

Studies on extracellular polysaccharide matrix and metabolites produced by selective white rot fungus

**(Graduate School of Agriculture,
Laboratory of Biomass Conversion, RISH, Kyoto University)**

Daisuke Suzuki

Wood biomass conversion has been receiving a great deal of attention as one of measures to solve the environmental problems caused by excessive use of fossil fuels. To convert wood biomass by enzymatic saccharification and fermentation, degradation of lignin network is necessary because cell wall polysaccharides are covered with lignin in lignified plant cell walls. One potential approach to degrade lignin prior to the saccharification and fermentation is to use ligninolytic systems of white rot fungi. Among the numerous fungi so far isolated, a white rot fungus, *Ceriporiopsis subvermispota* is characterized as one of the best biopulping fungi that degrade lignin without intensive damage of cellulose. Previous studies revealed that the selective ligninolysis by this fungus is catalyzed by low molecular mass compounds at a site far from extracellular enzymes and fungal hyphae. To elucidate the molecular mechanism of the selective ligninolysis by this fungus, the author focused on functions of fungal sheath (extracellular polysaccharide matrix) interfacing the wood and hyphae, and analyzed structures of the sheath and metabolites trapped in the polysaccharide matrix.

C. subvermispota was cultivated on beech wood specimens placed on PDA. The decayed specimens were fixed by rapid freezing, followed by the treatment with 2 % osmium tetroxide. The wood specimens were stained with uranium acetate/lead citrate, and then subjected to observation by transmission electron microscopy (TEM). For the chemical analysis of sheath, *C. subvermispota* was cultured in a SDW medium at 28°C for 4 weeks. Then, the culture was separated into sheath and fungal body by filtration. The filtrate was dialyzed and then lyophilized. Chemical structure and molecular weight distribution of the sheath were analyzed by MALDI-TOF-MS, GPC, NMR, methylation by Hakomori's method and determination of neutral sugar composition. Metabolites involved in the sheath were analyzed by ESI-LCMS. These microscopic and chemical analyses revealed unique structural features of the sheath and sheath-inherent metabolites produced by *C. subvermispota*.