

OR211*The functional implications of Termitomyces domestication on fungus-growing termite gut microbiomes***Michael Poulsen**, Haofu Hu, Cai Li, Saria Otani, Duur Aanen, Jacobus Boomsma, Guojie Zhang

Approximately 30 MYA, the ancestors of the higher termite sub-family Macrotermitinae and the basidiomycete fungus *Termitomyces* joined forces in what was to become one of the most sophisticated plant biomass decomposition symbioses on Earth. At that time, the termites had already lost their Protist gut symbionts and replaced them with bacteria, but the degree to which the innovation of fungiculture induced a functional shift in the gut microbiota has remained unclear. We used 16S pyrosequencing to describe the community composition of the core gut microbiota associated with the Macrotermitinae and offer the first metagenomic insight into the functional roles of these gut communities. Focusing on the carbohydrate-active enzymes (CAZymes) encoded by *Termitomyces* and gut microbes in *Macrotermes natalensis*, we show that the gut bacteria primarily contribute enzymes for the final digestion of simple polysaccharides after *Termitomyces* has degraded the more complex carbohydrates. We also provide the first comparative analysis of the enzymatic potential of gut microbiota for decomposing fungal cell walls in *Macrotermes natalensis* and *Odontotermes yunnanensis*. Despite belonging to different termite genera and occurring on different continents, the gut communities had remarkably similar enzyme profiles for this function. The bacterial genera making these enzymes are consistently over-represented in fungus-growing termites relative to other higher termites that have a higher preponderance of cellulolytic bacteria. The shift in gut metagenome function after *Termitomyces* domestication thus appears to involve both complementary division of labor and targeted digestion of the novel food offered by *Termitomyces*.