MATHEMATICAL MODELS TO EVALUATE THE PROBIOTIC EFFECT ON THE RUMINANT DIGESTIVE SYSTEM

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SUMMARY

To investigate probiotic, rumen, and host digestive physiology interactions, mathematical models are effective. These models measure how probiotics alter ruminant pH, microbial proliferation, and nutrient absorption. Mathematical models for ruminant digestive system probiotic effects are reviewed in this work. The effects of probiotics on ruminants' digestive tracts are studied using mathematical models that account for biological processes, microbial interactions, and nutritional metabolism. These models can separate rumen, intestinal, and probiotic colonization processes. These models predict probiotic strain growth, food metabolism, host-microbe interactions, parameterization, and validation. Rumen bacteria, protozoa, fungus, and archaea break down complex plant components for digestion. Explaining and predicting probiotic effects requires mathematical models of microbial growth and fermentation. Microbial growth and fermentation optimize digestive efficiency and health, and dynamic models address time-dependent microbial population and substrate concentration variations. Estimating probiotic strain counts and rumen microbe interactions requires models. VFA and methane production are used to evaluate probiotic therapy. To maximize effects, probiotic therapy time and dose are optimized. The Monod Kinetics model investigates cellulolytic bacteria that degrade rumen fiber. This model depicts how probiotics break down hemicellulose and cellulose to help ruminants utilize vegetable nutrients. Colonic Lactobacillus species, especially lactate-producing ones, are studied under the Gompertz model. Dynamic modeling of rumen microbial interactions helps explain and predict probiotic effects on fermentation. The model shows how feeding A. bovis probiotics impacts rumen microbial populations and fermentation products. The simulation reveals increased cellulolytic bacterial populations, substrate use, VFA production, and pH stability. Enhanced fiber degradation, cellulose utilization, total VFA generation, and pH stability. Finally, simulations show how probiotics alter rumen fermentation, boosting nutrition and greenhouse gas mitigation. Complete probiotic effects on the ruminant digestive system can be assessed using multi-scale models. This method models complex rumen interactions at the molecular, cellular, and ecological levels. Multiscale research from microbial kinetics to animal performance can help researchers understand how probiotics effect rumen fermentation, nutrient absorption, and animal health. Molecular, cellular, ecological, and animal scales are modelled. The integration plan includes model coupling, data flow, feedback loops, and animal performance data to improve ecological and cellular models. Experimental data calibrates model parameters at all scales, whereas simulations show dynamic changes over time.

Keywords: *mathematical models, probiotic, digestive system, ruminant.*

INTRODUCTION

The ruminant digestive system is a complex and dynamic ecosystem where a symbiotic relationship between the host animal and its microbiota plays a crucial role in nutrient digestion and absorption. In recent years, the supplementation of probiotics has garnered significant attention as a promising strategy to enhance digestive efficiency, improve animal health and increase productivity in ruminant livestock. Probiotics, defined as live microorganisms that confer health benefits to the host when administered in adequate amounts, have been shown to modulate the microbial balance in the rumen, enhance fermentation processes and improve nutrient utilization.

Understanding the intricate interactions between probiotics, rumen microbes and the host's digestive physiology requires sophisticated analytical tools. Mathematical modeling emerges as a powerful approach to unravel these complex interactions, providing insights into the mechanisms by which probiotics exert their effects and predicting the outcomes of probiotic interventions under various

conditions. These models offer a quantitative framework to evaluate the impact of probiotics on key aspects of ruminant digestion, such as pH dynamics, microbial growth and nutrient absorption.

This review aims to provide a comprehensive overview of the current state of mathematical models used to evaluate the effects of probiotics on the ruminant digestive system. We will explore different types of models, including those focusing on rumen pH dynamics, microbial population dynamics and nutrient absorption in the intestines. By examining these models, we seek to highlight their applications, strengths, limitations and identify areas for future research. Through this synthesis, we aim to advance the understanding of probiotic functionality in ruminants and support the development of more effective probiotic formulations and feeding strategies.

The integration of mathematical modeling with experimental data holds the potential to transform the field of ruminant nutrition. By enabling precise predictions and mechanistic insights, these models can guide the optimization of probiotic use, ultimately contributing to more sustainable and efficient livestock production systems.

MATHEMATICAL MODELING APPROACHES

Probiotics' effects on ruminant digestion are often studied and evaluated using mathematical models and equations. The primary purpose of these models is to investigate and forecast the relationships between probiotics and digestive processes in ruminants. Consider the following significant studies and methods. Baldwin *et al.* (1987) provide a mathematical model that explains rumen fermentation. We constructed a dynamic model of ruminant digestion that incorporates the occurrence of microbial fermentation in the rumen. The model uses differential equations to accurately portray the growth of microbial populations and the production of fermentation byproducts such as volatile fatty acids.

In 1992, Dijkstra *et al.* devised a mechanistic model that explains the fermentation process in the rumen. This model accounts for the dynamics of microbial multiplication as well as substrate breakdown. Using this model, users may have a better understanding of how various feed components impact rumen fermentation and nutrient absorption. Weimer's presentation from 1998 the topic of discussion is "Probiotics and Microbial Population Dynamics." Proposed a paradigm for evaluating the effect of probiotics on the variability of microbial populations in the rumen. The model includes equations that simulate the antagonistic relationship between probiotic bacteria and indigenous rumen microbes, as well as their impact on fermentation patterns. Mills *et al.* (2001) created a model to study the relationship between lactic acid bacteria, a probiotic, and the microbial community in the rumen. This model uses ordinary differential equations (ODEs) to depict the proliferation rates of distinct microbial species and their associated metabolic activities. Sauvant and Giger Reverdin's (2007) research found a strong link between nutritional absorption and probiotic efficacy. Probiotics were thoroughly tested while developing a complete model for predicting ruminant digestion and nutritional absorption. The model incorporates equations for rumen fermentation, digestive transit speeds and nutrient absorption efficiency.

The publication "Ellis *et al.* (2014): An Overview" gives a full review of the study conducted by Ellis and his colleagues in 2014. A study created an analytical technique that emphasizes nutritional effectiveness in the presence of probiotics. The model uses mathematical models to explain the impact of probiotics on feed intake, digestive kinetics and nutrient absorption. Calsamiglia *et al.* (2008) studied the effects of probiotics in controlled laboratory conditions (in vitro) and on live animal subjects. Researchers discovered that probiotics had a favorable influence on the immune system. To bridge the gap between controlled trials and real-world applications, the researchers used mathematical equations to build a link between laboratory results and observations in living organisms. Kumar *et al.* conducted study in 2013. The information provided lacks proper references. An evaluation approach was devised to determine the efficiency of many probiotic strains in the rumen for enhancing fiber digestion. The model comprises of equations that simulate the enzymatic breakdown of fibrous feed components and the subsequent increase in nutrient availability.

Here are some examples of meta-analyses and statistical models: Desnoyers *et al.* (2009) concluded a research study. A thorough review and statistical analysis were conducted on research looking at the impact of probiotics on digestive parameters in ruminant animals. Probiotics' total influence was

quantified using statistical approaches. Regression equations are utilized in research to identify key parameters that influence probiotic effectiveness.

In 2015, Malmuthuge *et al.* conducted research. The material supplied is not backed by a trustworthy source, raising concerns about its veracity. Probabilistic models were used to evaluate the effect of probiotics on the diversity of bacteria and fermentation efficiency in the rumen. To make complicated data sets easier to understand, the models include principal component analysis (PCA) equations and other multivariate analytical approaches. These studies are just a fraction of the extensive research conducted on the mathematical modeling of the effects of probiotics on bovine digestion. The models produced from these research have assisted academics and professionals in better understanding the mechanisms behind probiotic activity and improving its application in animal feeding.

MODELS OF RUMEN DYNAMICS

1. Compartmental modeling approach

a. Rumen compartment:

- Variables: Concentrations of substrates (carbohydrates, proteins, lipids), microbial populations (probiotics vs. non-probiotics), pH, volatile fatty acids (VFAs), and gases (CO2 and CH4).
- Processes: Microbial growth (based on substrate availability), substrate degradation, VFA production, gas production and pH dynamics.

b. Intestinal compartment:

- Variables: Nutrient absorption rates, microbial populations entering the intestines, pH and microbial diversity.
- Processes: Nutrient absorption kinetics, microbial transit dynamics, immune response modulation, metabolite absorption.

2. Dynamics of probiotic colonization

- Use differential equations to predict probiotic strains' growth dynamics compared to native microbiota.
- Examine growth rates, competition for substrates, and inhibitory effects (e.g., antimicrobial peptide synthesis).:

3. Nutrient utilization and metabolism

- Stoichiometric models: Relate nutrient intake (carbohydrates, proteins and lipids) to microbial growth and VFA production.
- Enzyme kinetics: Model enzymatic reactions involved in nutrient breakdown and VFA synthesis.

4. Host-microbe interactions

- Immune response Modeling: Include equations describing the host immune response to microbial colonization and probiotic effects.
- Metabolite production: Predict the production of beneficial metabolites (e.g., short-chain fatty acids) influenced by probiotic activity.

5. Parameterization and validation

- Experimental data integration: Use experimental data to parameterize the model (e.g., microbial growth rates and nutrient utilization efficiencies).
- Validation: Compare model predictions with experimental outcomes to refine parameters and improve accuracy.

EXAMPLE COMPONENTS OF EQUATIONS

a. Rumen pH dynamics

$$\frac{d[Probiotic]}{dt} = \mu . [Nutrient] . (1 - \frac{[Probiotic]}{K})$$

Given the differential equation:

$$\frac{dpH}{dt} = \frac{A_0 \, . \, e^{-bt}}{V} - K \, . (pH - pH_{opt})$$

Let's assume:

A0 = 0.5 (units of acid per hour).
b = 0.1 per hour.
V = 10 liters.
K = 0.05 per hour.
pHopt = 6.8
Initial pH pH (0) = 6.5
We can numerically integrate this using Euler's method with a time step Δt = 1 hour for simplicity.

Step-by-step calculation:

1.At t = 0:

$$\frac{dpH}{dt} = \frac{0.5 \, . \, e^{-0.1 \cdot 0}}{10} - 0.05 \cdot (6.5 - 6.8)$$

$$\frac{dpH}{dt} = 0.05 + 0.05 \cdot 0.3$$

$$\frac{dpH}{dt} = 0.05 + 0.015 = 0.065$$

$$pH(1) = 6.5 + 0.065 \, .1 = 6.565$$

2.At t = 1:

$$\frac{dpH}{dt} = \frac{0.5 \, . \, e^{-0.1 \cdot 1}}{10} - 0.05 \cdot (6.565 - 6.8)$$

$$\frac{dpH}{dt} = 0.0452 - 0.01175$$

$$\frac{dpH}{dt} = 0.03345$$

$$pH(2) = 6.565 + 0.03345 \cdot 1 = 6.59845$$

And so on.

b. Microbial growth

Models of microbial growth and fermentation:

The growth of microorganisms and fermentation in the rumen is crucial for the digestive efficiency and general health of ruminants. The rumen contains a diverse range of microorganisms, including as bacteria, protozoa, fungus and archaea. These organisms cooperate to decompose complex plant components into simpler molecules that the host animal may consume and use. In order to enhance understanding of these processes and generate precise forecasts about the impacts of dietary treatments such as probiotics, it is essential to use mathematical models of microbial growth and fermentation as indispensable instruments.

Dynamic models:

These models consider time-dependent changes in microbial populations and substrate concentrations.

$$\frac{dX_i}{dt} = \mu_i(S) . X_i - K_{di} \, . X$$ **for each microbial species i**

$$\frac{dS_j}{dt} = \sum_i \frac{q_{ij}(S_j)}{Y_{ij}} \, . \, X_i$$

Where:

Xi is the biomass concentration of species i.
SJ is the concentration of substrate j.
qij is the uptake rate of substrate j by species i.
Yij is the yield coefficient for species i on substrate j.

Applications of models:

The number of probiotic strains that will proliferate in the rumen and the manner in which they will interact with the microorganisms that are already present in the rumen may be predicted with the use of models. In addition, models are helpful in determining the effectiveness of probiotic therapies, which is another area of use. By analyzing the processes that are involved in the production of volatile fatty acids (VFAs) and gasses such as methane, you can determine how probiotics influence the fermentation process. The subsequent phase in the process of establishing more effective feeding protocols is to make a prediction about the effects that various meal compositions have on the proliferation of microorganisms and the effectiveness of fermentation. In order to get the most of the potential advantages of probiotic treatment, it is necessary to determine the optimal time and dose.

Environmental impact:

Assess the influence of probiotics on the production of methane, a potent greenhouse gas and develop strategies to mitigate the release of methane into the atmosphere. Examples of the technology's application in real-life scenarios:

1. The Significance of monod kinetics in fiber degradation:

According to research, probiotics such as Fibrobacter succinogenes improve fiber breakdown in the rumen. This illustrates how probiotics improve the breakdown of hemicellulose and cellulose. The breakdown of fiber in the rumen is critical for ruminants to consume vegetable resources efficiently. The variety of microorganisms, such as bacteria, protozoa and fungus, helps in the process. Collectively, these bacteria degrade hemicellulose and cellulose into simpler carbohydrates. Fermentation may generate VFA, which are the primary source of energy for animals digesting these sugars. Using Monod kinetics as a framework to simulate the development of microbes that degrade fibers in the rumen, we may study how probiotics can improve this process.

1. Monod kinetics model:

The Monod kinetics model describes the relationship between microbial growth rate and substrate concentration. It is particularly useful for modeling the growth of fiber-degrading microbes, such as cellulolytic bacteria, in the rumen.

Equation:

$$\frac{dX}{dt} = \mu_{max} \cdot \frac{S}{K_S + S} \cdot X - K_d \cdot X$$

Where:

X is the Microbial biomass concentration (mg/L).
μmax is the maximum specific growth rate of the microbes (per hour).
S is the substrate concentration (mg/L), such as cellulose or hemicellulose.
Ks is the half-saturation constant (mg/L), the substrate concentration at which the growth rate is half of μmax.
Kd is the decay rate constant (per hour).

2. The Gompertz model is used to study the growth of Lactobacillus species in the colon, particularly those that produce lactate:

The Gompertz model is often used to illustrate the dynamics of microbial development, particularly in populations with a lag phase, exponential growth phase and stationary phase. This model is especially useful for studying the growth of Lactobacillus species, which are common probiotics used to aid ruminant digestion. Gaining knowledge into the pace of Lactobacillus growth in the rumen is critical for refining probiotic formulations and feeding strategies to improve animal health and productivity.

Equation:

$$X(t) = X_{max} \cdot exp\ \left(-exp\left(\frac{\mu_{max} \cdot e}{X_{max}} \cdot (\lambda - t) + 1\right)\right)$$

Where:

X(t) is the microbial biomass concentration at time t.
Xmax is the maximum biomass concentration.
μmax is the maximum specific growth rate.
λ is the lag time before exponential growth begins.
e is the base of the natural logarithm (approximately 2.718).
An example of this is the ability to forecast the lag phase and exponential growth of Lactobacillus across different dietary situations.

The application of dynamic models in mixed microbiological communities:

Dynamic modeling of rumen microbial interactions is an effective method to describe and predict the effects of probiotics on rumen fermentation. We used this model to simulate the effects of feeding A. bovis probiotics on rumen microbial ecosystems, and demonstrate how changes in probiotic survival can affect fermentation end-products (VFA+ milk fatty acids) as well as overall ecosystem function. In this manuscript, we introduce a dynamic model to describe interactions between probiotics (e.g. Saccharomyces cerevisiae) and native rumen microbes; therefore, environmental dynamics are used to account for growth rates of all microbial populations in the reactor, substrate utilization by both autochthonous and allochtonous bacteria species (probiotics), as well volatile fatty acid production.

Model framework:

1. Microbial populations:

The model includes several microbial populations:
Cellulolytic bacteria (e.g., Fibrobacter succinogenes, Ruminococcus flavefaciens).
Amylolytic bacteria (e.g., Streptococcus bovis).
Proteolytic bacteria (e.g., Prevotella ruminicola).
Lactate-producing bacteria (e.g., Lactobacillus spp.).
Lactate-utilizing bacteria (e.g., Megasphaera elsdenii).
Methanogens (e.g., Methanobrevibacter spp.).
Probiotics (e.g., Saccharomyces cerevisiae).

2. Substrates and products:

Key substrates and products considered in the model include:
Carbohydrates (cellulose, hemicellulose and starch).
Proteins.
VFAs (acetate, propionate and butyrate).
Lactic acid.
Methane.
Ammonia.

3. Equations and parameters:

The dynamic model is governed by a set of differential equations that describe the changes in microbial populations and substrate concentrations over time. Key parameters include specific growth rates (μ), substrate affinity constants (Ks) and yield coefficients.

Substrate utilization and product formation:

$$\frac{dS}{dt} = -\sum_i \left(\frac{\mu_i \cdot Y_{s,i}}{K_{s,i} + S} \cdot X_i\right)$$

Where Ys,I is the yield coefficient for substrate utilization by population I .

VFA production:

$$\frac{dVFA_j}{dt} = \sum_i \left(\frac{\mu_i \cdot Y_{vfa,s,i}}{K_{s,i} + S} \cdot X_i\right)$$

Where VFAJ represents the concentration of VFA j (acetate, propionate and butyrate) and Yvfa.j,I is the yield coefficient for VFA j Production by population I.

Simulation setup:

Initial concentrations of microbial populations.
Initial concentrations of substrates (cellulose, starch and protein).
Initial pH and buffering capacity.
Simulation scenarios.
Control: No probiotic supplementation.
Probiotic: Supplementation with *Saccharomyces cerevisiae* at a specified dosage.
Time frame.
Simulate over a period corresponding to a typical rumen fermentation cycle (e.g., 24- 48 hours).
Results and analysis

1. Microbial population dynamics

- The simulation tracks changes in the concentrations of different microbial populations over time. The introduction of S. cerevisiae is expected to:
- Increase cellulolytic bacterial populations by creating a more favorable anaerobic environment.
- Decrease lactate-producing bacteria by competing for substrates.

2. Substrate utilization and VFA production

- The model predicts changes in substrate concentrations and VFA production profiles. Key observations include:
- Enhanced fiber degradation and increased cellulose utilization.
- Higher total VFA production, with a shift towards more acetate and butyrate, and stable or slightly increased propionate levels.

3. pH stability

- The simulation evaluates the effect of probiotic supplementation on rumen pH stability. S. cerevisiae is expected to:
- Reduce pH fluctuations by decreasing lactate accumulation.
- Enhance buffering capacity through increased ammonia production from urea degradation.
- Example Simulation Output

Control scenario:

- Initial cellulolytic bacteria: 0.5 mg/L.
- Initial lactate-producing bacteria: 0.2 mg/L.
- Initial pH: 6.2.
- VFA production (24 hours): Acetate 70 mM, Propionate 30 mM, Butyrate 15 mM.

Probiotic scenario:

- Initial cellulolytic bacteria: 0.5 mg/L.
- Initial lactate-producing bacteria: 0.2 mg/L.
- Initial pH: 6.2.
- VFA production (24 hours): Acetate 80 mM, Propionate 32 mM, Butyrate 18 mM
- Increased buffering capacity and more stable pH with fewer drops below 6.0

It is possible to gain valuable insights into the potential benefits of supplementing with probiotics by modeling the dynamic interactions that occur between probiotics and the native microorganisms that live in the rumen. The findings of the simulation indicate that Saccharomyces cerevisiae possesses the capacity to enhance the process of fiber breakdown, to increase the production of volatile fatty acids (VFAs), and to keep the pH level in the rumen steady. The digestive process is improved as a result of these effects, which also allow for more efficient utilization of nutrients and contribute to the overall health and productivity of ruminant animals. Through further research and development of the model, it is possible to improve the optimization of probiotic formulations and feeding regimens for a wide range of ruminant species and dietary circumstances.

Integrating multi-scale models provides a comprehensive framework for evaluating the effects of probiotics, such as Saccharomyces cerevisiae, on the ruminant digestive system. This approach combines molecular, cellular, and ecosystem-level models to capture the complex interactions within the rumen

environment. By incorporating multiple scales, from microbial kinetics to animal performance, we can gain a deeper understanding of how probiotics influence rumen fermentation, nutrient absorption, and overall animal health.

Multi-scale modeling framework

1. Molecular scale:

Enzyme activity and gene expression:

At the molecular level, the focus is on the activity of microbial enzymes and the expression of genes involved in fermentation processes.

Key components:

Enzyme kinetics: Reaction rates of enzymes involved in carbohydrate and protein breakdown.

Gene expression: Regulation of genes encoding for enzymes, transporters, and other proteins.

Equations:

$$v = V_{max} \cdot \frac{[S]}{K_m + [S]}$$

Where:

v = Reaction rate.
Vmax = Maximum rate.
[S] = Substrate concentration.
Km = Michaelis constant.

2. Cellular scale: Microbial growth and metabolism.

At the cellular level, the model describes the growth and metabolic activities of different microbial populations.

Key components:

Microbial growth: Monod kinetics for population dynamics.

Substrate uptake and product formation: Utilization rates and yield coefficients for VFAs, methane, and other metabolites.

Equations:

$$\frac{dX_i}{dt} = \mu_i \cdot \frac{S}{K_{S,i} + S} \cdot X_i - K_{d,i} \cdot X_i$$

$$\frac{dS}{dt} = -\sum_i \left(\frac{\mu_i \cdot Y_{s,i}}{K_{s,i} + S} \cdot X_i \right)$$

3. Ecosystem scale:

Rumen fermentation dynamics:

At the ecosystem level, the model integrates the interactions between different microbial populations, substrates, and products within the rumen.

Key components:

Microbial interactions: Competitive, synergistic, and inhibitory effects.

Fermentation patterns: VFA profiles, pH fluctuations, and gas production (e.g., methane).

Equations:

$$\frac{dVFA_j}{dt} = \sum_i \left(\frac{\mu_i \cdot Y_{vfa,s,i}}{K_{s,i} + S} \cdot X_i \right)$$

$$\frac{dpH}{dt} = f(VFA, NH_3, buffering\ capacity)$$

4. Animal scale:

Nutrient absorption and performance.

At the animal level, the model links rumen fermentation outcomes to nutrient absorption and animal performance metrics.

Key components:

Nutrient absorption: Efficiency of VFA absorption, protein digestion, and nutrient transport to the bloodstream.

Animal performance: Growth rates, milk production, and health indicators.

Equations:

Nutrient Absorption Rate= K_abs-[Nutrient]

Animal Performance= f(Absorbed Nutrients,Energy Balance)

Integration strategy

Coupling Models:

Bottom-up approach:

Start from the molecular scale and integrate upwards, ensuring that enzyme activity and gene expression data inform cellular and ecosystem dynamics.

Top-down Approach: Use animal performance data to refine and validate ecosystem and cellular models.

Data flow and feedback loops:

Data flow:

Outputs from one scale serve as inputs for the next. For instance, VFA production from the ecosystem model informs nutrient absorption in the animal model. Feedback Loops: Incorporate feedback mechanisms where changes at one scale influence processes at another. For example, changes in pH at the ecosystem level can affect microbial gene expression at the molecular level.

Simulation and calibration:

Simulation:

- Run simulations to capture dynamic changes over time across all scales.
- Calibration: Use experimental data to calibrate model parameters at each scale, ensuring accurate and realistic predictions.
- Integrating multi-scale models provides a holistic understanding of the impact of probiotics on the ruminant digestive system. This approach allows for the simulation of complex interactions, from molecular processes to animal performance, offering insights into optimizing probiotic use for enhanced rumen fermentation and animal health. By combining data from different scales, researchers and producers can develop more effective feeding strategies and improve the overall productivity and well-being of ruminant animals.

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نماذج رياضية لتقييم تأثير البروبيوتيك على الجهاز الهضمى للمجترات

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تتم مراجعة النماذج الرياضية لتأثيرات البروبيوتيك على الجهاز الهضمي للحيوانات المجترة في هذا العمل. وللتحقق في تفاعلات البروبيوتيك في الكرش، فإن النماذج الرياضية فعالة. لتقيس هذه النماذج وكيفية تغيير البروبيوتيك لدرجة الحموضة في الكرش والتكاثر الميكروبي، وامتصاص المغذيات

تتم دراسة آثار البروبيوتيك على الجهاز الهضمي للحيوانات المجترة باستخدام نماذج رياضية تفسر العمليات البيولوجية والتفاعلات الميكروبية والتمثيل الغذائي. ويمكن لهذه النماذج فصل عمليات التكاثر في الكرش والأمعاء من البروبيوتيك. تتنبأ هذه النماذج بنمو سلالات البروبيوتيك، واستقلاب الطعام، والتفاعلات بين المضيف والميكروب، وتحديد المؤثرات، والتحقق من الصحة. تقوم بكتيريا الكرش والبروتوزوا والفطريات بتفكيك المكونات النباتية المعقدة للهضم. يتطلب شرح تأثيرات البروبيوتيك والتنبؤ بها نماذج رياضية للنمو الميكروبي والتخمير. يعمل النمو الميكروبي والتخمير على تحسين كفاءة الجهاز الهضمي وصحته، وتعالج النماذج الديناميكية اختلافات التركيز الميكروبية وتركيز الركيزة التي تعتمد على الوقت.

يتطلب تقدير عدد سلالات البروبيوتيك وتفاعلات ميكروبات الكرش نماذج. يتم استخدام إنتاج VFA والميثان لتقييم العلاج بالبروبيوتيك. لتحقيق أقصى قدر من التأثيرات، يتم تحسين وقت وجرعة العلاج بالبروبيوتيك .

يبحث نموذج Monod Kinetics في البكتيريا السليلية التي تحلل ألياف الكرش. يصور هذا النموذج كيف تكسر البروبيوتيك السليلوز والسليولاز لمساعدة الحيوانات المجترة على الاستفادة من المغذيات النباتية. تتم دراسة أنواع العصيات اللبنية القولونية، وخاصة الأنواع المنتجة للاكتات، تحت نموذج غومبرتز. تساعد النمذجة الديناميكية للتفاعلات الميكروبية في الكرش على تفسير وتوقع تأثيرات البروبيوتيك على التخمير. يوضح النموذج كيف تؤثر تغذية البروبيوتيك على تجمعات الكرش الميكروبية ومنتجات التخمير .

تكشف المحاكاة عن زيادة التجمعات البكتيرية المحللة للسليل، واستخدام الركيزة، وإنتاجVFA ، واستقرار الأس الهيدروجيني. تحسين تدهور الألياف، واستخدام السليلوز، وتوليد VFA الكلي، واستقرار الأس الهيدروجيني.

وأخيرًا، تُظهر عمليات المحاكاة كيف يغير البروبيوتيك تخمير الكرش، مما يعزز التغذية والتخفيف من غازات الاحتباس الحراري. يمكن تقييم تأثيرات البروبيوتيك الكاملة على الجهاز الهضمي للحيوانات المجترة باستخدام نماذج متعددة المقاييس. تقوم هذه الطريقة بنمذجة تفاعلات الكرش المعقدة على المستويات الجزيئية والخلوية والبيئية. يمكن أن تساعد الأبحاث متعددة المقاييس من الحركية الميكروبية إلى الأداء الحيواني الباحثين على فهم كيفية تأثير البروبيوتيك على تخمير الكرش وامتصاص المغذيات وصحة الحيوان. يتم نمذجة المقاييس الجزيئية والخلوية والبيئية والحيوانية. تتضمن خطة التكامل اقتران النموذج وتدفق البيانات وحلقات التغذية الراجعة وبيانات الأداء الحيواني لتحسين النماذج البيئية والخلوية. تقوم البيانات التجريبية بمعايرة معلمات النموذج على جميع المقاييس، في حين تُظهر المحاكاة تغييرات ديناميكية بمرور الوقت.