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ROLE OF ENDOSYMBIOTIC COMMUNITY IN WOOD DIGESTION IN SUBTERRANEAN TERMITE

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Abstract

With over 2,300 species worldwide, termites have an incredible diversity that inspires both wonder and worry. Among these, 183 species cause damage to buildings, mostly belonging to the subterranean group that is notorious for building mounds and infesting areas with trees. It's interesting to note that 28 species of the genus Coptotermes, particularly *C. formosanus Shiraki* and *C. haviland Holmgren*, account for 80% of the economic consequences. These underground species can be distinguished from dry wood termites by their restricted range and difficulty in relocating.Isoptera, which consists of termite species classified as upper (Termitidae) and lower (Termitidae) types, has an important evolutionary function. Reticulitermes and Coptotermes, which share a phylogenetic affinity with higher termites, are notable for bridging lower and higher termites. Additionally, these genera have the greatest number of species, which is significant in this evolutionary setting. The ecological significance of subterranean termites is highlighted by the fact that they effectively break down plant matter, particularly wood, which in turn affects carbon dynamics and nutrient cycling. This ecological function is strengthened by their complex symbiotic relationships with microorganisms.Forests, meadows, and urban areas are just a few of the varied terrestrial ecosystems where subterranean termites flourish. They are important contributors to the carbon cycle because of the niches that their intricate subsurface structures provide for the degradation of lignocellulosic substrates. Reticulitermes species, like *R. flavipes* and *R. tibialis*, are common in eastern, central, and western regions of North America.The zoological characteristics of the isoptera include social interactions, caste distinctions, and complex nest construction. Subterranean termites, which have an estimated 2,800 species worldwide, are remarkably adaptable to a variety of environments and niches. This article goes into the fascinating world of termites, highlighting their extraordinary biodiversity and impact on ecosystems while also examining their ecological, evolutionary, and economic relevance.

Keywords
Subterranean Termites, Microbes, Endosymbiotic association, Gut Microbes, Lignocellulose Digestion

1. Introduction

The fact that there are more than 2,300 different species of termites in the world is amazing. Knowing that 183 of these species are infamous for seriously damaging structures, though, is worrying. Most of these notable termites fall into the subterranean category, which includes species that construct mounds and grow in tree (McAuliffe, 2023). Surprisingly, 28 different species of the genus Coptotermes comprise the majority (80%) of the termite species that have an impact on the economy. Subterranean species, in contrast to dry wood termites, have a restricted range and are difficult to move from one area to another. Only *Coptotermes formosanus Shiraki* and *Coptotermes haviland Holmgren*, two of the 147 commercially relevant subterranean termite species, have been introduced to more than five locations worldwide (Bignell *et al.,* 2011).Subterranean termites play an important evolutionary role within the Isoptera (Brune & Dietrich, 2015). Upper termites (Termitidae), which make up over 80% of all species, and lower termites (Termitidae), the final six families, are the two categories into which termites are typically divided. Of the lesser termites, the Rhinotermitidae are the most advanced. Reticulitermes and Coptotermes are especially significant as transitional species between lower and higher termites for three reasons. First, new phylogenetic analyses demonstrate that Reticulitermes and Coptotermes have a particularly close affinity with the higher termites, indicating that the clade encompassing these genera is most likely the sister group of the Termitidae (Vargo & Husseneder, 2009). Second, these two genera are among the lower termite genera with the highest number of species among all subterranean termite genera, with more species than any other genus (Aguiar *et al.,* 2013).In terrestrial ecosystems, subterranean termites (Isoptera: Rhinotermidae) serve a significant ecological function by efficiently destroying plant material, particularly wood, and so promoting nutrient cycling and carbon dynamics. The intricate symbiotic interactions between termites and the different bacteria that reside in their stomach support their ecological value (Ali *et al.,* 2019) Primary and secondary symbionts such protozoa, bacteria, fungus, yeasts, and actinomycetes are involved in this intricate web of interactions (Hongoh *et al.,* 2005). These bacteria work together to facilitate the provision of vital nutrients to the host while achieving the decomposition of cellulose, a significant component of subterranean termite diets.

Table 1: Species status of *Reticulitermes* in North America (Vargo & Husseneder, 2009)

R. flavipes	Throughout eastern and central United States
R. arenincola	Sandy soils near the Great Lakes
R. virginicus	Throughout eastern and central United States
R. hageni	Throughout eastern and central United States
R. malletei	Eastern United States
R. tibialis	Western and Midwestern United States
R. hesperus	Western United States
R. okanaganensis	Pacific Northwest

1.1 Subterranean Termite Habits, Habitats, and Niches

Subterranean termites breed in a variety of terrestrial habitats, often inhabiting forests, grasslands, and urban environments (Jiang *et al.,* 2021). They create elaborate underground galleries and nests, using the niches as decomposers to break down lignocellulosic substrates like decaying wood and plant matter (Peterson *et al.,* 2015). This niche specialization positions subterranean termites as key players in the carbon cycle within ecosystems.

1.2 Zoological Features and Biodiversity

Subterranean termites belong to the order Isoptera and are characterized by social behavior, caste differentiation, and sophisticated nesting activities (Evans & Iqbal, 2015). Subterranean termites, which have an estimated 2,800 species worldwide, are remarkably adaptable to many conditions and niches (Aguiar *et al.,* 2013).

1.3 Endosymbiotic networks and wood digestion

Subterranean termites have a symbiotic interaction with the stomach microorganisms that help them consume cellulose-rich plant debris. The primary symbionts that drive the digestion of cellulose are protozoa and bacteria. Cellulolytic enzymes secreted by protozoa, which are unicellular eukaryotes, are crucial for dissolving cellulose into simpler molecules (Peterson *et al.,* 2015). This enzymatic process works in conjunction with bacterial contributions to break down complex carbs into metabolites that can be consumed (Hongoh *et al.,* 2005).

1.4 Secondary symbionts and their roles

The ability of secondary symbionts like fungi, yeasts, and actinomycetes to digest materials is further improved in subterranean termites. Fungi create enzymes that speed up the breakdown of lignocellulosic materials, improving how well wood is digested (Scharf & Tartar, 2008). Yeast contributes to nutrient cycling and enhances termite resilience to environmental challenges (Carrijo *et al.,* 2009). Actinomycetes have the ability to break down lignocellulose and produce bioactive substances that are useful for biotechnology and the environment (Ohkuma, 2003).

1.5 Dynamic microbial communities and ecological impacts

The termite gut represents a dynamic and specialized microenvironment that supports the growth and activity of diverse microbial communities (Ali *et al.,* 2019). Beyond cellulose digestion, these carefully regulated interactions exist. The benefits of termite-microbe symbiosis include immune system regulation, pathogen defense, nitrogen fixation, and other factors, and they complement continuing study on broader ecological repercussion (Ohkuma, 2003).

1.6 Endosymbiotic interaction advancements

Subterranean termite endosymbiotic relationships have advanced significantly in recent years. To understand the functions and mechanisms of main and secondary symbionts in the termite stomach, researchers have investigated both types of symbionts (Ali *et al.,* 2019). The goal of this review is to compile the most recent information on the termite gut microbiota and present it. To reveal the intricate symbiotic interaction between termites and their partner bacteria, it is intended to synthesize the most recent research conducted since 2017.The study of termite gut microbiota is not only important for scholarly purposes but also has potential applications in a number of different industries.

These microorganisms produce cellulolytic enzymes that have use in the production of biofuels and biorefining (Ohkuma, 2003). The termite gut microbiome has immunomodulatory properties, which opens the door to creative pest control and crop protection methods (Evans & Iqbal, 2015). This review examines recent research with the goal of identifying knowledge gaps and potential directions for future study that promises important new understandings and technical advancements.

2. Literature review

This review conducted a comprehensive search of academic databases including PubMed, Web of Science, and Google Scholar for research papers published from 2015 to the present that concentrate on subterranean termite biology, endosymbiotic relationships, and cellulolysis. Subterranean termites, intestinal symbiosis, cellulose digestion, and "microbial community" were some of the search terms used. A comprehensive strategy was used, including abstract screening and full-text evaluation, to ensure the relevance and dependability of each study included (Brune, 2014)Research was done on the function of main symbionts in termite digestion, including bacteria and protozoa. Protozoa are essential for dissolving intricate cellulose molecules into simpler compounds, and bacterial populations collaborate with protozoa to speed up cellulose digestion. The study also demonstrated the significance of secondary symbionts for improving subterranean termite digestion and general health, including fungi, yeasts, and actinomycetes (Korb *et al.,* 2019)Metagenomics and high-throughput sequencing are two recent methodological innovations that have completely changed how we think about the termite gut microbiota. These cutting-edge methods give researchers a unique perspective on the variety and possible uses of commensal microorganisms in the gut (Hervé *et al.*, 2020). These discoveries not only expand our knowledge of termite-microbe interactions but also have the potential to be used in biotechnology for things like enzyme engineering and the creation of sustainable biofuels.The review provides a thorough overview of specific studies on primary and secondary symbionts with the goal of shedding light on the dynamic nature of termite-microbe interactions and their crucial role in forming terrestrial ecosystems. It draws attention to the intricate relationships between termites and bacteria and how these relationships affect the wider ecological implications (Peterson *et al.*, 2015).Complex symbiotic relationships in the subterranean termite gut affect broader ecological and evolutionary dynamics beyond digestion (Mathooko & Aswani, 2005).Through the symbiotic digestion of cellulose, underground termites contribute significantly to the carbon cycle. Microbes in termite guts affect greenhouse gas emissions by helping to sequester carbon. Termites discharge their collected carbon into the environment by destroying plant debris. This mechanism could have an impact on how terrestrial ecosystems function and how climate change is mitigated (Peterson *et al.,* 2015). Additionally, commensal microbe's destruction of cellulose-rich wood promotes the recycling of nutrients and the cycling of vital elements in the environment (Brune, 2014). This nutrient cycle not only supports termite colonies but also contributes to the health and sustainability of the surrounding ecosystem.The evolutionary interaction between subterranean

termites and their gut microbes is a subject of great interest. It shows co-adaptation between termite hosts and their symbionts (Hongoh *et al.,* 2005). This coevolution has produced specialized adaptations over time, including the cellulolytic enzymes produced by symbiotic bacteria and protozoa that allow termites to use cellulose-rich materials. The intricate dance of natural selection and co-evolution that formed termite digestive techniques is reflected in this complex interaction.Beyond ecological studies, the knowledge acquired from studying termite-microbe interactions has wider implications. Potential uses for the enzymatic capacities of symbiotic bacteria are in biotechnology. The application of termite gut enzymes in various industrial processes, such as the production of biofuel and biorefining, was emphasized by Scharf and Tartar (2008). Enzymes derived from termite gut microbiota provide fresh opportunities for resource sustainability (Scharf & Tartar, 2008).Additionally, controlling termite symbionts may open the door for cutting-edge pest management techniques. The prospect of using the intimate connection between termites and their symbionts to build specialized pest management methods was considered by Brune and Dietrich (2015). By upsetting the symbiotic balance, researchers hope to reduce the harm caused by termites to crops and structures (Brune & Dietrich, 2015).Even while current study has clarified many elements of the interactions between termites and microbes, there are still some exciting options to look into. Symbiont network stability may be revealed through research on the molecular mechanisms that control termite immunological reactions to symbionts (Korb *et al.,* 2019). In addition, it is anticipated that understanding the interactions in communication and metabolism between primary and secondary symbionts will show the intricacy of symbiotic relationships (Hervé *et al*., 2020).Modern techniques like single-cell sequencing and metatranscriptomics may be incorporated to better clarify the functional roles of various microbial species within the termite gut ecosystem (Biswas & Sarkar, 2018). Understanding the ecological resilience of termites also requires research into how environmental factors like habitat destruction and climate change affect interactions between termites and microbes (Hongoh *et al.*, 2005). Researchers will learn more about the intricate symbiotic relationships of the subterranean termite gut, discover new ecological insights, and further the practical application of this interesting field of study by exploring these unexplored areas (Otani *et al.,* 2014).

3. Methodology

This review seeks to give a thorough summary of recent studies that concentrate on cellulolysis, endosymbiotic connections, and subterranean termite biology. The research papers published between 2015 and the present were found using a systematic search of academic databases, such as PubMed, Web of Science, and Google Scholar. The search terms used were carefully chosen to address many facets of the research topic, including "subterranean termites," "intestinal symbiosis," "cellulose digestion," and "microbial community."

3.1 Primary Symbionts: Protozoa and Bacteria:

3.1.1 Nutritional cycling and cellulolytic enzymes

Protozoa and bacteria, the primary symbionts in the termite stomach, are crucial for the digestion of

cellulose and the cycling of nutrients. In a study published in 2019, Ali *et al.* explore the intricate ways by which termite protozoa produce cellulolytic enzymes and break down intricate plant components. This procedure promotes nutrient recycling in the ecosystem in addition to supporting termite nutrition. Termite intestinal bacteria also aid in the lignocellulose's breakdown. According to a study, numerous bacterial populations play different roles in the breakdown of tough plant polymers. These bacteria create enzymes that efficiently break down both hemicellulose and cellulose by targeting particular parts of plant cell walls (Ali *et al.*, 2019).Ali *et al.,* 2019 by using cellulose traps, subterranean termites were first removed from Al-Haraga hamlet in Egypt's Fayoum Governorate. Transported to the microbiology lab, the collected samples were identified using their morphological traits. Cellulase-producing bacteria were recovered using a mineral salt medium that contained carboxymethylcellulose (CMC) as the only carbon source after macerating the termite workers' guts. Spotting and well diffusion assays were used to characterize the isolates and check for their ability to break down cellulosic materials. By quantifying the amount of reducing sugar released from CMC using the DNS method, enzyme activity was evaluated.The morphological and physiological characteristics of the promising isolates were investigated for identification and characterization. By extracting genomic DNA and utilizing universal primers in PCR to amplify the 16S rDNA genes, molecular identification was carried out. Unweighted pair group method with arithmetic mean (UPGMA) was used to build a phylogenetic tree after the retrieved sequences were matched with those in the GenBank database.In conclusion, bacteria that break down cellulose were successfully recovered from the gut of the subterranean termite species *Psammotermes hypostoma*. The isolates were identified using morphological and genetic traits, and enzymatic assays were used to measure their cellulolytic activity. This research illuminates the termite gut-derived bacterial isolates capacity to produce cellulase. Table 2 shows the morphological and biochemical characteristics of the five selected isolates. Three isolates were identified as Gram-positive bacteria and two isolates were identified as Gram-negative bacteria. All isolates were able to grow in aerobic conditions. Isolate AFC3 was a motile and spore forming small rods, slightly tapered and curved with a circular greenish yellow colony on nutrient agar that identified as S. maltophilia. Isolates AFC2 and AFC4 were characterized as motile bacilli, while AFC5 was a motile and spore forming long rods, irregular with a brown colony on nutrient agar that identified as B. cereus. Isolate AFC1 was a motile and spore forming Long rods, slightly tapered and curved with a circular cream colony and greenish yellow colony on nutrient agar, indicating that AFC1 belonged to the genus Paenibacillus (Ali *et al., 2019).*

Table 2: Colony morphology of the bacteria isolated from termite gut contents (Ali *et al*., 2019)

No.	Isolates	Color	Shape	Size (mm)	Elevation	Opacity
1	AFC 1	Cream	Circular	1-2	Convex	Opaque
2	AFC 2	White	Oval	1-2	Flat	Opaque
3	AFC 3	Greenish Yellow	Circular	3	Circular	Opaque

4	AFC 4	Unpigmented	Compact	2-3	Compact	Opaque
5	AFC 5	Brown	Irregular	3-4	Flat	Opaque

3.1.2 Functional and phylogenetic diversity

The termite gut contains a very diverse range of bacteria and protozoa, according to recent developments in sequencing technology. The taxonomic diversity of termite-associated bacteria and their functional role in the digestion of lignocellulose were thoroughly examined. Researchers have established the existence of many bacterial strains that play particular roles in the degradation of intricate plant material (Breznak & Brune, 1994). This study looked at the relationship between functional diversity in termite protozoa and the dietary preferences of several termite species. Their findings revealed a nuanced interaction between host nutrition, protozoan variety, and the effectiveness of cellulose digestion. Fungal, yeast, and actinomycete secondary symbionts (Jiang *et al.,* 2021)

3.1.3 Degradation of fungi and lignocellulose

Other secondary symbionts that improve termite digestion and nutrient intake include yeasts, fungi, and actinomycetes. In a 2015 study, Brune and Dietrich looked into the termite gut's microbial populations' potential for use in several processes. They found numerous fungal enzymes that contribute to host feeding and the breakdown of lignocellulosic material (Brune & Dietrich, 2015).Yeast in the gut of termites is important for nutrient cycling and resilience. Carrijo *et al.,* 2009 investigated the role of termite-associated yeast in nitrogen fixation and nutrient conversion. The significance of these yeasts in helping termites better adapt to challenging environmental conditions was demonstrated by their findings (Carrijo *et al.,* 2009).The investigation was carried out in the 2,862.28-hectare Parque Estadual da Serra de Jaraguá in Jaraguá, Goiás, Brazil, which is surrounded by rural holdings, primarily cattle farms. The cerrado vegetation inside the park has been conserved, but the surrounding areas have had their landscapes changed. Two zones were examined for termites: "Cerrado sensu stricto," which has few trees, bushes, forbs, and native grasses, and "Pasture," which is a nearby area that was once cerrado but has since been turned into a pasture for *Brachiaria brizantha* grass. Sampling involved placing linear transects, each with 10 quadrats (5 x 2 metres), at least 50 metres from the area's edge and 30 metres apart. Within quadrats, the search for termites included a variety of environments, such as epigeous nests, soil surfaces, litter, plant stalks, and downed branches. 20 cm-deep trenches were excavated after the inspection to look for termites in the soil. Per quadrat, two collectors put in 30 minutes. Small, widely spaced quadrats were employed to prevent duplication. To avoid overestimating abundance, species that occurred in the same quadrat were treated as one colony. Termites were collected, stored in 70% alcohol, and identified using the Universidade Federal de Goiás (UFG) collection and existing references. Based on their feeding habits, termites were divided into four functional groups: humivorous, xylophagous, grass/litter feeders, and intermediates. This strategy included meticulous collection, thorough sampling, species identification, functional grouping based on

feeding behaviour, and species identification (Carrijo *et al.,* 2009).The Shannon-Wiener diversity index was employed in the study to combine richness and abundance to analyse termite diversity in Brazil's Parque Estadual da Serra de Jaraguá. Richness was measured using species accumulation curves and compared between "Cerrado" and "Pasture" richness averages using resampling and bootstrap technique. Beta diversity, which represents species turnover between environments, was assessed by the Jaccard's index.29 different species of termites were found in total, with 64 colonies and 21 species in the cerrado and 46 colonies and 17 species in the pasture. Cerrado displayed greater richness, but bootstrap comparisons revealed no appreciable changes. The qualitative shift in species composition revealed 12 unique species to the cerrado, 8 exclusive species to the grassland, and 9 coexisting species. Richness and composition of species were impacted by habitat alteration, with humivorous species thriving in the older pasture (Carrijo *et al.,* 2009; Hongoh, 2010).The study demonstrated termite diversity patterns and composition changes as a result of habitat alterations using diversity indices, resampling, accumulation curves, and qualitative analysis. The findings improve our knowledge of the variables affecting termite colonies in various situations.Actinomycetes are also receiving interest because of the possible biotechnological uses for them. According to Yan *et al.,* (2018), termite-associated actinomycetes have a special metabolic pathway that produces bioactive substances with ecological and biotechnological value *(Otani et al*., 2014).New insights with wider ecological and practical consequences are promised by ongoing research on termite-microbe interactions. Metagenomics and metatranscriptomics, two cutting-edge omics methods, offer previously uncommon perspectives on the functions and interactions of microbial species in the termite gut (Hervé *et al.,* 2020).Another crucial research area is figuring out how termite-microbe interactions alter as a result of environmental changes like habitat destruction and climate change (McAuliffe, 2023). Investigation is needed into the possible impacts of symbiotic network modifications on termite behavior, physiology, and ecosystem performance.

4. Results

Focusing on publications from 2015 to the present, this review summarises current research on subterranean termite biology, cellulolysis, and endosymbiotic connections. A thorough search was conducted using key words including "subterranean termites," "intestinal symbiosis," "cellulose digestion," and "microbial community" in databases like PubMed, Web of Science, and Google Scholar.The termite stomach's cellulose digestion and nutrient cycling depend heavily on primary symbionts, protozoa, and bacteria. The production of cellulolytic enzymes by termite protozoa, which aid in the breakdown of plant components for nutrient recycling, was studied by Ali *et al*. (2019). Each intestinal bacterium targets particular plant cell wall constituents to aid in the breakdown of lignocellulose (Ali *et al*., 2019).A complex link between host nutrition, protozoan variety, and cellulose digestion efficiency was revealed by a study of the functional diversity of termite-associated bacteria and protozoa (Hervé *et al*., 2020). As secondary symbionts, yeasts, fungi, and actinomycetes improve termite digestion and

resistance (Brune & Dietrich, 2015). According to research by Carrijo *et al*. (2009), termite-associated yeasts are helpful in the cycling of nutrients and in adapting to difficult conditions (Carrijo *et al*., 2009).Researchers in Brazil's Parque Estadual da Serra de Jaraguá used the Shannon-Wiener index, species accumulation curves, resampling, and bootstrap techniques to evaluate termite diversity. With unique compositions in both cerrado and pasture, cerrado showed a higher species richness. In older pastures, humivorous species were more prevalent due to habitat alterations that had an impact on species richness and composition (Carrijo *et al*., 2009).Through cutting-edge techniques like metagenomics and metatranscriptomics, current research investigates termite-microbe interactions (Hervé *et al*., 2020). It is critical to look into how these interactions react to environmental changes (McAuliffe, 2023) since doing so can reveal potential effects on termite physiology, behaviour, and ecosystem function.The breakdown of cellulose is significantly influenced by the variety of microbial symbionts found in termite bellies, especially bacteria and protozoa. Enzymes produced by these bacteria aid in the breakdown of lignocellulose into simpler carbohydrates, which benefits the termite host as well as the microbes themselves. various termite species support various microbial communities, indicating that the symbiosis between termites and their stomach microorganisms is also species-specific (Evans & Iqbal, 2015; Otani *et al*., 2014). According to phylogenomic research, a range of prokaryotic lineages are present in the gut microbiota of higher termites, which is essential for effective digestion (Hervé *et al*., 2020).Espeland's *et al*., (2010) research concentrated on the processes by which termites and other herbivorous insects break down cellulose using their symbiotic microorganisms. Their results highlight how important these interactions have been for evolution in helping termites to use lignocellulosic substrates, which in turn affects their ecological roles as decomposers in terrestrial environments (Espeland *et al*., 2010).

5. Conclusion

In the end, the intricate symbiotic interactions found in the subterranean termite gut have fascinated researchers and offered insightful information about numerous ecological, evolutionary, and biotechnological issues. To help an ecosystem function, primary symbionts like bacteria and protozoa interact dynamically with secondary symbionts like fungi, yeasts, and actinomycetes to break down cellulose-rich material. It significantly affects how well termites perform.This paper provides a detailed overview of the termite gut microbiota and highlights the numerous functions that these microorganisms play in the digestion of cellulose, nutrient cycling, and possible applications in biofuels and pest control. The complexity of these symbiotic connections and their significance in a wider ecological context has been highlighted by research over the past ten years.

5.1 Future directions and unanswered questions

Digging deeper into the complex world of termite-microbe interactions reveals several avenues for future research. Understanding the mechanisms that determine the stability and resilience of these symbiotic networks under changing environmental conditions remains an important challenge. In addition, the poorly understood functional roles of microbial actors and the complex communication

between primary and secondary symbionts provide exciting opportunities for exploration (Peterson *et al*., 2015).Moreover, the evolutionary dynamics that have shaped these interrelationships over millions of years require further study. Genomic and metagenomic studies can provide insight into the coevolution of termite hosts and their symbionts and shed light on the genetic adaptations that have led to their successful collaboration.

5.2 Practical applications and their implications

The insights gained from studying termite-microbe interactions go beyond theoretical knowledge and are of practical importance. Enzymes produced by these microbial communities could revolutionize industries such as biofuels and biorefining. Harnessing the cellulose-degrading ability of termite intestinal symbionts has the potential to contribute to sustainable and renewable resource utilization (Biswas & Sarkar, 2018)Furthermore, insights into interactions between termites and microbes may pave the way for innovative approaches in pest control and crop protection. Understanding how symbiotic networks operate allows researchers to develop targeted strategies to control termite populations while minimizing environmental impact (Vargo & Husseneder, 2009)Finally, the symbiotic interactions in the subterranean termite stomach comprise a sophisticated dance between the host animals and their companion bacteria. The realm of termite gut microbiota is rich of options, from contributing to food cycling and carbon dynamics to offering potential solutions in biotechnology and pest management. We can anticipate ground-breaking discoveries that will influence both our understanding of ecology and the practical use of microbial partnerships as researchers continue to unlock the secrets of this intricate ecosystem.

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