
Stack Stack Dupe Dupe Yu Hu Flt !!LINK!!

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[1/1/15 00:00:00:000 utc] 00000001
systemerr r java.lang.throwable [1/1/15
00:00:00:000 utc] 00000001 systemerr r at
java.thread.dumpstack(thread.java:434)
[1/1/15 00:00:00:000 utc] 00000001
systemerr r at com.ibm.ws.hamanager.runtim
e.runtimeproviderimpl.panicjvm(runtimeprovid
erimpl. the simplest configuration is called a
stack, but there are also other types of
cisternal organizations that feature non-equal
stack cisternae. in this case, the stacked
cisternae are not produced regularly but
randomly. armillaria mellea is a well-known
pathogenic basidiomycetes. armillaria has no
sexual stage. armillaria mellea is a
cosmopolitan organism that forms and
reproduces mycelium in soil. this fungus has a
long history of use in traditional medicines
(szabo and kubiela 1999 ). in fact, it is used for
cough, asthma, diarrhea, dysentery,
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tuberculosis, lymphoma, and abscesses. clinical studies have shown that the decoction of the fruit bodies of *armillaria mellea* is a powerful tool against bronchial asthma and allergic rhinitis, and is considered to have an efficacy equivalent to that of antihistamines and corticosteroids (he et al. 2000). similarly, caskin is a traditional chinese medicine. as per the chinese pharmacopoeia, it is used for the treatment of asthma and chronic cough, rheumatic arthralgia, gout and lumbago. like the rest of the basidiomycete family, the spores of *armillaria mellea* are hydrophobic and are responsible for the pathogenesis and spread of the disease. the spores of *armillaria* are used as a diagnostic marker for the identification of species. characterization of the biology and taxonomy of *armillaria mellea* has received a lot of attention over the past few decades. studies on the cellular biology of *armillaria mellea* have explored its infection cycle, including the potential to cause human disease. a detailed understanding of the infection process will help the development of strategies to prevent human infections. *armillaria mellea* is a fungus that is often found in the logs of decaying trees. it also commonly exists in the soil under the roots of its host tree. however, *armillaria mellea* does not grow well in pure culture. *armillaria mellea* can only be grown in soil and under a host tree.

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this is the second of the evolutionary patterns predicted by the model that evolution of stacked golgi cisternae is predicted to proceed via loss of the stacking factor and the appearance of orthologues of the proteins necessary for unstacking. to test the model, we first identify the orthologues of these proteins in non-metazoan organisms, then study their presence in taxonomic groups that are predicted to have stacked or unstacked golgi. note that in the case of hrd1, the tm domains of yeast orthologues were predicted to face the lumen, whereas the orthologues in other organisms (including other fungi) were predicted to face the cytosol (additional file 2 : figure s1). a representative genomes are shown, with species phylogeny shown (according to the taxonomy tree, figure 2 and additional file 7 : figure s2). b gfp-tagged protein expressed in live cells (top row) and immunolocalization (bottom row) showing the absence of protein in stacked golgi. the boxed region in the top row is shown in higher magnification in the left-hand image in each pair. scale bars: 10 μ m. note the continuity of the tubule in the left-hand image of each pair, indicating that these structures are not cisternae of the golgi. filled arrows indicate the distribution of the protein. open arrows indicate the localization of the protein, which is clearly cytosolic. dashed arrows indicate the position of the golgi. c cog functional category of the proteins identified as necessary for unstacking. d percentage of proteins in each cog functional category that are predicted to

be necessary for unstacking. e percentage of proteins in each cog functional category that are predicted to be present in unstacked golgi. f percentage of proteins in each cog functional category that are present in stacked golgi. note that, in the case of hrd1, the tm domains of yeast orthologues were predicted to face the lumen, whereas the orthologues in other organisms (including other fungi) were predicted to face the cytosol. g the predicted presence or absence of the proteins identified in figure 1a as necessary for unstacking, in each taxonomic group shown. the data are compiled in additional file 7 : table s4.

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