(36)

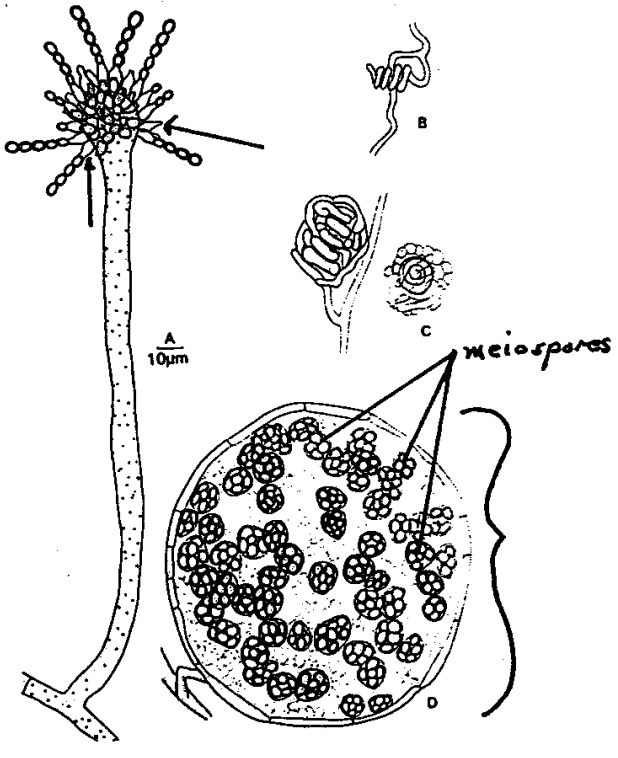
NAME _____

EXAM I
February 23, 1994
MIC 321

Directions: All explanations, definitions, and descriptions should be presented in good English. This means complete sentences should be used except when lists or fill-in-the-blanks are required. Spelling of mycological terms should be accurate. Slight misspellings may be overlooked, but major misspellings will result in wrong answers.

1. (1 pt per blank; 20 pts total) Identifications of structures and their essential basic function and/or their taxonomic significance to fungi or to fungal-like protoctistans. In the blanks provided identify with no more than one or two mycological terms each structure (as indicated by arrow(s) or bracket(s), and then with a word or short phrase describe its function (e.g., cytokinesis, asexual reproduction, meiosporangium, etc.) and/or its relevance to phylogeny (classification) at the rank(s) requested.

a.



a. structure (as indicated by bracket)

_____

b. class _____

c. phylum_____

d. structure as indicated by arrows

_____

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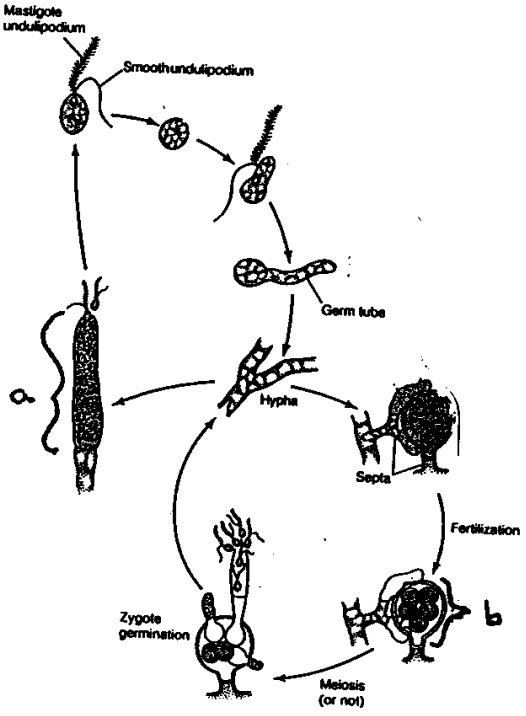
b.



e. structure (as indicated by bracket a)

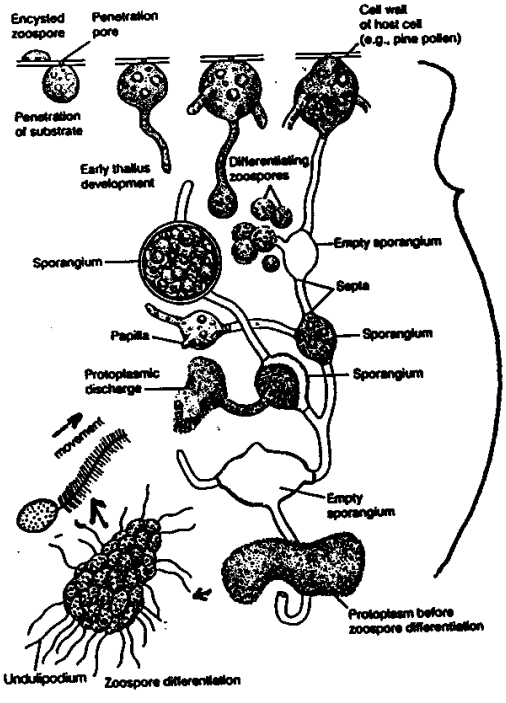
_____

f. structure (as indicated by bracket b)

_____

g. phylum_____

c.



h. type of thallus (as indicated by bracket)

_____

i. phylum_____

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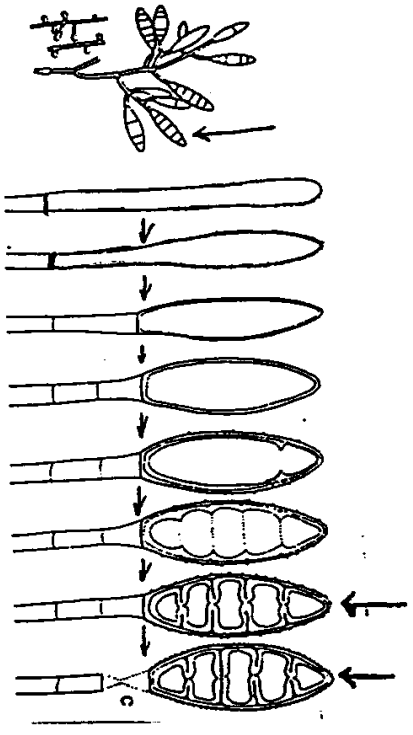
d.



i. structure (as indicated by horizonal arrows)

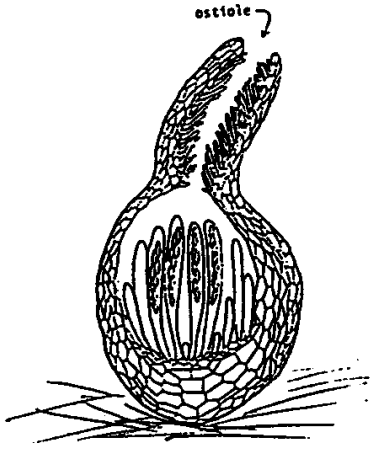
_____

j. form-class_____

k. form-phylum_____

e.

_____



l. structure (be specific)_____

m. function_____

_____

n. class_____

o. subdivision_____

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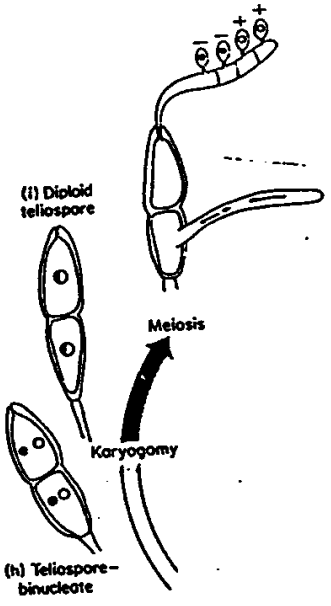
f.



p. structures (as indicated by pluses and minuses

_____

q. function_____

_____

r. phylum_____

s. subphylum_____

2. (1 pt per blank; 40 pts total) Fill in the blanks.

a. The all inclusive definition of a fungus as a _____, _____ and _____ organism, which has cell walls, typically reproduces sexually and/or asexually by producing spores, and grows either reproductively by budding and nonreproductively by hyphal apical tip elongation may have to be modified in the future in some way to exclude most or all organisms that produce _____ during their life cycle.

b. The various taxa of the members of the Kingdom Fungi are easily distinguished by specific suffixes. Identify these suffixes for the following:

1. class _____

2. subkingdom _____

3. division/phylum _____

c. Fungal nutrition is said to be greatly facilitated by _____ enzymes that depolymerize complex natural products that serve as substrates for carbon and energy.

d. Organisms currently included in the four phyla/divisions _____, _____, _____, and _____ were not too many years ago uniformly classified in the single fungal class Phycomycetes, because most produced their mitotically derived, and flagellate reproductive propagules in a cell called a/an _____.

e. Fungi that produce nonflagellated, endogenous mitospores called _____ and exogenous karyospores known as _____ are currently classified in the phylum/division _____.

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f. Fungal-like Protoctista that produce zoospores with an anterior tinsel-type flagellum are classified in the phylum/division _____.

g. Fungal-like Protoctista that produce endogenous karyospores known as _____ and heterokont zoospores with one whiplash and one tinsel-type flagellum are classified in the phylum/division _____.

h. Fungi that produce exogenous meiospores known as _____ on a cell known as a _____ are classified in the phylum/division _____.

i. Yeast and hyphal fungi that do not produce multihyphal aggregate structures in association with their endogenous meiospores are classified into the subdivision _____.

j. Fungi that produce deeply lobed or septate basidia in association with their exogenous meiospores are classified into the class _____.

k. Budding single cell fungi that are not known or observed to produce meiospores are included in the form-class _____ of the division/phylum _____.

l. Anamorphic fungi that form multihyphal aggregate, tissue-like structures, in association with their conidia-producing structures, are included in the form-class _____.

m. The thallus of some fungi consists of a branching system of walled tubes called _____, which grow by _____ _____ (two words) and by _____.

n. Species of *Allomyces, Achyla* and *Rhizopus* are common members of three different divisions/phyla. These three taxa are _____, _____, and _____, respectively (the word, respectively, means that the divisions you list must be in the same order as the genera listed).

o. Fungi that produce spores which upon germination directly give rise to basidia are usually classified between the two orders _____ and _____.

p. Fungi like *Saccharomyces cerevisiae* and some fungal-like protists which convert their whole body into a reproductive cell are said to be _____.

q. Fungi and fungal-like protists that have multiple reproductive centers associated with their thalli are said to be _____,

r. Multinucleate haploid hyphal fungi having sexually compatible mating genes in the same cytoplasm but in different mitotically dividing nuclei are said to be _____.

s. Sporangia that are reduced in size to the point where they contain only a relatively few sporangiospores are called _____ or _____.

3. (10 pts) On the answer sheets provided, diagram the sequence of hyphal apical growth and branching that occurs among some Basidiomycota and perpetuates the dikaryotic condition. Make sure your diagrams are accurate and well labelled. To save time, do not diagram any structures and events associated with karyogamy and meiosis.

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4. (15 pts) On the answer sheets provided, write a paragraph that describes in some detail the concept of thallic versus blastic conidiogenesis. Include in your paragraph mention of the relevance to this concept of the terms holoblastic, phialidic, annellidic, holothallic, holoarthric and enteroarthic and how each of these terms defines specifically a different type of conidiogenesis.

5. (15 pts) In one of last year's Science magazines, an article was published titled "Monophyletic Origins of the Metazoa: An Evolutionary Link with Fungi". The abstract associated with that paper and the paper's one Figure are reproduced below for your information. Although the phylogeny presented in Fig. 1 includes only the fungal-like protists *Dictyostelium discoidium* (Acrasiomycota), *Achlya bisexualis* (Oomycota) and *Blastocladiella emersonii* (Chytidiomycota) and the fungi *Athelia bombacina* (Homobasidiomycotina), *Saccharomyces cerevisiae* (Hemiascomycotinia), and *Aureobasidium pullulans* (Blastomycete), demonstrate your familiarity with current concepts of the relationships of the members of the Kingdom Fungi with each other and with other kinds of organisms by writing about and evaluating the data in Fig. 1. In other words, in an essay of an appropriate length critically evaluate the phylogeny depicted by presenting evidence in its favor and its general agreement with the concepts put forth by Whitaker, Margulis and Schwartz, and by Cavalier-Smith.

Monophyletic Origins of the Metazoa: An Evolutionary Link with Fungi

Patricia O. Wainright, Gregory Hinkle, Mitchell L. Sogin,* Shawn K. Stickel

A phylogenetic framework inferred from comparisons of small subunit ribosomal RNA sequences describes the evolutionary origin and early branching patterns of the kingdom Animalia. Maximum likelihood analyses show the animal lineage is monophyletic and includes choanoflagellates. Within the metazoan assemblage, the divergence of sponges is followed by the Ctenophora, the Cnidaria plus the placozoan *Trichoplax adhaerens*, and finally by an unresolved polychotomy of bilateral animal phyla. From these data, it was inferred that animals and fungi share a unique evolutionary history and that their last common ancestor was a flagellated protist similar to extant choanoflagellates.

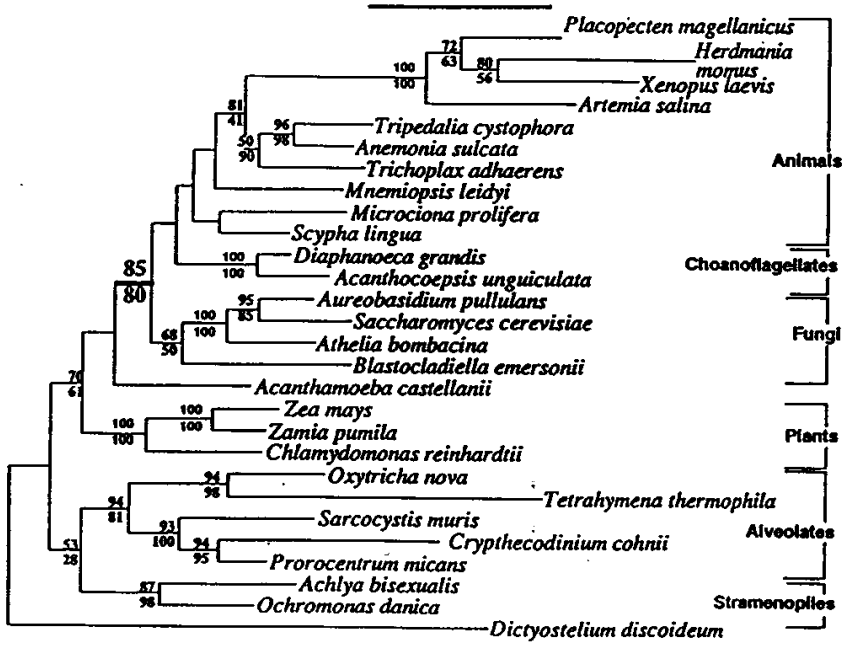

Fig. 1. Relation between animals, fungi, plants, and other eukaryotic groups inferred from complete 16*S*-like rRNAs. A computer-assisted method was used to align the 16*S*-like rRNA sequences from animals, plants, fungi, stramenopiles, alveolates, and other protist groups that diverged at the crown of the eukaryotic tree (*8*). Maximum likelihood methods (*10, 12*) were used to infer a molecular phylogeny with the use of sites that could be unambiguously aligned. The percentage of 110 bootstrap resamplings that support topological elements in maximum likelihood inferences is shown above the branches. The percentage of 200 neighbor-joining bootstrap replicates that corroborate topological elements in the figure is shown below the branches. The root of the tree is placed within the *Dictyostelium discoideum* lineage (*4, 5*). Confidence levels below 50% are not indicated.