ISSN 2518-1432 (Online); ISSN 2227-4782 (Print) https://doi.org/10.21856/j-PEP.2026.2.06

GUT MICROBIOTA AND ITS ROLE IN THE DEVELOPMENT OF ENDOCRINE DISEASES: ENDOCRINE AND PHARMACOLOGICAL ASPECTS*

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Over the past decade, concepts of endocrine homeostasis regulation have undergone substantial changes. The classical endocrinological view, which considered hormonal regulation exclusively as interactions between endocrine glands and their peripheral targets, has been expanded by new evidence [1–3] on the role of gut microbiota (GM) as an active participant in endocrine regulation. The microbial community inhabiting the human gastrointestinal tract is now regarded not only as a factor in digestion or immune responses, but also as a functionally significant component of the endocrine system that can modulate hormonal balance and metabolic processes [4].

At present, numerous studies convincingly demonstrate that GM can be viewed as a distinct organ that directly contributes to the functioning of the body as a whole [5, 6].

GM is a complex ecosystem comprising trillions of microorganisms with high metabolic potential [7]. Metabolites produced by the microbiota, including short-chain fatty acids (SCFAs; acetate, propionate, butyrate), secondary bile acids (deoxycholic acid, lithocholic acid), tryptophan-derived metabolites (indole, indole-3-propionic acid), trimethylamine (TMA) and its oxide (TMAO), as well as microbial-derived lipopolysaccharides (LPS), serve as signalling molecules with hormone-like activity. They interact with receptor systems of target cells, influence gene expression, and participate in the regulation of glucose, lipid, and energy metabolism-key processes that lie at the center of clinical endocrinology.

One of the most important aspects of microbiota-endocrine interactions is the effect of GM on insulin secretion and insulin tissue sensitivity. Accumulated experimental and clinical data indicate that disturbances in gut microbiota composition are associated with the development of insulin resistance, which is considered a central pathogenetic link in most endocrine disorders, including type 2 diabetes mellitus (T2DM),

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* The study was initiated by the authors.
The authors declared that this study received no financial support.
The authors guarantee full responsibility for all the information published herein.
The authors guarantee absence of competing interests and their own financial interest when carrying out the research and writing the article.
The manuscript was received by the editorial staff 22.02.2026.

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obesity, and metabolic syndrome. In this context, microbiota acts not merely as a background factor but as an active modifier of the organism's endocrine responses [8]. Therefore, GM may be considered an active endocrine organ.

An important direction of modern research is the study of the role of GM in the regulation of the incretin system, particularly the secretion of glucagon-like peptide-1 (GLP-1) and other intestinal hormones that are crucial for maintaining glycemic control. Impairment of incretin responses is a characteristic feature of endocrine-metabolic diseases, further underscoring the importance of the microbiota as a component of endocrine regulation.

Beyond metabolic effects, GM participates in regulating the hypothalamic-pituitary-adrenal (HPA) axis, affecting cortisol secretion and the body's adaptive responses to stress. This is particularly relevant to endocrinology, as chronic activation of the stress response is considered a risk factor for the development of endocrine pathology, including insulin resistance, thyroid dysfunction, and reproductive disorders. [8–12].

Equally important is the role of GM in thyroid hormone metabolism and the formation of immune tolerance. Evidence suggests that microbiota may influence the bioavailability of micronutrients required for thyroid hormone synthesis and modulate immune mechanisms underlying autoimmune thyroid diseases. Thus, the concept of the gut-thyroid axis is increasingly discussed in the context of endocrine pathology [11, 13, 14].

Taken together, GM emerges as a previously underestimated component of endocrine regulation that integrates metabolic, hormonal, and immune signalling pathways. Recognition of its role substantially expands modern concepts of endocrine disease pathogenesis and provides a theoretical basis for developing new approaches to prevention and treatment in clinical endocrinology [15].

Viewing GM as an integral component of endocrine regulation necessitates a detailed analysis of its interactions with key hormonal systems. Given the multifaceted metabolic and signalling potential of microbiota, its effects are realized not in isolation but through modifying the function of major hormonal axes that determine energy balance, adaptive responses, and reproductive health.

The **aim** of the review: to summarize current experimental and clinical data on the role of the intestinal microbiota as an integral component of endocrine regulation, to determine its importance in the formation of hormonal and metabolic homeostasis, to reveal the mechanisms of dysbiosis in the pathogenesis of major endocrine diseases (T2DM, obesity, thyroid and reproductive pathology) based on a systematic analysis of modern scientific publications indexed in international scientometric databases Scopus, Web of Science Core Collection, PubMed/MEDLINE, Embase, Google Scholar, etc., and to substantiate the prospects of microbiota-oriented approaches in the personalization of endocrine pharmacotherapy.

The next section analyses the role of GM in maintaining hormonal homeostasis, with an emphasis on systems most relevant to clinical endocrinology [13, 16–18].

Gut microbiota and hormonal homeostasis. Hormonal homeostasis results from finely balanced interactions between central and peripheral endocrine axes (including the hypothalamic-pituitary axes and their target glands), metabolic tissues (such as adipose tissue, liver, skeletal muscle), and signalling molecules of diverse origin. In this context, GM serves as an integrative regulatory link that can influence hormone secretion, peripheral hormone action, metabolism, and feedback within endocrine axes. Microbiota effects are mediated through the production of bioactive metabolites, including short-chain fatty acids (acetate, propionate, butyrate), secondary bile acids, indole derivatives, and lipopolysaccharides, modulation of immune responses, regulation of the intestinal barrier, and changes in hormone receptor sensitivity [17, 19].

Insulin and incretins. One of the best studied domains of GM-endocrine interactions is the regulation of glucose homeostasis. GM directly affects enteroendocrine cells that produce incretin hormones, including GLP-1, glucose-dependent insulinotropic polypeptide (GIP), peptide YY (PYY), and cholecystokinin (CCK), peptides involved in the postprandial insulin response [17].

Microbial metabolites, particularly SCFAs, act as signalling molecules that activate specific receptor systems, stimulating incretin secretion and, consequently, insulin secretion. Therefore, microbiota indirectly determines the efficiency of insulin responses and the sensitivity of peripheral tissues to insulin [20].

With dysbiosis, reduced incretin activity, increased intestinal barrier permeability, and systemic endotoxemia, chronic low-grade inflammation is observed. These processes are considered key mechanisms in the development of insulin resistance – the central pathogenetic link of T2DM and other metabolic endocrine disorders.

Alterations in the microbiota profile lead to a diminished incretin response, worsening postprandial insulin secretion and weakening glucagon suppression. At the same time, the endocrine function of adipose tissue changes, including adipokine secretion that is critical for regulating insulin sensitivity [21, 22].

In addition, GM affects the HPA axis, resulting in altered cortisol secretion. Cortisol directly influences gluconeogenesis and insulin resistance. Thus, microbiota is integrated into a complex network of endocrine signalling pathways, dysregulation of which underlies T2DM pathogenesis [23].

Available data on the role of GM in T2DM pathogenesis indicate that its impact extends beyond impaired glucose homeostasis to a broader spectrum of endocrine and metabolic disturbances.

Obesity is central among them. Today, it is viewed not only as a risk factor but also as an independent endocrine disease characterised by adipose tissue dysfunction, disturbed adipokine secretion, and chronic low-grade inflammation.

Because insulin resistance, inflammation, and disrupted hormonal signalling are shared pathogenetic links between T2DM and obesity, GM appears to be an integrating regulator of these conditions. It influences adipose tissue endocrine function, energy balance, and neurohumoral mechanisms controlling appetite, which underlie its key role in the development and progression of obesity [24–27].

Accordingly, the next section focuses on the role of GM in the endocrine regulation of adipose tissue and its significance in obesity pathogenesis.

Obesity as an endocrine disease: the role of microbiota. The modern concept of obesity goes beyond excess fat accumulation and considers it a chronic endocrine disease characterized by disturbed adipokine secretion, hormonal resistance (primarily insulin resistance and leptin resistance), and systemic inflammation. GM is an important pathogenetic factor that determines the development and progression of these disturbances [28].

Dysbiosis promotes increased energy harvest from food, altered appetite regulation, activation of inflammatory cascades, and impaired endocrine function of adipose tissue. As a result, a vicious pathogenetic cycle forms in which microbiota, adipose hormones, and endocrine signalling pathways mutually reinforce adverse metabolic effects.

From an endocrinological perspective, this allows GM to be considered a key modifier of the endocrine characteristics of obesity (including altered adipokine secretion, insulin resistance, leptin resistance, and chronic low-grade inflammation), opening new opportunities for pathogenetically substantiated therapeutic approaches [29–30].

In modern endocrinology, adipose tissue is regarded as a highly active endocrine organ that synthesizes a wide range of hormones and bioactive molecules regulating energy balance, insulin sensitivity, appetite, and systemic inflammation. Impaired endocrine function of adipose tissue is a key pathogenetic link in obesity, which is increasingly classified as an independent endocrine disease. In this context, GM serves as a central regulator, integrating metabolic, immune, and hormonal mechanisms [1, 2].

Gut microbiota and leptin regulation. Adiponectin as a mediator of microbiota-associated endocrine dysfunction. Leptin is one of the key hormones secreted by adipose tissue and regulates appetite, energy expenditure, and neuroendocrine signalling between the periphery and the central nervous system. In obesity, hyperleptinemia accompanied by leptin resistance is typical — a state in which excessive energy intake persists despite high hormone levels [15, 25–27].

GM influences the leptin system through several mechanisms. First, microbial metabolites can modulate leptin expression in adipocytes. Second, dysbiosis is associated with chronic low-grade inflammation that disrupts leptin receptor signalling. Third, microbiota indirectly affect central appetite-regulation mechanisms via the gut-brain axis.

Thus, disruption of microbiota balance contributes to the development of leptin resistance, a key endocrine mechanism that maintains obesity and associated metabolic disorders.

Adiponectin is an adipose tissue hormone with pronounced insulin-sensitizing, anti-inflammatory, and anti-atherogenic properties. Unlike leptin, adiponectin levels decrease in obesity, which promotes insulin resistance and metabolic disturbances.

GM affects adiponectin secretion by regulating adipose tissue inflammation and altering metabolic signalling. Reduced microbial diversity and impaired production of bioactive metabolites are associated with decreased adiponectin expression, which exacerbates endocrine dysfunction of adipose tissue [31, 32].

In this context, microbiota determines the balance between pro- and anti-inflammatory hormonal signals, thereby influencing the course of obesity and its complications.

Chronic low-grade inflammation as an endocrine mechanism. Chronic low-grade systemic inflammation is a fundamental link in the pathogenesis of T2DM. GM plays a leading role in its initiation and maintenance. Disruption of the microbial balance increases intestinal epithelial permeability and translocates bacterial products that activate immune cells and trigger a cascade of pro-inflammatory reactions [3, 7, 15].

From an endocrine perspective, inflammation directly affects tissue hormone sensitivity. Pro-inflammatory mediators impair insulin receptor signalling, suppress incretin responses, and promote resistance to other metabolic hormones.

This creates a vicious cycle in which dysbiosis sustains inflammation and inflammation sustains endocrine dysfunction [27, 33].

GM is therefore considered a key trigger of endocrine-mediated chronic inflammation that determines the course and progression of T2DM.

Role of microbiota in the pathogenesis of type 2 diabetes mellitus. Insulin resistance as a central link in microbiota-associated pathogenesis. T2DM is a complex multifactorial endocrine disease whose pathogenesis combines insulin resistance, progressive pancreatic beta-cell dysfunction, and chronic low-grade inflammation. In recent years, GM has been considered a key pathogenetic modifier integrating metabolic, immune, and hormonal mechanisms involved in T2DM development and progression [15, 29, 30, 34, 35].

Insulin resistance is the defining feature of T2DM and one of the most important mechanisms through which GM influences disease development. Disturbances in microbiota composition are accompanied by decreased SCFA-producing bacteria and disruption of intestinal barrier integrity. This leads to increased entry of bacterial components into the systemic circulation and the formation of metabolic endotoxemia.

At the level of endocrine regulation, dysbiosis reduces insulin receptor sensitivity in the liver, muscle, and adipose tissue, thereby disrupting physiological insulin signalling. As a consequence, insulin requirements increase, leading to compensatory hyperinsulinemia and progressive beta-cell exhaustion. Thus, GM is not only a background factor but an active participant in the formation of insulin resistance — the key endocrine hallmark of T2DM [36–39].

GM actively regulates major endocrine signalling pathways that control glucose homeostasis. Its metabolites influence enteroendocrine cell function, incretin secretion, and insulin signalling cascades.

Through SCFA production and interactions with GPR41 (G-protein-coupled receptor 41), GPR43 (G-protein-coupled receptor 43), and TLR4/5/9 (Toll-like receptors 4, 5, and 9), GM regulates secretion of appetite and metabolism hormones, including ghrelin, leptin, insulin, glucagon-like peptides (GLP-1, GLP-2), peptide YY, cholecystokinin, and serotonin [21, 40–43]. Microbiota metabolites affect intestinal enteroendocrine cells, pancreatic beta-cells, adipocytes, and enterochromaffin cells, thereby

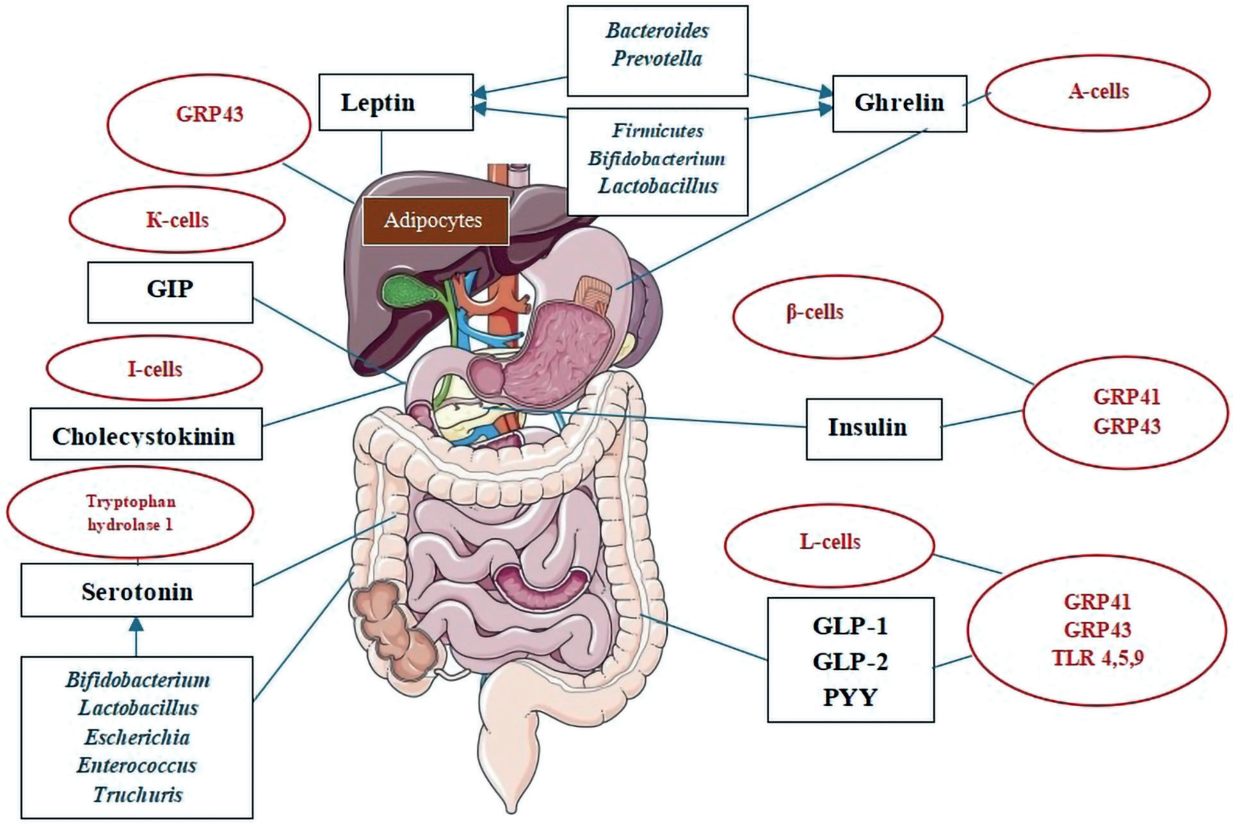

Fig. 1. Mechanisms of receptor-mediated and enzymatic interactions between gut microbiota and the endocrine system.

Notes: Bioactive metabolites of gut microbiota interact with receptor structures GPR41, GPR43, and Toll-like receptors TLR4, TLR5, and TLR9, initiating intracellular signalling cascades that regulate hormone production. SCFAs participate in the modulation of serotonin synthesis by inhibiting the activity of tryptophan hydroxylase-1. In addition, direct effects of specific gut microbiota representatives on the hormone-producing function of enteroendocrine cells have been described. GIP–glucose-dependent insulinotropic polypeptide, GLP-1, GLP-2–glucagon-like peptides 1 and 2, PYY-peptide YY.

integrating microbiota with neuroendocrine regulation of metabolism (Fig. 1) [22, 44–47].

The illustration was created using graphical elements from Servier Medical Art, available under the Creative Commons Attribution 3.0 Generic license, and the digestive system image was subsequently adapted for scientific use.

Microbiota and thyroid diseases. The thyroid gland plays a central role in regulating basal metabolic rate, energy homeostasis, and metabolic adaptation. Thyroid dysfunction is associated with a wide spectrum of systemic endocrine and metabolic disorders. Over recent years, interest in the role of GM in the pathogenesis of thyroid diseases has increased, leading to the concept of the gut-thyroid axis. According to current views, microbiota can influence both immune mechanisms underlying autoimmune thyroid diseases and peripheral thyroid hormone metabolism [14, 48].

Regulation of thyroid homeostasis is another important aspect of GM-endocrine interactions. Microbiota participates in micronutrients required for thyroid hormone synthesis, particularly iodine, selenium, iron, and zinc for thyroid hormone synthesis and affects immune mechanisms that determine tolerance to thyroid antigens [49].

Altered microbiota composition is associated with increased intestinal barrier permeability and immune activation, which may contribute to the development of autoimmune thyroid disease. In this context, the gut-thyroid axis concept explains the relationship between dysbiosis and thyroid pathology through systemic endocrine regulation. In addition, the microbiota may affect peripheral thyroid hormone metabolism, altering bioavailability and hormonal activity in target tissues [50, 51].

Autoimmune mechanisms of microbiotathyroid interactions. Autoimmune thyroid diseases are the most common form of thyroid pathology and a major problem in clinical endocrinology. Current evidence indicates that GM plays a key role in establishing immune tolerance and regulating immune responses, both of which are essential for the regulation of autoimmune processes.

Disruption of microbiota composition is accompanied by reduced intestinal barrier function and increased epithelial permeability. This creates conditions for the translocation of microbial antigens and the activation of the immune system, potentially leading to loss of tolerance to thyroid antigens. Chronic immune activation promotes low-grade systemic inflammation, an important trigger of autoimmune thyroid pathology.

From an endocrinological perspective, the ability of microbiota to influence the balance between pro- and anti-inflammatory immune reactions is particularly important. Dysbiosis is associated with the predominance of pro-inflammatory mechanisms, creating a favourable environment for autoimmune thyroid damage. Thus, GM is considered an immunoenhancer that determines individual susceptibility to autoimmune thyroid disease [20, 52].

Role of gut microbiota in thyroid hormone metabolism. In addition to immune mechanisms, GM participates in the regulation of thyroid hormone metabolism, influencing their bioavailability and peripheral activity. Microbiota can modulate micronutrient metabolism required for thyroid hormone synthesis, particularly iodine and selenium, which are critical for normal thyroid function.

Moreover, the microbiota affects the peripheral conversion of thyroid hormones, altering the ratio of biologically active to less active hormone forms. Dysbiosis may alter thyroid homeostasis even in the absence of structural thyroid lesions, a clinically relevant finding.

From an endocrine perspective, this allows GM to be viewed as a modulator of peripheral thyroid hormone sensitivity and an influence on the clinical phenotype of thyroid diseases. This approach may explain variability in clinical manifestations of thyroid dysfunction and individual differences in response to therapy.

Analysis of the role of GM in thyroid diseases underscores its importance not only as a pathogenetic factor but also as a modulator of hormonal homeostasis at different levels of endocrine regulation. Changes in microbiota composition and functional activity may determine variability of endocrine disease manifestations and influence the effectiveness of standard therapeutic approaches [48, 53].

Sex hormones. GM participates in the regulation of sex hormone metabolism, affecting their circulation, bioavailability, and receptor interactions. Microbial enzyme systems can modify hormonal molecules, altering their activity and half-life [6].

Disruption of microbial balance is associated with reproductive endocrine disorders, including polycystic ovary syndrome, characterized by hyperandrogenism, insulin resistance, and chronic inflammation. In this case, microbiota acts as a shared pathogenetic factor integrating metabolic and reproductive endocrine disturbances.

Therefore, regulation of sex hormone homeostasis cannot be considered in isolation from GM status, emphasizing its significance in modern endocrinology [16, 18, 40, 41].

Overall, GM is a multifunctional regulator of hormonal homeostasis that affects key endocrine axes, including insulin, stress, thyroid, and reproductive systems. Disturbances in microbial balance trigger systemic hormonal shifts that lay the groundwork for the development and progression of endocrine diseases.

Cortisol and the hypothalamic-pituitary-adrenal axis. GM plays an important role in regulating the HPA axis, which ensures adaptation to stressors. The composition and functional status of microbiota can modulate both basal cortisol levels and cortisol secretion in response to stress [19, 23].

Disruption of microbial balance is associated with chronic activation of the HPA axis, leading to elevated cortisol levels. Prolonged hypercortisolemia has well-known endocrine consequences, including insulin resistance, disturbances of fat and protein metabolism, and dysfunction of thyroid and reproductive systems [52, 53]. Thus, GM is considered a factor that shapes individual stress reactivity and indirectly influences the risk of endocrine diseases associated with chronic stress.

Microbiota as a determinant of response to endocrine pharmacotherapy (i.e., pharmacological treatment of endocrine diseases, including antidiabetic, thyroid, and hormonal therapies). The effectiveness of pharmacotherapy in endocrinology is characterized by substantial interindividual variability in clinical response, which cannot always be explained by differences in dosing, treatment duration, or disease severity. Over recent years, evidence has accumulated that GM is an important modifier of responses to endocrine pharmacotherapy, influencing both pharmacokinetic and pharmacodynamic mechanisms of drug action.

From an endocrinological perspective, this allows microbiota to be considered an additional regulator of hormonal treatment responses, which is crucial for therapy personalization.

Variability of response to endocrine therapy: the role of microbiota. One of the most clinically significant problems in endocrine pharmacotherapy is the variability in therapeutic response among patients with similar clinical characteristics. GM can influence this variability through several interrelated mechanisms.

First, the microbiota may modify drug bioavailability by altering intestinal absorption. Impairment of epithelial barrier function and changes in microbial composition can lead to unstable systemic drug concentrations, particularly for hormonal and metabolic agents with narrow therapeutic windows.

Second, GM can indirectly affect hormone receptor sensitivity and the activity of intracellular signalling pathways. In such cases, even adequate drug concentrations may be insufficient to achieve a clinical effect because endocrine responses at the target tissue level are impaired.

Third, dysbiosis is associated with chronic low-grade systemic inflammation, an independent factor that reduces the effectiveness of endocrine therapy. Inflammatory mediators can suppress hormonal signalling, which is especially relevant for the treatment of T2DM, obesity, and thyroid diseases [51, 53, 54].

Thus, the state of the gut microbiota determines not only the risk of endocrine disease development but also the individual response profile to pharmacotherapy.

Potential of microbiota-oriented adjunct strategies. Given the growing understanding of the role of the microbiota in endocrine pharmacotherapy, the development of adjunct strategies to restore microbial balance and enhance the effectiveness of standard treatment is particularly important.

Microbiota-oriented approaches are not considered alternatives to standard endocrine therapy but rather additional tools for optimising hormonal responses. Correction of dysbiosis may reduce systemic inflammation, improve hormone sensitivity, and stabilize metabolic processes, thereby increasing the clinical effectiveness of pharmacotherapy.

From an endocrine perspective, interventions targeting the microbiota may modify not only symptomatic manifestations but also deeper pathogenetic mechanisms underlying hormonal dysfunction. This opens the door to personalized treatment regimens in which microbiota status is considered among the criteria for selecting and adjusting therapy.

CONCLUSIONS

The gut microbiota is an important regulator of endocrine homeostasis, influencing hormone secretion, tissue hormone sensitivity, and immune-inflammatory mechanisms. Disturbances in microbiota composition and functional activity play a key role in the pathogenesis of major endocrine diseases, including type 2 diabetes mellitus, obesity, and thyroid disorders.

Contemporary research indicates that gut microbiota not only contribute to the development of endocrine pathology but also determine individual responses to pharmacotherapy. Considering microbiota as a therapeutic target opens new opportunities for personalized treatment approaches and optimization of clinical outcomes.

Integration of microbiota-oriented strategies into clinical endocrinology has significant potential to improve the prevention and treatment of endocrine diseases and represents a promising direction for further scientific and clinical research.

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Gut microbiota (GM) is increasingly recognized as an integral component of endocrine regulation, contributing to the maintenance of hormonal and metabolic homeostasis. The microbial community of the gastrointestinal tract functions as a metabolically active system capable of producing a wide range of bioactive compounds, including short-chain fatty acids, secondary bile acids, and other signalling molecules with hormone-like activity. These compounds interact with receptor systems in target cells and modulate endocrine signalling pathways. In preparing this paper, we performed a systematic analysis of contemporary scientific publications indexed in international scientometric databases, which allowed us to synthesize current experimental and clinical evidence on the role of gut microbiota in the pathogenesis of endocrine diseases. Dysbiosis is associated with the development of insulin resistance, impaired incretin responses, chronic low-grade systemic inflammation, and metabolic endotoxemia, which are key pathogenetic links in type 2 diabetes mellitus (T2DM) and obesity. We discuss the impact of microbiota on the endocrine function of adipose tissue, leptin and adiponectin secretion, and appetite regulation via the gut-brain axis. We analyze GM involvement in the hypothalamic-pituitary-adrenal (HPA) axis, its influence on cortisol secretion, and organismal adaptive responses to stress. The role of microbiota in thyroid hormone metabolism, immune tolerance, and the development of autoimmune thyroid diseases is highlighted within the concept of the gut-thyroid axis. Particular attention is paid to interactions between the microbiota and sex hormones, and to their relevance to polycystic ovary syndrome and reproductive endocrine disorders. We also consider GM's capacity to modify the pharmacokinetics and pharmacodynamics of endocrine medications, thereby influencing interindividual variability in therapeutic response. The potential of microbiota-oriented adjunct strategies as a tool for personalizing endocrine pharmacotherapy and optimizing the prevention and treatment of endocrine diseases is emphasized.

The aim of the review: to summarize current experimental and clinical data on the role of the intestinal microbiota as an integral component of endocrine regulation, to determine its importance in the formation of hormonal and metabolic homeostasis, to reveal the mechanisms of dysbiosis in the pathogenesis of major endocrine diseases (T2DM, obesity, thyroid and reproductive pathology) based on a systematic analysis of modern scientific publications indexed in international scientometric databases Scopus, Web of Science Core Collection, PubMed/MEDLINE, Embase, Google Scholar, etc., and to substantiate the prospects of microbiota-oriented approaches in the personalization of endocrine pharmacotherapy.

Keywords: gut microbiota, endocrine homeostasis, insulin resistance, type 2 diabetes mellitus, obesity, thyroid hormones, sex hormones, dysbiosis, incretins, review.

КИШКОВА МІКРОБІОТА ТА ЇЇ РОЛЬ У РОЗВИТКУ ЕНДОКРИННИХ ЗАХВОРЮВАНЬ: ЕНДОКРИННО-ФАРМАКОЛОГІЧНІ АСПЕКТИ

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Кишкова мікробіота (КМ) розглядається як інтегральний компонент ендокринної регуляції, що бере участь у підтриманні гормонального та метаболічного гомеостазу організму. Сукупність мікроорганізмів травного тракту функціонує як метаболічно активна система, здатна продукувати широкий спектр біологічно активних сполук, зокрема коротколанцюгові жирні кислоти, вторинні жовчні кислоти та інші сигнальні молекули з гормоноподібною дією, які взаємодіють із рецепторними системами клітин-мішеней та модулюють ендокринні сигнальні шляхи. У процесі підготовки даної роботи було здійснено системний аналіз сучасних наукових публікацій, проіндексованих у міжнародних наукометричних базах, що дозволило узагальнити актуальні експериментальні й клінічні дані щодо ролі кишкової мікробіоти в патогенезі ендокринних захворювань. Показано, що дисбіоз асоціюється з формуванням інсулінорезистентності, порушенням інкретинової відповіді, хронічним системним запаленням низької інтенсивності та метаболічною ендотоксемією, які є ключовими патогенетичними ланками розвитку цукрового діабету 2 типу (ЦД2) та ожиріння. Розглянуто вплив мікробіоти на ендокринну функцію жирової тканини, секрецію лептину і адипонектину, а також регуляцію апетиту через вісь «кишківник–мозок». Проаналізовано участь КМ у функціонуванні осі гіпоталамус–гіпофіз–наднирники, її вплив на секрецію кортизолу та адаптаційні реакції організму на стрес. Висвітлено роль мікробіоти в метаболізмі тиреоїдних гормонів, формуванні імунної толерантності та розвитку автоімунних захворювань щитоподібної залози в межах концепції осі «кишківник–щитоподібна залоза». Окрему увагу приділено взаємодії мікробіоти зі статевими гормонами та її значенню в патогенезі синдрому полікістозних яєчників і репродуктивних ендокринних порушень. Розглянуто здатність КМ модифікувати фармакокінетику й фармакодинаміку ендокринних лікарських засобів, визначаючи індивідуальну варіабельність терапевтичної відповіді. Підкреслено перспективність мікробіота-орієнтованих ад'ювантних стратегій як інструменту персоналізації ендокринної фармакотерапії та оптимізації профілактики й лікування ендокринних захворювань.

Мета огляду: узагальнити актуальні експериментальні та клінічні дані щодо ролі кишкової мікробіоти як інтегрального компонента ендокринної регуляції, визначити її значення у формуванні гормонального та метаболічного гомеостазу, розкрити механізми участі дисбіозу в патогенезі основних ендокринних захворювань (цукрового діабету 2 типу, ожиріння, тиреоїдної та репродуктивної патології) на основі системного аналізу сучасних наукових публікацій, проіндексованих у міжнародних наукометричних базах даних Scopus, Web of Science Core Collection, PubMed/MEDLINE, Embase, Google Scholar та ін., а також обґрунтувати перспективи мікробіота-орієнтованих підходів у персоналізації ендокринної фармакотерапії

Ключові слова: кишкова мікробіота, ендокринний гомеостаз, інсулінорезистентність, цукровий діабет 2 типу, ожиріння, тиреоїдні гормони, статеві гормони, дисбіоз, інкретини, огляд.