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论 文

子囊菌较担子菌具有更快的进化速率和更高的物种多样性

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摘要　研究表明, 在一些进化分支或有机体之间存在着核苷酸或氨基酸替代速率差异. 越来越多的证据表明, 种群内的中性分子突变与物种多样化相关. 超过 98%的陆生真菌属于子囊菌门和担子菌门, 而且前者的物种多样性明显多于后者. 获得了地衣型真菌红脐鳞的 21 种蛋白编码基因序列, 并应用这些及 GenBank 中的相关序列进行了随后的分析. 建立了 3 组矩阵: (1) 13 种真菌, 包括 105 种蛋白编码基因; (2) 9 种真菌, 包括 21 种蛋白编码基因; (3) 299 种真菌的 nu LSU rDNA 序列. 应用这些数据, 检测了子囊菌门与担子菌门以及子囊菌内部主要纲之间的基因替代速率. 蛋白质数据和 nu LSU rDNA 数据分析显示, 子囊菌的基因替代速率显著快于担子菌; 而且在子囊菌内部, 物种丰富的粪壳菌纲进化速率最快, 物种数量较少的锤舌菌纲进化最慢. 结果提示, 子囊菌的快速进化不是得益于互惠共生、生态条件、无性繁殖、代谢速率或者短世代时间, 而可能是由奠基者效应引起的. 这是物种数量与进化速率相关的又一证据, 与奠基者效应是导致物种丰富的分支进化速率较快的主要原因的假说相吻合.

关键词
进化速率
氨基酸替代
核苷酸替代
真菌进化
物种多样性
奠基者效应

众所周知, 不同生物类群的物种多样性具有非常大的差异, 有些世系仅仅包括 1 个幸存种, 有些世系却具有庞大的物种数量, 如拥有超过 350000 个物种的甲虫(Coleoptera)[1]. 世系的年龄、适应性辐射和关键特征的进化常常被用来解释该现象发生的原因[2~5]. 许多研究表明, 物种间的进化速率存在差异[6~11], 而精确的分子钟(如果其确实存在)却很少被观察到[12,13]. 研究表明, 生物分类群的进化速率与某些因素有关, 例如, 个体大小和代谢速率[14~19], 世代时间[20~25], 共生关系[9,11,26]或环境条件[27,28]. 此外, 也有研究者提出了进化速率与物种分化速率的相关性. 支持这一相关性存在的证据正在逐渐增加[29~34]. 基于种群生物学和种群进化学理论[35~38]的物种形成速率假说[31]对这一相关性进行了解释. 如果物种形成发生于小边缘种群, 遗传漂变将造成该种群的快速遗传改变, 同时导致奠基者效应的发生[35]. 在不同的世系中, 如

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果成种方式和其发生的频率不同, 则会造成相关世系在进化速率上的差异. 实际上, 间断平衡理论甚至预测物种分化速率与基因替代速率的相关性是普遍存在的[39~41].

作为动物界的姊妹群, 真菌界是一个物种丰富的、重要的生物类群[42]. 陆生真菌与其他有机体形成共生和寄生关系, 是陆地生态系统的重要组成部分, 同时又是陆地上最重要的有机分解者[43]. 超过 98%的已知真菌都属于子囊菌门和担子菌门[44,45]. 这两个门是姊妹群, 而且位于真菌进化树的顶端[46]. 它们的物种数量不同, 子囊菌门的物种数量是担子菌门的 2 倍还多(表 1)[45]. 而且, 由于未描述的真菌更多地属于子囊菌门, 所以这两个门物种数量的实际差异可能更大[47,48].

如果间断平衡理论是正确的, 那么子囊菌门和担子菌门的物种数量存在显著差异意味着两者的基因组进化速率同样存在显著差异. 因此, 对这两个门的进化速率进行了比较分析. 主要应用 GenBank 中已经完成基因组测序工作的可用真菌序列. 在子囊菌门中有一个重要的地衣型共生类群, 茶渍纲(Lecanoromycetes)[49~54]. 关于此纲, GenBank 中还没有足够数量的蛋白质基因序列能够用于本文的研究. 之前, 曾研究过此纲的一个地衣型真菌, 红脐鳞(*Rhizoplaca chrysoleuca*)的遗传多样性[55]. 本实验测定了红脐鳞中 21 种线性遗传的(orthologous)蛋白质基因片段序列, 并且将其与 GenBank 中其他真菌的相关序列进行联合分析. 组建了 3 个不同的数据集: 其中两个由多个线性遗传的蛋白质基因构成(包括 9 种真菌的 21 种基因数据集, 和包括 13 种真菌的 105 种基因数据集); 另外一个数据集包括 299 种真菌的核糖体大亚基 DNA(nu LSU rDNA)序列. 利用这些数据检验了子囊菌门和担子菌门以及子囊菌门内部各主要纲(表 1)之间的进化速率是否存在显著性差异.

1 材料与方法

1.1 取样和比对

红脐鳞中线性遗传的蛋白质基因片段通过随机测定其 EST 文库的 1000 个克隆获得. 该工作由北京华大基因公司完成. 这些随机测定的 cDNA 片段通过 DNAMAN 4.0(Lynnon Biosoft)软件被翻译成蛋白质序列. 这些蛋白质片段通过 GenBank 的相似性搜索(Blastp)被鉴定, 其中 21 种线性遗传的蛋白质片段被

表 1 研究所涉及物种数量及其分类地位[45]

纲/门	纲或门中已知科和种的数量	纲和门中被 nu LSU rDNA 数据集所涉及的科和种的数量	蛋白质数据所涉及的真菌	21 种蛋白质数据	105 种蛋白质数据
子囊菌门	327/64163	170/201	–	–	–
座囊菌纲	90/19010	44/44	*Phaeosphaeria nodorum*	+	+
散囊菌纲	27/3401	17/26	*Aspergillus fumigatus*	+	+
			Coccidioides immitis	+	+
茶渍纲	77/14199	40/40	*Rhizoplaca chrysoleuca*	+	–
锤舌菌纲	19/5587	15/27	*Sclerotinia sclerotiorum*	+	+
盘菌纲	16/1684	11/21	–	-	–
粪壳菌纲	64/10564	38/38	*Gibberella zeae*	+	+
			Magnaporthe grisea	+	+
			Neurospora crassa	+	+
酵母菌纲(外类群)	–	5/5	*Yarrowia lipolytica*	+	–
担子菌门	177/31515	91/94	*Coprinopsis cinerea*	–	+
			Cryptococcus neoformans	–	+
			Laccaria bicolor	–	+
			Malassezia globosa	–	+
			Ustilago maydis	–	+
毛霉亚门(外类群)	–	–	*Rhizopus oryzeae*	–	+
壶菌门(外类群)	–	4/4	–	–	–

用来分析. 这 21 种蛋白质序列及其相应的基因序列已递交 GenBank(序列接收号为 HM007281~HM007304).

所有 299 种真菌的 nu LSU rDNA 序列, 以及红脐鳞和 *Rhizopus oryzae* 之外真菌的蛋白质基因序列全部来自 GenBank(详见网络版附表 1~3). *Rhizopus oryzae* 的蛋白质基因序列来自网站: http://www.broadinstitute.org/ science/data.

用 ClustalX 1.81[56]软件进行序列比对, Mega 4[57]软件进行蛋白质序列的拼接及缺失和错误位点的删除.

1.2 进化速率差异的检测

PAML 3.14b 软件包[58]中的 Baseml 和 Codonml 程序被用于进化速率的显著性差异比较. 似然率检验法[59]被用于该项分析. 子囊菌门与担子菌门进化速率的同质性检验包括了两个数据集, 105 种蛋白质数据集和 nu LSU rDNA 数据集; 子囊菌内各纲间进化速率的同质性检验除了上述两个数据集外, 还包括 21 种蛋白质的数据. 比较在 2-速率模型和 3-速率模型间进行. 2-速率模型假设两个目标分支具有相同的进化速率, 外类群则不同; 3-速率模型假设两个目标分支和外类群均具有不同的进化速率.

1.3 进化距离的计算

nu LSU rDNA 数据集中进化距离的计算应用了 Mega 4[57]软件中的 MCLM 法[60](maximum composite likelihood method). 矩阵中缺失和错误位点的处理选择了成对删除. 最终的矩阵包含了 1129 bp. 各目标类群到外类群的平均进化距离的显著性差异分析选择了 SPSS 13.0 软件包中的单因素多组数据统计分析法(one-way ANOVA).

囊括 9 种真菌的 21 种蛋白质矩阵最终包含了 3879 个氨基酸; 囊括 13 种真菌的 105 种蛋白质矩阵最终包含了 39279 个氨基酸.

1.4 相对进化速率的计算

每对分支间的相对进化速率通过 Mega 4[57]软件计算的进化距离获得. 基于蛋白质数据的进化距离计算通过 Mega 4[57]软件中的泊松校正法[61](Poisson correction method)获得.

2 结果与分析

2.1 子囊菌门与担子菌门以及子囊菌各纲间进化速率的显著性差异

应用似然率检验法测定了子囊菌门与担子菌门以及子囊菌内各纲间进化速率的显著性差异. 为了确定两个分支间的进化速率是否存在差异, 在进行似然率统计分析时比较了 2-速率模型和 3-速率模型的 Ln L 值差异(LRT).

为了比较子囊菌门与担子菌门的进化速率差异, 分析了两个数据集, 105 种蛋白质数据集和 nu LSU rDNA 数据集. 前者包括 7 种子囊菌和 5 种担子菌, 以及作为外类群的 1 种毛霉亚门真菌(表 1). 后者包括 196 种子囊菌和 94 种担子菌, 以及作为外类群的 4 种壶菌(表 1). 基于这两个数据集的分析结果表明, 子囊菌门与担子菌门的进化速率存在显著差异, 前者快于后者(表 2).

同样的 nu LSU rDNA 数据集和 105 种蛋白质数集被用于比较子囊菌内各纲的进化速率差异. 此外, 21 种蛋白质数据集也被用于该项分析. 此 21 种蛋白质数集包括 105 种蛋白质数据集中的所有子囊菌样品和 1 种茶渍纲地衣型真菌, 以及作为外类群的 1 种酵母纲真菌(表 1). 基于这 3 个数据集的分析都表明, 粪壳菌纲子囊菌较其他纲子囊菌具有更快的进化速率. 此外, 基于 nu LSU rDNA 数据集的分析还显示, 散囊菌纲具有第二快的进化速率, 锤舌菌纲的进化速率最慢, 其他 3 个纲(茶渍纲、座囊菌纲和盘菌纲)具有第三快的进化速率(表 2).

2.2 进化距离

应用 Baseml 和 Codonml 程序的进化速率差异分析, 需要首先提供一个系统进化树. 由于 nu LSU rDNA 数据集拥有很大的样品量和相对有限的核苷酸位点, 基于此数据集很难构建理想的系统进化树. 考虑到系统进化树的拓扑结构在一定程度上会影响进化速率显著性差异分析的结果, 基于该数据集比较了子囊菌门与担子菌门以及子囊菌内各纲到外类群的进化距离.

为了比较子囊菌门与担子菌门到外类群的进化距离, 分析了两个 nu LSU rDNA 数据集. 其中一个与进化速率显著性差异分析的数据集完全相同, 另外一个自上述数据集中排除了子囊菌中进化最快的粪壳

菌纲. 基于这两个数据集的分析都显示, 子囊菌到壶菌的进化距离显著大于担子菌(表 3). 结果表明, 子囊菌与担子菌到外类群进化距离的差异不是由于子囊菌内个别纲的进化速率变化所造成的. 图 1 显示了子囊菌与担子菌每个样品到壶菌的进化距离的差异.

为比较子囊菌内各纲进化距离的差异, 应用 nu LSU rDNA 数据集中的所有 196 种子囊菌样品, 选择了酵母菌亚门的 5 种真菌作为外类群(表 1). 依据进化速率显著性差异分析结果, 将子囊菌分成4个类群进行进化距离比较: 粪壳菌纲、散囊菌纲、锤舌菌纲和第 4 个类群(茶渍纲、座囊菌纲和盘菌纲). 结果显示, 这 4 个类群彼此间到外类群的进化距离都存在显著性差异(表 3). 该结果与进化速率的差异分析结果相一致.

3 讨论

基于不同的方法和3个不同的数据集, 本研究清楚地证明了子囊菌门的分子进化速率显著快于担子菌门. 同时阐明了子囊菌内某些纲之间的进化速率同样存在着显著性差异. 本文为子囊菌门及粪壳菌纲进化速率的加快提供了统计学证据. 但是, 在此之前已有研究表明, 某些担子菌[11,26]和子囊菌[9,27]的小分支同样具有加快的进化速率. 这些小分支进化速率的加快被认为与共生或生态条件有关. 子囊菌门与担子菌门以及本实验所涉及的子囊菌各纲间的生态条件并没有一致差异. 而且, 子囊菌内物种数量最丰富的 3 个纲, 座囊菌纲、茶渍纲和粪壳菌纲的共生关系完全不同. 茶渍纲的绝大多数真菌与绿藻或蓝细菌形成地衣型共生关系, 而座囊菌纲的地衣型种类非常少, 粪壳菌纲中的地衣型真菌更是完全缺失[62]. 因此, 地衣型共生的发生似乎并不能合理解释本实验所观察到的进化速率差异.

通常情况下, 造成核苷酸替代速率加快的因素有两种: 正向选择或基因组替代速率的普遍加快. 为

表 2　应用 PAML 软件的速率模型比较(d*f*=1, *P*<0.05 示差异显著)

类群	数据集	Ln L(null)2-速率模型	Ln L(alt.)3-速率模型	LRT	*P*	相对速率
子囊菌门 *vs.* 担子菌门	105 种蛋白质	−527398.204058	−527312.526435	85.677623	<0.0001	1∶0.824
	nu LSU rDNA	−65068.740739	−65062.100412	6.640327	<0.01	1∶0.724
粪壳菌纲 *vs.* 散囊菌纲	105 种蛋白质	−527560.318578	−527402.805448	157.51313	<0.0001	1∶0.859
	21 种蛋白质	−27015.482279	−27001.819130	13.663149	<0.001	1∶0.763
	nu LSU rDNA	−64998.459349	−64970.501967	27.957382	<0.0001	1∶0.536
粪壳菌纲 *vs.* 茶渍纲	21 种蛋白质	−24678.859250	−24662.406111	16.453139	<0.0001	1∶0.925
	nu LSU rDNA	−65040.207085	−64974.290373	65.916712	<0.0001	1∶0.435
粪壳菌纲 *vs.* 座囊菌纲	105 种蛋白质	−527547.627172	−527410.509802	137.11737	<0.0001	1∶0.960
	21 种蛋白质	−24815.434902	−24805.185578	10.249324	<0.01	1∶0.963
	nu LSU rDNA	−65025.983459	−64978.705730	47.277729	<0.0001	1∶0.409
粪壳菌纲 *vs.* 锤舌菌纲	105 种蛋白质	−527783.148246	−527434.405216	348.74303	<0.0001	1∶0.813
	21 种蛋白质	−24305.693655	−24274.466383	31.227272	<0.0001	1∶0.792
	nu LSU rDNA	−65035.747310	−64975.958430	59.78888	<0.0001	1∶0.299
粪壳菌纲 *vs.* 盘菌纲	nu LSU rDNA	−65019.466588	−64978.806885	40.659703	<0.0001	1∶0.412
散囊菌纲 *vs.* 茶渍纲	nu LSU rDNA	−65063.689716	−65056.385849	7.303867	<0.01	1∶0.782
散囊菌纲 *vs.* 座囊菌纲	nu LSU rDNA	−65068.612580	−65067.109686	1.502894	>0.1	–
散囊菌纲 *vs.* 锤舌菌纲	nu LSU rDNA	−65062.767258	−65040.574709	22.192549	<0.0001	1∶0.603
散囊菌纲 *vs.* 盘菌纲	nu LSU rDNA	−65068.264591	−65064.268406	3.996185	<0.05	1∶0.702
茶渍纲 *vs.* 座囊菌纲	nu LSU rDNA	−65054.212621	−65051.467129	2.745492	>0.05	–
茶渍纲 *vs.* 锤舌菌纲	nu LSU rDNA	−65032.323634	−65028.335008	3.988626	<0.05	1∶0.735
茶渍纲 *vs.* 盘菌纲	nu LSU rDNA	−65053.936657	−65052.906898	1.029759	>0.1	–
座囊菌纲 *vs.* 锤舌菌纲	nu LSU rDNA	−65050.186493	−65039.104095	11.082398	<0.001	1∶0.767
座囊菌纲 *vs.* 盘菌纲	nu LSU rDNA	−65063.346948	−65063.045087	0.301861	>0.1	–
盘菌纲 *vs.* 锤舌菌纲	nu LSU rDNA	−65042.811015	−65035.001269	7.809746	<0.01	1∶0.887

表 3　每个类群到外类群进化距离的均值检验(nu LSU rDNA 数据集, $P<0.05$ 示差异显著)

类群	外类群	样品量	均值	最小值	最大值	P	相对速率
子囊菌门	壶菌门	196	0.211	0.182	0.289	0.000	1∶0.824
担子菌门		94	0.181	0.149	0.212		
子囊菌门(不包括粪壳菌纲)	壶菌门	158	0.200	0.182	0.237	0.000	1∶0.804
担子菌门		94	0.181	0.149	0.212		
粪壳菌纲	酵母菌亚门	38	0.201	0.179	0.243	0.000	–
散囊菌纲		26	0.149	0.137	0.160		
茶渍纲, 座囊菌纲, 盘菌纲		104	0.135	0.112	0.161		
锤舌菌纲		27	0.124	0.113	0.159		

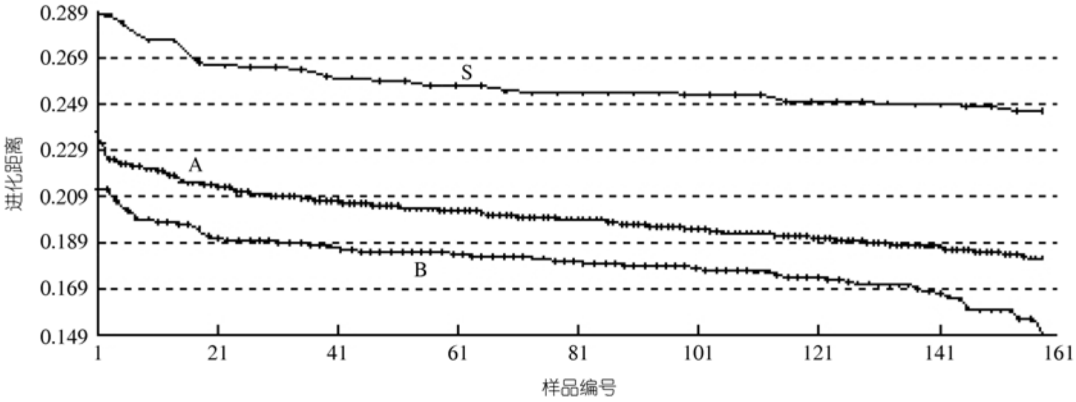

图 1　每个样品到外类群的平均进化距离(nu LSU rDNA 数据集)

相关类群的样品是按进化距离递减的次序由 1~158 平均分布的. S: 粪壳菌纲(38 种); A: 子囊菌门(158 种, 不包括粪壳菌纲); B: 担子菌门(94 种). 壶菌门的外类群包括 *Boothiomyces macroporosum*, *Kappamyces laurelensis*, *Rhizophlyctis harderi* 和 *Rozella* sp.

了检验正向选择存在的可能性, 比较了 105 种蛋白质编码基因数据集中的同义替代和非同义替代速率的差异(详见网络版附表 4). 没有证据表明正向选择的存在. 说明基因组替代速率的普遍加快导致了子囊菌进化速率的加快. 可能由多种因素造成, 包括无性型[63]、代谢速率[64]、较短的世代时间[65]或奠基者效应[35]. 缺少有性繁殖被认为加快了内共生细菌的进化速率[63,66]. 实际上, 子囊菌的无性型物种多于担子菌[67]. 然而, 由于散囊菌纲的无性型种类多于粪壳菌纲, 但是前者的进化速率却慢于后者, 因此有性繁殖的缺失似乎也不能解释本实验所观察到的进化速率差异. 同时, 也没有证据表明子囊菌和担子菌的代谢速率或世代时间存在普遍差异[68]. 所以奠基者效应成为造成本文所研究真菌世系进化速率差异的最可能原因. 子囊菌门的物种数量明显多于担子菌门的事实也支持这一解释.

4　结论

提供了生物世系的物种数量与其进化速率相关的又一证据. 这在子囊菌门与担子菌门之间是确实存在的. 关于子囊菌内各纲间的比较分析表明, 子囊菌进化速率的加快并非得益于共生、生态条件、无性型、代谢速率或更短的世代时间, 而更可能主要是奠基者效应. 这与间段平衡理论相一致. 该理论认为, 边域模型是物种形成的主要方式. 由于遗传漂变, 边域物种形成所涉及的小隔离群体将经历更快的遗传改变, 从而随着时间的推移, 物种形成过程将会加快其所在分支的分子进化速率. 尽管物种形成模式还包括边域模式以外的异域模式、邻

域模式、同域模式或成种基因的突变等, 但本研究表明, 子囊菌与它的姊妹群担子菌相比具有更丰富的物种多样性和更快的进化速率, 符合间段平衡假说.

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附表 1　105 种蛋白质编码基因的样品

蛋白质	*Aspergillus fumigatus*	*Coccidioides immitis*	*Coprinopsis cinerea*	*Cryptococcus neoformans*	*Gibberella zeae*	*Laccaria bicolor*	*Magnaporthe grisea*	*Malassezia globosa*	*Neurospora crassa*	*Phaeosphaeria nodorum*	*Sclerotinia sclerotiorum*	*Ustilago maydis*	*Rhizopus oryzae*
Vacuolar protein sorting-associated protein 26	XP_751625	XP_001247863	EAU83945	XP_776046	XP_381331	EDR10318	XP_362384	XP_001731425	EAA35892	EAT77623	XP_001592543	EAK82921	RO3G_03069
vacuolar ATP synthase catalytic subunit A	XP_748105	XP_001242551	EAU88427	XP_775506	XP_387180	EDR11023	XP_362504	XP_001732794	EAA32337	EAT81520	XP_001595698	EAK80890	RO3G_01898
pre-mRNA splicing factor (Prp8)	XP_749438	XP_001245132	EAU86045	XP_778129	XP_382712	EDR13411	XP_359533	XP_001732213	EAA33717	EAT91945	XP_001595120	EAK82591	RO3G_01072
gamma tubulin MipA	XP_752709	XP_001241990	EAU88379	XP_772622	XP_390169	EDR13746	XP_368283	XP_001729231	EAA28357	EAT82125	XP_001598808	EAK84729	RO3G_11100
Centromere/microtubule-binding protein cbf5	XP_754061	XP_001242479	EAU92842	XP_775935	XP_387382	EDR15040	XP_367607	XP_001729376	EAA31591	EAT83460	XP_001590061	EAK80867	RO3G_15034
triosephosphate isomerase	XP_753309	XP_001239740	EAU86629	XP_775227	XP_386878	EDR10156	XP_364060	XP_001732054	EAA29827	EAT76573	XP_001587441	EAK84286	RO3G_03048
translation initiation factor 2 alpha subunit	XP_754274	XP_001246338	EAU89116	XP_773976	XP_386396	EDR08279	XP_001404451	XP_001729265	EAA32669	EAT79164	XP_001585956	EAK82336	RO3G_13185
threonyl-tRNA synthetase	XP_751461	XP_001248022	EAU80442	XP_776995	XP_381424	EDR10518	XP_361008	XP_001729744	EAA30565	EAT80431	XP_001587735	EAK86112	RO3G_06614
T-complex protein 1, zeta subunit	XP_754660	XP_001248128	EAU91603	XP_773781	XP_386489	EDR09063	XP_361383	XP_001731930	EAA29712	EAT80679	XP_001591294	EAK83388	RO3G_13197
T-complex protein 1, eta subunit	XP_750420	XP_001244568	EAU92308	XP_778256	XP_386482	EDR15287	XP_360767	XP_001732682	EAA29703	EAT76803	XP_001586957	EAK81214	RO3G_10956
T-complex protein 1, delta subunit	XP_754830	XP_001248566	EAU88477	XP_774369	XP_380734	EDR14879	XP_363656	XP_001728916	EAA34893	EAT76083	XP_001597630	EAK83741	RO3G_14969
T-complex protein 1, beta subunit,	XP_749924	XP_001238899	EAU82336	XP_777942	XP_385954	EDR09515	XP_365277	XP_001730993	EAA30290	EAT88787	XP_001595013	EAK87115	RO3G_03092
T-complex protein 1, alpha subunit	XP_755937	XP_001246551	EAU88242	XP_776254	XP_385426	EDR10956	XP_366138	XP_001728987	EAA26670	EAT78684	XP_001590906	EAK82142	RO3G_05866
splicing factor 3B subunit 1	XP_755711	XP_001245212	EAU90529	XP_774063	XP_387227	EDR14089	XP_368888	XP_001731366	EAA34811	EAT88157	XP_001596870	EAK82854	RO3G_07617
small monomeric GTPase SarA	XP_750243	XP_001245464	EAU88667	XP_777426	XP_386822	EDR03200	XP_369847	XP_001731788	EDO65417	EAT85260	XP_001591874	EAK87233	RO3G_05258
signal recognition particle protein SRP54	XP_747957	XP_001242701	EAU88500	XP_775089	XP_389140	EDR14856	XP_369487	XP_001730607	EAA31407	EAT77106	XP_001595676	EAK83583	RO3G_13370
methyltransferase	XP_750530	XP_001243369	EAU88807	XP_778233	XP_385904	EDR14902	XP_363121	XP_001732469	EAA35697	EAT88653	XP_001594354	EAK82606	RO3G_15486
DUF652 domain protein	XP_749469	XP_001241339	EAU91589	XP_775101	XP_387375	EDR08878	XP_362746	XP_001731785	EAA32079	EAT89089	XP_001596852	EAK80884	RO3G_13163
60S ribosome biogenesis protein Nip7	XP_756040	XP_001239792	EAU92678	XP_777449	XP_387138	EDR15126	XP_368762	XP_001730043	EAA27993	EAT76236	XP_001589048	EAK86086	RO3G_09534
rRNA processing protein (Rrp20)	XP_750535	XP_001243372	EAU88852	XP_777870	XP_381521	EDR14785	XP_359641	XP_001730122	EAA32853	EAT88982	XP_001594483	EAK84633	RO3G_00885
RIO1 family protein kinase	XP_753477	XP_001239555	EAU93038	XP_776475	XP_389960	EDR15017	XP_367194	XP_001730876	EAA32736	EAT78642	XP_001590865	EAK86208	RO3G_04042
cytosolic large ribosomal subunit protein L7A	XP_751177	XP_001247914	EAU86554	XP_772335	XP_388654	EDQ99374	XP_362167	XP_001732654	EAA30992	EAT86044	XP_001598059	EAK80786	RO3G_14825
ribonucleotide reductase small subunit RnrA	XP_753417	XP_001239725	EAU84682	XP_772723	XP_385585	EDR13226	XP_369893	XP_001730759	EAA33584	EAT82336	XP_001595401	EAK87225	RO3G_12051
DNA replication factor C subunit　Rfc4	XP_747574	XP_001248860	EAU92758	XP_774249	XP_387376	EDR15164	XP_367615	XP_001730833	EDO65226	EAT91453	XP_001598347	EAK81118	RO3G_16283
secretory pathway gdp dissociation inhibitor	XP_755448	XP_001240816	EAU92695	XP_774160	XP_386342	EDR15137	XP_367212	XP_001731580	EAA32823	EAT79915	XP_001589137	EAK81128	RO3G_03976
pyruvate kinase	XP_750636	XP_001240869	EAU93215	XP_776923	XP_387704	EDR16037	XP_362480	XP_001729750	EAA30602	EAT92314	XP_001594760	EAK81542	RO3G_08020
proteasome component Pup2	XP_755476	XP_001241019	EAU92402	XP_772516	XP_386335	EDR15938	XP_367205	XP_001731866	EAA32830	EAT91216	XP_001589129	EAK86958	RO3G_13946
phosphatidylinositol:UDP-GlcNAc transferase subunit PIG-A	XP_753063	XP_001243553	EAU82881	XP_775674	XP_381136	EDR04632	XP_361459	XP_001731545	EAA28961	EAT90228	XP_001588529	EAK82847	RO3G_07782
phenylalanyl-tRNA synthetase beta chain, cytoplasmic	XP_749491	XP_001245059	EAU84898	XP_773126	XP_381280	EDR12918	XP_361980	XP_001729085	EAA27845	EAT92087	XP_001594633	EAK82585	RO3G_11637
L-ornithine aminotransferase Car2	XP_751911	XP_001240799	EAU87983	XP_773582	XP_385722	EDR09594	XP_369877	XP_001729938	EAA27181	EAT88909	XP_001587988	EAK84399	RO3G_12123
mitochondrial processing peptidase beta subunit	XP_752790	XP_001243696	EAU85792	XP_774411	XP_381039	EDR13198	XP_361057	XP_001731874	EAA36444	EAT81329	XP_001593250	EAK86965	RO3G_04336
peptide N-myristoyl transferase (Nmt1)	XP_752019	XP_001241626	EAU88866	XP_772024	XP_389573	EDR14336	XP_367304	XP_001732829	EAA30036	EAT92391	XP_001594233	EAK83827	RO3G_06862
lysyl-tRNA synthetase	XP_750655	XP_001247536	EAU90925	XP_773851	XP_388937	EDR11645	XP_359811	XP_001731476	EAA28399	EAT82803	XP_001595938	EAK82995	RO3G_14000
lipoic acid synthetase precursor	XP_754950	XP_001246687	EAU92837	XP_773405	XP_389620	EDR15648	XP_001522320	XP_001732059	EAA35490	EAT91765	XP_001589458	EAK85510	RO3G_01981
isoleucyl-tRNA synthetase	XP_752741	XP_001243953	EAU91061	XP_778214	XP_390898	EDR11511	XP_360677	XP_001731519	EAA26778	EAT80885	XP_001585648	EAK83034	RO3G_12153
isocitrate dehydrogenase Idp1	XP_754749	XP_001240510	EAU84027	XP_777363	XP_390523	EDR10319	XP_367343	XP_001730822	EAA26614	EAT91095	XP_001593497	EAK86993	RO3G_13820
iron-sulfur protein subunit of succinate dehydrogenase Sdh2	XP_753605	XP_001241858	EAU82988	XP_774483	XP_385786	EDR13751	XP_369077	XP_001729560	EAA35916	EAT88556	XP_001594577	EAK81918	RO3G_03816
IMP dehydrogenase	XP_749494	XP_001245055	EAU87620	XP_777938	XP_381037	EDR09420	XP_361156	XP_001730522	EAA35740	EAT91916	XP_001587025	EAK83736	RO3G_14462
GTP-binding protein YchF	XP_752347	XP_001239251	EAU85656	XP_776732	XP_382940	EDR08546	XP_361880	XP_001728946	EAA35430	EAT85562	XP_001592250	EAK86999	RO3G_07275
GMP synthase	XP_748432	XP_001239961	EAU83257	XP_772762	XP_390534	EDR09233	XP_368325	XP_001732749	EAA30515	EAT84008	XP_001595541	EAK84975	RO3G_02515
glycine-tRNA ligase	XP_754040	XP_001242329	EAU86846	XP_774702	XP_387134	EDQ99825	XP_369806	XP_001729902	EAA28055	EAT83336	XP_001598549	EAK84392	RO3G_11381
succinate dehydrogenase subunit Sdh1	XP_754832	XP_001248568	EAU81873	XP_773861	XP_387537	EDR13384	XP_369076	XP_001729428	EDO65095	EAT76087	XP_001591238	EAK81956	RO3G_13321
translation initiation factor eIF-6	XP_754031	XP_001242313	EAU85399	XP_773008	XP_385604	EDR08495	XP_363745	XP_001730047	EAA29796	EAT90992	XP_001591620	EAK87150	RO3G_13353
peptide chain release factor eRF/aRF, subunit 1	XP_754064	XP_001242476	EAU88180	XP_776668	XP_387103	EDR11251	XP_369751	XP_001730088	EAA28060	EAT83625	XP_001598524	EAK85196	RO3G_00516
translation elongation factor EF-Tu	XP_752585	XP_001239381	EAU93042	XP_774180	XP_387358	EDR15015	XP_362579	XP_001729762	EAA32277	EAT82586	XP_001597967	EAK81523	RO3G_01455
translation elongation factor G1	XP_752015	XP_001241630	EAU83626	XP_776356	XP_381567	EDR02488	XP_363639	XP_001731326	EAA36106	EAT92120	XP_001589746	EAK86751	RO3G_07529
ATP dependent RNA helicase (Sub2)	XP_747814	XP_001239034	EAU92983	XP_777578	XP_388839	EDR15710	XP_001522452	XP_001729648	EAA35657	EAT76998	XP_001593842	XP_761087	RO3G_15740
DNA-directed RNA polymerase III, beta subunit,	XP_749996	XP_001242390	EAU87529	XP_773994	XP_381019	EDR09689	XP_370487	XP_001731706	EAA27959	EAT91415	XP_001595664	EAK83484	RO3G_12315
DNA replication licensing factor Mcm5	XP_748090	XP_001242563	EAU93404	XP_777467	XP_386953	EDR15422	XP_363062	XP_001730681	EAA32301	EAT77199	XP_001591048	EAK85924	RO3G_10698
diphthamide biosynthesis protein	XP_755576	XP_001245771	EAU84561	XP_777602	XP_380812	EDR14729	XP_360694	XP_001732172	EAA34196	EAT85141	XP_001588209	EAK84039	RO3G_16190
dimethyladenosine transferase	XP_749024	XP_001247217	EAU87730	XP_773062	XP_385225	EDR09459	XP_368993	XP_001729060	EAA31554	EAT76682	XP_001593673	EAK83482	RO3G_14104

英文版见: Wang H Y, Guo S Y, Huang M R, et al. Ascomycota has faster evolutionary rate and higher species diversity than Basidiomycota (Fungi). Sci China Life Sci, 2010, 53, in press

附表 1(续)

蛋白质	*Aspergillus fumigatus*	*Coccidioides immitis*	*Coprinopsis cinerea*	*Cryptococcus neoformans*	*Gibberella zeae*	*Laccaria bicolor*	*Magnaporthe grisea*	*Malassezia globosa*	*Neurospora crassa*	*Phaeosphaeria nodorum*	*Sclerotinia sclerotiorum*	*Ustilago maydis*	*Rhizopus oryzae*
dihydrolipoamide succinyltransferase	XP_755064	XP_001248359	EAU89463	XP_777242	XP_388146	EDR10293	XP_360606	XP_001729588	EAA30207	EAT78149	XP_001587717	EAK82572	RO3G_06527
ATP-dependent RNA helicase	XP_750371	XP_001244087	EAU88082	XP_773820	XP_384204	EDR11265	XP_001411591	XP_001732004	EAA27679	EAT84178	XP_001592326	EAK82902	RO3G_03957
ATP-dependent RNA helicase HAS1	XP_751498	XP_001246788	EAU88940	XP_777235	XP_384526	EDR16076	XP_370007	XP_001732565	EAA29692	EAT86830	XP_001588603	EAK85282	RO3G_07575
cytochrome C1/Cyt1	XP_749957	XP_001238954	EAU90205	XP_774726	XP_380737	EDR05656	XP_360371	XP_001729525	EAA34520	EAT88545	XP_001586215	EAK85488	RO3G_08415
tRNA splicing protein (Spl1)	XP_754202	XP_001246354	EAU88735	XP_776031	XP_390225	EDR14351	XP_368477	XP_001732187	EAA29943	EAT76535	XP_001598849	EAK86015	RO3G_11728
CTP synthase	XP_748988	XP_001246057	EAU82860	XP_776312	BAA33767	EDR12113	XP_367634	XP_001729415	EAA28496	EAT79715	XP_001589075	EAK81142	RO3G_03216
cell division control protein Cdc48	XP_756045	XP_001239786	EAU90639	XP_773075	XP_385706	EDR14459	XP_359584	XP_001732423	EAA27769	EAT82668	XP_001595101	EAK81798	RO3G_07895
DEAD-box RNA helicase Dhh1/Vad1	XP_755058	XP_001248331	EAU89171	XP_776581	XP_390967	EDR08188	XP_360845	XP_001730716	EAA30775	EAT80597	XP_001588066	EAK84197	RO3G_06550
spartyl-tRNA synthetase Dps1	XP_749394	XP_001248036	EAU93029	XP_776192	XP_384730	EDR15009	XP_001522528	XP_001729396	EAA35505	EAT91850	XP_001589717	EAK85319	RO3G_04619
alanyl-tRNA synthetase	XP_747195	XP_001248510	EAU91282	XP_774788	XP_381082	EDR11794	XP_361064	XP_001731546	EAA36461	EAT88464	XP_001593079	EAK82846	RO3G_07558
adenylosuccinate synthetase AdB	XP_752913	XP_001243896	EAU88944	XP_776751	XP_385363	EDR03268	XP_367061	XP_001731021	EAA30951	EAT76814	XP_001593669	EAK84757	RO3G_08252
adenylate kinase	XP_750499	XP_001248754	EAU81921	XP_772932	XP_390913	EDR11223	XP_368186	XP_001732798	EAA27017	EAT91128	XP_001597412	EAK83143	RO3G_13367
adenosylhomocysteinase	XP_752379	XP_001239289	EAU81357	XP_775643	XP_385791	EDR10213	XP_359622	XP_001732329	EAA33210	EAT85768	XP_001596998	EAK84912	RO3G_07184
60S ribosomal protein L4	XP_748041	XP_001242607	EAU83110	XP_773160	XP_387362	EDR09812	XP_362607	XP_001728871	EAA31868	EAT80905	XP_001597207	EAK83947	RO3G_09581
60S ribosomal protein L19	XP_755133	XP_001247141	EAU93376	XP_774059	XP_390050	EDR00720	XP_001404186	XP_001729625	EAA30828	EAT89870	XP_001595641	EAK82415	RO3G_04235
60S ribosomal protein L17	XP_752811	XP_001243753	EAU86083	XP_771988	XP_382047	EDR13793	XP_364349	XP_001731924	EAA32243	EAT90522	XP_001586516	EAK86962	RO3G_01574
60S ribosomal protein L11	XP_752052	XP_001239964	EAU90374	XP_773228	XP_381257	EDR14488	XP_367849	XP_001730226	EAA36404	EAT88761	XP_001586298	EAK85026	RO3G_09340
60S ribosomal protein L1	XP_752537	XP_001243105	EAU92198	XP_775117	XP_387100	EDR08282	XP_362251	XP_001731247	EAA28529	EAT85593	XP_001598446	EAK85891	RO3G_16218
60S ribosomal protein P0	XP_750257	XP_001245443	EAU85302	XP_774147	XP_387003	EDR08463	XP_362022	XP_001728628	EAA28947	EAT77462	XP_001584828	EAK86939	RO3G_09023
40S ribosomal protein S8e	XP_750180	XP_001245539	EAU91660	XP_774458	XP_380807	EDR08803	XP_360708	XP_001731848	EAA34193	EAT77032	XP_001588292	EAK84649	RO3G_04360
40S ribosomal protein S3Ae	XP_754085	XP_001242450	EAU84719	XP_777512	XP_387656	EDR12827	XP_370422	XP_001728782	EAA26738	EAT83615	XP_001598109	EAK85901	RO3G_12122
40S ribosomal protein S0	XP_754290	XP_001244060	EAU91101	XP_773962	XP_391081	EDR11584	XP_001406293	XP_001731370	EAA27604	EAT86783	XP_001587181	EAK83011	RO3G_04736
proteasome regulatory particle subunit Rpt2	XP_753929	XP_001242204	EAU85352	XP_775283	XP_382204	EDR08470	XP_360102	XP_001730706	EAA32354	EAT83263	XP_001591603	EAK83732	RO3G_10320
proteasome regulatory particle subunit Rpt1	XP_754831	XP_001248567	EAU88428	XP_774476	XP_380735	EDR11355	XP_363655	XP_001732793	EAA34894	EAT76084	XP_001597631	EAK80891	RO3G_11342
proteasome regulatory particle subunit Rpt5	XP_750366	XP_001244098	EAU86097	XP_772095	XP_391773	EDR13340	XP_001403458	XP_001732254	EAA28255	EAT84531	XP_001596943	XP_760694	RO3G_03248
proteasome regulatory particle subunit Rpt6	XP_746652	XP_001241366	EAU82882	XP_772972	XP_381781	EDR04627	XP_363454	XP_001732083	EAA34118	EAT90722	XP_001597447	EAK81907	RO3G_12232
proteasome component Pup3	XP_752084	XP_001239915	EAU92531	XP_777884	XP_381412	EDR15819	XP_362106	XP_001731296	EAA35245	EAT89142	XP_001586346	EAK80963	RO3G_16220
proteasome component Pup1	XP_749622	XP_001247301	EAU81477	XP_776879	XP_380543	EDR09720	XP_362084	XP_001729238	EAA34801	EAT78113	XP_001584802	EAK86392	RO3G_00008
proteasome component Pre9	XP_750785	XP_001247565	EAU90883	XP_774604	XP_385541	EDR12033	XP_362705	XP_001731725	EAA29550	EAT80099	XP_001587697	EAK83098	RO3G_16334
6-phosphogluconate dehydrogenase Gnd1	XP_750696	XP_001247382	EAU92918	XP_772874	XP_381287	EDR09736	XP_369069	XP_001728891	EAA35723	EAT76717	XP_001589237	EAK83747	RO3G_01672
alpha-ketoglutarate dehydrogenase complex subunit Kgd1	XP_751665	XP_001247826	EAU85723	XP_777169	XP_384485	EDR13583	XP_001408601	XP_001731922	EAA34012	EAT78214	XP_001593012	EAK85720	RO3G_08761
translation release factor eRF3	XP_749613	XP_001247604	EAU84760	XP_774637	XP_388779	EDR12396	XP_368795	XP_001730065	EAA31180	EAT79373	XP_001596056	EAK86098	RO3G_13821
pre-mRNA splicing factor RNA helicase	XP_753488	XP_001239544	EAU81615	XP_774927	XP_390933	EDR10006	XP_361419	XP_001731936	EAA27287	EAT85898	XP_001589848	EAK82057	RO3G_08924
60S ribosomal protein L7	XP_746575	XP_001240725	EAU88749	XP_566981	XP_382718	EDR14897	XP_359540	XP_001732427	XP_962950	EAT86244	XP_001597919	XP_759725	RO3G_16080
proteasome component Pre6	XP_748127	XP_001242525	EAU88401	XP_775738	XP_387458	EDR10996	XP_369957	XP_001729803	EAA28095	EAT81628	XP_001591078	EAK86352	RO3G_10410
transketolase TktA	XP_752720	XP_001239980	EAU88185	XP_570402	XP_390174	EDR10917	XP_365769	XP_001731824	XP_961414	EAT82418	XP_001588699	XP_761114	RO3G_13067
t-complex protein 1, gamma subunit (Cct3)	XP_754318	XP_001244016	EAU92138	XP_567673	XP_386161	EDR13239	XP_370142	XP_001730709	XP_956627	EAT86746	XP_001592815	XP_762214	RO3G_03228
AAA family ATPase Rvb2/Reptin	XP_749991	XP_001242359	EAU92476	XP_566914	XP_386436	EDR15378	XP_360630	XP_001732143	XP_963328	EAT90854	XP_001597906	XP_760373	RO3G_07845
phosphoglycerate kinase PgkA	XP_752401	XP_001239296	EAU88439	XP_571947	XP_384168	EDR11030	XP_359714	XP_001728700	XP_962430	EAT85787	XP_001596913	XP_761018	RO3G_08041
translation elongation factor EF-1 alpha subunit	XP_750388	XP_001244267	EAU93024	XP_568462	XP_388987	EDR15006	XP_361098	XP_001732312	XP_964868	EAT80707	XP_001594091	XP_757071	RO3G_15351
DNA-directed RNA polymerase III largest subunit	XP_754189	XP_001246195	EAU80581	XP_571468	XP_390036	EDR04865	XP_362032	XP_001730008	XP_956571	EAT91146	XP_001588093	XP_762303	RO3G_12475
DNA polymerase delta catalytic subunit Cdc2	XP_755997	XP_001239851	EAU90154	XP_772922	XP_387351	EDR05542	XP_362488	XP_001728836	XP_961558	EAT82147	XP_001587512	XP_757605	RO3G_03762
TFIIH complex helicase Rad3	XP_752761	XP_001243936	EAU88545	XP_566880	XP_384471	EDR14295	XP_360589	XP_001732571	XP_956536	EAT82740	XP_001589884	XP_760298	RO3G_12052
deoxyhypusine synthase	XP_748168	XP_001242489	EAU84757	XP_567440	XP_380499	EDR12843	XP_364328	XP_001732398	XP_963241	EAT83590	XP_001597869	XP_756218	RO3G_10161
prolyl-tRNA synthetase	XP_755936	XP_001246550	EAU81430	XP_569307	XP_385425	EDR09277	XP_366137	XP_001729319	XP_955907	EAT78685	XP_001590907	XP_757002	RO3G_08732
arsenite translocating ATPase ArsA	XP_754484	XP_001244255	EAU93342	XP_567863	XP_390067	EDR15466	XP_364690	XP_001731054	XP_960897	EAT86334	XP_001593411	XP_759985	RO3G_11494
ribosomal protein L16a	XP_750349	XP_001244411	EAU93058	XP_568413	XP_382275	EDR15024	XP_360074	XP_001730190	XP_961587	EAT77902	XP_001591799	XP_757073	RO3G_15704
proteasome regulatory particle subunit (RpnK)	XP_749475	XP_001245086	EAU84677	XP_566594	XP_380957	EDR12356	XP_369606	XP_001732491	XP_964366	EAT92004	XP_001592900	XP_757688	RO3G_06585
GTP binding protein	XP_750305	XP_001244472	EAU84685	XP_569574	XP_387417	EDR12813	XP_360356	XP_001731642	XP_957275	EAT80854	XP_001591529	XP_759154	RO3G_15244
prohibitin	XP_755243	XP_001247251	EAU86052	XP_566440	XP_381295	EDR13797	XP_365041	XP_001730682	XP_964487	EAT82909	XP_001589275	XP_761177	RO3G_13787
AAA family ATPase Pontin	XP_751754	XP_001247704	EAU82356	XP_566529	XP_385326	EDR08315	XP_361484	XP_001730521	XP_955769	EAT76964	XP_001593913	XP_762348	RO3G_15559
DNA replication factor C subunit Rfc3	XP_748155	XP_001242497	EAU90493	XP_771880	XP_386203	EDR14578	XP_001414254	XP_001729496	XP_963397	EAT76168	XP_001597346	XP_760770	RO3G_03308
cell division control protein 2 kinase	XP_750689	XP_001247390	EAU81687	XP_569525	XP_388644	EDR06007	XP_363436	XP_001729871	XP_960117	EAT79379	XP_001596080	AAP94021	RO3G_05995
karyopherin alpha subunit	XP_755944	XP_001243434	EAU93208	XP_570493	XP_387317	EDR14943	XP_367135	XP_001730902	XP_960652	EAT82614	XP_001587480	XP_760972	RO3G_11023

附表 2　21 种蛋白质编码基因的样品

蛋白质	*Rhizoplaca chrysoleuca*	*Aspergillus fumigatus*	*Coccidioides immitis*	*Gibberella zeae*	*Magnaporthe grisea*	*Neurospora crassa*	*Phaeosphaeria nodorum*	*Sclerotinia sclerotiorum*	*Yarrowia lipolytica*
Malate dehydrogenase	HM007281	XP_748936	XP_001246025	XP_382637	XP_364559	XP_958408	XP_001796362	XP_001585256	XP_502909
Mitochondrial Hsp70 chaperone	HM007284	XP_755328	XP_001244995	XP_386330	XP_361717	XP_961753	XP_001803790	XP_001589111	XP_501940
Cytosolic hydroxymethyltransferase	HM007285	XP_755116	XP_001247153	XP_390049	XP_001404185	XP_960065	XP_001793492	XP_001595640	XP_503153
Translation elongation factor 1-alpha	HM007287, HM007304	XP_750388	XP_001244267	XP_388987	XP_361098	XP_964868	XP_001801902	XP_001594091	XP_501628
Peptidyl-prolyl cis-trans isomerase	HM007288	XP_749504	XP_001245045	XP_380953	XP_366228	XP_001728468	XP_001790747	XP_001593362	XP_501664
Aminopeptidase	HM007289	XP_751922	XP_001241125	XP_388516	XP_366388	XP_959172	XP_001793910	XP_001594581	XP_500893
ATP synthase F1, beta subunit	HM007290	XP_753589	XP_001242378	XP_384488	XP_360642	XP_963253	XP_001791943	XP_001591168	XP_500475
Glyceraldehyde-3-phosphate dehydrogenase GpdA	HM007291	XP_748145	XP_001242378	XP_384488	XP_360642	XP_963253	XP_001791924	XP_001591168	XP_500475
Vacuolar ATP synthase subunit d1	HM007292	XP_754283	XP_001244066	XP_391083	XP_370510	XP_956842	XP_001792129	XP_001587183	XP_505487
60S ribosomal protein L20	HM007293	XP_750201	XP_001245490	XP_381692	XP_361110	XP_963936	XP_001801850	XP_001592983	XP_505817
mRNA-nucleus export ATPase (Elf1)	HM007294	XP_747719	XP_001239067	XP_388708	XP_001522177	XP_958018	XP_001798057	XP_001593480	XP_500490
40S ribosomal protein Rps16	HM007295	XP_755383	XP_001244905	XP_384312	XP_359488	XP_964828	XP_001798536	XP_001598002	XP_500817
Transketolase TktA	HM007296, HM007301	XP_752720	XP_001239980	XP_390174	XP_365769	XP_961414	XP_001800365	XP_001588699	XP_503628
60S ribosomal protein L3	HM007298	XP_755517	XP_001245984	XP_386465	XP_360650	XP_963317	XP_001806656	XP_001598836	XP_502097
Rho GTPase Rho1	HM007299	XP_750583	XP_001244593	XP_384576	XP_367251	XP_956761	XP_001795250	XP_001595777	XP_504289
Cytochrome c	HM007300	XP_755643	XP_001245655	XP_391057	XP_370188	XP_956486	XP_001805810	XP_001598900	XP_502612
Molecular chaperone and allergen Mod-E/Hsp90/Hsp1	HM007282, HM007297	XP_747926	XP_001245288	XP_382190	XP_370262	XP_961298	XP_001791544	XP_001591945	XP_501578
Ribosomal protein S23 (S12)	HM007302	XP_752311	XP_001243230	XP_390909	XP_368178	XP_956255	XP_001795358	XP_001588322	XP_500301
Alternative oxidase AlxA	HM007303	XP_749637	XP_001247280	XP_381518	XP_001403506	XP_962086	XP_001793620	XP_001596660	XP_502637
Mitochondrial peroxiredoxin PRX1	HM007283	XP_751969	XP_001241702	XP_387712	XP_362792	XP_959621	XP_001791462	XP_001594896	XP_500241
Cobalamin-independent methionine synthase MetH/D	HM007286	XP_752090	XP_001244621	XP_391001	XP_370215	XP_957152	XP_001934603	XP_001588472	XP_503874

附表 3　核 LSU rDNA 的样品

nu LSU rDNA	种	科	目	纲	门
EU940084	D_Acrospermum_compressum	Acrospermaceae	Acrospermales	Dothideomycetes	Ascomycota
AY004336	D_Botryosphaeria ribis	Botryosphaeriaceae	Botryosphaeriales	Dothideomycetes	Ascomycota
AY004337	D_Microxyphium_citri	Capnodiaceae	Capnodiales	Dothideomycetes	Ascomycota
DQ678074	D_Davidiella tassiana	Davidiellaceae	Capnodiales	Dothideomycetes	Ascomycota
EU019274	D_Penidiella_columbiana	incertae sedis	Capnodiales	Dothideomycetes	Ascomycota
DQ246232	D_Mycosphaerella flexuosa	Mycosphaerellaceae	Capnodiales	Dothideomycetes	Ascomycota
AY016366	D_Piedraia_hortae	Piedraiaceae	Capnodiales	Dothideomycetes	Ascomycota
EF134949	D_Schizothyrium pomi	Schizothyriaceae	Capnodiales	Dothideomycetes	Ascomycota
GU301874	D_Teratosphaeria_jonkershoeken	Teratosphaeriaceae	Capnodiales	Dothideomycetes	Ascomycota
AY004342	D_Stylodothis_puccinioides	Dothideaceae	Dothideales	Dothideomycetes	Ascomycota
AY016359	D_Columnosphaeria fagi	Dothioraceae	Dothideales	Dothideomycetes	Ascomycota
AY541493	D_Hysteropatella_clavispora	Hysteriaceae	Hysteriales	Dothideomycetes	Ascomycota
AY541492	D_Farlowiella carmichaeliana	incertae sedis	incertae sedis	Dothideomycetes	Ascomycota
DQ678083	D_Helicomyces roseus	Tubeufiaceae	incertae sedis	Dothideomycetes	Ascomycota
DQ384104	D_Zopfia rhizophila	Zopfiaceae	incertae sedis	Dothideomycetes	Ascomycota
GU301796	D_Aliquandostipite_khaoyaiensi	Aliquandostipitaceae	Jahnulales	Dothideomycetes	Ascomycota
DQ678060	D_Elsinoe_veneta	Elsinoaceae	Myriangiales	Dothideomycetes	Ascomycota
AY016365	D_Myriangium_duriaei	Myriangiaceae	Myriangiales	Dothideomycetes	Ascomycota
DQ678081	D_Lophium mytilinum	Mytilinidiaceae	Mytilinidiales	Dothideomycetes	Ascomycota
FJ469672	D_Rhytidhysteron rufulum	Patellariaceae	Patellariales	Dothideomycetes	Ascomycota
GU301793	D_Aigialus_grandis	Aigialaceae	Pleosporales	Dothideomycetes	Ascomycota
AY538339	D_Arthopyrenia_salicis	Arthopyreniaceae	Pleosporales	Dothideomycetes	Ascomycota
DQ384102	D_Curreya pityophila	Cucurbitariaceae	Pleosporales	Dothideomycetes	Ascomycota
DQ384090	D_Delitschia_didyma	Delitschiaceae	Pleosporales	Dothideomycetes	Ascomycota
AB524621	D_Roussoella hysterioides	Didymosphaeriaceae	Pleosporales	Dothideomycetes	Ascomycota

附表 3(续)

nu LSU rDNA	种	科	目	纲	门
AY016363	D_Lojkania enalia	Fenestellaceae	Pleosporales	Dothideomycetes	Ascomycota
FJ515646	D_Didymella vitalbina	incertae sedis	Pleosporales	Dothideomycetes	Ascomycota
GU301822	D_Keissleriella_cladophila	Lentitheciaceae	Pleosporales	Dothideomycetes	Ascomycota
DQ470946	D_Leptosphaeria_maculans	Leptosphaeriaceae	Pleosporales	Dothideomycetes	Ascomycota
AB521737	D_Lindgomyces_ingoldianus	Lindgomycetaceae	Pleosporales	Dothideomycetes	Ascomycota
DQ782384	D_Lophiostoma_arundinis	Lophiostomataceae	Pleosporales	Dothideomycetes	Ascomycota
DQ678065	D_Massaria platani	Massariaceae	Pleosporales	Dothideomycetes	Ascomycota
AY016356	D_Bimuria_novaezelandiae	Melanommataceae	Pleosporales	Dothideomycetes	Ascomycota
DQ678086	D_Montagnula opulenta	Montagnulaceae	Pleosporales	Dothideomycetes	Ascomycota
EF590318	D_Phaeosphaeria nodorum	Phaeosphaeriaceae	Pleosporales	Dothideomycetes	Ascomycota
AY004340	D_Phaeotrichum_benjaminii	Phaeotrichaceae	Pleosporales	Dothideomycetes	Ascomycota
AY004341	D_Pleomassaria_siparia	Pleomassariaceae	Pleosporales	Dothideomycetes	Ascomycota
AY544645	D_Cochliobolus heterostrophus	Pleosporaceae	Pleosporales	Dothideomycetes	Ascomycota
AY004343	D_Westerdykella_cylindrica	Sporormiaceae	Pleosporales	Dothideomycetes	Ascomycota
AY016357	D_Byssothecium_circinans	Teichosporaceae	Pleosporales	Dothideomycetes	Ascomycota
DQ678067	D_Lepidosphaeria nicotiae	Testudinaceae	Pleosporales	Dothideomycetes	Ascomycota
AB524620	D_Quadricrura_septentrionalis	Tetraplosphaeriaceae	Pleosporales	Dothideomycetes	Ascomycota
DQ678072	D_Trematosphaeria_pertusa	Trematosphaeriaceae	Pleosporales	Dothideomycetes	Ascomycota
DQ384100	D_Metacoleroa dickiei	Venturiaceae	Pleosporales	Dothideomycetes	Ascomycota
AY004339	E_Ceramothyrium_carniolicum	Chaetothyriaceae	Chaetothyriales	Eurotiomycetes	Ascomycota
AY004338	E_Capronia_mansonii	Herpotrichiellaceae	Chaetothyriales	Eurotiomycetes	Ascomycota
AJ507323	E_Phaeococcomyces_chersonesos	Herpotrichiellaceae	Chaetothyriales	Eurotiomycetes	Ascomycota
AF346420	E_Glyphium_elatum	Incertae sedis	Chaetothyriales	Eurotiomycetes	Ascomycota
DQ470987	E_Caliciopsis_orientalis	Coryneliaceae	Coryneliales	Eurotiomycetes	Ascomycota
DQ782908	E_Monascu_purpureus	Elaphomycetaceae	Eurotiales	Eurotiomycetes	Ascomycota
FJ358291	E_Xeromyces_bisporus	Elaphomycetaceae	Eurotiales	Eurotiomycetes	Ascomycota
FJ358281	E_Chromocleista_malachitea	Trichocomaceae	Eurotiales	Eurotiomycetes	Ascomycota
FJ358278	E_Aspergillus_fumigatus	Trichocomaceae	Eurotiales	Eurotiomycetes	Ascomycota
GU332517	E_Dolabra_nepheliae	Incertae sedis	Incertae sedis	Eurotiomycetes	Ascomycota
FJ358273	E_Arachnomyces_glareosus	Arachnomycetaceae	Onygenales	Eurotiomycetes	Ascomycota
FJ358275	E_Ascosphaera_apis	Ascosphaeraceae	Onygenales	Eurotiomycetes	Ascomycota
FJ358282	E_Ctenomyces_serratus	Arthrodermataceae	Onygenales	Eurotiomycetes	Ascomycota
AY062120	E_Trichophyton_interdigitale	Arthrodermataceae	Onygenales	Eurotiomycetes	Ascomycota
FJ358283	E_Eremascus_albus	Eremascaceae	Onygenales	Eurotiomycetes	Ascomycota
FJ358286	E_Leucothecium_emdenii	Gymnoascaceae	Onygenales	Eurotiomycetes	Ascomycota
FJ358284	E_Gymnoascus_reesii	Gymnoascaceae	Onygenales	Eurotiomycetes	Ascomycota
FJ358288	E_Shanorella_spirotricha	Onygenaceae	Onygenales	Eurotiomycetes	Ascomycota
FJ358287	E_Onygena_corvina	Onygenaceae	Onygenales	Eurotiomycetes	Ascomycota
DQ782909	E_Spiromastix_warcupii	Onygenaceae	Onygenales	Eurotiomycetes	Ascomycota
DQ782906	E_Anisomeridium_polypori	Monoblastiaceae	Pyrenulales	Eurotiomycetes	Ascomycota
EF411063	E_Pyrenula_aspistea	Pyrenulaceae	Pyrenulales	Eurotiomycetes	Ascomycota
DQ823103	E_Pyrgillus_javanicus	Pyrenulaceae	Pyrenulales	Eurotiomycetes	Ascomycota
EF411062	E_Granulopyrenis_seawardii	Requienellaceae	Pyrenulales	Eurotiomycetes	Ascomycota
EF643805	E_Bagliettoa_parmigera	Verrucariaceae	Verrucariales	Eurotiomycetes	Ascomycota
EF643774	E_Staurothele_drummondii	Verrucariaceae	Verrucariales	Eurotiomycetes	Ascomycota
AY640939	L_Acarospora_bullata	Acarosporaceae	Acarosporales	Lecanoromycetes	Ascomycota
DQ986774	L_Placynthiella_uliginosa	Agyriaceae	Agyriales	Lecanoromycetes	Ascomycota
AF356658	L_Baeomyces_placophyllus	Baeomycetaceae	Baeomycetales	Lecanoromycetes	Ascomycota
DQ986791	L_Candelaria_concolor	Candelariaceae	Candelariales	Lecanoromycetes	Ascomycota
AY640956	L_Maronea_constans	Fuscideaceae	incertae sedis	Lecanoromycetes	Ascomycota
AY533006	L_Hymenelia_lacustris	Hymeneliaceae	incertae sedis	Lecanoromycetes	Ascomycota
AF279376	L_Arthrorhaphis_citrinella	Arthrorhaphidaceae	Lecanorales	Lecanoromycetes	Ascomycota
AY533011	L_Sporastatia_testudinea	Catillariaceae	Lecanorales	Lecanoromycetes	Ascomycota
AY584640	L_Cladonia_caroliniana	Cladoniaceae	Lecanorales	Lecanoromycetes	Ascomycota
AY584653	L_Crocynia_pyxinoides	Crocyniaceae	Lecanorales	Lecanoromycetes	Ascomycota
AY584651	L_Lopezaria_versicolor	Incertae sedis	Lecanorales	Lecanoromycetes	Ascomycota
DQ973028	L_Ophioparma_lapponica	Ophioparmaceae	Lecanorales	Lecanoromycetes	Ascomycota
AY584641	L_Xanthoparmelia_conspersa	Parmeliaceae	Lecanorales	Lecanoromycetes	Ascomycota
DQ883798	L_Heterodermia_vulgaris	Physciaceae	Lecanorales	Lecanoromycetes	Ascomycota

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nu LSU rDNA	种	科	目	纲	门
DQ314902	L_Porpidia_flavocaerulescens	Porpidiaceae	Lecanorales	Lecanoromycetes	Ascomycota
AY533009	L_Psora_rubiformis	Psoraceae	Lecanorales	Lecanoromycetes	Ascomycota
AY533010	L_Rhizocarpon_geminatum	Rhizocarpaceae	Lecanorales	Lecanoromycetes	Ascomycota
AY453643	L_Leifidium_tenerum	Sphaerophoraceae	Lecanorales	Lecanoromycetes	Ascomycota
AY533002	L_Stereocaulon_vesuvianum	Stereocaulaceae	Lecanorales	Lecanoromycetes	Ascomycota
AY452504	L_Calicium_adspersum	Caliciaceae	Lecanorales	Lecanoromycetes	Ascomycota
DQ986746	L_Lecanora_contractula	Lecanoraceae	Lecanorales	Lecanoromycetes	Ascomycota
AY532990	L_Cecidonia_umbonella	Lecideaceae	Lecanorales	Lecanoromycetes	Ascomycota
DQ986762	L_Niebla_cephalota	Ramalinaceae	Lecanorales	Lecanoromycetes	Ascomycota
AF356662	L_Petractis_clausa	Gyalectaceae	Ostropales	Lecanoromycetes	Ascomycota
DQ912346	L_Coccocarpia_domingensis	Coccocarpiaceae	Peltigerales	Lecanoromycetes	Ascomycota
AY424212	L_Leptogium_gelatinosum	Collemataceae	Peltigerales	Lecanoromycetes	Ascomycota
AY584655	L_Lobaria_scrobiculata	Lobariaceae	Peltigerales	Lecanoromycetes	Ascomycota
AY584656	L_Nephroma_parile	Nephromataceae	Peltigerales	Lecanoromycetes	Ascomycota
AY584657	L_Peltigera_degenii	Peltigeraceae	Peltigerales	Lecanoromycetes	Ascomycota
AF356674	L_Placynthium_nigrum	Placynthiaceae	Peltigerales	Lecanoromycetes	Ascomycota
DQ917419	L_Fuscopannaria_mediterranea	Pannariaceae	Peltigerales	Lecanoromycetes	Ascomycota
AF329171	L_Ochrolechia_balcanica	Ochrolechiaceae	Pertusariales	Lecanoromycetes	Ascomycota
AF356679	L_Thamnolia_subuliformis	Icmadophilaceae	Pertusariales	Lecanoromycetes	Ascomycota
DQ782907	L_Pertusaria_dactylina	Pertusariaceae	Pertusariales	Lecanoromycetes	Ascomycota
AY584648	L_Letrouitia_domingensis	Letrouitiaceae	Teloschistales	Lecanoromycetes	Ascomycota
AY584650	L_Megalospora_tuberculosa	Megalosporaceae	Teloschistales	Lecanoromycetes	Ascomycota
AY584647	L_Teloschistes_exilis	Teloschistaceae	Teloschistales	Lecanoromycetes	Ascomycota
AF279405	L_Porina_guentheri	Porinaceae	Trichotheliales	Lecanoromycetes	Ascomycota
AY648106	L_Rhizoplacopsis_weichingii	Rhizoplacopsidaceae	Umbilicariales	Lecanoromycetes	Ascomycota
DQ782912	L_Umbilicaria_mammulata	Umbilicariaceae	Umbilicariales	Lecanoromycetes	Ascomycota
DQ470960	Le_Bulgaria_inquinans	Bulgariaceae	Helotiales	Leotiomycetes	Ascomycota
DQ470942	Le_Mollisia_cinerea	Dermateaceae	Helotiales	Leotiomycetes	Ascomycota
AY064705	Le_Neofabraea_alba	Dermateaceae	Helotiales	Leotiomycetes	Ascomycota
DQ470967	Le_Pezicula_carpinea	Dermateaceae	Helotiales	Leotiomycetes	Ascomycota
AY487098	Le_Pilidium_concavum	Dermateaceae	Helotiales	Leotiomycetes	Ascomycota
DQ470981	Le_Microglossum_rufum	Geoglossaceae	Helotiales	Leotiomycetes	Ascomycota
AY544656	Le_Chloroscypha_enterochroma	Helotiaceae	Helotiales	Leotiomycetes	Ascomycota
AY544680	Le_Crinula_caliciiformis	Helotiaceae	Helotiales	Leotiomycetes	Ascomycota
DQ470944	Le_Cudoniella_clavus	Helotiaceae	Helotiales	Leotiomycetes	Ascomycota
AF356694	Le_Fabrella_tsugae	Hemiphacidiaceae	Helotiales	Leotiomycetes	Ascomycota
AY789415	Le_Hyaloscypha_daedaleae	Hyaloscyphaceae	Helotiales	Leotiomycetes	Ascomycota
DQ227262	Le_Hyphodiscus_hymeniophilus	Hyaloscyphaceae	Helotiales	Leotiomycetes	Ascomycota
AY544674	Le_Lachnum_bicolor	Hyaloscyphaceae	Helotiales	Leotiomycetes	Ascomycota
AY544679	Le_Chaetomella_acutiseta	Incertae sedis	Helotiales	Leotiomycetes	Ascomycota
AY544644	Le_Leotia_lubrica	Leotiaceae	Helotiales	Leotiomycetes	Ascomycota
DQ470978	Le_Lambertella_subrenispora	Rutstroemiaceae	Helotiales	Leotiomycetes	Ascomycota
AY789423	Le_Mitrula_paludosa	Sclerotiniaceae	Helotiales	Leotiomycetes	Ascomycota
AY544683	Le_Monilinia_fructicola	Sclerotiniaceae	Helotiales	Leotiomycetes	Ascomycota
FJ176874	Le_Vibrissea_truncorum	Vibrisseaceae	Helotiales	Leotiomycetes	Ascomycota
AY541491	Le_Myxotrichum_deflexum	Myxotrichaceae	incertae sedis	Leotiomycetes	Ascomycota
DQ470988	Le_Pseudeurotium_zonatum	Pseudeurotiaceae	incertae sedis	Leotiomycetes	Ascomycota
AF279379	Le_Cudonia_circinans	Cudoniaceae	Rhytismatales	Leotiomycetes	Ascomycota
AY541496	Le_Spathularia_flavida	Cudoniaceae	Rhytismatales	Leotiomycetes	Ascomycota
DQ470954	Le_Meria_laricis	Rhytismataceae	Rhytismatales	Leotiomycetes	Ascomycota
DQ470949	Le_Potebniamyces_pyri	Rhytismataceae	Rhytismatales	Leotiomycetes	Ascomycota
AF356696	Le_Rhytisma_acerinum	Rhytismataceae	Rhytismatales	Leotiomycetes	Ascomycota
FJ176895	Le_Thelebolus_caninus	Thelebolaceae	Thelebolales	Leotiomycetes	Ascomycota
AY544678	P_Ascobolus_crenulatus	Ascobolaceae	Pezizales	Pezizomycetes	Ascomycota
FJ176870	P_Saccobolus_dilutellus	Ascobolaceae	Pezizales	Pezizomycetes	Ascomycota
DQ470966	P_Eleutherascus_lectardii	Ascodesmidaceae	Pezizales	Pezizomycetes	Ascomycota
DQ247799	P_Caloscypha_fulgens	Caloscyphaceae	Pezizales	Pezizomycetes	Ascomycota
AY544673	P_Gyromitra_californica	Discinaceae	Pezizales	Pezizomycetes	Ascomycota
AY544652	P_Barssia_oregonensis	Helvellaceae	Pezizales	Pezizomycetes	Ascomycota

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nu LSU rDNA	种	科	目	纲	门
AY544655	P_Helvella_compressa	Helvellaceae	Pezizales	Pezizomycetes	Ascomycota
AY544667	P_Disciotis_venosa	Morchellaceae	Pezizales	Pezizomycetes	Ascomycota
AY544665	P_Morchella_elata	Morchellaceae	Pezizales	Pezizomycetes	Ascomycota
AY544664	P_Morchella_esculenta	Morchellaceae	Pezizales	Pezizomycetes	Ascomycota
AY544666	P_Verpa_conica	Morchellaceae	Pezizales	Pezizomycetes	Ascomycota
DQ470948	P_Peziza_vesiculosa	Pezizaceae	Pezizales	Pezizomycetes	Ascomycota
AY544668	P_Sarcosphaera_crassa	Pezizaceae	Pezizales	Pezizomycetes	Ascomycota
AY544654	P_Aleuria_aurantia	Pyronemataceae	Pezizales	Pezizomycetes	Ascomycota
AY544661	P_Cheilymenia_stercorea	Pyronemataceae	Pezizales	Pezizomycetes	Ascomycota
DQ247806	P_Scutellinia_scutellata	Pyronemataceae	Pezizales	Pezizomycetes	Ascomycota
DQ470961	P_Rhizina_undulata	Rhizinaceae	Pezizales	Pezizomycetes	Ascomycota
EF494056	P_Phymatotrichopsis_omnivora	Rhizinaceae	Pezizales	Pezizomycetes	Ascomycota
AY544658	P_Pithya_cupressina	Sarcoscyphaceae	Pezizales	Pezizomycetes	Ascomycota
AY544647	P_Sarcoscypha_coccinea	Sarcoscyphaceae	Pezizales	Pezizomycetes	Ascomycota
FJ176877	P_Tuber_gibbosum	Tuberaceae	Pezizales	Pezizomycetes	Ascomycota
DQ438186	Y-Sporopachydermia_cereana	Dipodascaceae	Saccharomycetales	Saccharomycetes	Ascomycota
DQ518995	Y-Myxozyma_udenii	Lipomycetaceae	Saccharomycetales	Saccharomycetes	Ascomycota
EF550320	Y-Pichia_mississippiensis	Pichiaceae	Saccharomycetales	Saccharomycetes	Ascomycota
EU011594	Y-Ambrosiozyma_platypodis	Saccharomycopsidaceae	Saccharomycetales	Saccharomycetes	Ascomycota
DQ442681	Y-Trichomonascus_ciferrii	Trichomonascaceae	Saccharomycetales	Saccharomycetes	Ascomycota
AY780054	S_Camarops_amorpha	Boliniaceae	Boliniales	Sordariomycetes	Ascomycota
AY761081	S_Togninia_novaezealandiae	Calosphaeriaceae	Calosphaeriales	Sordariomycetes	Ascomycota
AY544685	S_Carpoligna_pleurothecii	Chaetosphaeriaceae	Chaetosphaeriales	Sordariomycetes	Ascomycota
AY346276	S_Coniochaetidium_savoryi	Coniochaetaceae	Coniochaetales	Sordariomycetes	Ascomycota
AF408339	S_Microthia_havanensis	Cryphonectriaceae	Diaporthales	Sordariomycetes	Ascomycota
AY818964	S_Gnomonia_gnomon	Gnomoniaceae	Diaporthales	Sordariomycetes	Ascomycota
AF408364	S_Harknessia_lythri	incertae sedis	Diaporthales	Sordariomycetes	Ascomycota
AF362567	S_Melanconis_stilbostoma	Melanconidaceae	Diaporthales	Sordariomycetes	Ascomycota
AF408386	S_Valsa_ceratosperma	Valsaceae	Diaporthales	Sordariomycetes	Ascomycota
AY490788	S_Ceriosporopsis_halima	Halosphaeriaceae	Halosphaeriales	Sordariomycetes	Ascomycota
AY686634	S_Bionectria_ochroleuca	Bionectriaceae	Hypocreales	Sordariomycetes	Ascomycota
EU334679	S_Beauveria_bassiana	Cordycipitaceae	Hypocreales	Sordariomycetes	Ascomycota
FJ176861	S_Emericellopsis_maritima	incertae sedis	Hypocreales	Sordariomycetes	Ascomycota
AB067709	S_Cordyceps_sinensis	Ophiocordycipitaceae	Hypocreales	Sordariomycetes	Ascomycota
AF218207	S_Metarhizium_anisopliae	Clavicipitaceae	Hypocreales	Sordariomycetes	Ascomycota
AF510497	S_Hypocrea_jecorina	Hypocreaceae	Hypocreales	Sordariomycetes	Ascomycota
AY489727	S_Stephanonectria_keithii	Nectriaceae	Hypocreales	Sordariomycetes	Ascomycota
AY489720	S_Niesslia_exilis	Niessliaceae	Hypocreales	Sordariomycetes	Ascomycota
DQ471018	S_Apiospora_montagnei	Apiosporaceae	incertae sedis	Sordariomycetes	Ascomycota
DQ286199	S_Glomerella_cingulata	Glomerellaceae	incertae sedis	Sordariomycetes	Ascomycota
DQ493955	S_Magnaporthe_grisea	Magnaporthaceae	incertae sedis	Sordariomycetes	Ascomycota
DQ470950	S_Papulosa_amerospora	Papulosaceae	Incertae sedis	Sordariomycetes	Ascomycota
AY780077	S_Sinosphaeria_bambusicola	Thyridiaceae	Incertae sedis	Sordariomycetes	Ascomycota
DQ522856	S_Lulworthia_grandispora	Lulworthiaceae	Lulworthiales	Sordariomycetes	Ascomycota
FJ176888	S_Gondwanamyces_capensis	Ceratocystidaceae	Microascales	Sordariomycetes	Ascomycota
DQ470979	S_Ambrosiella_xylebori	Microascaceae	Microascales	Sordariomycetes	Ascomycota
DQ470955	S_Ophiostoma_piliferum	Ophiostomataceae	Ophiostomatales	Sordariomycetes	Ascomycota
DQ286206	S_Colletotrichum_crassipes	Phyllachoraceae	Phyllachorales	Sordariomycetes	Ascomycota
AY346257	S_Annulatascus_triseptatus	Annulatascaceae	Sordariales	Sordariomycetes	Ascomycota
AF431950	S_Cephalotheca_sulfurea	Cephalothecaceae	Sordariales	Sordariomycetes	Ascomycota
AY346305	S_Zopfiella_ebriosa	Chaetomiaceae	Sordariales	Sordariomycetes	Ascomycota
AY436419	S_Lasiosphaeris_hispida	Lasiosphaeriaceae	Sordariales	Sordariomycetes	Ascomycota
AY346301	S_Sordaria_macrospora	Sordariaceae	Sordariales	Sordariomycetes	Ascomycota
FJ176892	S_Nigrospora_oryzae	mitosporic	Trichosphaeriales	Sordariomycetes	Ascomycota
AF431949	S_Cainia_graminis	Amphisphaeriaceae	Xylariales	Sordariomycetes	Ascomycota
AY780068	S_Duradens_sp	Clypeosphaeriaceae	Xylariales	Sordariomycetes	Ascomycota
DQ470964	S_Diatrype_disciformis	Diatrypaceae	Xylariales	Sordariomycetes	Ascomycota
AY544676	S_Xylaria_acuta	Xylariaceae	Xylariales	Sordariomycetes	Ascomycota
DQ911601	B_Leucoagaricus_barssii	Agaricaceae	Agaricales	Agaricomycetes	Basidiomycota

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nu LSU rDNA	种	科	目	纲	门
DQ071728	B_Limacella_glioderma	Amanitaceae	Agaricales	Agaricomycetes	Basidiomycota
DQ470820	B_Plicaturopsis_crispa	Atheliaceae	Agaricales	Agaricomycetes	Basidiomycota
DQ457660	B_Conocybe_lactea	Bolbitiaceae	Agaricales	Agaricomycetes	Basidiomycota
DQ071735	B_Macrotyphula_fistulosa	Clavariaceae	Agaricales	Agaricomycetes	Basidiomycota
EU600883	B_Inocybe_sp	Cortinariaceae	Agaricales	Agaricomycetes	Basidiomycota
AY820890	B_Crepidotus_versutus	Crepidotaceae	Agaricales	Agaricomycetes	Basidiomycota
AY380407	B_Rhodocybe_aureicystidiata	Entolomataceae	Agaricales	Agaricomycetes	Basidiomycota
U66435	B_Hygrocybe_citrinopallida	Hygrophoraceae	Agaricales	Agaricomycetes	Basidiomycota
DQ071709	B_Bovista_nigrescens	Lycoperdaceae	Agaricales	Agaricomycetes	Basidiomycota
DQ071741	B_Omphalotus_illudens	Omphalotaceae	Agaricales	Agaricomycetes	Basidiomycota
DQ071722	B_Pleurotus_ostreatus	Pleurotaceae	Agaricales	Agaricomycetes	Basidiomycota
AY634279	B_Pluteus_romellii	Pluteaceae	Agaricales	Agaricomycetes	Basidiomycota
DQ457661	B_Coprinopsis_atramentaria	Psathyrellaceae	Agaricales	Agaricomycetes	Basidiomycota
DQ071725	B_Schizophyllum_commune	Schizophyllaceae	Agaricales	Agaricomycetes	Basidiomycota
DQ987904	B_Tubaria_serrulata	Strophariaceae	Agaricales	Agaricomycetes	Basidiomycota
AY639434	B_Marasmiellus_palmivorus	Tricholomataceae	Agaricales	Agaricomycetes	Basidiomycota
DQ144610	B_Amyloathelia_crassiuscula	Atheliaceae	Atheliales	Agaricomycetes	Basidiomycota
AY634277	B_Auricularia_sp	Auriculariaceae	Auriculariales	Agaricomycetes	Basidiomycota
AY645056	B_Exidia_uvapsassa	Exidiaceae	Auriculariales	Agaricomycetes	Basidiomycota
DQ831025	B_Pseudohydnum_gelatinosum	Hyaloriaceae	Auriculariales	Agaricomycetes	Basidiomycota
AY684158	B_Boletellus_projectellus	Boletineae	Boletales	Agaricomycetes	Basidiomycota
EU118643	B_Leucogyrophana_mollusca	Coniophoraceae	Boletales	Agaricomycetes	Basidiomycota
DQ534669	B_Gomphidius_roseus	Gomphidiaceae	Boletales	Agaricomycetes	Basidiomycota
AY586659	B_Hygrophoropsis_aurantiaca	Hygrophoropsidaceae	Boletales	Agaricomycetes	Basidiomycota
AY645059	B_Paxillus_vernalis	Paxillaceae	Boletales	Agaricomycetes	Basidiomycota
AJ440941	B_Serpula_lacrymans	Serpulaceae	Boletales	Agaricomycetes	Basidiomycota
AY586715	B_Suillus_luteus	Suillaceae	Boletales	Agaricomycetes	Basidiomycota
DQ071746	B_Tapinella_panuoides	Tapinellaceae	Boletales	Agaricomycetes	Basidiomycota
AY885164	B_Waitea_circinata	Ceratobasidiaceae	Cantharellales	Agaricomycetes	Basidiomycota
AY885163	B_Multiclavula_mucida	Clavulinaceae	Cantharellales	Agaricomycetes	Basidiomycota
DQ863692	B_Phlebia_chiricahuaensis	Corticiaceae	Corticiales	Agaricomycetes	Basidiomycota
AJ583431	B_Gloeophyllum_abietinum	Gloeophyllaceae	Gloeophyllales	Agaricomycetes	Basidiomycota
AY647207	B_Gomphus_clavatus	Gomphaceae	Gomphales	Agaricomycetes	Basidiomycota
AY635770	B_Hydnochaete_duportii	Hymenochaetaceae	Hymenochaetales	Agaricomycetes	Basidiomycota
U66452	B_Contumyces_rosella	Incertae sedis	Hymenochaetales	Agaricomycetes	Basidiomycota
U66432	B_Loreleia_marchantiae	Incertae sedis	Hymenochaetales	Agaricomycetes	Basidiomycota
U66441	B_Sphagnomphalia_brevibasidiat	Incertae sedis	Hymenochaetales	Agaricomycetes	Basidiomycota
DQ911614	B_Auriscalpium_vulgare	Auriscalpiaceae	Polyporales	Agaricomycetes	Basidiomycota
AY635771	B_Cyphella_digitalis	Cyphellaceae	Polyporales	Agaricomycetes	Basidiomycota
DQ071727	B_Fistulina_hepatica	Fistulinaceae	Polyporales	Agaricomycetes	Basidiomycota
AJ583428	B_Donkioporia_expansa	Fomitopsidaceae	Polyporales	Agaricomycetes	Basidiomycota
DQ208413	B_Ganoderma_lucidum	Ganodermataceae	Polyporales	Agaricomycetes	Basidiomycota
AF506469	B_Scytinostroma_odoratum	Lachnocladiaceae	Polyporales	Agaricomycetes	Basidiomycota
DQ071736	B_Phyllotopsis_nidulans	Lentinaceae	Polyporales	Agaricomycetes	Basidiomycota
DQ457673	B_Hydnopolyporus_fimbriatus	Meripilaceae	Polyporales	Agaricomycetes	Basidiomycota
AY629320	B_Polyporus_squamosus	Polyporaceae	Polyporales	Agaricomycetes	Basidiomycota
AY629315	B_Pterula_echo	Pterulaceae	Polyporales	Agaricomycetes	Basidiomycota
AY629321	B_Sparassis_crispa	Sparassidaceae	Polyporales	Agaricomycetes	Basidiomycota
EU118658	B_Xenasmatella_ardosiaca	Xenasmataceae	Polyporales	Agaricomycetes	Basidiomycota
AY684166	B_Albatrellus_higanensis	Albatrellaceae	Russulales	Agaricomycetes	Basidiomycota
DQ234539	B_Bondarzewia_montana	Bondarzewiaceae	Russulales	Agaricomycetes	Basidiomycota
AF506430	B_Echinodontium_tinctorium	Echinodontiaceae	Russulales	Agaricomycetes	Basidiomycota
DQ457665	B_Epithele_typhae	Epitheliaceae	Russulales	Agaricomycetes	Basidiomycota
AF506439	B_Gloeocystidiellum_formosanum	Gloeocystidiellaceae	Russulales	Agaricomycetes	Basidiomycota
EU118625	B_Dentipellis_leptodon	Hericiaceae	Russulales	Agaricomycetes	Basidiomycota
EU118634	B_Hyphodontiella_multiseptata	Hyphodermataceae	Russulales	Agaricomycetes	Basidiomycota
EU118662	B_Phlebiopsis_flavidoalba	Meruliaceae	Russulales	Agaricomycetes	Basidiomycota
EU118621	B_Cyphellostereum_laeve	Podoscyphaceae	Russulales	Agaricomycetes	Basidiomycota
EU118670	B_Steccherinum_ochraceum	Steccherinaceae	Russulales	Agaricomycetes	Basidiomycota

附表 3(续)

nu LSU rDNA	种	科	目	纲	门
DQ521406	B_Sebacina_incrustans	Sebacinaceae	Sebacinales	Agaricomycetes	Basidiomycota
AY586635	B_Bankera_fuligineoalba	Bankeraceae	Thelephorales	Agaricomycetes	Basidiomycota
AY634276	B_Polyozellus_multiplex	Thelephoraceae	Thelephorales	Agaricomycetes	Basidiomycota
AY586724	B_Typhula_phacorrhiza	Typhulaceae	Thelephorales	Agaricomycetes	Basidiomycota
AY586720	B_Trechispora_nivea	Sistotremataceae	Trechisporales	Agaricomycetes	Basidiomycota
AY745730	B_Bensingtonia_ciliata	Agaricostilbaceae	Agaricostilbales	Agaricostilbomycetes	Basidiomycota
DQ831021	B_Phleogena_faginea	Phleogenaceae	Atractiellales	Atractiellomycetes	Basidiomycota
DQ832205	B_Sakaguchia_dacryoidea	Incertae sedis	Erythrobasidiales	Cystobasidiomycetes	Basidiomycota
DQ831020	B_Naohidea_sebacea	Incertae sedis	Naohideales	Cystobasidiomycetes	Basidiomycota
AY586643	B_Cerinomyces_crustulinus	Cerinomycetaceae	Dacrymycetales	Dacrymycetes	Basidiomycota
DQ831032	B_Rhamphospora_nymphaeae	Rhamphosporaceae	Doassansiales	Exobasidiomycetes	Basidiomycota
DQ663687	B_Entyloma_calendulae	Entylomataceae	Entylomatales	Exobasidiomycetes	Basidiomycota
AY745714	B_Tilletiopsis_washingtonensis	Entylomataceae	Entylomatales	Exobasidiomycetes	Basidiomycota
DQ667151	B_Exobasidium_rhododendri	Exobasidiaceae	Exobasidiales	Exobasidiomycetes	Basidiomycota
AY745713	B_Tilletiopsis_minor	Tilletiariaceae	Georgefischeriales	Exobasidiomycetes	Basidiomycota
DQ832196	B_Rhodotorula_hinnulea	Incertae sedis	Microstromatales	Exobasidiomycetes	Basidiomycota
EF551316	B_Rhodotorula_nothofagi	Incertae sedis	Microstromatales	Exobasidiomycetes	Basidiomycota
DQ832244	B_Tilletia_controversa	Tilletiaceae	Tilletiales	Exobasidiomycetes	Basidiomycota
AY629313	B_Colacogloea_peniophorae	Incertae sedis	Incertae sedis	Microbotryomycetes	Basidiomycota
AY745728	B_Kriegeria_eriophori	Incertae sedis	Incertae sedis	Microbotryomycetes	Basidiomycota
AY646098	B_Leucosporidium_scottii	Leucosporidiaceae	Leucosporidiales	Microbotryomycetes	Basidiomycota
DQ789982	B_Microbotryum_violaceum	Microbotryaceae	Microbotryales	Microbotryomycetes	Basidiomycota
DQ831009	B_Mixia_osmundae	Mixiaceae	Mixiales	Mixiomycetes	Basidiomycota
AY646099	B_Insolibasidium_deformans	Platygloeaceae	Platygloeales	Pucciniomycetes	Basidiomycota
AY745696	B_Kuehneola_uredinis	Phragmidiaceae	Pucciniales	Pucciniomycetes	Basidiomycota
DQ419920	B_Auriculoscypha_anacardiicola	Septobasidiaceae	Septobasidiales	Pucciniomycetes	Basidiomycota
DQ831016	B_Mrakia_frigida	Cystofilobasidiaceae	Cystofilobasidiales	Tremellomycetes	Basidiomycota
EF551318	B_Guehomyces_pullulans	Incertae sedis	Cystofilobasidiales	Tremellomycetes	Basidiomycota
DQ836002	B_Trichosporon_lignicola	Incertae sedis	Cystofilobasidiales	Tremellomycetes	Basidiomycota
AY586653	B_Elmerina_holophaea	Aporpiaceae	Tremellales	Tremellomycetes	Basidiomycota
DQ645514	B_Asterotremella_humicola	Tremellaceae	Tremellales	Tremellomycetes	Basidiomycota
AY745724	B_Malassezia_pachydermatis	Incertae sedis	Malasseziales	Ustilaginomycetes	Basidiomycota
DQ846888	B_Ustanciosporium_standleyanum	Cintractiaceae	Ustilaginales	Ustilaginomycetes	Basidiomycota
DQ094784	B_Ustilago_tritici	Ustilaginaceae	Ustilaginales	Ustilaginomycetes	Basidiomycota
DQ273824	C_Kappamyces_laurelensis	Kappamycetaceae	Rhizophydiales	Chytridiomycetes	Chytridiomycota
DQ273823	C_Boothiomyces_macroporosum	Terramycetaceae	Rhizophydiales	Chytridiomycetes	Chytridiomycota
DQ273766	C_Rozella_sp.	Incertae sedis	Spizellomycetales	Chytridiomycetes	Chytridiomycota
DQ273775	C_Rhizophlyctis_harderi	Spizellomycetaceae	Spizellomycetales	Chytridiomycetes	Chytridiomycota

附表 4　基于 105 种蛋白质基因密码子的中性替代分析 [a)]

	1	2	3	4	5	6	7	8	9	10	11	12	13
1. *Gibberella zeae*		−184.317	−142.743	−226.836	−117.516	−191.803	−148.869	−113.929	−137.833	−129.891	−164.784	−160.468	−180.596
2. *Magnaporthe grisea*	0.000		−188.521	−227.962	−117.358	−120.369	−193.850	−144.449	−125.675	−87.916	−200.894	−135.379	−186.449
3. *Neurospora crassa*	0.000	0.000		−177.944	−178.191	−112.182	−123.331	−113.202	−94.598	−141.345	−116.777	−100.106	−121.007
4. *Sclerotinia sclerotiorum*	0.000	0.000	0.000		−133.105	−196.832	−243.138	−177.307	−234.438	−108.635	−220.575	−133.662	−162.847
5. *Aspergillus fumigatus*	0.000	0.000	0.000	0.000		−247.560	−155.108	−111.981	−119.304	−100.577	−174.783	−94.895	−171.981
6. *Coccidioides immitis*	0.000	0.000	0.000	0.000	0.000		−156.800	−141.129	−124.953	−111.981	−135.773	−103.759	−195.702
7. *Phaeosphaeria nodorum*	0.000	0.000	0.000	0.000	0.000	0.000		−175.179	−84.938	−142.238	−124.861	−181.418	−159.492
8. *Malassezia globosa*	0.000	0.000	0.000	0.000	0.000	0.000	0.000		−191.895	−128.378	−176.426	−136.619	−131.781
9. *Ustilago maydis*	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		−114.146	−164.587	−143.049	−233.382
10. *Cryptococcus neoformans*	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		−116.655	−177.228	−157.077
11. *Laccaria bicolor*	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		−293.352	−260.705
12. *Coprinopsis cinerea*	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		−164.899
13. *Rhizopus oryzae*	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	

a) 假设 dN=dS 存在的可能性(*P* 值)显示于对角线的下方. dS 和 dN 分别是指同义和非同义替代数. $P<0.05$ 示差异显著(5%水平)的存在. dN-dS 的统计结果被显示于对角线上方. 此分析应用了 MEGA 4 软件中的 Nei-Gojobori 方法. 在 105 种蛋白质编码基因的矩阵中最终包括了 39279 个位点(缺失和错误位点被全部删除). 自展检验进行了 1000 次重复