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Foulongne-Oriol, M., Spataro, C., Savoie, J.-M.

Novel microsatellite markers suitable for genetic studies in the white button mushroom Agaricus bisporus

(2009) *Applied Microbiology and Biotechnology*, pp. 1-11. Article in Press.

UR1264 Mycologie et Sécurité des aliments, INRA, Centre de Recherche Bordeaux-Aquitaine, BP 81, Villenave d'Ornon cedex, 33883, France

Abstract

Co-dominant microsatellite molecular markers were obtained from the Agaricus bisporus cultivated mushroom. Their potential for both the molecular characterisation of commercial strains and the monitoring of the intraspecific genetic variation was demonstrated. The analysis of 673 unique sequences issued from public database and 59 from an enriched A. bisporus genomic library resulted in the development of a total of 33 single sequence repeat or microsatellite (SSR) markers. Their usefulness for genetic analysis was assessed on 28 strains, which include six cultivars representative of traditional lineage, two hybrids and 20 strains originating from wild populations. A. bisporus SSR markers displayed each from two to ten alleles, with an average of 5.6 alleles per locus. The observed heterozygosity ranged from 0 to 0.88. Cluster analysis resulting from SSR fingerprintings was in agreement with published A. bisporus population structure. A combination of only three selected SSR markers was sufficient to discriminate unambiguously 27

out of 28 distinct genotypes. However, the two genetically related hybrids were not distinguishable. Multiplexing was tested, and up to seven loci could be genotyped simultaneously. We are therefore reporting the first development in A. bisporus of a set of microsatellite markers powerful and suitable for genetic analysis. © 2009 Springer-Verlag.

Author Keywords
Agaricus bisporus; Genetic diversity; SSR; Strain typing

Document Type: Article in Press
Source: Scopus

Sha, T.[a] , Xu, J.[b] , Palanichamy, M.G.[a] , Zhang, H.-B.[a] , Li, T.[a] , Zhao, Z.-W.[a] , Zhang, Y.-P.[a]

Genetic diversity of the endemic gourmet mushroom Thelephora ganbajun from south-western China

(2008) *Microbiology*, 154 (11), pp. 3460-3468.

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Abstract

The ectomycorrhizal fungus Thelephora ganbajun is an endemic gourmet mushroom in Yunnan province, south-western China. However, despite its widespread consumer appeal, nutritional value and potential ecological role in natural forests, very little is known about its genetics, diversity and ecology. In this study, we investigated DNA

sequence variation at the internal transcribed spacer (ITS) regions among 156 specimens collected from 23 sites of nine regions in Yunnan Province. Our analysis identified a total of 34 ITS haplotypes and these haplotypes were clustered into five distinct phylogenetic groups. The evolutionary divergences among these clades are similar to or greater than many known sister species pairs within the genus Thelephora and the closely related genus Tomentella. Among the 34 ITS haplotypes, 22 were represented by one specimen each and the remaining 12 were each shared by two or more specimens. The most common haplotype contained 68 specimens distributed in 21 of the 23 sites, a result consistent with gene flow among geographical populations. However, analysis of molecular variance (AMOVA) revealed low but significant genetic differentiation among local and regional populations. Interestingly, the Mantel test identified that the extent of genetic differentiation was not significantly correlated with geographical distance. Our study revealed significant genetic divergence within Th. ganbajun and limited but detectable gene flow among geographical populations of this endemic ectomycorrhizal gourmet mushroom. © 2008 SGM.

Document Type: Article
Source: Scopus

Yang, H.[a] , Wu, J.[a] , Chen, X.[b] , He, Y.[b]
A new study on variety discrimination of fragrant mushrooms using genetic algorithm
(2008) *Proceedings of the World Congress on Intelligent Control and Automation (WCICA)*, art. no. 4594300, pp. 8697-8701.

[a] College of Information Engineering, Zhejiang University of Technology, Hangzhou 310032
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Abstract
The potential of genetic algorithm (GA) as a new way for the variety discrimination of fragrant mushrooms was evaluated. First, the visual/near infrared spectral data ranging from 375nm to 1025nm were collected by a spectrometer and then analyzed by principle component analysis (PCA) for space clustering. The resulting accumulative credibility of 94.37% based on the first three principle components (PCs) signifies that it is possible to establish a 3-D model for the variety discrimination of fragrant mushrooms. A new method which combines PCA with 3-D division planes established by genetic algorithm (GA) was proposed. In the test, a number of 195 samples from three varieties of fragrant mushrooms were examined, in which 150 samples were selected randomly for model-building and other 45 for model-prediction with the recognition rate over 91%. It proves feasible to adopt GA for the machine recognition of various fragrant mushrooms. © 2008 IEEE.

Author Keywords
Fragrant mushroom; Genetic algorithm; Principle component analysis; Space clustering; Visible-near infrared spectra

Document Type: Conference Paper
Source: Scopus

Miyazaki, K.[a] , Huang, F.[b] , Zhang, B.[b] , Shiraishi, S.[b] ,

Sakai, M.[c] , Shimaya, C.[d e] , Shishido, K.[f]

Genetic map of a basidiomycete fungus, Lentinula edodes (shiitake mushroom), constructed by tetrad analysis

(2008) *Breeding Science*, 58 (1), pp. 23-30.

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Abstract

We constructed a framework map of the edible mushroom Lentinula edodes (shiitake mushroom) using tetrad analysis. The map is based on the segregation of 264 randomly amplified polymorphic DNA (RAPD) markers, 14 structural genes, 1 expressed sequence tag (EST) marker, 2 mating factors (matA and matB), and 8 sequence-characterized amplified regions (SCARs) among 92 basidiosporic strains in 23 tetrads. We identified 11 linkage groups on a support

interval of a minimal LOD score of 3.0 and a maximum distance of 25 centimorgans (cM). The length of the 11 linkage groups (LGs) ranged from 157.2 cM to 24.4 cM, and they covered a distance of 908.8 cM. One of the quantitative trait loci controlling the vegetative growth rate on potato dextrose agar (PDA) for L. edodes was detected between the markers D18CCA-360t and S08-1000c on LG2.

Author Keywords
Framework map; Lentinula edodes; Quantitative trait loci; Tetrad analysis

Document Type: Article
Source: Scopus

Xu, J.[a b c] , Sha, T.[b] , Li, Y.-C.[a] , Zhao, Z.-W.[b] , Yang, Z.L.[a]
Recombination and genetic differentiation among natural populations of the ectomycorrhizal mushroom Tricholoma matsutake from southwestern China
(2008) *Molecular Ecology*, 17 (5), pp. 1238-1247. Cited 2 times.

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Abstract

Effective conservation and utilization strategies for natural biological resources require a clear understanding of the natural populations of the target organisms. Tricholoma matsutake is an ectomycorrhizal mushroom that forms symbiotic associations with plants and plays an important ecological role in natural forest ecosystems in many parts of the world. It is also an economically very important gourmet mushroom. Because no artificial cultivation is available, natural populations of this species are under increasing threats, primarily from habitat disturbance and destruction. Despite its economical and ecological importance, little is known about its genetics and population biology. Here, using 14 polymerase chain reaction-restriction fragment length polymorphism markers, we analysed 154 strains from 17 geographical locations in southwestern China, a region where over 25% of the global T. matsutake harvest comes from. Our results revealed abundant genetic variation within individual populations. The analyses of gene and genotype frequencies within populations indicated that most loci did not deviate from Hardy-Weinberg equilibrium in most populations and that alleles among loci were in linkage equilibrium in the majority of the local populations. These results are consistent with the hypothesis that sexual reproduction and recombination play an important role in natural populations of this species. Our analyses indicated low but significant genetic differentiation among the geographical populations, with a significant positive correlation between genetic distance and geographical distance. We discuss the implications of our results to the ecology and resource management of this species. © 2008 The Authors.

Author Keywords
Biodiversity; Conservation; Fungi; Matsutake mushroom; PCR-RFLP; SNP

Document Type: Article
Source: Scopus

Badalyan, S.M.[a] , Hughes, K.W.[b] , Sakeyan, C.Z.[a] , Helmbrecht, E.[b]

Morphology, growth characteristics, and genetic variability of the edible medicinal mushroom Flammulina velutipes (W. Curt.: Fr.) singer collections

(2006) *International Journal of Medicinal Mushrooms*, 8 (3), pp. 263-278.

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[b] Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN 37996, United States

Abstract
Mycelial micro- and macromorphology and growth characteristics, laccase activity tests, pigmentation, teleomorph formation, and genetic variability of 31 collections of the edible medicinal mushroom Flammulina velutipes have been investigated. The strains were isolated from fruiting bodies collected in different geographical regions and wood substrates. Two morphological types (A, B) and three subtypes (A1, A2, A-B) of mycelial colonies with different growth parameters were described in F. velutipes collections on different agar media. Correlations between morphological types and growth characteristics of colonies with substrate nature and geographical origination of strains have been revealed. However, in order to evaluate species-specific media responses for the described mycelial morphotypes,

further research with more strains is required. Mycelial macromorphology and growth parameters were more variable than the described microstructures (form, shape of clamp cells and crystals, asexual spores). Significant correlation between the mycelial morphotypes and genetic variability of screened F. velutipes strains has not been revealed. Genes for morphological and cultural variability may be unlinked to genes for the nuclear ribosomal repeat. Collections of putative F. velutipes were confirmed by rDNA-ITS sequencing to be F. velutipes with the exception of four collections as follows: SB71 (Armenia) is a hybrid or unknown biotype; collections SBIV-1 (Armenia) and SB317 (Germany) are identified as F. elastica; and R12 (Russia) as F. rossica. High genetic diversity was observed in Armenian collections of F. velutipes when compared to collections from Eurasia. At least 16 haplotypes were recovered in Armenian collections. This sequence diversity may be a consequence of the survival of an ancient genetic variation in the Caucasus and Armenia during the glaciation period, while in Europe, the genetic variation was extirpated. A subset of Armenian genetic diversity of F. velutipes is found in Europe. Morphological and growth characteristics of mycelium will assist in further biotechnological cultivation of F. velutipes. High genetic variability of Armenian collections may be used for improvement of strains to obtain novel biotech products and health-enhancing functional food additives from this valuable medicinal mushroom. © 2006 by Begell House, Inc.

Author Keywords
Flammulina velutipes; Genetic variability; Growth parameters; Macromorphology; Medicinal mushroom; Micromorphology; Mycelium

Document Type: Article
Source: Scopus

Zhang, J.X.[a b] , Huang, C.Y.[a] , Ng, T.B.[c] , Wang, H.X.[b]

Genetic polymorphism of ferula mushroom growing on Ferula sinkiangensis

(2006) *Applied Microbiology and Biotechnology*, 71 (3), pp. 304-309. Cited 4 times.

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[b] State Key Laboratory for Agrobiotechnology, Department of Microbiology, China Agricultural University, Beijing, 100094, China

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

Abstract

Mating tests, internal transcribed spacer (ITS) sequence analysis, intergenic spacer 1-restriction fragment length polymorphism (IGS1-RFLP), IGS1 sequence analysis, and IGS2-RFLP analysis were carried out on isolates of 17 morphologically different Pleurotus mushrooms collected on Ferula sinkiangensis. The isolates were divided, based on mating tests and ITS sequence analysis, into two groups identical to P. eryngii var. ferulae and P. nebrodensis, respectively. Single spores from these two groups were incompatible, but those from P. eryngii var. ferulae and P. eryngii were compatible and combined to produce 56.25% dikaryon mycelia with clamp connections. The ITS of P. eryngii var. ferulae and P. nebrodensis (GenBank accession no. AY311408) were both 638 bp in size but differed by 3% in sequence. P. eryngii var. ferulae and P. eryngii (GenBank accession no. AY368658) were identical in ITS size and

sequence. P. nebrodensis was the dominant population of Pleurotus mushroom growing on F. sinkiangensis. It exhibited genetic diversity. The two species could also be distinguished by IGSI-RFLP, similar to identification by mating tests and ITS sequence analysis. Difference in IGS1-RFLP existed between P. eryngii var. ferulae and P. nebrodensis. The sequence difference reached 2.28%. Both IGS1 size and IGS1-RFLP were similar among the different samples of P. nebrodensis. The 17 isolates were separated into five types based on IGS2 size and IGS2-RFLP, with both interspecies and extraspecies differences. P. nebrodensis exhibited polymorphism and was divided into four types. These results agreed with macroscopic differences. IGS2 might be the effective domain of genetically polymorphic ribosomal DNA in P. nebrodensis mushrooms found in Xinjiang, China. © Springer-Verlag 2005.

Document Type: Article
Source: Scopus

Neves, M.A.[a] , Kasuya, M.C.M.[b] , Araújo, E.F.[b] , Leite, C.L.[c] , Camelini, C.M.[a] , Ribas, L.C.C.[a] , De Mendonça, M.M.[a d]

Physiological and genetic variability of commercial isolates of culinary-medicinal mushroom Agaricus brasiliensis S. Wasser et al. (Agaricomycetideae) cultivated in Brazil

(2005) *International Journal of Medicinal Mushrooms*, 7 (4), pp. 553-563.

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Abstract

Agaricus brasiliensis S. Wasser et al. ("Cogumelo medicinal"), a culinary-medicinal mushroom native to Brazil, is cultivated mostly for exports. Strain characteristics influence productivity, but little is known about ecological and genetic variation among commercial strains. We examined six strains of A. brasiliensis to determine the characteristics of colony growth and genetic variability. Two colony growth studies were conducted: (1) on ordinary laboratory media, malt extract agar, and potato dextrose agar at several incubation temperatures (20°, 25°, 28°, 30° C); (2) on minimal media supplemented with glucose) at three pH (6.0, 7.0, 8.0). We also evaluated linear growth on "race tubes" filled with commercial compost (at 28° C). Generally, strain 22, commonly considered by producers to have low productivity, tended to grow the slowest on both media at all temperatures, with significant differences in rates found between it and all other strains on both media at 30° C. At pH 6.0, strain 22 grew more slowly than strains 21, 23, and 24 and presented similar rates to strains 33 and 34. At pH 8.0, no isolate was able to grow. Strain 22 also grew the slowest in race tubes. PCR-RFLPs of the ITS region identified all strains as A. brasiliensis. RAPD patterns identified two groupings: strain 22 and all other strains. Even though we

found low genetic variability, important strain characteristics (e.g., low colonization rate) considered related to productivity were detected for strain 22. We conclude that five of the strains may belong to the same ecological/genetic biotype. Low variability among Brazilian commercial strains might suggest a common origin of a single isolate recently brought into cultivation. © 2005 by Begell House, Inc.

Author Keywords
Agaricus brasiliensis; Culinary-medicinal mushrooms; Genetic variability; Intraspecific variability; Mycelium growth rate

Document Type: Article
Source: Scopus

Lakhanpal, T.N., Rana, M.
Medicinal and nutraceutical genetic resources of mushrooms
(2005) *Plant Genetic Resources: Characterisation and Utilisation*, 3 (2), pp. 288-303. Cited 2 times.

Department of Biosciences, Himachal Pradesh University, Summer Hill, Shimla-171 005, India

Abstract
Mushrooms are the fungi that have been used as food since time immemorial. Nutritionally they are a valuable source of health food, which is low in calories, and rich in carbohydrates, essential amino acids, fibre, important vitamins and minerals. Mushrooms have also been used in medicine for centuries in the Orient but their potential as health potentiators and elicitors of immune system is recent. In the last two decades there has been an upsurge on the use

of mushrooms as nutraceuticals and many edible species have been thoroughly investigated and authenticated for medicinal use. The species that have been properly analysed for medicinal value are: Ganoderma lucidum (Reishi), Lentinus edodes (Shiitake), Grifola frondosa (Maitake), Agaricus blazei (Himematsutake), Cordyceps militaris (Caterpillar fungus), Pleurotus ostreatus (Oyster mushroom) and Hericium erinaceous (Lions mane). There are many more species of cultivated and wild edible and non-edible mushrooms that have been analysed for both their nutritional and nutraceutical components but to a lesser extent than those listed above. The active constituents found in mushrooms are polysaccharides, dietary fibres, oligosaccharides, triterpenoids, peptides and proteins, alcohols and phenols, and mineral elements such as zinc, copper, iodine, selenium and iron, vitamins, amino acids etc. These have been found to boost the immune system, have anti-cancerous properties, act as anti-hypercholesterolaemic and hepato-protective agents, show anti-HIV activity and anti-viral activity, and ameliorate the toxic effect of chemo- and radiotherapy. Many of the species are known to be aphrodisiacs. Many commercial products from these mushrooms are available in the market. Prominent among these are: Lentinan from Lentinus edodes, Concord Sunchih and Reishi Plus from Ganoderma lucidum, Grifon from Grifola frondosa and Didanosine from Cordyceps militaris. The nutraceuticals have been found to relieve the stress and pressure of modern society by stimulating both basic and secondary immune responses of the immune system. There are more than 5000 species of mushrooms recorded from all over the world out of which around 2000 are identified as edible. A large number of the species are yet to be analysed for their nutraceutical/medicinal potential. © NIAB 2005.

Author Keywords

Anti-cancerous agents; Bioactive compounds; Functional foods; Immunomodulators; Medicinal mushrooms; Mushroom; Nutraceutical mushrooms; Nutraceuticals

Document Type: Review
Source: Scopus

Shnyreva, S.V.[a] , Belokon, Y.S.[b] , Belokon, M.M.[b] , Altukhov, Yu.P.[b]

Interspecific genetic variability of the oyster mushroom Pleurotus ostreatus as revealed by allozyme gene analysis

(2004) *Genetika*, 40 (8), pp. 1068-1080.

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Abstract

Allozyme variation in natural populations of basidiomycetes fungus Pleurotus ostreatus (88 individuals) from three regions of central Russia was studied. The species was shown to have 92.86% of polymorphic allozyme loci and expected heterozygosity He = 0.49. The mean number of alleles per locus was 3.5. The genetic differences among populations were supported by F-statistics (FST = 0.750). The low level of inbreeding (F IS = 0.018) suggests that the P. ostreatus populations are panmictic, and the main reproduction mode involves basidiospores dispersing at long distances. Using cluster analysis, geographically isolated populations and intersterile groups were differentiated within the complex P.

ostreatus species.

Document Type: Article
Source: Scopus

Martin, P.[a] , Muruke, M.[b] , Hosea, K.[b] , Kivaisi, A.[b] , Zerwas, N.[a] , Bauerle, C.[a c]

A rapid PCR-RFLP method for monitoring genetic variation among commercial mushroom species

(2004) *Biochemistry and Molecular Biology Education*, 32 (6), pp. 390-394. Cited 2 times.

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[b] Applied Microbiology Unit, Department of Botany, University of Dar es Salaam, Dar es Salaam, Tanzania

[c] Biology Department, Hamline University, 1536 Hewitt Avenue, St. Paul, MN 55104, United States

Abstract
We report the development of a simplified procedure for restriction fragment length polymorphism (RFLP) analysis of mushrooms. We have adapted standard molecular techniques to be amenable to an undergraduate laboratory setting in order to allow students to explore basic questions about fungal diversity and relatedness among mushroom species. The streamlined protocols allowed students to practice important molecular techniques within the context of self-designed investigative projects. This laboratory experience provided opportunities for students to practice strategies for examining molecular diversity among species.

Author Keywords
Biotechnology education; Mushrooms; Phylogenetic analysis; RFLP analysis

Document Type: Article
Source: Scopus

James, T.Y.[a] , Liou, S.-R.[a b] , Vilgalys, R.[a]

The genetic structure and diversity of the A and B mating-type genes from the tropical oyster mushroom, Pleurotus djamor

(2004) *Fungal Genetics and Biology*, 41 (8), pp. 813-825. Cited 11 times.

[a] Department of Biology, Box 90338, Duke University, Durham, NC 27708, United States
[b] Dept. of Neurobiology and Behavior, SUNY at Stony Brook, Stony Brook, NY 11794-5245, United States

Abstract
In most heterothallic mushroom species, inbreeding is avoided by an incompatibility system determined by two loci each with multiple alleles (the A and B mating-type loci). In this study we investigated the genetic structure of the mating-type loci in the tropical oyster mushroom Pleurotus djamor using both positional cloning and degenerate PCR methods. DNA sequences from genomic regions cosegregating with the mating-type loci of P. djamor revealed homeodomain transcription factors (A) and pheromone receptors (B), suggesting the genetic basis for mating-type determination in P. djamor is the same as in the model mushroom species. Three pheromone receptors were detected in a single homokaryotic isolate of P. djamor. Only

one pair of homeodomain genes was detected in the A mating-type region. It is hypothesized that the A mating-type locus of P. djamor is comprised of only one homeodomain pair, which may explain the lower number of A mating-type alleles relative to other mushroom species. © 2004 Elsevier Inc. All rights reserved.

Document Type: Article
Source: Scopus

Shnyreva, A.V.[a] , Belokon, Yu.S.[b] , Belokon, M.M.[b] , Altukhov, Yu.P.[b]

Interspecific genetic variability of the oyster mushroom Pleurotus ostreatus as revealed by Allozyme gene analysis

(2004) *Russian Journal of Genetics*, 40 (8), pp. 871-881. Cited 1 time.

[a] Department of Mycology and Algology, Moscow State University, Moscow, 119992 Russia
[b] Vavilov Inst. of General Genetics, Russian Academy of Sciences, Moscow, 119333 Russia

Abstract

Allozyme variation in natural populations of basidiomycete fungus Pleurotus ostreatus (88 individuals) from three regions of central Russia was studied. The species was shown to have 92.86% of polymorphic allozyme loci and expected heterozygosity He = 0.49. The mean number of alleles per locus was 3.5. The genetic differences among populations were supported by F-statistics (FST = 0.750). The low level of inbreeding (FIS = 0.018) suggests that the P. ostreatus

populations are panmictic, and the main reproduction mode involves basidiospores dispersing at long distances. Using cluster analysis, geographically isolated populations and intersterile groups were differentiated within the complex P. ostreatus species.

Document Type: Article
Source: Scopus

Singh, S.K., Upadhyay, R.C., Kamal, S., Tiwari, M.
Mushroom cryopreservation and its effect on survival, yield and genetic stability
(2004) *Cryo-Letters*, 25 (1), pp. 23-32. Cited 3 times.

Natl. Research Centre for Mushroom, Chambaghat, Solan (HP)-173213, India

Abstract
Mycelial stock cultures of Agaricus bisporus, A. bitorquis, Pleurotus flabellatus, P. sajor-caju, P. ostreatus, P. sapidus, Auricularia polytricha, Lentinula edodes, Morchella esculenta and Volvariella volvacea were maintained by frequent subculturing at an interval of two months and separately as wheat grain spawn in liquid nitrogen with 15% glycerol. Preservation of mushroom stock cultures as wheat grain spawn under liquid nitrogen proved to be the better method of maintenance. The percent recoveries of stored samples were unchanged from the first recovery after six months to the last recovery after 42 months in nine out of 11 stock cultures preserved under liquid nitrogen. However, a marginal decline in survival of 10 % was recorded in Auricularia polytricha and Volvariella volvacea. Yields before preservation of mushroom stock cultures and after 30 months of preservation exhibited static biological efficiency and fruitbody

weight. The comparison of Random Amplified Polymorphic DNA (RAPD) and Internal Transcribed Spacers (ITS) PCR amplified products did not exhibit DNA fragment variation in banding patterns at the intraspecific level during preservation of stock cultures by either method. The modified cryopreservation protocol and experimental demonstration of genetic stability of stock cultures reported here validate the use of mushroom cryopreservation techniques and supports studies on genetic stability of preserved biological materials.

Author Keywords
Cryopreservation; Genetic stability; ITS; Mushroom; RAPD

Document Type: Article
Source: Scopus

Reuter, J.E.[a] , Nardine, T.M.[a] , Penton, A.[a] , Billuart, P.[a] , Scott, E.K.[a] , Usui, T.[b] , Uemura, T.[b c] , Luo, L.[a]

A mosaic genetic screen for genes necessary for Drosophila mushroom body neuronal morphogenesis

(2003) *Development*, 130 (6), pp. 1203-1213. Cited 43 times.

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Abstract

Neurons undergo extensive morphogenesis during development. To systematically identify genes important for different aspects of neuronal morphogenesis, we performed a genetic screen using the MARCM system in the mushroom body (MB) neurons of the Drosophila brain. Mutations on the right arm of chromosome 2 (which contains ~20% of the Drosophila genome) were made homozygous in a small subset of uniquely labeled MB neurons. Independently mutagenized chromosomes (4600) were screened, yielding defects in neuroblast proliferation, cell size, membrane trafficking, and axon and dendrite morphogenesis. We report mutations that affect these different aspects of morphogenesis and phenotypically characterize a subset. We found that roadblock, which encodes a dynein light chain, exhibits reduced cell number in neuroblast clones, reduced dendritic complexity and defective axonal transport. These phenotypes are nearly identical to mutations in dynein heavy chain Dhc64 and in Lis1, the Drosophila homolog of human lissencephaly 1, reinforcing the role of the dynein complex in cell proliferation, dendritic morphogenesis and axonal transport. Phenotypic analysis of short stop/kakapo, which encodes a large cytoskeletal linker protein, reveals a novel function in regulating microtubule polarity in neurons. MB neurons mutant for flamingo, which encodes a seven transmembrane cadherin, extend processes beyond their wild-type dendritic territories. Overexpression of Flamingo results in axon retraction. Our results suggest that most genes involved in neuronal morphogenesis play multiple roles in different aspects of neural development, rather than performing a dedicated function limited to a specific process.

Author Keywords
Axon; Cytoskeleton; Dendrite; Pleiotropy; Polarity

Document Type: Review

Source: Scopus

Staniaszek, M.[a d] , Marczewski, W.[b] , Szudyga, K.[a] , Maszkiewicz, J.[a] , Czaplicki, A.[c] , Qian, G.[e]

Genetic relationship between Polish and Chinese strains of the mushroom Agaricus bisporus (Lange) Sing., determined by the RAPD method

(2002) *Journal of Applied Genetics*, 43 (1), pp. 43-47.

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[b] Plant Breed. Acclimatization Inst., Młochów, Poland

[c] Plant Breed. Acclimatization Inst., Radzików, Poland

[d] Res. Institute of Vegetable Crops, ul. Konstytucji 3 Maja 1/3, 96-100 Skierniewice, Poland

Abstract

The genetic relationship between twenty-six strains of Agaricus bisporus were analysed by the RAPD (random amplified polymorphic DNA) method. DNA amplification was performed with the use of twelve arbitrary 10-mer primers. Four primers, which gave polymorphic band patterns were chosen for RAPD analysis. In total, they gave 24 distinguishable bands, of which nine were polymorphic. The conducted research showed that there is a great genetic similarity among the examined strains. Low polymorphism of the strains may be a proof of a limited genetic pool used in the cultivation of those strains.

Author Keywords

Genetic diversity; Mushroom strains; RAPD

Document Type: Article

Source: Scopus

Juarez del Carmen, S.[a] , Largeteau-Mamoun, M.L.[a] , Rousseau, T.[b] , Regnault-Roger, C.[c] , Savoie, J.-M.[a]
Genetic and physiological variation in isolates of Verticillium fungicola causing dry bubble disease of the cultivated button mushroom, Agaricus bisporus
(2002) *Mycological Research*, 106 (10), pp. 1163-1170. Cited 4 times.

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Abstract
The objectives of this study were to examine genetic variation, physiological dissimilarities and diversity in pathogenicity between Verticillium fungicola var. aleophilum and var. fungicola and within a population of six V. fungicola var. fungicola strains responsible for dry bubble outbreaks on mushroom farms. Genetic variability was investigated using random amplification of polymorphic DNA (RAPD). Mycelial growth rate, extracellular enzyme production and susceptibility to hydrogen peroxide were used to examine physiological dissimilarities. Variation in pathogenicity was studied both in vitro and during mushroom cultivation. All the physiological properties studied indicated that var. aleophilum isolates were potentially more efficient than var. fungicola isolates for rapid colonisation of the mushroom cultivation

medium. They could then interact more efficiently with Agaricus bisporus to produce dry bubble disease. RAPD analysis confirmed that all the French isolates belonged to var. fungicola, and two isolates were distinguishable from the homogeneous group constituted by the others. These isolates had a higher mycelial growth rate and lower extracellular enzyme activities in liquid media, except for chitinases. Their spores were more susceptible to germination inhibition by hydrogen peroxide, and they were responsible for higher levels of affected mushrooms. The two varieties might be regarded as pathotypes that are geographically isolated, and variation in isolates of var. fungicola might have consequence for mushroom growers.

Document Type: Article
Source: Scopus

Hoi-Shan, K.[a b] , Hai-Lou, X.[a b]

Construction of a genetic linkage map of shiitake mushroom Lentinula Edodes strain L-54

(2002) *Journal of Biochemistry and Molecular Biology*, 35 (5), pp. 465-471. Cited 6 times.

[a] Department of Biology, Chinese University of Hong Kong, Hong Kong, Hong Kong
[b] School of Chemical and Life Sciences, Singapore Polytechnic, 500 Dover Road, Singapore 139651, Singapore

Abstract

From fruiting bodies of L. edodes strain L-54, single-spore isolates (SSIs) were collected. Two parental types of L-54 were regenerated via monokaryotization. By means of random-amplified polymorphic DNA (RAPD), DNA samples

from L-54, its two parental types, and 32 SSIs were amplified with arbitrary primers. Dedikaryotization was demonstrated, and 91 RAPD-based molecular markers were generated. RAPD markers that were segregated at a 1:1 ratio were used to construct a linkage map of L. edodes. This RAPD-linkage map greatly enhanced the mapping of other inheritable and stable markers [such as those that are linked to a phenotype (the mating type), a known gene (priA) and a sequenced DNA fragment (MAT)] with the aid of mating tests, bulked-segregant analysis, and PCR-single-strand conformational polymorphism. These markers comprised a genetic map of L. edodes with 14 linkage groups and a total length of 622.4 cM.
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Author Keywords
Genetic map; Genetic mapping; Lentinula edodes; Random-amplified polymorphic DNA (RAPD)

Document Type: Article
Source: Scopus

Xu, J., Desmerger, C., Callac, P.
Fine-scale genetic analyses reveal unexpected spatial-temporal heterogeneity in two natural populations of the commercial mushroom Agaricus bisporus
(2002) *Microbiology*, 148 (5), pp. 1253-1262. Cited 7 times.

Department of Biology, McMaster University, 1280 Main Street West, Hamilton, Ont. L8S 4K1, Canada

Abstract
This study examined the fine-scale genetic variation of the commercial mushroom, Agaricus bisporus, over 2 years at two sites in France. One site was a meadow fertilized with

horse manure and disturbed regularly by humans; the other was a Monterey cypress forest free of human disturbance. Altogether, 50 mushrooms were collected and analysed for mitochondrial and nuclear genetic variation marked by RFLPs and multilocus enzyme electrophoretic polymorphisms. Population samples from these two sites were genetically different and both sites contained high levels of genetic diversity. No identical genotypes were found at either site between the 2 years and there was little evidence for extensive vegetative clonality for this species. Contrary to expectations, very limited evidence of pseudohomothallic reproduction was found. Results from tests of Hardy-Weinberg equilibrium and genotypic equilibrium showed that outcrossing and recombination have played significant roles in both populations. The results demonstrated spatial-temporal genetic heterogeneity of A. bisporus in natural populations.

Author Keywords
Fungi; Modes of reproduction; Molecular markers; Population structure

Document Type: Article
Source: Scopus

Terashima, K., Matsumoto, T., Hasebe, K., Fukumasa-Nakai, Y.
Genetic diversity and strain-typing in cultivated strains of Lentinula edodes (the shii-take mushroom) in Japan by AFLP analysis
(2002) *Mycological Research*, 106 (1), pp. 34-39. Cited 11 times.

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Japan

Abstract
Amplified fragment length polymorphism (AFLP) analysis is based on selective PCR (polymerase chain reaction) amplification of genomic DNA restriction fragments. The present study was performed to: (1) assess the extent of AFLP variation among major cultivated strains of Lentinula edodes (the shii-take mushroom) in Japan; (2) evaluate the usefulness of AFLP as genetic marker for typing the cultivated strains; and (3) infer the genetic relatedness among them. Six AFLP primer pairs detected a total of 304 DNA fragments in a sample of 13 cultivated strains for wood log cultivation and 2 strains for sawdust cultivation, of which 179 DNA fragments (58.9% of detected fragments) were polymorphic between two or more strains. These polymorphic DNA fragments could differentiate all of the cultivated strains. Cluster analysis and principle coordinate analysis based on AFLP data showed two distinct groups; one group was composed of the strains in which fruiting occurred during the middle to low temperature period from autumn to next spring under outdoor wood log cultivation, and the other strains in which fruiting could be induced in the summer under outdoor cultivation and strains for sawdust cultivation under indoor air-controlled condition.

Document Type: Article
Source: Scopus

Wang, Y.[a] , Wright, N.J.D.[a] , Guo, H.-F.[a] , Xie, Z.[b] , Svoboda, K.[a] , Malinow, R.[a] , Smith, D.P.[c] , Zhong, Y.[a]
Genetic manipulation of the odor-evoked distributed neural activity in the Drosophila mushroom body

(2001) *Neuron*, 29 (1), pp. 267-276. Cited 47 times.

[a] Cold Spring Harbor Lab, 1 Bungtown Road, Cold Spring Harbor, NY 11724, United States

[b] Department of Biological Sciences and Biotechnology, Tsinghua University, Beijing, China

[c] Department of Pharmacology, University of Texas, Southwestern Medical Center, Dallas, TX 75235, United States

Abstract

Odor-induced neural activity was recorded by Ca2+ imaging in the cell body region of the Drosophila mushroom body (MB), which is the second relay of the olfactory central nervous system. The signals recorded are mainly from the cell layers on the brain surface because of the limited penetration of Ca2+-sensitive dyes. The densely packed cell bodies and their accessibility allow visualization of odor-induced population neural activity. It is revealed that odors evoke diffused neural activities in the MB. Although the signals cannot be attributed to individual neurons, patterns of the population neural activity can be analyzed. The activity pattern, but not the amplitude, of an odor-induced population response is specific for the chemical identity of an odor and its concentration. The distribution pattern of neural activity can be altered specifically by genetic manipulation of an odor binding protein and this alteration is closely associated with a behavioral defect of odor preference. These results suggest that the spatial pattern of the distributed neural activity may contribute to coding of odor information at the second relay of the olfactory system.

Document Type: Article
Source: Scopus

Kurusu, M.[a] , Nagao, T.[a] , Walldorf, U.[b] , Flister, S.[c] , Gehring, W.J.[c] , Furukubo-Tokunaga, K.[a]

Genetic control of development of the mushroom bodies, the associative learning centers in the Drosophila brain, by the eyeless, twin of eyeless, and dachshund genes

(2000) *Proceedings of the National Academy of Sciences of the United States of America*, 97 (5), pp. 2140-2144. Cited 55 times.

[a] Institute of Biological Sciences, University of Tsukuba, Tsukuba 305-8572, Japan

[b] Institute of Genetics, University of Hohenheim, Garbenstrasse 30, D-70599 Stuttgart, Germany

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Abstract

Mushroom bodies (MBs) are the centers for olfactory associative learning and elementary cognitive functions in the Drosophila brain. By high- resolution neuroanatomy, we show that eyeless (ey), twin of eyeless, and dachshund (dac), which are implicated in eye development, also are expressed in the developing MBs. Mutations of ey completely disrupted the MB neuropils, and a null mutation of dac resulted in marked disruption and aberrant axonal projections. Genetic analyses demonstrated that, whereas ey and dac synergistically control the structural development of the MBs, the two genes are regulated independently in the course of MB development. These data argue for a distinct combinatorial code of regulatory genes for MBs as compared

with eye development and suggest conserved roles of Pax6 homologs in the genetic programs of the olfactory learning centers of complex brains.

Document Type: Article
Source: Scopus

Fukuda, M.
Diversity of genetic resources in the shiitake mushroom, Lentinula edodes
(1999) *Nippon Nogeikagaku Kaishi*, 73 (6), pp. 626-628.

Faculty of Agriculture, Shinshu University, Minamiminowa, Nagano 399-4598, Japan

Author Keywords
Genetic resources; Isozyme; Lentinula edodes; Mitochondrial DNA; Ribosomal DNA

Document Type: Article
Source: Scopus

McKay, G.J.[a d] , Egan, D.[b] , Morris, E.[c] , Scott, C.[c] , Brown, A.E.[a]
Genetic and morphological characterization of Cladobotryum species causing cobweb disease of mushrooms
(1999) *Applied and Environmental Microbiology*, 65 (2), pp. 606-610. Cited 6 times.

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5PX, United Kingdom
[b] Environ. Rsrc. Management Laboratory, Faculty of Agriculture, University College Dublin, Dublin, Ireland
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[d] Department of Applied Plant Science, Queen's University of Belfast, Agriculture and Food Science Centre, Newforge Lane, Belfast, BT9 5PX, United Kingdom

Abstract
Cladobotryum dendroides (= Dactylium dendroides) has hitherto been regarded as the major causal agent of cobweb disease of the cultivated mushroom, Agaricus bisporus. Nucleotide sequence data for the internal transcribed spacer (ITS) regions of four Cladobotryum/Hypomyces species reported to be associated with cobweb disease, however, indicate that the most common pathogen is now C. mycophilum. This cobweb pathogen varies somewhat in conidial septation from published descriptions of C. mycophilum and lacks the distinctive colony odor. ITS sequencing revealed minor nucleotide variation which split isolates of the pathogen into three subgroups, two comprising isolates that were sensitive to methylbenzimidazole carbamate (MBC) fungicides and one comprising MBC-resistant isolates. The MBC-resistant isolates, which were only obtained from Ireland and Great Britain, clustered together strongly in randomly amplified polymorphic DNA (RAPD) PCR analysis, suggesting that they may be clonal. The MBC-sensitive isolates were more diverse. A RAPD fragment of 800 to 900 bp, containing a microsatellite and found in the MBC-resistant isolates, also indicated their clonal nature; the microsatellites of these isolates contained the same number of GA repeats. Smaller, polymorphic microsatellites, similarly comprising GA repeats, in the MBC-sensitive isolates in

general correlated with their geographic origin.

Document Type: Article
Source: Scopus

Stoop, J.M.H.[a b] , Mooibroek, H.[a]
Advances in genetic analysis and biotechnology of the cultivated button mushroom, Agaricus bisporus
(1999) *Applied Microbiology and Biotechnology*, 52 (4), pp. 474-483. Cited 7 times.

[a] Agrotechnological Research Institute, ATO-DLO, P.O. Box 17, NL-6700 AA Wageningen, Netherlands
[b] DuPont Agricultural Biotechnology, Experimental Station E402/5241, P.O. Box 80402, Wilmington, DE 19880, United States

Abstract
During the last decade several major breakthroughs have been achieved in mushroom biotechnology, which greatly enhanced classical mushroom breeding. DNA-based technologies such as restriction fragment length polymorphisms and randomly amplified polydisperse DNA sequences have allowed for a measure of genetic diversity, for the isolation of homokaryons, for the determination of inheritance of nuclear and mitochondrial markers, and for the production of a genetic linkage map. The recent availability of ready-to-use and affordable DNA technologies has resulted in a substantial increase in the number of Agaricus bisporus genes that have been identified and characterized. A major breakthrough was achieved in 1996 when the first successful and stable transformation system of A. bisporus was reported. Together, the availability of an increasing number of

known genes and the possibility to produce transgenic mushrooms will result in a better understanding of the molecular, physiological and biochemical processes that are essential for mushroom production, shelf life and quality aspects such as flavor, texture and disease resistance. Some potential targets for strain improvement are discussed, such as the genes involved in brown discoloration, substrate utilization, carbon and nitrogen metabolism, and fruit body development.

Document Type: Short Survey
Source: Scopus

Muthumeenakshi, S.[a c] , Brown, A.E.[a b] , Mills, P.R.[a b c]
Genetic comparison of the aggressive weed mould strains of Trichoderma harzianum from mushroom compost in North America and the British Isles
(1998) *Mycological Research*, 102 (4), pp. 385-390. Cited 16 times.

[a] Department of Applied Plant Science, Queen's University of Belfast
[b] Applied Plant Science Division, Dept. of Agric. for Northern Ireland, Newforge Lane, Belfast BT9 5PX, United Kingdom
[c] Dept. Plant Pathol. and Microbiol., HRI, Wellesbourne, Warwick, CV35 9EF, United Kingdom

Abstract
Genetic characterization of 15 aggressive weed mould strains that were identified morphologically as Trichoderma harzianum (sensu Rifai) from mushroom compost in commercial units in North America (designated T. harzianum

group 4) was undertaken using various molecular techniques. RFLP analysis of rDNA revealed homogeneity among these strains; a tow level of polymorphism was detected in mitochondrial DNA. RAPD analysis also indicated a very high degree of homogeneity among the T. harzianum group 4 strains. Nucleotide sequence determination of the rDNA internal transcribed spacer (ITS) I revealed five base pair differences between T. harzianum groups 4 and 2. Comparison of molecular data on T. harzianum group 4 with that of T. harzianum group 2, which caused green mould epidemics in the mushroom industries of the British Isles, indicated that T. harzianum group 4 is not the same as group 2.

Document Type: Article
Source: Scopus

Xu, J.[a d] , Kerrigan, R.W.[b] , Callac, P.[c] , Horgen, P.A.[a] , Anderson, J.B.[a]

Genetic structure of natural populations of Agaricus bisporus, the commercial button mushroom

(1997) *Journal of Heredity*, 88 (6), pp. 482-488. Cited 25 times.

[a] Department of Botany, University of Toronto, Erindale College, Mississauga, Ont. L5L 1C, Canada

[b] Research Department, Sylvan Spawn Laboratory, Inc., Kittanning, PA, United States

[c] INRA-CTC, Stn. de Rech. sur les Champignons, 33883 Villenave d'Ornon, France

[d] Department of Microbiology, Duke University, Medical Center, Durham, NC 27710, United States

Abstract
Agaricus bisporus (Lange) Imbach, the familiar button mushroom of commerce, is a major vegetable crop around the world. In the past 10 years a significant world-wide effort has been made to collect Agaricus germ plasm from the wild. Here we report the genetic analysis of a collection of 342 isolates from 12 locations. For 10 nuclear loci marked by RFLPs, we found high genetic diversity in all geographic populations. Among the 342 isolates, three different analyses of genetic diversity were carried out: the first on the total sample of 342 isolates, the second on a subset of 108 'cultivar- like' isolates shown previously to carry either of the two mitochondrial DNA haplotypes found in cultivated strains, and the third on the other 234 isolates that carry a diversity of mtDNA haplotypes not found in cultivated strains. We found that the samples of cultivar-like isolates from various locations were genetically more similar among themselves and to the cultivars than to the samples of other isolates from the same locations. Furthermore, the cultivar-like samples showed no evidence of genetic differentiation between continents and between regions within a continent. In contrast, samples of other isolates showed significant differentiation at the same levels of the geographic hierarchy. A comparison of gene frequencies was consistent with the occurrence of hybridization between the cultivar-like and the other strains in the coastal California population. Analyses of genetic diversity and genetic distance were all consistent with the historical record that cultivars and cultivar-like strains in the wild originated from Western Europe.

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

Hibbett, D.S., Donoghue, M.J.
Implications of phylogenetic studies for conservation of genetic diversity in shiitake mushrooms [Implicaciones de estudios filogeneticos en la conservacion de la diversidad genetica de hongos shiitake]
(1996) *Conservation Biology*, 10 (5), pp. 1321-1327. Cited 30 times.

Harvard University Herbaria, 22 Divinity Avenue, Cambridge, MA 02138, United States

Abstract
We consider the impact of recent molecular phylogenetic analyses on conservation issues for shiitake mushrooms. Based on mating compatibility, shiitake has been considered a single species. Lentinula edodes sensu lato. Phylogenetic analyses of ribosomal RNA internal transcribed spacers (Hibbett et al. 1995), however, suggest that shiitake is composed of four distinct lineages. Thus, under a phylogenetic species concept, four species of shiitake should be recognized. A classification of shiitake based on a phylogenetic species concept would convey information about evolutionary relationships and distribution of genetic variation, whereas a classification based on a biological species concept would lack such information. This is a clear case in which new insights into phylogenetic relationships can

be used to target areas for conservation action and formulate international agricultural policies. At the heart of our argument is the belief that the basic units of both taxonomy and conservation should be unique evolutionary lineages of organisms identified through phylogenetic studies.

Document Type: Review
Source: Scopus

De Belle, J.S.[a] , Heisenberg, M.[b]

Expression of Drosophila mushroom body mutations in alternative genetic backgrounds: A case study of the mushroom body miniature gene (mbm)

(1996) *Proceedings of the National Academy of Sciences of the United States of America*, 93 (18), pp. 9875-9880. Cited 74 times.

[a] Max-Planck-Inst. F. Biol. Kybernetik, Spemannstrasse 38, D-72076 Tübingen, Germany

[b] Theodor-Boveri-Inst. F. B., Lehrstuhl für Genetik, Universität Würzburg, Am Hubland, D-97074 Würzburg, Germany

Abstract

Mutations in 12 genes regulating Drosophila melanogaster mushroom body (MB) development were each studied in two genetic backgrounds. In all cases, brain structure was qualitatively or quantitatively different after replacement of the 'original' genetic background with that of the Canton Special wild-type strain. The mushroom body miniature gene (mbm) was investigated in detail, mbm supports the maintenance of MB Kenyon cell fibers in third instar larvae and their regrowth during metamorphosis. Adult mbm1

mutant females are lacking many or most Kenyon cell fibers and are impaired in MB-mediated associative odor learning. We show here that structural defects in mbm1 are apparent only in combination with an X-linked, dosage- dependent modifier (or modifiers). In the Canton Special genetic background, the mbm1 anatomical phenotype is suppressed, and MBs develop to a normal size. However, the olfactory learning phenotype is not fully restored, suggesting that submicroscopic defects persist in the MBs. Mutant mbm1 flies with full-sized MBs have normal retention but show a specific acquisition deficit that cannot be attributed to reductions in odor avoidance, shock reactivity, or locomotor behavior. We propose that polymorphic gene interactions (in addition to ontogenetic factors) determine MB size and, concomitantly, the ability to recognize and learn odors.

Author Keywords
brain anatomy; genetic modifiers; odor learning; olfaction; walking

Document Type: Article
Source: Scopus

Kerrigan, R.W., Carvalho, D.B., Horgen, P.A., Anderson, J.B.
Indigenous and introduced populations of Agaricus bisporus, the cultivated button mushroom, in eastern and western Canada: Implications for population biology, resource management, and conservation of genetic diversity
(1995) *Canadian Journal of Botany*, 73 (12), pp. 1925-1938. Cited 17 times.

Sylvan Spawn Laboratory Inc.,Dept Res., 1163 Winfield Rd, Cabot, PA 16023, United States

Document Type: Article
Source: Scopus

Kay, E., Vilgalys, R.
Spatial distribution and genetic relationships among individuals in a natural population of the oyster mushroom Pleurotus ostreatus
(1992) *Mycologia*, 84 (2), pp. 173-182. Cited 26 times.

Dept. of Botany, Duke Univ., Durham, C 27706, USA

Abstract
Spatial distribution of 60 heterokaryons in a natural population of Pleurotus ostreatus was examined through study of their somatic incompatibility interactions and analysis of mating compatibility factors. Results implicate basidiospore dispersal as a primary mechanism for dikaryon establishment. -from Authors

Source: Scopus

Guerineau
Selected topics from the Congress on the Genetics of Industrial Microorganisms (GIM): From genetic plasticity to edible mushrooms
(1991) *Research in Microbiology*, 142 (4), pp. 357-358.

Institute de Genetique et Microbiologie, Universite Paris-XI, CNRS URA 1354, 91405 Orsay, France

Document Type: Conference Paper
Source: Scopus

May, B., Royse, D.J.

Genetic variation and joint segregation of biochemical loci in the common meadow mushroom, Agaricus campestris

(1982) *Biochemical Genetics*, 20 (11-12), pp. 1165-1173. Cited 7 times.

Dep. Plant Pathol., Pennsylvania State Univ., University Park, PA 16802, United States

Document Type: Article
Source: Scopus

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