Whole Grain Consumption and Gut Microbiota: Implications for Metabolic Health

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Abstract: Whole grain consumption has known beneficial effects for health. However, the interplay of whole grain consumption, the human gut microbiota, and metabolic health needs to be further unraveled. This paper aims to describe the interplay of whole grain consumption and gut microbiota for metabolic health. It is a narrative literature review. The journals were selected from PubMed, Science Direct, and Google Scholar. It was found that whole grain consumption could modulate the production of short-chain fatty acids. Whole grains contain phenolic acid, flavonoids, and plant sterols. The composition, diversity, structure, and metabolites of gut microbiota might be changed by whole grain consumption. Whole grain consumption might improve glucose metabolism, enhance immune function, and reduce inflammation. Glucose intolerance and insulin resistance might be reduced. Intestinal inflammation could be alleviated. In conclusion, whole grain consumption can improve gut health, better blood glucose control, and potentially reduced inflammation.

1 INTRODUCTION

The gut microbiota is essential in metabolic health and diet. Fermentation of dietary fibre is facilitated by gut microbial communities. The result of intestinal fermentation is Short Chain Fatty Acid (SCFA). Some SCFA such as propionate, acetetate, and butyrate influence endocrine system, adipogenesis, glucose homeostasis, lipid oxidation, gluconeogenesis, and gut barrier integrity. These mechanisms might protect against metabolic diseases (hypertension, type 2 diabetes, and cardiovascular health) (Fava et al., 2019).

The gut microbiota is important in bile acid metabolism and change pathways involved in metabolic health. Metabolic disease risk might be diminished due to small phenolic compound. Molecular cross-talk might occur between host and the gut microbiota (Fava et al., 2019).

Metabolic syndrome (MetS) might cause cardiovascular and cerebrovascular diseases. Research suggests that differences in gut microbiota composition between individuals with MetS and healthy individuals can lead to development of MetS. The interaction between gut microbiota and host metabolism is influenced by various factors, including inflammation, short-chain fatty acid metabolism, and bile acid metabolism. However, the relationship between gut microbiota and MetS remains controversial in humans and requires further research (Liu et al., 2025).

Given the increasing prevalence of MetS globally, research on gut microbiota has become crucial. A balanced gut microbiota plays a vital role in maintaining homeostasis and preventing metabolic diseases. However, further studies are needed to understand how gut microbiota can be manipulated to prevent and treat MetS (Oda, 2018).

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2 METHOD

It is a narrative literature review. The journals were selected from PubMed, Science Direct, and Google Scholar. The publication date was 2015-2025. The articles were included if the title and abstract included 2 out of 3 keywords (grain, microbiota, metabolic health). The articles were excluded if the full text articles were not availables in English. From 32 articles reviewed, there were 15 articles chosen based on the inclusion criteria.

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3 RESULT

Grain consumption

It was found that whole grain consumption could modulate the production of short-chain fatty acids. Whole grains contain phenolic acid, flavonoids, and plant sterols. The composition, diversity, structure, and metabolites of gut microbiota might be changed by whole grain consumption. Whole grain consumption might improve glucose metabolism, enhance immune function, and reduce inflammation. Glucose intolerance and insulin resistance might be reduced. Intestinal inflammation could be alleviated (Fava et al., 2019).

The gut microbiota is essential in maintaining the balance of the body's metabolic processes. An imbalance of the gut microbiota, also known as dysbiosis. Dysbiosis might cause some metabolic disorders such as dyslipidemia, insulin resistance, and obesity (Wang et al., 2020).

Short-chain fatty acids (SCFAs), gut barrier, and bile acid

The gut microbiota influences the host's metabolism through several mechanisms. The gut microbiota helps maintain the integrity of gut barrier. The translocation of toxins and undigested food particles into the bloodstream are prevented. Short-chain fatty acids (SCFAs) are produced by the gut microbiota. SCFAs play a key role in regulating glucose and lipid metabolism, insulin sensitivity, and inflammation. Bile acids are produced by the liver and stored in the gallbladder, play a crucial role in lipid digestion and absorption. The gut microbiota influences bile acid metabolism, which can impact glucose and lipid metabolism (Wang et al., 2020).

Gut microbiota

The gut microbiota, composed of up to 1000 species of bacteria, plays a crucial role in human health by producing metabolites that can have positive or negative effects on the host. These metabolites can influence inflammation, oxidation, pain relief, and energy production, among other physiological processes. An imbalance of the gut microbiota, or dysbiosis, can lead to extensive physiological changes and increase the risk of metabolic syndrome (Wang et al., 2020).

Studies have found differences in the gut microbiome between healthy and obese individuals, with changes in the composition and function of the microbiota contributing to obesity and insulin resistance. Specific bacteria, such as Enterobacter cloacae, have been linked to obesity and metabolic disease. These findings suggest that the gut microbiota is an important environmental factor in regulating fat storage and metabolism, and may be a potential target for the prevention and treatment of obesity and related disorders (Tomas et al., 2016; Wang et al., 2020).

Gut microbiota and metabolic health

Gut microbiota dysbiosis is linked to hyperglycemia, a key component of metabolic syndrome (MetS). Reduced abundance of beneficial bacteria like butyrate-producing bacteria, are associated with type 2 diabetes (T2DM). Butyrate, a short-chain fatty acid produced by gut microbiota, has beneficial effects on gut health, inflammation, and metabolism. However, more research is needed to fully understand the relationship between gut microbiota and hyperglycemia (Wang et al., 2020; Zhou et al., 2019).

Dyslipidemia, characterized by abnormal lipid or lipoprotein levels in the blood, is linked to gut microbiota imbalance. Research has shown that high-glucose or high-fructose diets can alter the gut microbiome, leading to dyslipidemia and lipid accumulation. Studies in both mice and humans have found associations between gut microbiota composition and lipid metabolic disorders, including changes in diversity and abundance of specific taxa. The gut microbiome has been estimated to explain a significant proportion of variation in body mass index, triglycerides, and HDL levels (Wang et al., 2020).

Individuals with hypertension have reduced gut microbiota diversity and an imbalance in the ratio of certain bacterial populations. Studies in both animals and humans have found that gut microbiota alterations can contribute to the development of hypertension, and that transplanting gut microbiota from hypertensive individuals into healthy mice can transfer elevated blood pressure. These findings suggest a direct link between the gut microbiota and blood pressure regulation (Li et al., 2017).

Hyperuricemia, a key factor in gout and metabolic syndrome, is linked to gut microbiota imbalance. Studies have shown that individuals with hyperuricemia have altered gut microbiota composition, including changes in the abundance of certain bacterial populations such Bacteroides, while Fecalibacterium prausnitzii and Bifidobacterium pseudocatenulatum are diminished. These changes may contribute to the development of hyperuricemia and related disorders (Guo et al., 2016; He et al., 2025).

Non-alcoholic fatty liver disease (NAFLD) is a common chronic liver disease closely linked to metabolic syndrome. Research suggests that gut microbiota imbalance plays a crucial role in NAFLD development. Studies have identified specific bacteria, such as Klebsiella pneumoniae, that may contribute to NAFLD pathogenesis. The gut-liver axis is thought to be a key factor, with disruption of the gut barrier leading to bacterial translocation, immune activation, and liver inflammation (Wang et al., 2020).

Obstructive sleep apnea hypopnea syndrome (OSAHS) is a sleep disorder linked to gut microbiota disorders. Research has shown that intermittent hypoxia can alter the gut microbiome composition, with changes in the abundance of certain bacterial populations, such as increased Firmicutes and decreased Bacteroidetes and Proteobacteria. These changes may contribute to the development of OSAHS (Ko et al., 2019; Moreno-Indias et al., 2015; Zmora et al., 2019).

Balance among nutrition (grain), microbiota, and metabolic health

Nutritional guidelines emphasized on more grain for health reasons. Grain could be fermented by the gut microbiota and produces SCFA. SCFA shown beneficial effects on inflammation and insulin resistance. This condition might lower the prevalence of diabetes and obesity. Grain consumption will improve insulin resitance and control body weight (lower body fat) (Aslam et al., 2026; Ray & Shankaran, 2026; Van Kalkeren et al., 2026).

4 CONCLUSIONS

The gut microbiota plays a critical role in the development and progression of metabolic syndrome. Metabolic syndrome is a global health issue characterized by risk factors like obesity, hyperglycemia, and hypertension. If untreated, it can lead to diseases like non-alcoholic fatty liver disease (NAFLD) and obstructive sleep apnea hypopnea syndrome (OSAHS). The development of MetS is linked to factors like insulin resistance, chronic inflammation, and gut microbiota disorder. The gut microbiota plays a crucial role in maintaining human health and is involved in regulating metabolism, immune function, and gene expression.

REFERENCES

Aslam, H., Trakman, G., Dissanayake, T., Todd, E., Harrison, P., Alby, C., Jabeen, T., Gamage, E., Travica, N., Marshall, S., Ruusunen, A., Rocks, T., Marx, W., Berk, M., O’Neil, A., McGuinness, A. J., Jennings, L., Jacka, F. N., & Dawson, S. L. (2026). Dietary interventions and the gut microbiota: A systematic literature review of 80 controlled clinical trials. Journal of Translational Medicine, 24(1), 39. https://doi.org/10.1186/s12967-025-07428-9

Fava, F., Rizzetto, L., & Tuohy, K. M. (2019). Gut microbiota and health: Connecting actors across the metabolic system. Proceedings of the Nutrition Society, 78(02), 177–188. https://doi.org/10.1017/S0029665118002719

Guo, Z., Zhang, J., Wang, Z., Ang, K. Y., Huang, S., Hou, Q., Su, X., Qiao, J., Zheng, Y., Wang, L., Koh, E., Danliang, H., Xu, J., Lee, Y. K., & Zhang, H. (2016). Intestinal Microbiota Distinguish Gout Patients from Healthy Humans. Scientific Reports, 6(1), 20602. https://doi.org/10.1038/srep20602

He, J., He, Y., Li, J., Ma, G., Li, Y., Xie, J., He, C., Feng, X., Jia, K., Li, W., Wang, M., Tang, A., Tian, T., Liao, X., Li, W., Yan, F., Zhang, Y., Cao, X., Zhang, Y., … Wang, Q. (2025). Habitual coarse grain intake, gut microbiota, and hyperuricemia in individuals with or at risk of metabolic syndrome: A post-hoc analysis. Nutrition, Metabolism and Cardiovascular Diseases, 104126. https://doi.org/10.1016/j.numecd.2025.104126

Ko, C.-Y., Liu, Q.-Q., Su, H.-Z., Zhang, H.-P., Fan, J.-M., Yang, J.-H., Hu, A.-K., Liu, Y.-Q., Chou, D., & Zeng, Y.-M. (2019). Gut microbiota in obstructive sleep apnea–hypopnea syndrome: Disease-related dysbiosis and metabolic comorbidities. Clinical Science, 133(7), 905–917. https://doi.org/10.1042/CS20180891

Li, J., Zhao, F., Wang, Y., Chen, J., Tao, J., Tian, G., Wu, S., Liu, W., Cui, Q., Geng, B., Zhang, W., Weldon, R., Auguste, K., Yang, L., Liu, X., Chen, L., Yang, X., Zhu, B., & Cai, J. (2017). Gut microbiota dysbiosis contributes to the development of hypertension. Microbiome, 5(1), 14. https://doi.org/10.1186/s40168-016-0222-x

Liu, H., Xu, X., Yao, Z., Kang, J., Shen, Y., & Liu, W. (2025). Association between the dietary index for gut microbiota and metabolic syndrome in adults: The mediating role of body mass index. Frontiers in Nutrition, 12, 1598664. https://doi.org/10.3389/fnut.2025.1598664

Moreno-Indias, I., Torres, M., Montserrat, J. M., Sanchez-Alcoholado, L., Cardona, F., Tinahones, F. J., Gozal, D., Poroyko, V. A., Navajas, D., Queipo-Ortuño, M. I., & Farré, R. (2015). Intermittent hypoxia alters gut microbiota diversity in a mouse model of sleep apnoea. European Respiratory Journal, 45(4), 1055–1065. https://doi.org/10.1183/09031936.00184314

Oda, E. (2018). Historical perspectives of the metabolic syndrome. Clinics in Dermatology, 36(1), 3–8. https://doi.org/10.1016/j.clindermatol.2017.09.002

Ray, S., & Shankaran, P. (2026). Nutrition and the gut microbiome: A symbiotic dialogue influencing health and disease. Frontiers in Nutrition, 13, 1761992. https://doi.org/10.3389/fnut.2026.1761992

Tomas, J., Mulet, C., Saffarian, A., Cavin, J.-B., Ducroc, R., Regnault, B., Kun Tan, C., Duszka, K., Burcelin, R., Wahli, W., Sansonetti, P. J., & Pédron, T. (2016). High-fat diet modifies the PPAR-γ pathway leading to disruption of microbial and physiological ecosystem in murine small intestine. Proceedings of the National Academy of Sciences, 113(40). https://doi.org/10.1073/pnas.1612559113

Van Kalkeren, C. A., Adam, T. C., & Blaak, E. E. (2026). Gut Microbiome-Associated Effects of Plant-Based Diets on Glucose Homeostasis, Body Composition, and Cognitive Function: A Scoping Review. Advances in Nutrition, 17(4), 100610. https://doi.org/10.1016/j.advnut.2026.100610

Wang, P.-X., Deng, X.-R., Zhang, C.-H., & Yuan, H.-J. (2020). Gut microbiota and metabolic syndrome. Chinese Medical Journal, 133(7), 808–816. https://doi.org/10.1097/CM9.0000000000000696

Zhou, W., Xu, H., Zhan, L., Lu, X., & Zhang, L. (2019). Dynamic Development of Fecal Microbiome During the Progression of Diabetes Mellitus in Zucker Diabetic Fatty Rats. Frontiers in Microbiology, 10, 232. https://doi.org/10.3389/fmicb.2019.00232

Zmora, N., Suez, J., & Elinav, E. (2019). You are what you eat: Diet, health and the gut microbiota. Nature Reviews Gastroenterology & Hepatology, 16(1), 35–56. https://doi.org/10.1038/s41575-018-0061-2