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# Carbohydrate-Rich Dietary Fiber, Gut Health and Systemic Inflammation

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**ABSTRACT**

**Chronic low-grade systemic inflammation (CLGSI) is a fundamental pathophysiological driver of a spectrum of metabolic dysfunctions, including obesity, insulin resistance, and type 2 diabetes. A key instigator of this inflammatory state is a compromised intestinal epithelial barrier, often characterized by increased paracellular permeability. This "leaky gut" phenotype facilitates the translocation of microbial-derived products, such as lipopolysaccharides (LPS), from the intestinal lumen into systemic circulation, a phenomenon termed metabolic endotoxemia. From a carbohydrate chemistry perspective, dietary fiber comprises a diverse class of non-digestible polysaccharides and oligosaccharides, with varying degrees of polymerization and glycosidic linkages that resist enzymatic hydrolysis in the human small intestine. These complex carbohydrates serve as a crucial substrate for colonic microbial fermentation. This hypothetical research article elucidates the intricate relationship between the chemical structure of dietary fibers, their metabolic fate in the gut, and their physiological impact on gut barrier integrity and systemic inflammation. A simulated randomized controlled trial is proposed to investigate the effects of a high-fiber dietary intervention, rich in fermentable polysaccharides, on gut barrier function. We hypothesize that the microbial fermentation of these carbohydrates yields beneficial short-chain fatty acids (SCFAs)—primarily acetate, propionate, and butyrate—which act as signaling molecules and energy substrates for colonocytes. This process is posited to enhance the expression of tight junction proteins (e.g., zonulin-1, occludin) and reduce systemic LPS levels, thereby mitigating CLGSI. The findings of this study are discussed in the context of sustainable metabolic health management, highlighting how a diet rich in complex, non-digestible carbohydrates can concurrently improve human well-being and contribute to environmental sustainability. This framework underscores the therapeutic potential of carbohydrate-based dietary interventions in the amelioration of chronic inflammatory diseases.**

***Keywords-*** Dietary Fiber, Systemic Inflammation, Short-Chain Fatty Acids (SCFAs), Lipopolysaccharides (LPS), Glycosidic Linkages, Colonic Fermentation.

## I. INTRODUCTION

Metabolic syndrome, a cluster of conditions including obesity, insulin resistance, and dyslipidemia, has reached epidemic proportions globally, posing a significant public health challenge. While genetic predisposition and lifestyle factors like diet and physical inactivity are well-established contributors, an emerging paradigm highlights the critical role of the gut-liver axis and chronic low-grade systemic inflammation (CLGSI) in its pathogenesis.

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### *1.1. Dietary Fiber and its Classification*

From a carbohydrate chemistry perspective, dietary fiber is a heterogeneous group of plant-derived carbohydrate polymers and lignin that are not hydrolyzed by the endogenous enzymes of the human small intestine. These molecules are primarily classified based on their physicochemical properties, particularly their solubility in water. Soluble fibers, such as pectins, β-glucans, and inulin, form viscous gels in water and are typically fermentable by the colonic microbiota. Their chemical structures often contain a mix of glycosidic linkages, such as the β-(1→4) linkages in pectin and the β-(1→3) and β-(1→4) linkages in β-glucans, which are accessible to microbial enzymes. In contrast, insoluble fibers, including cellulose and some hemicelluloses, are largely non-viscous and poorly fermented. Their rigid structures, characterized by robust β-(1→4) glycosidic linkages, provide bulk and facilitate intestinal transit.

### *1.2. The Gut Microbiota and Its Role in Health*

The human colon harbours a dense and diverse microbial ecosystem, known as the gut microbiota, which plays a pivotal role in host physiology. This microbial community is essential for nutrient salvage from undigested food, maturation of the immune system, and resistance against pathogenic colonization. A disruption in the composition and function of this microbial community, a state referred to as dysbiosis, is frequently observed in metabolic diseases. The availability of fermentable carbohydrates, i.e., dietary fiber, is a primary determinant of the microbiota's structure and metabolic output.

### *1.3. Gut Barrier Function and Metabolic Endotoxemia*

The intestinal epithelium acts as a selective barrier, regulating the passage of nutrients while preventing the translocation of harmful luminal substances. The integrity of this barrier is maintained by tight junctions (TJs), multiprotein complexes that seal the paracellular space between epithelial cells. A compromised barrier, or "leaky gut," allows bacterial components, notably lipopolysaccharides (LPS) from the outer membrane of Gram-negative bacteria, to translocate into the portal and systemic circulation. This condition, known as metabolic endotoxemia, serves as a potent trigger for systemic inflammation.

### *1.4. Systemic Inflammation and Chronic Diseases*

Metabolic endotoxemia initiates a cascade of pro-inflammatory signaling by activating Toll-like receptor 4 (TLR4) on immune cells and adipocytes. This leads to a state of CLGSI, characterized by elevated circulating levels of pro-inflammatory cytokines such as tumor necrosis factor-alpha (TNF-α) and interleukin-6 (IL-6). This persistent inflammation disrupts insulin signaling pathways, impairs glucose uptake, and promotes adipose tissue dysfunction, thereby directly contributing to the development of insulin resistance and type 2 diabetes.

## II. LITERATURE REVIEW

### *2.1. Fiber's Impact on Gut Microbiota Composition and Diversity*

Dietary fiber serves as a key prebiotic, a non-digestible food component that selectively stimulates the growth and/or activity of beneficial bacteria in the colon. A diet rich in fermentable carbohydrates has been shown to increase the abundance of key saccharolytic genera, such as *Bifidobacterium* and the butyrate-producer *Faecalibacterium prausnitzii*. This shift in microbial community structure and increased diversity are often depleted in individuals consuming a low-fiber, high-fat Western diet.

### *2.2. Short-Chain Fatty Acids (SCFAs) as Mediators of Gut Health*

The anaerobic fermentation of dietary fibers by the colonic microbiota produces short-chain fatty acids (SCFAs), with acetate ($CH_3COO^-$), propionate ($CH_3CH_2COO^-$), and butyrate ($CH_3CH_2CH_2COO^-$) being the most abundant. These small organic acids serve as crucial mediators of host-microbe interactions. Butyrate is particularly vital, as it is the preferred energy source for colonocytes and is essential for maintaining the integrity and function of the intestinal epithelial barrier. Its role extends to regulating oxygen consumption in the colonic lumen, thereby favoring the growth of strict anaerobic bacteria. The SCFAs are readily absorbed into circulation, where acetate and propionate are involved in hepatic gluconeogenesis and appetite regulation, respectively.

### *2.3. Evidence Linking Gut Barrier Dysfunction to Systemic Inflammation*

Preclinical and clinical studies have robustly linked a compromised intestinal barrier to CLGSI. In a seminal study, high-fat feeding in mice induced gut permeability, leading to increased plasma LPS levels and subsequent adipose tissue inflammation. In humans, elevated circulating LPS levels and markers of gut permeability, such as zonulin, have been consistently reported in individuals with obesity and metabolic syndrome, and these levels correlate with inflammatory markers like C-reactive protein (CRP).

### *2.4 Dietary Interventions and Metabolic Health Outcomes*

Clinical trials have demonstrated that increasing dietary fiber intake can effectively improve metabolic health parameters. A randomized controlled trial showed that a diet rich in whole grains significantly improved insulin sensitivity and reduced inflammatory markers in obese subjects. The direct mechanistic link, particularly the role of SCFA-mediated gut barrier restoration, requires further elucidation in human intervention studies.

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# III. METHODOLOGY

### *3.1. Study Design and Participants*

This study is designed as a double-blind, randomized controlled trial to evaluate the effects of a high-fiber dietary intervention on gut barrier function and systemic inflammation. A total of 60 participants (aged 30-55 years) with features of metabolic syndrome (e.g., body mass index (BMI) ≥25 kg/m$^2$, mild hyperglycemia) will be recruited. Participants will be randomly allocated to either the intervention group (n=30) or the control group (n=30) for 12 weeks.

### *3.2. Dietary Intervention*

The intervention group will be prescribed a high-fiber diet, aiming for a daily intake of ≥35 g, with a focus on fermentable fibers from whole grains, legumes, fruits, and vegetables. Participants will receive structured dietary counselling and meal plans to ensure compliance. The control group will continue their habitual low-fiber diet (estimated ≤15 g/day) and receive general health advice. Physical activity levels will be monitored and maintained in both groups to control for confounding factors.

### *3.3 Sample Collection and Analysis*

Blood and stool samples will be collected at baseline and the end of the 12-week intervention.

**3.3.1. Blood Samples:**

- **Inflammatory markers:** High-sensitivity C-reactive protein (hs-CRP), interleukin-6 (IL-6), and tumor necrosis factor-alpha (TNF-α) will be measured using ELISA.
- **Metabolic markers:** Fasting glucose and insulin will be measured to calculate HOMA-IR (Homeostatic Model Assessment for Insulin Resistance) as a proxy for insulin sensitivity. A full lipid panel will also be assessed.
- **Gut permeability markers**: Plasma levels of zonulin, a key regulator of TJs, and LPS-binding protein (LBP), a reliable surrogate marker for circulating LPS, will be quantified.

**3.3.2. Stool Samples:**

- **Microbiota composition:** The 16S rRNA gene sequencing will be performed on faecal DNA to assess bacterial diversity and the relative abundance of specific taxa.
- **SCFA concentration:** Faecal concentrations of acetate, propionate, and butyrate will be measured using gas chromatography (GC).

### *3.4. Statistical Analysis*

Paired t-tests will be used to compare within-group changes from baseline to endpoint, while independent t-tests will be used for between-group comparisons. Pearson correlation coefficients will be calculated to determine the linear relationship between changes in fiber intake, SCFA production, gut permeability markers, and inflammatory cytokines. A p-value of $< 0.05$ will be considered statistically significant.

# IV. RESULTS AND DISCUSSION

### *4.1. Changes in Gut Microbiota Composition (Simulated Results)*

At the 12-week endpoint, the intervention group demonstrated a significant increase in the relative abundance of *Bifidobacterium* and *Faecalibacterium prausnitzii* compared to baseline ($p < 0.01$) and the control group ($p < 0.05$). The control group showed no significant changes. These simulated findings are consistent with the well-established prebiotic effect of fermentable fibers, which selectively promote the growth of beneficial, SCFA-producing bacteria.

### *4.2. SCFA Production and Gut Permeability (Simulated Results)*

Faecal butyrate concentrations in the intervention group increased significantly by an average of 45% ($p < 0.001$). This increase was strongly and inversely correlated with plasma zonulin levels ($r=-0.72$, $p<0.001$), suggesting that elevated butyrate production directly contributes to the strengthening of intestinal TJs. Furthermore, the intervention group experienced a 30% reduction in plasma LBP levels ($p < 0.01$), providing direct evidence of a decrease in metabolic endotoxemia. These results underscore the critical role of the microbial fermentation of complex carbohydrates in fortifying the intestinal barrier.

### *4.3. Modulation of Systemic Inflammatory Markers (Simulated Results)*

The high-fiber dietary intervention led to a significant reduction in key markers of systemic inflammation. hs-CRP levels decreased by 25% ($p < 0.01$) and IL-6 levels decreased by 20% ($p < 0.05$) in the intervention group compared to the control group. A strong positive correlation was observed between the reduction in plasma LBP and the decrease in inflammatory markers ($r=0.65$, $p<0.01$), highlighting a clear causal link between a restored gut barrier and the attenuation of systemic inflammation. These findings align with previous research demonstrating the anti-inflammatory properties of high-fiber diets.

### *4.4. Discussion of Findings in the Context of Sustainable Management*

Our simulated data presents a compelling case for adopting dietary fiber as a cornerstone of metabolic health management. This intervention does not rely on costly pharmaceutical therapies but on a fundamental dietary shift towards fiber-rich, plant-based foods. This approach offers a sustainable model for public health on multiple fronts:

**4.4.1. Economic Sustainability:** Promoting cost-effective fiber sources like legumes and whole grains can reduce healthcare expenditures associated with the management of chronic diseases.

**4.4.2.** Environmental Sustainability: Diets rich in plant-based foods have a significantly lower environmental footprint in terms of greenhouse gas emissions, land use, and water consumption compared to animal-based diets.

**4.4.3.** Food System Resilience: Emphasizing diverse fiber-rich crops supports agricultural biodiversity and reduces reliance on resource-intensive monocultures.

The observed improvements in gut barrier function and systemic inflammation demonstrate that dietary fiber is a critical modulator of host-microbe interactions that can profoundly influence disease trajectory.

## V. CONCLUSION

This hypothetical research article elucidates the powerful interplay between the carbohydrate chemistry of dietary fiber, its metabolic fate in the gut, and its subsequent impact on gut barrier integrity and systemic inflammation. The simulated results from a randomized controlled trial suggest that a high-fiber diet can effectively enhance gut barrier function, reduce metabolic endotoxemia, and ameliorate CLGSI, thus offering a robust, evidence-based strategy for managing metabolic health. These findings hold significant implications for sustainable public health management, advocating for a dietary approach that benefits both human well-being and planetary health. Future research should focus on the long-term effects of diverse fiber interventions and their practical integration into sustainable food systems.

## REFERENCES

[1] Ajani, U. A., Ford, E. S., & Mokdad, A. H. (2004). Dietary fiber and C-reactive protein: findings from national health and nutrition examination survey data. *The Journal of nutrition*, *134*(5), 1181–1185. https://doi.org/10.1093/jn/134.5.1181

[2] Ambroselli, D., Masciulli, F., Romano, E., Catanzaro, G., Besharat, Z. M., Massari, M. C., Ferretti, E., Migliaccio, S., Izzo, L., Ritieni, A., Grosso, M., Formichi, C., Dotta, F., Frigerio, F., Barbiera, E., Giusti, A. M., Ingallina, C., & Mannina, L. (2023). New Advances in Metabolic Syndrome, from Prevention to Treatment: The Role of Diet and Food. *Nutrients*, 2023, *15*(3), 640. https://doi.org/10.3390/nu15030640

[3] Amisi C. A. Markers of insulin resistance in Polycystic ovary syndrome women: An update. World journal of diabetes, 2022, 13(3), 129–149. https://doi.org/10.4239/wjd.v13.i3.129

[4] Belete, R., Ataro, Z., Abdu, A., & Sheleme, M. Global prevalence of metabolic syndrome among patients with type I diabetes mellitus: a systematic review and meta-analysis. *Diabetology & metabolic syndrome*, 2021, 13 (1), 25. https://doi.org/10.1186/s13098-021-00641-8

[5] Canfora, E. E., Jocken, J. W., & Blaak, E. E. Short-chain fatty acids in control of body weight and insulin sensitivity. Nature reviews. Endocrinology, 2015, 11(10), 577–591. https://doi.org/10.1038/nrendo.2015.128

[6] Cani, P. D., Amar, J., Iglesias, M. A., Poggi, M., Knauf, C., Bastelica, D., Neyrinck, A. M., Fava, F., Tuohy, K. M., Chabo, C., Waget, A., Delmée, E., Cousin, B., Sulpice, T., Chamontin, B., Ferrières, J., Tanti, J. F., Gibson, G. R., Casteilla, L., Delzenne, N. M., … Burcelin, R. Metabolic endotoxemia initiates obesity and insulin resistance. Diabetes, 2007, 56(7), 1761–1772. https://doi.org/10.2337/db06-1491

[7] Cani, P. D., Bibiloni, R., Knauf, C., Waget, A., Neyrinck, A. M., Delzenne, N. M., & Burcelin, R. Changes in gut microbiota control metabolic endotoxemia-induced inflammation in high-fat diet-induced obesity and diabetes in mice. Diabetes, 2008, 57(6), 1470–1481. https://doi.org/10.2337/db07-1403

[8] Czarnowski, P., Mikula, M., Ostrowski, J., & Żeber-Lubecka, N. Gas Chromatography-Mass Spectrometry-Based Analyses of Fecal Short-Chain Fatty Acids (SCFAs): A Summary Review and Own Experience. Biomedicines, 2024, 12(8), 1904. https://doi.org/10.3390/biomedicines12081904

[9] de La Serre, C. B., Ellis, C. L., Lee, J., Hartman, A. L., Rutledge, J. C., & Raybould, H. E. Propensity to high-fat diet-induced obesity in rats is associated with changes in the gut microbiota and gut inflammation. American journal of physiology. Gastrointestinal and liver physiology, 2010, 299(2), G440–G448. https://doi.org/10.1152/ajpgi.00098.2010

[10] Dreher M. L. Whole Fruits and Fruit Fiber Emerging Health Effects. Nutrients, 2018, 10(12), 1833. https://doi.org/10.3390/nu10121833

[11] Fasano A. Zonulin, regulation of tight junctions, and autoimmune diseases. *Annals of the* New York Academy of Sciences, 2012, 1258(1), 25–33. https://doi.org/10.1111/j.1749-6632.2012.06538.x

[12] Fung, T. T., Hu, F. B., Pereira, M. A., Liu, S., Stampfer, M. J., Colditz, G. A., & Willett, W. C. Whole-grain intake and the risk of type 2 diabetes: a prospective study in men. The American journal of clinical nutrition, 2002, 76(3), 535–540. https://doi.org/10.1093/ajcn/76.3.535

[13] Gibson, G. R., Hutkins, R., Sanders, M. E., Prescott, S. L., Reimer, R. A., Salminen, S. J., Scott, K., Stanton, C., Swanson, K. S., Cani, P. D., Verbeke, K., & Reid, G. Expert consensus document: The International Scientific

Association for Probiotics and Prebiotics (ISAPP) consensus statement on the definition and scope of prebiotics. Nature reviews. Gastroenterology & hepatology, 2017, 14(8), 491–502. https://doi.org/10.1038/nrgastro.2017.75

[14] Giovannini, S., Onder, G., Liperoti, R., Russo, A., Carter, C., Capoluongo, E., Pahor, M., Bernabei, R., & Landi, F. (2011). Interleukin-6, C-reactive protein, and tumor necrosis factor-alpha as predictors of mortality in frail, community-living elderly individuals. Journal of the American Geriatrics Society, 2011, 59(9), 1679–1685. https://doi.org/10.1111/j.1532-5415.2011.03570.x

[15] Hall, C. V., Hepsomali, P., Dalile, B., Scapozza, L., & Gurry, T. (2024). Effects of a diverse prebiotic fibre blend on inflammation, the gut microbiota and affective symptoms in metabolic syndrome: a pilot open-label randomised controlled trial. The British journal of nutrition, 2024, 132(8), 1002–1013. https://doi.org/10.1017/S0007114524002186

[16] Holscher H. D. Dietary fiber and prebiotics and the gastrointestinal microbiota. Gut microbes, 2017, 8(2), 172–184. https://doi.org/10.1080/19490976.2017.1290756

[17] Hu, Y., Ding, M., Sampson, L., Willett, W. C., Manson, J. E., Wang, M., Rosner, B., Hu, F. B., & Sun, Q. Intake of whole grain foods and risk of type 2 diabetes: results from three prospective cohort studies. *BMJ (Clinical research ed.), 2020, 370,* m2206. https://doi.org/10.1136/bmj.m2206

[18] Ioniță-Mîndrican, C. B., Ziani, K., Mititelu, M., Oprea, E., Neacșu, S. M., Moroșan, E., Dumitrescu, D. E., Roșca, A. C., Drăgănescu, D., & Negrei, C. Therapeutic Benefits and Dietary Restrictions of Fiber Intake: A State of the Art Review. Nutrients, 2022, 14(13), 2641. https://doi.org/10.3390/nu14132641

[19] Kadam, P., Shahi, S., Singh, S. K. (2024) Transforming Medicine: A Comprehensive Review of Artificial Intelligence in Healthcare, *African Journal of Biological Sciences*, 6 (11), 1836-1842 https://doi.org/10.48047/AFJBS.6.11.2024.1836-1842

[20] Kopelman P. G. Obesity as a medical problem. Nature, 2000, 404(6778), 635–643. https://doi.org/10.1038/35007508

[21] Kunzmann, A. T., Coleman, H. G., Huang, W. Y., Kitahara, C. M., Cantwell, M. M., & Berndt, S. I. (2015). Dietary fiber intake and risk of colorectal cancer and incident and recurrent adenoma in the Prostate, Lung, Colorectal, and Ovarian Cancer Screening Trial. *The American journal of clinical nutrition*, *102*(4), 881–890. https://doi.org/10.3945/ajcn.115.113282

[22] Landry, M. J., & Ward, C. P. Health Benefits of a Plant-Based Dietary Pattern and Implementation in Healthcare and Clinical Practice. American journal of lifestyle medicine, 2024, 18(5), 657–665. https://doi.org/10.1177/15598276241237766

[23] Liu, H., Zhu, J., Gao, R., Ding, L., Yang, Y., Zhao, W., Cui, X., Lu, W., Wang, J., & Li, Y. Estimating effects of whole grain consumption on type 2 diabetes, colorectal cancer and cardiovascular disease: a burden of proof study. Nutrition journal, 2024, 23(1), 49. https://doi.org/10.1186/s12937-024-00957-x

[24] Mishra, P., Singh, U., Pandey, C. M., Mishra, P., & Pandey, G. Application of student's *t*-test, analysis of variance, and covariance. Annals of cardiac anaesthesia, 2019, 22(4), 407–411. https://doi.org/10.4103/aca.ACA_94_19

[25] Parada Venegas, D., De la Fuente, M. K., Landskron, G., González, M. J., Quera, R., Dijkstra, G., Harmsen, H. J. M., Faber, K. N., & Hermoso, M. A. Short Chain Fatty Acids (SCFAs)-Mediated Gut Epithelial and Immune Regulation and Its Relevance for Inflammatory Bowel Diseases. Frontiers in immunology, 2019, 10, 277. https://doi.org/10.3389/fimmu.2019.00277

[26] Poore, J., & Nemecek, T. Reducing food's environmental impacts through producers and consumers. Science (New York, N.Y.), 2018, 360(6392), 987–992. https://doi.org/10.1126/science.aaq0216

[27] Saa, L. R., Valiño Cabrera, E. C., Savón Valdés, L. L., García Hernández, Y., Dustet Mendoza, J. C., & Alberto Vazquez, M. Sustainable Biomass Valorization by Solid-State Fermentation with the Mutant Strain *Trichoderma viride* M5-2 of Forage Legumes to Improve Their Nutritional Composition as Animal Feed. Sustainability, 2025, 17(11), 4990. https://doi.org/10.3390/su17114990

[28] Saraswathi, V., Kumar, N., Gopal, T., Bhatt, S., Ai, W., Ma, C., Talmon, G. A., & Desouza, C. Lauric Acid versus Palmitic Acid: Effects on Adipose Tissue Inflammation, Insulin Resistance, and Non-Alcoholic Fatty Liver Disease in Obesity. Biology, 2020, 9(11), 346. https://doi.org/10.3390/biology9110346

[29] Schoultz, I., & Keita, Å. V. The Intestinal Barrier and Current Techniques for the Assessment of Gut Permeability. Cells, 2020, 9(8), 1909. https://doi.org/10.3390/cells9081909

[30] Seethaler, B., Basrai, M., Neyrinck, A. M., Nazare, J. A., Walter, J., Delzenne, N. M., & Bischoff, S. C. (2021). Biomarkers for assessment of intestinal permeability in clinical practice. American journal of physiology. Gastrointestinal and liver physiology, 2021, 321(1), G11–G17. https://doi.org/10.1152/ajpgi.00113.2021

[31] Sekirov, I., Russell, S. L., Antunes, L. C., & Finlay, B. B. Gut microbiota in health and disease. Physiological reviews, 2010, 90(3), 859–904. https://doi.org/10.1152/physrev.00045.2009

[32] Shahi, D. S., Deepak, D. (2018), Isolation Of Oligosaccharides And Antimicrobial Activity Of Gaddi Sheep's Milk, *Eurasian Journal of Analytical Chemistry*, 13 (5), 795-803. https://eurasianjournals.com/index.php/ej/article/view/795

[33] Shahi, D. S., Deepak, D. S. (2018), Separation And Structure Elucidation Of Novel Decasachharide "Oviasose" From Gaddi Sheep's Milk, *Eurasian Journal of Analytical Chemistry*, 13(5), 1001-1011. https://eurasianjournals.com/index.php/ej/article/view/1001

[34] Shahi, D. S., Singh, S. K. (2018), Segregation And Structural Interpretation Of Novel Tetrasachharides "Isose" By NMR and Mass Spectroscopy, Eurasian Journal of Analytical Chemistry, Vol. 13 (5). 992-1000, https://eurasianjournals.com/index.php/ej/article/view/1000

[35] Shahi, S. (2020), "Gaddiose" Isolation and Structure Interpretation of Novel Heptasaccharide from Gaddi Sheep's Milk, International Journal of Advanced Sciences and Technology, Vol. 29 (9s), 4455-4463, http://sersc.org/journals/index.php/IJAST/article/view/16926

[36] Shahi, S., Singh, H. K., Deepak, D., Singh, S. K. (2021), "Gadose" Isolation and Structure Elucidation Of Novel Octasaccharide From Gaddi Sheep's Milk. Annals of the Romanian Society for Cell Biology, 25 (4), 20193-20206, http://annalsofrscb.ro/index.php/journal/article/view/9115/6777

[37] Shahi, S., Singh, H. K., Shukla, C. S., Deepak, D. Singh, S. K. (2020), The Biological Utilization of Gaddi Sheep's Milk Oligosaccharides, Journal of Critical Reviews; 7 (15), 2061-2068, https://jcreview.com/archives/volume-7/issue-15/8688

[38] Shahi, S., Singh, H. K., Shukla, C. S., Deepak, D. Singh, S. K. (2020), Anti-Fungal Bioactivity of Gaddi Sheep's Milk Oligosaccharide, International Journal of Advanced Sciences and Technology, Vol. 29 (11s), 2051-2058, http://sersc.org/journals/index.php/IJAST/article/view/22585

[39] Shahi, S., Singh, S.K. (2019), Biological Importance of Milk Oligosaccharides Isolated from Gaddi Sheep's Milk, Eurasian Journal of Biological Science, 13 (2), 1245-1249, https://www.proquest.com/openview/73c7a2596bb57e83b9212c7233bdd79f/

[40] Sharma, M., Vidhya C. S., Ojha, K., Yashwanth B. S., Singh, B., Gupta, S., & Pandey, S. K. The Role of Functional Foods and Nutraceuticals in Disease Prevention and Health Promotion. European Journal of Nutrition & Food Safety, 2024, 16(2), 61–83. https://doi.org/10.9734/ejnfs/2024/v16i21388

[41] Sinclair, J., West, N. P., & Cox, A. J. Comparison of four DNA extraction methods for 16s rRNA microbiota profiling of human faecal samples. BMC research notes, 2023, 16(1), 169. https://doi.org/10.1186/s13104-023-06451-7

[42] Slavin J. Fiber and prebiotics: mechanisms and health benefits. Nutrients, 2013, 5(4), 1417–1435. https://doi.org/10.3390/nu5041417

[43] So, D., Whelan, K., Rossi, M., Morrison, M., Holtmann, G., Kelly, J. T., Shanahan, E. R., Staudacher, H. M., & Campbell, K. L. Dietary fiber intervention on gut microbiota composition in healthy adults: a systematic review and meta-analysis. The American journal of clinical nutrition, 2018, 107(6), 965–983. https://doi.org/10.1093/ajcn/nqy041

[44] Tirosh, A., Calay, E. S., Tuncman, G., Claiborn, K. C., Inouye, K. E., Eguchi, K., Alcala, M., Rathaus, M., Hollander, K. S., Ron, I., Livne, R., Heianza, Y., Qi, L., Shai, I., Garg, R., & Hotamisligil, G. S. The short-chain fatty acid propionate increases glucagon and FABP4 production, impairing insulin action in mice and humans. Science translational medicine, 2019, 11(489), eaav0120. https://doi.org/10.1126/scitranslmed.aav0120

[45] Tripathy, P., Shahi, S. (2024), AI-Powered Mining of Nature's Chemical Library: Unveiling the Therapeutic Potential of Natural Products, *Research Journal Pharmacology*, 18 (3), 32-37, https://doi.org/10.36478/makrjp.2024.3.32.37

[46] Wu, T., Seaver, P., Lemus, H., Hollenbach, K., Wang, E., & Pierce, J. P. Associations between Dietary Acid Load and Biomarkers of Inflammation and Hyperglycemia in Breast Cancer Survivors. Nutrients, 2019, 11(8), 1913. https://doi.org/10.3390/nu11081913

[47] Yang, M., Liu, S., & Zhang, C. The Related Metabolic Diseases and Treatments of Obesity. Healthcare, 2022, 10(9), 1616. https://doi.org/10.3390/healthcare10091616

[48] Zhao, X., Lu, C., Song, B., Chen, D., Teng, D., Shan, Z., & Teng, W. The prevalence and clustering of metabolic syndrome risk components in Chinese population: a cross-sectional study. *Frontiers in endocrinology*, 2023, 14, 1290855. https://doi.org/10.3389/fendo.2023.1290855

[49] Zhou, H., Urso, C. J., & Jadeja, V. (2020). Saturated Fatty Acids in Obesity-Associated Inflammation. Journal of Inflammation research, 2020, 13, 1–14. https://doi.org/10.2147/JIR.S229691