

**Characterization of genes involved in the lignin degradation  
from a new white-rot fungus, *Phellinus* sp. SKM2102**

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The production of ethanol from lignocellulosics has received much attention due to immense potential for conversion of renewable biomaterials into biofuels and chemicals. Since lignin makes the access of cellulolytic enzymes to cellulose difficult, it is necessary to decompose the network of lignin prior to the enzymatic hydrolysis. Recently, we have isolated a new white-rot fungus which has been characterized as the best fungus for the pretreatments of enzymatic saccharification of Japanese cedar wood. The fungus, designated *Phellinus* sp. SKM2102, exhibits high pretreatment effects for enzymatic saccharification of wood similar to those of a selective lignin-degrading fungus, *Ceriporiopsis subvermispota* [1]. The former exhibits less weight decrease in holocellulose than the latter. However, profiles of their metabolites, such as fatty acids, are different, reflecting the differences in gene expression involved in the fatty acid metabolism of these strains. Therefore, we focus on the fatty acid metabolism, especially the biosynthesis of unsaturated fatty acids because unsaturated fatty acids are precursors of lipid peroxidation in the selective lignin degradation by *C. subvermispota* [2]. On the other hand, we have found that strain SKM2102 possesses activities of ligninolytic enzymes, such as laccase and manganese peroxidase [3]. In order to establish basic understandings of the lignin-degrading system, we cloned fatty acid desaturase, laccase and manganese peroxidase genes from *Phellinus* sp. SKM2102 by PCR-based method.

REFERENCES

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