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Liu, X.[b] , Ding, S.[a b b]

Molecular characterization of a new acetyl xylan esterase (AXEII) from edible straw mushroom Volvariella volvacea with both de-O-acetylation and de-N-acetylation activity

(2009) *FEMS Microbiology Letters*, 295 (1), pp. 50-56.

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Abstract

A new Volvariella volvacea gene encoding a carbohydrate esterase (CE) family 4 acetyl xylan esterase (AXE) (designated as VvaxeII) was cloned and characterized. The coded polypeptide had 253 amino acid residues, with the first 19 serving as a secretion signal peptide. The VvaxeII transcript levels were high when the fungus was grown on oat spelt xylan, cellobiose, microcrystalline cellulose, carboxymethyl-cellulose, lactose, galactose, and chitin from crab as carbon sources. The recombinant VvAXEII produced by expression of VvaxeII in Pichia pastoris exhibited activity toward acetylated oat spelt xylan and various chitinous substrates, but was totally inactive against artificial aromatic acetates such as β-nitrophenyl, 4-methylumbelliferyl, and α-naphthyl acetates. Enzyme-catalyzed hydrolysis was maximal at pH 7.0 and 60 ° C, and reciprocal plots revealed an apparent Km value of 1.42 mg mL -1 and a Vmax value of

833 IU μmol-1 protein using glycol chitin as a substrate. The recombinant VvAXEII requires activation by bivalent cations such as Co2+ and Mg2+. Interestingly, the recombinant VvAXEII showed no deacetylation activity to fully acetylated monosaccharides such as xylose tetraacetate. © 2009 Federation of European Microbiological Societies. Published by Blackwell Publishing Ltd. All rights reserved.

Author Keywords
Acetyl xylan esterase; Carbohydrate esterase family 4; Volvariella volvacea

Document Type: Article
Source: Scopus

Sharma, V.P.[a b] , Sharma, S.R.[a]

Molecular identification and cultivation of the black poplar culinary-medicinal mushroom agrocybe aegerita (V. Brig.) Singer (Agaricomycetideae)

(2009) *International Journal of Medicinal Mushrooms*, 11 (1), pp. 87-91.

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[b] National Research Centre for Mushrooms, ICAR, Solan-173213 (Himachal Pradesh)

Abstract

The nucleotide sequence is obtained by amplification of the ITS region of rDNA identified as Agrocybe aegerita. Cultivation of A. aegerita was carried out on two substrates, namely, wheat straw and sawdust. Sawdust proved to be the better substrate because it resulted in 67.66% biological

efficiency as compared to 56.25% for wheat straw. Supplementation with wheat bran resulted in increased biological efficiency on both substrates, the highest being on sawdust with 10% wheat bran (74.33% biological efficiency).
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Author Keywords
Agrocybe aegerita; Biological ef? ciency; Medicinal mushrooms; Molecular characterization; Supplements; Yield

Document Type: Article
Source: Scopus

Hibbett, D.S.[a] , Matheny, P.B.[a b]
The relative ages of ectomycorrhizal mushrooms and their plant hosts estimated using Bayesian relaxed molecular clock analyses
(2009) *BMC Biology*, 7, art. no. 13, .

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Abstract
Background: Ectomycorrhizae (ECM) are symbioses formed by polyphyletic assemblages of fungi (mostly Agaricomycetes) and plants (mostly Pinaceae and angiosperms in the rosid clade). Efforts to reconstruct the evolution of the ECM habit in Agaricomycetes have yielded vastly different results, ranging from scenarios with many relatively recent origins of the symbiosis and no reversals to the free-living condition; a single ancient origin of ECM and many subsequent transitions

to the free-living condition; or multiple gains and losses of the association. To test the plausibility of these scenarios, we performed Bayesian relaxed molecular clock analyses including fungi, plants, and other eukaryotes, based on the principle that a symbiosis cannot evolve prior to the origin of both partners. As we were primarily interested in the relative ages of the plants and fungi, we did not attempt to calibrate the molecular clock using the very limited fossil record of Agaricomycetes. Results: Topologically constrained and unconstrained analyses suggest that the root node of the Agaricomycetes is much older than either the rosids or Pinaceae. The Agaricomycetidae, a large clade containing the Agaricales and Boletales (collectively representing 70% of Agaricomycetes), is also significantly older than the rosids. The relative age of Agaricomycetidae and Pinaceae, however, is sensitive to tree topology, and the inclusion or exclusion of the gnetophyte Welwitschia mirabilis. Conclusion: The ancestor of the Agaricomycetes could not have been an ECM species because it existed long before any of its potential hosts. Within more derived clades of Agaricomycetes, there have been at least eight independent origins of ECM associations involving angiosperms, and at least six to eight origins of associations with gymnosperms. The first ECM symbioses may have involved Pinaceae, which are older than rosids, but several major clades of Agaricomycetes, such as the Boletales and Russulales, are young enough to have been plesiomorphically associated with either rosids or Pinaceae, suggesting that some contemporary ECM partnerships could be of very ancient origin. © 2009 Hibbett and Matheny; licensee BioMed Central Ltd.

Document Type: Article
Source: Scopus

Islam, M.M.[a b]

Molecular cloning, expression and characterization of a serine proteinase from Japanese edible mushroom, Grifola frondosa: Solving the structure - Function anomaly of a reported aminopeptidase

(2008) *Electronic Journal of Biotechnology*, 11 (4), .

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Abstract

The N-terminal amino acid sequence of an aminopeptidase from Japanese edible mushroom, Grifola frondosa, was reported to have high similarity with that of a serine proteinase from basidiomycete, Agaricus bisporous (Nishiwaki and Hayashi, 2001). The full-length cDNA and the corresponding genomic DNA of the enzyme were cloned, based on the reported N-terminal amino acid sequence. The predicted open reading frame (ORF) of the cloned cDNA, encoding a product of 379 amino acids, was expressed in E. coli using pET expression vector. The expressed pro-enzyme (40 kDa) underwent autolysis to produce the mature protein (30 kDa) and a pro-peptide (10 kDa). The mature protein and the pro-peptide remained tightly bound to each other and could not be separated by Ni-NTA metal affinity chromatography or Q-Sepharose ion-exchange chromatography. The enzyme was inactive in the bound form. Upon treatment with subtilisin, the bound pro-peptide was further hydrolyzed and a high serine proteinase activity was recovered. No aminopeptidase activity was detected at any

stage of the protein processing. These results clearly indicated that the N-terminal amino acid sequence and the function of the reported aminopeptidase were not derived from the same protein entity and hence caused the structure-function anomaly. © 2008 by Pontificia Universidad Católica de Valparaíso.

Author Keywords
5′-RACE; cDNA; Genomic DNA; Maitake; Refolding

Document Type: Article
Source: Scopus

Ding, S.[a b], Cao, J.[a], Zhou, R.[a], Zheng, F.[a]

Molecular cloning, and characterization of a modular acetyl xylan esterase from the edible straw mushroom Volvariella volvacea

(2007) *FEMS Microbiology Letters*, 274 (2), pp. 304-310. Cited 1 time.

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Abstract

A new Volvariella volvacea gene encoding an acetyl xylan esterase (designated as Vvaxe1) was cloned and expressed in Pichia pastoris. The cDNA contained an ORF of 1047 bp encoding 349 amino acids with a calculated mass of 39 990 Da. VvAXE1 is a modular enzyme consisting of an N-terminal signal peptide, a catalytic domain, and a cellulose-binding domain. The amino acid sequence of the enzyme exhibited a

high degree of similarity to cinnamoyl esterase B from Penicillium funiculosum, and acetyl xylan esterases from Aspergillus oryzae, Penicillium purpurogenum, and Aspergillus ficuum. Recombinant acetyl xylan esterase released acetate from several acetylated substrates including β-d-xylose tetraacetate and acetylated xylan. No activity was detectable on p-nitrophenyl acetate. Enzyme-catalyzed hydrolysis of 4-methylumbelliferyl acetate was maximal at pH 8.0 and 60° C, and reciprocal plots revealed an apparent Km value of 307.7 μM and a V max value of 24 733 IU μmol-1 protein. ReAXE1 also exhibited a capacity to bind to Avicel and H3PO4 acid-swollen cellulose. © 2007 Federation of European Microbiological Societies.

Author Keywords
Acetyl xylan esterase; Characterization; Volvariella volvacea

Document Type: Article
Source: Scopus

Ding, S.[a b d] , Ge, W.[a] , Buswell, J.A.[a c]

Molecular cloning and transcriptional expression analysis of an intracellular β-glucosidase, a family 3 glycosyl hydrolase, from the edible straw mushroom, Volvariella volvacea

(2007) *FEMS Microbiology Letters*, 267 (2), pp. 221-229. Cited 1 time.

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[c] Institute of Edible Fungi, Shanghai Academy of Agricultural Sciences, Shanghai, China
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Abstract

A β-glucosidase, with a molecular mass of 95 kDa, was isolated from extracts of Volvariella volvacea mycelium grown on crystalline cellulose. Degenerate primers based on the N-terminal sequences of purified β-glucosidase and two protease-generated peptides were used to generate cDNA fragments encoding a portion of the β-glucosidase gene (bgl), and rapid amplification of cDNA ends was used to obtain full-length cDNA clones. The cDNA of bgl contained an ORF of 2586 bp coding for 862 amino acids. Alignment of the deduced amino-acid sequence of β-glucosidase with deduced amino acid sequences of other microbial β-glucosidases showed the highest overall homology with glycoside hydrolase family 3 β-glucosidases from fungi. Transcripts of bgl were detected in total RNA extracted from mycelium grown on cellulose and cellobiose, and from mycelium pre-grown for 72 h in basal medium containing 1% (w/v) sorbitol following addition of α-lactose, β-lactose, cellobiose, d- xylose, l-sorbose, β-gentiobiose, sophorose or d-galactose. Addition of l-sorbose and d-glucosamine to mycelium grown on 1% (w/v) crystalline cellulose greatly increased the level of bgl expression. bgl Was expressed at various stages of the mushroom developmental cycle (substrate colonization to mature fruit body), although the number of bgl transcripts in pinhead and button stages was slightly smaller. © 2006 Federation of European Microbiological Societies.

Author Keywords

β-glucosidase; Cellulase gene expression; Intracellular;

Volvariella volvacea

Document Type: Article
Source: Scopus

Khan, M.T.H.[a b c] , Choudhary, M.I.[b] , Ather, A.[c] , Rahman, A.U.[b]

Modelling of the mushroom tyrosinase and its molecular dynamic (MD) simulations experiments in room and elevated temperatures and the docking interactions with nucleotides

(2006) *Minerva Biotecnologica*, 18 (4), pp. 171-179.

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Abstract

In the present works, the modelling of the mushroom tyrosinase enzyme have been done and validated. Then after the energy minimization, the molecular dynamics (MD) simulation, without water molecules, of the model at room (300 K) and elevated (1000 K) temperatures have also been done and the deviation of kinetic, potential and the total energy were calculated. Finally using the same model preliminary docking experiments have done with aptameric DNA (ssDNA), where it was shown that the enzyme virtually

interact with the nucleotide at least at two points with C32, with ASP76 and GLY313 where the distances calculated were 7.43 and 3.55 Å, respectively. So the closest interaction point is GLY313 with C32.

Author Keywords
Docking; Modelling; Molecular dynamic; Mushroom tyrosinase; Simulations

Document Type: Article
Source: Scopus

Singh, S.K.[a] , Doshi, A.[b] , Yadav, M.C.[a] , Kamal, S.[a]
Molecular characterization of specialty mushrooms of western Rajasthan, India
(2006) *Current Science*, 91 (9), pp. 1225-1230.

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Abstract
Eighteen specialty mushroom germplasm accessions were collected from Udaipur (Rajasthan) and characterized using DNA fingerprinting and ribosomal rRNA gene sequencing. Phylogenetic analyses based on RAPD profiles and nucleotide sequence of 5.8S rRNA gene along with its spacer regions revealed variation of inter-generic and intra-species isolates among accessions. Based on ITS sequence polymorphism, seven isolates were identified as Podaxis pistillaris, four as Phellinus igniarius, one as Gymnopilus subearlei and six as

Phellorinia herculea. The similarity matrix revealed very high intra-species homology (99.5-100%) and significant inter-generic diversity (21.2-37.7%). G. subearlei and P. herculea have been discovered as new additions to the Indian basidiomycetes biodiversity.

Author Keywords
ITS; Molecular taxonomy; Mushroom; Phylogenetic analysis; Sequences polymorphism

Document Type: Article
Source: Scopus

Singh, S.K., Sharma, V.P., Sharma, S.R., Kumar, S., Tiwari, M.

Molecular characterization of Trichoderma taxa causing green mould disease in edible mushrooms

(2006) *Current Science*, 90 (3), pp. 427-431. Cited 1 time.

National Research Centre for Mushroom (ICAR), Chambaghat, Solan 173 213, India

Abstract
Trichoderma taxa associated with green mould disorder of edible mushrooms were isolated from both fruit bodies and substrates of Agaricus bisporus, A. bitorquis, Calocybe indka, Ganoderma lucidum, Lentinula edodes, Pleurotus sajor-caju, and Volvariella volvacea. Emerged fruiting bodies in the affected portion of the substrate were badly spotted, brownish in colour and reduced in both growth rate and yield performance. Microscopic examination of cultures revealed significant differences in fungal morphology, but were difficult to designate as Trichoderma species. The nucleotide sequence comparisons of 5.8S rRNA gene using BLAST network

facilitated molecular identification and genetic cataloguing of 18 Trichoderma isolates into two taxa, namely T. harzianum and T. virens. RAPD primers exhibited both inter- and intra-specific variations among the test isolates and separated them into eight distinct phylogenetic sub-clades. The present study underlines the potential threat of green mould disorders in cultivated mushrooms and validates existence of significant intraspecific diversity in isolates of both T. harzianum and T. virens.

Author Keywords
Edible mushrooms; Green mould disease; Molecular identification; Trichoderma

Document Type: Article
Source: Scopus

Singh, S.K.[a b] , Rai, R.D.[a] , Kamal, S.[a]

Molecular identification of some medicinally important aphyllophorales mushrooms based on ITS rDNA sequences and RAPD data

(2005) *International Journal of Medicinal Mushrooms*, 7 (4), pp. 565-572.

[a] National Research Centre for Mushroom (ICAR), Chambaghat, Solan, HP, India
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Abstract

Analysis of genetic relationship of important Aphyllophorales germplasm accessions of the National Research Centre for Mushroom, Solan, India, was conducted using RAPD and ITS

rDNA sequences. RAPD profiles exhibited significant variations among Trametes versicolor, Tyromyces chioneus, and Ganoderma species. The resulting RAPD-based phylogram grouped Ganoderma spp. accessions into four clades. Phylogeny inferred from ITS rDNA sequence distinguished Trametes versicolor, Tyromyces chioneus, and Ganoderma spp. at the generic level due to different lengths and variations of the 5.8S rDNA conserved region. At the intrageneric level, Ganoderma accessions were divided into two distinct groups based on nucleotide substitution in ITS-1 and ITS-2 regions. It is presumed that some of the Ganoderma sp. samples might be G. lucidum. Single nucleotide substitutions turned out to be more useful for genetic cataloguing of isolates within a species than sequence alignment using NCBI databse. © 2005 by Begell House, Inc.

Author Keywords
5.8S rRNA gene; Aphyllophorales; Ganoderma; Gene sequencing; Trametes; Tyromyces

Document Type: Article
Source: Scopus

Yang, N.[a c] , Tong, X.[b] , Xiang, Y.[a] , Zhang, Y.[a] , Liang, Y.[a b c] , Sun, H.[b] , Wang, D.-C.[a]

Molecular character of the recombinant antitumor lectin from the edible mushroom Agrocybe aegerita

(2005) *Journal of Biochemistry*, 138 (2), pp. 145-150. Cited 6 times.

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[b] State Key Laboratory of Virology, College of Life Science, Wuhan University, Wuhan, 430072, China

[c] Graduate School of Chinese Academy of Sciences, Beijing 100039, China

Abstract
The lectin from Agrocybe aegerita (AAL) has been found to possess potent tumor-suppressing function and tumor cell apoptosis-inducing activity. In this paper, we report the full sequence, the active expression of the gene encoding AAL at a high level and bioassay of the binding property with lactose, apoptosis-inducing activity and DNase activity of recombinant AAL (rAAL). The results reveal that AAL is a member of the galectin family and the dimeric form is the active unit for the functional performance. The rAAL showed comparable tumor cell apoptosis-inducing activity with the wild AAL but no DNase activity at all. The molecular characters revealed by this study are significant for the in-depth investigation of the functional mechanism of this interesting protein. © 2005 The Japanese Biochemical Society.

Author Keywords
Antitumor; Apoptosis; Galectin; Homodimer; Mushroom

Document Type: Article
Source: Scopus

Buswell, J.A., Chen, M.
Cultivation, biochemical, molecular biological and medical aspects of the culinary-medicinal straw mushroom Volvariella volvacea (Bull.:Fr.) singer (Agaricomycetideae)
(2005) *International Journal of Medicinal Mushrooms*, 7 (1-

2), pp. 157-166. Cited 5 times.

Edible Fungi Institute, Shanghai Academy of Agricultural Sciences, Shanghai 201106, China

Abstract
Key features associated with the cultivation of Volvariella volvacea, the edible straw mushroom, in a modern Chinese cultivation facility are described. Our current understanding of the biochemistry and molecular biology of V. volvacea cellulases and laccases, and the evidence supporting important roles for these enzymes in substrate utilization and fruit body development, is presented. Problems arising from low temperature-associated autolysis of the mushroom mycelium and fruit body and changes in gene expression that occur in V. volvacea mycelium during cold shock are detailed and analyzed. Various bioactive components isolated from V. volvacea are identified and ascribed medicinal properties reviewed. © 2005 by Begell House, Inc.

Author Keywords
Cellulases; Cold-shock proteins; Cryopreservation; Laccase; Medicinal properties; Mushroom cultivation; Volvariella volvacea

Document Type: Review
Source: Scopus

Xia, L.[a] , Chu, K.T.[b] , Ng, T.B.[b]
A low-molecular mass ribonuclease from the brown oyster mushroom
(2005) *Journal of Peptide Research*, 66 (1), pp. 1-8. Cited 1 time.

[a] Department of Life Sciences, Shenzhen University, Shenzhen, China
[b] Department of Biochemistry, Faculty of Medicine, Chinese University of Hong Kong, Shatin, Hong Kong

Abstract

A ribonuclease, with a molecular mass of 9 kDa and an N-terminal sequence resembling the sequence of a fragment of tRNA/rRNA cytosine-C5-methylase and a fragment of a alanyl-tRNA synthetase, was isolated from fresh fruiting bodies of the brown oyster mushroom Pleurotus ostreatus. The ribonuclease was purified using a very simple protocol that comprised ion-exchange chromatography on carboxymethyl (CM)-cellulose and affinity chromatography on Affi-gel blue gel. Subsequent gel filtration by fast protein liquid chromatography on Superdex 75 and sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis revealed that the ribonuclease was purified after the first two chromatographic steps. The ribonuclease was adsorbed on CM-cellulose and Affi-gel blue gel. The ribonuclease exhibited the highest activity toward poly A, lower activity toward poly C, slight activity toward poly G, and indiscernible activity toward poly U. The enzyme was stimulated upon exposure to 1 μM Mg2+ and 10 μM Zn2+, but was inhibited by the following ions at 10 mM: Ca 2+, Mg2+, Zn2+, Cu2+, Fe 2+, Mn2+, and Fe3+. The ribonuclease required a pH of 8.0 and a temperature of 50-70 ° C to express maximal activity. It had a Km of 60 μM toward yeast tRNA. It lacked mitogenic and HIV-1 reverse transcriptase inhibiting activities, but exerted antiproliferative activity toward leukemia L1210 cells.
Copyright Blackwell Munksgaard, 2005.

Author Keywords

Brown oyster mushroom; Fruiting body; Purification; Ribonuclease

Document Type: Article
Source: Scopus

Zaidman, B.-Z.[a b] , Yassin, M.[a b] , Mahajna, J.[b] , Wasser, S.P.[a]

Medicinal mushroom modulators of molecular targets as cancer therapeutics

(2005) *Applied Microbiology and Biotechnology*, 67 (4), pp. 453-468. Cited 50 times.

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Abstract
Empirical approaches to discover anticancer drugs and cancer treatments have made limited progress in the past several decades in finding a cure for cancer. The expanded knowledge of the molecular basis of tumorigenesis and metastasis, together with the inherently vast structural diversity of natural compounds found in mushrooms, provided unique opportunities for discovering new drugs that rationally target the abnormal molecular and biochemical signals leading to cancer. This review focuses on mushroom low-molecular-weight secondary metabolites targeting processes such as apoptosis, angiogenesis, metastasis, cell cycle regulation, and signal transduction cascades. Also discussed in this review are

high-molecular-weight polysaccharides or polysaccharide-protein complexes from mushrooms that appear to enhance innate and cell-mediated immune responses, exhibit antitumor activities in animals and humans, and demonstrate the anticancer properties of selenium compounds accumulated in mushrooms. © Springer-Verlag 2005.

Document Type: Short Survey
Source: Scopus

Yan, P.-S.[a] , Luo, X.-C.[b] , Zhou, Q.[b]

RAPD molecular differentiation of the cultivated strains of the jelly mushrooms, Auricularia auricula and A. polytricha

(2004) *World Journal of Microbiology and Biotechnology*, 20 (8), pp. 795-799.

[a] Institute of Applied Mycology, Laiyang Agricultural University, Laiyang, Shandong 265200, China
[b] State Key Lab. of Agro-Microbiology, Ctrl. China Agricultural University, Wuhan 430070, China

Abstract

Auricularia mushrooms are the fourth most important cultivated mushrooms in the world, with a unique jelly taste and horizontal-septated basidium which are significantly different from other cultivated mushrooms. Differentiation of commercial cultivated strains is difficult to conduct, due to the lack of useful distinguishable characters. In this study, we used the RAPD technique to differentiate 11 commercial strains of A. auricula and five commercial strains of A. polytricha and one white-fruitbody mutant strain, and to characterize their genetic diversity. Results showed that all

the strains tested could be differentiated by pooled RAPD data, and even one individual primer (S10) could also discriminate all tested strains. RAPD analysis could differentiate strains having identical rDNA RFLP and supports the classification of the white-fruitbody mutant to the species of A. polytricha. Genetic similarity analysis and grouping derived from RAPD markers reveals a high level of genetic diversity of commercial strains of Auricularia auricula and A. polytricha. Therefore, the RAPD technique can provide a powerful tool to discriminate the commercial Auricularia strains and offer the molecular information useful for breeding systems.

Author Keywords
Heterobasidiomycetes; Jelly fungus; Molecular identification; Wood ear mushroom

Document Type: Article
Source: Scopus

Park, H.-G.[b] , Ko, H.-G.[b] , Kim, S.H.[a] , Park, W.-M.[b]
Molecular identification of Asian isolates of medicinal mushroom Hericium erinaceum by phylogenetic analysis of nuclear ITS rDNA
(2004) *Journal of Microbiology and Biotechnology*, 14 (4), pp. 816-821. Cited 7 times.

[a] Department of Microbiology, Institute of Basic Science, Dankook University, Cheonan, Chungnam 330-714, South Korea
[b] Sch. of Life Sciences/Biotechnology, Korea University, Seoul 136-701, South Korea

Abstract
A reliable molecular phylogenetic method to identify Hericium erinaceum, the most industrially valuable species in the Hericium genus, was established. Sequencing and phylogenetic analyses of the PCR-amplified ITS and 5.8S rDNA from Hericium fungi, including 6 species and 23 isolates, showed that variation in nucleotide sequences and size exists in both ITS1 and ITS2 regions, but not in the 5.8S region. These two ITS regions provided different levels of information on the relationship of H. erinaceum to other Hericium species. Based on the ITS1 sequence, both the parsimony and neighbor joining trees clearly distinguished Asian H. erinaceum isolates from other Hericium species and isolates. The intraspecific divergence of the ITS2 region was suitable to dissect the Asian H. erinaceum isolates into a few groups. © The Korean Society for Microbiology and Biotechnology.

Author Keywords
Hericium erinaceum; Intraspecific variation; ITS1-5.8S-ITS2; Medicinal mushroom; Nuclear ribosomal DNA; Phylogenetic identification

Document Type: Article
Source: Scopus

Wang, H.X.[a] , Ng, T.B.[b]
Purification of a novel low-molecular-mass laccase with HIV-1 reverse transcriptase inhibitory activity from the mushroom Tricholoma giganteum
(2004) *Biochemical and Biophysical Research Communications*, 315 (2), pp. 450-454. Cited 17 times.

[a] Department of Microbiology, China Agricultural University, State Key Lab. of Agrobiotechnology, Beijing, China
[b] Department of Biochemistry, Faculty of Medicine, Chinese University of Hong Kong, Shatin, New Territories, Hong Kong

Abstract
A laccase with a novel N-terminal sequence, a low molecular mass of 43kDa smaller than those of previously reported laccases, a pH optimum of 4, and a temperature optimum at 70° C was isolated from fresh fruiting bodies of the mushroom Tricholoma giganteum. The activity of the enzyme rose steadily from 20 to 50° C, increased very slowly from 50 to 70° C, and fell slightly when the temperature was further increased to 80° C. The activity of the laccase underwent little changes over the pH range 3.0-5.0. However, the enzyme activity dwindled to nothing after exposure to 100° C for 10min and when the ambient pH was 7 or above. The procedure used for purifying the enzyme included ion exchange chromatography on DEAE-cellulose, affinity chromatography on Affi-gel blue gel, ion exchange chromatography on CM-cellulose, and FPLC-gel filtration on Superdex 75. The laccase was unadsorbed on DEAE-cellulose and adsorbed on Affi-gel blue gel and CM-cellulose. It inhibited HIV-1 reverse transcriptase with an IC50 of 2.2μM.
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Author Keywords
Fruiting bodies; Isolation; Laccase; Mushroom; Tricholoma giganteum

Document Type: Article
Source: Scopus

Zervakis, G.I.[a] , Moncalvo, J.-M.[b] , Vilgalys, R.[c]

Molecular phylogeny, biogeography and speciation of the mushroom species Pleurotus cystidiosus and allied taxa

(2004) *Microbiology*, 150 (3), pp. 715-726. Cited 20 times.

[a] Natl. Agricultural Res. Foundation, Institute of Kalamata, Lakonikis 87, 24100 Kalamata, Greece

[b] Ctr. for Biodiversity/Conserv. Biol., Royal Ontario Museum/Dept. of Botany, University of Toronto, 100 Queen's Park, Toronto, Ont. M5S 2C6, Canada

[c] Department of Biology, Duke University, Durham, NC 27708, United States

Abstract

Members of the mushroom genus Pleurotus form a heterogeneous group of edible species of high commercial importance. Subgenus Coremiopleurotus includes taxa that produce synnematoid fructifications (anamorphic state). Several species, subspecies and varieties have been described in Coremiopleurotus. These taxa are discriminated by minute morphological differences and correspond to Pleurotus cystidiosus sensu lato. A worldwide geographical sampling of Coremiopleurotus taxa and nucleotide sequence data from the internal transcribed spacer of the nuclear rRNA genes (ITS) were used to produce a molecular phylogeny for the group. Also conducted were new interfertility studies, and a summary of the mating data currently available in the literature is provided. Both ITS phylogeny and mating data supported the distinction between Pleurotus australis (a species apparently endemic to New Zealand and Australia) and P. cystidiosus sensu lato. Within P. cystidiosus sensu lato, ITS phylogeny showed a deep split between Old and New

World isolates and clearly distinguished four distinct clades that strongly corresponded to the geographical origin of the strains. In the Old World, one clade is composed of isolates from Europe and Africa, and one clade is composed of isolates from Asia (including collections from Hawaii). In the New World, one clade is restricted to isolates from Mexico, and one clade includes all the authors' North America isolates, one collection from Japan and one collection from South Africa. Mating data revealed a high level of interfertility among strains of P. cystidiosus sensu lato, except that isolates from Mexico were nearly fully intersterile with the other collections. Nucleotide sequence divergence in the ITS1-5.8S rDNA-ITS2 regions among intercompatible P. cystidiosus collections was very high (0-6.9 %) in comparison to that reported in other biological species of basidiomycetes (0-3 %), indicating significant genetic divergence between geographically isolated populations of the P. cystidiosus group. The phylogenetic species concept, as well as molecular, mating and geographical evidence, was used to recognize five species in the subgenus Coremiopleurotus: P. australis (in New Zealand and Australia), Pleurotus abalonus (in Asia and Hawaii), Pleurotus fuscosquamulosus (in Africa and Europe), Pleurotus smithii (in Mexico) and Pleurotus cystidiosus sensu stricto (in North America). However, geographical boundaries between these species are not strict, as rare events of long distance dispersal have occurred. © 2004 SGM.

Document Type: Review
Source: Scopus

Chen, S., Wei, G., Buswell, J.A.
Erratum: Biochemical and molecular characterization of a laccase from the edible straw mushroom, Volvariella volvacea (European Journal of Biochemistry (2004)

271 (318-328))
(2004) *European Journal of Biochemistry*, 271 (5), p. 1063.

Document Type: Erratum
Source: Scopus

Chen, S.[a] , Ge, W.[a] , Buswell, J.A.[a b]
Molecular cloning of a new laccase from the edible straw mushroom Volvariella volvacea: Possible involvement in fruit body development
(2004) *FEMS Microbiology Letters*, 230 (2), pp. 171-176. Cited 10 times.

[a] Department of Biology, Chinese University of Hong Kong, Shatin, New Territories, Hong Kong
[b] Ctr. Intl. Serv. Mushroom Biotech., Chinese University of Hong Kong, Shatin, New Territories, Hong Kong

Abstract
Cloning of a laccase-encoding cDNA from the edible straw mushroom, Volvariella volvacea, was performed using reverse transcription-polymerase chain reaction (RT-PCR) and rapid amplification of cDNA ends. The cDNA of the putative laccase gene (lac4) consisted of 1689 bp, including an open reading frame encoding a 23-amino acid signal peptide at the N-terminal end and a 540-amino acid mature protein with a predicted molecular mass of 58 173 Da and a pI value of 6.1. The 10 histidine residues and one cysteine residue required to co-ordinate the four copper atoms at the active site of the protein were all conserved. The amino acid sequence of V. volvacea lac4 has a high degree of identity with other basidiomycete laccases. Transcription of the laccase gene was analysed by RT-PCR and, unlike many other laccase genes,

shown to be regulated independently of either copper or aromatic compounds under the test conditions. However, the laccase gene is strongly expressed during that part of the mushroom developmental cycle involving fruit body morphogenesis. © 2003 Federation of European Microbiological Societies. Published by Elsevier B.V. All rights reserved.

Author Keywords
Edible mushroom; Fruit body development; Gene expression; Laccase; Mushroom; Regulation; Volvariella volvacea

Document Type: Article
Source: Scopus

Chen, S.[a] , Ge, W.[a] , Buswell, J.A.[a b]
Biochemical and molecular characterization of a laccase from the edible straw mushroom, Volvariella volvacea
(2004) *European Journal of Biochemistry*, 271 (2), pp. 318-328. Cited 19 times.

[a] Department of Biology, Ctr. Intl. Serv. Mushroom Biotech., Chinese University of Hong Kong, Shatin, New Territories, Hong Kong
[b] Edible Fungi Institute, 35 Nanhua Road, Shanghai 201106, China

Abstract
We have isolated a laccase (lac1) from culture fluid of Volvariella volvacea, grown in a defined medium containing 150 μM CuSO4, by ion-exchange and gel filtration chromatography. Lac1 has a molecular mass of 58 kDa as

determined by SDS/PAGE and an isoelectric point of 3.7. Degenerate primers based on the N-terminal sequence of purified lac1 and a conserved copper-binding domain were used to generate cDNA fragments encoding a portion of the lac1 protein and RACE was used to obtain full-length cDNA clones. The cDNA of lac1 contained an ORF of 1557 bp encoding 519 amino acids. The amino acid sequence from Ala25 to Asp41 corresponded to the N-terminal sequence of the purified protein. The first 24 amino acids are presumed to be a signal peptide. The expression of lac1 is regulated at the transcription level by copper and various aromatic compounds. RT-PCR analysis of gene transcription in fungal mycelia grown on rice-straw revealed that, apart from during the early stages of substrate colonization, lac1 was expressed at every stage of the mushroom developmental cycle defined in this study, although the levels of transcription varied considerably depending upon the developmental phase. Transcription of lac1 increased sharply during the latter phase of substrate colonization and reached maximum levels during the very early stages (primordium formation, pinhead stage) of fruit body morphogenesis. Gene expression then declined to ≈20-30% of peak levels throughout the subsequent stages of sporophore development.

Author Keywords
Edible mushroom; Gene expression; Laccase; Volvariella volvacea

Document Type: Article
Source: Scopus

Shnyreva, A.V.[a] , Belokon, Yu.S.[b] , Belokon, M.M.[c]
Differentiation between commercial strains of oyster

and button mushrooms using molecular markers
(2003) *Genetika*, 39 (11), pp. 1461-1469.

[a] Department of Mycology and Algology, Lomonosov Moscow State University, Moscow, 119992, Russian Federation
[b] Vavilov Institute of General Genetics, Russian Academy of Sciences, Moscow, 119899, Russian Federation

Abstract
Analysis of commercial strains of two edible mushrooms, Pleurotus ostreatus and Agaricus bisporus, using PCR and isozyme electrophoresis techniques allowed us to differentiate groups of genetically similar and distant strains. Among the commercial strains of P. ostreatus, the level of genetic variation was higher suggesting a broader genetic basis employed in breeding of this mushroom. The cultivars and hybrids of, A. bisporus, showed a higher level of homology. The isozyme markers (nonspecific esterase, leucinaminopeptidase, and phosphoglucoisomerase) are recommended for identification of the commercial strains of edible mushrooms.

Document Type: Article
Source: Scopus

Shnyreva, A.V.[a] , Belokon', Yu.S.[b] , Belokon', M.M.[b]
Differentiation between commercial strains of oyster and button mushrooms using molecular markers
(2003) *Russian Journal of Genetics*, 39 (11), pp. 1232-1239.

[a] Department of Mycology and Algology, Moscow State University, Moscow, 119992 Russia

[b] Vavilov Inst. of General Genetics, Russian Academy of Sciences, Moscow, 119899 Russia

Abstract
Analysis of commercial strains of two edible mushrooms, Pleurotus ostreatus and Agaricus bisporus, using PCR and isozyme electrophoresis techniques allowed us to differentiate groups of genetically similar and distant strains. Among the commercial strains of P. ostreatus, the level of genetic variation was higher suggesting a broader genetic basis employed in breeding of this mushroom. The cultivars and hybrids of A. bisporus showed a higher level of homology. The isozyme markers (nonspecific esterase, leucinaminopeptidase, and phosphoglucoisomerase) are recommended for identification of the commercial strains of edible mushrooms.

Document Type: Article
Source: Scopus

Bougnoux, M.-É.
Molecular typing of mushrooms [Typage moléculaire des champignons]
(2003) *Annales de l'Institut Pasteur/Actualites*, (17), pp. 75-87.

Document Type: Review
Source: Scopus

Covic, A.[a] , Goldsmith, D.J.A.[b] , Gusbeth-Tatomir, P.[a] , Volovat, C.[a] , Dimitriu, A.G.[c] , Cristogel, F.[c] , Bizo, A.[d]
Successful use of Molecular Absorbent Regenerating System (MARS) dialysis for the treatment of fulminant

hepatic failure in children accidentally poisoned by toxic mushroom ingestion

(2003) *Liver International*, 23 (SUPPL. 3), pp. 21-27. Cited 20 times.

[a] Dialysis Center, C.I. Parhon University Hospital, Blvd. Carol 1st No. 50, Iasi 6600, Romania

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[c] St Mary's Children Hospital, Iasi, Romania

[d] University Hospital, Paediatric Clinic, Cluj, Romania

Abstract

Background: Acute liver failure (ALF) as a result of mushroom poisoning is associated with a high mortality (particularly in children), despite optimal medical therapy (OMT), including charcoal haemoperfusion and haemodiafiltration. MARS is a new, cell-free, extracorporeal liver assistance method utilizing an albumin dialysate for the removal of albumin-bound toxins. Methods: We describe the first series in the literature (also first MARS treatments in Romania) with ALF because of mushroom poisoning in children (M/F =2/4, age= 7-16 years). Liver function was evaluated pre-MARS and 15-min post-MARS, 24 h following each treatment and 30 days post-MARS. Findings: All patients had severe hepatic dysfunction: hepatic encephalopathy (HE; four grade II, one grade III, one grade IV), ALT=4082 (3400-5600)IU/L, bilirubin = 6.3 (2-10) mg/dL, prothrombin time (PT) = 52.5 (23-141) s. MARS was uneventful and well-tolerated. Two 6-h sessions per patient were performed with a similar immediate impact on liver tests: mean drop in ALT of -33 and -35%, respectively, and in bilirubin of -39 and -36%, respectively. ALT levels 24 h following MARS-1, remained unchanged but continued to drop by a further -28% following MARS-2. By contrast, all patients

had a significant rebound in bilirubin (+39%) 24 h following MARS-1; however, following MARS-2 a rebound was seen only in two cases (+220%). PT improved by 37% after MARS-1 and normalized in four patients after MARS-2. Outcome: Four patients survived and completely recovered the hepatic function. Negative prognostic markers: lack of complete correction of PT, continuous rebound and increase in bilirubin, and lack of improvement in HE post-MARS-1. Survival in six well-matched cases, treated by OMT = 0/6 ($P < 0.05$). Conclusions: MARS is a safe and highly effective depurative therapy in children with ALF. Survival is predicted only by the impact/results of the initial MARS sessions and not by any of the baseline parameters.

Author Keywords
Acute hepatic failure; Albumin dialysis; Children; MARS system; Mushroom poisoning

Document Type: Article
Source: Scopus

Tateno, H., Goldstein, I.J.
Molecular Cloning, Expression, and Characterization of Novel Hemolytic Lectins from the Mushroom Laetiporus sulphureus, Which Show Homology to Bacterial Toxins
(2003) *Journal of Biological Chemistry*, 278 (42), pp. 40455-40463. Cited 17 times.

Dept. of Biological Chemistry, Univ. of Michigan Medical School, Ann Arbor, MI 48109-0606, United States

Abstract
We describe herein the cDNA cloning, expression, and characterization of a hemolytic lectin and its related species

from the parasitic mushroom Laetiporus sulphureus. The lectin designated LSL (L. sulphureus lectin), is a tetramer composed of subunits of ~35 kDa associated by non-covalent bonds. From a cDNA library, three similar full-length cDNAs, termed LSLa, LSLb, and LSLc, were generated, each of which had an open reading frame of 945 bp encoding 315 amino acid residues. These proteins share 80-90% sequence identity and showed structural similarity to bacterial toxins: mosquitocidal toxin (MTX2) from Bacillus sphaericus and α toxin from Clostridium septicum. Native and recombinant forms of LSL showed hemagglutination and hemolytic activity and both activities were inhibited by N-acetyllactosamine, whereas a C-terminal deletion mutant of LSLa (LSLa-D1) retained hemagglutination, but not hemolytic activity, indicating the N-terminal domain is a carbohydrate recognition domain and the C-terminal domain functions as an oligomerization domain. The LSL-mediated hemolysis was protected osmotically by polyethylene glycol 4000 and maltohexaose. Inhibition studies showed that lacto-N-neotetraose (Galβ1-4GlcNAcβ1-3Galβ1-4Glc) was the best inhibitor for LSL. These results indicate that LSL is a novel pore-forming lectin homologous to bacterial toxins.

Document Type: Article
Source: Scopus

Wu, B.F., Yang, J.Y., Jiang, C.Q., Huang, R.H., Liu, W.W.
Blood purification, plasma exchange and molecular adsorbents recycling system recur the amanita phalloides mushroom poisoning patients with severe hepatic damage
(2003) *Zhonghua gan zang bing za zhi = Zhonghua ganzangbing zazhi = Chinese journal of hepatology*, 11 (8), p. 507.

12th People's Hospital, Guangzhou 510620, China.

Document Type: Article
Source: Scopus

Sun, N.K., Song, K.B.
Effect of nonthermal treatment on the molecular properties of mushroom polyphenoloxidase
(2003) *Journal of Food Science*, 68 (5), pp. 1639-1643. Cited 4 times.

Dept. of Food Science and Technology, Coll. of Agric. and Life Sciences, Chungnam Natl. Univ., Daejeon, 305-764, South Korea

Abstract
To elucidate the mechanism of inactivation of mushroom polyphenoloxidase (PPO) by nonthermal treatment, PPO solutions were irradiated up to 10 kGy or pressurized at 600 MPa and 800 MPa, respectively. PPO activities were significantly affected by γ irradiation, and treatment at 5 kGy decreased the activity by 93%. Treatment of PPO at 600 MPa decreased the activity slightly, yet 10 and 20 min treatments at 800 MPa decreased the activities by 28% and 43%, respectively. Circular dichroism study showed that nonthermal treatment altered the ellipticity values in the range of 210 and 225 nm, resulting in decrease of the ordered structure. Fluorescence spectroscopy indicated that nonthermal treatment quenched the emission intensity.

Author Keywords
γ; Circular dichroism; Fluorescence spectroscopy; High pressure; Irradiation; Polyphenoloxidase

Document Type: Article
Source: Scopus

Vane, C.H.[a] , Drage, T.C.[b] , Snape, C.E.[b]

Biodegradation of oak (Quercus alba) wood during growth of the shiitake mushroom (Lentinula edodes): A molecular approach

(2003) *Journal of Agricultural and Food Chemistry*, 51 (4), pp. 947-956. Cited 21 times.

[a] British Geological Survey, Kingsley Dunham Centre, Keyworth, Nottingham NG12 5GG, United Kingdom
[b] Sch. of Chem., Environ./Mining Eng., University of Nottingham, Nottingham, NG7 2RD, United Kingdom

Abstract
The chemical transformations that occur during growth of the shiitake mushroom (Lentinula edodes) on oak (Quercus alba) were investigated to improve mushroom cultivation and utilization of the spent substrate. Oak logs were decayed by L. edodes over 8 years, during which time they were sampled at six intervals (30, 40, 66, 76, 77, and 101 months). Fresh and decayed oak samples were analyzed using solid-state 13C NMR and pyrolysis-gas chromatography-mass spectrometry as well as off-line thermochemolysis with tetramethylammonium hydroxide. Degraded oak exhibited lower carbon contents and increased oxygen content compared to the control. Solid-state 13C NMR analysis revealed that polysaccharides were the major component of both fresh and decayed oak but that L. edodes mediated the preferential loss of cellulose and xylans as compared to lignin, which remained in an altered form. Several trends point

toward the degradation of lignin, including a decrease in the proportion of syringyl units as compared to guaiacyl units and a reduction in side-chain length. An increase in guaiacyl and syringyl acid-to-aldehyde ratios occurred with growth, which suggested that the fungus had caused oxidation of Cα-Cβ bonds. The overall effect of L. edodes on oak is similar to that of many white-rot fungi, which simultaneously degrade all cell wall components.

Author Keywords
Degradation; Lentinula edodes; Lignin; Oak; Polysaccharide; Pyrolysis; Quercus alba; Shiitake mushroom; Solid-state ^{13}C NMR; Thermochemolysis

Document Type: Article
Source: Scopus

Xu, J.[a] , Rao, J.R.[b] , Millar, B.C.[a] , Elborn, J.S.[c d] , Evans, J.[e] , Barr, J.G.[e] , Moore, J.E.[a]

Improved molecular identification of Thermoactinomyces spp. associated with mushroom worker's lung by 16S rDNA sequence typing

(2002) *Journal of Medical Microbiology*, 51 (12), pp. 1117-1127. Cited 6 times.

[a] N. Ireland Public Health Laboratory, Department of Bacteriology, Belfast City Hospital, Belfast BT9 7AD, United Kingdom

[b] Applied Plant Science Division, Department of Agriculture, Newforge Lane, Belfast BT9 5PX, United Kingdom

[c] Department of Respiratory Medicine, Belfast City Hospital, Belfast BT9 7AD, United Kingdom

[d] Department of Respiratory Medicine, Queen's University of Belfast, Royal Victoria Hospital, Grosvenor Road, Belfast BT12 6BA, United Kingdom

[e] Reg. Mycology Reference Laboratory, Department of Microbiology, Royal Group of Hospitals, Grosvenor Road, Belfast BT12 6BA, United Kingdom

Abstract

Mushroom worker's lung (MWL) is a hypersensitivity pneumonitis or allergic alveolitis caused by a type III IgG-mediated immunopathogenic inflammatory reaction in the host due to the inhalation of several thermophilic organisms, including Thermoactinomyces spp. It is difficult to distinguish phenotypically the eight species of this genus; therefore, this study sought to develop an improved molecular means of identifying Thermoactinomyces spp. associated with MWL by partial 16S rDNA PCR amplification and direct sequencing. Hypervariable regions within the 16S rRNA gene, which could be employed as signature sequences of the eight individual species, were identified and employed with highly conserved flanking primers to allow initial PCR amplification, before direct DNA sequencing of the 16S rDNA amplicons. A novel 24-mer 16S rDNA oligonucleotide upstream primer was designed from in silico alignments of all Thermoactinomyces spp. and was employed in combination with downstream (reverse) 16S rDNA primers. This permitted the successful identification of all four isolates associated with mushroom workers' lung. The method may be useful in the identification of Thermoactinomyces spp. associated with allergic alveolitis or pneumonitis associated with occupational exposure in agricultural and horticultural environments.

Document Type: Article
Source: Scopus

Sun, N., Lee, S., Song, K.B.

Effect of high-pressure treatment on the molecular properties of mushroom polyphenoloxidase

(2002) *LWT - Food Science and Technology*, 35 (4), pp. 315-318. Cited 7 times.

Department of Food Science and Technology, College of Agriculture, Chungnam National University, Taejon, 305-764, South Korea

Abstract

To elucidate the mechanism of pressure-induced denaturation of mushroom polyphenoloxidase (PPO), the enzyme was treated under 600 and 800 MPa, respectively, and its molecular properties such as secondary and tertiary structure were examined. High-pressure inactivation of the enzyme increased with pressure level and treatment time. Circular dichroism study showed that high-pressure treatment decreased the negative ellipticity values in the range 210-225 nm, resulting in change of the secondary structure of the enzyme. Fluorescence emission intensities also decreased with increase of high pressure and processing time, indicating changes in the tertiary structure of the enzyme. This study clearly shows that high-pressure treatment significantly alters the molecular properties of the enzyme. © 2002 Elsevier Science Ltd. All rights reserved.

Author Keywords

High-pressure treatment; Molecular properties; Polyphenoloxidase

Document Type: Article
Source: Scopus

Brauer, D., Kimmons, T., Phillips, M.

Effects of management on the yield and high-molecular-weight polysaccharide content of shiitake (Lentinula edodes) mushrooms

(2002) *Journal of Agricultural and Food Chemistry*, 50 (19), pp. 5333-5337. Cited 4 times.

Dale Bumpers Small Farms Res. Center, Agricultural Research Service, United States Dept. of Agriculture, 6883 South Highway 23, Booneville, AR 72927, United States

Abstract

Shiitake (Lentinula edodes (Berk.) Pegler) mushroom production in the United States has increased greatly over the last twenty years. Additional expansion of the shiitake mushroom market should be possible if the product can be marketed as a functional food, i.e., a food that has health-promoting effects beyond its nutritional value. High-molecular-weight polysaccharides (HMWP) including lentinan in shiitake may promote human health. This study was conducted to determine if management protocols influence the HMWP of shiitake mushrooms. Results indicate that measuring the total carbohydrate content of water-extractable, ethanol-insoluble polysaccharides was a simple way to estimate HMWP. Results also indicate that log-grown shiitake contained more HMWP than did substrate-grown shiitake. Among log-grown shiitake, both mushroom strain and tree species influenced HMWP content. The results suggest that there is considerable variation among shiitake mushrooms in HMWP content and that production protocols influenced the HMWP content of mushrooms.

Author Keywords

Carbohydrates; Growth conditions; Lentinan; Lentinula edodes; Log-grown; Shiitake mushroom; Strain; Substrate-grown; Tree species

Document Type: Article
Source: Scopus

Edvinsson, T.[a] , Elvingson, C.[a] , Arteca, G.A.[b]
Effect of compression on the molecular shape of polymer mushrooms with variable stiffness
(2002) *Journal of Chemical Physics*, 116 (21), pp. 9510-9517. Cited 7 times.

[a] Department of Physical Chemistry, Uppsala University, Box 532, S-751 21 Uppsala, Sweden
[b] Département de Chimie et Biochimie, Laurentian University, Sudbury, Ont. P3E 2C6, Canada

Abstract
The effect of compression on the molecular shape of polymer mushrooms with variable stiffness was discussed. Polymer mushroom is a single chain that is permanently anchored to a flat surface by an end point. Compression was introduced by confining the chains inside an infinite slab with parallel hard walls. The chain's size and its entanglement complexity were analyzed using Monte Carlo simulations. Results showed that flexible polymer with strong self-attraction sustained high compression without deforming and the polymers that were either too rigid or too weakly self-attracting were flattened by slight compression.

Document Type: Article
Source: Scopus

Kamada, T.

Molecular genetics of sexual development in the mushroom Coprinus cinereus

(2002) *BioEssays*, 24 (5), pp. 449-459. Cited 33 times.

Department of Biology, Faculty of Science, Okayama University, Okayama 700-8530, Japan

Abstract

Sexual development in the mushroom Coprinus cinereus is under the control of two mating type loci, A and B. When two haploid homokaryons with compatible alleles at both A and B loci are mated, the coordinated activities of A- and B-regulated pathways lead to formation of a mycelium termed the dikaryon, in which the two nuclei from the mating partners pair in each cell without fusing. The dikaryon is a prolonged mycelial stage that can be induced to develop a multicellular structure, the mushroom, under proper environmental conditions. The two nuclei fuse in specialized cells on the mushroom and immediately undergo meiosis to complete the sexual life cycle, it has been established recently that the A genes encode two classes of homeodomain proteins while the B genes encode pheromones and their receptors. More recently, molecular genetics has been used to reveal genes that work downstream of the mating type genes to regulate dikaryon formation, mushroom morphogenesis, and meiosis. © 2002 Wiley Periodicals, Inc.

Document Type: Review
Source: Scopus

Shishido, K.

Molecular mechanism of fruiting-body formation in the basidiomycete mushroom
(2002) *Nippon Nogeikagaku Kaishi*, 76 (10), pp. 951-953.

Author Keywords
A kinase; Developmental regulation; Lentinula edodes; Target gene; Transcription factor

Document Type: Article
Source: Scopus

Krüger, D., Binder, M., Fischer, M., Kreisel, H.
The lycoperdales. A molecular approach to the systematics of some gasteroid mushrooms
(2001) *Mycologia*, 93 (5), pp. 947-957. Cited 17 times.

University of Tennessee, Department of Botany, 437 Hesler Biology Building, Knoxville, TN 37996-1100, United States

Abstract
Based on selected taxa of Lycoperdales and Geastrales, phylogeny and delimitation of several gasteroid mushroom genera were investigated using RFLP and sequence analysis of 18S rDNA and ITS rDNA (ITS1-5.8S-ITS2). Support for an Agaricales-Lycoperdales relationship was found, the Geastrales being clearly separated from this lineage. Within the Lycoperdales, Lycoperdon was found to be polyphyletic, whereas Bovista appeared to be monophyletic.

Author Keywords
Basidiomycotina; Bovistella; Calvatia; Capillitium; Gasteromycetes; Geastrum; Lycoperdon; Morganella; Mycenastrum; Myriostoma; Vascellum

Document Type: Article
Source: Scopus

Pennisi, E.
A molecular approach to mushroom hunting
(2001) *Science*, 293 (5532), pp. 1027-1028.

Document Type: Note
Source: Scopus

Hibbett, D.S.[a b]
Shiitake mushrooms and molecular clocks: Historical biogeography of Lentinula
(2001) *Journal of Biogeography*, 28 (2), pp. 231-241. Cited 19 times.

[a] Harvard University Herbaria, 22 Divinity Avenue, Cambridge, MA 02138, United States
[b] Department of Biology, Clark University, 950 Main Street, Worcester, MA 01610-1477, United States

Abstract
Aim: Fungi make up a large, ecologically important group of eukaryotes that has been neglected in historical biogeography. In this study, molecular phylogenies and molecular clock dating were used to infer historical biogeography of the shiitake genus, Lentinula Earle, which occurs in both the Old World and New World. The major goals of this study were to determine if the Old World and New World groups are monophyletic, and whether the Old World/New World disjunction is the result of vicariance or long distance dispersal. Location: Collections studied are from

Asia, Australasia, the Gulf Coast region of North America, the Caribbean, Central America, and northern South America. Methods: Phylogenetic trees were inferred with nuclear large subunit (nuc-Isu) ribosomal DNA (rDNA) and internal transcribed spacer (ITS) sequences. Molecular clock dating was performed using trees derived from nuc-Isu rDNA and mitochondrial small-subunit (mt-ssu) rDNA sequences. Rate constancy was tested with maximum likelihood, and clocks were calibrated using evidence from fossils or other molecular clock studies, or according to expected ages under different historical biogeographic scenarios. Results: Analyses of ITS and nuc-Isu rDNA sequences suggest that there are seven species of Lentinula worldwide, which occur in two main clades, one in the New World the other in the Old World. Rate constancy cannot be rejected in nuc-Isu rDNA, but can be rejected in mt-ssu rDNA. Both genes suggest that the Old World/New World disjunction could be due to fragmentation of an ancient Laurasian range. An alternative Gondwanan hypothesis is not supported by the molecular clock age estimates. Main conclusions: Only one long distance dispersal event must be invoked in Lentinula, that being between Australia and New Zealand. Despite having airborne spores, it appears that long distance dispersal is rare in Lentinula. This may also be true in other fungi, which are therefore excellent candidates for historical biogeographic studies using molecular characters.

Author Keywords
Beringia; Biogeography; Fungi; Lentinula; Maximum likelihood; Molecular clock; Phylogeny

Document Type: Conference Paper
Source: Scopus

Ramírez, L.[a] , Muez, V.[a b] , Alfonso, M.[a] , García Barrenechea, A.[a] , Alfonso, L.[a] , Pisabarro, A.G.[a]

Use of molecular markers to differentiate between commercial strains of the button mushroom Agaricus bisporus

(2001) *FEMS Microbiology Letters*, 198 (1), pp. 45-48. Cited 8 times.

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[b] Gurelan, Huarte-Pamplona, Spain

Abstract

Agaricus bisporus is an edible basidiomycete cultivated industrially for food production. Different spawn and mushroom producers use genetically related A. bisporus strains frequently marketed as different products. In this paper we show that the use of suitable molecular markers reveals the high level of genetic homology of commercial strains of A. bisporus, and allows, at the same time, to distinguish between them. In the course of this work, a molecular marker potentially linked to the agronomic character 'mushroom weight' has been identified by bulked segregant analysis. © 2001 Federation of European Microbiological Societies.

Author Keywords

Agaricus bisporus; Bulked segregant analysis; Button mushroom; Molecular marker; Strain typing

Document Type: Article

Source: Scopus

Wang, H.[a b] , Ng, T.B.[b c]

Isolation and characterization of velutin, a novel low-molecular-weight ribosome-inactivating protein from winter mushroom (Flammulina velutipes) fruiting bodies

(2001) *Life Sciences*, 68 (18), pp. 2151-2158. Cited 36 times.

[a] Department of Microbiology, China Agricultural University, Beijing, Beijing, China

[b] Department of Biochemistry, Faculty of Medicine, Chinese University of Hong Kong, Shatin, Hong Kong

[c] Chinese University of Hong Kong, Department of Biochemistry, Faculty of Medicine, Shatin, NT, Hong Kong

Abstract

From the fruiting bodies of the edible mushroom Flammulina velutipes a single-chained ribosome inactivating protein with a molecular weight of 13.8 kDa was isolated with a procedure involving ion exchange chromatography on DEAE-cellulose and SP-Sepharose and affinity chromatography on Affi-gel blue gel. The protein was novel in that it possessed a molecular weight lower than those of previously reported RIPs and that it was capable of inhibiting human immunodeficiency virus (HIV-1) reverse transcriptase, β-glucosidase and β-glucuronidase. Its N-terminal sequence exhibited a certain degree of similarity to those of plant ribosome inactivating proteins. © 2001 Elsevier Science Inc.

Author Keywords

Fruiting body; Mushroom; Ribosome-inactivating protein

Document Type: Article

Source: Scopus

Collopy, P.D., Largeteau-Mamoun, M.L., Romaine, C.P., Royse, D.J.

Molecular phylogenetic analyses of Verticillium fungicola and related species causing dry bubble disease of the cultivated button mushroom, agaricus bisporus

(2001) *Phytopathology*, 91 (9), pp. 905-912. Cited 12 times.

Department of Plant Pathology, Pennsylvania State University, University Park, PA 16802, United States

Abstract

Molecular phylogenetic analyses were performed on 40 isolates of Verticillium fungicola collected from various Pennsylvania mushroom farms in 1999 and 28 isolates of Verticillium spp. collected during the last 50 years from various geographic locations. Sequence analysis of internal transcribed spacers 1 and 2 (ITS1 and ITS2) and 5.8S regions of the nuclear ribosomal DNA (rDNA) transcriptional unit and analysis of random amplified polymorphic DNA (RAPD) data were performed for the 68 isolates of Verticillium spp. Identical rDNA sequences were obtained for all 40 Pennsylvania isolates collected during 1999, 13 North American isolates collected during the last 50 years, and the ex-type strain of V. fungicola var. aleophilum. Sequence analysis of European isolates revealed a close relationship to the ex-type strain V. fungicola var. fungicola. No European-like isolates of V. fungicola var. fungicola were detected in the collection of North American isolates examined. Results from six decamer RAPD primers strongly indicate the presence of a clonal population of V. fungicola among Pennsylvania isolates. In addition, RAPD data delineated a Korean isolate (DC130) and ex-type strain V. fungicola var. aleophilum from the

North American group. Virulence assays, based on spore inoculation of mushroom pilei, revealed variation corresponding to each neighbor-joining and RAPD grouping. All isolates with rDNA sequence and RAPD grouping similarity to ex-type strains V. fungicola var. aleophilum and V. fungicola var. fungicola displayed the highest level of virulence. Based on rDNA sequence and RAPD analyses, isolates displaying reduced or no virulence were distantly related to these two varieties. All results obtained for the analyses of ex-type strain U. fungicola var. flavidum suggested that this fungal isolate should not be considered a variety of V. fungicola, but rather a distinct species.

Author Keywords
Acremonium strictum; Helicoon sessile; Nectria inventa; Orbilia luteorubella; Tolypocladium parasiticum; V. tenerum

Document Type: Article
Source: Scopus

Barroso, G.[a] , Sonnenberg, A.S.M.[b] , Van Griensven, L.J.L.D.[b] , Labarère, J.[a]

Molecular cloning of a widely distributed microsatellite core sequence from the cultivated mushroom Agaricus bisporus

(2000) *Fungal Genetics and Biology*, 31 (2), pp. 115-123. Cited 5 times.

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Horst, Netherlands

Abstract
An Agaricus bisporus microsatellite with the tetranucleotide motif TATG tandemly repeated was isolated from an A. bisporus library enriched in repeated sequences. The use of the 16-mer oligonucleotide (TATG)4 indicates that many loci contain nearby copies of the microsatellite in opposite orientations. The wide distribution of the microsatellite in the A. bisporus genome was assessed (i) by polyacrylamide gel electrophoresis of the products generated by directed amplification of microsatellite-region DNA (DAMD) and (ii) by hybridization of these products with A. bisporus chromosomes separated by pulsed-field gel electrophoresis. This is, to our knowledge, the first microsatellite reported in the cultivated edible mushrooms. DAMD-PCR products were generated using DNA of three Pleurotus species (P. pulmonarius, P. sajor-caju, and P. florida), indicating that (TATG)4 repeats are also present in these cultivated species. The variability found within closely related strains indicates that such microsatellites are useful in fingerprinting and studying genetic variability in wild and commercial mushrooms. © 2000 Academic Press.

Author Keywords
Agaricus bisporus; Basidiomycota; Directed amplification of microsatellite-region DNA (DAMD); Microsatellite; Mushroom; Pleurotus

Document Type: Article
Source: Scopus

Whiteford, J.R., Thurston, C.F.
The molecular genetics of cultivated mushrooms

(2000) *Advances in Microbial Physiology*, 42, pp. 1-23. Cited 5 times.

Division of Life Sciences, King's College London, Franklin-Wilkins Building, 150 Stamford Street, London SE1 8WA, United Kingdom

Abstract
The types, economic significance and methods of production of the principal cultivated mushrooms are described in outline. These organisms are all less than ideal for conventional genetic analysis and breeding, so molecular methods afford a particular opportunity to advance our understanding of their biology and potentially give the prospect of improvement by gene manipulation. The sequences described are limited to those found in GenBank by August 1999. The gene sequences isolated from the white button mushroom Agaricus bisporus, the shiitake Lentinula edodes, the oyster mushrooms Pleurotus spp., the paddy straw mushroom Volvariella volvacea and the enotake Flammulina velutipes are described. The largest group are genes from A. bisporus, which includes 29 for intracellular proteins and 12 for secreted proteins. In comparison, only a total of 26 sequences can be reported for the other cultivated species. A. bisporus is also the only cultivated species for which molecular karyotyping is already supported by reliable markers for all 13 of its chromosomes.

Document Type: Article
Source: Scopus

Rai, D.R.[a b] , Masuda, R.[a] , Saito, M.[a]
Effect of Modified Atmosphere Packaging on Low

Molecular Weight Carbohydrates of Oyster Mushrooms
(2000) *Journal of Food Science and Technology*, 37 (4), pp. 384-387. Cited 1 time.

[a] Food Packing Laboratory, National Food Research Institute, Min. of Agric., Forest. and Fish., 2-1-2, Kannondai, Tsukuba, Ibaraki, 305-8642, Japan

[b] Div. Agric. Struct. Environ. Contr., Ctrl. Inst. Post-harvest Eng. T., Punjab Agric. University Campus, Ludhiana-141 004, India

Abstract

Experiments were conducted to study the effect of modified atmosphere packaging on low molecular weight carbohydrates of oyster mushrooms (Pleurotus ostreatus), during post-harvest storage at 5 and 15° C, using highly permeable micro-perforated oriented polypropylene (OPP) film and ordinary OPP film packages. Changes in sugar and sugar alcohol contents among different treatments were measured, using high performance liquid chromatography (HPLC) technique. Among free sugars, trehalose content was observed to be varying between pileus and stipe portion of the mushroom, in response to in-pack gaseous environment. Increases in pileus and stipe portions trehalose and total sugar content were observed for mushrooms packaged in micro-perforated film packages at both the storage temperatures of 5° and 15° C, while they reduced in ordinary OPP film packages and the reduction was observed to be more in stipes than pileus, indicating that low O2 (0.4%) and high CO2 (12 to 13%) observed in these packages had more adverse effect on stipe portion trehalose and total sugar content. Among sugar alcohols, only mannitol was found to be affected under low O2 and high CO2 conditions, prevailing in ordinary OPP film packages at both

the storage temperatures.

Author Keywords
Free sugars; Micro-perforated films; Modified atmosphere packaging; Oyster mushroom; Post-harvest storage; Sugar alcohols

Document Type: Article
Source: Scopus

Kamalov, L.S., Agzamova, M.A., Aripova, S.F., Isaev, M.I.
Low-molecular-weight mushroom metabolites. IV. Slightly polar components of Stachybotrys alternans
(2000) *Chemistry of Natural Compounds*, 36 (2), pp. 170-172. Cited 1 time.

S. Yu. Yunuson Inst. of the C., Acad. of Sci. of the Rep. of U., Tashkent, Uzbekistan

Abstract
Slightly polar fractions of low-molecular-weight metabolites of Stachybotrys alternans contain 10 components: 2(E)-decenal, 2(E)-undecenal, ionol, ethylpalmitate, ethylstearate, ethyloleinate, palmitic, stearic, and oleinic acids, and ergosterol.

Author Keywords
Ergosterol; Fatty acids; Stachybotrys alternans

Document Type: Article
Source: Scopus

Kamalov, L.S., Agzamova, M.A., Aripova, S.F., Isaev, M.I.

Low-molecular-weight mushroom metabolites. V. Eburicoic acid from Polyporus ailanthus
(2000) *Chemistry of Natural Compounds*, 36 (1), pp. 72-75. Cited 3 times.

S. Yu. Yunusov Inst. of the C., Acad. of Sci. of the Rep. of U., Tashkent, Uzbekistan

Abstract
The triterpene acid isolated from Polyporus ailanthus (Aphyllophorales) is identified as eburicoic acid on the basis of 1H and 13C NMR, electron-impact mass, and IR spectra.

Author Keywords
Mushrooms; Triterpene acid

Document Type: Article
Source: Scopus

Zhao, J., Kwan, H.S.
Characterization, molecular cloning, and differential expression analysis of laccase genes from the edible mushroom Lentinula edodes
(1999) *Applied and Environmental Microbiology*, 65 (11), pp. 4908-4913. Cited 53 times.

Department of Biology, Chinese University of Hong Kong, Shatin, N.T., Hong Kong

Abstract
The effect of different substrates and various developmental stages (mycelium growth, primordium appearance, and fruiting-body formation) on laccase production in the edible mushroom Lentinula edodes was studied. The cap of the

mature mushroom showed the highest laccase activity, and laccase activity was not stimulated by some well-known laccase inducers or sawdust. For our molecular studies, two genomic DNA sequences, representing allelic variants of the L. edodes lac1 gene, were isolated, and DNA sequence analysis demonstrated that lac1 encodes a putative polypeptide of 526 amino acids which is interrupted by 13 introns. The two allelic genes differ at 95 nucleotides, which results in seven amino acid differences in the encoded protein. The copper-binding domains found in other laccase enzymes are conserved in the L. edodes Lac1 proteins. A fragment of a second laccase gene (lac2) was also isolated, and competitive PCR showed that expression of lac1 and lac2 genes was different under various conditions. Our results suggest that laccases may play a role in the morphogenesis of the mushroom. To our knowledge, this is the first report on the cloning of genes involved in lignocellulose degradation in this economically important edible fungus.

Document Type: Article
Source: Scopus

Murata, H.

Molecular cloning of glpFKRD of a mushroom-pathogenic bacterium, Pseudomonas tolaasii strain PT814: Induction of an avirulent mutant carrying a single mini-Tn5km 1 insertion in glpD

(1999) *Mycoscience*, 40 (4), pp. 353-358.

Division of Bio-Resource Development, Forestry/Forest Products Res. Inst., P.O. Box 16, Tsukuba-Norin 305-8687, Japan

Abstract

Pseudomonas tolaasii strain PT814 causes brown blotch disease in cultivated mushrooms. A pleiotropic avirulent mutant was isolated by mini-Tn5km 1 insertion mutagenesis. The insertion was localized in an open reading frame (ORF) predicted to encode sn-glycerol-3-phosphate dehydrogenase (glpD). ORFs that should encode its regulator, kinase, and facilitator were also identified as the glp gene cluster in the bacterium. The data suggest that the glp system may contribute to the ecology of this pathogen.

Author Keywords
GlpD; GlpFKRD; Mini-Tn5km 1; Pathogenicity; Pleurotus ostreatus; Pseudomonas tolaasii

Document Type: Article
Source: Scopus

Kersten, M.A.S.H.[a] , Müller, Y.[b] , Baars, J.J.P.[c] , Op Den Camp, H.J.M.[a] , Van Der Drift, C.[a] , Van Griensven, L.J.L.D.[c] , Visser, J.[b] , Schaap, P.J.[b]

NAD+-dependent glutamate dehydrogenase of the edible mushroom Agaricus bisporus: Biochemical and molecular characterization

(1999) *Molecular and General Genetics*, 261 (3), pp. 452-462. Cited 7 times.

[a] Dept. of Microbiol./Evolutionary B., Faculty of Science, University of Nijmegen, Toernooiveld 1, NL-6525 ED Nijmegen, Netherlands
[b] Sect. Molec. Genet. of Indust. M., Wageningen Agricultural University, Dreijenlaan 2, NL-6703 HA, Wageningen, Netherlands

[c] Mushroom Experimental Station, P.O. Box 6042, NL-5960 AA, Horst, Netherlands

Abstract
The NAD+-dependent glutamate dehydrogenase (NAD-GDH) of Agaricus bisporus, a key enzyme in nitrogen metabolism, was purified to homogeneity. The apparent molecular mass of the native enzyme is 474 kDa comprising four subunits of 116 kDa. The isoelectric point of the enzyme is about 7.0. K(m) values for ammonium, 2-oxoglutarate, NADH, glutamate and NAD+ were 6.5, 3.5, 0.06, 37.1 and 0.046 mM, respectively. The enzyme is specific for NAD(H). The gene encoding this enzyme (gdhB) was isolated from an A. bisporus H39 recombinant λ phage library. The deduced amino acid sequence specifies a 1029-amino acid protein with a deduced molecular mass of 115,463 Da, which displays a significant degree of similarity with NAD-GDH of Saccharomyces cerevisiae and Neurospora crassa. The ORF is interrupted by fifteen introns. Northern analysis combined with enzyme activity measurements suggest that NAD-GDH from A. bisporus is regulated by the nitrogen source. NAD-GDH levels in mycelium grown on glutamate were higher than NAD-GDH levels in mycelium grown on ammonium as a nitrogen source. Combined with the kinetic parameters, these results suggest a catabolic role for NAD-GDH. However, upon addition of ammonium to the culture transcription of the gene is not repressed as strongly as that of the gene encoding NADP-GDH (gdhA). To date, tetrameric NAD-GDHs with large subunits, and their corresponding genes, have only been isolated from a few species. This enzyme represents the first NAD-GDH of basidiomycete origin to be purified and is the first such enzyme from basidiomycetes whose sequence has been determined.

Author Keywords
Agarcius bisporus; Gene structure; Molecular cloning; NAD^+-specific glutamate dehydrogenase

Document Type: Article
Source: Scopus

Ospina-Giraldo, M.D., Royse, D.J., Chen, X., Romaine, C.P.
Molecular phylogenetic analyses of biological control strains of Trichoderma harzianum and other biotypes of Trichoderma spp. associated with mushroom green mold
(1999) *Phytopathology*, 89 (4), pp. 308-313. Cited 27 times.

Department of Plant Pathology, Pennsylvania State University, University Park, PA 16802, United States

Abstract
A polymerase chain reaction-amplified DNA containing the internal transcribed spacer (ITS)-1, 5.8S, and ITS-2 regions of the nuclear ribosomal DNA transcriptional unit was sequenced for 81 isolates of Trichoderma spp. associated with mushroom culture or used for biological control of plant pathogens. Phylogenetic analyses revealed that the biocontrol isolates were more closely related to an isolate of T. harzianum biotype 1 (Th1) than to the aggressive biotypes 2 and 4. Th1 has been isolated from mushroom compost but is not the cause of widespread green mold epidemics that have occurred during the last 12 years in Europe and North America. Three isolates of T. harzianum obtained from shiitake (Lentinula edodes; Shi1B and S3-96) and maitake (Grifola frondosa; Mail) substrates were placed within the biocontrol group. We also found evidence suggesting that

some isolates of T. harzianum originally identified as Th4 from Pennsylvania are more closely related to Th2 from Europe. Finally, considering the wide range in sequence distribution of our samples, we propose that the consensus sequence found in this investigation be used as the reference sequence for further studies involving the identification and taxonomy of T. harzianum.

Author Keywords
Agaricus bisporus; ITS sequences; Systematics

Document Type: Article
Source: Scopus

De Groot, P.W.J.[a] , Visser, J.[a] , Van Griensven, L.J.L.D.[b] , Schaap, P.J.[a]

Biochemical and molecular aspects of growth and fruiting of the edible mushroom Agaricus bisporus

(1998) *Mycological Research*, 102 (11), pp. 1297-1308. Cited 8 times.

[a] Sect. Molec. Genet. Indust. M., Wageningen Agricultural University, Dreijenlaan 2, NL-6703 HA, Wageningen, Netherlands
[b] Mushroom Experimental Station, P.O. box 6042, NL-5960 AA, Horst, Netherlands

Abstract
The introduction of recombinant DNA technology in the field of mushroom research has resulted in the cloning and characterization of a large number of genes. In order to study the genetics of compost colonization of A. bisporus, genes

encoding enzymes involved in utilization of this substrate have been isolated. In addition, a number of genes which are induced in fruit bodies during fruit body development have been cloned and they will provide more insight in the genetics of this economically important aspect of the life cycle. Other genes that were cloned encode proteins of basic biochemical routes. They provide knowledge on the importance and regulation of these routes in the life cycle of A. bisporus and add to knowledge on the general architecture of A. bisporus genes. Here we present an overview of the currently available biochemical and molecular data of A. bisporus and we discuss the importance of the available genes as genetic markers for breeding purposes.

Document Type: Article
Source: Scopus

Castle, A.[a d] , Speranzini, D.[a e] , Rghei, N.[a] , Alm, G.[b] , Rinker, D.[b] , Bissett, J.[c]

Morphological and molecular identification of Trichoderma isolates on North American mushroom farms

(1998) *Applied and Environmental Microbiology*, 64 (1), pp. 133-137. Cited 29 times.

[a] Brock University, St. Catharines, Ont. L2S 3A1, Canada

[b] Hort. Research Institute of Ontario, Vineland Station, Ont. LOR 2E0, Canada

[c] E. Cereal and Oilseed Res. Centre, Central Experimental Farm, Ottawa, Ont. K1A 0C6, Canada

[d] Department of Biological Sciences, Brock University, St. Catharines, Ont. L2S 3A1, Canada

[e] Ontario Ministry of Agriculture, Food and Rural Affairs, Ridgetown Coll. of Agric. Technology, Ridgetown, Ont. N0P 2C0, Canada

Abstract
Green mold disease (causal agent, Trichoderma) has resulted in severe crop losses on mushroom farms worldwide in recent years. We analyzed 160 isolates of Trichoderma from mushroom farms for morphological, cultural, and molecular characteristics and classified these isolates into phenotypic groups. The most common group comprised approximately 40% of the isolates and was identified as a strain of Trichoderma harzianum. This group was consistently recovered from farms with severe green mold disease but not from farms with little or no problem. In addition, the strain identified as the major cause of green mold disease in Ireland and the United Kingdom grouped with these North American isolates in having very similar randomly amplified polymorphic DNA patterns.

Document Type: Article
Source: Scopus

Arteca, G.A.
Molecular shape changes in compressed polymer mushrooms with variable excluded volume
(1997) *Anales de Quimica*, 93 (4), pp. 237-245. Cited 3 times.

Département de Chimie et Biochimie, Laurentian University - Université Laurentienne, Ramsey Lake Road, Sudbury, Ont. P3E 2C6, Canada

Abstract
The behaviour of polymer chains at interfaces is central to the understanding of adhesion and lubrication, among other topics. Experiments and computer simulations indicate that boundary conditions may have remarkable effects on the nature of the conformers accessible to a polymer. Yet the effect of configurational rearrangements on the mean molecular shape of a polymer is far from trivial and is only beginning to be understood. In this work, we study the changes in molecular shape that accompany configurational transitions induced by compression. We deal with the regime of a single chain grafted to a flat surface (a "polymer mushroom"). We consider a chain of constant length compressed between two flat surfaces. For this model, we analyze the changes in molecular size and chain entanglements due to two factors: (i) a variable wall separation (compression), and (ii) a variable excluded volume interaction (or solvent quality). We have analyzed how the changes in shape descriptors relate to the "size" of the configurational space. Our results indicate the presence of shape transitions for moderate values of the monomermonomer interaction and strong compressions. In these transitions, the molecular size passes through a minimum and the chain entaglements are maximized, although at different values of the geometrical confinement. We provide an interpretation of this difference in terms of the changes in configurational space during compression. Our results reinforce the notion that a full understanding of transitions in polymer shape requires the use of two or more independent shape descriptors. © Springer-Verlag Ibérica 1997.

Author Keywords
Asphericity; Conformational transitions; Entanglements; Grafted polymers; Molecular shape

Document Type: Article
Source: Scopus

Kersten, M.A.S.H.[a] , Müller, Y.[b] , Op den Camp, H.J.M.[a] , Vogels, G.D.[a] , Van Griensven, L.J.L.D.[c] , Visser, J.[b] , Schaap, P.J.[b]

Molecular characterization of the glnA gene encoding glutamine synthetase from the edible mushroom Agaricus bisporus

(1997) *Molecular and General Genetics*, 256 (2), pp. 179-186. Cited 15 times.

[a] Department of Microbiology, Faculty of Science, University of Nijmegen, Toernooiveld 1, NL-6525 ED Nijmegen, Netherlands

[b] Sect. Molec. Genet. Indust. M., Wageningen Agricultural University, Dreijenlaan 2, NL-6703 HA Wageningen, Netherlands

[c] Mushroom Experimental Station, P.O. Box 6042, NL-5960 AA Horst, Netherlands

Abstract

The gene encoding glutamine synthetase (glnA) was isolated from an Agaricus bisorus H39 recombinant λ phage library. The deduced A. bisporus glutamine synthetase amino acid sequence contains 354 residues. The amino acid sequence is very similar to that derived from the gene coding for glutamine synthetase of the yeast Saccharomyces cerevisiae. The open reading frame is interrupted by four introns. Northern analysis revealed that transcription of the gene is repressed upon addition of ammonium to the culture but the

repression was not as strong as that of the gene encoding NADP+-dependent glutamate dehydrogenase (gdhA). Enzyme activities are low in the presence of ammonium, glutamine and albumin and do not correlate with the mRNA levels revealed by Northern analysis. This suggests that glutamine synthetase expression in A. bisporus is also post-transcriptionally regulated by the nitrogen source.

Author Keywords
Agaricus bisporus; Gene structure; Glutamine synthetase; Molecular cloning; Mushroom

Document Type: Article
Source: Scopus

Yasuda, T., Shishido, K.
Aggregation of yeast cells induced by the Arg-Gly-Asp motif-containing fragment of high-molecular-mass cell-adhesion protein MFBA, derived from the basidiomycetous mushroom Lentinus edodes
(1997) *FEMS Microbiology Letters*, 154 (2), pp. 195-200. Cited 7 times.

Department of Life Science, Fac. of Bioscience and Biotechnology, Tokyo Institute of Technology, Nagatsuta, Midori-ku, Yokohama 226, Japan

Abstract
A fruiting body-specific cDNA mfbAc, derived from the basidiomycete Lentinus edodes, has been shown to encode a high-molecular-mass (2157 amino acids) cell-adhesion protein MFBA containing the Arg-Gly-Asp (RGD) motif. A 425-amino-acid fragment containing the RGD motif of MFBA (designated MFBA(582-1006) peptide) produced in

Escherichia coli exhibited cell-adhesion and spreading activity toward mammalian cells and cell-aggregation activity toward basidiomycetous hyphal cells via the RGD sequence. Here we investigated the biological activity of MFBA(582-1006) peptide in Saccharomyces cerevisiae. The DNA sequence encoding MFBA(582-1006) peptide, introduced into the yeast using an expression vector, resulted in a marked aggregation of the yeast cells. The aggregation was almost completely abolished by replacement of the RGD motif by an RGE motif in the peptide sequence.

Author Keywords
Arg-Gly-Asp (RGD) motif; Basidiomycete; Cell aggregation; Yeast

Document Type: Article
Source: Scopus

Chaure, P.T.[a] , Casselton, L.A.[a] , Connerton, I.F.[b]
Molecular analysis of the isocitrate lyase gene (acu-7) of the mushroom Coprinus cinereus
(1997) *Gene*, 184 (2), pp. 185-187. Cited 3 times.

[a] Department of Plant Sciences, University of Oxford, South Parks Road, Oxford, OX1 3RB, United Kingdom
[b] Dept. of Food Macromolec. Sciences, Institute of Food Research, Reading, RG6 6BZ, United Kingdom

Abstract
The nucleotide sequence of the structural gene for isocitrate lyase (acu-7) is presented and features of its coding sequence and predicted protein are described. Several motifs were identified within the promoter region which are potentially

involved in transcriptional regulation. Surprisingly, some of these occur within the coding sequence of an adjacent gene of unrelated function that terminates within 371 bp upstream from acu-7. The sequence of this second gene identified an N-acetylglucosamine-1-phosphate transferase.

Author Keywords
Amino acid sequence; Gene structure; Isocitrate lyase; N-acetylglucosamine-1-phosphate transferase

Document Type: Article
Source: Scopus

Thorn, G.

Molecular genetic characterization of bacterial isolates causing brown blotch on cultivated mushrooms in Japan

(1996) *Mycoscience*, 37 (4), pp. 409-416. Cited 5 times.

Center for Microbial Ecology, Michigan State University, East Lansing, MI, United States

Abstract
The polymerase chain-reaction (PCR) was used to amplify 16S ribosomal DNA (16S rDNA) from bacteria, identified as Pseudomonas tolaasii or P. fluorescens, causing brown blotch on cultivated mushrooms in Japan. PCR-amplified 16S rDNA was analyzed on the basis of nucleotide sequence and restriction fragment length polymorphisms (RFLP) to determine the specific identity of isolates. Banding patterns obtained through PCR using primers corresponding to repetitive extragenic palindromic sequences of enteric bacteria (REP-PCR) were used to determine the relatedness of conspecific isolates. All P. tolaasii isolates and a mushroom

pathogen identified as P. fluorescens had identical RFLP patterns end partial 16S sequences, and are considered conspecific. An isolate of P. fluorescens from creamery wastes (IFO 3507) differed slightly from isolates of P. tolaasii in both 16S sequence (0.8%) and RFLP patterns (d = 0.08), and had almost entirely different REP-PCR bands (d=O.88-1.0). Phylogenetic analyses based on 16S sequences indicated that P. tolaasii and P. fluorescens are close members of Pseudomonas sensu stricto. REP-PCR shows promise in characterizing isolates pathogenic on different mushroom crops. Two isolates of P. tolaasii pathogenic on Pleurotus ostreatus had identical banding patterns, but three isolates from Lentinula ododes showed the greatest diversity.

Author Keywords
Agaricus brunnescens; bacterial disease; Lentinula edodes; Pseudomonas fluorescens; Pseudomonas tolaasii; REP-PCR

Document Type: Article
Source: Scopus

Kondoh, O.[a] , Muto, A.[a c] , Kajiwara, S.[a d] , Takagi, J.[b] , Saito, Y.[b] , Shishido, K.[a]

A fruiting body-specific cDNA, mfbAc, from the mushroom Lentinus edodes encodes a high-molecular-weight cell-adhesion protein containing an Arg-Gly-Asp motif

(1995) *Gene*, 154 (1), pp. 31-37. Cited 27 times.

[a] Department of Life Science, Tokyo Institute of Technology, Nagatsuta, Midori-ku, Yokohama 227, Japan
[b] Department of Biological Science, Tokyo Institute of

Technology, Nagatsuta, Midori-ku, Yokohama 227, Japan
[c] Institute of Medical Science, University of Tokyo, 4-6-1 Shiroganedai, Minato-ku, Tokyo 108, Japan
[d] Central Laboratories for Key Technology, Kirin Brewery Co., Ltd., 1-13-5 Fukuura, Kanazawa-ku, Yokohama 236, Japan

Abstract
A cDNA clone (designated mfbAc), encoding 2157 amino acids (aa), was isolated from a mature fruiting-body cDNA library of the edible mushroom Lentinus edodes. The mfbA transcript was abundant in mature fruiting bodies, detectable in immature fruiting bodies but absent in earlier developmental stages and in the vegetative mycelium. Although more abundant in the pileus than the stipe, only low levels were found in the gill tissue. The deduced MFBA protein (234.5 kDa) contained a cell-surface attachment-promoting Arg-Gly-Asp (RGD) motif. MFBA was produced in Escherichia coli using a maltose-binding protein (MBP) fusion vector, but it was cleaved into four fragments even in a protease-deficient host. A 425-aa MFBA peptide containing the RGD motif (named MFBA(582-1006) peptide) was successfully produced using the phage T7 expression system. This MFBA(582-1006) peptide exhibited a cell adhesion and spreading activity toward mammalian cells. This activity of the MFBA fragment was competitively inhibited by the Gly-Arg-Gly-Asp-Ser-Pro peptide but not by the Gly-Arg-Gly-Glu-Ser-Pro peptide, showing that the RGD motif of MFBA is essential for the cell-binding activity.

Author Keywords
Discoidin I; Fibronectin; Mammal; N-glycosylation; Northern blotting; Promoter; Recombinant DNA; RGD; Spread morphology

Document Type: Article
Source: Scopus

Shishido, K.
Recent advance in molecular biology of the basidiomycetous mushrooms
(1994) *Tanpakushitsu kakusan koso. Protein, nucleic acid, enzyme*, 39 (6), pp. 906-919.

Department of Life Science, Faculty of Bioscience and Biotechnology, Tokyo Institute of Technology, Yokohama, Japan.

Document Type: Review
Source: Scopus

Muthumeenakshi, S., Mills, P.R., Brown, A.E., Seaby, D.A.
Intraspecific molecular variation among Trichoderma harzianum isolates colonizing mushroom compost in the British Isles
(1994) *Microbiology*, 140 (4), pp. 769-777. Cited 70 times.

Horticulture Research International, Wellesbourne, Warwick CV35 9EF, United Kingdom

Abstract
The genetic diversity in Trichoderma harzianum isolates from mushroom compost was assessed using various molecular techniques. Restriction fragment length polymorphism (RFLP) analysis of ribosomal DNA (rDNA) and mitochondrial DNA (mtDNA) divided the 81 isolates into three major groups, 1, 2 and 3. There was no variation within a group in rDNA, while a low degree of polymorphism was detected in mtDNA. Random

amplified polymorphic DNA (RAPD) analysis of 30 randomly chosen isolates, with six primers, in general confirmed the RFLP groups. Nucleotide sequence determination of rDNA internal transcribed spacer (ITS) 1 revealed three distinct ITS types, 1, 2 and 3, possessed by isolates from the respective groups 1, 2 and 3. Based on these molecular data, group 2 isolates, which are aggressive colonizers of mushroom compost, could be clearly distinguished from the isolates belonging to the other two groups.

Author Keywords
Molecular variation; Mushroom compost; Systematics; Trichoderma harzianum

Document Type: Article
Source: Scopus

Bhaskaran, R., Yu, C.

NMR spectra and restrained molecular dynamics of the mushroom toxin viroisin

(1994) *International Journal of Peptide and Protein Research*, 43 (4), pp. 393-401. Cited 3 times.

Department of Chemistry, National Tsing Hua University, Hsinchu 30043, Taiwan

Abstract
The conformation of viroisin, the monocyclic toxic heptapeptide of the virotoxin family from mushroom Amanita virosa, was analysed using two-dimensional nuclear magnetic resonance spectroscopy and restrained molecular dynamics simulations. All proton signals were completely assigned, and interproton distances were determined using data from rotating-frame nuclear Overhauser enhancement. The

backbone dihedral angles were deduced from measurements of coupling constants. The temperature dependence of the amide proton chemical shifts provided information about hydrogen bonding. Six probable solution conformations of viroisin were derived from the use of distance geometry and restrained molecular dynamics based on a set of distance constraints obtained from experimental data. The results of the structural analysis indicate that viroisin has a well ordered conformation in solution. In all these conformations the functional groups essential for toxicity orient themselves in the same direction so as to bind to the target proteins. This feature is consistent with previous results about the formation of a hydrophobic pocket on one side of the molecule.

Author Keywords
distance geometry; mushroom toxin viroisin; restrained molecular dynamics; solution conformation; three-dimensional structure; two-dimensional NMR

Document Type: Article
Source: Scopus

Rainey, P.B., Brodey, C.L., Johnstone, K.
Identification of a gene cluster encoding three high-molecular-weight proteins, which is required for synthesis of tolaasin by the mushroom pathogen Pseudomonas tolaasii
(1993) *Molecular Microbiology*, 8 (4), pp. 643-652. Cited 17 times.

NERC Inst. Virol./Environm Microbiol, Mansfield Road, Oxford OX1 3SR, United Kingdom

Abstract

The extracellular lipodepsipeptide toxin tolaasin is the primary disease determinant of pathogenicity of Pseudomonas tolaasii on the cultivated mushroom, Agaricus bisporus. Transposon mutagenesis of P. tolaasii NCPPB 1116 with Tn5-generated 5000 chromosomal insertions of which 35 (0.7%) were tolaasin negative and 12 (0.25%) produced a reduced amount of tolaasin. In addition, TnphoA mutagenesis yielded a single tolaasin-negative mutant which was phoA active. Restriction enzyme mapping of mutant DNAs by Southern hybridization analysis revealed that the majority of Tn5 insertions were confined to a single genetic locus of approximately 65 kbp. Pulsed-field gel electrophoresis of representative Tn5 mutant DNAs showed that this region is at one end of a 640 kbp PacI chromosomal fragment and that the P. tolaasii genome is 6.7 Mbp. SDS-PAGE analysis of protein extracts from wild-type P. tolaasii demonstrated the presence of three high-molecular-weight proteins (designated TL1, TL2 and TL3). Alterations in the presence of these proteins, as well as apparently truncated forms of the 465 kDa (TL1), 440 kDa (TL2) and 435 kDa (TL3) proteins were observed in some mutants, enabling the direction and order of the transcriptional units to be determined. Two other Tn5 mutations were also identified which resulted in a toolasin-negative phenotype, but which did not affect the expression of TL1, TL2, or TL3. One of these mutants is linked to the TL-cluster, but the other is located outside this region. It is concluded that at least five genetic loci, including encoding TL1, TL2 and TL3, are required for tolaasin synthesis.

Document Type: Article
Source: Scopus

Bonzli, P., Gerig, J.T.
Conformational analysis of the mushroom toxin

phallacidin by 1H NMR spectroscopy and restrained molecular dynamics
(1990) *Journal of the American Chemical Society*, 112 (10), pp. 3719-3726. Cited 7 times.

Department of Chemistry, University of California, Santa Barbara, CA 93106, United States

Document Type: Article
Source: Scopus

Bönzli, P., Gerig, J.T.
Conformational analysis of the mushroom toxin phallacidin by 1H NMR spectroscopy and restrained molecular dynamics
(1990) *Journal of the American Chemical Society*, 112 (10), pp. X-3725. Cited 1 time.

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Abstract
A conformational study of the toxin phallacidin [cyclo(Val1-erythro-3-hydroxy-D-Asp2-Cys 3-cis-4-hydroxy-Pro4-Ala5-2-mercapto-Trp 6-4,5-dihydroxy-Leu7)cyclic(3 → 6) sulfide] has been carried out using PMR spectroscopy and molecular dynamics simulations. An assignment of most of the resonances of the heptapeptide has been achieved, and internuclear distance information has been obtained from rotating frame NOE experiments. Temperature dependences of the amide NH chemical shifts and amide hydrogen-deuterium exchange rates were also examined. Energy minimization and molecular dynamics studies, carried out with the available experimental information as constraints,

define the orientations of those parts of the heptapeptide identified as being essential for toxicity and suggest that these groups can maintain their relative orientations in spite of high flexibility in some parts of the peptide backbone.

Document Type: Article
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Maddaluno, J.F., Faull, K.F.
Inhibition of mushroom tyrosinase by 3-amino-L-tyrosines: Molecular probing of the active site of the enzyme
(1988) *Experientia*, 44 (10), pp. 885-887. Cited 13 times.

Pasarow Analytical Neurochemical Facility, Nancys Pritzker Laboratory of Behavioral Neurochemistry, Department of Psychiatry and Behavioral Sciences, Stanford University School of Medicine, Stanford, 94305, California, United States

Abstract
We report the ability of 3-amino-L-tyrosine to act as a fully reversible competitive inhibitor of mushroom tyrosinase. The inhibition is linked to the ortho-aminophenol structure, and a coppe bridging mechanism in the active site is proposed. © 1988 Birkhäuser Verlag Basel.

Author Keywords
3-amino-L-tyrosine; di-copper active site; Mushroom tyrosinase inhibition; ortho-aminophenols

Document Type: Article
Source: Scopus

Smith, N.P.
From mushrooms to molecular biology. 100 years of skin tumours with particular reference to cutaneous lymphoma
(1988) *British Journal of Dermatology*, 119 (4), pp. 487-494.

Institute of Dermatology, St. John's Hospital for Diseases of the Skin, London WC2H 7BJ, United Kingdom

Document Type: Article
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Nakamura, H., Iitaka, Y., Kurasawa, S.
The crystal and molecular structure of a dibromo derivative of MS 3: a glyoxalase I inhibitor produced by a mushroom, Stereum hirsutum
(1976) *Agricultural and Biological Chemistry*, 40 (9), pp. 1781-1784. Cited 2 times.

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