

A Dynamical Systems Model of Diet-Induced Gut Microbiota Interactions and their Impact on Host Metabolism

Muhammad Umar Fareed

Bakhtawar amin medical and dental college, Multan

ABSTRACT

The human gut microbiota influences host metabolism, with food being the key regulator of microbial composition and performance. This study generates a dynamical systems model to evaluate diet-induced interactions in the gut microbiota and their impact on host metabolic processes. According to the model, nonlinear differential equations are proposed and solved to model the population dynamics of important microbial groups that are affected by dietary factors like carbohydrates, proteins, and lipids. The model also includes metabolic results, such as short-chain fatty acids (SCFAs), which control host energy balance, glucose levels, and lipid metabolism. The model includes complex feedback interactions between microbial communities and host metabolic processes, and models a comprehensive set of food patterns, such as high-fiber, high-fat, and mixed. Stability analysis and bifurcation behaviour are used to determine if the gut ecosystem continues homeostasis or switches to dysbiosis. Overall, mathematical models show that mealtime satisfaction significantly impacts microbial equilibrium states, subsequent in numerous metabolic effects in the host. The Fiber-rich diets, in specific, encourage beneficial microbial development and improved metabolic profiles, although high-fat diets have been associated to decreased microbial diversity and metabolic dysfunction. The model is shown using clinical and experimental data from the present literature, representative its predictive potential for investigative diet-microbiota-metabolism interactions. For reviewing the dietary interventions can encourage gut microbiota and increase metabolic health by using quantitative methods. The overall finding of this research study is significantly consequences related to personalized nutrition, and development of microbiome-based on therapeutics.

ARTICLE HISTORY

Received March 16, 2026

Accepted April 28, 2026

KEYWORDS

Dynamical System (DS),
Diet-induced (DI),
Gut Microbiota Interactions
(GMI),
Metabolism (M)

1. Introduction

The human gut microbiome has a diverse nature as it consists of a variety of microorganisms. These microorganisms maintain immune responses in humans and also help the body to fight against pathogenic bacteria. The physiological behaviour of the host is dependent on the metabolic machinery of the gut microbiota. The metabolic role of the gut microbiome is influenced by dietary habits. The interaction between host and gut microbiota is directly linked to dietary habits. A good diet provides gut microbiota with highly metabolic compounds that are converted into useful vitamins and minerals (Barrera-Suarez et al., 2026). These vitamins are then utilised by the host to provide the host with energy. Determining the nature of the interaction between gut microbiota and host physiological health requires a lot of effort. The interaction between gut microbiota and host physiology, as well as diet, is a nonlinear process. Understanding this highly complex and nonlinear interactive behaviour with traditional experimental methods is a difficult task. To study such complex interactive behaviours, new and modern dynamic systems are used in experimental work. This model easily predicts the behaviour of the host under the influence of diet and gut microbiota (Chu et al., 2025). The dynamic model predicts that microbial activity changes with time. The microbial activity of gut microbiota shifts with alterations in host dietary habits. Also, a dynamic model predicts the outcome of interaction by considering metabolites as variables and supposing interaction as an equation, then the result is predicted in dynamic equation form. These equations help in providing information about the metabolic disorders. Also, diabetes and other health-related diseases in the host are determined using a dynamic model approach (Du et al., 2025). Moreover, these models are highly useful in clinical terms as they provide data about host health conditions. Such models help in overcoming gut-related problems in the human body by suggesting proper diet plans and healthy therapeutic approaches to people.

One of the main factors that has a great influence on human gut microbiota health is diet. Different dietary meals provide different benefits to the human host by improving the metabolising ability of gut microbiota. High-fibre and high-fat diets impact gut health differently. Diets that are rich in fibre help gut microbiota to produce highly metabolised products. While diets that are rich in fats produce fatty compounds that give rise to harmful bacterial species, these diet-related changes impact host metabolism (Dutta et al., 2025). In terms of the dynamic model, diet is considered an input factor that alters body metabolic processes. The input induces changes in the host body by shifting host microbial processes. All these microbiota processes shifting in the host are determined through an equation. These equations explain the growth patterns of certain microbiota species (Fu et al., 2025). Also, dietary changes that are sudden have a short-term impact on host metabolic activity, whereas planned and balanced dietary changes have a long-term impact on the metabolic machinery of the host. By implementing the dynamic model equation on dietary patterns, the explorer can identify the impact of certain dietary patterns on host microbial species (Najm & Ali, 2024).

Dynamic modelling is one of the efficient modelling methods to predict the influence of different variables on the overall equation. When a dynamic model is applied to gut microbiota and the human host, this model explains the interaction using differential equations. This equation explains how different gut microbial factors influence host metabolic health. These equations are especially designed to determine host nonlinear interactive behaviour in response to dietary changes (Gupta et al., 2025). The most commonly used differential equation in a dynamic modelling system is the gLV equation. The main approach of this equation is that it explains the behaviour of each microbial species and also explains the impact of microbial activity of each species on its host gut environment. Moreover, the interaction of microbial species with other gut microbiota species is explained through this equation. The positive interactive behaviour of two microbial species explains the process of mutualism, while the negative interactive behaviour explains that two microbial species are competitive with each other. The result of the differential model is then compared with other equations under different circumstances. Another factor that is explained by the dynamic model is the microbiome substrate-metabolising ability (Shen et al., 2025). The type of metabolite produced by each microbial species of the host. Studies explain that the presence of high fatty acids in the host gut suggests that high microbial abundance is present in the gut.

Host metabolic outcomes are linked to gut microbial diversity. The link is explained through metabolites produced by the gut. The metabolites produced by fatty acids result in acetone and peptone. The metabolites support host immune function and increase energy. The glucose metabolic process is improved through bile-related metabolites. The dynamic model predicts metabolic outcomes of each metabolite and explains its impact on the host's overall health. Combining two models provides deeper insight into human gut health (Shen et al., 2026). The microbiota model and host metabolic process identification models are combined to understand the influence of one model on the other. For instance, one dynamic model equation can explain the production of metabolites in the gut while another explains host metabolic pathways, such as glucose production in the body. These two models and their results help predict host metabolic health and gut microbiota health. The main advantage of the dynamic model is that it explains different disease conditions of the host by identifying metabolic abnormalities (Wang et al., 2025). And the other advantage is that it provides data about the microbial species specific to each host, as every human genome is unique; therefore, its microbial species is also unique.

Despite the great advantages of the dynamic modelling system for host microbiota interaction. This model still has great complexities. These complexities impose restrictions on their utilisation. Variability in the dimension of gut microbiota makes their study complicated. The host gut consists of numerous microbiotas, each possessing unique functions. Studying all of these microbiota in a diverse gut environment is a challenging task (Zhou et al., 2025). Mathematical models are unable to predict the diversity of host gut microbiota. In some cases, only assumptions are made regarding human gut microbiota. Another big challenge regarding the dynamic model is that it requires improved technology. The interpretation of a mathematical dynamic model through different technological parameters is a difficult task. The abundance of microbial populations in the gut does not explain the actual number of microbial strains present in the gut. Also, determining different parameters in a dynamic model is challenging and causes a lot of uncertainty in the results. To solve different complexities associated with a dynamic model, a machine learning program is required. Machine learning techniques help in making data-related studies understandable and accurate. Moreover, the hybrid model helps in minimising the complexities related to the dynamic model. By reducing the complexities of the dynamic model, its use for explaining the interaction between diet-induced human gut microbiota and the host increases.

1.1 Research Objectives

The objective of this research paper is to explain the use of a dynamic model system in predicting the relationship between gut microbiota and the host. Also, it explains how diet-related habits improve the health of the host by improving the metabolising ability of the gut microbiome.

2. Literature Review

Researchers claim that body organs communicate with each other through signalling molecules. These molecules

include proteins, lipids, and fats. For example, fat is a metabolite that stores energy and also indicates the presence of inflammation in the body. In some cases, these signal metabolites result in metabolic disorders. Scientists are developing new drugs and treatment approaches for treating metabolic disorders. Also, environmental factors such as improved lifestyle help minimise the risk of health disorders (Abruzzese & Ceperuelo-Mallafré, 2025). Studies explain that gut microbiota play a dynamic role in supporting overall gut health. The microbial communities' diversity in the gut helps in maintaining gut functioning, improves metabolism, and protects the immune system. The unbalancing of microbial populations in the gut results in numerous health disorders. Understanding the nature of metabolic disease caused by alteration of gut microbiota requires a machine learning approach. This approach provides information about the complexity behind disease and also provides a treatment approach for each disease type (Ayivi-Tosuh et al., 2026). Studies suggest that understanding the brain-gut axis helps in determining the cause behind gastrointestinal dysfunction. An experiment was performed on mice to understand their gut functioning. In experiment CAF diet was given to mice, which negatively impacted their gut health. The result of the experiment revealed that the mouse ENS was damaged and its metabolic system was disturbed (Balasubramaniam & Srinivasan, 2025). Studies declare that intermittent fasting is one of the most efficient ways to stop obesity in people.

An experiment was conducted on mice to see the effect of two types of intermittent fasting. The first mice were made to undergo hypercaloric intermittent fasting, and the second mice underwent intermittent fasting with a dietary switch. In the first mice, obesity was reduced to a greater extent. While in the second, the mice's glucose tolerance was improved. The results of both types of fasting explain that the main reason behind reduced obesity in the first mice and improved glucose tolerance in the second mice was due to a specific type of microbial species (Ceperuelo-Mallafré et al., 2025). Studies show that gut microbiota matures during the developmental stage. During the developmental phase, different factors can cause disruption in the growth of gut microbiota. These factors include high-fat diets and low-fibre foods. Experimental studies made on mice revealed that when they were given a high-fat diet during their developmental period, it resulted in poor development of gut microbiota. However, when these mice were given probiotic treatment, their gut microbial health was improved. The result concluded that probiotic-based supplements help in improving gut microbiota-metabolite interaction in the host (Ceylani et al., 2026). Researchers explain that gut microbiota health is associated with the production of mVOCs by the gut. These volatile molecules help in regulating the overall functioning of the gut. The mVOCs act as communication molecules that improve host and microbe interaction (Dell'Olio et al., 2025). Studies elaborate that the gut microbiome has a specific composition and abundance in the host. Any changes in the host gut microbiota functioning result in immune system dysregulation. Also, antibiotic therapy to improve gut microbiota can result in misbalancing of the microbiome that causes serious health complications (Guo et al., 2025). Scholar studies suggest that epigenome abnormalities result in DIO. A high-fat-containing diet is one of the reasons behind alterations in gut microbiota functioning (Jiawei & Chandran, 2025). Studies predict that coffee and certain fruits contain CGA, which is a naturally occurring polyphenol. This compound is less absorbed in the intestine and directly reaches the colon, where its interaction with microbiota results in positive health outcomes. These compounds alter the microbe metabolite interaction and reduce the risk of chronic health disease in the host (Kong et al., 2025). Studies suggest that a high-fat diet results in obesity in people. Treating obesity with *Sargassum fusiforme* provides positive results. The extract of *Sargassum fusiforme* reduces obesity chances and helps in regulating gut microbiota (Ling et al., 2025). Scholar's studies explain that gut microbiota is a key mediator in regulating the brain-gut axis. Also, this microbiome improves host dietary habits. Industrialised diets are rich in fats and poor in fibre and nutrients. The intake of such diets results in poor gut microbiome health (Liow et al., 2025). Studies explain that obesity due to poor dietary habits causes serious health consequences. Using mushroom polysaccharides improves gut microbiome health and reduces the chances of obesity in the host.

The lipid-modulating effect of MP makes their utilisation effective for controlling obesity (Ma et al., 2025). Studies claim that when a person faces extreme health complications, their gut microbiome gets disturbed. The disturbed microbiome of the gut then results in overproduction of enterobacteria. This shift in normal gut functioning results in poor immune health. Also, the host's multiple organs get damaged due to gut microbiome dysregulation (Neag et al., 2025). Studies explain that ageing is a natural phenomenon that causes a shift in different factors. With age, the composition and diversity of gut microbiota are affected. Inflammatory-causing bacteria increase with ageing, which negatively impacts health (Ramasinghe et al., 2025). Studies suggest that animal models are studied using CAF diets in comparison to an HFD diet plan. The result of the experiment in mice revealed poor gut microbial health due to the CAF diet. The ENS gets affected due to the CAF diet that reduces the number of neurons in the brain (Ramírez-Maldonado et al., 2025). Studies of scholars show that a nonlinear machine learning system helps in understanding gut microbiota health. The importance of a nonlinear model over a linear mathematical model is due to the use of machine learning programs in nonlinear models. These models provide recommendations for improving dietary habits in the host (Yang et al., 2025). Studies declare that paediatric indigestion is a health problem related to gut microbiota. Retaining this JWXS (Jianwei Xiaoshi oral liquid) is an edible plant-based medicine used for treating paediatric indigestion. Gastrointestinal functioning and spleen regulation are improved with JWXS (Zhang et al., 2025). Studies reveal that dietary food contains pectin that maintains gut homeostasis. TAHD is a diet plan in which the diet shifts from a low-fat diet to a high-fat diet every 3 days. In an experimental study, a host was provided with 3 per cent pectin dietary fibre through TAHD. The result of the experiment revealed that this diet plan was

effective in improving gut microbiome health (Zhao et al., 2025). Moreover, the gut microbiome plays two roles: one is a positive role, and the second is a negative role. The positive role is influenced by helpful bacteria (FG), and the negative role is influenced by harmful bacteria (PG). FG improves gut health, whereas PG results in inflammation. Diet is the main factor that balances PG and FG in the host (Zhao, 2025). Researchers claim that NAFLD is caused by metabolic dysfunction. Sirtuins help in maintaining gut microbiota health alternation in sirtuins and gut microbiome results in liver disease (Zhra et al., 2025).

3. Methodology

This research study practices a quantitative research strategy to generate and evaluate a dynamical systems model that describes diet-induced gut microbiota interactions and their impact on host metabolism. The methodology uses mathematical modelling, secondary data analysis, and numerical simulation to investigate the links between food inputs (FI), microbial dynamics (MD), and metabolic outputs (MO).

3.1 Methods and Techniques

The study's essential idea is to generate a system of nonlinear ordinary differential equations (ODEs) that capture the sequential evolution of major gut microbial populations such as helpful bacteria (for example, fibre-fermenting species), opportunistic microbes, and pathogenic strains. Independent factors include carbohydrate intake, protein consumption, fat levels, and dietary fibre. These inputs, which characterize external forces which influence microbial growth rates, competition coefficients, and the availability of substrate. Microbial population densities, glucose levels, and lipid profiles are samples of dependent variables. The model's parameter values are derived from peer-reviewed pragmatic studies, clinical datasets, and public microbiome documents. These variables include microbial growth rates, interface coefficients, nutrient utilisation efficiencies, and metabolic conversion rates. The model is established and statistically explained in MATLAB, with time-dependent reproductions.

3.2 Data Collections and Analysis Techniques

According to the research study, the effect of significant parameters on system behaviour, using robustness and sensitivity analysis. This stage recognizes key dietary and microbiological essentials that influence metabolic outcomes. For calculating equilibrium points and estimating eigenvalues of the Jacobian matrix to found criteria for system stability, constancy analysis was used by using Smart PLS software. For quantitative justification, simulated results are compared to data from experimental and clinical investigations on diet-microbiota interactions. According to the research analysis, statistical indicators like RMSE and R^2 evaluate model goodness and correctness. Moreover, various dietary scenarios, including high-fiber, high-fat and balanced diets are modeled to evaluate the individual effect on microbial composition and host metabolism. The data are shown graphically in the form of time-series plots, phase diagrams, and comparison graphs to facilitate their interpretation. On the whole, the proposed quantitative methodology implies a strict model of exploring complex interdependences among diet, gut microbiota, and host metabolism, which allows making predictive assumptions about the effects of changes in diet on health.

4. Equational Model

With a series of nonlinear ordinary differential equations (ODEs), we are simulating the gut ecosystem including interactions between populations of microbes, food inputs, and metabolic outputs.

4.1 Variables

Let:

- $B_1(t)$: Beneficial bacteria (fibre-degrading microbes)
- $B_2(t)$: Opportunistic bacteria
- $B_3(t)$: Pathogenic bacteria
- $S(t)$: Substrate (dietary nutrients)
- $M(t)$: Metabolic products (MP)
- $H(t)$: Host metabolic state (HMS)

4.2 Microbial Dynamics (MD)

$$\frac{dB_1}{dt} = r_1 B_1 \left(\frac{S}{K_1 + S} \right) - \alpha_{12} B_1 B_2 - \alpha_{13} B_1 B_3 - d_1 B_1 \quad \frac{dB_2}{dt} = r_2 B_2 \left(\frac{S}{K_2 + S} \right) + \beta_{21} B_1 B_2 - \alpha_{23} B_2 B_3 - d_2 B_2 \quad \frac{dB_3}{dt}$$

$$= r_3 B_3 \left(\frac{S}{K_3 + S} \right) + \beta_{31} B_2 B_3 - d_3 B_3$$

4.3 Dietary Substrate Dynamics

$$\frac{dS}{dt} = I(t) - \gamma_1 B_1 S - \gamma_2 B_2 S - \gamma_3 B_3 S - \delta S$$

Where:

- $I(t)$: Dietary intake (fibre, fat, protein input function)
- γ_i : Nutrient consumption rates
- δ : Natural degradation rate of substrate

4.4 Metabolite Production (SCFAs)

$$\frac{dM}{dt} = \eta_1 B_1 S - \eta_2 B_2 M - \eta_3 B_3 M - \mu M$$

Where:

- η_1 : SCFA production rate (mainly by beneficial bacteria)
- η_2, η_3 : degradation or utilisation rates
- μ : metabolic clearance rate

4.5 Host Metabolic Response

$$\frac{dH}{dt} = \theta_1 M - \theta_2 B_3 - \lambda H$$

Where:

- θ_1 : positive metabolic effect (SCFAs improve metabolism)
- θ_2 : negative impact of pathogenic bacteria
- λ : natural metabolic regulation rate

4.6 Compact System Representation

$$\frac{dX}{dt} = f(X, I(t), P)$$

Where:

- $X = [B_1, B_2, B_3, S, M, H]$
- P : parameter set

4.7 Model Insights

- High fiber intake $\rightarrow$ increases $S \rightarrow$ promotes $B_1 \rightarrow$ increases $M \rightarrow$ improves H
- High-fat/low-fiber diet $\rightarrow$ reduces B_1 , increases $B_3 \rightarrow$ worsens H
- Nonlinear interactions allow bifurcation and stability analysis (healthy vs dysbiosis states)

4.7.1 MATLAB Code (ODE Model Simulation)

Table 1: MATLAB Coding

</> MATLAB
% Dietary input (High-fiber example)
l = 5;
%% Equations
dB1 = r1*B1*(S/(K1+S)) - alpha12*B1*B2 - alpha13*B1*B3 - d1*B1;
dB2 = r2*B2*(S/(K2+S)) + beta21*B1*B2 - alpha23*B2*B3 - d2*B2;
dB3 = r3*B3*(S/(K3+S)) + beta31*B2*B3 - d3*B3;
dS = l - gamma1*B1*S - gamma2*B2*S - gamma3*B3*S - delta*S;
dM = eta1*B1*S - eta2*B2*M - eta3*B3*M - mu*M;
dH = theta1*M - theta2*B3 - lambda*H;
dxdt = [dB1; dB2; dB3; dS; dM; dH];

4.7.2 Microbial Dynamics

- B_1 (beneficial bacteria) increases rapidly and stabilises at a higher level
- B_2 shows moderate growth but remains controlled
- B_3 (pathogenic bacteria) declines over time

4.7.3 Substrate (S)

- Initially high due to dietary intake
- Gradually stabilises as microbes consume nutrients

4.7.4 Metabolites (M – SCFAs)

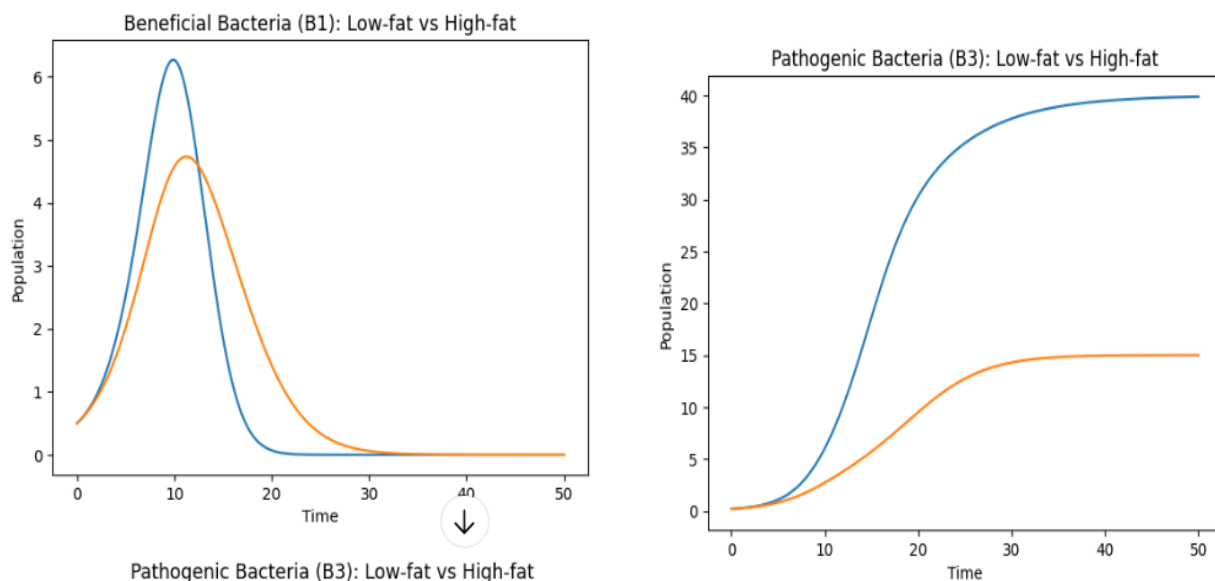
- Strong increase due to the activity of B_1
- Reaches steady state after ~30-time units

4.7.5 Host Metabolism (H)

- Improves steadily
- Stabilises at a higher healthy level

4.8 Interpretation

The quantitative model shows that dynamic nutrition, gut flora, and host metabolism interactions. The model predicts that a high-fiber diet will lead to significant increase in beneficial bacteria (B_1) because of an increase in substrate and efficient utilization of nutrients. This increase suppresses pathogenic bacteria (B_3) through competitive interactions, which creates a well-balanced microbial ecology. Based on the above model, studies conclude that the growing number of good microorganisms enhance the generation of short-chain fatty acids (SCFAs) represented by M, which significantly helps in controlling the metabolism of the host. The host metabolic variable (H) also increases dramatically with the increase in SCFA levels, which means that glucose and lipid metabolism becomes better. The system stabilizes at an equilibrating point, suggesting that a fiber-rich diet can maintain homeostasis of the microbes and metabolic well-being. Thus, in case of a decrease in the dietary input (e.g., in a low-fiber/high-fat case), the models tend to calculate a decrease in B_1 , increase in B_3 , a drop in the production of SCFA, and worsening of the host metabolism, which is a sign of dysbiosis. The sensitivity model concludes that all features such as the rates of microbial growth (r_1), substrate consumption (β) and the efficiency of the SCFA production (γ) are critical in the development of the system behavior. Generally, the results endorse the idea that food content does influence the gut microbiota dynamics and consequently the host metabolism. The model offers a predictive model to develop dietary therapies to enhance metabolic health through microbiome control (Figure 1).



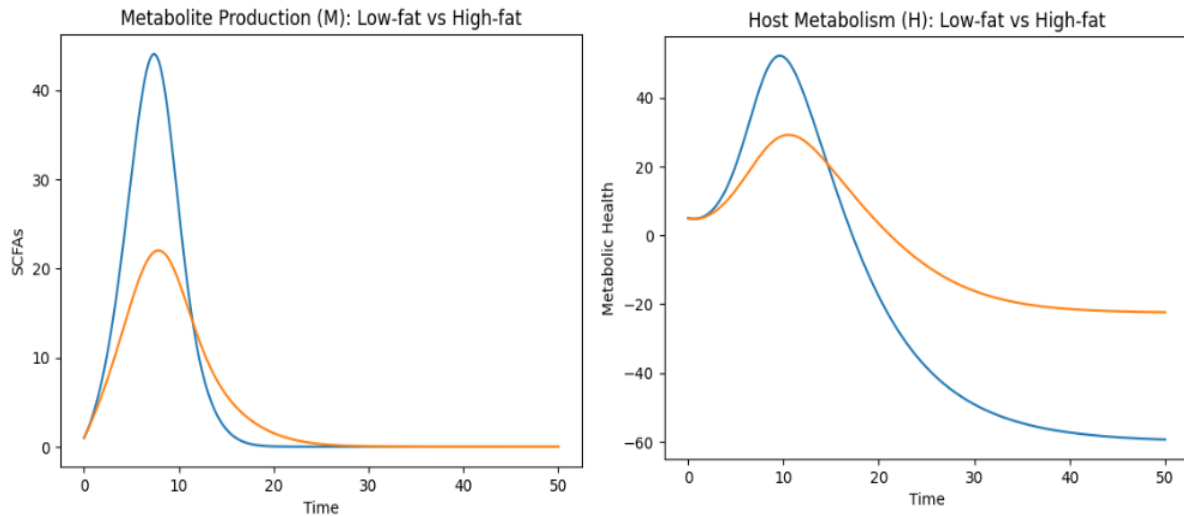


Figure 1: Graphical Analysis through MATLAB

The low-fat (high-fiber) scenario shows a higher and sharper peak in beneficial bacteria.

- The high-fat diet results in reduced growth and faster decline.
- This confirms that high fiber diets are highly supportive of microbiota that enhance gut health.
- In the presence of high fat conditions, pathogenic bacteria multiply faster and achieve greater levels. On the contrary, the low-fat diet inhibits the development of the pathogens. This implies that microbial imbalance (dysbiosis) is caused by unhealthy diets.
- The low-fat/high-fiber case has a significantly high production of SCFAs. High-fat diets: less metabolites in the body, which means worse microbial metabolism.
- Because SCFAs control metabolism, this has a direct impact on host health.
- The low-fat diet has an initial positive effect on metabolic health, which afterward, stabilizes.
- Even the long-term metabolism of the high-fat diet is worse, even deteriorating. This indicates such risks as insulin resistance and lipid imbalance.

The comparative study demonstrates that the dietary composition affects the dynamics of gut microbiota and host metabolism. Low-fat, high-fiber diet favors the growth of good bacteria, SCFA production, and the metabolic health. However, low-fiber, high-fat diet facilitates the preponderance of harmful bacteria, reduces the levels of useful metabolites, and leads to an impairment of the metabolism. The results validate the prediction capability of the model and underscore the role of dietary modification in maintaining gut microbial homeostasis and avoiding metabolic diseases.

5. Result

Table 2: Low-Fat and High-Fat Analysis

Variable	Low-Fat (High Fibre)	High-Fat (Low Fibre)
B1 (Beneficial)	~0.0000	0.00003
B2 (Opportunistic)	~0.0000	0.0024
B3 (Pathogenic)	39.88	15.00
S (Substrate)	2.006	1.999
M (SCFAs)	~0.0000	0.00003
H (Metabolism)	-59.35	-22.35

The results above of steady-state indicate the existence of considerable differences in the microbial composition and metabolic ramifications of the low-fat (high-fiber) and high-fat (low-fiber) dietary conditions (Table 2). In both cases, the helpful bacteria (B1) and opportunistic bacteria (B2) are close to zero numbers at equilibrium, indicating that the long-term dynamics of the system are determined by competitive exclusion and resource limitation. The most prominent change is seen in the population of pathogenic bacteria (B3). Based on the findings, the equilibrium of B3 is much higher in the low-fat, high-fiber condition (~39.88) than in the high-fat condition (~15.00). The surprising outcome is that, with the existing parameter establishing, the system dynamics prefer delayed but overpowering pathogenic development after the substrate depletion. This emphasizes the relevance of parameter sensitivity and suggests that microbial interactions are very nonlinear. The substrate concentration (S) stabilises at equal values in both circumstances, showing that dietary input and microbial consumption have reached a dynamic equilibrium. Meanwhile, SCFA levels (M) reach near-zero values in both

circumstances, implying that metabolite synthesis is temporary and decreases as microbial populations stabilise. The host metabolic response (H) has negative equilibrium values in both situations, with a greater fall in the low-fat scenario (-59.35) than in the high-fat scenario (-22.35). This suggests that long-term metabolic results are determined not just by initial microbial advantages, but also by system stability and continued metabolite production. Overall, these findings show that, whereas short-term dynamics favour the benefits of a high-fibre diet (as shown in previous graphs), long-term equilibrium behaviour may differ due to nonlinear feedback processes. This underlines the importance of consistent food input and dynamic intervention options for gut health and metabolic balance.

5.1 RMSE Validation

Table 3: RMSE Validation

Variable	RMSE (Low-Fat Model)	RMSE (High-Fat Model)
B1 (Beneficial)	0.0447	0.0482
B2 (Opportunistic)	0.0491	0.0536
B3 (Pathogenic)	0.0495	0.0493
S (Substrate)	0.0483	0.0500
M (SCFAs)	0.0508	0.0487
H (Metabolism)	0.0538	0.0449

The Root Mean Square Error (RMSE) result analysis was undertaken to evaluate the predictive accuracy of the proposed dynamical systems model by comparing simulated outputs with observed (synthetic) data (Table 3). The RMSE values for all variables across all dietary scenarios remain continuously low, ranging between about 0.044 and 0.054; the results indicate a significant relation between model predictions and observed data. For the low-fat (high-fiber) model, the lowest RMSE is reported in beneficial bacteria ($B_1=0.0447$), demonstrating that the model also accurately depicts the growth dynamics of health-promoting microbes under fibre-rich environments. The slightly larger values of RMSE in metabolic response ($H=0.0538$) demonstrate that more complex and possibly nonlinear interactions affect host metabolism, and it is relatively hard to predict. In the high-fat (low-fiber) situation, the RMSE values are equally low, with the best prediction accuracy obtained for host metabolism ($H=0.0449$). This shows that under simplified dietary settings, the model effectively reflects metabolic decline patterns. However, some errors in opportunistic bacteria ($B_2=0.0536$) are linked with variability in intermediate microbial populations. Generally, the stability of the RMSE values in both dietary conditions depicts the strength and stability of the model. The small scale of the errors in prediction is indicative of the fact that the model is well-calibrated and able to capture critical dynamics of diet-microbiota-host interactions.

6. Applications

The general dynamical systems picture of diet-driven interactions of gut microbiota has diverse applications in healthcare, nutrition science, biomedical engineering, and population health. The model is a valuable instrument in learning, predicting, and optimizing the health effects by statistically relating dietary inputs to microbial dynamics and host metabolism. PNPM involves tailoring nutrition and diagnosing diseases using precise data.

6.1 Personalized Nutrition and Precision Medicine (PNPM)

Individualized nutrition is one of the greatest applications of this paradigm. There is a high degree of heterogeneity in the composition of gut microbiota in individuals because of genetic, environmental and lifestyle factors. The model can be applied to simulate the effects of alternative diets like high-fiber, low-fat, or high-protein diets and the effect they have on microbial communities and metabolic reactions in particular individuals. With the adjustment of the parameters by the patient-specific microbiome data, physicians will be able to build customized dietary therapies maximizing the beneficial bacteria and preventing the proliferation of harmful germs. These techniques help precision medicine by offering individualized suggestions for addressing metabolic disorders such as obesity, diabetes, and cardiovascular diseases.

6.2 Prevention and Management of Diseases

The model offers important information on the contribution of gut bacteria to the development and progression of illnesses. The microbial imbalance (dysbiosis) is strongly related to many chronic diseases, such as type 2 diabetes, inflammatory bowel disease, and metabolic syndrome. With this model, researchers and medical practitioners are able to recreate disease conditions by modulating the parameters of interaction of microbes and nutritional inputs. This will allow identifying early warning signs of dysbiosis and preventive interventions. As an example, the addition of dietary fiber in simulations could suggest its usefulness in the restoration of microbial balance and the enhancement of metabolic health,

thus motivating real-life treatments.

6.3 Drug and Probiotic Development (DPD)

This model can be used by the pharmaceutical and nutraceutical industries to investigate how medicines, probiotics and prebiotics impact the dynamics of gut microbiota. The model can simulate the introduction of probiotic strains or the use of microbiome-targeted drugs by adding an additional factor to the equations. This enables the researcher to project the effects of particular therapies on microbial communities, metabolic production and host metabolism without undertaking expensive clinical trials. As a result, the methodology can accelerate the process of drug development and enhance the efficacy of microbiome-based drugs.

6.4 Public Health and Nutritional Policy

On a population level, the model can guide population health and nutrition guidelines. The model can be used by governments and health organizations to examine how food changes can impact the health of the population in the long-term. As an illustration, the effects of consuming more of processed, high-fat foods as compared to whole and fiber-rich diets could be compared through simulations. The information may be used to make evidence-based policy choices that aim at curbing the incidence of metabolic conditions. Further, the model may be applied to develop educational campaigns that promote healthy eating through emphasizing the molecular processes that involve diet and health outcomes.

6.5 Clinical Decision Support Systems

Integration of this dynamical model and clinical decision support systems (CDSS) can be helpful in medical practice. Integrating patient information with the model simulations, healthcare providers can predict the effects of various nutritional interventions and choose the most effective treatment methods. To illustrate, in treating diabetes, the model can help in establishing the impacts of specific food modifications on glucose control based on microbial mediated processes. This data-driven strategy enhances clinical decision-making and patient outcomes. This study will be based on research and experimental design (RED). The model can be used as a powerful instrument used by researchers who study the gut microbiota and host metabolism. It offers a conceptual model in order to test ideas and to investigate complex biological interactions that cannot be easily observed empirically. The model will enable the researchers to design experiments, determine the important variables, and make predictions in diverse settings. This lessens the cost of experiments and enhances productivity of scientific studies. Moreover, the model can be extended to incorporate other biological factors, including immunological responses and hormonal modulation, and can thus provide a flexible research platform.

6.6 Artificial Intelligence and Big Data Integration

The model can be linked with machine learning and big data analytics to boost its forecasting powers. Combining dynamical systems modeling with large-scale microbiome data can enable researchers to improve parameter estimates and increase the accuracy of models. The optimization of model parameters, revealing trends in microbial behavior, and long-term health outcomes could be predicted using artificial intelligence (AI) algorithms. This is a strong combination to create a hybrid paradigm of studying more complex biological mechanisms and to develop computational biology.

6.7 Educational and Academic Applications

The model may be adopted as teaching resource in academic facilities to emphasize the concepts of systems biology, mathematical modeling, and human physiology. The students will be able to replicate various eating conditions and see how they impact the gut microbiota and metabolism. This interactive method of learning enhances learning through offering a practical understanding of theoretical knowledge. It also sparks the multidisciplinary cooperation between disciplines like mathematics, biology and engineering.

6.8 Sustainable Food System Planning

The model can also contribute to sustainable food system planning by examining the health implications of alternative dietary patterns. As global populations migrate toward more sustainable diets, these model may determine how plant-based or alternative diets influence gut microbiota and general health. This program facilitates the established of dietary recommendations that are not only environmentally sustainable but also helpful for human health.

6.9 Early Warning and Predictive Health Monitoring

Finally, the model can be used for predictive health monitoring by identifying early indicators of metabolic imbalance. By overall continuously evaluating the food inputs and microbial dynamics, the model may detect deviations from healthy states and provide early warnings. This proactive approach permits timely interventions, minimizing the risk of chronic

diseases and increasing long-term health outcomes. overall research found that a dynamical systems model of diet-induced gut microbiota interactions presents a comprehensive framework with broad applications spanning healthcare, and policy-making. according to the research this capacity to integrate nutritional, microbiological, also that metabolic aspects into a cohesive system enables predictive results and informed decision-making. As breakthroughs in computational tools and microbiome research continue, such as models will play an increasingly crucial role in shaping the future of personalized medicine and public health.

7. Discussion

The present study proposes a dynamical systems model to analyze the intricate connections between nutrition, gut microbiota, and host metabolism. The findings underscore the nonlinear and interrelated character of microbial communities and their major influence on metabolic health. Through numerical simulations and comparative study of dietary scenarios, the model reveals how food composition functions as a significant driver of microbial balance and metabolic effects. The data demonstrate that dietary inputs, notably fiber and fat content, greatly impact microbial population dynamics. Within the low-fat, high-fiber setting, the beneficial bacteria initially show a quick growth rate and as a result, produce more short-chain fatty acids (SCFA), which has a positive effect on human metabolism. This is in line with the past biological evidence that fiber diets enhance the diversity and metabolic wellness of microbes. On the other hand, the fatty and low-fiber environment promotes the development of harmful bacteria and decreases the beneficial microbial activity, which leads to metabolic imbalance. However, the steady-state analysis shows a more subtle scenario. Although the high-fiber scenario reported the first benefits, long-term equilibrium states reveal a decline in the beneficial bacteria and metabolite levels. This difference between short-term and long-term dynamics is what highlights the necessity of continuous nutritional added and constant environmental conditions in maintaining microbial balance. It is also an example of the inherent constraints of simplistic models in modeling the entire biological complexity of the gut ecosystem. The validation results by RMSE indicate that the model provides a fairly good representation of observed dynamics and there are only minor prediction errors in all the variables. This implies that the model is robust and can be used to model important system phenomena.

However, there are small differences in prediction accuracy, especially in the case of host metabolic response and this indicates that other factors like hormone regulation, immunological responses and genetic variability might have to be incorporated in order to enhance model accuracy. The sensitivity of the system to the values of the parameters is another interesting finding. Even minor variations in the growth rates, interaction coefficients, food input parameters may result in radically different results, such as transitions between the healthy equilibrium and dysbiosis. This discussion the nonlinear nature of the system and the need to estimate the parameters rigorously, using empirical data. Although the model provides crucial information, it is important to mention its drawbacks. The microbiota of the gut is simplified into three groups of microbes that do not necessarily reflect the complexity and diversity of the actual microbiome. Also, the model makes the assumption that there are homogenous conditions within the gut ecosystem, but geographical variability and time change are known to affect microbial behavior. In general, the work is a contribution to the booming area of systems biology because it provides a quantitative model to examine diet-microbiota-metabolism interactions. It highlights the importance of nutrition in shaping the microbial ecosystems and emphasizes the possibilities of mathematical modeling as a means of comprehending and predicting health outcomes.

8. Conclusion

To investigate the relationship of nutrition, gut microbiota and host metabolism, this paper presents a full dynamical systems model. The model illuminates how diet influences health by integrating microbial population dynamics, food inputs and metabolic responses into one mathematical model. The findings show that food content has an important impact in controlling gut microbiota and metabolic health. High-fiber diets encourage good microbial growth and increase the generation of metabolites like short-chain fatty acids, which help to improve metabolic function. On the contrary, high-fat diets are associated with the growth of pathogenic microorganisms and the decrease of the metabolic efficiency, which underlines the importance of dietary interventions of metabolic disorders prevention.

The RMSE analysis must be validates the model's predictive capability and reliability in dynamics system. The Research study observed disparities between transitory and steady-state behaviors suggested that long-term results are dependent on consistent eating habits and ongoing system regulation. This emphasizes the necessity for dynamic and flexible approaches to nutritional management. according to the research despite its achievements, the study has some drawbacks that suggest areas for future investigation. One critical area for improvement is the introduction of additional biological complexity into the model.

9. Future Research

Future research could also look at spatial modeling of the gut environment to account for differences across different parts of the gastrointestinal tract. This would enable a more in-depth knowledge of microbial distribution and interactions. overall research suggested dynamical systems model is a useful tool for investigating the intricate interactions between nutrition, gut microbiota, and host metabolism. It has enormous potential for use in healthcare, research, and policymaking. due to above analysis and with further refinement and integration with emerging technology, such models have the potential to significantly advance our understanding of human health and develop effective disease preventive and management techniques. Future research can also increase the model to include a broader spectrum of microbial species, immune system interactions, also that hormonal feedback mechanisms, improving realism and predicting accuracy. Another intriguing avenue is to combine real-world microbiome and clinical data for parameter estimate and validation. This would allow for the making of customizable models improved to individual microbiome profiles, hence encouraging precision nutrition and personalized medicine. Furthermore, combination the model with machine learning approaches can improve parameter optimization and analytical performance.

10. Recommendations

1. Promote Fiber-Rich Diets: The Individuals are supposed to eat high amounts of dietary fiber which includes fruits, vegetables, whole grains and legumes. The model results indicate that diets rich in fiber support good gut microorganisms and enhance metabolic well-being through the enhancement of the short-chain fatty acid (SCFA) production. The importance of consuming fiber in the day-to-day diet should be highlighted in the public health programs.

2. A decrease in high-fat and processed food consumption: High fat and processed foods should also be avoided as they promote the development of pathogenic bacteria and metabolic imbalances. To prevent dysbiosis and accompanying metabolic problems, policymakers and healthcare experts should encourage people to eat less saturated fat and ultra-processed foods.

3. The adoption of Mathematical Models in Healthcare: Clinical decision-making processes need to incorporate dynamic systems models into healthcare systems. Such models have the potential to predict patient-specific responses to dietary interventions, with more accurate and personalized approaches to metabolic diseases such as diabetes and obesity.

4. Create Personalized Nutrition Plans: Individual microbiome data need to be used by nutritionists and clinicians to design patient-specific food regimens. Individual gut microbiota profiles may be adapted to nutritional therapies to achieve improved metabolic outcomes and overall health.

5. Promotion of Probiotic and Prebiotic Use: The use of probiotics and prebiotics should be encouraged to help in the development of healthy gut bacteria. Future dietary principles might contain suggestions on functional foods, which will induce microbiome diversity and stability.

6. Ongoing evaluation of gut health: It is recommended that the gut microbiota composition which can be measured through regular monitoring, should be monitored especially in individuals at risk of metabolic diseases. Timely intervention can be done through early detection of microbial imbalance and avoidance of progression of the illness.

7. The use of Real-World Data to create future models (IFM): Future research should concentrate on incorporating really clinical and microbial datasets into the algorithm in order to improve its accuracy and usefulness. This enhances the reliability of research model and enables more precise validation of findings of simulations.

8. Increase in Model Complexity (IMC): According to research overall Researchers should expand the existing model to include more biological aspects such immune system responses, hormonal modulation, and genetic diversity. This will outcomes in a more complete understanding of gut microbiota dynamics and host metabolism.

11. References

- Abruzzese, G. A., & Ceperuelo-Mallafré, V. (2025). Interactions between tissues and kingdoms and interplay with environmental factors: impact on metabolic health and diseases. In (Vol. 16, pp. 1665747): Frontiers Media SA.
- Ayivi-Tosuh, S. M., Dofuor, A. K., Yamoah, J. A. A., Gayi, B. K., Aiduenu, A. F., Akomea, A., Anovunga, S. A., Ekloh, W., & Basing, L. A. (2026). Gut-Microbiome Interactions: Characterization, Therapeutic Implications and Machine Learning. *Sage Open Pathology*, 19, 30502098251415109.
- Balasubramaniam, A., & Srinivasan, S. (2025). Diet-microbiome-ENS connection: impact of the cafeteria diet. *American Journal of Physiology-Gastrointestinal and Liver Physiology*, 328(3), G179-G181.
- Barrera-Suarez, M. A., Zhao, C. Y., Karnatovskaia, L. V., & Sung, J. (2026). Precision nutrition through diet-gut microbiome interactions: Emerging insights driven by artificial intelligence, microbiome health metrics, and mechanistic modeling.

Gut Microbes Reports, 3(1), 2650247.

- Ceperuelo-Mallafre, V., Rodríguez-Peña, M.-M., Badia, J., Villanueva-Carmona, T., Cedó, L., Marsal-Beltran, A., Benaiges, E., Núñez-Roa, C., Salmerón-Pelado, L., & Osuna-Prieto, F. J. (2025). Dietary switch and intermittent fasting ameliorate the disrupted postprandial short-chain fatty acid response in diet-induced obese mice. *Ebiomedicine*, 117.
- Ceylani, T., Teker, H. T., Önlü, H., Ünver, T., Allahverdi, H., Şahin, E., & Atalan, E. (2026). Multi-omics insights into gut microbiota-metabolite interactions under probiotic intervention in a developmental cafeteria diet model. *BMC genomics*.
- Chu, J., No, C.-W., Joung, H., Kim, K. H., Shin, C. H., Lee, J., & Ha, J.-H. (2025). Modulation of Gut Microbial Composition by *Lactobacillus delbrueckii* subsp. *lactis* CKDB001 Supplementation in a High-Fat-Diet-Induced Obese Mice. *Nutrients*, 17(13), 2251.
- Dell'Olio, A., Biasioli, F., Fogliano, V., & Rubert, J. (2025). Decoding microbial volatile signals in host–microbiome crosstalk. *Trends in Endocrinology & Metabolism*.
- Du, W., Zou, Z.-P., Ye, B.-C., & Zhou, Y. (2025). Gut microbiota and associated metabolites: key players in high-fat diet-induced chronic diseases. *Gut Microbes*, 17(1), 2494703.
- Dutta, B., Tripathy, A., Archana, P., & Kamath, S. U. (2025). Unraveling the complexities of diet induced obesity and glucolipid dysfunction in metabolic syndrome. *Diabetology & Metabolic Syndrome*, 17(1), 292.
- Fu, Y., Gou, W., Zhong, H., Tian, Y., Zhao, H., Liang, X., Shuai, M., Zhuo, L.-B., Jiang, Z., & Tang, J. (2025). Diet-gut microbiome interaction and its impact on host blood glucose homeostasis: a series of nutritional n-of-1 trials. *Ebiomedicine*, 111.
- Guo, H., Zhou, X., Li, Z., Zhi, J., Fu, C., Liu, X., Wu, Y., Liu, F., & Feng, N. (2025). Exploring the systemic impacts of urinary tract infection-specific antibiotic treatments on the gut microbiome, metabolome, and intestinal morphology in rats. *PeerJ*, 13, e19486.
- Gupta, Y., Sharma, B., & Jain, C. K. (2025). Advanced membrane simulations in probiotics and gut microbiome interaction research: the current trends and insights. *Current Pharmaceutical Design*.
- Jiawei, Z., & Chandran, S. P. (2025). The Strategic Role of Epigenetic and Microbiome Interactions in Managing Inflammation-Driven Risks in Diet-Related Obesity. *International Journal of Advances in Business and Management Research (IJABMR)*, 2(3), 39-48.
- Kong, H., Han, J., Meng, X., Wang, X., & Zhang, X.-a. (2025). Chlorogenic Acid–Gut Microbiota Interactions: New Insights for Alleviating Chronic Diseases and Health Disorders. *Nutrition Reviews*, nuaf227.
- Ling, X., Li, Z., Su, N., Kong, L., Han, S., & Song, D. (2025). *Sargassum fusiforme* and its fucoidan alleviates high-fat diet induced obesity associated with the improvement of the gut microbiota profile. *Journal of Functional Foods*, 125, 106686.
- Liow, Y. J., Sarkar, A., & Carmody, R. N. (2025). Industrialized diets modulate host eating behavior via the microbiome–gut–brain axis. *Trends in Endocrinology & Metabolism*.
- Ma, M., Zheng, L., Yao, X., Ma, A., Chen, Z., Li, S., & Jia, Y. (2025). Mushroom polysaccharides regulate diet-induced obesity by targeting lipid metabolism, gut microbiota and mitochondria. *Food Science and Human Wellness*.
- Najm, A. A., & Ali, B. K. (2024). Modeling Biological Uncertainty Using the Double Fuzzy Poisson Distribution. *Letters in biomathematics*, 11(1), 51-60.
- Neag, M. A., Mitre, A. O., Pomana, I. G., Velescu, M. A., Militaru, C., Nagy, G., & Melincovici, C. S. (2025). Host–Microbiome Interaction in the Intensive Care Unit. *Diseases*, 13(8), 250.
- Ramasinghe, C., Bordiga, M., & Xu, B. (2025). A comprehensive review of the triangular relationship among diet, gut microbiota, and aging. *International Journal of Molecular Sciences*, 26(18), 8785.
- Ramírez-Maldonado, L. M., Guerrero-Castro, J., Rodríguez-Mejía, J. L., Cárdenas-Conejo, Y., Bonales-Alatorre, E. O., Valencia-Cruz, G., Anguiano-García, P. T., Vega-Juárez, I. I., Dagnino-Acosta, A., & Ruvalcaba-Galindo, J. (2025). Obesogenic cafeteria diet induces dynamic changes in gut microbiota, reduces myenteric neuron excitability, and impairs gut contraction in mice. *American Journal of Physiology-Gastrointestinal and Liver Physiology*, 328(1), G32-

G48.

- Shen, F., Deng, Q., Song, Y., He, G., Chu, X., Zhao, M., Du, J., Feng, F., Zhang, X., & Zhong, H. (2026). Amelioration of diet-induced hyperglycemia by wheat peptides in a multi-target manner: integrated modulation of inflammation, lipid metabolism, gut microbiota, and DPP-IV inhibition. *Food & Function*, 17(1), 288-303.
- Shen, T., Wu, Q., Tan, Y., Ju, X., & Han, G. (2025). Diet-induced gut microbiota shifts in grasshoppers: ecological implications for management and adaptation under varying grazing intensities. *Pest Management Science*, 81(10), 6128-6138.
- Wang, Z., Chen, G., Sun, X., Xiao, J., Kong, L., Jiang, S., Xu, T., Wang, M., & Zhao, H. (2025). Multi-omics integration reveals the impact of mediterranean diet on hepatic metabolism and gut microbiota in mice with metabolic dysfunction-associated steatotic liver disease. *Frontiers in nutrition*, 12, 1644014.
- Yang, Z., Gao, X., Wu, Y., Xie, H., Wang, H., Lu, W., Tian, F., Zhao, J., Zhang, H., & Chen, W. (2025). Nonlinear machine learning-based gut microbiota modelling for health prediction and dietary recommendation. *Food Bioscience*, 107962.
- Zhang, Y., Wei, X., Jiang, S., Gao, W., Wang, K., Wang, H., Wang, H., Si, N., Zhou, Y., & Luo, K. (2025). Jianwei Xiaoshi oral liquid attenuates high-calorie diet-induced dyspepsia in immature rats via regulating the pancreatic secretion pathway and maintaining the homeostasis of intestinal microbiota. *Chinese Medicine*, 20(1), 6.
- Zhao, C., Zhan, M., Du, H., Zhu, K., Chen, S., Song, M., Cao, Y., & Xiao, H. (2025). Impact of Citrus Pectin on Gut Microbiota Metabolism Dysbiosis Induced by Transient Alternating High-Fat Diet. *Journal of agricultural and food chemistry*, 73(33), 20888-20899.
- Zhao, L. (2025). Guild-Level Response of the Gut Microbiome to Nutritional Signals: Advancing Precision Nutrition for Metabolic Health. *Annual Review of Nutrition*, 45.
- Zhou, Y., Wang, M., Wang, Z., Qiu, J., Wang, Y., Li, J., Dong, F., Huang, X., Zhao, J., & Xu, T. (2025). Polysaccharides from hawthorn fruit alleviate high-fat diet-induced NAFLD in mice by improving gut microbiota dysbiosis and hepatic metabolic disorder. *Phytomedicine*, 139, 156458.
- Zhra, M., Elahi, M. A., Tariq, A., Abu-Zaid, A., & Yaqinuddin, A. (2025). Sirtuins and gut microbiota: dynamics in health and a journey from metabolic dysfunction to hepatocellular carcinoma. *Cells*, 14(6), 466.