

Complete genomes of uncultured bacterial endosymbionts of cellulolytic protists in the gut of termites

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A metagenome approach is beneficial for grasping functions of the microbial community as a whole, but usually very difficult to know the activities of its individual constituents. The genome analysis of a targeting single species in the community is preferable particularly in order to understand its precise function and interaction with another. The microbial community in the gut of termites comprises both cellulolytic flagellated protists and diverse prokaryotes, which are responsible for the efficient degradation of recalcitrant lignocellulose. The complex nature of the community and formidable unculturability of the most members have hampered detailed microbial studies. Comprehensive phylogenetic and in situ identifications of the community members based on culture-independent analyses of rRNA gene sequences reveal that the community is highly structured but conserved within a termite species. Nevertheless, these studies still provide little information about their functions because the community contained enormous novel microbial diversity. A prominent feature of the community is the species-specific associations of a variety of bacterial species with the cells of gut flagellates as endosymbionts in the cytoplasm and/or ectosymbionts on the cell surface. The voluminous cellulolytic flagellates and their endosymbionts, ones of the most abundant bacteria of the community, likely play central roles in the gut metabolisms. The complete genome sequences of the two species of the endosymbionts determined after whole genome amplifications starting from small amounts of the manually isolated cells reveal their functions, symbiotic interactions, and adaptative evolution. The metabolic functions of the host flagellates are investigated through the meta-EST (Expressed Sequence Tags) analysis. These advances have gradually unveiled how this symbiotic complex functions to efficiently utilize lignocellulose.