

OR214*Cellulose catabolism in the gut of the termite, Hodotermopsis sjostedti***Gaku Tokuda, Jun Kikuchi**

Increasing evidence for the presence of endogenous cellulase genes in many invertebrates has raised intriguing questions on the mechanisms by which they digest cellulose and the role played by gut symbionts in their metabolism. Although DNA- and RNA-based approaches have provided important insights in recent decades, we are still far from a comprehensive understanding of in situ digestive processes of these invertebrates. In this talk, we present the first comprehensive metabolomic investigation of ¹³C-labeled cellulose digestion in a termite. Two-dimensional nuclear magnetic resonance analyses of the gut extract resolve 256 signals, which are assigned to 46 known metabolites. Temporal and spatial variations of these signals along the gut segments provide the first direct evidence for immediate cellulose breakdown by endogenous cellulases in insects, and the previously neglected contribution of hindgut bacteria, which we show phosphorylate cellodextrins or cellobiose. Temporal ordination analyses of the metabolites along the gut segments show that essential amino acid acquisition by termites is most likely occurring via digestion of microbes. Soil-burrowing behavior contributed to accumulation of amino acids and essential minor minerals, providing firm evidence for the nutritional importance of soil to these insects. These findings provide the first comprehensive metabolic network analysis of an insect gut and reveal the temporal transitions of cellulose-derived catabolites along the gut and with respect to the intestinal cellulolytic symbiosis. Our techniques with ¹³C-labeled cellulose should be applicable to diverse xylophagous insects to understand their digestive processes and will greatly contribute to shedding light on the complex metabolic networks in symbioses.