




REVIEW ARTICLE

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Bacterial diversity from soil-feeding termite gut and their potential application

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Abstract

Purpose High population growth and the expansion of industry from time to time produce a large amount of waste/pollution, which harms global environmental health. To overcome the above problems, soil feeding (mound/nest) builders of termite gut bacteria execute thriving since they can be obtained easily, available, and at low costs. The purpose of this review is to provide evidence of bacteria in the soil feeding termite gut and its potential role in various applications including reduction of methane gas emission, bio bricks/production of bricks, biomedicine, biocontrol (promising tool for sustainable agriculture), and bio-fertilizer (improve the fertility of the soil) and plant growth promote effectiveness all year.

Methods This review was progressive in that it assessed and produced peer-reviewed papers related to bacteria in the soil feeding termite gut and its potential role in different applications for an environmentally sound. Based on the findings of reputable educational journals, articles were divided into four categories: methods used to distributions of soil-feeding termites, termite caste system, bacterial diversity, and strain improvement of bacteria in the termite guts for enhanced multipurpose and techniques.

Results The bacterial diversity from termite guts of soil feeding termite caste systems/differentiations is vital for snowballing day to day due to their low cost and no side effect on the public health and environment becoming known improvement of the microbial bacteria rather than other microbes. So termites function as “soil engineers” in tropical agroforestry ecosystems that are of great benefit for economic importance to greener approach.

Conclusion The present findings indicate that recovery was chosen as an appreciable bring out the bacteria in the soil feeding termite gut and its potential application of termite mounds/nests biotechnological applications. Because of the large amount of nutrients that have built up in termite embankment soil feeding, this type of termite is now known as a “gold-leaf excavation” for bacterial concentrations. This provides the assertion that termite insects are important from an ecological standpoint since they aid in nutrient flows in the ecosystem as a useful tool for various species.

Keywords Bacteria, Bacteriocins, Termite gut, Mound, Soil engineers

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Background

The termite order (*Isoptera*) was formed from the Greek words “isos” meaning equal and “pteron” meaning wing, as mature termites have equal-sized front and hind wings. Termites, sometimes known as “white ants” by the general public, do not have a tight phylogenetic relation with ants (Turner 2011; Howard and Thorne 2010; Heyde et al. 2021). Termites are considered to have evolved in the late Jurassic, with an evolutionary surge in the early Cretaceous. This fast-evolving eusocial group produced delicate microecosystems in Cretaceous terrestrial ecosystems by forming close relationships with biological communities and the surrounding environment. Although termite fossil records do provide insight into their subsequent diversification in the Cretaceous (Zhao et al. 2021; Bezerra et al. 2021).

Higher termites have a distinct and complex digestive system in which digestive enzymes generated by termites' hosts and gut symbionts play an important role in lignocellulosic material metabolism (Tokuda and Watanabe 2007; Banerjee et al. 2022). Termites are “ecosystem engineers” because they play an important role in the biotransformation and alteration of soil physicochemical and morphological features. The difference between mound soil qualities and surrounding surface soil properties at various soil depths is characteristic of termite mounds (Bera et al. 2020). They influence plant community production and composition by tunneling, organic matter decomposition and deposition (saliva and feces), and soil distribution (Omofunmi et al. 2017; Ahmad et al. 2018).

Mound-building termites decisively and substantially alter the soil conditions within termite mounds (Bignell 2019). Termites can alter soil populations of bacteria and functions by feeding, nest construction, littering, and affecting the physicochemical characteristics of mounds, all of which are important ecosystem functions in the face of global climate change (Chiri et al. 2021; Yan et al. 2021). Higher termites that feed on soil have radial and axial gradients in their physical and chemical features (such as pH, O₂, and H₂ partial pressure) and different microbial community densities and structures. Although 60% of the species of termites that are known to exist eat on soil, less is known about how they degrade biomass in comparison to their wood-feeding counterparts (Marynowska et al. 2023).

Termite mounds provide an important habitat for a wide range of microorganisms. The methods of microbial community building in termite mounds remain unknown, reducing our ability to predict the biological roles of this mound-associated microbiota. The new evidence indicates that temperature-based deterministic selection, rather than unpredictable mechanisms,

dominated microbial community assembly in termite mounds to a substantial extent (Chen et al. 2021a, b). In the termite's gut, different species of bacteria with various functions have been isolated and identified. Among them were hemicellulose-degrading bacteria, lignolytic bacteria, cellulolytic bacteria, aromatics-degrading bacteria, and nitrogen-fixing bacteria (Rajan et al. 2022).

The approaches of bacterial diversity assembly in soil-feeding termites remain unresolved, hampering our capacity to predict the biological activities of this soil-feeding-associated microbiota in an environment of global changes. This review embarks with an overview of soil-feeding termites, followed by a distribution of soil-feeding termites, termite caste systems, bacterial diversity of termite gut, strain improvement of bacteria from soil feeding termite, their application, and future trends of soil feeding termites.

Overview of soil-feeding termites

Soil feeding termites and their characteristics

The potential of termites to digest lignocellulose depends mostly on mutualistic symbiosis with different intestinal microbes, such as bacteria and archaea. In the case of *Termitidae*, “higher” termites and flagellate protists in basal lineages “lower” termites. Higher termites constitute more than 80% of the termite species. Compared to ruminants, termites are reported to degrade wood more efficiently and remove 74–99% cellulose and 65–87% hemicellulose from wood (Brune 2014).

Changes in soil-feeding termite (mound builder) microbial and biochemical characteristics may influence soil nutrient availability because microorganisms play an important role in elemental cycling and are sensitive to changes in soil conditions (Maharjan et al. 2017). A mound builder of termites is a pile of earth created by termites that resembles a little hill. Termite mounds are so sturdy and stable under their weight (with a safety factor of 100 for triangular shape and 50 for trapezoidal shape) that they can remain intact for hundreds of thousands of years (Omofunmi and Oladipo 2018).

Termites play an important role as “soil engineers” in tropical agroforestry environments. However, little is known about their role in phosphorus (P) cycling. The present findings and result of the study on the contribution of termite activity to P enrichment in the mounds (Lin et al. 2023).

In many humid habitats, termites construct visible structures known as mounds. Termite mounds are millimeter-sized structures constructed from mounds. They are mostly made of organic materials and clay components that are cemented together by termites' feces, saliva, and other secretions (Jouquet et al. 2015; Chauhan et al. 2017). Loundoungou termite mounds, for example,

include a conical architecture. This structure is typical of savannah termite mounds and reflects the strategy used by savannah colonies to deal with severe solar radiation and wind load (Fagundes et al. 2021).

Those (typically the vast majority) can have their ability to reproduce repressed, allowing them to reversibly or irreversibly adapt behaviorally and anatomically for other activities like defense, foraging, construction, or child rearing (Bignell 2019).

The use of molecular genetics technologies to explore species identification and distribution, population differentiation, colony social structure, and eating behavior is an important trend in termite research. *Macrotermes* (*M.natalensis*) conical mounds of medium size, *M.herus* relatively low closed dome mounds, and massive closed and comparatively dome-shaped mounds which could belong to *M. herus* or *M. falciger* were revealed in Central Ethiopia. In contrast to the other regions, Southern Ethiopia has a higher number of species and more diverse mounds. *M. jenneli*, *M.michaelseni*, *M. falciger*, and *M. natalensis*, as well as an undetermined species (*M.spA*) were found in the area (Debelo 2018).

Termite mounds are rich in natural nanoparticles, and their physicochemical, geochemical, mineralogical, and biological features differ from those of the surrounding soils. Even though termite mounds play important ecological and environmental roles such as soil formation and global climate change, the nano-scale structures formed by the associated organic mineral complexes are still poorly understood due to technical constraints (Enagbonma and Babalola 2019a, b; Apori et al. 2020; Duran-Bautista et al. 2020; Eze et al. 2020). Phosphorus (P) is found in soils in both organic and inorganic forms, ranging from ionic forms in solution to extremely stable complexes containing organic matter and clay minerals (Bera et al. 2020).

Termites create mounds under, above, or connected to a limb or stem of a tree (arboreal) and are named after their termite colony. Mounds, while similar in shape and size for many species, can change in shape and size according to micro-environmental conditions. Production rates vary by three to four orders of magnitude depending on termite species and dietary preferences, such as wood, grass, soil, or fungus feeding (Korb and Thorne 2017; Aiki et al. 2020; Sanchez-Garcia et al. 2020). *Bacillota* (74%), such as *Bacillus subtilis*, *Proteobacteria* (22%), such as *Azotobacter*, and *Actinobacteria* (3%), such as *Streptomyces*, are the most common phyla of culturable bacteria found in termite mound soil (Adebajo et al. 2021).

The enhancement of soil organic matter and micro- and macronutrients in mounds relative to their surroundings is mostly related to the speciation of

microbial communities. Mounds have larger relative abundances of *Copiotrophic* microorganisms, which support nutrient-rich habitats, and lower relative abundances of oligotrophic microbes, which prefer nutrient-limited circumstances (Baker et al. 2020). Soil-feeding termites eat organic stuff (such as humus, minerals, and litter) and construct their nests out of feces mixed with coarse inorganic soil particles. Soil-feeding termites, for example, have an impact on soil characteristics predominantly through feces regrowth in clay-organic complexes (Tuma et al. 2022).

Termites are the most important decomposers (insects) in tropical forests, tropical savanna, and desert environments. The majority of them are degraded wood and other cellulose-based materials (*Macrotermitinae*, *Termitinae*, and *Nasutitermitinae* subfamilies), redistribute soil materials, and hence affect physical soil qualities such as texture (*Macrotermitinae*, *Termitinae*, and *Nasutitermitinae* subfamilies). *Macrotermes* sp. Holmgren/*Termitidae: Macrotermitinae*, water infiltration rates, and organic matter and nutrient recycling, e.g. Holmgren's *Odontotermes/Termitidae: Macrotermitinae* (Lo and Eggleton 2010).

Termite mounds, it was discovered, are “hot spots” of P nutrient, which is a feasible source of available P for cash crops if smallholders can effectively use abandoned mound soils while conserving active mounds without destroying termite habitats (Apori et al. 2020; Van Thuyne and Verrecchia 2021). The spatial layout of complex agroforestry around termite mounds based on soil fertility gradients is critical for nutrient management (Tilahun et al. 2021). Termite clay soil's consistency and plasticity are within the typical range of 25 to 35, indicating modest plasticity. The presence of organic content and a larger percentage of enzymes in termite mound soil may explain the liquid limit measurement (Umara et al. 2023).

Distribution of soil-feeding termites in different mounds arena

Termites are tropical insects with a complicated social structure. Lower temperatures related to greater latitudes and altitudes limit their geographical distribution. Currently, Ethiopia has made it possible to make pretty definitive assertions about the distribution of species in the country and the damage they inflict (Wood 1991; Beyene and Getu 2021). Farmers were aware that different sorts (species) of termites existed, and they only knew termites as a single creature. Even they realize that a colony is made up of different castes, and they can identify some of them by certain characteristics, such as the queen (haadhoo—the mother), soldiers (diimtuu Kan Nama ciniintu—the red-colored which bites humans), and alates by

flying behavior (roobaan jireettii—the ones who appear during rain) (Debelo and Degaga 2015).

Coptotermes gestroi (Wasmann) and *Coptotermes formosanus* (Shiraki) are the most common subterranean termites (*Rhinotermitidae*) on the planet. *C. gestroi*'s widespread distribution had just been found in the last decade when multiple junior synonyms for this tropical termite were resolved (Grace 2014). Because of the warmth of these places, termite mounds (which are formed by termites) are common (Makonde et al. 2015).

There were a total of 13 nests identified. Four *Amitermes guineensis* arboreal nests and 9 *Macrotermes bellicosus* epigeal nests, i.e., 2 types of nests (Akpesse et al. 2022). Its findings compare to those of Boga et al. (2015) reported 165 termite mounds at the National Centre of Floristic (NCF) on the Cocody campus, 119 aboveground and 46 arboreal. This abundance of biogenic structure is justified by the tremendous activity of termite colonies, which have steadily regenerated the NCF forest over 51 years. The distribution of the ecologically important termite genus *Macrotermes* (*M*) over a South African savanna land-use gradient, with quantification of the effects of land-use change on mound densities, heights, and spatial patterning. Despite extensive anthropogenic landscape disturbance, termite mounds persisted and shared several commonalities with mounds in unaltered areas (Davies et al. 2020).

Termite mounds are heaping piles of soil built by termites that can be found all over the world between 47° Northern and 47° Southern latitudes. In the tropical rain forest, they are highly common (Claudius and Duna 2017). Termite mounds are common in Africa, particularly in Nigeria and Ghana (Mahamat and Azeko 2018).

In Ethiopia, 63 termite species from 25 genera have been recorded, accounting for around 6.3% of African termite diversity, an adequate estimate given the broad range and climate suitability (Debelo 2018). All of the Ethiopian fauna identification work was based on the fauna of other parts of Africa. The most important components of soil insect biomass contribute significantly to the ecosystem's effective functioning. Currently, *M. subhyalinus* and *M. herus* are the only two species of termites of the genus *Macrotermes* recorded in Ethiopia (including seven species: *M. herus* from Western, *M. subhyalinus*, *M. natalensis*, and *M. herus* from Central; *M. michaelsoni*, *M. jeanneli*, *M. natalensis*, *M. falciger*, and *Macrotermes* SpA (an unidentified sp.) from Southern Ethiopia (Jembere et al. 2017; Debelo 2018, 2020).

Termites have a significant impact on the ecology at the landscape level in Africa. Termites transfer soil particles, water, and nutrients, influencing the chemical and physical qualities of the soil. As a result, termites have been dubbed "ecosystem engineers" (Wisselink et al. 2020).

Many termite species (for example, *M. michaelsoni*, *M. natalensis*, *Odontotermes transvaalensis*) in Africa; *O. obesus*, *O. redemanni*, *M. convulsionarius* in Asia; *Amitermes meridionalis* in Australia, *Syntermes dirus* in South America) build large epigeal mounds that are typical of tropical landscapes (Chakraborty et al. 2020). Paejaroen et al. (2021) discovered other species in the genus *Globitermes* and *Microcerotermes* building enormous epigeal mounds in Thailand's tropics, implying that more species may be involved in the eventual form of a mound.

Currently, there are over 3000 termite species that have been reported in the world (Devi et al. 2007). Nests/mounds from 28 termite colonies were gathered during several sampling campaigns in South America and Africa in 2019 and 2020 (Chen et al. 2021a, b). The first sampling location is located in French Guiana, in the Sinnamary River (503'N, 5302.76' E), and is characterized by hot and humid weather all year with two dry seasons and two rainy seasons. Termites are among the oldest social insects on the planet, dating back over 250 million years (Krishna et al. 2013; Colas et al. 2020; Li and Pan 2021).

Termites have a global distribution due to their adaptation to a high degree of resource specialization, which allows them to be familiar with a wide range of nutritional, foraging, and nesting habits (Fisher et al. 2019). In this sense, subterranean termites are known as economically significant species that face an 80% loss worldwide, notably in tropical, subtropical, and temperate habitats.

According to Bhanupriya et al. (2022), studied that *M. obesi* was the most common species among soil feeders (SF), accounting for 30% of all occurrences, followed by *O. obesus* (25%), *O. guptai* (16%), *O. gurdaspurensis* (13%), *O. assmuthi* (10%), and *O. giriensis* (6%). *Amitermes belli* accounted for 21% of all soil-wood intermediate feeders (S/WF), with *M. beelsoni* (19%), *M. Cameroni* (16%), *M. newmani* (14%), and *O. feae*, *O. parvidens*, *O. redemanni*, and *M. baluchistanicus* accounting for the remaining 19%.

Gergonne et al. (2023) studied soil-feeding termite species, which are abundant in this environment. a secondary encounter that occurred after the lineages' allopatric split, emphasizing the possible significance of the northern Andes' recent environment change. On the west coast of Colombia, there was a sympatry zone for two alleged sister-species termites, *E. neotenicus* and *E. chagresi*, and it is reported a complex pattern of their genetic and geographic history using an integrative approach.

Soil feeding of termite caste systems

The termite caste system is a complex process influenced by a variety of inherent and extrinsic factors that have perplexed researchers for decades. Over the last decade,

advances in molecular, genomic, and integrative or “systems” biology have substantially aided efforts to understand this process (Eggleton 2010). The reproductive division of labor, which involves developmental regulation of the reproductive organs, is a key component of eusocial insect societies. However, whereas caste systems are critical for building social structure in termites, one of the primary eusocial insect families, little is known about reproductive organ development during caste distinction (Oguchi et al. 2016).

All castes of social insects have diverse morphologies suitable to their functions and engage in social interactions. The acquisition of caste-specific features was a significant milestone in the evolution of social insects. Nonetheless, understanding of the genetic bases and developmental mechanisms that give birth to these features remains restricted. Using RNAi, a comparative study of termites (*Zootermopsis nevadensis*) and cockroaches revealed that caste-specific cuticular pigmentation was caused by different expression patterns of “key genes” in the tyrosine metabolic pathway dopamine decarboxylase, NBAD synthase, acetyltransferase, and laccase 2 (Masuoka and Maekawa 2016).

Rasheed et al. (2019) studied those endo cuticular protein genes of alate adults, laborers, and soldiers in a comparative transcriptome analysis of *Reticulitermes aculabialis*. Termite caste distinction is one of the most visible examples of facultative polyphenism in animals, in which individuals exhibit diverse phenotypes despite having the same genetic background. Termites typically have three castes with distinct phenotypes: workers, soldiers, and reproductives shown in Table 1 below (Sanchez-García et al. 2020; Zhao et al. 2021; Bezerra et al. 2021).

Termites are eusocial insects that live in colonies that divide into reproductives, workers, and soldiers. Soldiers are trained for defense but are costly to maintain because they cannot care for themselves and must be fed and groomed by others. Several species’ soldiers impact foraging behavior by acting as scouts who initiate foraging or by influencing worker behavioral plasticity during food exploration (McCarthy et al. 2023).

The bacterial isolates obtained from termite worker and soldier has more cultural isolates (Kakkar et al. 2015). Their social structure differs greatly from that of bees and ants. Only the reproductive castes (kings and queens) are adults in a termite society, whereas workers and soldiers are larvae of males and females. Termite workers and soldiers can mature into reproductives, unlike bees and ants, whose workers are unable to replace their queens. Termites have traditionally been classified as either higher or lower termites: higher termites are members of the family *Termitidae*, which contains around 80% of all

termite species, whereas lower termites are members of other families shown in Fig. 1 below (Bucek et al. 2019; Chouvenc et al. 2021).

Bacterial diversity in the gut of soil-feeding termites

The microbial diversity of termite nests was investigated in this study using bacterial tag-encoded *Amplicon pyrosequencing* in both culture-dependent and culture-independent. Researchers used the bacterial tag-encoded FLX amplicon pyrosequencing (bTEFAP) method to examine the microbial diversity of a termitarium (Manjula et al. 2014). Tag-encoded FLX-amplicon pyrosequencing (TEFAP) has been used to assess functional genes as well as bacterial, archaeal, fungal, and algal genes. By using the new bTEFAP method, were able to sequence the ribosomal RNA genes of microorganisms (hereafter focused on bacteria) without the inherent bias of culture methods. This allowed us to assess bacterial diversity (Andreotti et al. 2011; Sun et al. 2011).

In the culture-independent and culture-dependent methods respectively, 10,793 and 4777 high-quality reads were produced. The earlier method identified *Proteobacteria* 32% and *Actinobacteria* 20% as the most prominent phyla, but the latter method revealed *Bacillota* 74% and *Proteobacteria* 22%. Because the metagenomic approach examined all of the termitarium’s diversity of bacteria while the culture-dependent conduct only looked at a small portion of it, there may be a significant difference between the two approaches’ assessments of the diversity of microbes (Manjula et al. 2014).

Mound-associated bacteria are different from classical symbionts in several ways. For example, they are generalist bacteria that can live both free-living and mound-associated lifestyles. They are also recruited and maintained in order through termite nest-building and digestive activities. However, strong arguments have been made that mammals can consistently acquire microbial symbionts if symbionts are widely dispersed and promiscuous interactions may arise (Moran and Sloan 2015; Chouvenc et al. 2018).

The occurrence of *Bacteroidetes*, *Bacillota*, *Spirochaetes*, *Chloroflexi*, *Nitrospirae*, *Planctomycetes*, *Proteobacteria*, *Tenericutes*, *Actinobacteria*, and *Deinococcus* has been recorded by several studies. The high amount of organic matter in the termite mound may be the cause of the soil’s high bacterial diversity (Enagbonma and Babalola 2019a). In the soil of termite mounds, the *Verrucomicrobia*, *Fibrobacteres*, *Chlorobi*, *Elusimicrobia*, *Candidate Division WS3*, *Acidobacteria*, *Synergistetes*, *Cyanobacteria*, WCHB 1–60, *Chlamydiae*, and *Gemmatimonadetes* phyla have been identified (Costa et al. 2013).

Table 1 Some differences and characteristics of soil-feeding termite castes

Caste systems	The role and activity of castes	Reference
Soldier termites	The whole <i>Isoptera</i> clade is eusocial for the possession of a caste of soldiers. Judging from phylogeny, soldiers evolved once in a basal lineage ancestral to all living termites	Roisin and Korb 2010
	As for soldier differentiation, some endocrine mechanisms may cause sex-specific differences in gonad development in these types of termites	Oguchi et al. 2016
	Taxonomic characters found in soldier caste present conspicuously reliable features for diversity investigations	Himmi et al. 2020
	The principle of caste differentiation of reproductive division between the reproductive individuals that monopolize reproduction (queens and kings) and their non-reproductive helpers such as workers and defense specialists known as soldiers	Thompson and Chernyshova 2020
	Termite soldier groups were searched more intensively and encountered more food sources simultaneously than other castes and more efficient perception of changes in food availability and redirecting to more profitable patches	do Sacramento et al. 2020
Worker termites	The size of the worker termites is related to physiological factors, such as nutrition and energy expenditure, and mainly to the quantity and quality of food, although the results are contrasting	Dahlsjö et al. 2015
	Workers fill many important roles, which include nest construction, food collection, nest-mate care, and hygienic activity within the nest	
	Workers termite has limited visual capabilities and communicates with nest mates primarily via olfactory channels to convey pheromonal and other chemical cues	Sun et al. 2019
	Worker termites masticate soil and water to create mud, as a subtle and complex combination of moisture and granular materials	
	As the young workers ingest forage material and the old workers consume the mature comb, the changes in diet influence the bacterial composition of the gut	Otani et al. 2019
	The primary sequence and spatial expression pattern of <i>Orco</i> and <i>5-HTT</i> in workers, which are respectively, associated with chemosensation and neurotransmission in insects	Sun et al. 2019
Specifically, workers are wingless individuals lacking compound eyes with a pronotum that is trapezoidal	Shi et al. 2021	
Termite reproductives	Termite colonies are almost always headed by a single pair of reproductives that develop from workers generally via a single molt within the natal nest; they lack several adult traits, such as wings and compound eyes	Korb 2018
	Termite reproductive live deep inside the nest of the central area (e.g., 'royal chamber' in a few species) of an enclosed and protected mound or nest (subterranean, epigeal, or arboreal) safe from predation	Tasaki et al. 2021
	Reproductive dominance of termites is often achieved via chemical communication through (CHCs) (other compounds can also be involved). Queen CHCs have been proposed to function as fertility signals across social insects to affect the behavior and physiology of colony members	Lin et al. 2021; Masuoka et al. 2021

CHCs cuticular hydrocarbons; 5-HTT serotonin transporter gene, *orco* olfactory receptor co-receptor

The gut of the lower termite *Psammodermes hypostoma* was studied by Ali et al. (2019) to isolate five symbiotic bacterial strains and establish their function in the breakdown of cellulose. Based on biochemical testing and analysis of the 16S rRNA gene sequence, these bacterial strains were identified as *Paenibacillus lactis*, *Lysinibacillus macrolides*, *Stenotrophomonas maltophilia*, *Lysinibacillus fusiformis*, and *Bacillus cereus*.

Different as part of the three termites under investigation have been shown to contain bacteria from ten different families. About 68.1% of the isolates belonged to the genus *Enterobacteriaceae*, followed by *Yersiniaceae* (10.6%) and *Moraxellaceae* (9%). *A. pakistanicus* and *Macrotermes* sp. bacteria that were recovered belonged to four different families. Only the gut of *Macrotermes*

sp. contained members of the *Streptococcaceae*, *Microbacteriaceae*, and *Weeksellaceae* families. The majority of the termites under study belonged to the *Bacillales* and *Micrococcaceae* families, which were unique to the digestive tracts of *O. longignathus* and *A. pakistanicus*, respectively. However, the other bacteria displayed term-specific distribution (Xie et al. 2023).

The bacterial phyla *Pseudomonadota* and *Bacillota* are frequently found in those three insect families, but their compositions differ at lower taxonomic levels. Eusocial insects have distinctive gut bacterial communities that are shared by all host species, albeit the stability of these communities varies according to the physiology and ecology of the hosts. In contrast to "generalists" like the majority of ant species, species with "narrow dietary

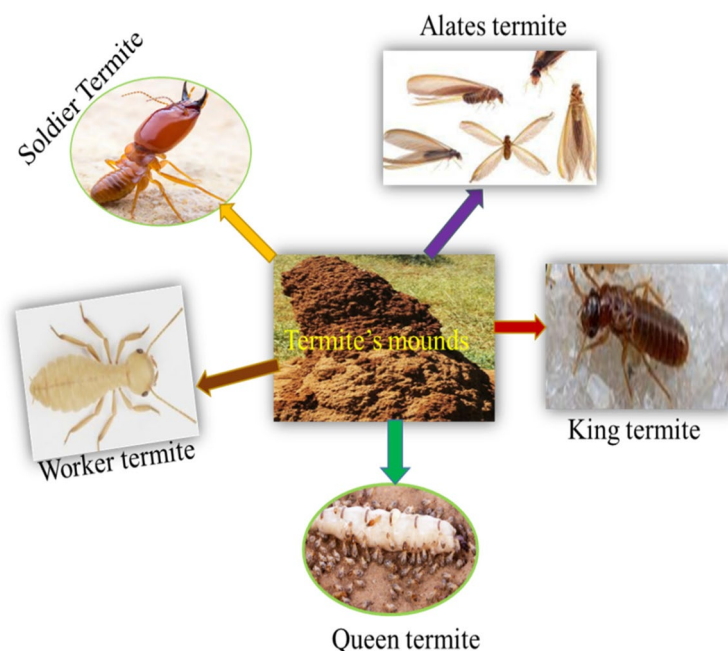


Fig. 1 Termite caste systems (Matsuura et al. 2018; Oguchi and Miura 2023)

habits” like eusocial bees have very stable and intraspecific microbial communities (Suenami et al. 2023).

Strain improvement of bacteria from soil-feeding termites

Termite guts and nests have complex microbial ecosystems. There is, however, limited data on the comparative investigation of termites in the gut and nest-associated microbial communities. Manjula et al. (2016) studied that used high-throughput sequencing of the V3 hypervariable region of 16S rDNA to investigate and compare the bacterial diversity of termites in the gut and nest.

The entire digestive system of a termite can successfully investigate various regions of a termite gut system evolved with salivary glands, foregut, midgut, and hindgut for total RNA isolation and high-throughput RNA sequencing. An in-depth “omics” investigation of the various organs in the termite gut digestive system will show the biocatalytic network in each portion as well as the detailed mechanisms for biomass breakdown (Eggleton 2010; Geng et al. 2018).

According to Ayerofe et al. (2019), studied three potential lignin degraders identified as *Bacillus* sp.,

Lysinibacillus sp. and *Acinetobacter* sp. were successfully isolated. These strains have been shown to metabolize kraft lignin and produce the three essential ligninolytic enzymes laccase, manganese peroxidase, and lignin peroxidase. Furthermore, the G+:G- ratio in the live mounds was generally higher and lower than in the surrounding surface soils and subsoils, and the

G+: G- ratio was significantly related to soil nutrients. They support that the G+ to G- bacteria ratio reflects the nutritional state of the soil, with a higher percentage of G+ bacteria suggesting a deficiency in nutrients (Xia et al. 2019).

Actinobacteria are highly prevalent in taxonomic metabarcoding using 16S amplicon sequencing, which exhibits comparable tendencies to metagenomic bacterial annotations. Contrarily, *Proteobacteria* do not. *Nasutitermes* belong to the class *Actinomycetia*, either to the genera *Grylotalpicola* in three examples or *Mycobacterium* in the last. *Streptosporangiales* were found to be the most common orders in several of the sequenced soil feeders. The literature has already discussed variations in both sequencing approaches’ results (Rausch et al. 2019).

According to the metagenomic study of several termite guts, *Spirochaetota* is the most common bacterial phyla. By investigating the 16S rRNA gene sequence, the termite gut bacteria have been identified and grouped into the phyla *Spirochaetota* such as *Bacteroidetes*, *Bacillota*, *Fibrobacteres*, *Proteobacteria*, *Actinobacteria*, and *Elusimicrobia* (Liu et al. 2019a, b; Victorica et al. 2020).

Actinobacteriota and candidate phylum *Dormibacterota* make up an average of 71% and 6.8% (57% and 7.5% depending on amplicon sequencing) of the bacteria in the mounds of the three most common termite feeding groups in Australia, according to metagenome analysis. The majority of the mound-enriched *Actinobacteriota*, *Dormibacterota*, and *Acidobacteriota* bacteria can grow

mixotrophically using organic and inorganic substances, according to the metabolic annotation of Metagenome-assembled genomes, which supports the aforementioned result (Chiri et al. 2021).

Furthermore, miRNAs were found to be involved in the regulation of insect behavior. MiR-8 and miR-429 govern virus-induced climbing behavior in cotton bollworms by controlling BrZ2 expression (Zhang et al. 2018). *Thermalin*, gram-negative binding protein 2 (GNBP2), selenium-binding protein, and transglutaminase (TG) gene silencing in termites has been demonstrated to drastically limit antifungal activity and therefore infection mortality (Zhao et al. 2021). Termites eat lignocellulose or soil in collaboration with particular stomach bacteria. The investigators created gut metagenomes for 145 termite species (Arora et al. 2022). The 129 most complete metagenomes were used to study the functional evolution of termite gut microbiota, revealing that gut prokaryotic genes involved in the main nutritional functions are found in all termites, which indicates that these genes were already present in the common ancestor of modern termites. The gut microbes possessed a similar set of carbohydrate and nitrogen metabolism genes across the termite phylogenetic tree (Arora et al. 2022).

In Penang, Malaysia, a metagenomic dataset of gut microbial DNA from the lower group of subterranean termites, *Coptotermes gestroi*, and the higher groups, *Globitermes sulphureus* and *Macrotermes gilvus*, was generated. Each species has two replicates that were read using Next-Generation Sequencing

(Illumina MiSeq) and processed using QIIME2. There were 210,248 sequences in *C.gestroi*, 224,972 in *G. sulphureus*, and 249,549 in *M. gilvus* in the results. The sequence data were submitted to the NCBI Sequence Read Archive (SRA) with the BioProject identifier PRJNA896747. The bacterial diversity analysis showed that Bacteroidota is the most abundant phylum in *C.gestroi* and *M.gilvus*, while *Spirochaetota* is prevalent in *G.sulphureus* (Shamsuri and Ab Majid 2023).

Termite groups with miRNAs targeted had lower behavioral and physiological disease defenses at both the group and individual levels, indicating broad-spectrum suppression of termite social immunity. By targeting miRNAs, termite groups died at a high rate after fungal contamination, implying that miRNAs could be used as termiticides to improve biological control of termites by weakening their social immunity. As a result, miRNAs may be regarded as novel targets for insect pest control (Liu et al. 2023).

Potential application of soil-feeding termite guts bacteria

Termite mound soils could be used as a bulking agent and for silo construction for short-term grain storage. Furthermore, some bacteria isolated from termite mound soil could be utilized in an eco-friendly way as a potential material for antimicrobial production, biofertilizers, and biocontrol Fig. 2 below (Enagbonma and Babalola 2019a, b).

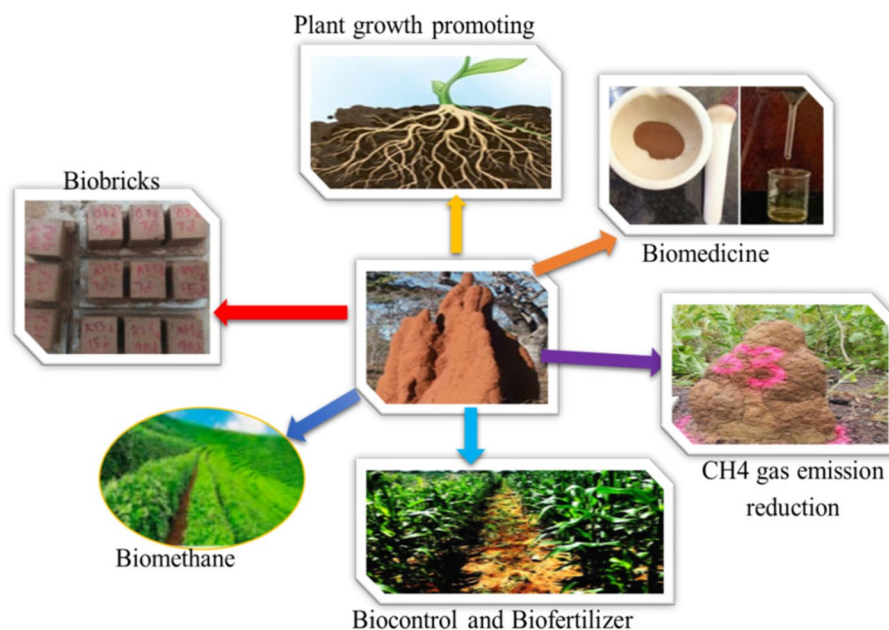


Fig. 2 Some potential applications of soil-feeding termites (Enagbonma and Babalola 2019b; Li and Greening 2022)

Termites have beneficial effects on the soils they inhabit and are the most important soil bioturbators; they excavate organic materials and mineral particles from different depths of their parent soil, which they mix with their saliva and excretions to form building materials when constructing their mounds (Enagbonma et al. 2020). Termites store SOM and plant nutrients in their nests, mounds, galleries, and other structures for extended periods, resulting in increased organic carbon, C/N ratio, Ca, Mg, K, and P in mounds (Devi and Thakur 2018; Oluleye et al. 2020).

A high concentration of greenhouse gases in the atmosphere contributes to global warming. Termites

emit methane gas, which is produced by the fermentation of organic materials during mound creation. Termite mounds emit around 580Tg of methane per year shown in Table 2 below (Eze et al. 2020; Li and Greening 2022). Termite mounds contain a ventilation system that allows gases produced by symbiotic and insect life during respiration and transpiration to escape, and this process regulates byproduct concentrations inside the chambers. The termites in the nest move about during foraging activities and can digest cellulose complexes outside of the mounds (Quevedo et al. 2021).

Table 2 Some potential applications of termite mounds

Items	Importance of soil feeding termites in different environments	Reference
CH ₄ gas emission reduction	Termite mounds mitigate emissions of methane (CH ₄) by aerobic CH ₄ oxidizing bacteria (methanotrophs) significantly and are responsible for ~ 1 to 3% of global CH ₄ emissions	Nauer et al. 2018
	The evidence from mounds confirmed that methanotrophs mitigate between 20 and 80% of termite-derived CH ₄ before emission to the atmosphere	Chiri et al. 2020
	By putting economic weight on CH ₄ production in the breeding goal, selective breeding can reduce the CH ₄ intensity even by 24% by the EU	de Haas et al. 2021
Biomedicine	The antibacterial activity of <i>Litchi chinensis</i> wood vinegar against <i>S. aureus</i> , <i>Acinetobacter baumannii</i> , and <i>P. aeruginosa</i> due to its high phenolic compositions for biomedical	Yang et al. 2016
	Antibacterial against food spoilage microorganisms including <i>Escherichia coli</i> ATCC 25922, and <i>Pseudomonas aeruginosa</i> ATCC 27853 by Kirby–Bauer disc diffusion and microdilution	Witasari et al. 2022
	Microbes isolated from soil, water, sewage, and sediments are potential sources of antibacterial and antifungal agents against a whole range of bacterial pathogens resistant to drugs	Dimri et al. 2020
Bioblocks	Thus, termite mounds are clay-rich sites and the composition of many chemical elements is greater than surrounding soils	Eze et al. 2020
	An important habitat for an enormous diversity of microorganisms and is used for making bricks, geochemical prosperity, pottery, and plastering of houses	Pandey and Upadhyay 2021
	Used as a construction material for pozzolanic crucial activities by empirical and traditional without a clear scientific explanation behind its usage (calcined termites)	
Biocontrol and biofertilizer	DsRNA is considered a new generation of RNA biopesticides with great potential for biological control. For example, feeding <i>Spodoptera littoralis</i> (<i>Boisduval</i>) larvae sl 102 dsRNA enhanced the toxicity of Bt	Caccia et al. 2020
	Termites are considered pests and biological control is an environmentally friendly alternative to reduce pesticide contamination	Coêlho et al. 2023
	The soil conditions created by termite mounds are also sufficiently fertile to enable the recruitment and development of new tree species that have higher water and nutrient requirements than the original savannah tree community	Davies et al. 2016
Plant growth promoting	Active involvement in bioturbation and pedogenesis, organic litter degradation and decomposition, water infiltration and runoff, nutrient cycling, soil animal and microbial diversity, and vegetation growth and diversity	Eze et al. 2020
	<i>Bacillus cereus</i> TSH77 and <i>Bacillus endophyticus</i> TSH42 isolated from termite mound soils were used to bacterial the rhizome of <i>Curcuma longa</i> . Both strains showed remarkable (PGP) activities	Chauhan et al. 2017
	Improving sunflower yield requires a better understanding of structural, functional, and plant-growth promotion, conservation of ecosystem function, and sustainable agriculture	Li et al. 2022
	Play an important role in soil ecology; transporting and mixing soil and organic material from different horizons (enrich the crop field with available nitrogen, total phosphorous, and an organic carbon than the adjacent soil)	Devi and Thakur 2018
	Beneficial to the environment, mainly as efficient decomposers of organic matter for plant growth promotion	Santos 2020

Bacteria in soil feeding termites as reducing methane (CH₄) gas emission

Many termite species construct nests and mounds out of soil. Aerobic CH₄ oxidizing bacteria (methanotrophs) considerably reduce termite CH₄ emissions. These species' mounds have previously been shown to oxidize a significant amount of termite-produced CH₄. *Tumulitermes pastinator* mounds, for example, appear to be largely inactive, although a high fraction of termite-derived CH₄ can be oxidized in the soil beneath mounds due to mound facilitation of CH₄ movement (Nauer et al. 2018).

Methanogenesis in termite hindgut is thought to be contributing to 11% of the methane emissions from natural sources, or around 3% of the total world methane emissions (Liu et al. 2019a, b). Termite mounds have recently been shown to reduce about half of termite methane (CH₄) emissions; however, the aerobic CH₄ oxidizing bacteria (methanotrophs) responsible for this consumption remain unidentified. The rate constant of CH₄ oxidation, as well as the porosity of the mound material, were found to be strongly positively related to the abundance of termite mound methanotrophic communities (Chiri et al. 2020).

Two approaches were used to assess the contribution of termites to the ecosystem's CH₄ budget. Termite mound emission estimates were integrated with local termite mound density figures, yielding an estimate of 0.15–0.71 nmol CH₄ m² s⁻¹ emitted by termite mounds on average 15. In addition, the termite CH₄ emission factor from this investigation was merged with termite density numbers, yielding a termite-emitted CH₄ estimate of 1.0 nmol m² s⁻¹ (Van Asperen et al. 2021).

Methane is a greenhouse gas that contributes to global warming. Over the first 20 years after emission into the atmosphere, it is 80 times more powerful at heating the world than carbon dioxide. It indicates that the concentration in the atmosphere is increasing at an alarming rate, both naturally and intentionally from many sources. Climate change and climate chemistry have devastating effects on people (Black et al. 2021).

Carbon dioxide and methane concentrations in the atmosphere have increased from 350 to 410 ppm (28%) and 1100 to 1875 ppb (70%), respectively, since 1950. Methane is 28 times more potent as a greenhouse gas than carbon dioxide after 100 years and 80 times more potent after 10–20 years (Black et al. 2021). The balance between CH₄ generation and CH₄ oxidation after release determines CH₄ emissions by mound-building termites. Given that these insects' (termites') intestines include bacteria that oxidize CH₄ (methanotrophs), the CH₄ produced is immediately discharged into the environment. However, the bacteria present in the termite mound

material can act as a CH₄ sink by oxidizing these greenhouse gases (Oliveira et al. 2021).

The global warming potential of N₂O is 298 times greater than that of CO₂, implying that N₂O is approximately 88% more effective at retaining heat in the troposphere than CH₄, raising concerns about the potential for termite infestation of degraded soils and indicating the need for soil restoration (Quevedo et al. 2021).

Bacteria in soil feeding termites as biomedicine

In the biomedical sciences, antibiotics have been the primary source to fight against bacterial colonization, but the indiscriminate use of such medications has led to the development of antimicrobial resistance (AMR), which is currently one of the most serious threats in medicine (Patil et al. 2021). The low number of described genes at BactiBase or AnhyDeg indicates the potential of these termite nest microbial communities for being a source of novel genes that can be used in fighting antimicrobial resistance (Bacteriocins) (Fan et al. 2021).

Many termite species build nests and mounds out of soil material. Soils are generally sinks for atmospheric methane and harbor active methanotrophs, thus, termite mounds appear to be obvious sites for methane oxidation. Termite mound soil obtained in the environment. However, the extraction of termite mound soil significantly impacted various environmental purposes and also determined the various functional groups present in the selected soil. Recent studies of termite mound soil studies revealed that they proved various biomedical properties and applications (Farias et al. 2021).

The feeding habits of termites, as well as maybe some termite-active antimicrobial strategies, are creating a set of conditions that allow the growth of specific types of genera, which will carry out the required set of community functions, in this case, the metabolism of aromatic amino acids. Its study included terpene as a selective metabolite, which possesses antibacterial capabilities and is released by *Nasutitermes*, since both have been established in the literature. The defensive or protective component of feces was thoroughly examined (Cole et al. 2021).

Insect detoxification and antioxidant systems frequently work with the immune system, reducing the risk of toxins and ROS during host–pathogen interactions (Syazwan et al. 2021). Sawadogo et al. (2023) studied the isolation of bacteria from *M. bellicosus* termite mound material and the antibacterial activity of the isolates. The study emphasized antibacterial activity, which inhibits the growth of dangerous bacteria (*Bacillus subtilis*, *Escherichia coli*, *Micrococcus luteus*, *Pseudomonas aeruginosa*, and *Staphylococcus aureus*) and fungi (*Aspergillus niger* and *Candida albicans*).

Antibacterial activity

Termite mound soil extract has been shown to have significant antibacterial activity against a wide range of bacterial strains including clinically isolated multidrug-resistant pathogens. Gram-negative and gram-positive bacterial strains of *Escherichia coli*, *Pseudomonas*, *Bacillus subtilis*, and *Staphylococcus aureus* were examined against termite mound soil extract in this investigation (Aidoo et al. 2021). Bhadra et al. (2015) studied that used a hydrothermal technique to build nanoarrays on the surface of commercially pure grade-2 titanium surfaces that mimicked the dragonfly's surface. They tested the antibacterial effect of the modified surfaces on *Pseudomonas aeruginosa* and *Pseudomonas aureus* cells and showed that 50% of *Pseudomonas aeruginosa* and 20% of *S. aureus* cells were destroyed after contact with the surface.

Mahdi et al. (2020a) studied and isolated various antibacterial compounds from *Macrotermes bellicosus* soldier termites that inhibited Gram-positive *Staphylococcus aureus* bacteria as well as Gram-negative *E. coli* and *Pseudomonas aeruginosa*. As a result, more research is needed to determine the composition and diversity of antibacterial compounds obtained from termite mound-associated microorganisms.

Antifungal activity against termite mound soil

Normal termite activity involves stimulating immune genes to strengthen physiological defenses, which increases antifungal ability. The physiological defenses of termites were negatively impacted by miRNA dysregulation (Liu et al. 2015). Termite colonies typically contain 48 *Streptomyces* morphotypes, according to analysis of 3348 isolates from 20 nests in eight distinct locales; no morphotypes were shared between locations, and many isolates revealed broad-spectrum antifungal activity (Chouvenc et al. 2018).

The optimum antifungal activity was found in the termite mound soil and measured at 150 l. The DMSO extract of termite mound soil was found to inhibit *Candida albicans* (21 mm). According to Mahdi et al. (2020b), the termite mound soil was well-chosen and revealed considerable fungi-inhibitory capacity.

As a result, the termites' overall antifungal activity was a reliable sign of their physiological disease defenses. Recent research revealed that in addition to immunological genes, genes involved in carbohydrate metabolism and antioxidants have been shown to play a significant role in the antifungal activity of termites (Liu et al. 2020; Zhao et al. 2021).

Anti-inflammatory activity

The proportion of denaturation inhibition increased gradually as termite mound soil concentration rose.

The maximum denaturation inhibition of 28.39% was attained with a concentration of 500 g of termite mound soil (Azab et al. 2016). Termite mound soil was effective in preventing denaturation of the BSA protein at a concentration of at least 100 µg reported by (Karthick and Sheela 2023). The termite nests of *Nasutitermes* spp. and *Macrotermes* spp. are used for anti-inflammatory activity, while those of *Trinervitermes* spp. and *Nasutitermes* spp. are used to cure diarrhoea and fractures, and for their toning effect. The presence of xyloglucan, a hemicellulose in the wall of dicotyledons that shortens the frequency and length of diarrhea, in termite mounds may account for their medicinal properties (Ouango et al. 2022).

Bacteria in soil feeding termite as bioblocks/production of bricks

Even though previous studies revealed a significant improvement in strength, CTM concrete needs more water to reach a standard consistency, indicating that it has a preference for water. According to Claudia and Duna (2017) studied that termite mound material is pozzolanic and can be used in place of cement in concrete. The price of conventional building materials has risen gradually while the bulk of the population continues to live below the poverty line; as a result, these materials are now unaffordable. As a result, both rural and urban communities need to look for affordable, locally available environmentally friendly building materials that don't sacrifice quality (Toubal Seghir et al. 2020).

This encouraged mounds to use inexpensive supplies, like termite mound clay, in place of or in addition to more traditional ones. Due to their binding capabilities and the fact that termite mounds are rich in silica and alumina, the characteristics of termite mound soil make them appropriate as building materials (Jouquet et al. 2020).

Bricks also used in shaping lateritic bricks for construction purposes produce better results than using regular clay. Legese et al. 2021 found that their performances were superior to those of regular clay soil even while building storage facilities and stabilizing soil (Assam et al. 2016). Alabandan et al. (2016) reported that termite hill soils include clay, which is made up of inorganic minerals and water and is fire and combustible-resistant. The mounds are constructed in two levels, with the outer layer being porous to allow for optimal termite ventilation and the inner layer being dense and sturdy (Zachariah et al. 2020).

The current study uses termite construction methods as inspiration to develop a material for building organically cemented mound structures. The termite mound under investigation was constructed from a mixture of soil particles, termite saliva, and cellulase enzyme, which

breaks down cellulose into beta-glucose or shorter polysaccharides and oligosaccharides. There is a need to look for alternative materials that will have less of an impact on the environment because the world is experiencing massive pollution during the processes of producing materials, and building, and demolishing buildings (Sangaet al. 2022). The application of response surfaces methodology (RSM) to improve the incorporation of calcined termite mound material into mortar and concrete. The amount of calcined termite mound material used as cement replacement in mortar and concrete ranged from 5 to 15%, with 5% intervals (Konitufe et al. 2023).

The construction industries will benefit from alternative replacements for conventional buildings and construction materials, which present environmental problems. The natural termite mound clay was obtained, calcined, and ground to a 75-mm fineness. Calcined Termite Mound (CTM) was used in various concrete mixes to partially replace Ordinary Portland cement, with a range of 0 to 25% replacement at a step size of 5%, and recycled concrete aggregates (RCA) were also used to partially replace coarse natural aggregate (NA), with replacement rates of 20%, 40%, 60%, 80%, and 100% by weight.

Bacteria in soil feeding termites as biocontrol and biofertilizer

Microbial inoculants have recently been used as an environmentally friendly method of reducing or combating plant diseases (Ayitso et al. 2015). According to Menichetti et al. (2014), studied that the daily activities of termites that feed on litter are the primary driving element in the circulation of nutrients in soil occupied by them. Furthermore, *Bacillus* spp., *Citrobacter freundii*, *Azotobacter chroococcum*, and *Pseudomonas aeruginosa* solubilized phosphate, phosphorus, and IAA, which adds to their suitability as agricultural biocontrol agents. Plants respond to their environment via hormones such as ethylene, gibberellin, cytokines, auxins, and abscisic acid. Plant growth-promoting rhizobacteria are bacteria in the rhizosphere that have a major influence on plant physiology (Alori et al. 2017).

Curcuma longa L. rhizome rot diseases were reduced when three strains of these bacteria were used. Antifungal activity was also demonstrated by *Staphylococcus saprophyticus* and *Bacillus methylotrophicus* isolated from termite mounds against *Fusarium oxysporum*, *Alternaria brassicae*, *Rhizoctonia solani*, *Sclerotium rolfsii*, and *Colletotrichum truncatum* (Devi and Thakur 2018). Bacterial diversity in the rhizosphere can protect plants from infections and promote tolerance to abiotic stresses, plant growth promotion, biocontrol, biofertilizer, and yield (Meena et al. 2014; Li et al. 2020).

Reduced radial growth of the test fungus (*F. oxysporum*) showed termitarium biocontrol activity. Among the 57 plant growth-promoting isolates, three showed the potential to suppress *Fusarium oxysporum*. *Bacillus* sp. (56.1%) from household down-layer termite mound soil demonstrated the highest P.I. driven by diffusible compound secretion, while *Azotobacter chroococcum* from household down-layer termite mound soil revealed the lowest biocontrol activity on *Fusarium oxysporum* 46.0% (Adebajo et al. 2021).

A key component of biological control is the use of RNAi when combined with Entomopathogens. Termites' innate and social immunity makes them resistant to most diseases, and using RNAi technology to decrease this immunity in conjunction with entomopathogens may be beneficial for biological control. Termicin silencing in *O. formosanus* termites using RNAi elevated SM1 toxicity considerably (Feng et al. 2022).

Because of the nutrient richness of termite mound soil, small-scale farmers frequently use it to improve the soil quality of their farmland, believing that it will increase crop yield (Deke et al. 2016). As a result, examining bacteria with these distinct genes in the soil population of bacteria can lead to the identification of novel secondary metabolic features that can be exploited as biofertilizers in soils and plants to boost resistance to pathogenic attacks. Previous studies have shown the diversity and abundance of genes associated with antibiotic resistance (Wang et al. 2013; Enagbonma and Babalola 2020).

During the growing stage of sunflowers, major bacterial phyla were detected in the rhizosphere and bulk soil. The attraction of these bacterial phyla to form a community within the rhizosphere could explain their presence. Most of the bacterial phyla determined in the rhizosphere of sunflower, soybean, wheat, and maize were previously identified (Alawiye and Babalola 2021; Igiehon et al. 2021). To identify potential biocontrol candidates for the management of enigmatic feeding pests such as termites, the potential of different indigenous Entomopathogenic Nematodes (EPN) species, as well as their optimal dosages and application times, requires further elucidation in both laboratory and field experiments (Aslam et al. 2023).

Bacteria in soil feed termites in improving plant growth promoting

Some bacteria isolated from termite mound soils with numerous plant growth-promoting activities, such as *Achromobacter*, *Agrobacterium*, *Azotobacter*, *Bacillus*, *Burkholderia*, *Flavobacterium*, *Micrococcus*, *Pseudomonas*, *Rhizobium*, can aid in plant production tailoring by inducing nutrient uptake, plant growth, and yield via a variety of mechanisms (Istina et al. 2015).

Devi and Thakur (2018) reported that during laboratory tests, 21 isolates from the genera *Bacillus* and *Alcaligenes* produced 0.6–47.56 g/mL of indole acetic acid, 12 isolates produced 9.27–65.48% SU of *Siderophores*, and 13 isolates produced ammonia in peptone broth and showed HCN production. It is essential to use modern approaches to uncover novel genes that encode significant metabolic pathways with several vital functions important for plant development and sustainable agriculture (Klimek et al. 2016; Kumar and Dubey 2020).

Reports on plant growth-promoting bacteria associated with sunflower plants for better productivity are rare in South Africa, possibly due to few investigations on sunflower plants employing next-generation sequencing techniques. As a result, it is critical to identify bacterial community structures in sunflower rhizosphere soils using the 16S rRNA gene and their related predictive functions (Yadav et al. 2017; Lu et al. 2020). The dominance of the bacterial community in LTR over other samples may reflect the agricultural relevance of this bacterial family, whereas the main bacterial community in the KRPR site is key plant growth-promoting bacteria. Similarly, the majority of these families have previously been demonstrated to positively promote sunflower growth (Tseng et al. 2021; Majeed et al. 2018).

Determining the physicochemical parameters of anthill and termite mound soils and their combinations with conventional topsoil, as well as assessing their effects on aubergine and okra germination, growth, and yield performance under screen house conditions. In comparison to the control, aubergine and okra grown on anthill and termite mound soils, as well as their combinations with regular top soils, had higher fresh whole plant and root biomass (Turay et al. 2022).

Antagonism using diffusible substance technique and antagonistic activity of cell-free culture filtrate of bacterial isolates against *Ralstonia solanacearum* and *Fusarium oxysporum* were used to test the activities of plant growth-promoting bacteria. From the 27 soil samples, 200 bacterial isolates were recovered. *Bacillus* spp. was the most common isolate. Of the 200 bacterial isolates tested, 57 passed the phosphate solubilization, potassium solubilization, and indole acetic acid production tests. Six of the 57 isolates displayed antagonistic activity against *Fusarium oxysporum*, while 7 isolates antagonized *Ralstonia solanacearum* (Adebajo et al. 2021).

Future trends of termite mounds

To illustrate a hypothesis that the high nutrient concentrations in termite mound soils influence a complex diversity of microorganisms, the compositional and

diversity of bacteria in termite mound soils were compared to the surrounding soils. This review used shotgun sequencing to discover that *Proteobacteria* and *Actinobacteria* significantly predominated the soils found in termite mounds and the surrounding soils, respectively. *Tenericutes*, *Bergeyella*, *Gloeotheca*, *Thalassospira*, and *Glaciecola* were found to be unique to the soils found in termite mounds (Enagbonma et al. 2020).

The current understanding of the bacterial communities in the guts of some higher termite species from the *Syntermitinae*, *Apicotermitinae*, *Termitidae*, and *Nasutitermitinae* subfamilies had previously received little research. Bacterial 16S rRNA gene amplicons were sequenced at high throughput, yielding 4,086,163 reads that were then filtered to 10,000 reads per library and assigned to 8069 bacterial OTUs defined at 97% sequence similarity (Marynowska et al. 2020).

Victorica et al. (2020) studied the metagenomic analysis of bacterial gut microbiota of two higher termites, *Cortaritermes fulviceps* and *Nasutitermes aquilinus*. Both termite species accommodated *Spirochaetes*, *Bacillota*, *Proteobacteria*, *Fibrobacteres*, and *Bacteroidetes* as abundant bacterial phyla. *Spirochaetes* were found to be the predominant (47%) bacterial phyla in both the termite species. Additionally, mound builders termite gut bacteria have a sixfold better capacity for nitrate reduction than soil bacteria, indicating that they may flip between aerobic and anaerobic respiration to adjust to changes in oxygen supply (Chiri et al. 2021).

The bacterium uses a full pmoCAB operon to encode a particulate methane monooxygenase. The bacteria can also use the serine cycle and the H4MPT pathway to consume carbon generated from CH₄, and it can conserve energy by utilizing two terminal oxidases for aerobic respiration. Other recently sequenced USC bacteria have these fundamental metabolic characteristics (Pratscher et al. 2018; Tveit et al. 2019). The potential of termite gut microbiota for the biomethanation of lignocellulosic biomass can be further demonstrated with improved knowledge of termites and their related symbionts. Additional details will emerge as omics technology improves, which will also help us better understand one of the most effective natural lignocellulosic biomass utilization systems (Bhujbal et al. 2021).

The nutrient cycle and other ecological processes can be modified by termite population structure and activity density. However, it is still uncertain how termites are distributed spatially and how densely they are active in tropical woods. In a 1-ha (100 m 100 m) plot; it examined the geographical distribution patterns of the termite feeding groups and species, their co-occurrence pattern, and their correlation with the environmental parameters (Thant et al. 2023).

Termite-associated bacteria are an important source for the identification of new antibiotics with a variety of 'one health' applications. Termite mound communities have antibiotic resistance genes as well, which is probably due to bacteria and fungi eliminating each other. Nevertheless, despite the large concentrations of natural products and biosynthetic gene clusters seen, mounds are said to have lower amounts of antibiotic-resistance genes than the nearby soils (Yan et al. 2021).

Van Thuyne and Verrecchia's (2021) reported that no conclusive findings can be made about the impact of termite activity on mound stability. The worker and soldier castes' morphological characteristics that were related to the insect's overall size showed the largest percentages of coefficient of variation. As a result, they are less useful for determining how termites respond functionally to coverage changes. The unique microbial communities found in the live termite mounds are intermediate in abundance between the top and deep soils surrounding them, and they have a greater F: B ratio than those soils do. The termites' redistribution of organic resources or subsequent changes in the physiochemical characteristics (water content, pH, and EC) may have an effect on the microbial populations in the mounds (Chen et al. 2023).

An integrative multi-omics approach for the first time at the holobiont level to study the highly compartmentalized gut system of the soil-feeding higher termite *Labiotermes labralis*. It relied on 16S rRNA gene community profiling, metagenomics and (meta) transcriptomics to uncover the distribution of functional roles, in particular those related to carbohydrate hydrolysis, across different gut compartments and among the members of the bacterial community *Bacillota* phylum, whose abundance gradually decreased towards the posterior segments of the hindgut, in favor of *Bacteroidetes*, *Proteobacteria* and *Verrucomicrobia* the host itself (Marynowska et al. 2023).

Although nest material is a byproduct of termite feces and the surrounding soil, the stratification indicated by the bacterial and fungal taxonomical profiles is likely explained by diet and phylogenetic relatedness. Even the differences between soil-feeding termites' nests from both African sites were minor studied; however, the bacterial and fungal taxonomical identities point towards a stratification mainly owed to diet and phylogenetic relatedness, which is potentially explained since nest material is a product of termite feces and surrounding soil (González Plaza and Hradecký 2023).

With 16S rRNA gene sequencing, Nwachukwu et al. (2023) studied that on the functions of various rhizospheric bacterial communities in the promotion of plant growth and health providing potential for improving efficient and environmentally friendly techniques for increasing agricultural yield by manipulating

microorganisms. Between the rhizosphere and bulk soil at each site, there were differences in the dominant bacterial groups.

Conclusion

It is crucial for sustaining the need for a more green economy to feed, shelter, and lifestyle the world's booming human population without affecting the environment or the public's health. Alternative safe solutions are required due to the significant health and environmental issues caused by the use of greenhouse gases (particularly methane emissions), high diseases high costs of medicine, chemical fertilizers, and pesticides, and the high cost of building materials and quality of construction globally. Therefore, this review focused on the use of soil-feeding termites of mound builder and their bacterial guts to reduce methane gas emission, biomedicine, made bio block (improve the effectiveness of bio-bricks and brick produce), biocontrol and biofertilizer and boost plant growth promoting in various fields. Harnessing soil-feeding termites for potential regulatory mechanisms of bacterial diversity involved in significant growth of the environmental quality is essential for the success of the future. Because there are so many different bacteria, it is used that efforts be made to study the novel groups of bacterial diversity in soil-feeding termites of mound/nests. By attempting so, it may be possible to identify different bacteria that have the potential to be used in biotechnological and/or industrial applications.

Abbreviations

AMR	Antimicrobial resistance
CTM	Calcined termite mound
NCF	National Center of Floristic
GNBP2	Gram-negative binding protein 2
PET	Poly(ethylene terephthalate)
RSM	Response surfaces methodology
EPNa	Entomo pathogenic Nematodes

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