

Termites evolved complex bioreactors 30 million years ago

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A termite soldier overlooking the fungus farm. Credit: Saria Otani

Achieving complete breakdown of plant biomass for energy conversion in industrialized bioreactors remains a complex challenge, but new research shows that termite fungus farmers solved this problem more than 30 million years ago. The new insight reveals that the great success of termite farmers as plant decomposers is due to division of labor between a fungus breaking down complex plant components and gut bacteria contributing enzymes for final digestion.

Sophisticated Management in Termite Fungus Farms

Fungus-farming termites are dominant plant decomposers in (sub)tropical Sub-Saharan Africa and Southeast Asia, where they in some areas decompose up to 90% of all dead [plant material](#). They achieve near-complete plant [decomposition](#) through intricate multi-stage cooperation between the *Termitomyces* fungi and [gut](#) bacteria, with the termites managing these symbionts by providing gut compartments and nest infrastructure. Researchers at the Centre for Social Evolution, Department of Biology, University of Copenhagen and Beijing Genomics Institute (BGI, China) discovered this by analyzing plant decomposition genes in the first genome sequencing of a [fungus](#)-farming termite and its fungal crop, and bacterial gut communities.

Termites manage their fungus farm in a highly structured way. Older termite workers collect plant material and bring it to the nest. Younger workers eat the plant material together with *Termitomyces* fungal spores, and this plant-spore mix is defecated as a new layer of fungus garden. Within the garden, *Termitomyces* rapidly grows on the plant substrate until it is utilized, after which older termites consume the fungus garden. By then, nearly all organic matter has been broken down.

"While we have so far focused on the fungus that feeds the termites, it is now clear that termite gut bacteria play a major role in giving the symbiosis its high efficiency", says Associate Professor Michael

Poulsen, who spearheaded the work. "But it took a massive effort of sequencing the genome of the termite itself, its fungus, and several gut metagenomics to analyze the enzymes involved in plant decomposition", adds Assistant Professor Guojie Zhang, who made the [genome sequencing](#) happen at BGI Shenzhen.



A termite queen, king and workers. Credit: Saria Otani

A Symbiotic Community Optimized for Efficient Plant Decomposition

A remarkable 86% of all the glycoside hydrolase enzyme families known from living organisms were present in the farming symbiosis. The fungus coded for enzymes needed to handle complex carbohydrates, while gut microbes contributed enzymes for the final digestion of oligosaccharides. The first gut passage, thus, mainly serves to inoculate the plant substrate with fungal spores, while [gut bacteria](#) play a prominent digestive role during second gut passage.

Termite colonies are founded by a single queen and king that disperse by air, but lose their wings when locking themselves up for life in an underground royal chamber. As the colony grows, the queen swells up to gigantic proportions and becomes an egg-laying machine.

The royal pair may survive for decades and maintain a very large colony of short-lived workers and soldiers, who take care of all colony duties. The metagenomic analyses of the queen gut showed that it contained a highly simplified bacterial community lacking plant decomposition enzymes. This suggests that the royal pair is exempt from decomposition duties and receives a high-quality fungal diet from their workers.

More information: Complementary symbiont contributions to plant decomposition in a fungus-farming termite. *Proceedings of the National Academy of Sciences*, 2014. www.pnas.org/content/early/2014/10/01/1319718111.abstract

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