

## Abstract of thesis

Thesis title Characterization of *Pleurotus ostreatus* mutants defective in lignin degradation using reverse genetic and comparative transcriptomic analyses  
(逆遺伝学および比較トランスクリプトーム解析を用いたヒラタケリグニン分解不全変異株の特性評価)

ウー ホンリー

Name WU HONGLI

White-rot fungi efficiently degrade lignin and thus play a pivotal role in the global carbon cycle. However, molecular mechanisms underlying the transcriptional regulation of lignocellulolytic genes are largely unknown. *Pleurotus ostreatus* is one of the white-rot fungi frequently used in molecular genetics and genomic studies because various molecular genetic tools and well-annotated genome databases are available. In previous studies, mutations in four genes, namely *wtr1*, *chd1*, *pex1*, and *gat1*, were shown to abrogate wood lignin-degrading ability in *P. ostreatus* on beech wood sawdust medium (BWS). Here, comparative transcriptional analyses of these mutants on BWS was conducted. Using RNA-seq and bioinformatics analysis, intriguing transcriptional shifts were observed that putative ligninolytic genes highly expressed in parental strains were significantly downregulated in the mutant strains, whereas, many putative cellulolytic and xylanolytic genes were upregulated. Furthermore, the author newly identified a mutation in the gene *hir1* which encodes putative histone chaperone complex, caused remarkably reduction of the lignin-degrading ability. This is the first study of HIRA homologous protein in Agaricomycetes, turning out to be a modifier to affect ligninolytic, cellulolytic, and xylanolytic system in *P. ostreatus*. Moreover, rice straw substrate was applied to reveal that these transcriptional shifts are not substrate-dependent but regulation patterns on different substrates are distinct. This study is the first work in Basidiomycetes elucidating the transcriptional alterations in ligninolysis-deficient mutants, which will not only facilitate the utilization of this species in various industrial processes, but also contribute to studying ligninolytic regulation mechanisms common in white-rot fungi.