

**Characterization of lipid-biosynthetic genes from a lignin-degrading fungus,
*Ceriporiopsis subvermispora***

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A selective white rot fungus, *Ceriporiopsis subvermispora* selectively degrades lignin in wood with minimum damage of cellulose. So far, we have analyzed functions and biosynthesis of lipid-related metabolites, which may play a key role in the lignin degradation of *C. subvermispora*. In this study, in order to clarify the lipid metabolism involved in the selective lignin degradation, we have cloned two genes encoding long acyl-CoA synthetases (*Cs*-ACSLs), which esterify long-chain fatty acid to long acyl-CoA in the key step of fatty acid utilization. These *Cs*-ACSLs have two functional domains characteristic of other already-known ACSLs, but no transmembrane domains. Although the *Cs*-ACSLs are phylogenetically similar to some ACSLs derived from basidiomycetes, there is an evolutionary distance between *Cs*-ACSLs and ACSLs derived from a lignin-degrader, *Phanerochaete chrysosporium*. Furthermore, we heterogeneously overexpressed *Cs*-ACSLs in *Escherichia coli* and purified them as His-tagged fusion proteins. On the other hand, a *Cs*-ACSL-gene was inducibly transcribed when *C. subvermispora* was grown on medium supplemented with a lignin fragment and at low temperatures. This induction pattern was partially similar to that of other genes involved in the fatty acid synthesis.