

Isolation and Sequencing of the cDNA Encoding β -tubulin from *Pleurotus sajor-caju*

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여름느타리버섯으로부터 β -tubulin cDNA의 분리 및 염기서열 결정

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ABSTRACT: The cDNA encoding β -tubulin of *Pleurotus sajor-caju* was isolated using an internal gene segment probe amplified by polymerase chain reaction (PCR) of genomic DNA and by cDNA library screening. The cDNA was consisted of 1560 nucleotides(nt), including a 5'-untranslation region (UTR) of 27nt, an open reading frame (ORF) of 1341nt, and a 3'-UTR of 191nt. The ORF encoded a protein of 446 amino acids(aa), which shows over 80% homology with β -tubulins of other filamentous fungi. Southern hybridization analysis showed that there were two isotypes of β -tubulin genes in *P. sajor-caju*. Through sequence analysis we found that β -tubulin had a unusual Cys¹⁶⁵ residue, which might be a significant factor for the insensitivity of fungi to fungicide benomyl.

KEYWORDS: Basidiomycetes, Benomyl resistance, *Pleurotus sajor-caju*, β -tubulin

Microtubules are basic elements of cytoskeleton and they take part in essential cellular functions such as cell division, motility, and transport. Consequently, their protein components are abundant and present in all eukaryotic cells. Tubulin, a heterodimer formed by two different subunits, α and β , is the major constituents of microtubules. Comparison of full length amino acid sequences indicates that β -tubulins are highly conserved polypeptides in all eukaryotic organisms (Hepler and Palevitz, 1974; Cleveland and Sullivan, 1985; Fosket, 1992; Alberts *et al.*, 1994).

In fungi the cloning and characterization of β -tubulin genes have been widely reported in

ascomycetes, deuteromycetes and yeasts but no β -tubulin genes have yet been reported in edible mushrooms (Orbach *et al.*, 1986; May *et al.*, 1987; Russo *et al.*, 1992).

Fungicide benomyl interferes with mitosis in fungi by binding to tubulin (Fujimura *et al.*, 1994). Molecular characterization of benomyl resistant mutants in *Aspergillus nidulance*, *Neurospora crassa* and *Saccharomyces cerevisiae* provides evidences that benomyl resistance is due to point mutations of β -tubulin and common mutation sites are known (Orbach *et al.*, 1986; Koenraadt *et al.*, 1992; Fujimura *et al.*, 1994). In many fungi, benomyl resistance has been used as a dominant selection marker in genetic transformation. The development of genetic transformation system in edible mushroom, *Pleu-*

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rotus species is necessary for breeding and molecular biology studies (Henson *et al.*, 1988; Bernier *et al.*, 1989; Seip *et al.*, 1990; Cooley *et al.*, 1991; Nowak and Kuck, 1994). We started a program of cloning and sequencing the β -tubulin gene of *P. sajor-caju* in order to develop the benomyl resistant β -tubulin *in vitro*. The benomyl resistant β -tubulin can be used as selection marker for vector.

In the present paper, we report the full sequences of the cDNA encoding β -tubulin in *P. sajor-caju* and comparison with those of other fungi and benomyl resistant β -tubulin.

Materials and Methods

Enzymes and Chemicals

Restriction enzymes and modifying enzymes were obtained from Promega and used as recommended by supplier. [α - 35 S]dATP and [α - 32 P]dCTP were purchased from Amersham. The sequencing kit was purchased from USBiochemical, USA. Other chemicals were purchased from the Sigma Chemical Co.

Strains and media

The *P. sajor-caju* (MGL 2084) stocked at National Institute of Agricultural Science and Technology was grown in mushroom complete medium at 30°C (MCM; Bennett and Lasure, 1991). The *E. coli* strain was XL 1Blue MRF^r.

cDNA library construction

Total RNA was isolated from submerged-grown mycelia by the method using Cesium Chloride (Ullrich *et al.*, 1977). Polyadenylate-containing [poly(A)+] RNA was isolated from total RNA using poly(A)Quik mRNA isolation kit (Stratagene) and cDNA library was constructed using ZAPII cDNA synthesis kit (Stratagene) and Gigapack II kit (Stratagene). The kits were used as recommended by supplier.

Polymerase chain reaction

PCR amplification of *P. sajor-caju* genomic DNA was performed with oligo deoxynucleotide primers (upstream primer 5'-GAGGAAT-TCCCAGACCGTATGATG-3', downstream primer 5'-TACAAGCTGGGTTTCTTGTAC-TACCGAC-3') used in *Venturina velutipes* for β -tubulin gene cloning. PCR reaction was carried out in a thermal cycler (Perkin Elmer Cetus) for 40 cycles with each cycle consisting of 94°C for 1 min to denature the template, 55°C for 1 min for primer annealing and 72°C for 2 min for polymerization.

Plaque hybridization and Southern hybridization

Pleurotus sajor-caju mycelia cDNA library was screened with a PCR product encoding the β -tubulin conservative region as probe. Approximately 200,000 phages from the cDNA library were screened with the probe labelled with ECL hybridization kit (Amersham). Hybridization and washing were performed as recommended from supplier.

DNA sequencing and homology analysis

DNA sequencing was performed by the dideoxy chain termination method of Sanger *et al.* with [α - 35 S]dATP. DNA homology analysis was carried out with Dnasis program (HITACHI) and Genbank database (NIH). Amino acid homology analysis was performed with Prosis program (HITACHI) and Swiss-plot database.

Southern blot analysis

An insert fragment of Myc7tub clone was labelled by random primer labelling system (promega) with [α - 32 P]dCTP. The labelled DNA was used for hybridization at 65°C with a blotted DNA fragment on a nylon membrane by the procedure of Southern (1975).

1 GCC AAT CCG TCC TCC ATC CTC ATC TAT ATG CCG GAA ATC CTC CAG CTT CAG ACT GGC CAG
 61 TGT CCG AAC CAA ATT GGT GGC AAG TTC TGG GAG GTT GTT TCC GAT GAG CAT GGA ATC GAG
 121 CCG GAT GGT CTG TAC TAC GGC AAC AAT GAC CTC CAA CTC GAG CCG ATC TCT GTC TAC TAC
 181 AAC GAG GTC GGA CCG AAC AAG TAC GGT CCG CCA GCT GTC CTC GAT CTC GAG CCG GGT
 241 ACC ATG GAT TGG TGG CCG TGG GGC CCA CTG GGC AGC CTT TTC CCG CCA GAC AAC TTT GTC
 301 TTT GGT CAG AGT GGA GGC GGT AAT AAC TGG GGC AAA GGG CAT TAT ACG GAG GGC GCT GAA
 361 CTC GAT GAT GCC GTT CTC GAT GGT GTG CCG AAG GAG GCT GAG GGC AGG GAT TGT CTG CAA
 421 GGT TTC CAG ATC ACC CAC TGT CTA GGT GGT GAA ACT GGT GGC GAT ATG GGT ACA CTT TTG
 481 ATC TCC AAA ATT CBT GAG GAA TAT CCG GAC CCA ATG ATG TCC ACA TAT TCC GGT TTT CCA
 541 AGT CCG AAG GTA TGG GAC ACT GTT GTC GGT GAG CCG TAC AAC CCG ACG CTC TCC GTC CAC CAA
 601 CTT GTC GAG AAT TCC GAC GAG ACT TJC TGT ATT GAT AAC GAG GCT CTC TAC GAC ATC TGT
 661 TTC CCG ACT CTC AAA CTC AGG AGA CCG ACC TAC GGC GAT CTC AAC CAT CTC ATC TCA ATT
 721 GTC ATG TCA GGC ATT ACA ACT TGT TTA CCA TCC CTT GGT CAA CTC AAC TGG GAT CTG AGA
 781 AAG TGG GCC GTC AAC ATG GTT CTT TTC CCG GTC CTT CAT TTC TJC ATG GCT GGC GTT TGC
 841 CCG CTC ACC GCA CCA GGA AGC CAA CAA TAT TCC GCC GTC AGC GTC CTT GAG TGG ACC CAG
 901 CAA ATG TTC GAC GCG AAG AAC ATG ATG GCT CCG TGG GAT CCG CCG GAT GGC GGC TAC CTC
 961 ACT GGT GCT GCC GTC TTC GGT GGC AAA GTA TGG TGG AAG GAA TGC GAA GAG CAA ATG CAG
 1021 AAC GTC CAG AAC AAA AAC TCT GCC TAC TTC GTG GAG TGG ATC CCG AAT AAC GTC CTT ACT
 1081 GCC CAA TGT GAC ATT CCA CCG CCG GGA TGC AAG ATG AAC GGC GTT ACC TTC TTG GGC AAC TGG
 1141 ACC GGC ATC CAA GAA CTC TTC AAG GGT GTC AAC GAC CAA TTC CCG GCT ATG TTC AAG CCG
 1201 AAG GCT TTC TTG CAT TGG TAC ACG CAA GAG GGT ATG GAC GAG ATG GAG TTC ACG GAG GGC
 1261 GAA TCA AAC ATG CAG GAT CTT GTC GCT GAA TAC CAA CAA TAC CAG GAT GCT ACT GGC GAT
 1321 GAG GAA GAG GGT GAA TAC GAA GAG GAA CCG GCT A GAA GAA GAA CAG TGA TCA ATG GAT TGT
 1381 CTG TAT GGC CCA CTG CAG TCG CCG GGT AAA TCG TAC CTA CCT TCT CCA TAT TGC TCT TCA
 1341 GCA TGT TAC GCT CTT TCA TTT CTC TAT ATG GAT GTC TGA ATA AAT TGC CTT TTA TCA GCA

Fig. 1. Nucleotide sequence and the deduced amino-acid sequence of the *P. sajor-caju* β -tubulin cDNA.

The consensus sequences of poly A signal are underlined. The sequence was determined by following the protocol for sequencing double stranded templates using sequenase from USB, and by using [α - 35 S] dATP as a label. The sequence is available in the Genbank database under accession no. U64720.

Results and Discussion

PCR amplification of the β -tubulin gene

Optimal annealing temperature in PCR yielded only one band at about 500bp on a gel (data not shown). This PCR product showed the same size estimated in *V. velutipes*.

Isolation of cDNA clones encoding β -tubulin and sequencing analysis

Twenty positive clones were selected in 200, 000 plaques and one of five positive clones that carried suitable insert size was further analyzed and was named My7tub. The cDNA

Table 1. Amino acid sequence homology among Myc7tub clone and β -tubulin isolated from 5 different species

| Species | % ^a |
|--------------------------------|----------------|
| <i>Schizophyllum commune</i> | 93 |
| <i>Homo sapiencie</i> | 86 |
| <i>Drosophila melanogaster</i> | 83 |
| <i>Neurospora crassa</i> | 82 |
| <i>Arabidopsis thaliana</i> | 80 |

^aSequences were collected from the SWISS-PLOT Databank and comparison was made with PROSIS (Hitachi) software.

was consisted of a 5'-UTR of 27 nt, an ORF of 1341nt, and a 3'-UTR of 191nt (Fig. 1). The 3'-UTR had a consensus AATAA polyadenylation signal 16nt upstream from the polyadenylation site. The deduced aa sequence of the ORF shows over 70% homology with β -tubulins of various organisms such as human, *Drosophila*, *Neurospora*, and *Arabidopsis* (Table 1). Guanidine moiety of GTP is now known to bind to β -tubulin within the sequence AI(v) LVDLEPGTMDSVR, between aa 63-77 and β -tubulin of *P. sajor-caju* has 100% identity to these aa sequences in the same region (Linse and Mandelkow, 1988). The carboxylterminal region has recently been shown to be involved in the binding of microtubule associated proteins (MAPs). The acidic nature of carboxylterminal region is thought to form the basis for the interaction of MAPs with tubulin. In β -tubulin of *P. sajor-caju* the aa of carboxylterminal region also includes a high number of glutamic acid residues (Vallee *et al.*, 1990).

Benzimidazole fungicides such as carben-dazim, thiabendazole, nocodazole and benomyl, interfere mitosis in fungi by binding to β -tubulin. Ala¹⁶⁵ to Val, Phe¹⁶⁷ to Tyr, and Glu¹⁹⁸ to Gly changes in aa sequences commonly confer to resistance to a benomyl sensitivity in many fungi (Orbach *et al.*, 1986; Jung and Oakley., 1990). In contrast, the β -tubulin of *P. sajor-caju* has a Cys¹⁶⁵ residue which is un-

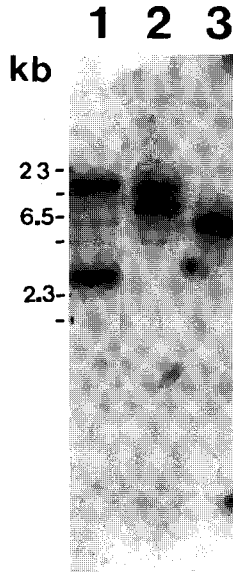


Fig. 2. Southern blot analysis of *Pleurotus sajor-caju* genomic DNA probed with the fragment of the Myc7tub clone digested with *EcoRI* 5g of genomic DNA prepared *Pleurotus sajor-caju* was separated on 0.8% agarose gel and transferred. Genomic DNA was digested with *EcoRI* (Lane 1), *HindIII* (Lane 2) and *EcoRV* (Lane 3). The fragment of myc7tub-clone was labelled with [α - 32 P]dCTP (3000Ci/mmol) by the random primer labelling system (Promega). The blot was prehybridized at 65°C in a solution containing 0.1% SDS, 6X SSC, 5X Denharts solution, 50 mM Tris-HCl (pH 7.6), 100 μ g/ml salmon sperm DNA for at least 1h and then hybridized in the same solution plus the denaturated probe for 16 hr. The blots were washed twice with 2X SSC and 0.1% SDS for 10 min each time at room temperature, twice with a solution containing 1X SSC and 0.1% SDS for 20 min at 65°C and twice with 0.5X SSC and 0.1% SDS for 20 min at 65°C.

usual among β -tubulins of other fungi except for the slime mold and *Schizophyllum commune*. These three fungi which have a Cys¹⁶⁵ residue in their β -tubulin show benomyl insensitivity. It suggests that the presence of Cys¹⁶⁵ residue in β -tubulin results in the insensitivity of *S. commune*, *P. sajor-caju* and slime molds (Burland *et al.*, 1988; Wenen-

skoid *et al.*, 1988).

Southern blot analysis

Genomic DNA was isolated from *P. sajor-caju* and digested with *EcoRI*, *HindIII*, *EcoRV*. The total DNA fragments were transferred to nylon membrane and then hybridized with a cDNA fragment of Myc7tub clone digested with *EcoRI*. Genomic DNA digested with *EcoRI* and *HindIII* showed a double signal at about 2.7 kb, 12 kb, 9 kb, and 8 kb, respectively (Fig. 2). This suggests that two different isotypes of β -tubulin are present in *P. sajor-caju*.

적 요

여름느타리버섯 균사체의 cDNA library로부터 β -tubulin 유전자를 분리하여 염기서열을 분석하였다. 분리된 β -tubulin cDNA 유전자는 27nt의 5'-untranslation region과 1341nt의 open reading frame, 191nt의 3'-untranslation region으로 구성되어 있었다. ORF는 445개의 아미노산들로 구성되어 있으며, 동물, 식물, 사상균에서 보고된 β -tubulin과 80% 이상의 상동성을 보였다. 분리된 Myc7tub clone을 사용하여 Southern hybridization 한 결과 여름느타리버섯에는 두 가지의 isotype β -tubulin이 존재할 것으로 생각된다.

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