S, *et al.* Understanding aging through the lense of gut microbiome. *Explor Res Hypothesis Med.* 2024;9(4):294–307. DOI: [10.14218/ERHM.2024.00008](https://doi.org/10.14218/ERHM.2024.00008)

- [2] Ghosh TS, Shanahan F, O'Toole PW. The gut microbiome as a modulator of healthy ageing. *Nat Rev Gastroenterol Hepatol*. 2022;19(9):565–84. DOI: [10.1038/s41575-022-00605-x](https://doi.org/10.1038/s41575-022-00605-x)
- [3] Yang M, Zhai G, Li J, Song Y, Gao Y, Shi Y, et al. Systematic review and meta-analysis: Changes of gut microbiota before and after menopause. *Evid Based Complement Alternat Med*. 2022;2022:3767373. DOI: [10.1155/2022/3767373](https://doi.org/10.1155/2022/3767373)
- [4] Zhang Y, Wang X, Li W, Yang Y, Wu Z, Lyu Y, et al. Intestinal microbiota: A new perspective on delaying aging? *Front Microbiol*. 2023;14:1268142. DOI: [10.3389/fmicb.2023.1268142](https://doi.org/10.3389/fmicb.2023.1268142)
- [5] Ragonnaud E, Biragyn A. Gut microbiota as the key controllers of healthy aging of elderly people. *Immun Ageing*. 2021;18:2. DOI: [10.1186/s12979-020-00213-w](https://doi.org/10.1186/s12979-020-00213-w)
- [6] Zhang F, Aschenbrenner D, Yoo JY, Zuo T. The gut mycobiome in health, disease, and clinical applications in association with the gut bacterial microbiome assembly. *Lancet Microbe*. 2022;3(12):e969–83. DOI: [10.1016/S2666-5247\(22\)00203-8](https://doi.org/10.1016/S2666-5247(22)00203-8)
- [7] Deng L, Wu Y, Li X, Zhang J, Huang R, Chen Q, et al. Gut microbiota characteristics in healthy ageing and longevity: Evidence from elderly adults in China. *Microorganisms*. 2025;13(7):1657. DOI: [10.3390/microorganisms13071657](https://doi.org/10.3390/microorganisms13071657)
- [8] Ai X, Huang C, Liu Q, Duan R, Ma X, Li L, et al. Gut microbiome dynamics and functional shifts in healthy aging: Insights from a metagenomic study. *Front Microbiol*. 2025;16:1629811. DOI: [10.3389/fmicb.2025.1629811](https://doi.org/10.3389/fmicb.2025.1629811)
- [9] Wang Y, Qu Z, Chu J, Han S. Aging gut microbiome in healthy and unhealthy aging. *Aging Dis*. 2024;16:980–1002. DOI: [10.14336/AD.2024.0331](https://doi.org/10.14336/AD.2024.0331)
- [10] World Health Organization. Ageing and health [Internet]. [cited 2025 November 12]. Available from: <https://www.who.int/health-topics/ageing>
- [11] Order of the Ministry of Health of the Kyrgyz Republic No. 421. On Holding a Seminar on Storage, Preparation of Nutrient Media, Quality Control of Research, and Office Work in Bacteriological Laboratories [Internet]. 2010 August 20 [cited 2025 February 19]. Available from: https://prg.kz/Document/?doc_id=30842501
- [12] Order of the Ministry of Health of the Kyrgyz Republic No. 104. On Approval of Methodological Recommendations for Ensuring the Safety of Work in Laboratories when Working with Microorganisms of Pathogenicity Groups I-IV [Internet]. 2010 March 15 [cited 2025 March 16]. Available from: https://continent-online.com/Document/?doc_id=30973294
- [13] The World Medical Association. Declaration of Helsinki: Ethical Principles for Medical Research Involving Human Subjects [Internet]. [cited 2024 December 30]. Available from: <https://surl.lu/athpzg>
- [14] Sommer F, Bäckhed F. The gut microbiota – masters of host development and physiology. *Nat Rev Microbiol*. 2013;11(4):227–38. DOI: [10.1038/nrmicro2974](https://doi.org/10.1038/nrmicro2974)
- [15] Valles-Colomer M, Falony G, Darzi Y, Tigchelaar EF, Wang J, Tito RY, et al. The neuroactive potential of the human gut microbiota in quality of life and depression. *Nat Microbiol*. 2019;4(4):623–32. DOI: [10.1038/s41564-018-0337-x](https://doi.org/10.1038/s41564-018-0337-x)
- [16] Zhernakova A, Kurilshikov A, Bonder MJ, Tigchelaar EF, Schirmer M, Vatanen T, et al. Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. *Science*. 2016;352(6285):565–69. DOI: [10.1126/science.aad3369](https://doi.org/10.1126/science.aad3369)
- [17] Rinninella E, Raoul P, Cintoni M, Franceschi F, Miggiano GAD, Gasbarrini A, et al. What is the healthy gut microbiota composition? A changing ecosystem across age, environment, diet, and diseases. *Microorganisms*. 2019;7(1):14. DOI: [10.3390/microorganisms7010014](https://doi.org/10.3390/microorganisms7010014)
- [18] Hur KY, Lee MS. Gut microbiota and metabolic disorders. *Diabetes Metab J*. 2015;39(3):198–203. DOI: [10.4093/dmj.2015.39.3.198](https://doi.org/10.4093/dmj.2015.39.3.198)
- [19] Xu C, Zhu H, Qiu P. Aging progression of human gut microbiota. *BMC Microbiol*. 2019;19(1):236. DOI: [10.1186/s12866-019-1616-2](https://doi.org/10.1186/s12866-019-1616-2)
- [20] Claesson MJ, Cusack S, O'Sullivan O, Greene-Diniz R, de Weerd H, Flannery E, et al. Composition, variability, and temporal stability of the intestinal microbiota of the elderly. *Proc Natl Acad Sci USA*. 2011;108(Suppl 1):4586–91. DOI: [10.1073/pnas.1000097107](https://doi.org/10.1073/pnas.1000097107)
- [21] O'Toole PW, Jeffery IB. Gut microbiota and aging. *Science*. 2015;350(6265):1214–5. DOI: [10.1126/science.aac8469](https://doi.org/10.1126/science.aac8469)
- [22] Calder PC, Bosco N, Bourdet-Sicard R, Capuron L, Delzenne N, Doré J, et al. Health relevance of the modification of low grade inflammation in ageing (inflammageing) and the role of nutrition. *Ageing Res Rev*. 2017;40:95–119. DOI: [10.1016/j.arr.2017.09.001](https://doi.org/10.1016/j.arr.2017.09.001)
- [23] Fan Y, Pedersen O. Gut microbiota in human metabolic health and disease. *Nat Rev Microbiol*. 2021;19(1):55–71. DOI: [10.1038/s41579-020-0433-9](https://doi.org/10.1038/s41579-020-0433-9)
- [24] Nieto MR, Rus MJ, Areal-Quecuty V, Lubián-López DM, Simon-Soro A. Menopausal shift on women's health and microbial niches. *npj Womens Health*. 2025;3:3. DOI: [10.1038/s44294-024-00045-1](https://doi.org/10.1038/s44294-024-00045-1)

Улгайган жаштагы аялдардын ичеги микрофлорасынын курактык өзгөрүүлөрү

Бибигул Орунбаева

Биология илимдеринин кандидаты
Ош эл аралык медициналык университети
723500, Алымбек Датка көч., 428, Ош ш., Кыргыз Республикасы
Ош мамлекеттик университети
723500, Алымбек Датка көч., 331, Ош ш., Кыргыз Республикасы
<https://orcid.org/0000-0003-1922-6512>

Айнагуль Жумабаева

Окутуучу
Ош мамлекеттик университети
723500, Алымбек Датка көч., 331, Ош ш., Кыргыз Республикасы
<https://orcid.org/0009-0005-3922-6562>

Жазгул Абдырахманова

Окутуучу
Ош мамлекеттик университети
723500, Алымбек Датка көч., 331, Ош ш., Кыргыз Республикасы
<https://orcid.org/0000-0001-8706-6675>

Замирбек Арынов

Медицина илимдеринин кандидаты, доцент
Ош эл аралык медициналык университети
723500, Алымбек Датка көч., 428, Ош ш., Кыргыз Республикасы
Ош мамлекеттик университети
723500, Алымбек Датка көч., 331, Ош ш., Кыргыз Республикасы
<https://orcid.org/0000-0003-4115-6223>

Айсалкын Атамкулова

Окутуучу
Ош мамлекеттик университети
723500, Алымбек Датка көч., 331, Ош ш., Кыргыз Республикасы
<https://orcid.org/0009-0008-3065-6074>

Аннотация. Картаюу процесси организмдин функционалдык системаларында, анын ичинде тамак сиңирүү жана микробиологиялык чөйрөлөрдө терең өзгөрүүлөр менен коштолот. Өзгөчө мааниге ичеги микрофлорасында жүрүп жаткан процесстер ээ, анткени ал гомеостазды жана иммунологиялык туруктуулукту сактоодо негизги роль ойнойт. Бул изилдөөнүн максаты улгайган жана кары курактагы аялдардын ичеги микробиологиялык системаларынын өзгөчөлүктөрүн зат алмашуунун жашка байланыштуу кайра түзүлүшү жана организмдин резистенттүүлүгүнүн төмөндөшү шартында изилдөө болуп саналат. Изилдөө ичеги микрофлорасын талдоонун салттуу бактериологиялык ыкмаларын колдонуу менен жүргүзүлдү. Бул ыкмалар микроорганизмдерди бөлүп алуу, алардын сандык баасын аныктоо жана селективдүү жана дифференциалдык-диагностикалык азыктандыруучу чөйрөлөрдө идентификациялоону камтыйт. Изилдөө санитардык-гигиеналык жана этикалык нормаларды так сактоо менен аткарылды. Жүргүзүлгөн анализ улгайган курактагы аялдардын ичеги микробиотасынын курамында олуттуу өзгөрүүлөр болорун көрсөттү. Бул өзгөрүүлөр нормалдуу облигаттуу флора өкүлдөрүнүн санынын азайышы жана шарттуу-патогендик микроорганизмдердин, ошондой эле *Candida* уруусуна таандык ачыткы сымал козу карындардын үлүшүнүн көбөйүшү менен мүнөздөлөт. Сурамжыланган аялдардын көпчүлүгүндө I-II даражадагы дисбиотикалык бузулуулар белгиленип, бул ичегинин колонизациялык резистенттүүлүгүнүн төмөндөшүн далилдейт. Айрым учурларда *Candida* козу карындарынын көлөмү референттик көрсөткүчтөрдөн ашып, микробиоценоздун кандидоздук трансформациясына болгон тенденцияны көрсөттү. Аныкталган өзгөрүүлөр жашка байланыштуу физиологиялык жана метаболикалык факторлордун, ошондой эле тамактануу өзгөчөлүктөрүнүн биргелешкен таасири менен шартталган микробдук гомеостаздын бузулушун чагылдырат. Алынган жыйынтыктар ичеги микрофлорасы организмдин картаюу процесстеринин сезимтал көрсөткүчү болуп саналарын жана улгайган жана карылык курактагы аялдардын жашына байланыштуу трансформациялануусунун жана жалпы ден соолук абалынын маанилүү биомаркери катары каралышы мүмкүн экенин тастыктайт.

Негизги сөздөр: ичеги микробиотасы; чиритүүчү бактериялар; *Candida*; дисбиоз; геронтология; Өзгөн району

Возрастные изменения кишечной микрофлоры у женщин пожилых групп

Бибигул Орунбаева

Кандидат биологических наук

Ошский международный медицинский университет
723500, ул. Алымбек Датка, 428, г. Ош, Кыргызская Республика
Ошский государственный университет
723500, ул. Алымбек Датка, 331, г. Ош, Кыргызская Республика
<https://orcid.org/0000-0003-1922-6512>

Айнагуль Жумабаева

Преподаватель

Ошский государственный университет
723500, ул. Алымбек Датка, 331, г. Ош, Кыргызская Республика
<https://orcid.org/0009-0005-3922-6562>

Жазгул Абдырахманова

Преподаватель

Ошский государственный университет
723500, ул. Алымбек Датка, 331, г. Ош, Кыргызская Республика
<https://orcid.org/0000-0001-8706-6675>

Замирбек Арынов

Кандидат медицинских наук, доцент

Ошский международный медицинский университет
723500, ул. Алымбек Датка, 428, г. Ош, Кыргызская Республика
Ошский государственный университет
723500, ул. Алымбек Датка, 331, г. Ош, Кыргызская Республика
<https://orcid.org/0000-0003-4115-6223>

Айсалкын Атамкулова

Преподаватель

Ошский государственный университет
723500, ул. Алымбек Датка, 331, г. Ош, Кыргызская Республика
<https://orcid.org/0009-0008-3065-6074>

Аннотация. Процесс старения сопровождается глубокими изменениями в функциональных системах организма, в том числе в пищеварительной и микробиологической сферах. Особое значение приобретают процессы, происходящие в кишечной микрофлоре, поскольку именно она играет ключевую роль в поддержании гомеостаза и иммунологической устойчивости. Целью настоящего исследования являлось изучение особенностей кишечных микробиологических систем у женщин пожилого и старческого возраста в контексте возрастной перестройки обменных процессов и снижения резистентности организма. Исследование проводилось с использованием традиционных бактериологических методов анализа кишечной микрофлоры, включающих выделение, количественную оценку и идентификацию микроорганизмов на селективных и дифференциально-диагностических питательных средах при строгом соблюдении санитарно-гигиенических и этических норм. Проведённый анализ показал, что у женщин геронтологического возраста происходят выраженные изменения в составе кишечной микробиоты, характеризующиеся снижением количества представителей нормальной облигатной флоры и увеличением доли условно-патогенных микроорганизмов, а также дрожжеподобных грибов рода *Candida*. У большинства обследованных выявлены признаки дисбиотических нарушений I-II степени, что свидетельствует о снижении колонизационной резистентности кишечника. Увеличение содержания грибов рода *Candida* в ряде случаев превышало референтные значения, что указывает на тенденцию к кандидозной трансформации микробиоценоза. Выявленные изменения отражают нарушение микробного гомеостаза, обусловленное совокупным воздействием возрастных физиологических и метаболических факторов, а также особенностей питания. Полученные результаты подтверждают, что кишечная микрофлора является чувствительным индикатором процессов старения организма и может рассматриваться как важный биомаркер возрастных трансформаций и общего состояния здоровья женщин пожилого и старческого возраста.

Ключевые слова: кишечная микробиота; гнилостные бактерии; *Candida*; дисбиоз; геронтология; Узгенский район