

Two black fungi with industrial niches: *Acidomyces* and *Amorphotheca*

Walter Buzina¹, Martin Grube²

1 Institute of Hygiene, Microbiology and Environmental Medicine, Medical University Graz, Austria

2 Institute for Plant Sciences, Karl-Franzens University Graz, Austria

A new acidophilic *Scytalidium*¹

LYNNE SIGLER AND J. W. CARMICHAEL

University of Alberta Mold Herbarium and Culture Collection, Edmonton, Alberta

Accepted October 29, 1973

SIGLER, L., and J. W. CARMICHAEL. 1974. A new acidophilic *Scytalidium*. *Can. J. Microbiol.* **20**: 267-268.

A brown mold fungus was isolated from acid soil and from acid solutions in an industrial plant and a uranium mine. The only type of spores observed were arthroconidia. The morphology of the fungus is illustrated and it is described as a new species, *Scytalidium acidophilum*.

Starkey (1943): from acid solutions (pH 0.2-0.7) containing 4% copper sulfate used in an industrial plant

Ivarson (1972): from acidic uranium mine drainage water

Sigler (1974): from soil near a sulfur pile

CAN. J. MICROBIOL. VOL. 20, 1974



Starkey & Waksman (1943) first found *Acidomyces acidophilus* in extremely acidic, sulphate containing industrial water.

STARKEY, R. L. and S. A. WAKSMAN 1943. Fungi tolerant to extreme acidity and high concentrations of copper *J. Bacteriol.* **45**: 509-519.

Metabolically Active Eukaryotic Communities in Extremely Acidic Mine Drainage

Brett J. Baker,^{1*} Michelle A. Lutz,² Scott C. Dawson,³ Philip L. Bond,²
and Jillian F. Banfield^{1,4}

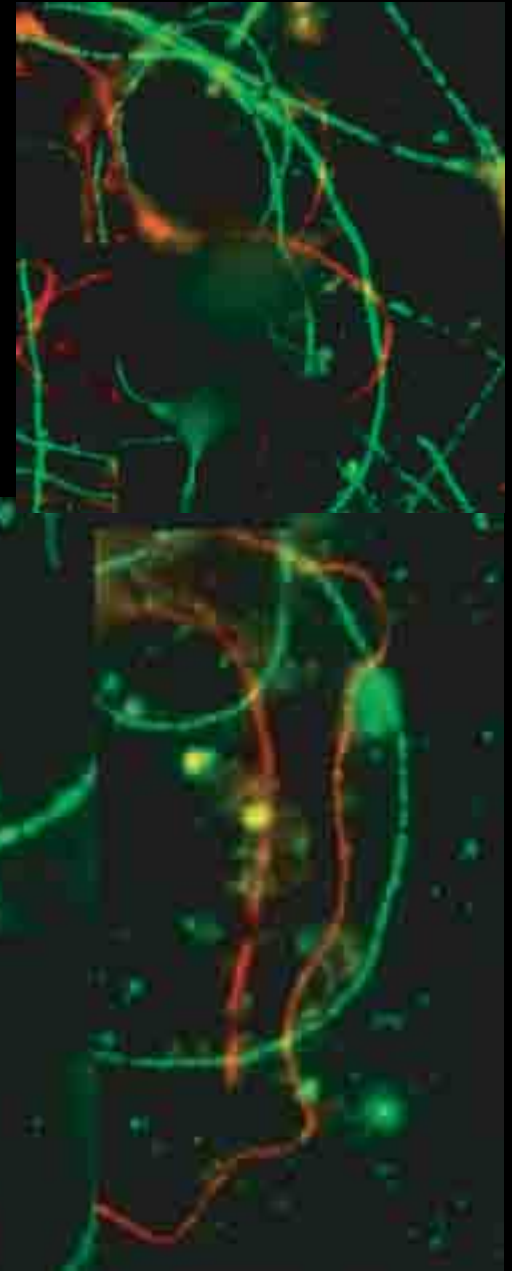
Department of Earth and Planetary Sciences,¹ Department of Cell and Molecular Biology,² and Environmental Sciences, Policy, and Management,³ University of California, Berkeley, California, and Department of Geology and Geophysics, University of Wisconsin, Madison, Wisconsin⁴

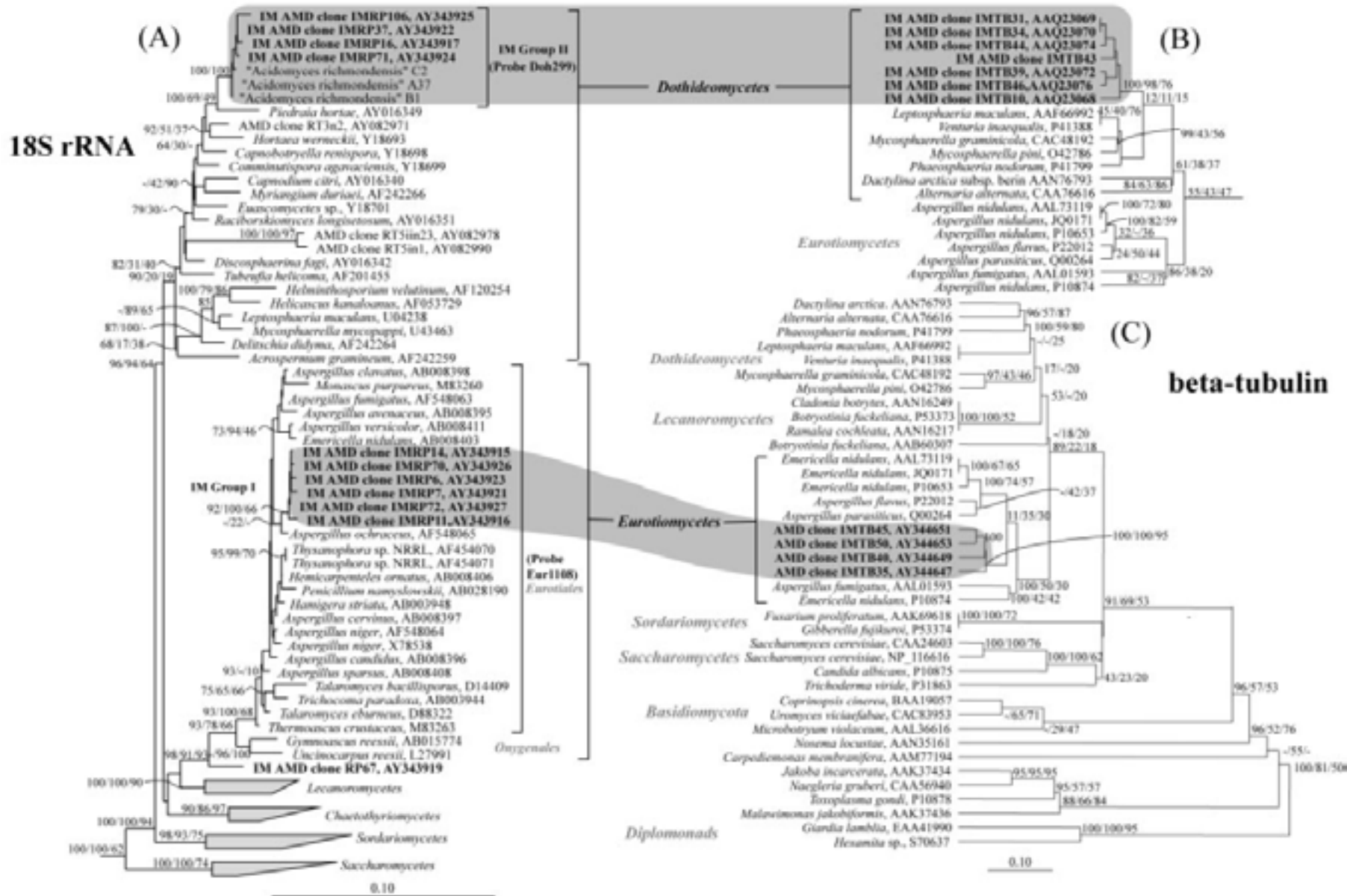
Acid mine drainage microbial communities contain microbial eukaryotes (both fungi and protists) that confer a biofilm structure and impact the abundance of bacteria and archaea.

Extremely acidic (pHs 0.8 to 1.38), warm (30 to 50°C), metal-rich (up to 269 mM Fe²⁺, 16.8 mM Zn, 8.5 mM As, and 4.1 mM Cu)

FISH analyses of five-way community, using Doh299 (Cy3 labeled, highlighting *Dothideomyces* in red), and Eur1108 (fluorescein isothiocyanate labeled, highlighting *Eurotiomyces* in green) rRNA probes.

There is significant nonspecific fluorescence in these images from the minerals (rounded objects) in the sample. Note that the *Eurotiomyces* (in green) are branched in several places and that the *Eurotiomyces* are more abundant than the *Dothideomyces*.

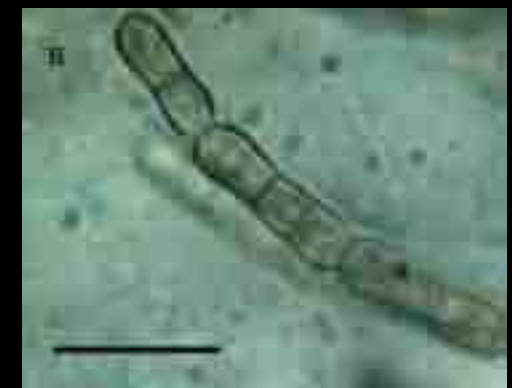
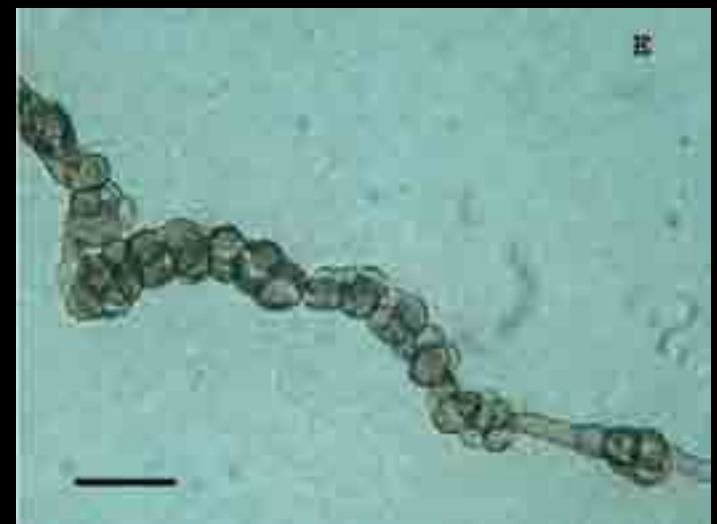




A *Rhodophyta* (red algae) lineage and organisms from the *Vahlkampfiidae* family were identified. The fungal 18S rRNA and tubulin gene sequences formed two distinct phylogenetic groups associated with the classes *Dothideomycetes* and *Eurotiomycetes*.

Drought meets acid: three new genera in a dothidealean clade of extremotolerant fungi

L. Selbmann^{1*}, G.S. de Hoog^{2,3}, L. Zucconi¹, D. Isola¹, S. Ruisi¹, A.H.G. Gerrits van den Ende², C. Ruibal², F. De Leo⁴, C. Urzi⁴ and S. Onofri¹



Acidomyces acidophilus strain CBS 899.87

B: Toruloid unbranched hyphae with melanised and thick-walled cells

E: Meristematic development of the hyphae

H: Chain of 1- 2- and 3- celled conidia

Molecular phylogeny based on SSU sequences indicating the positions of the clades in *Dothideomycetidae*; the described new genera were highlighted with coloured rectangles. The tree has been built with neighbour-joining algorithm in ARB package with 100 replications. Branches of the clades supported by a bootstrap value above 95 % are in bold.

Selbmann *et al.* 2008

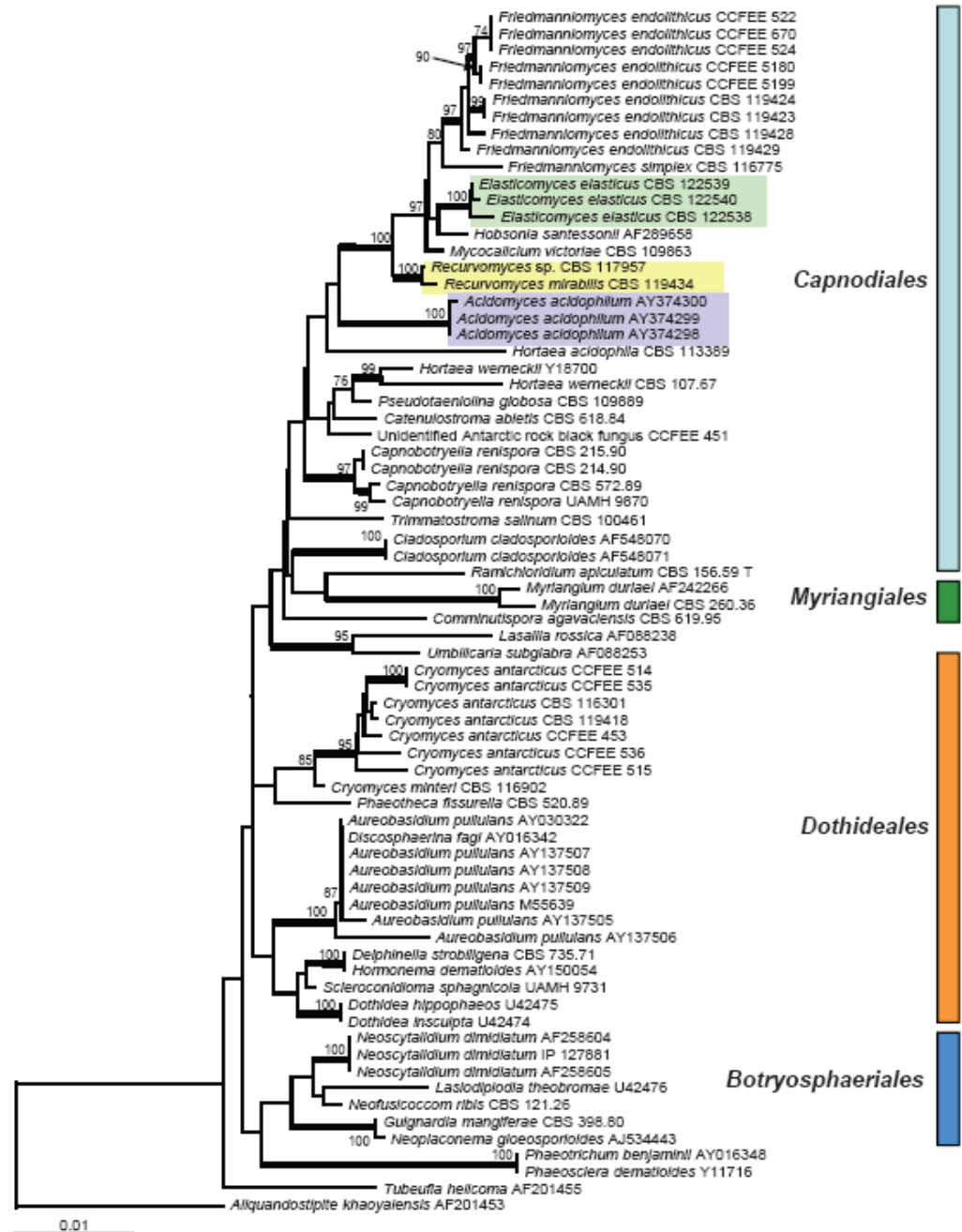


Table 3. Cultural preferences and salt tolerance of acidophilic strains.

Species	Strain no.	Cultural preferences								NaCl %			
		PGA	MEA	CzA	OA	1.2	1.5	3	5	7	10	12	
<i>Acidomyces acidophilus</i>	CS0 000.87	1.17±0.1	1.25±0.15	0.3±0.02	1.17±0.1	1.3±0.02	0.7±0.02	0.8±0.02	0.8±0	0.5±0	0.2±0.02	--	
	CS0 335.97	1.00±0.1	1.0±0.14	0.6±0.2	1.0±0.2	1.5±0.02	0.5±0.02	0.4±0.04	0.3±0.02	0.2±0.02	--	--	
	04 12851	2.0±0.14	1.8±0.14	1.3±0.2	1.8±0.1	1.6±0.02	1.6±0.02	1.6±0.02	0.7±0.02	0.6±0.04	--	--	
	04 11536	2.5±0.2	0.2±0.2	1.5±0.14	1.2±0.2	2.3±0.02	2.0±0.04	2±0.04	0.8±0.04	0.8±0.008	--	--	
	04 12001	1.6±0.14	2.3±0.2	1.7±0.1	1.5±0.2	1.0±0.04	0.6±0.02	0.6±0.02	0.6±0.02	0.3±0.02	--	--	

Growth on different media and salt concentration expressed as diameter of the colonies (Dn); -- = No growth.

Table 4. Thermal and pH preferences of acidophilic strains

Species	Strain no.	Thermal preferences (°C)								pH			
		4	10	16	25	30	37	4	5	7	9		
<i>Acidomyces acidophilus</i>	CS0 000.87	--	--	+	++	+	--	+	+	++	+	+	
	CS0 335.97	+	+	++	+	+	--	+	++	+	+	--	
	04 12851	+	+	++	++	+	--	+	++	+	+	--	
	04 11536	+	+	+	+	++	--	+	++	+	+	--	
	04 12001	+	+	+	++	+	--	+	++	+	+	--	

++ = maximum growth recorded; ++ = growth; + = weak growth; -- = no growth.

Seawater: 3.5%
Dead Sea: 30-35%



Selbmann *et al.* 2008

Salterns of Sečovlje (<http://www2.arnes.si/>)

FUNGI CAPABLE OF GROWING IN STRONGLY ACID MEDIA AND IN CONCENTRATED COPPER SULFATE SOLUTIONS

OWEN SLETTEN¹ AND C. E. SKINNER²

*Department of Bacteriology and Immunology, University of Minnesota, Minneapolis 14,
Minnesota*

J. Bacteriol. 56: 679–681, 1948

¹ Present address: Coca-Cola Bottling Company, 2035 S.E. University Avenue, Minneapolis 14, Minnesota.

² Present address: Department of Bacteriology and Public Health, Washington State College, Pullman, Washington.

Trichosporon cerebriforme

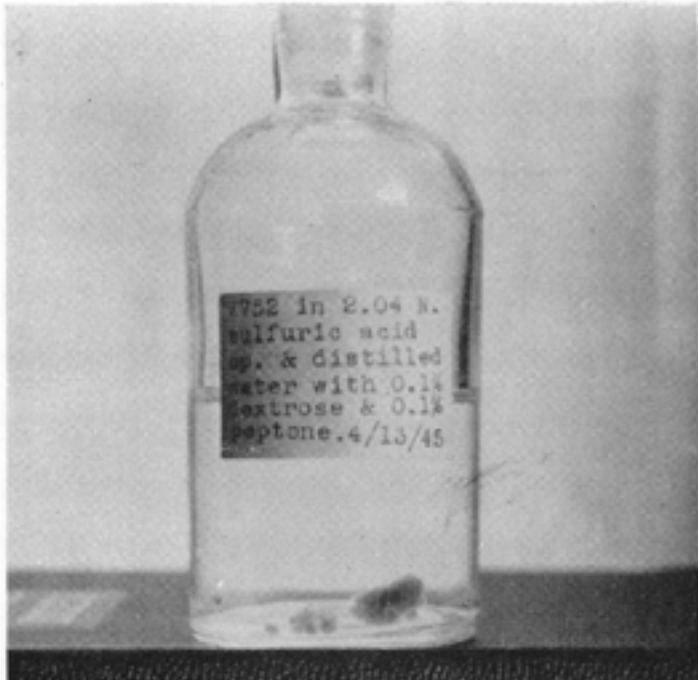
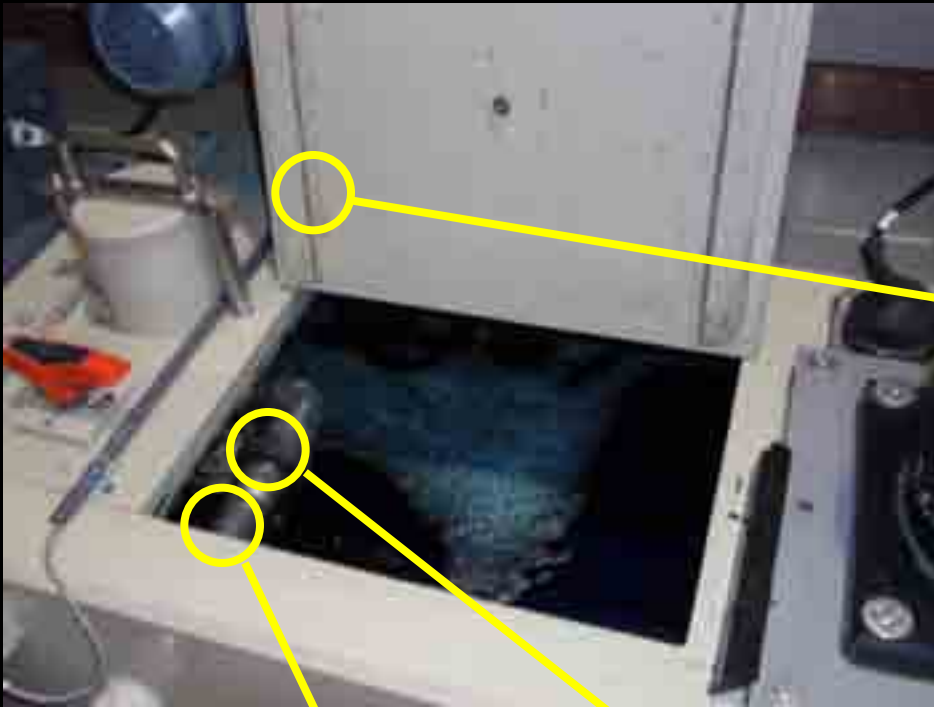


Figure 1. Growth of mold in 2 N sulfuric acid solution.

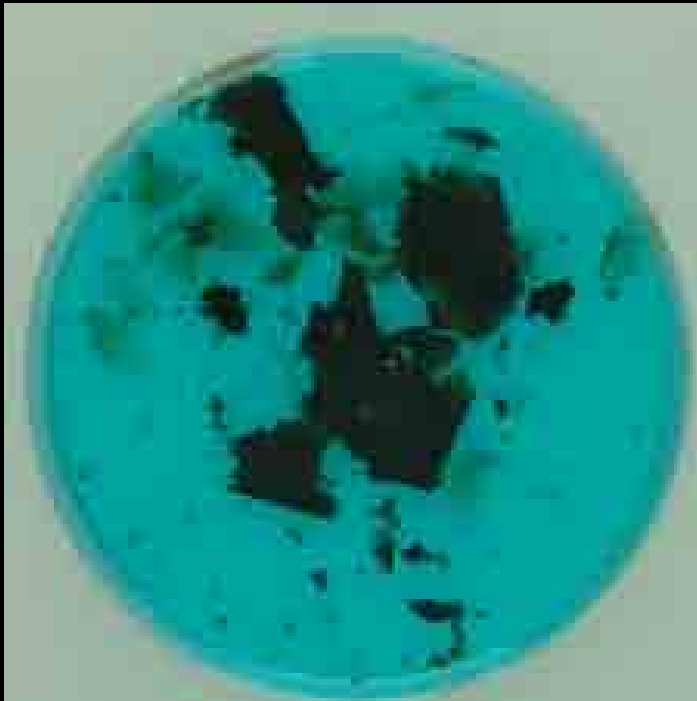
TABLE 1
Growth of two isolates of molds in acid media

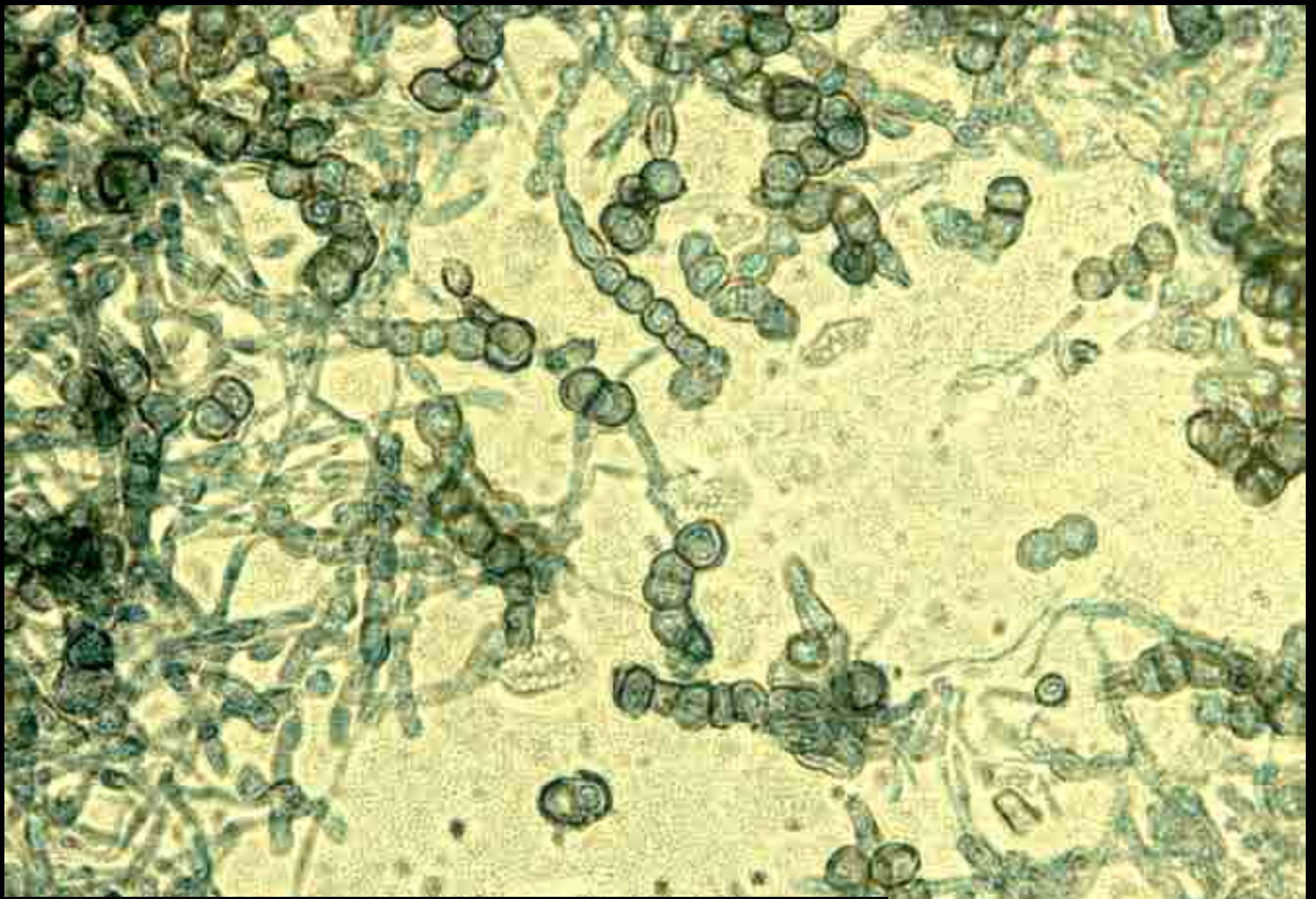
NUMBER OF ISOLATE	NORMALITY OF SULFURIC ACID	AGE OF GROWTH	AMOUNT OF GROWTH
		<i>days</i>	
7752	1.0	67	Fair
7752	1.47	67	Fair
7752	2.04	103*	Light
7752	2.04	103*	Fair
9024	1.0	58	Heavy
9024	1.47	58	Heavy
9024	2.04	58	Light

* No visible growth in 67 days.



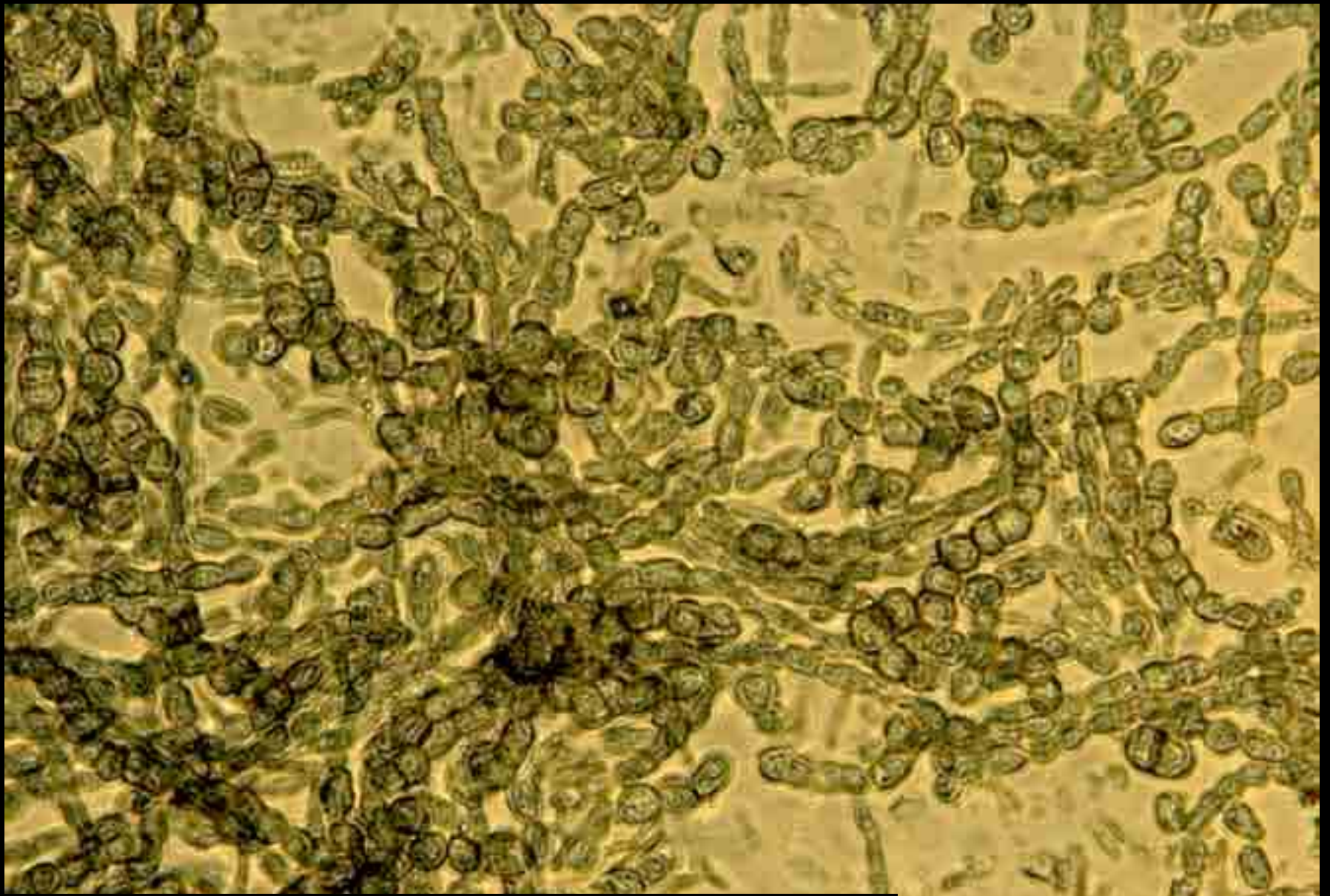
Galvanisation jar:
20% copper sulphate
pH = 0.5





Toruloid unbranched hyphae with melanised and thick-walled cells, meristematic development of the hyphae

10 μm



Toruloid unbranched hyphae with melanised and thick-walled cells, meristematic development of the hyphae

10 µm



Branched hyphae



Chain of 1-, 2- or 3-celled conidia



Chain of 1-, 2-or 3-celled conidia

Bispora sp. **EF001169** ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence
 Length=543

Source = 803 hits (4901), Expect = 0.0
 Identities = 490/490 (100%), Gaps = 0/490 (0%)
 Strand=Plus/Minus

```

Query 1:  GGGGTTTTACGGGGGGGGCCGCCGATACCCGCGAGGACTGAAAGAAATACCCGAC 60
             |||
Hit 1:  GGGGTTTTACGGGGGGGGCCGCCGATACCCGCGAGGACTGAAAGAAATACCCGAC 60

Query 41:  GCTGGGGAAGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 120
             |||
Hit 2:  GCTGGGGAAGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 120

Query 121: CCAATACCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
             |||
Hit 3:  CCAATACCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180

Query 181: ACCAGGGGGGGGCAATGPPGDTTCAAGATTGCTGATTTACTGAATTCGAAATTCAT 240
             |||
Hit 4:  ACCAGGGGGGGGCAATGPPGDTTCAAGATTGCTGATTTACTGAATTTGCAATTCAT 240

Query 241: TACTTAACGAAATGCTGATTTACTGAATTTACTGAATTTACTGAATTTACTGAAT 300
             |||
Hit 5:  TACTTAACGAAATGCTGATTTACTGAATTTACTGAATTTACTGAATTTACTGAAT 300

Query 301: AGTTTGGTTGATTTGCGCTTTTACGCTCAGACCGCTCGATAAGACCGGTTGTHAGAG 360
             |||
Hit 6:  AGTTTGGTTGATTTGCGCTTTTACGCTCAGACCGCTCGATAAGACCGGTTGTHAG 360

Query 361: GTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 420
             |||
Hit 7:  GTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 420

Query 421: GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 480
             |||
Hit 8:  GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 480

Query 481: GAGACCTTGT 490
             |||
Hit 9:  GAGACCTTGT 490
  
```

Feature Summary

```

LOCUS       EF001169                543 bp    DNA    Linear    SIM 04-080-0000
DEFINITION  Bispora sp. EF001169 ribosomal RNA gene, partial sequence;
            internal transcribed spacer 1, 5.8S ribosomal RNA gene, and
            internal transcribed spacer 2, complete sequence; and 28S ribosomal
            RNA gene, partial sequence.
ACCESSION   EF001169
VERSION     020000003  02/2008/2016
KEYWORDS
SOURCE      Bispora sp. EF001169
  ORGANISM  Bispora sp. EF001169
            Eukaryota; Fungi; Ascomycota; Sordariomycetes; Sordariomycetales;
            Sordariaceae.
REFERENCE   1  (bases 1 to 543)
            Wang, Q., Song, L., and Sun, F.
            Nucleotide analysis of Sordariomycetes which are used as
            wood rot
            JOURNAL   Mycol. Res.
            REFERENCE   2  (bases 1 to 543)
            Wang, Q., Song, L., and Sun, F.
            Nucleotide analysis
            JOURNAL   Submitted (17-JUN-2008) GenBank of Environment & Lake, China
            Beihai Lake Street Rd, Fuzhou, Fujian 350001, China
  
```

CBS 112.31

Price: 150 Euro (65.0 Euro for Academies, Universities, Education)

Taxon name:	Bispora effusa Peck
Identified by:	F.H. van Beyma
Previous names:	Bispora effusa
Other collection numbers:	VKM F-78
Deposited by:	R. Lurie, Feb 1931
Substrate:	mine timber
Country and locality:	South Africa

The creosote or diesel or kerosene fungus

Lindau has described *Hormodendrum resinae* (*Cladosporium resinae*) in 1907 from the resin of the conifer *Picea excelsa*.

In the late 1930's several people had observed a brown mould growing on pieces of wood such as poles and railroad ties impregnated with coal tar products (creosote) (Christensen *et al.*, 1942).

1939 an investigation was initiated by Christensen and his colleagues into the identity of this mould and its occurrence in nature. Their findings were published in 1942.



Studies on the 'Kerosene Fungus' *Cladosporium resinae* (Lindau) De Vries

Tuatara: Volume 19, Issue 2, May 1972

Part II. The Natural Habitat of *C. resinae*

by J. E. Sheridan, Jan Nelson and Y. L. Tan

Botany Department, Victoria University of Wellington

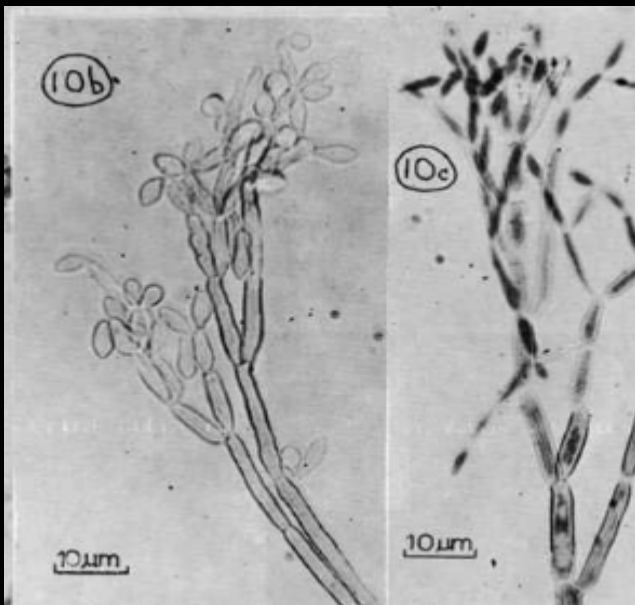
The natural habitat of the fungus may be resinous bark and wood, from where it was isolated first. It not only tolerates a far higher concentration of creosote and coal tar than other fungi, but is able to grow and reproduce with no other source of nourishment than in these environment.

Probencharakterisierung	Zahl der beprobten Orte	
	positiv	negativ
Boden unter Eiben (<i>Taxus baccata</i>)	10	9
" " Ahoen (<i>Acer spp.</i>)	0	8
" " Buche (<i>Fagus sylvatica</i>)	0	8
" " Kiefer (<i>Pinus spp.</i>)	1	9
" " <i>Pinus</i> neben <i>Taxus</i>	4	0
" " Robinie (<i>Robinia pseudoacacia</i>)	1	0
" " verschiedene andere Bäume	0	10
Harz von <i>Pinus sp.</i>	0	3
Boden einer früheren Teerfabrik	3	2
Gesamtzahl der beprobten Orte	19 (28 %)	49 (72 %)

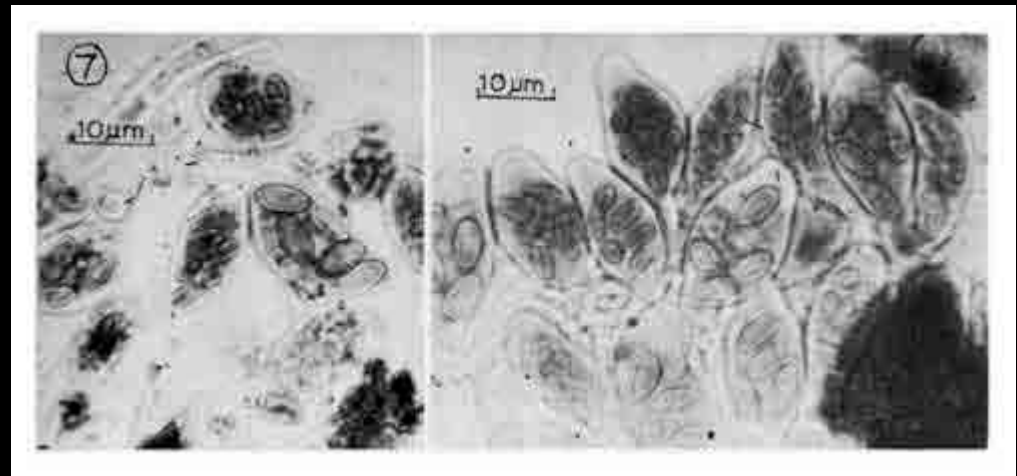
Tabelle 3.3: Vorkommen von *H. resinae* in Bodenproben und Harzen. Es wurden 68 verschiedene Orte in Berliner Parkanlagen und anderen Stellen Ostdeutschlands untersucht.

Fürst 1999

Christensen *et al.* 1942: *Hormodendrum resinae* (Lindau), an inhabitant of wood impregnated with creosote and coal tar. Am J Botany 29: 552-58



Hormoconis resinae



Amorphototheca resinae Asci and ascospores

Table 1. Nomenclature and synonymies for the creosote fungus and the resin fungus, showing the use of the same basionym for the two fungi. The 'false' names and synonymies for the anamorph of the resin fungus are indicated by **blue** text. The second nomenclatural solution described in the text would have the effect of switching the **blue** text to black for the creosote fungus, and to simultaneously switch the equivalent black text to **blue** for the mononematous synanamorph of the resin fungus. Holotypes we have examined, and the herbarium where they are deposited, are marked with exclamation points, and details of these specimens are noted in Materials and Methods

Creosote fungus

Teleomorph: *Amorphotheca resinae* Parberry, Australian J. Bot. 17: 340. 1969

Anamorph

Homodendrum resinae Lindau, in Rabenh. Krypt.-Fl., 2, 1 (Pflze) 8: 699. 1906 (B!)

≡ *Cladosporium resinae* (Lindau) G.A. de Vries, Antonie van Leeuwenhoek 21: 157. 1955

≡ *Hormoconis resinae* (Lindau) von Arx & G.A. de Vries, in von Arx, Verh. K. Ned. Akad. Wet., Afd. Natuurk. 61: 62. 1973

≡ *Cladosporium avellaneum* G.A. de Vries, Contribution to the knowledge of the genus *Cladosporium*, Uitg. Druk. Hollandia, p. 56. 1952

Resin fungus

Mononematous synanamorph:

Homodendrum resinae Lindau, in Rabenh. Krypt.-Fl., 2, 1 (Pflze) 8: 699. 1906 (B!)

≡ *Cladosporium resinae* (Lindau) G.A. de Vries, Antonie van Leeuwenhoek 21: 157. 1955

≡ *Hormoconis resinae* (Lindau) von Arx & G.A. de Vries, in von Arx, Verh. K. Ned. Akad. Wet., Afd. Natuurk. 61: 62. 1973

Synnemalous anamorph:

Sporocybe resinae (Fr.) Fr., Summa Veg. Scan. 2: 468. 1849

≡ *Racodum resinae* Fr., Obe. Mycol. 1: 216. 1815 (basionym) (B!)

≡ *Sporocybe resinae* (Fr.) Fr., Syst. Mycol. 3: 341. 1832

≡ *Dendryphion resinae* (Fr.) Corda, Icon. Fung. 6: 11. 1854

≡ *Stysanopsis resinae* (Fr.) Ferr., Flora Ital. Crypt., 1 (Fungi, Hyphales), p. 187. 1910

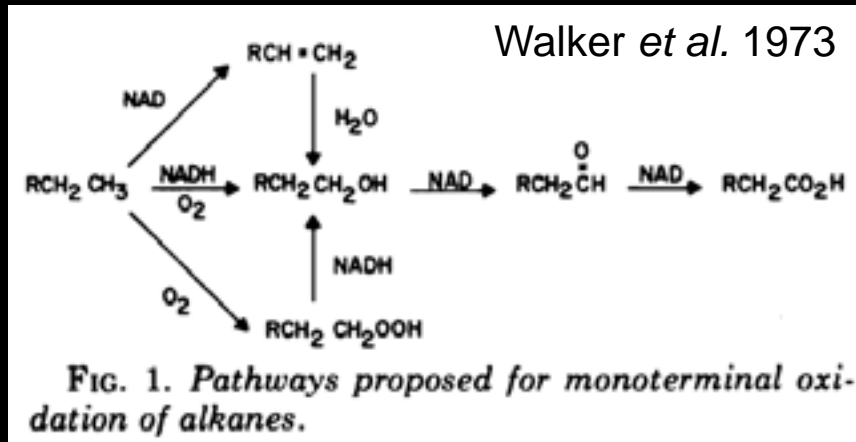
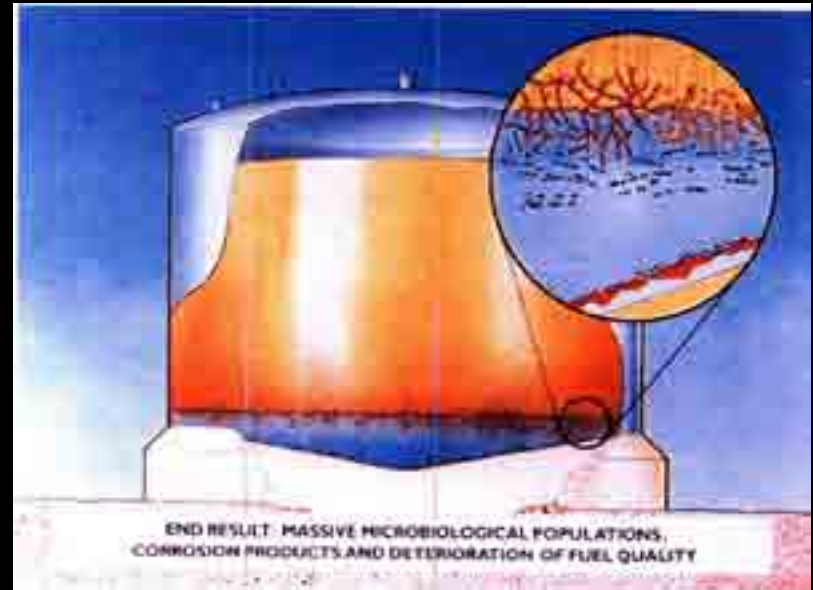
? = *Dematium nigrum* Link, Mag. ges. naturf. Fr. 3: 21. 1809 (B!)

≡ *Sporotrichum nigrum* (Link) Link, Mag. Ges. naturf. Fr. Berlin 7: 35. 1815

≡ *Pycnostysanus resinae* Lindau, Verh. Bot. Ver. Brandenb. 45: 160. 1904 (B!)

≡ *Stysanus resinae* (Lindau) Sacc., Syll. Fung. 18: 651. 1906

In the 1960's interest in this fungus revived with the implicating of *Amorphotheca resiniae* in contamination of jet aviation fuels and in corrosion of aircraft tanks.



P450-monooxygenase system is responsible for oxidation of RH to ROH

(H.-M. Fürst, Dissertation. TU Berlin 1999)

Amorphotheca resiniae can degrade alkanes (branched and unbranched), alkenes, cyclic alkanes and aromatic hydrocarbons, even ones difficult to digest. Best growth on C₁₀ to C₁₈, no growth on C₂₉ to C₃₄

H.-M. Fürst 1999

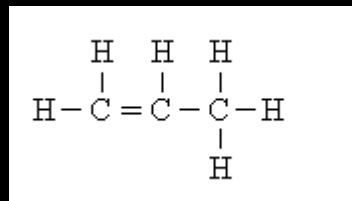
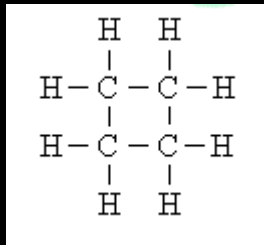
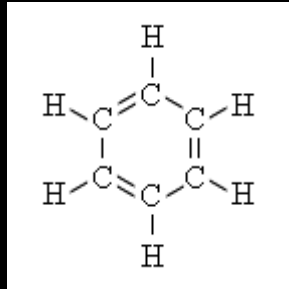
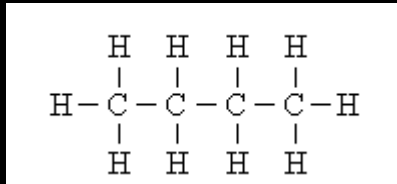


Table 1 - Fuel fractions obtained from crude oil

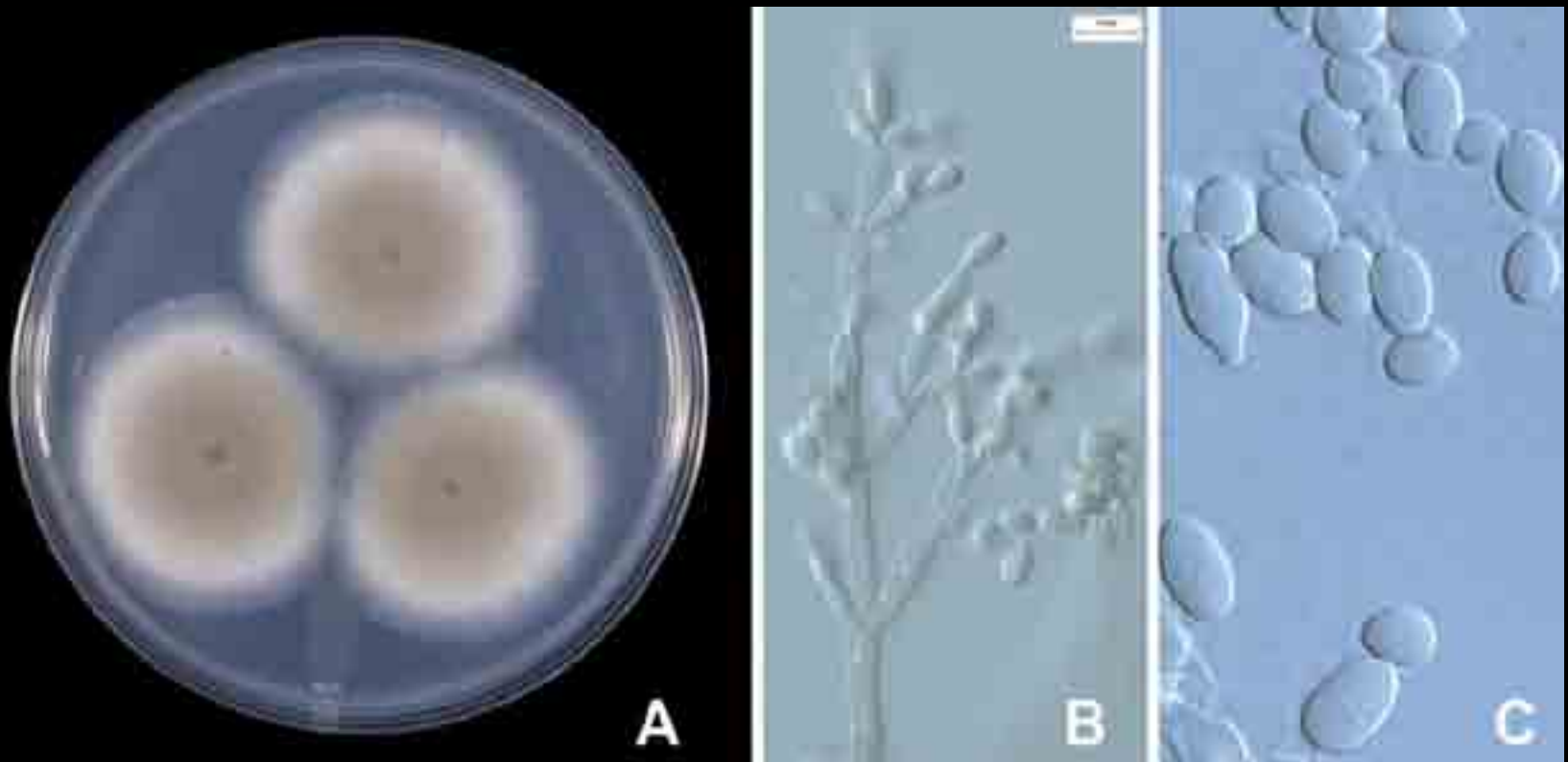
Fraction	C atoms	M. Wt.
Gas	1-4	16-58
Gasoline	5-12	72-170
Kerosene	10-16	156-226
Diesel	15-22	212-294

C.C. Gaylarde 1999



Taxonomy, nomenclature and phylogeny of three cladosporium-like hyphomycetes, *Sorocybe resiniae*, *Seifertia azaleae* and the *Hormoconis* anamorph of *Amorphotheca resiniae*

K.A. Seifert, S.J. Hughes, H. Boulay and G. Louis-Seize



Amorphotheca resiniae, colony characters and anamorph micromorphology. A. 10-d-old colony on PDA. B. Micromorphology of conidiophores, showing acropetal conidial chains, ramoconidia, and conidia. C. Conidia.

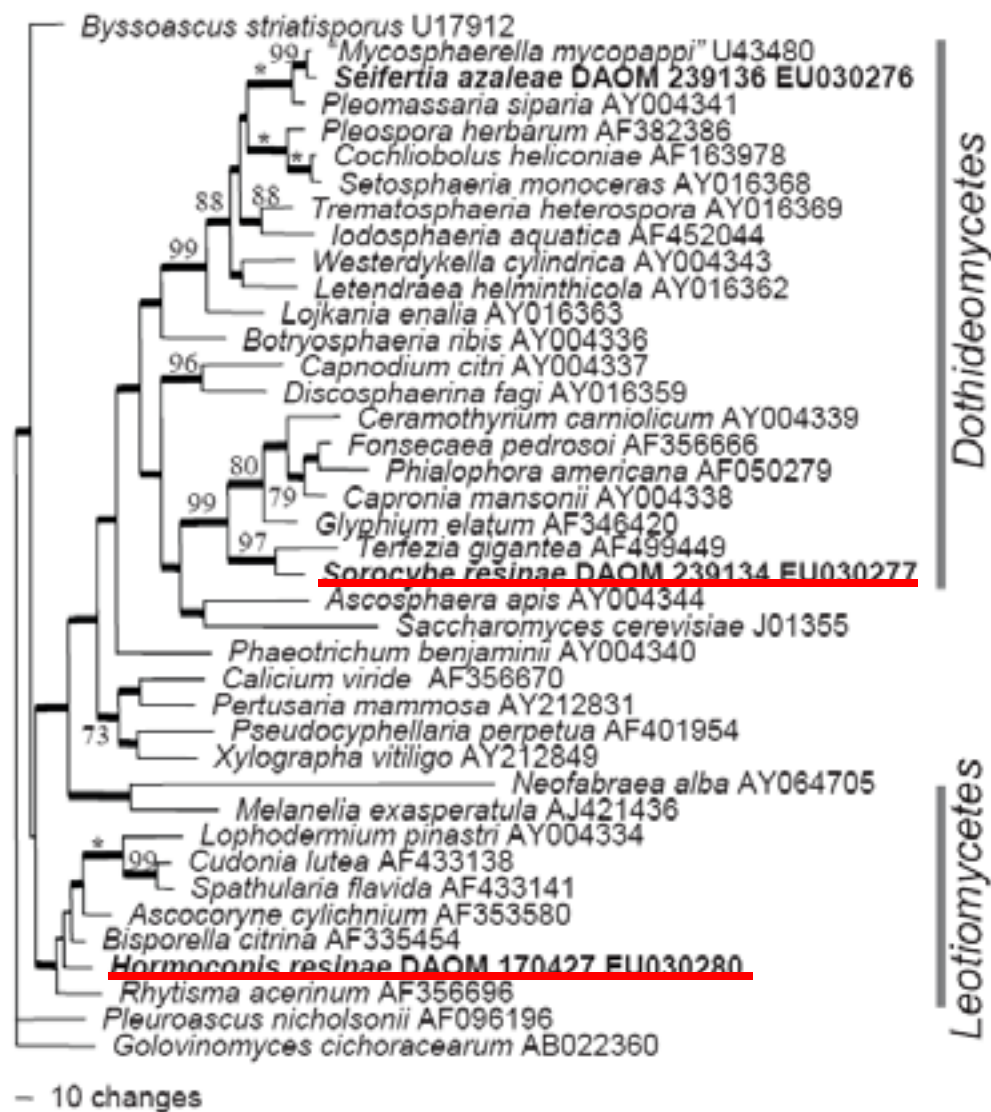


Fig. 4. Parsimony analysis of large subunit sequences, demonstrating the phylogenetic positions of *Amorphotheca resinae*, *Sorocybe resinae* and *Seifertia azaleae* (all shown in bold) in the Ascomycota. One of 12 equally parsimonious trees (1 888 steps, CI = 0.390, RI = 0.554, RC = 0.216, HI = 0.610) with *Golovinomyces cichoracearum* as the out-group. Bootstrap values above 70 % are shown at the relevant nodes, with an asterisk representing 100 % bootstrap support; branches with thick lines occurred in all equally parsimonious trees.



