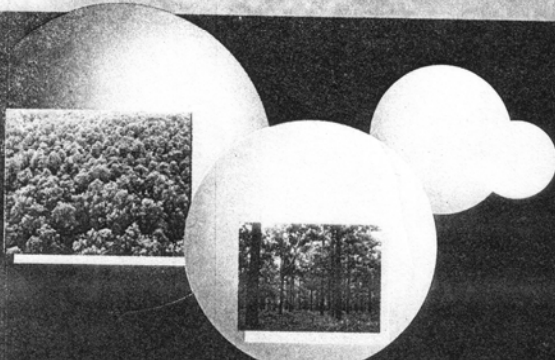
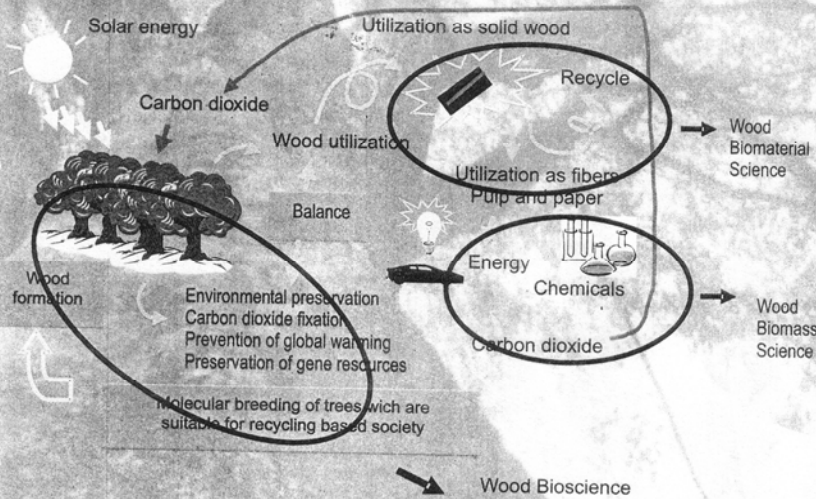


# Towards Ecology and Economy Harmonization of Tropical Forest Resources

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## Characterization of cDNA *FPICL1* Encoding Isocitrate Lyase from Wood-rotting Basidiomycete *Fomitopsis palustris*

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### Introduction

The brown-rot fungus *Fomitopsis palustris* acquires biochemical energy for vegetative growth by oxalate fermentation, in which isocitrate lyase (ICL, EC 4.1.3.1) constitutively replenishes the intermediates, glyoxylate and succinate to glyoxylate and short-cut TCA cycles, respectively. This role of *F. palustris* ICL is sharply distinct from the general function of ICLs that are important only in gluconeogenesis in microorganisms grown on C<sub>2</sub> compounds. Previously we purified and characterized ICL from *F. palustris*. The purified ICL is termed as FPICL1 in this study. We report here the characterization of cDNA (*FPICL1*) encoding FPICL1.

### Results and Discussion

We have determined sequence of cDNA (*FPICL1*) consisting of 1780 bp, corresponding to 539 amino acid residues encoding FPICL1. The predicted amino acid sequence was compared to ICLs of *Phanerochaete chrysosporium*, *Coprinus cinereus*, *A. nidulans*, *S. cerevisiae* revealing 83%, 79%, 63%, and 54% identity, respectively. The motif K39, R40, G41, T42 is a putative cAMP-dependent protein kinase phosphorylation site for the T residue and is found in acu7 of *C. cinereus*, and ICLs of *S. cerevisiae* and *Candida tropicalis*. Especially, ICL1 of *S. cerevisiae* has been proposed to be phosphorylated followed by inactivated in the presence of glucose. However, the motif KRGT in FPICL1 may not play the same role as that of *S. cerevisiae*, because no similar glucose repression was observed for FPICL1 in *F. palustris*. Thus, the role of the motif KRGT in FPICL1 is remaining to be elucidated. The carboxy terminal amino acids S-K-L, representing a peroxisomal targeting signal (PTS1), suggest a peroxisomal localization of FPICL1 in *F. palustris*.