



Mini Review

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# Termite Holobiont: Microbe Matters



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## Mini Review

And its been not much surprise that the prokaryotes have close alliance with eukaryotes because it apparently evolved from them [1]. Myriad microbial niches in nature forms exceptional microbial communities due to their interaction with habitats [2]. It led to a tremendous diversity of prokaryotes which essentially dominate and exploit all available microenvironments. Co-evolution partnership among animal-microbe partnership is ubiquitous from immunity, behavior, fitness, metabolism host development, speciation, circadian regulation and evolution. Lynn Margulis coined the term "holobiont" a combination of host, its microbiota and biotope [3].

The insect colon is one such niche contributes delineated habitats comprising a battery of intrinsic microorganisms. Termite (Isoptera) gut harbors strong affiliation towards the dense assemblage of complex microorganisms which assists in host digestion. Enigma towards understanding the intricacies about holobiont concept has been a major focus in the two decades [4]. These novel arthropods are the most efficient lignocellulosic degraders when compared to all other organisms. They are posterity of *Cryptocercus*, a wood-feeding cockroach and both are considered as a well-established lineage of insects.

The former is broadly categorized into two groups, lower and higher termites [5]. The lower termites have an unique symbiosis with cellular flagellates (protists) along with gut bacteria [6]. The higher termites the most prevalent termite families which are diversified over 85% of total genera. They lack eukaryote symbionts (protists) and their gut bacteria aid them in digestion while fungus outside. Apart from symbiotic relationship with gut microbiota the higher termites have an additional role of cultivating the *Termitomyces* fungi (class: Basidiomycete) in their abode for their nutritional fulfilment and lignocellulose degradation. It has unique feeding habits drives in shaping the phylogeny of peculiar gut microbial communities which outshines the other wood-feeding species [7]. Termite gut acts as an efficient bioreactor where the microbes aid in assimilation of

lingo cellulosic materials, converting into monosaccharides. The metabolic collaboration and co-evolution between the microbes and its host is still unclear. The phylogenetic diversity of the intestinal microbes was analyzed for 16S/18S rRNA sequences through traditional cultivation approaches. But it is often fail to acquire ecologically relevant organisms, either due to lack of appropriate cultivation technique or lack of expertise in formulating new media for growing recalcitrant microorganisms (Figure 1).

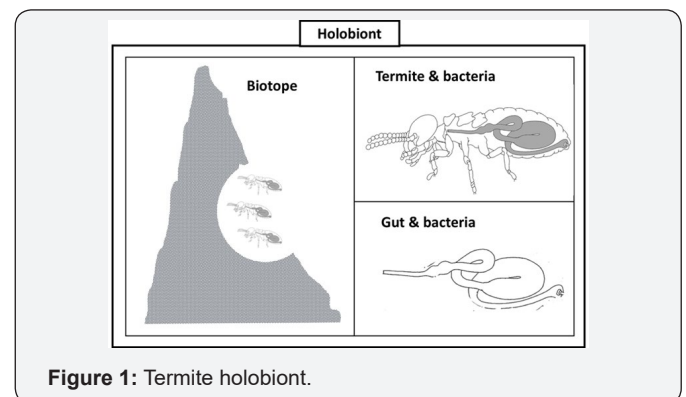


Figure 1: Termite holobiont.

Nowadays, High-throughput technologies are used towards the identification of microbial population through Illumina platform [8], Roche 454 pyrosequencing [9] and ion torrent [10]. Thus, the next generation sequencing technologies made evident on the guild between population dynamics within the termite gut. With sufficient sampling, in-depth sequencing highlights the pattern of different microbial lineages between the host species and their microhabitats. Further extending -omics studies will facilitate the mystery of intertwined invisible residents and their role in the digestion process of different feeding guilds. Conclusively, more commercial enzymes have been raised for successful degradation of lignocellulosic materials hitherto no such viable enzyme is cost effective. In this context, finding a promising model for the industrial conversion of lignocellulose to biofuels will shed light on these simple creatures and further considering as biological treasure trove.

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