International Journal of Research Studies on Environment, Earth, and Allied Sciences (IJRSEAS)
| Volume-2 Issue-4 |August-2025 | ISSN: 3066-0637 | Website: https://eesrd.us

The Role of Microbium in Animal Health

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Manuscript ID:
IJRSEAS-2025-020401

OPEN ACCESS

Quick Response Code:

Website: https://eesrd.us

DOI: 10.5281/zenodo.17090056

DOI Link:
https://doi.org/10.5281/zenodo.17090056

Volume: 2

Issue: 4

Pp. 1-3

Month: August

Year: 2025

E-ISSN: 3066-0637

Submitted: 06 July 2025

Revised: 10 July 2025

Accepted: 10 Aug 2025

Published: 31 Aug 2025

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How to cite this article:
Khan, R. S. A. (2025). The Role of Microbium in Animal Health. International Journal of Research Studies on Environment, Earth, and Allied Sciences, 2(4), 1–3.
https://doi.org/10.5281/zenodo.17090056

Abstract

The microbiome are the diverse community of microorganism present in the body of animals. They are made of many different micro organisms. They play an important role in the physiological functions and the overall health of the host. These microorganism may present in the digestive tract, respiratory tract, skin and other body tissues. This paper focuses on the complex relationship within the microbiome of the gut, how it is formed, mechanism of action and interaction with the host. The structure and the diversity of the gut microbes in the animals depends upon several factors such as, host's environment, temperature, pH, oxygen availability, diet of the host, genetic composition o the host, living conditions and the management of the animals. The imbalance in these gut microbial can cause problems in the digestive and the immune system of the animals resulting in the decreased productivity and decline in overall health of the animal. For better communication between the cells and the proper transportation between the various barriers such as intestinal wall and the blood-brain barrier, extracellular vesicles like exosomes are required. If these connections are disrupted, it may lead to the various disorders in the animals. Certain interventions like prebiotics, probiotics, microbial transplant and phage therapy helps to improve the animal health. phage therapy to modify the gut microbiota shows promising results for improving the animal health and food safety in poultry farming. The interplay between host environment, microorganism in the git and extracellular vesicles helps understanding how the host and the microbs interact and affects the health of animals and influence their productivity. More research in this field is needed to create better treatment and better ways to manage the gut health and overall well being of the animals.

Keywords: *Animal gut microbiome, extracellular vesicles, immune system , probiotics; prebiotics*

Introduction

The microorganisms present in the gut plays an important role in marinating the overall health in the wide range of animals ranging from insects to humans. There are many microorganisms which are beneficial and helps to improve the quality of life of the host. Drosophila is one of the best model for studying how hosts and their microbes interact because it's easy to change the microbes in the gut. The gut bacteria in flies are simple and can be grown and studied genetically, thus making it easier to understand their effect on the host's body processes. The growth process of Drosophila is studied during its early development. Since Drosophila and mammals have similar tissues and highly conserved physiological systems, findings from Drosophila studies are likely to give important insights into how hosts and gut microbes interact in more complex animals.

Neutralizing toxins and harmful substances, aiding in detoxification, and keeping us healthy are important roles of microorganisms. Using microorganisms in medical treatments is one of the major developments in the 21st century. Many studies have shown how crucial microbes and their communities are for human and animal health.

Respiratory Tract Microbiota:

The respiratory tract includes the nose, pharynx (nasopharynx, oropharynx), larynx, tonsils, hard palate, trachea, bronchi, bronchioles and the lungs. Each part has different collection of microbes. There are six main groups of bacteria that could be responsible for a healthy respiratory system in mammals these are Tenericutes, Proteobacteria, Firmicutes, Bacteroidetes, Fusobacteria, and Actinobacteria. The amount, type and the distribution of the microbes depends upon the part of the part of the tract. The respiratory tract includes nostrils, nasal cavity, pharynx, lartynx, trachea, bronchi and bronchioles. Each part consists of different community of the bacterias that live there. Fusobacteria are most commonly found in tonsils, Firmicutes are present more widespread in mouth area, including the floor and the hard palate. Proteobacteria are found in the nose, nasopharynx and oropharynx. The lower respiratory tract contains lesser microbes, these includes, Streptococcus, Veillonella and Prevoella.

The microbiota of respiratory tract acts in the protective manner. They help in preventing the growth of harmful pathogens, maintaining healthy immune system and maintain the normal physiological functions of the respiratory tract. The nostrils and the external nares are mostly exposed to the external environment. They are lined by keratinized epithelium which are present in the skin and contain sebaceous glands that secrete sebum. This environment favors the growth of lipophillic organisms such as Propionibacterium and the staphylococcus species. The nasopharyn has the stratified squamous epithelium as the lining epithelium. The bacterial communities are more diverse here than the nostrils. It includes, Haemophillus, Dolosigranulum, Streptococcus etc. The oropharynx is lined by non-keratinised stratified squamous epithelium, it have even broader spectrum of microorganisms than in nasopharynx. It includes Streptococcus species, Rothia, Neisseria etc. It also contain anaerobic bacteria like Prevotella, Leptotrichia, Fusobacterium and Veillonella.

Oral Microbiota:

The oral cavity contains the wide range of microorganisms. These microorganisms are distributed over the various part of the oral cavity such as tongue, tooth, gums, saliva and the buccal mucosa. These microbes are present in the hard surfaces of the teeth and also the soft tissues and the oral mucosa, it forms an intricate ecosystem. These microbes help in the digestion process and also help in maintaining the overall health of the body. Mutual communication, control mechanism and the Healthy interaction between the oral and the gut microbes is essential to maintain the health of the organism. On the flip side, imbalances leads to the various diseases like oral candidiasis, periodontal diseases and the tooth decay.

In a research conducted upon dogs, the presence of core microbiomes were identified, these mainly includes Porphyromonas species, which are influenced by the microenvironments in their mouths, promoting certain microbes while discouraging the rest. The canine oral microbiomes were moderately stable yet highly diverse. They showed wide range of microbiomes compared to the gut microbiomes.

Gut Microbiota:

The gut ecosystem is highly diverse and complex. The number of anaerobic bacteria are two to three times more than that of aerobic bacteria. The rumen, often described as th black box because of it's complexity have highly diverse microorganisms. The ruminal microbes acts as the crucial organ for hosting the trillions of microorganisms whose genetic makeup exceeds that of the host. The microbes influences the health of the host and h=the nutrition through specific metabolic function and making the ruminal microbiome closely linked to the host's pattern of digestion and metabolic balance. There are several studies that shows that different microbial groups significantly affects the efficiency if the feed, nitrogen breakdown and the production of methane in the ruminal animals.

Small Intestinal Microbiota:

Although the role of the small intestinal microbiome in processing food is still not entirely clear, it's known that the gut bacteria help the host adjust to changes in dietary fat by regulating the digestion process through intestinal epithelial mechanisms. The small intestine, which includes the duodenum, jejunum, and ileum, is primarily responsible for absorbing nutrients from food, particularly proteins and carbohydrates. Within these parts, complex microbial systems are essential for tasks like fermentation, vitamin production, and immune system regulation. Notably, in cattle, the jejunum is dominated by proteobacteria, while the Firmicutes phylum largely controls the other parts of the gastrointestinal tract. The jejunum contains a high number of Acetitomaculum, Lachnospiraceae, and Ruminococcus, whereas Enterobacteriaceae are common in the small intestine. The Firmicutes phylum increases significantly in the small intestine, reaching up to 80% of its presence, while the Bacteroidetes phylum decreases, going from 0.4 to 1.1% in comparison to the rumen. Other phyla, such as Proteobacteria, Actinobacteria, and Tenericutes, are present at lower levels. Important bacteria found in the small intestine include Butyrivibrio, Ruminococcus, Mogibacterium, Mitsuokella, Propionibacterium, Lactobacillus, and Bulleidia.

Large intestinal microbiota:

The large intestine plays an important role in absorbing water, vitamins, electrolytes, and other nutrients. Different sections of the large intestine have varied diversity of the microbes. In the cecum, the Firmicutes phylum dominates, making up about 70 to 81% of all phyla, while Bacteroidetes account for the rest, around 18 to 26%. Other phyla, such as Actinobacteria, Tenericutes, and Spirochetes, are also present. The main genera in the cecum include Prevotella, Coprococcus, Dorea, Ruminococcus, Blautia, Turicibacter, Clostridium, and Oscillospira. Similarly, the Firmicutes phylum is prevalent in the rectum. Common genera found in the rectum include Roseburia, Oscillospira, Clostridium, Bacteroides, Succinivibrio, Ruminococcus, Prevotella, Blautia, Turicibacter, and Coprococcus.

Conclusion:

In summary, this paper highlighted the distinct microbiomesof the oral cavity, respiratory tract, gut and the intestinal tract, emphasizing their individual as well as their combined influence on the health of the host. It also emphasizes the main role of gut microbiota in maintaining the various aspect of health and reproduction in animals. These complex relationships between the hst and their microbeshas significant implication throughout the lifecycle, metabolic and signaling pathways of the host. From the practical standpoint, these findings also focuses on the experimental models based on the microbiota offer promising ways to improve the health and the productivity in agricultural animals and enhances the reproductive outcome in medical application.

Acknowledgment

The author would like to express their sincere gratitude to J. A. T. Arts, Science and Commerce College (For Women), Malegaon, Dist. Nashik, Maharashtra, India for providing the necessary facilities and support to carry out this research.

We also thank Principal Dr. Salma Ab. Sattar J. A.T. Arts, Science and Commerce College (For Women), Malegaon for her valuable guidance and insightful suggestions during the course of this study.

Financial support and sponsorship

Nil.

Conflicts of interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

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