



Review Article

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Exploring the Role of Gut Microbiota in Endocrine Disorders: Mechanisms and Therapeutic Implications

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Abstract

Background: Endocrine disorders encompass a wide range of conditions affecting hormone secretion and function, with significant impacts on health and well-being. Emerging research suggests a pivotal role of the gut microbiota in modulating endocrine pathways, thereby influencing the development and progression of various endocrine disorders.

Objective: This review aims to elucidate the mechanisms through which gut microbiota influence endocrine disorders and explore potential therapeutic interventions targeting the gut microbiome.

Materials and Methods: A comprehensive literature search was conducted using electronic databases including PubMed, Google Scholar, and Web of Science. Keywords such as "gut microbiota," "endocrine disorders," "mechanisms," and "therapeutic implications" were utilized to identify relevant studies. Articles published up to January 2024 were included in this review.

Conclusion: The gut microbiota plays a crucial role in modulating endocrine function through various mechanisms including immune modulation, metabolism regulation, and neuroendocrine signaling. Dysbiosis of the gut microbiota has been associated with the pathogenesis of endocrine disorders such as obesity, diabetes, and thyroid dysfunction. Understanding the intricate interplay between gut microbiota and endocrine pathways opens avenues for novel therapeutic strategies including probiotics, prebiotics, and fecal microbiota transplantation. Further research is warranted to elucidate specific microbial targets and optimize therapeutic approaches for the management of endocrine disorders.

Keywords: Gut Microbiota; Endocrine Disorders; Dysbiosis; Therapeutic Interventions

Abbreviations: T2DM: Type 2 Diabetes Mellitus; AITD: Autoimmune Thyroid Diseases; PCOS: Polycystic Ovary Syndrome; FXR: Farnesoid X Receptor; TGR5: Takeda G-protein-coupled Receptor 5; LPS: Lipopolysaccharides; GLP-1: Glucagon-Like Peptide-1; PYY: Peptide YY; CCK: Cholecystokinin; HPA: Hypothalamic-Pituitary-Adrenal; FMT: Fecal Microbiota Transplantation; RCTs: Randomized Controlled Trials.

Introduction

Endocrine disorders, characterized by dysregulation of hormone production or action, pose significant health challenges globally. While traditional factors such as genetics and lifestyle have been implicated in their etiology, emerging research highlights the crucial role of the gut microbiota in modulating endocrine function. The human gut harbors a

Surbhi Tyagi and Saurabh Tyagi. Exploring the Role of Gut Microbiota in Endocrine Disorders: Mechanisms and Therapeutic Implications. Clin J Dia Care Control 2024, 6(1): 180052. diverse ecosystem of microorganisms, collectively known as the gut microbiota, which plays a pivotal role in maintaining host homeostasis and influencing various physiological processes [1-3]. The intricate interplay between intestinal microbiota and the endocrine system has garnered considerable attention in recent years. Understanding the mechanisms underlying this interaction is essential for unraveling the focalization of endocrine disorders and exploring novel therapeutic strategies. This review aimss to provide a comprehensive overview of the role of gut microbiota in endocrine disorders, focusing on the basic mechanisms and therapeutic implications.

Gut Microbiota Composition and Endocrine Health

The gut microbiota, a diverse community of microorganisms inhabiting the gastrointestinal tract, plays a analytic role in maintaining host health and regulating various physiological processes, including endocrine function. This intricate relationship involves bidirectional communication between the gut microbiota and the endocrine system, influencing hormone secretion, metabolism, and signaling pathways. Understanding the composition of the gut microbiota and its effect on endocrine health requires a detailed examination of microbial diversity, host-microbe interactions, and underlying mechanisms [4].

Microbial Diversity and Composition: The gut microbiota is composed of trillions of microorganisms, predominantly bacteria, but also including viruses, fungi, archaea, and other microbial species. Firmicutes, Bacteroidetes, Actinobacteria, and Proteobacteria are among the predominant bacterial phyla in the human gut, with species-level diversity influenced by numerous factors, including diet, genetics, age, geography, medications, and lifestyle [5,6]. Microbial composition varies along the length of the gastrointestinal tract, with distinct microbial communities inhabiting different regions, such as the stomach, small intestine, and colon. The colonic microbiota, in particular, harbors the highest microbial density and diversity, playing a crucial role in nutrient metabolism, fermentation, and host-microbe interactions [4-8].

Dysbiosis and Endocrine Disorders: Disruptions in gut microbiota composition and function, termed dysbiosis, have been implicated in the pathogenesis of various endocrine disorders, including obesity, type 2 diabetes mellitus (T2DM), autoimmune thyroid diseases (AITD), adrenal disorders, and polycystic ovary syndrome (PCOS). Dysbiosis may manifest as alterations in microbial diversity, abundance, community structure, and metabolic activity, leading to metabolic dysregulation, inflammation, and hormonal imbalances [9-13].

Material and Methods

For this review, a comprehensive literature search was conducted using electronic databases such as PubMed, Scopus,

and Web of Science. Keywords including "gut microbiota," "endocrine disorders," "dysbiosis," "metabolism," and "therapeutic interventions" were used to identify relevant articles published up to 2024. Studies investigating the role of gut microbiota in endocrine disorders, including both experimental and clinical research, were included. Relevant articles were screened based on their titles and abstracts, and full-text articles were retrieved for detailed evaluation. The selected articles were then analyzed to extract information on the mechanisms underlying the influence of gut microbiota on endocrine function and the therapeutic implications of modulating gut microbial composition. Data synthesis and interpretation were performed to generate insights into the current understanding of the topic and identify gaps in knowledge. The findings were organized into sections based on thematic content, and critical analysis was conducted to provide a comprehensive overview of the subject matter.

Mechanisms Underlying Gut Microbiota-Endocrine Interactions

The mechanisms underlying gut microbiota-endocrine interactions are multifaceted and involve intricate communication pathways between the gut microbiota, host cells, and various components of the endocrine system. Here's a detailed exploration of these mechanisms:

Metabolite Production

Short-Chain Fatty Acids: Gut bacteria ferment dietary fibers to produce SCFAs such as acetate, propionate, and butyrate. SCFAs act as signaling molecules that bind to G protein-coupled receptors (GPCRs) on enteroendocrine cells and other host cells, modulating hormone secretion and metabolic processes [7,14].

Bile Acids: Gut bacteria play a crucial role in bile acid metabolism, converting primary bile acids synthesized by the liver into secondary bile acids. Bile acids act as ligands for nuclear receptors such as the farnesoid X receptor (FXR) and the Takeda G-protein-coupled receptor 5 (TGR5), regulating glucose and lipid metabolism, as well as gut hormone secretion [15].

Neurotransmitters: Certain gut bacteria produce neurotransmitters such as serotonin, dopamine, and γ -aminobutyric acid (GABA), which can influence neuronal signaling in the enteric nervous system and the central nervous system, thereby affecting endocrine function and metabolic regulation [16-18].

Gut Barrier Function

The gut microbiota contributes to the maintenance of gut barrier integrity through the production of mucusdegrading enzymes, antimicrobial peptides, and tight junction proteins. Dysbiosis-induced disruption of the gut barrier can lead to increased intestinal permeability (leaky gut), allowing translocation of microbial products such as lipopolysaccharides (LPS) into the systemic circulation, triggering inflammation and endocrine dysfunction [16].

Enteroendocrine Cell Activation

Enteroendocrine cells scattered throughout the gastrointestinal tract sense luminal nutrients, microbial metabolites, and bacterial antigens through various receptors and sensory mechanisms. Activation of enteroendocrine cells leads to the secretion of hormones such as glucagon-like peptide-1 (GLP-1), peptide YY (PYY), cholecystokinin (CCK), and ghrelin, which regulate appetite, satiety, gastrointestinal motility, insulin secretion, and glucose homeostasis [17].

Immune Modulation

The gut microbiota interacts with the host immune system, influencing the balance between pro-inflammatory and anti-inflammatory responses. Dysbiosis-induced immune dysregulation can contribute to chronic low-grade inflammation, insulin resistance, and the development of endocrine disorders such as obesity and type 2 diabetes [16,17].

Microbial Endocrinology

Some gut bacteria produce hormones or hormone-like molecules that mimic host hormones or modulate host hormone signaling pathways. For example, certain bacteria can produce catecholamines or metabolize host hormones such as estrogen, affecting host physiology and endocrine function [18].

Genetic and Epigenetic Interactions

Host genetics and epigenetic factors can influence gut microbiota composition and function, while microbial metabolites and signaling molecules can in turn modulate host gene expression and epigenetic modifications, creating a bidirectional interaction between the gut microbiota and the host endocrine system [19]. Understanding these intricate mechanisms of gut microbiota-endocrine interactions provides insights into the pathophysiology of endocrine disorders and offers opportunities for developing microbiota-targeted interventions for disease prevention and treatment. However, further research is needed to elucidate the specific microbial species, metabolites, and signaling pathways involved in these interactions and their implications for human health.

Impact on Obesity and Metabolic Disorders

Obesity and metabolic disorders represent major public health challenges worldwide, characterized by aberrant

energy metabolism and dysregulated glucose and lipid homeostasis. Over the past decade, numerous studies have highlighted the significant influence of gut microbiota on obesity and metabolic health [20]. The gut microbiota participates in energy harvest and storage through the fermentation of dietary fibers and the production of SCFAs, which can modulate host metabolism and energy expenditure. Additionally, alterations in gut microbiota composition, termed dysbiosis, have been observed in individuals with obesity and metabolic syndrome, characterized by a decrease in microbial diversity and an overabundance of certain taxa, such as Firmicutes and a reduction in Bacteroidetes [21,22]. Dysbiosis-induced inflammation and metabolic endotoxemia contribute to insulin resistance, adipose tissue inflammation, and dyslipidemia, further exacerbating metabolic dysfunction.

Moreover, gut microbiota-derived metabolites, such as lipopolysaccharides (LPS), trimethylamine N-oxide (TMAO), and bile acids, exert profound effects on host metabolism and inflammation, thereby influencing the development of obesity and metabolic disorders. For instance, elevated levels of circulating LPS, stemming from gut dysbiosis and increased intestinal permeability, can trigger low-grade inflammation and insulin resistance. Similarly, TMAO, produced from dietary choline and carnitine by gut bacteria, has been implicated in the pathogenesis of atherosclerosis and cardiovascular disease by promoting macrophage foam cell formation and impairing cholesterol metabolism. Furthermore, the gut microbiota interacts with host appetite-regulating hormones, such as leptin and ghrelin, modulating food intake and energy balance. Dysbiosisinduced alterations in gut hormone signaling can contribute to appetite dysregulation and excessive weight gain. Collectively, these findings underscore the pivotal role of gut microbiota in obesity and metabolic disorders and highlight the therapeutic potential of targeting gut microbiota to mitigate these conditions [23,24].

Impact on Thyroid Function

The thyroid-gutaxis represents a bidirectional communication system wherein gut microbiota influence thyroid hormone metabolism and vice versa. Key mechanisms include:

Thyroid Hormone Metabolism

Gut microbiota contribute to the metabolism and recycling of thyroid hormones through deiodination processes, affecting systemic thyroid hormone levels and bioavailability [25].

Immune Modulation

Dysbiosis-induced inflammation and immune dysregulation may trigger autoimmune thyroid disorders, such as

Hashimoto's thyroiditis and Graves' disease, highlighting the role of gut microbiota in immune-mediated thyroid dysfunction [26].

Nutrient Absorption and Synthesis

Optimal nutrient absorption, particularly iodine, selenium, and tyrosine, is essential for thyroid hormone synthesis. Alterations in gut microbiota composition may impair nutrient uptake, compromising thyroid function [27].

Gut Barrier Integrity

Intestinal permeability, influenced by gut microbiota, plays a crucial role in preventing the translocation of harmful substances and antigens that could trigger autoimmune thyroiditis [28,29]. The elucidation of mechanisms underlying gut-thyroid axis interactions offers new insights into the pathogenesis and treatment of thyroid dysfunction. Continued research efforts are essential to translate these findings into clinical practice and improve patient outcomes in the realm of endocrine health.

Implications for Diabetes Management

The gut microbiota plays a pivotal role in the pathophysiology of diabetes mellitus, influencing insulin sensitivity, glucose metabolism, and systemic inflammation. Understanding the interplay between gut microbiota and diabetes holds significant implications for diabetes management:

Personalized Nutrition

Tailored dietary interventions based on an individual's gut microbiota profile can optimize glycemic control and metabolic parameters in diabetes management [30].

Microbiota-Based Therapeutics

Development of microbiota-based therapeutics, such as microbial-based drugs or microbial metabolite supplementation, may offer novel treatment approaches for diabetes by targeting gut dysbiosis [31].

Early Detection Biomarkers

Gut microbiota composition and activity can serve as potential biomarkers for early detection of diabetes risk and progression, enabling timely intervention and prevention strategies [32].

Integrated Approaches

Integrating gut microbiota modulation strategies into existing diabetes management protocols, including lifestyle interventions and pharmacotherapy, may enhance treatment efficacy and metabolic outcomes [33,34].

Role in Adrenal Disorders

Adrenal disorders encompass a range of conditions affecting the adrenal glands, including adrenal insufficiency, Cushing's syndrome, and adrenal tumors. While research on the connection between gut microbiota and adrenal disorders is still in its infancy, preliminary findings suggest significant interactions.

Adrenal Insufficiency

The adrenal glands play a crucial role in producing hormones such as cortisol and aldosterone, vital for regulating metabolism, immune function, and blood pressure. Disruptions in gut microbiota composition may influence adrenal hormone synthesis and secretion, contributing to adrenal insufficiency [35].

Cushing's Syndrome

Excess cortisol production characterizes Cushing's syndrome, often due to adrenal tumors or prolonged glucocorticoid therapy. Gut dysbiosis may exacerbate cortisol excess by modulating the hypothalamic-pituitary-adrenal (HPA) axis, leading to adrenal hyperactivity and dysregulation [36,37].

Adrenal Tumors

Although the direct link between gut microbiota and adrenal tumors remains unclear, emerging evidence suggests potential indirect effects through systemic inflammation, immune modulation, and metabolic alterations influenced by gut microbial composition [38,39].

Role in Polycystic Ovary Syndrome (PCOS)

Polycystic ovary syndrome (PCOS) is a common endocrine disorder characterized by hyperandrogenism, ovulatory dysfunction, and insulin resistance. Emerging evidence suggests that gut microbiota dysbiosis may contribute to the pathogenesis of PCOS. Alterations in gut microbial composition and function have been observed in women with PCOS, correlating with metabolic disturbances and reproductive dysfunction [40].

Mechanistically, gut dysbiosis in PCOS is associated with increased intestinal permeability, chronic lowgrade inflammation, and altered production of microbial metabolites. These perturbations contribute to insulin resistance, hyperandrogenism, and dysregulated ovarian function, hallmark features of PCOS [41]. Therapeutically, targeting gut microbiota may offer a novel approach for managing PCOS. Interventions such as probiotics, dietary fiber supplementation, and microbiota-targeted therapies hold promise in improving metabolic and reproductive 5

outcomes in women with PCOS by restoring microbial balance and ameliorating associated metabolic disturbances [42-44].

Confounding Factors

The composition of gut microbiota is influenced by various factors such as diet, genetics, age, and medication, which can confound the association between gut microbiota and endocrine disorders. For instance, dietary patterns significantly shape microbial diversity and function, and differences in diet across study populations can lead to variability in outcomes. Genetic factors also play a role in determining individual microbiota profiles and their metabolic capabilities. Additionally, age-related changes in gut microbiota composition and the use of medications such as antibiotics and probiotics can further complicate the interpretation of results. Addressing these confounding variables is essential for accurately assessing the relationship between gut microbiota and endocrine health.

Therapeutic Implications

Probiotics and Prebiotics: Targeted manipulation of the gut microbiota through probiotics (beneficial microorganisms) and prebiotics (substrates for beneficial microorganisms) holds promise for managing endocrine disorders. Probiotic supplementation has shown potential in improving insulin sensitivity and modulating immune responses in diabetes [45].

Dietary Interventions: Dietary modifications, such as fiberrich diets that promote microbial diversity, can positively influence gut microbiota composition and metabolic health. Personalized nutrition strategies based on individual microbiota profiles may optimize therapeutic outcomes [46,47].

Fecal Microbiota Transplantation (FMT): FMT, the transfer of fecal microbiota from a healthy donor to a recipient, represents an emerging therapeutic approach for restoring microbial balance and treating certain endocrine disorders. Clinical trials investigating FMT in conditions like obesity and metabolic syndrome are ongoing [48,49].

Methodological Limitations

While this review provides a comprehensive overview of the current understanding of gut microbiota and endocrine disorders, several methodological limitations should be considered. Firstly, there is a potential bias in study selection, as the inclusion criteria may inadvertently favor studies with positive findings, leading to publication bias. Secondly, methodological heterogeneity among the reviewed studies, including differences in study design, sample size, and microbial analysis techniques, could affect the reliability and generalizability of the findings. Thirdly, many studies rely on animal models or in vitro experiments, which may not fully replicate the complexities of human gut microbiotaendocrine interactions. Acknowledging these limitations is crucial for interpreting the results and drawing meaningful conclusions.

Future Directions

Future research in the field of gut microbiota and endocrine disorders should address several key areas to advance our understanding and translation of findings into clinical practice:

Longitudinal Cohort Studies

There is a need for long-term cohort studies to monitor changes in gut microbiota composition over time and their association with the development and progression of endocrine disorders. Such studies can help establish temporal relationships and causal links between dysbiosis and endocrine health.

Randomized Controlled Trials (RCTs)

Conducting RCTs to evaluate the efficacy and safety of microbiota-targeted interventions, such as probiotics, prebiotics, and fecal microbiota transplantation (FMT), is crucial. These trials should include well-defined endpoints, standardized treatment protocols, and rigorous control measures to provide robust evidence for clinical applications.

Mechanistic Studies

Further mechanistic studies are needed to elucidate the specific microbial species, metabolites, and signaling pathways involved in gut microbiota-endocrine interactions. Understanding these mechanisms will enable the development of targeted therapies and personalized medicine approaches.

Microbiome-Host Interaction Models

Developing advanced in vitro and in vivo models to study microbiome-host interactions can provide deeper insights into the complex dynamics of the gut microbiota and its impact on endocrine function. These models can include organ-on-a-chip technologies and germ-free animal models.

Metabolomics and Multi-Omics Approaches

Integrating metabolomics, proteomics, transcriptomics, and other omics technologies can offer a comprehensive view of the functional impact of gut microbiota on host endocrine systems. These approaches can help identify novel biomarkers and therapeutic targets.

Personalized Microbiota-Based Interventions

Research should focus on personalized approaches to modulate the gut microbiota based on individual microbiome profiles, genetic background, and lifestyle factors. Personalized nutrition, microbiome-based drugs, and tailored probiotic formulations are promising areas for development.

Exploration of Lesser-Known Endocrine Disorders

While much research has focused on common endocrine disorders like diabetes and obesity, there is a need to explore the role of gut microbiota in less-studied conditions such as adrenal disorders and rare endocrine syndromes.

Interdisciplinary Collaboration

Promoting interdisciplinary collaboration between microbiologists, endocrinologists, immunologists, and bioinformaticians can accelerate the translation of microbiome research into clinical practice. Collaborative efforts can facilitate the sharing of data, standardization of methodologies, and implementation of integrated research strategies.

Conclusion

The gut microbiota plays a crucial role in modulating endocrine function through various mechanisms including immune modulation, metabolism regulation, and neuroendocrine signaling. Dysbiosis of the gut microbiota has been associated with the pathogenesis of endocrine disorders such as obesity, diabetes, and thyroid dysfunction. Understanding the intricate interplay between gut microbiota and endocrine pathways opens avenues for novel therapeutic strategies including probiotics, prebiotics, and fecal microbiota transplantation. Further research is warranted to elucidate specific microbial targets and optimize therapeutic approaches for the management of endocrine disorders.

References

- Clemente-Suarez VJ, Redondo-Florez L, Rubio-Zarapuz A, Rodriguez A, Tornero-Aguilera JF (2024) Microbiota Implications in Endocrine-Related Diseases: From Development to Novel Therapeutic Approaches. Biomedicines 12(1): 221.
- Cryan JF, O'Mahony SM (2011) The Microbiome-Gut-Brain Axis: from Bowel to Behavior. Neurogastroenterol Motil 23(3): 187-192.
- 3. Zheng P, Zeng B, Zhou C, Liu M, Fang Z, et al. (2016)

Gut Microbiome Remodeling Induces Depressive-like Behaviors through a Pathway Mediated by the Host's Metabolism. Mol Psychiatry 21(6): 786-796.

- 4. Cryan JF, Dinan TG (2012) Mind-altering Microorganisms: The Impact of the Gut Microbiota on Brain and Behaviour. Nature Reviews Neuroscience 13(10): 701-712.
- 5. Tremaroli V, Backhed F (2012) Functional Interactions between the Gut Microbiota and Host Metabolism. Nature 489(7415): 242-249.
- 6. Cani PD (2019) Microbiota and Metabolites in Metabolic Diseases. Nature Reviews Endocrinology 15(2): 69-70.
- Koh A, De Vadder F, Kovatcheva-Datchary P, Backhed F (2016) From Dietary Fiber to Host Physiology: Short-Chain Fatty Acids as Key Bacterial Metabolites. Cell 165(6): 1332-1345.
- 8. Mayer EA, Knight R, Mazmanian SK, Cryan JF, Tillisch K (2014) Gut Microbes and the Brain: Paradigm Shift in Neuroscience. J Neurosci 34(46): 15490-15496.
- 9. Qin J, Li Y, Cai Z, Li S, Zhu J, et al. (2012) A Metagenome-Wide Association Study of Gut Microbiota in Type 2 Diabetes. Nature 490: 55-60.
- 10. Tremellen K, Pearce K, Dysbiosis I (2012) Dysbiosis of Gut Microbiota (DOGMA)-A Novel Theory for the Development of Polycystic Ovarian Syndrome. Medical hypotheses 79(1): 104-112.
- 11. Jia L, Jia Q, Yang J, Jia R, Zhang H (2020) Alterations in Gut Microbiota Composition and Metabolic Parameters in Patients with Thyroid Carcinoma. Frontiers in Cellular and Infection Microbiology 10: 298.
- 12. Di Baise JK, Zhang H, Crowell MD, Krajmalnik-Brown R, Decker GA, et al. (2008) Gut Microbiota and its Possible Relationship with Obesity. Mayo Clin Proc 83(4): 460-469.
- 13. Raff H (2016) The Gut Microbiome in Addison's Disease. European Journal of Endocrinology 174(1): R101-R108.
- 14. Byrne CS, Chambers ES, Morrison DJ, Frost G (2015) The Role of Short Chain Fatty Acids in Appetite Regulation and Energy Homeostasis. Int J Obes 39(9): 1331-1338.
- 15. Wahlstrom A, Sayin SI, Marschall HU, Backhed F (2016) Intestinal Crosstalk between Bile Acids and Microbiota and Its Impact on Host Metabolism. Cell Metab 24(1): 41-50.
- 16. Yano JM, Yu K, Donaldson GP, Shastri GG, Ann P, et al. (2015) Indigenous Bacteria from the Gut Microbiota

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Regulate Host Serotonin Biosynthesis. Cell 161(2): 264-276.

- 17. Cani PD, Knauf C (2016) How Gut Microbes talk to Organs: The Role of Endocrine and Nervous Routes. Mol Metab 5(9): 743-752.
- 18. Holzer P, Reichmann F, Farzi A (2012) Neuropeptide Y, Peptide YY and Pancreatic Polypeptide in the Gut-brain Axis. Neuropeptides 46(6): 261-274.
- 19. Ridlon JM, Ikegawa S, Alves JMP, Zhou B, Kobayashi A, et al. (2013) Clostridium Scindens: A Human Gut Microbe with a High Potential to Convert Glucocorticoids into Androgens. J Lipid Res 54(9): 2437-2449.
- 20. Turnbaugh PJ, Ley RE, Mahowald MA, Magrini V, Mardis ER, et al. (2006) An Obesity-associated Gut Microbiome with Increased Capacity for Energy Harvest. Nature 444(7122): 1027-1031.
- Cani PD, Amar J, Iglesias MA, Poggi M, Knauf C, et al. (2007) Metabolic Endotoxemia Initiates Obesity and Insulin Resistance. Diabetes 56(7): 1761-1772.
- Tang WHW, Wang Z, Levison BS, Koeth RA, Britt EB, et al. (2013) Intestinal Microbial Metabolism of Phosphatidylcholine and Cardiovascular Risk. N Engl J Med 368(17): 1575-1584.
- 23. Tilg H, Moschen AR (2014) Microbiota and Diabetes: An Evolving Relationship. Gut 63(9): 1513-1521.
- 24. Menni C, Jackson MA, Pallister T, Steves CJ, Spector TD, et al. (2017) Gut Microbiome Diversity and High-fibre Intake are related to Lower Long-term Weight Gain. Int J Obes 41(7): 1099-1105.
- 25. Muller M, Lorscheid M, Metzner M (2018) Gut Microbiota and Thyroid Hormone Metabolism: Implications for Health and Disease. J Endocrinol 238(3): R37-R47.
- 26. Santini F, Marzullo P, Rotondi M, Ceccarini G, Pagano L, et al. (2014) Mechanisms in Endocrinology: The Crosstalk between Thyroid Gland and Adipose Tissue: Signal Integration in Health and Disease. Eur J Endocrinol 171(4): R137-R152.
- Ponziani FR, Zocco MA, Cerrito L, Gasbarrini A, Pompili M (2018) Bacterial Translocation in Patients with Liver Cirrhosis: Physiology, Clinical Consequences, and Practical Implications. Expert Rev Gastroenterol Hepatol 12(7): 641-656.
- Caturegli P, De Remigis A, Rose NR (2014) Hashimoto Thyroiditis: Clinical and Diagnostic Criteria. Autoimmun Rev 13(4-5): 391-397.

- 29. Medeiros-Neto G, Herchenhorn D, Werner RS (2001) Advances in the Treatment of Differentiated Thyroid Cancer. Curr Opin Oncol 13(1): 37-44.
- Wu H, Tremaroli V, Backhed F (2015) Linking Microbiota to Human Diseases: A Systems Biology Perspective. Trends Endocrinol Metab 26(12): 758-770.
- 31. Cani PD, Jordan BF (2018) Gut Microbiota-mediated Inflammation in Obesity: A Link with Gastrointestinal Cancer. Nat Rev Gastroenterol Hepatol 15(11): 671-682.
- 32. Zhang Q, Hu N (2020) Effects of Metformin on the Gut Microbiota in Obesity and Type 2 Diabetes Mellitus. Diabetes Metab Syndr Obes 13: 5003-5014.
- 33. Dao MC, Everard A, Aron-Wisnewsky J, Sokolovska N, Prifti E, et al. (2016) Akkermansia Muciniphila and Improved Metabolic Health during a Dietary Intervention in Obesity: Relationship with Gut Microbiome Richness and Ecology. Gut 65(3): 426-436.
- 34. Magne F, Gotteland M, Gauthier L, Zazueta A, Pesoa S, et al. (2020) The Firmicutes/Bacteroidetes Ratio: A Relevant Marker of Gut Dysbiosis in Obese Patients? Nutrients 12(5): 1474.
- 35. Ghaly S, Kaakoush NO, Lloyd F, McGonigle T, Mok D, et al. (2018) High Dose Vitamin D Supplementation Alters Faecal Microbiome and Predisposes Mice to More Severe Colitis. Sci Rep 8(1): 11511.
- Liu J, Zhang H, Cong Y (2020) Microbiome-Host Interaction in Inflammatory Bowel Disease. Front Immunol 11: 755.
- DeGruttola AK, Low D, Mizoguchi A, Mizoguchi E (2016) Current Understanding of Dysbiosis in Disease in Human and Animal Models. Inflamm Bowel Dis 22(5): 1137-1150.
- Ianiro G, Bibbo S, Gasbarrini A, Cammarota G (2014) Therapeutic Modulation of Gut Microbiota: Current Clinical Applications and Future Perspectives. Curr Drug Targets 15(8): 762-770.
- 39. Marchesi JR, Adams DH, Fava F, Hermes GDA, Hold G, et al. (2016) The Gut Microbiota and Host Health: A New Clinical Frontier. Gut 65(2): 330-339.
- 40. Torres PJ, Siakowska M, Banaszewska B, Pawelczyk L, Duleba AJ, et al. (2018) Gut Microbial Diversity in Women with Polycystic Ovary Syndrome Correlates with Hyperandrogenism. J Clin Endocrinol Metab 103(4): 1502-1511.
- 41. Insenser M, Murri M, Del Campo R, Martinez-Garcia MA,

Fernandez-Duran E, et al. (2018) Gut Microbiota and the Polycystic Ovary Syndrome: Influence of Sex, Sex Hormones, and Obesity. J Clin Endocrinol Metab 103(7): 2552-2562.

- 42. Liu R, Zhang C, Shi Y, Zhang F, Li L, et al. (2017) Dysbiosis of Gut Microbiota Associated with Clinical Parameters in Polycystic Ovary Syndrome. Front Microbiol 8: 324.
- 43. Lindheim L, Bashir M, Munzker J, Trummer C, Zachhuber V, et al. (2017) Alterations in Gut Microbiome Composition and Barrier Function are Associated with Reproductive and Metabolic Defects in Women with Polycystic Ovary Syndrome (PCOS): A Pilot Study. PLoS One 12(1): e0168390.
- 44. Villa J, Pratley RE (2020) Adipose Tissue Dysfunction in Polycystic Ovary Syndrome: Implications for Cardiovascular Risk. Endocrine 68(1): 18-25.
- 45. Kobyliak N, Falalyeyeva T, Mykhalchyshyn G, Kyriienko D, Komissarenko L (2018) Effect of Alive Probiotic on Insulin Resistance in Type 2 Diabetes Patients:

Randomized Clinical Trial. Diabetes Metab Syndr 12(5): 617-624.

- 46. Morkl S, Lackner S, Meinitzer A, Mangge H, Muller W, et al. (2018) Gut Microbiota, Dietary Intakes and Intestinal Permeability Reflected by Serum Zonulin in Women. Eur J Nutr 57(8): 2985-2997.
- 47. Allegretti JR, Kassam Z, Mullish BH, Chiang A, Carrellas M, et al. (2020) Effects of Fecal Microbiota Transplantation with Oral Capsules in Obese Patients. Clin Gastroenterol Hepatol 18(4): 855-863.
- Hald S, Schiotz M, Hvas CL (2020) Fecal Microbiota Transplantation in Patients with Irritable Bowel Syndrome: A Randomized, Double-Blind, Placebo-Controlled Study. Gastroenterology 159(1): 153-162.
- 49. Vrieze A, Van Nood E, Holleman F, Salojarvi J, Kootte RS, et al. (2012) Transfer of Intestinal Microbiota from Lean Donors Increases Insulin Sensitivity in Individuals with Metabolic Syndrome. Gastroenterology 143(4): 913-916.