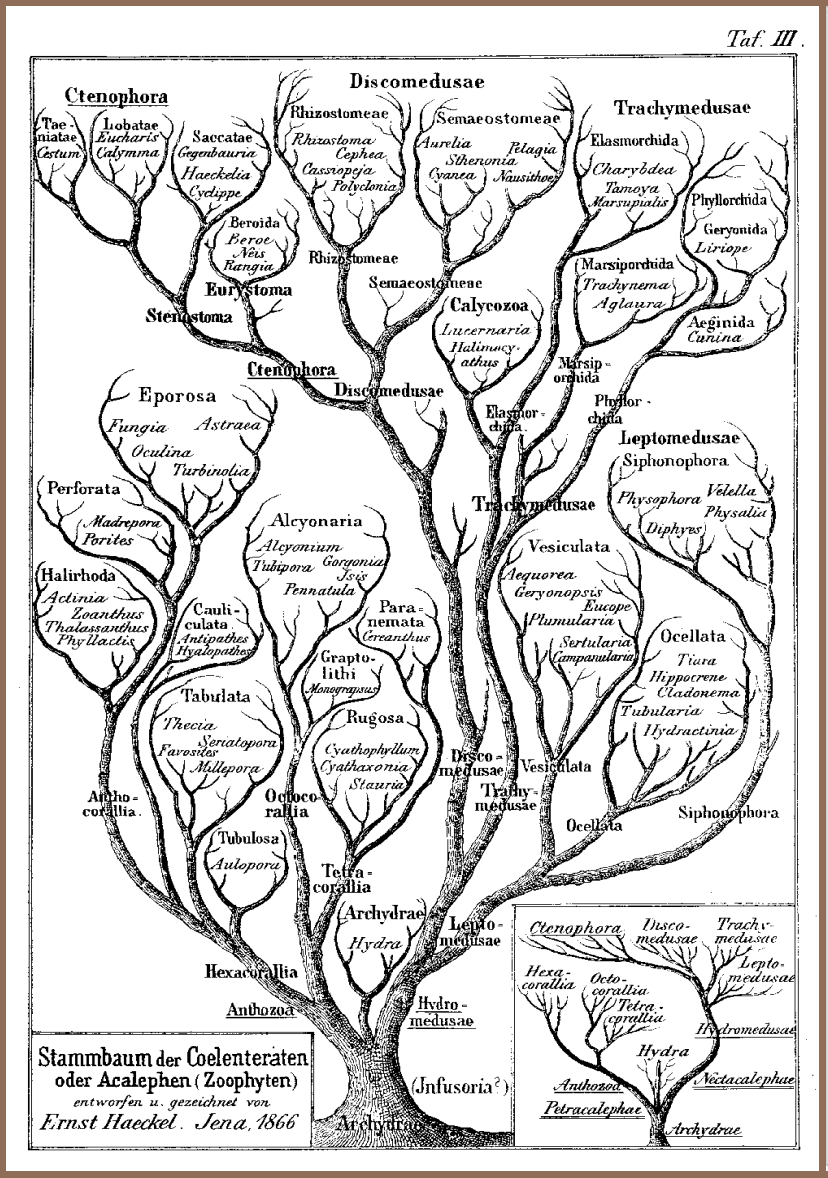
基因水平转移

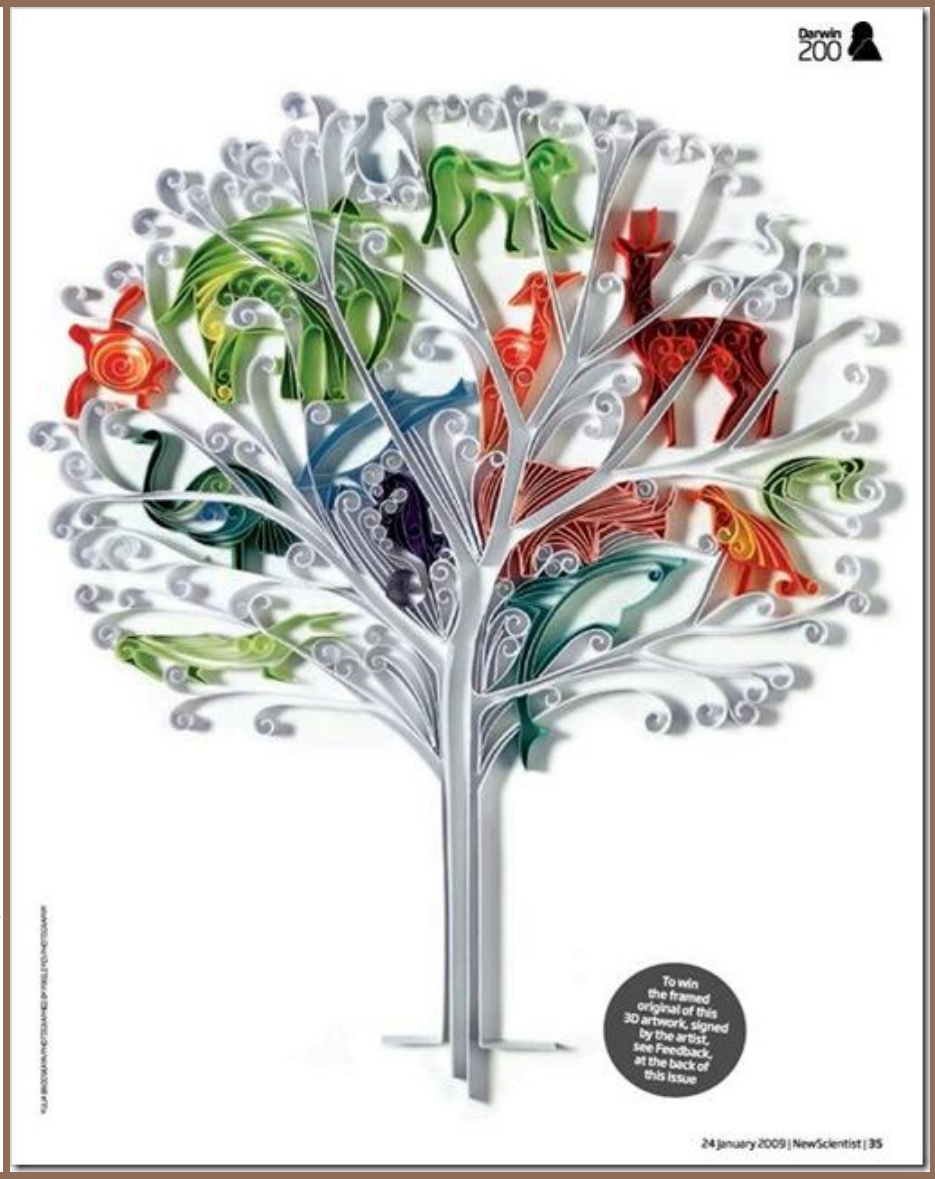
系统发育预测与实验验证

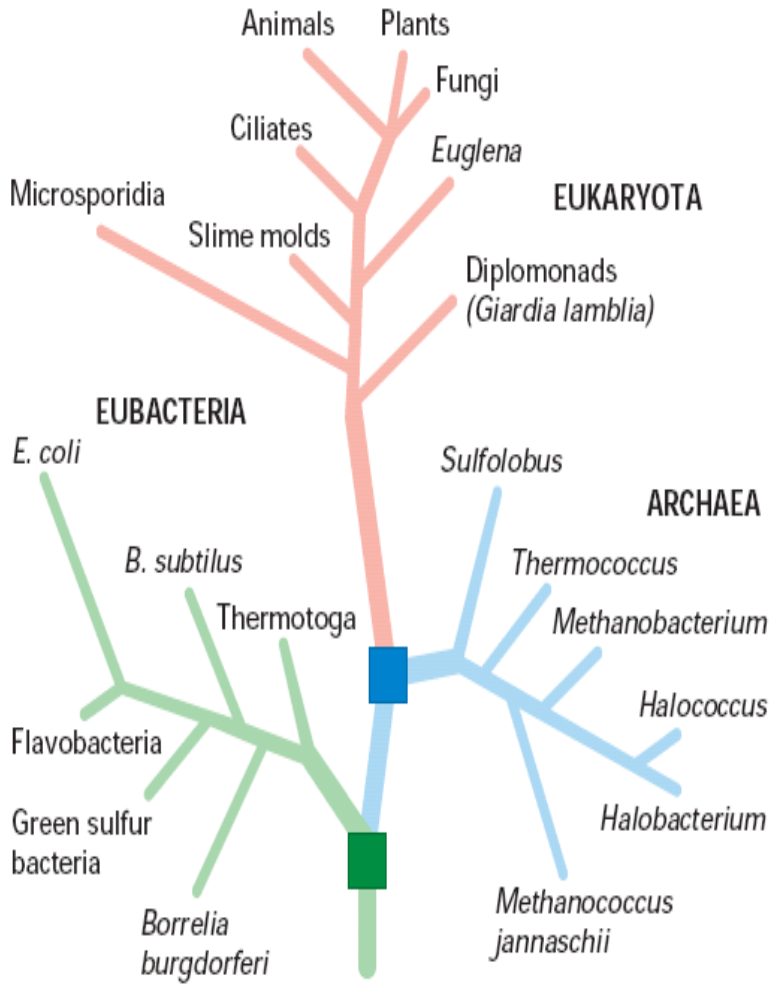
钟 扬

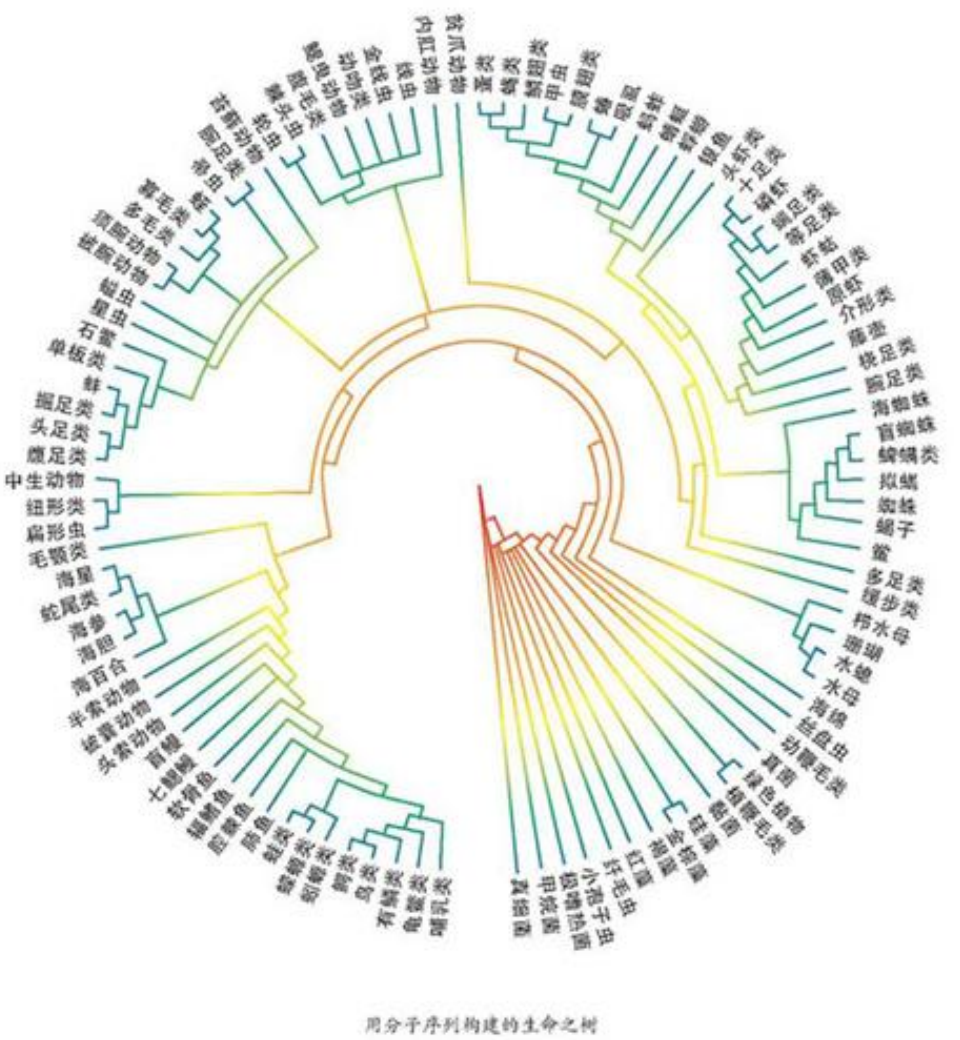
（西藏大学/复旦大学）

Tree of Life（生命之树）



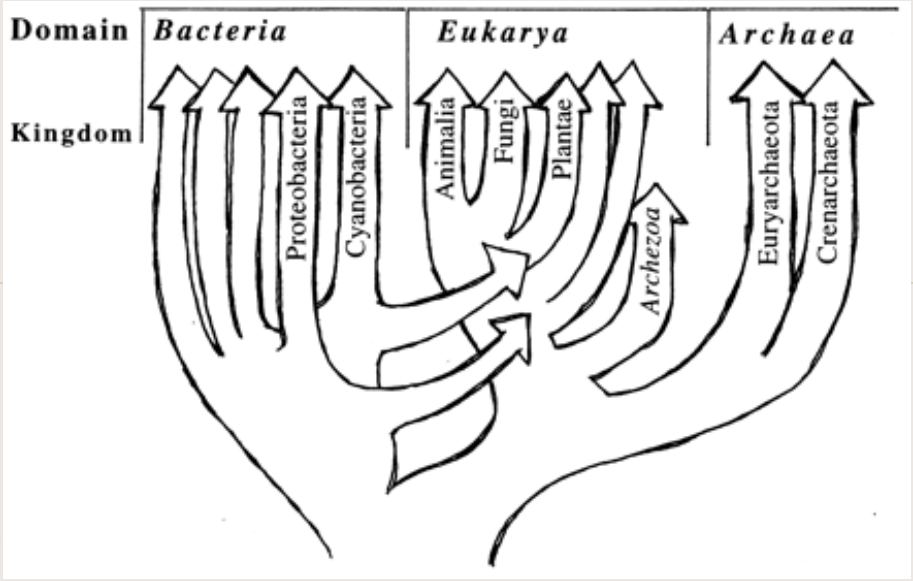




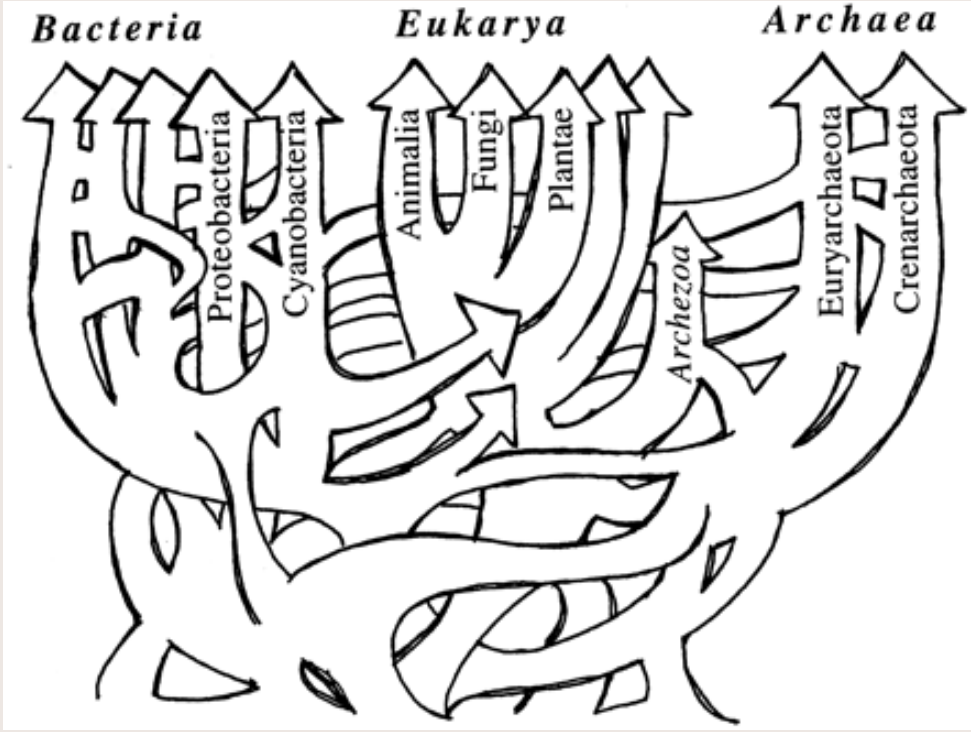


用分子序列构建的生命之树

细菌与生命之树


Domain
Kingdom
Bacteria
Eukarya
Archaea
Proteobacteria
Cyanobacteria
Animalia
Fungi
Plantae
Archezoa
Euryarchaeota
Crenarchaeota

网状树


Bacteria
Eukarya
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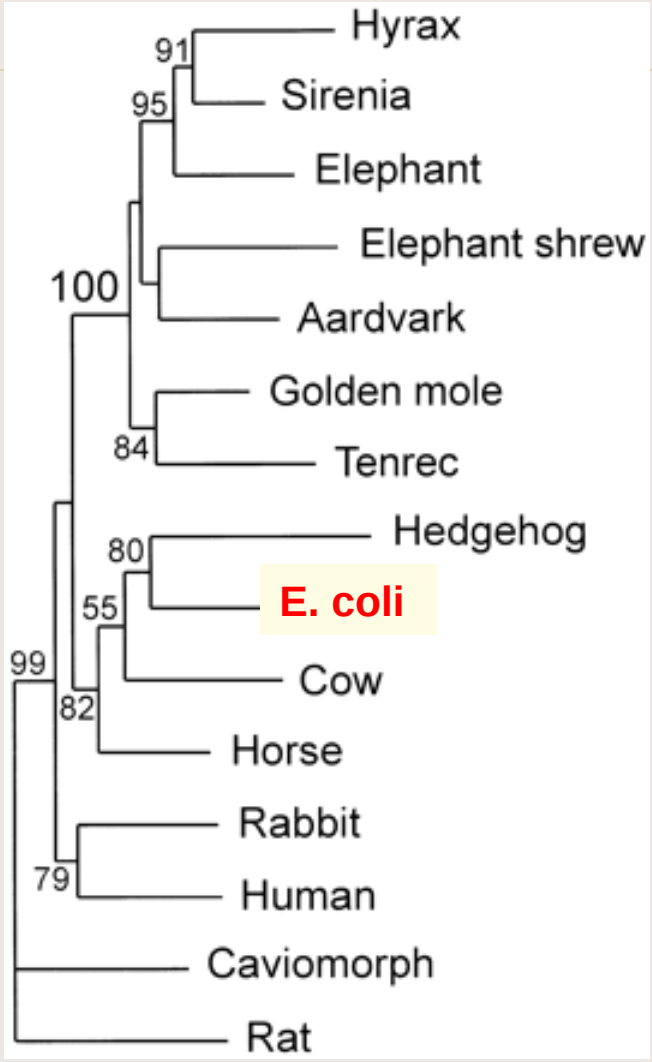
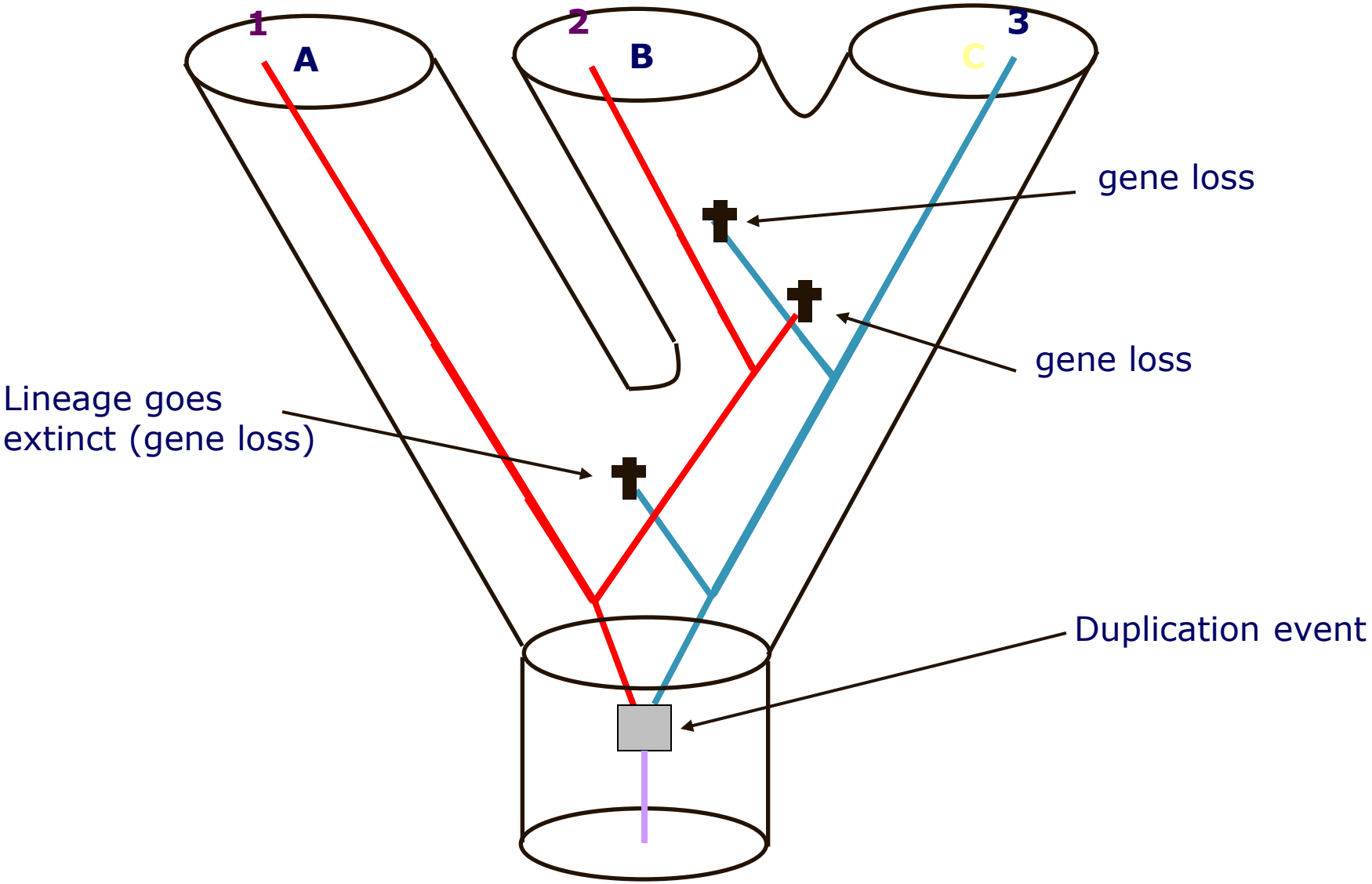
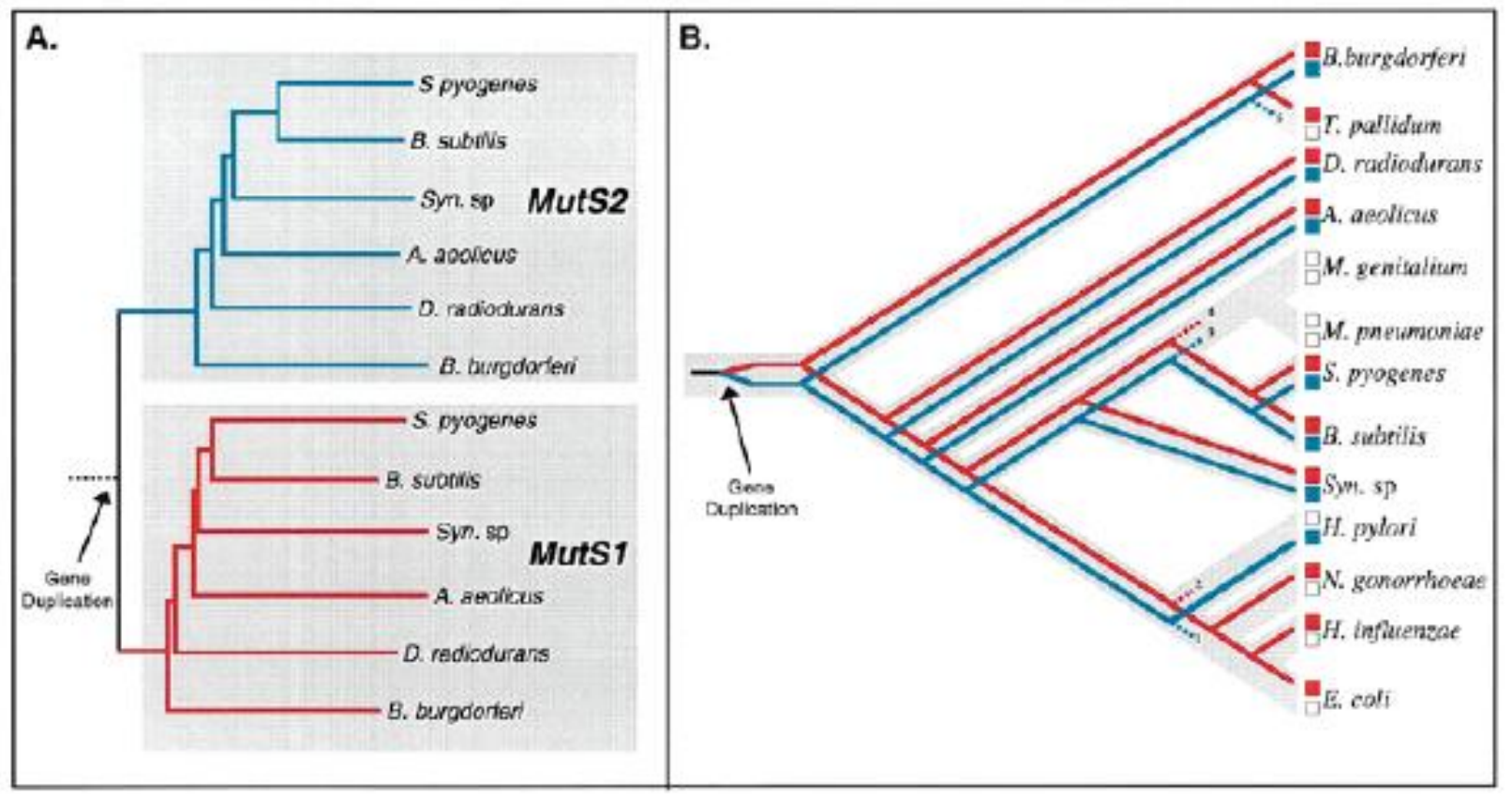
基因水平转移（Horizontal gene transfer）？



备择假设：基因丧失


1
A
2
B
3
C
gene loss
gene loss
Lineage goes
extinct (gene loss)
Duplication event

利用系统发育树了解基因重复和丧失



A. 基因树
B. 将基因树叠加在物种树上来鉴定基因重复和丧失

articles

Initial sequencing and analysis of the human genome

International Human Genome Sequencing Consortium*

* A partial list of authors appears on the opposite page. Affiliations are listed at the end of the paper.

The human genome holds an extraordinary trove of information about human development, physiology, medicine and evolution. Here we report the results of an international collaboration to produce and make freely available a draft sequence of the human genome. We also present an initial analysis of the data, describing some of the insights that can be gleaned from the sequence.

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Hundreds of genes appear to have resulted from horizontal gene transfer from bacteria…

2001 409:860-921 *Nature*

Genomics

Genes lost during evolution

One of the main conclusions presented by the International Human Genome Sequencing Consortium is that "hundreds of genes appear to have resulted from horizontal gene transfer from bacteria at some point in the vertebrate lineage"[1]. We noticed that a significant proportion of these human genes have closely related orthologues in the primitive eukaryote *Dictyostelium*. This observation supports independent gene loss in multiple lineages (worm, fly, yeast, plants) rather than horizontal gene transfer from bacteria.

The human genome sequence revealed 113 genes that share a high degree of identity with bacterial genes, but are absent in the completely sequenced genomes of *Caenorhabditis elegans*, *Drosophila melanogaster*, *Saccharomyces cerevisiae* and *Arabidopsis thaliana*[1]. Do these genes represent examples of horizontal gene transfer from bacteria to the vertebrate lineage, or were they present in both prokaryotes and early eukaryotes, but subsequently lost from all non-vertebrate eukaryotic lineages? Although this latter possibility may seem unlikely, we recently identified a gene in *Dictyostelium* that is clearly an orthologue of the gene that encodes soluble

2001 411:1013-1014 *Nature*

We used all 113 listed human genes to screen for homologous sequences in *Dictyostelium* (27 February 2001; see supplementary information). A TBLASTN screen of the *Dictyostelium* database yielded 36 sequences with expectation values of less than 10^{-10}. BLASTX analysis with the obtained *Dictyostelium* DNA sequences against GenBank identified 11 genes that represent clear *Dictyostelium* orthologues of human genes: the human sequences share a higher degree of identity with *Dictyostelium* than with bacterial sequences, and the bacterial sequences score more highly with respect to *Dictyostelium* than they do to humans (on the basis of BLAST expectation values). A further 17 *Dictyostelium* sequences share a high degree of identity with the human sequence, but are not obvious intermediates between the bacterial and vertebrate orthologues (see supplementary information). Thus, in at least 11 cases, the *Dictyostelium* and human genes have a common ancestor, eliminating the need to invoke horizontal gene transfer from bacteria.

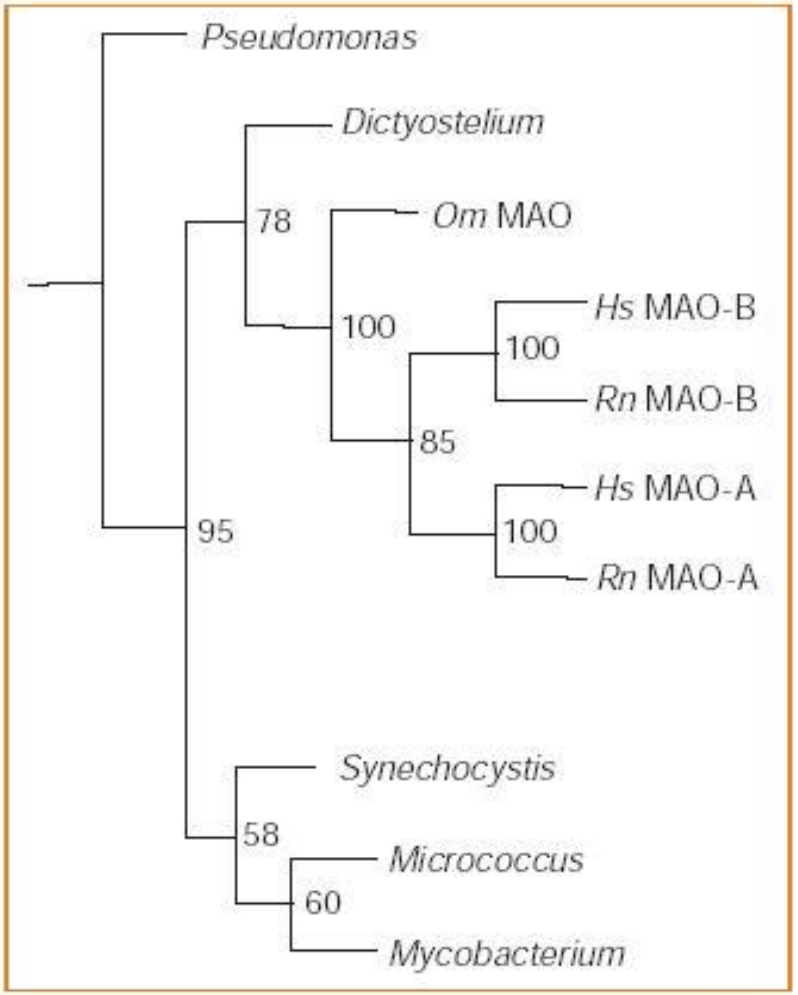


Figure 1 Phylogenetic analysis of monoamine oxidase (MAO). Numbers indicate values of bootstrap analysis ($n = 100$). Hs, *Homo sapiens*; Rn, *Rattus norvegicus* (rat); Om, *Oncorhynchus mykiss* (rainbow trout).

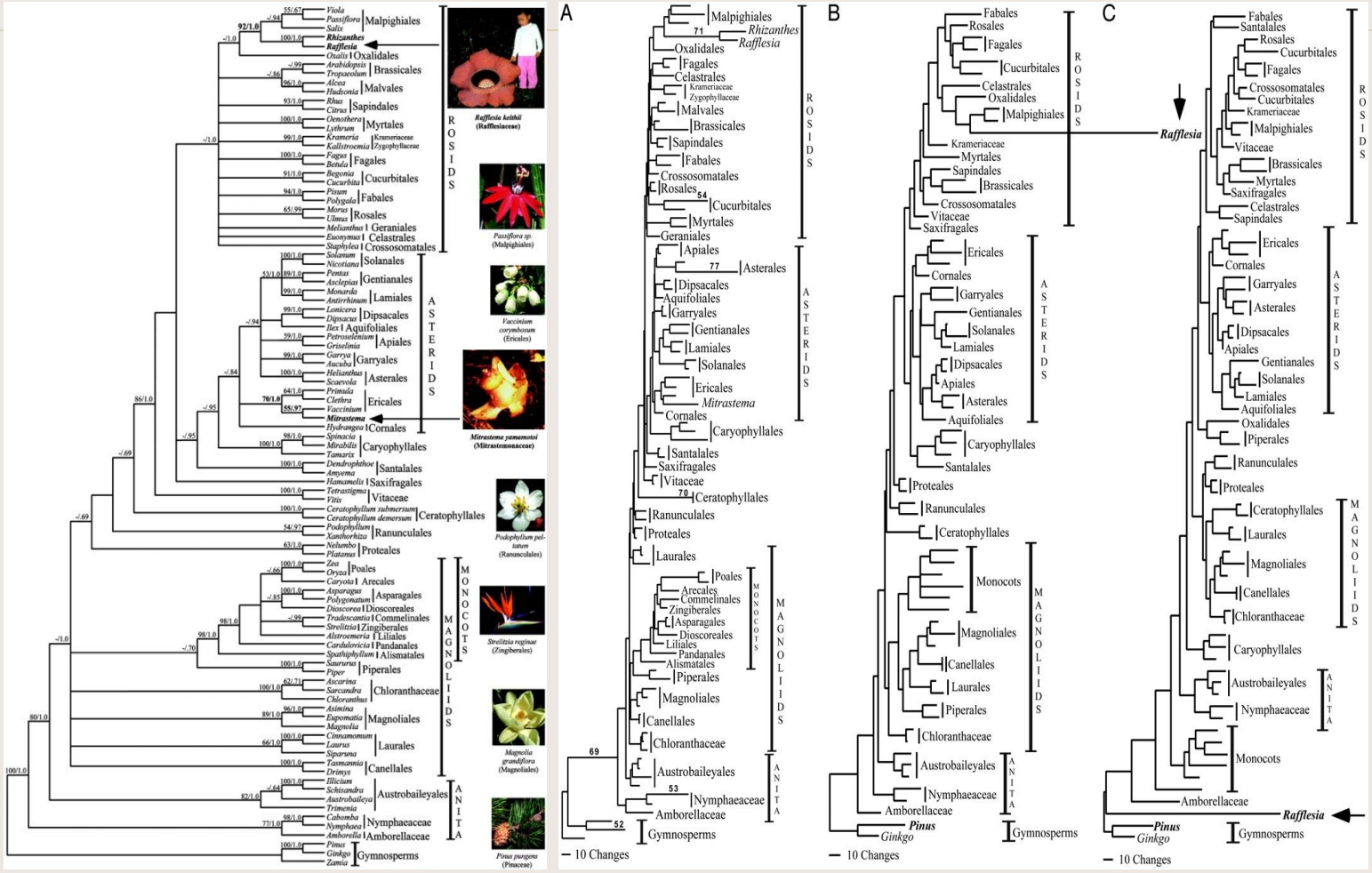
加入盘基网柄菌的**Blast**及系统发育分析

盘基网柄菌(*Dictyostelium discoideum*)
—— 真核生物中最简洁的基因组之一

Within the group of 113 genes proposed to have entered the human genome by horizontal gene transfer from bacteria, we have identified at least 11 that probably arose through normal evolution with gene loss in several lineages, suggesting that gene loss is not a rare event. With several ongoing genomic sequencing projects for lower eukaryotes, it will be interesting to see how many genes have truly undergone horizontal transfer.

大花草属（***Rafflesia***）

全寄生植物大花草的系统发育位置



基因水平转移：从早期陆地植物到被子植物的基出类群

Massive horizontal transfer of mitochondrial genes from diverse land plant donors to the basal angiosperm *Amborella*

Ulfar Bergthorsson†, Aaron O. Richardson, Gregory J. Young, Leslie R. Goertzen‡, and Jeffrey D. Palmer§

Department of Biology, Indiana University, Bloomington, IN 47405-3700

Contributed by Jeffrey D. Palmer, November 9, 2004

Several plants are known to have acquired a single mitochondrial gene by horizontal gene transfer (HGT), but whether these or any other plants have acquired many foreign genes is entirely unclear. To address this question, we focused on *Amborella trichopoda*, because it was already known to possess one hortzontally acquired gene and because it was found in preliminary analyses to contain several more. We comprehensively sequenced the mitochondrial protein gene set of *Amborella*, sequenced a variable number of mitochondrial genes from 28 other diverse land plants, and conducted phylogenetic analyses of these sequences plus those already available, including the five sequenced mitochondrial genomes of angiosperms. Results indicate that *Amborella* has acquired one or more copies of 20 of its 31 known mitochondrial protein genes from other land plants, for a total of 26 foreign genes, whereas no evidence for HGT was found in the five sequenced genomes. Most of the *Amborella* transfers are from other angiosperms (especially eudicots), whereas others are from nonangiosperms, including six striking cases of transfer from (at least three different) moss donors. Most of the transferred genes are intact, consistent with functionality and/or recency of transfer. *Amborella* mtDNA has sustained proportionately more HGT than any other eukaryotic, or perhaps even prokaryotic, genome yet examined.

Materials and Methods

We used primers for conserved regions of angiosperm mitochondrial genes in an attempt to PCR-amplify and sequence all mitochondrial protein genes from *A. trichopoda* (primer sequences available on request). Many *Amborella* reactions produced multiple bands, heterogeneous sequence, or unreadable sequence; these were cloned, and multiple (usually eight) clones were sequenced. This process yielded portions of 27 genes. We then used PCR to amplify and sequence as many of these 27 genes as possible, plus the four genes already sequenced from *Amborella* mtDNA, from 13 other angiosperms (see Fig. 5, which is published as supporting information on the PNAS web site, for taxa and sources) and three gymnosperms. For each of these plants, we carried out 80 PCRs with conserved mitochondrial primers. Selected genes were amplified and sequenced from 12 additional nonangiosperms. PCR was performed under the following conditions: 95°C for 2 min, 35 cycles of 95°C for 30 s, 55° or 52°C for 30 s, 72°C for 2 min, and 72°C for 5 min. PCR products were cleaned by using 2 μl of ExoSAP-IT (United States Biochemical). Sequences were generated by using an ABI 3730 (Applied Biosystems). Sequence traces were assembled and trimmed by using CODONCODE ALIGNER 1.3.2.

Sequences were aligned by using either BIOEDIT or SE-AL

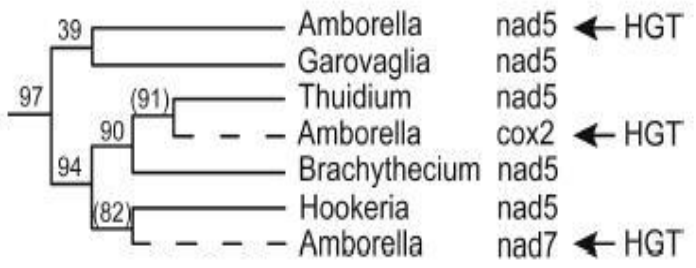


Fig. 2. *Amborella* acquired three genes from different moss donors. The solid parts of the cladogram and nonparenthetical bootstrap values are from the *nad5* intron phylogeny of Fig. 6. The dashed lines and other bootstrap values indicate the relationship to the indicated mosses of the moss-derived *cox2* and *nad7* genes of *Amborella*, as per the *cox2* gene tree of Fig. 1 and the *nad7* intron tree of Fig. 6.

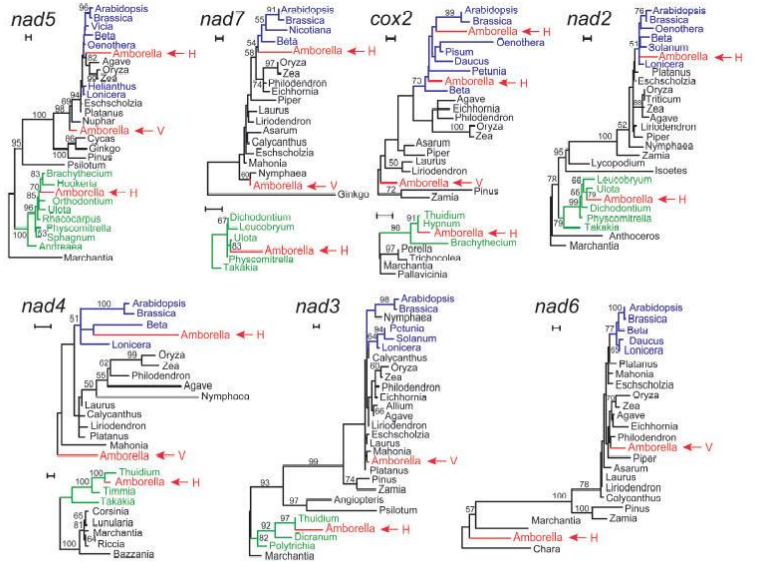


Fig. 1. Phylogenetic evidence for horizontal acquisition of genes from mosses and angiosperms in *Amborella*. Shown are ML trees. Bootstrap values (100 ML replicates) >50% are shown. H and V indicate *Amborella* genes of putatively horizontal and vertical transmission, respectively. *Amborella* genes are in red, core eudicot genes are in blue (basal eudicots commonly included are *Platanus*, *Eschscholzia*, and *Mahonia*), and moss genes are in green. Note that for *nad7*, *cox2*, and *nad4*, seed and nonseed plants were analyzed separately. Scale bars correspond to 0.01 substitutions per site.

Fig. 4. *A. trichopoda* leaf from a cloud forest at Massif de l'Aoupinié (Province Nord in New Caledonia) at 801 m altitude. Note the greenish bryophyte (liverwort) growth covering the leaf tip, and the small spots of lichens and other epiphytes elsewhere on the leaf. Photograph courtesy of Sean Graham, Centre for Plant Research, University of British Columbia, Vancouver.

高等植物间的基因水平转移：从菟丝子到番茄

Plant genetics

Gene transfer from parasitic to host plants

Plant mitochondrial genes are transmitted horizontally across mating barriers with surprising frequency, but the mechanism of transfer is unclear[1,2]. Here we describe two new cases of horizontal gene transfer, from parasitic flowering plants to their host flowering plants, and present phylogenetic and biogeographic evidence that this occurred as a result of direct physical contact between the two. Our findings complement the discovery that genes can be transferred in the opposite direction, from host to parasite plant[3].

Figure 2 A parasitic dodder (*Cuscuta californica*) in flower, with its haustoria penetrating a host tomato plant.

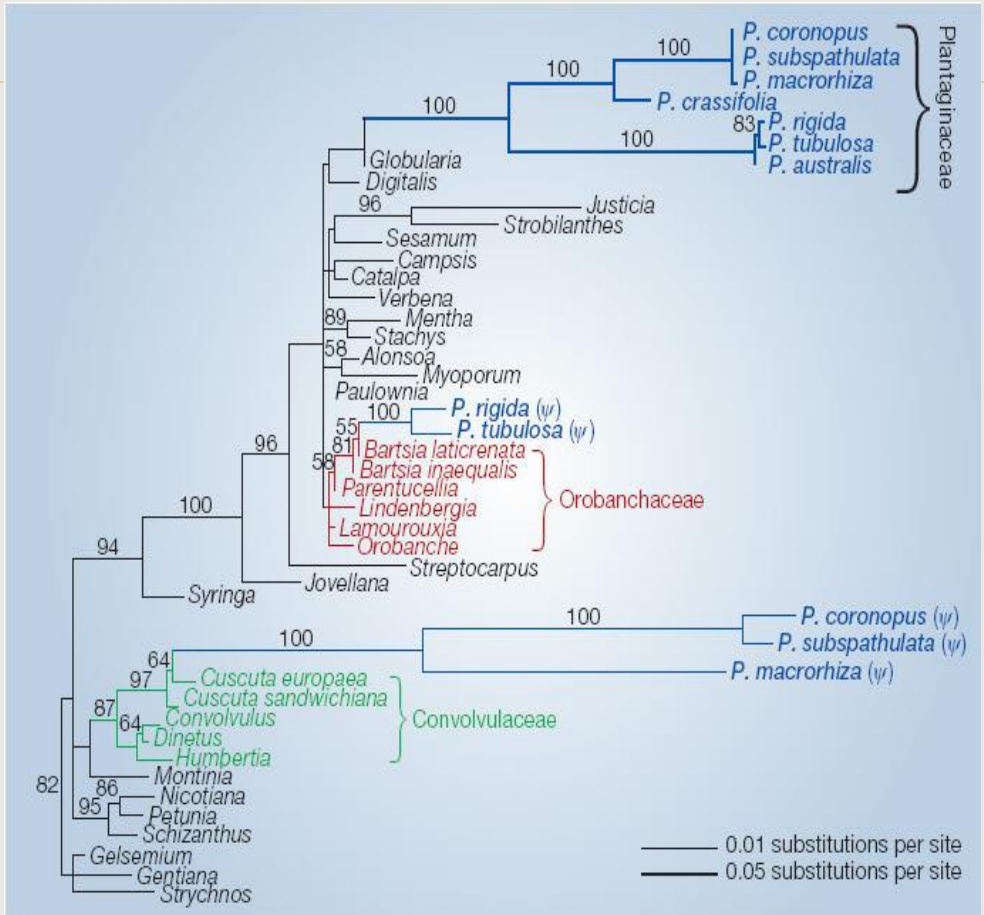


Figure 1 Phylogenetic evidence for two horizontal transfer events of the gene *atp1* into *Plantago* (blue). Seven *Plantago atp1* genes at the top of the maximum-likelihood tree are intact, vertically transmitted, and rapidly evolving (scale reduced by 80%). The other two sets of *Plantago atp1* genes are pseudogenes (ψ) acquired from parasitic plants in the Orobanchaceae (red) and Convolvulaceae (green). Bootstrap values of over 50% are shown. For methods, see supplementary information.

综述: 植物间的基因水平转移

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SPECIAL ISSUE PAPER

Horizontal gene transfer in plants

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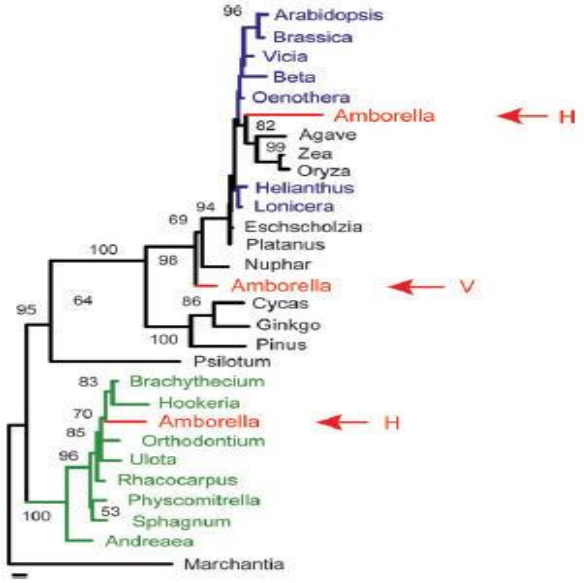

Fig. 3. Two transfers of *nad5* to *Amborella* from disparate plant donors. Maximum likelihood tree of *nad5* exons [reproduced from Bergthorsson *et al.* (2004), Copyright 2004 National Academy of Sciences, USA]. *Amborella* genes are shown in red, core eudicots genes in blue, and moss genes in green. Bootstrap values (100 ML replicates) >50% are shown. H, horizontally acquired gene; V, vertically inherited gene. The scale bar represents 0.01 nucleotide substitutions per site. The number of nucleotides in the alignment varies across genes as not all exons amplified for all sequences; vertically transmitted copy, 1238 nucleotides; angiosperm-derived copy, 601 nucleotides; moss-derived copy, 1062 nucleotides.

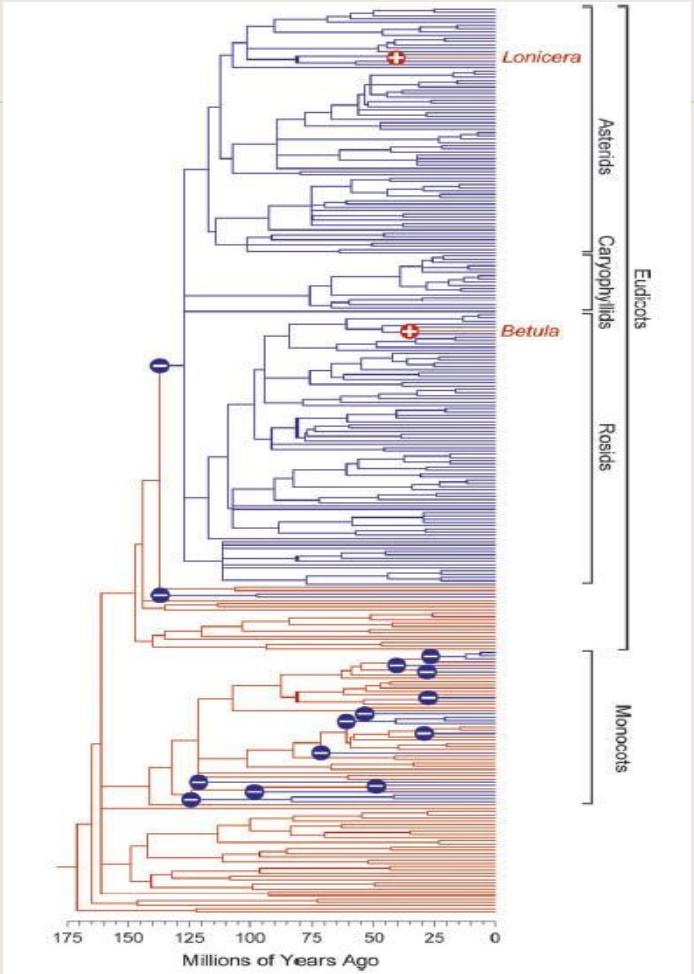

Fig. 1. Distribution of mitochondrial *rps11* among 280 flowering plants. Red and blue branches indicate the presence and absence, respectively, of *rps11* in the mitochondrial genome. Blue circles with minus signs indicate gene losses as inferred by parsimony; red circles with plus signs indicate putative recaptures of *rps11* by mtDNA. Modified from Bergthorsson *et al.* (2003). See Adams *et al.* (2002) for names of all 280 angiosperms represented by the tree.

Horizontal gene transfer of the algal nuclear gene *psbO* to the photosynthetic sea slug *Elysia chlorotica*

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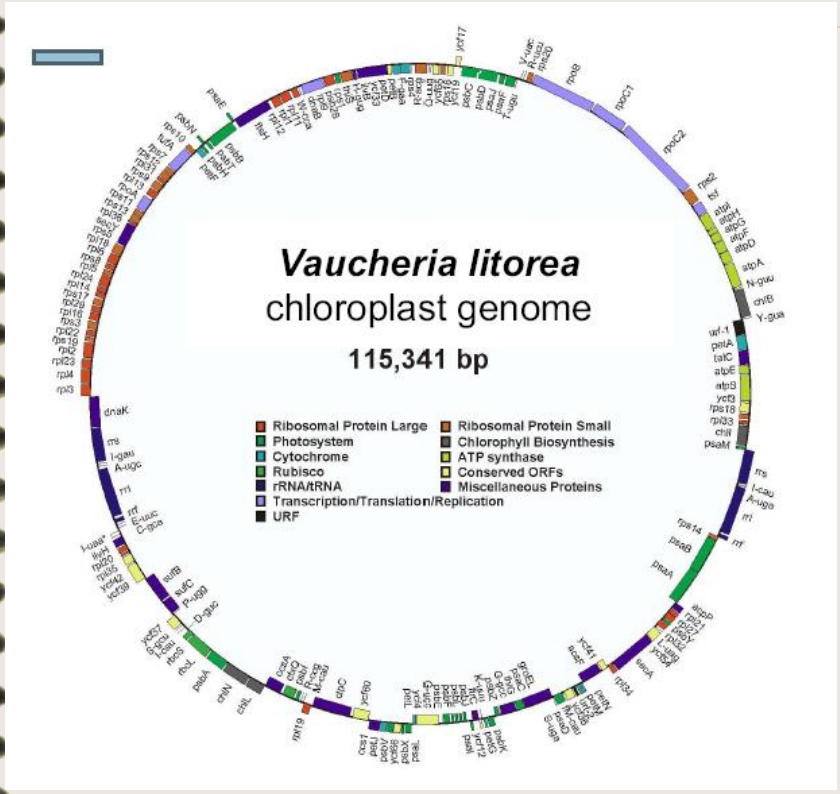
Edited by Lynn Margulis, University of Massachusetts, Amherst, MA, and approved September 17, 2008 (received for review June 9, 2008)

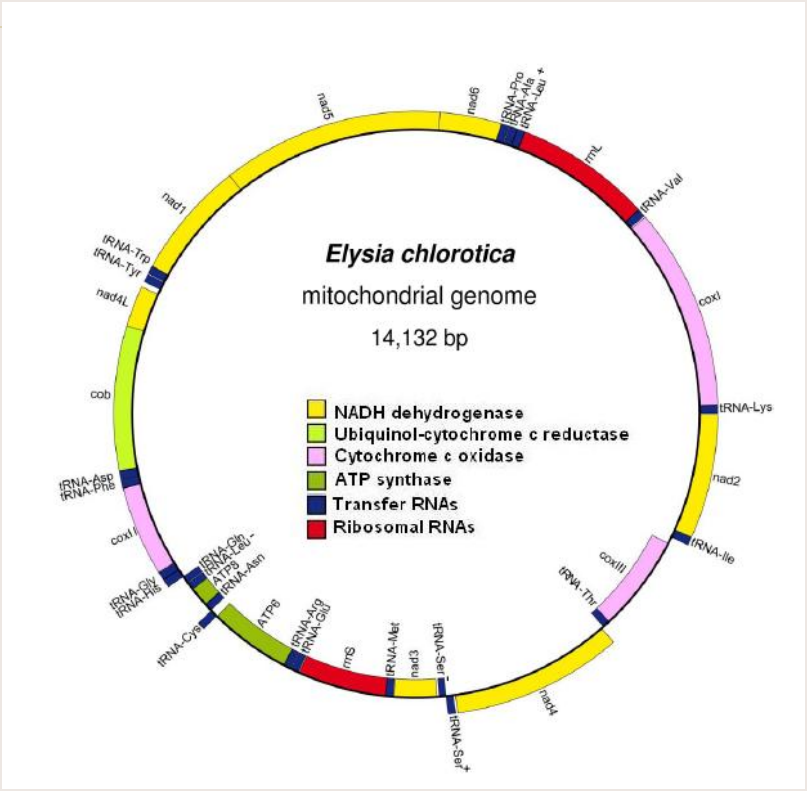
The sea slug *Elysia chlorotica* acquires plastids by ingestion of its algal food source *Vaucheria litorea*. Organelles are sequestered in the mollusc's digestive epithelium, where they photosynthesize for months in the absence of algal nucleocytoplasm. This is perplexing because plastid metabolism depends on the nuclear genome for >90% of the needed proteins. Two possible explanations for the persistence of photosynthesis in the sea slug are (*i*) the ability of *V. litorea* plastids to retain genetic autonomy and/or (*ii*) more likely, the mollusc provides the essential plastid proteins. Under the latter scenario, genes supporting photosynthesis have been acquired by the animal via horizontal gene transfer and the encoded proteins are retargeted to the plastid. We sequenced the plastid genome and confirmed that it lacks the full complement of genes required for photosynthesis. In support of the second scenario, we demonstrated that a nuclear gene of oxygenic photosynthesis, *psbO*, is expressed in the sea slug and has integrated into the germline. The source of *psbO* in the sea slug is *V. litorea* because this sequence is identical from the predator and prey genomes. Evidence that the transferred gene has integrated into sea slug nuclear DNA comes from the finding of a highly diverged *psbO* 3′ flanking sequence in the algal and mollusc nuclear homologues and gene absence from the mitochondrial genome of *E. chlorotica*. We demonstrate that foreign organelle retention generates metabolic novelty ("green animals") and is explained by anastomosis of distinct branches of the tree of life driven by predation and horizontal gene transfer.

20). Most of these latter examples are associated with parasitism or phagotrophy, including the elegant studies of HGT from the α-proteobacteria *Wolbachia* to insects and nematodes (16–18), and the finding of rhizobial-like genes in plant parasitic nematodes (19, 20). The exchange of genetic material between two eukaryotes is extremely rare, or at least not well documented to date. The best-studied cases include the transfer of mitochondrial DNA from achlorophyllous or epiphytic plants to the mitochondrial genome (mtDNA) of their closely related photosynthetic hosts (21), the exchange of transposons between two animal (22) or two plant (23) species, and the presence of plant genes in plant parasitic nematodes (in addition to the rhizobial genes discussed previously), which are hypothesized to be "defense" genes whose products protect the parasite from host detection (20).

The sacoglossan mollusc (sea slug) *Elysia chlorotica* represents a unique model system to study the potential for interdomain HGT between two multicellular eukaryotes—in this case, from a filamentous secondary (heterokont) alga (*Vaucheria litorea*) to a mollusc. This emerald green sea slug owes its coloring and photosynthetic ability to plastids acquired during herbivorous feeding (24–29). The plastids do not undergo division in the sea slug and are sequestered intracellularly in cells lining the finely divided digestive diverticula. The plastids continue to carry out photosynthesis, providing the sea slug with energy and carbon during its approximately 10-month life span (27, 28). Long-term plastid activity continues despite the absence of algal nuclei (27, 29), and hence a source of nuclear-encoded plastid-targeted

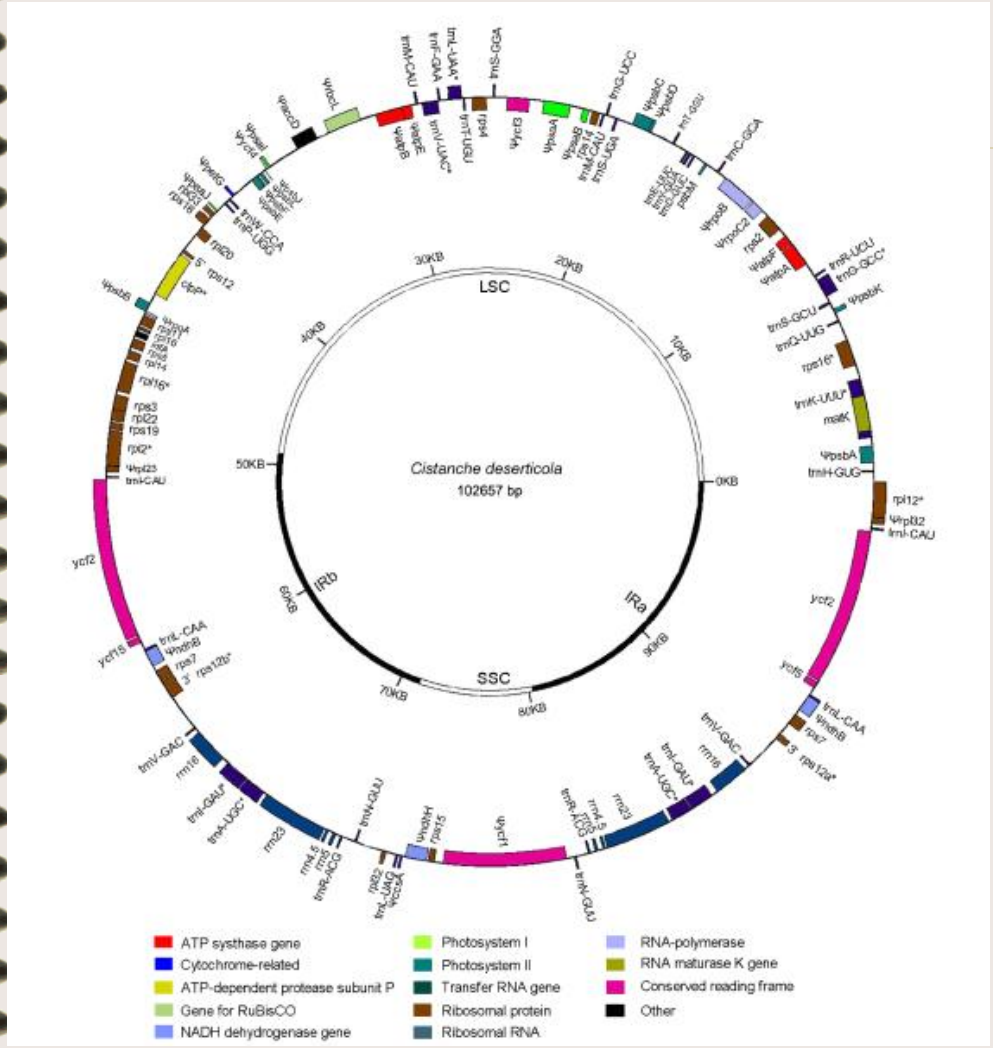

A
B
C
D

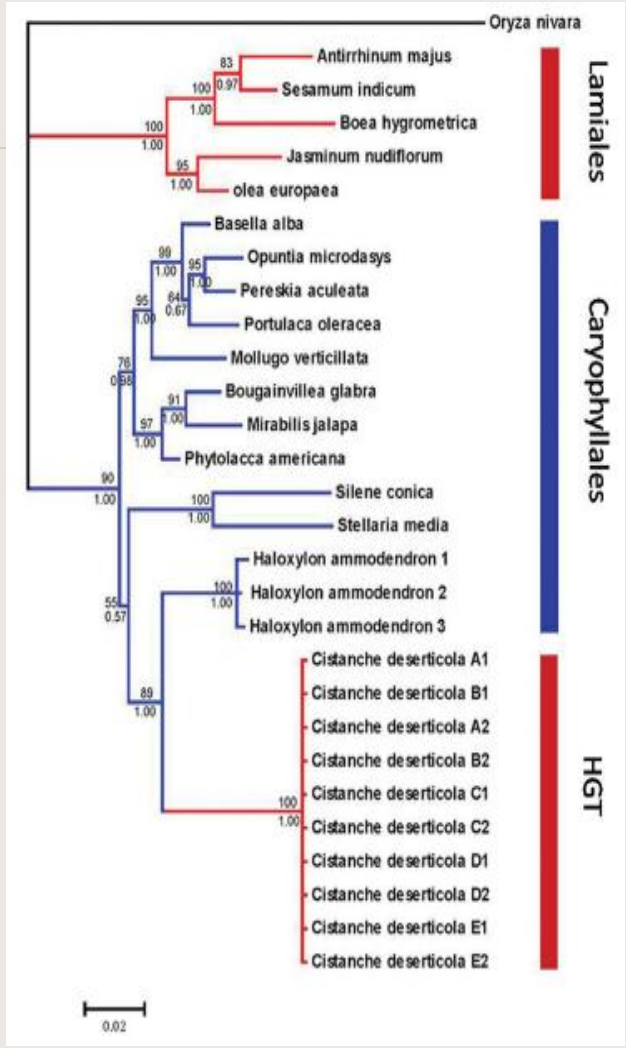

Vaucheria litorea
chloroplast genome
115,341 bp
Ribosomal Protein Large
Photosystem
Cytochrome
Rubisco
rRNA/tRNA
Transcription/Translation/Replication
URF
Ribosomal Protein Small
Chlorophyll Biosynthesis
ATP synthase
Conserved ORFs
Miscellaneous Proteins


Elysia chlorotica
mitochondrial genome
14,132 bp
NADH dehydrogenase
Ubiquinol-cytochrome c reductase
Cytochrome c oxidase
ATP synthase
Transfer RNAs
Ribosomal RNAs

肉苁蓉?

肉苁蓉与梭梭间的基因水平转移证据





叶绿体基因组结构与 ***rpoC2*** 基因水平转移

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PLOS | ONE

Complete Chloroplast Genome Sequence of Holoparasite *Cistanche deserticola* (Orobanchaceae) Reveals Gene Loss and Horizontal Gene Transfer from Its Host *Haloxylon ammodendron* (Chenopodiaceae)

Xi Li[1☯], Ti-Cao Zhang[1☯], Qin Qiao[1], Zhumei Ren[2], Jiayuan Zhao[1], Takahiro Yonezawa[1], Masami Hasegawa[1], M. James C Crabbe[3], Jianqiang Li[4]*, Yang Zhong[1,5]*

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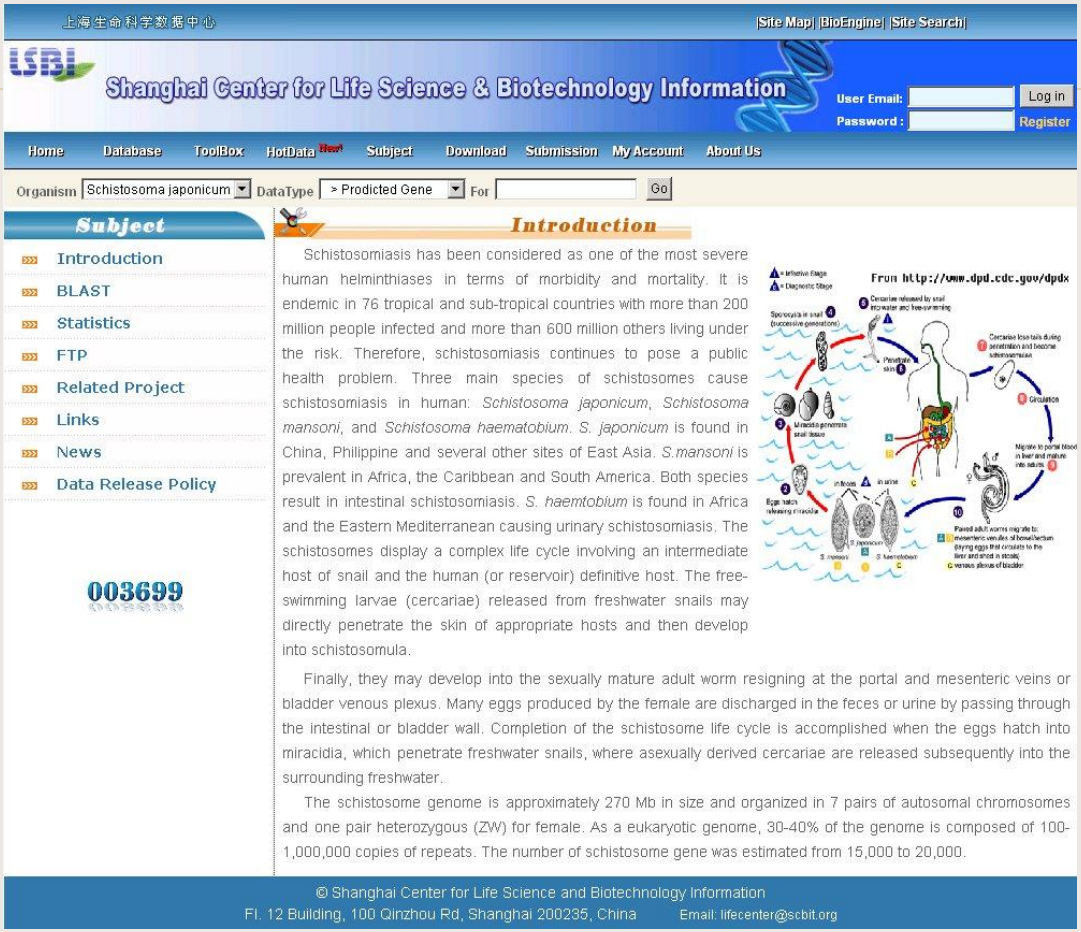
Abstract

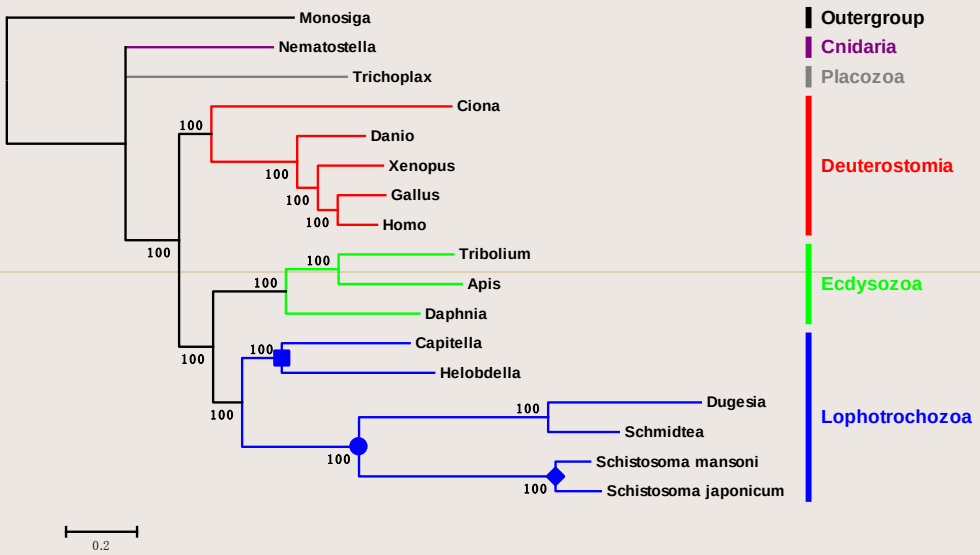
Background: The central function of chloroplasts is to carry out photosynthesis, and its gene content and structure are highly conserved across land plants. Parasitic plants, which have reduced photosynthetic ability, suffer gene losses from the chloroplast (cp) genome accompanied by the relaxation of selective constraints. Compared with the rapid rise in the number of cp genome sequences of photosynthetic organisms, there are limited data sets from parasitic plants.

Principal Findings/Significance: Here we report the complete sequence of the cp genome of *Cistanche deserticola*, a holoparasitic desert species belonging to the family Orobanchaceae. The cp genome of *C. deserticola* is greatly reduced both in size (102,657 bp) and in gene content, indicating that all genes required for photosynthesis suffer from gene loss and pseudogenization, except for *psb*M. The striking difference from other holoparasitic plants is that it retains almost a full set of tRNA genes, and it has lower *dN/dS* for most genes than another close holoparasitic plant, *E. virginiana*, suggesting that *Cistanche deserticola* has undergone fewer losses, either due to a reduced level of holoparasitism, or to a recent switch to this life history. We also found that the *rpo*C2 gene was present in two copies within *C. deserticola*. Its own copy has much shortened and turned out to be a pseudogene. Another copy, which was not located in its cp genome, was a homolog of the host plant, *Haloxylon ammodendron* (Chenopodiaceae), suggesting that it was acquired from its host via a horizontal gene transfer.

血吸虫?

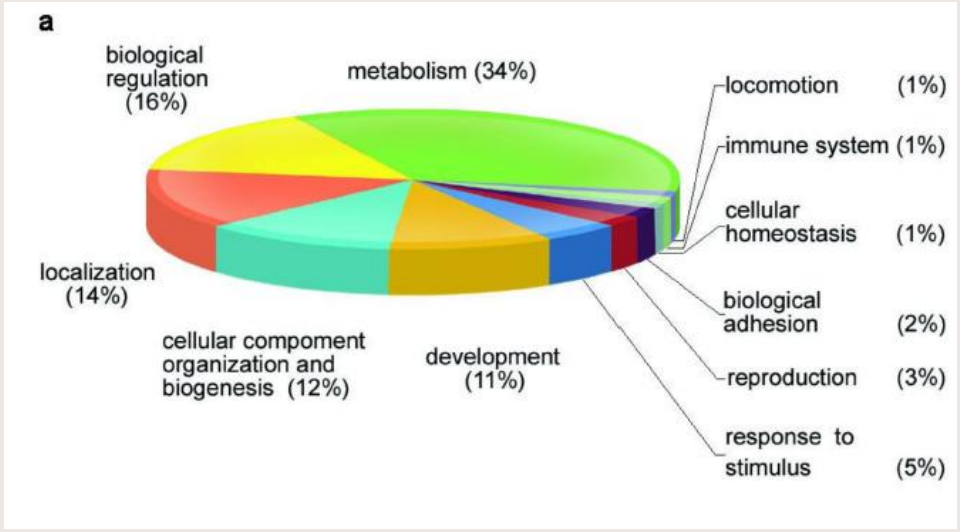


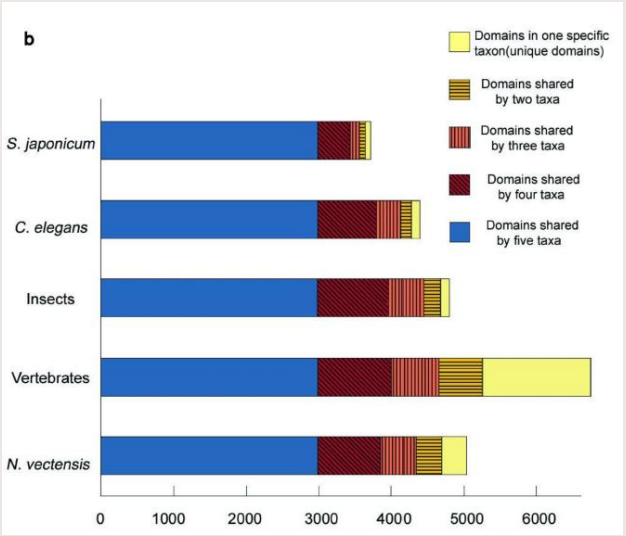
Genome data of *Schistosoma* at Shanghai Center for Bioinformation Technology (http://www.scbit.org/)

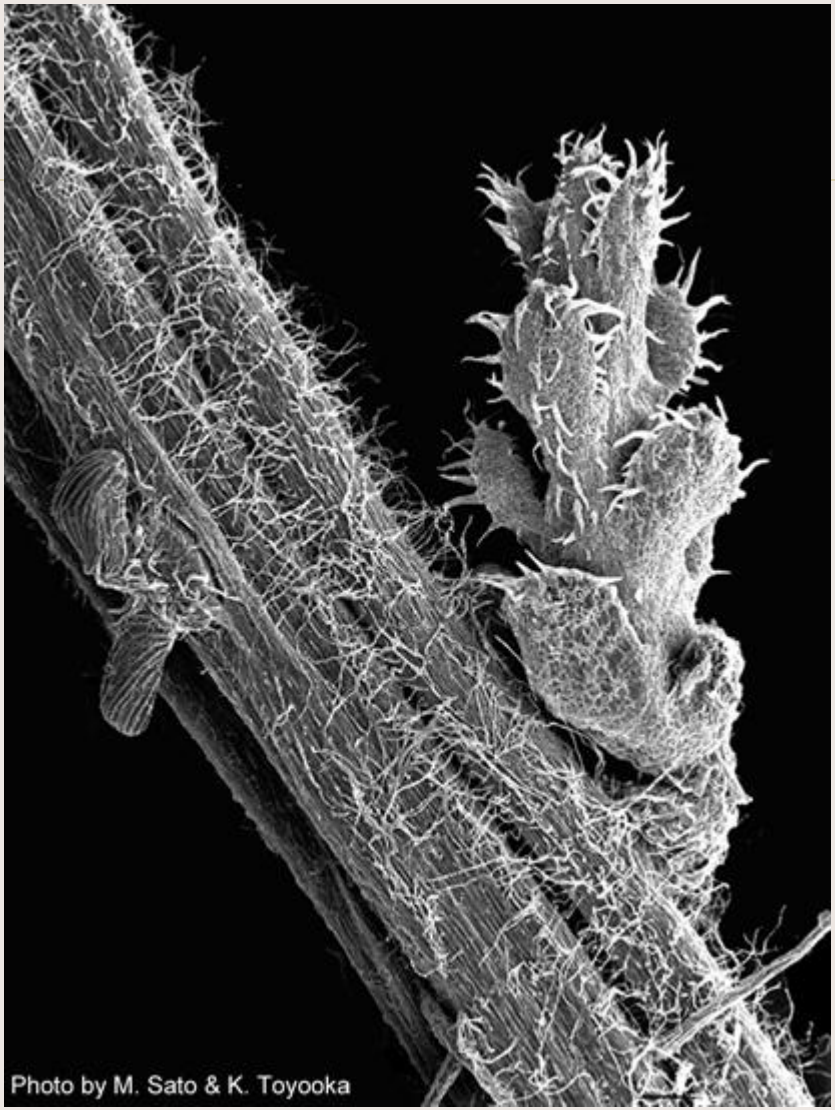


Zhou Y et al, 2009, *Nature*

Phylogenomics of metazoan（>300,000 bp)







黄独脚金（*Striga hermonthica*）
玄参科

Horizontal Gene Transfer by the Parasitic Plant *Striga hermonthica*

Satoko Yoshida,[1] Shinichiro Maruyama,[2] Hisayoshi Nozaki,[2] Ken Shirasu[1]*

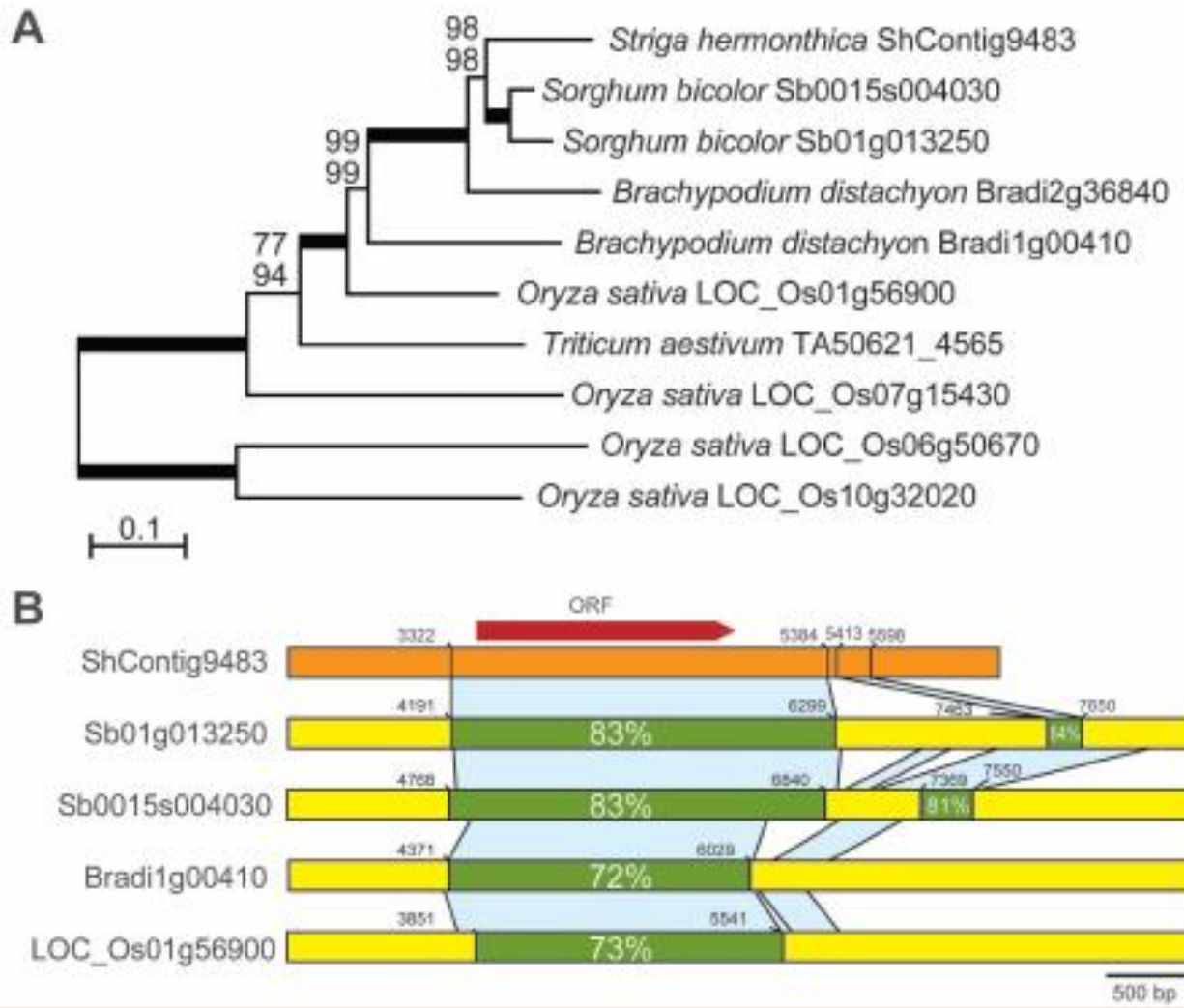
Horizontal gene transfer (HGT) plays an important role in genome evolution (*1*). In plants, the majority of reported cases of HGT have been limited to exchanges between plants and microbes, mitochondrial transfer, or the translocation of mobile elements among related species (*1*). Parasitic plants are known to be vectors of mitochondrial HGT, but it has been unclear whether they also mediate nuclear HGT (*1*, *2*).

Striga hermonthica (Del.) Benth. is a devastating parasitic plant that infests members of the grass family (Poaceae), including major crops such as sorghum (*Sorghum bicolor*) and rice (*Oryza sativa*). *S. hermonthica* belongs to the eudicot Orobanchaceae family of the order Lamiales (fig. S1) (*3*) and only infects monocot plants. Thus, we reasoned that we may be able to detect nuclear HGT, if it occurs, by identifying monocot-specific genes in the *S. hermonthica* genome. From a large-scale expressed sequence tag analysis of *S. hermonthica* (*4*), we found one gene, designated *ShContig9483*, which shows high similarity to genes in sorghum and rice but has no homologs in eudicots (fig. S2A and table S1) (*5*). Southern blot analysis revealed *ShContig9483* cross-hybridization signals from sorghum, and rice to a lesser extent, reflecting its lower similarity, whereas no signals were detected from other closely related plants in Orobanchaceae nor from any nonparasitic eudicots (fig. S2B). This indicates that *ShContig9483* most likely originated in the monocots before its transfer to *S. hermonthica*.

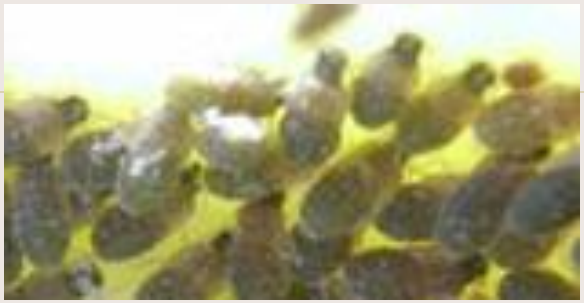
ShContig9483 encodes a 448–amino acid protein with unknown function. Phylogenetic analysis of *ShContig9483* and related protein-coding sequences clusters *S. hermonthica* with sorghum (Fig. 1A). This tree conflicts with the phylogenetic position of *Striga* (*3*), suggesting that *S. hermonthica* acquired *ShContig9483* from sorghum or a related grass species. The *S. hermonthica* genomic region containing *ShContig9483* resides near a nuclear gene encoding a putative cis-prenyltransferase (fig. S3A). In contrast to *ShContig9483*, this putative cis-prenyltransferase gene from *S. hermonthica* clusters with genes from other eudicot species (fig. S3B).

The genomic sequences of the sorghum homologs show similarities to the *ShContig9483* locus from about 150 base pairs (bp) up- and 800 bp downstream of the putative open reading frame (ORF), except for several insertions and deletions (Fig. 1B and fig. S4). The similarity to homologs from *Brachypodium* and rice covers a shorter region with lower identities (Fig. 1B). The high conservation of sequence between *S. hermonthica* and sorghum outside the ORF suggest that transfer was a relatively recent event. Indeed, a sequence highly similar to *ShContig9483* was found in *S. gesnerioides* but not in *Orobanche minor*, which is from a closely related genus (figs. S2B and S5). These data suggest that incorporation of the *ShContig9483* fragment occurred before speciation of *S. hermonthica* and *S. gesnerioides* but after differentiation of the genera *Striga* and *Orobanche*. Parasitic plants form an invasive organ called a haustorium, which interconnects their vasculature with that of their hosts to allow transfer of nutrients, water, and even mRNAs (*2*). Thus, one possibility is that *ShContig9483* was originally captured by *S. hermonthica* as mRNA or cDNA. Interestingly, we found 13 consecutive adenine (A) nucleotides at the 3′ end of the *ShContig9483* genomic region (fig. S4). This sequence may be indicative of a poly-A tail added to a transcriptional unit of the originally transferred gene. In any case, our comparative genomics analysis of a eudicot parasite and its monocot hosts presents a clear case for nuclear HGT. Because the method used in this study is limited to the

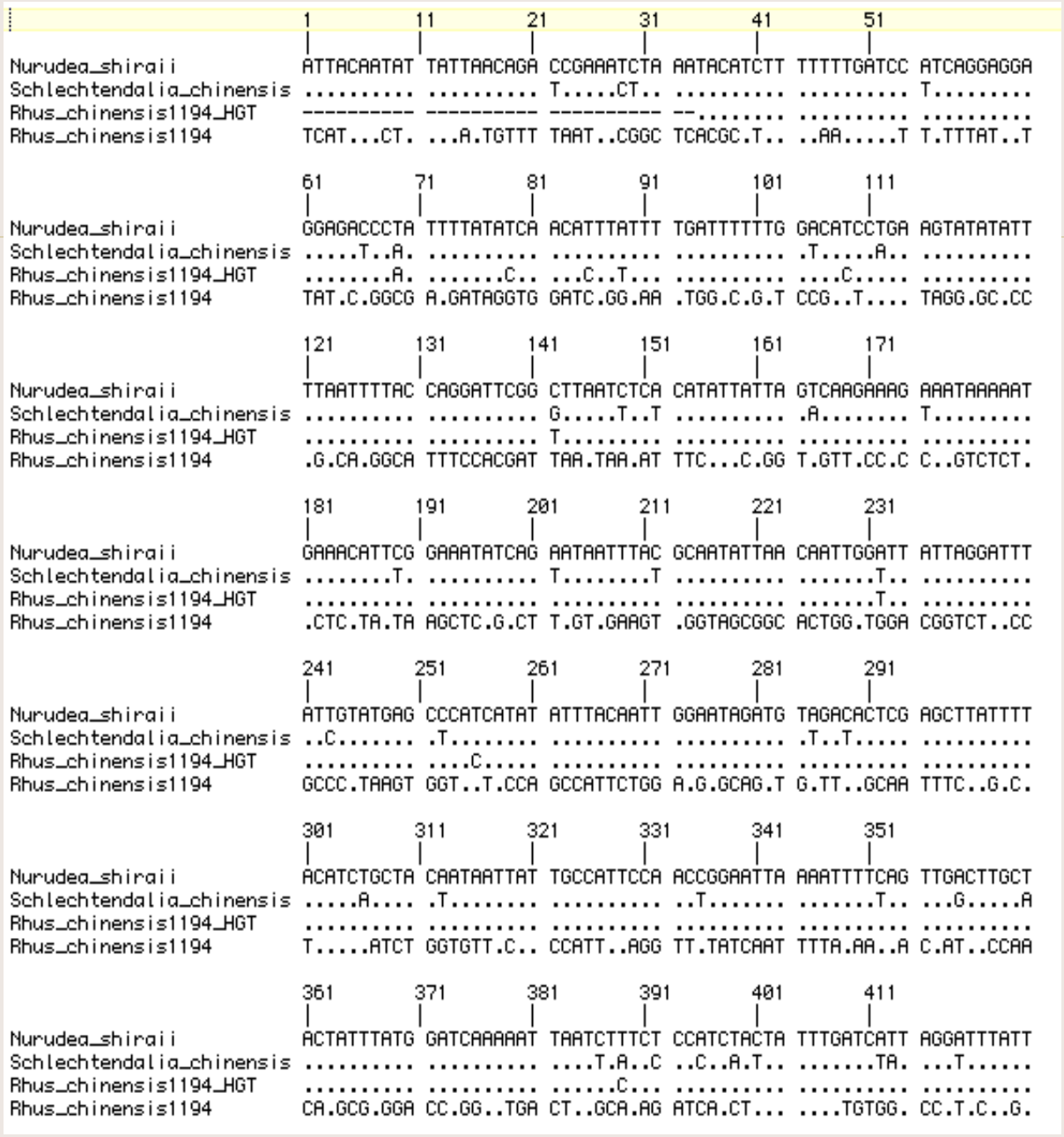
Science April 15, 2010

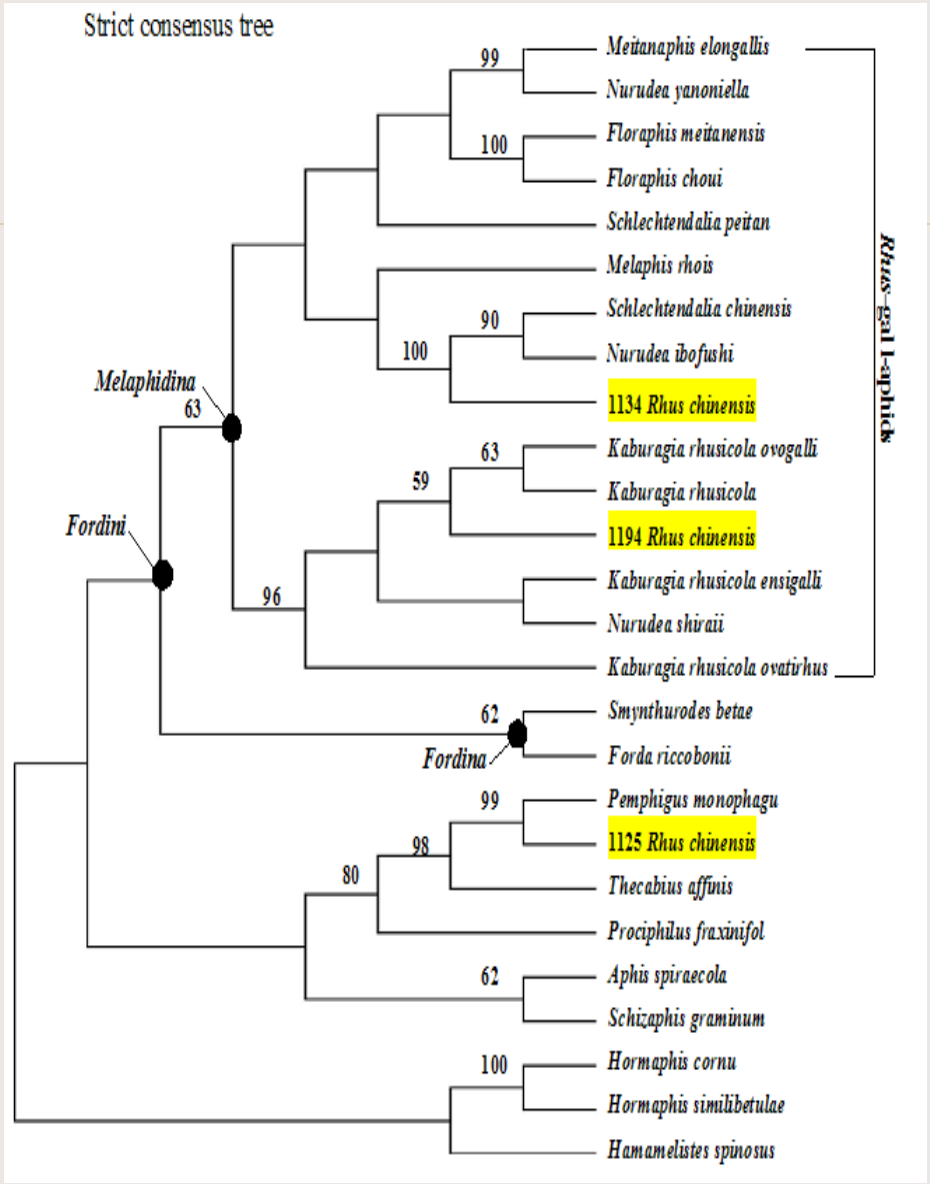

A
98
98
Striga hermonthica ShContig9483
Sorghum bicolor Sb0015s004030
99
99
Sorghum bicolor Sb01g013250
Brachypodium distachyon Bradi2g36840
77
94
Brachypodium distachyon Bradi1g00410
Oryza sativa LOC_Os01g56900
Triticum aestivum TA50621_4565
Oryza sativa LOC_Os07g15430
Oryza sativa LOC_Os06g50670
Oryza sativa LOC_Os10g32020
0.1
B
ORF
ShContig9483
Sb01g013250
Sb0015s004030
Bradi1g00410
LOC_Os01g56900
83%
83%
72%
73%
500 bp

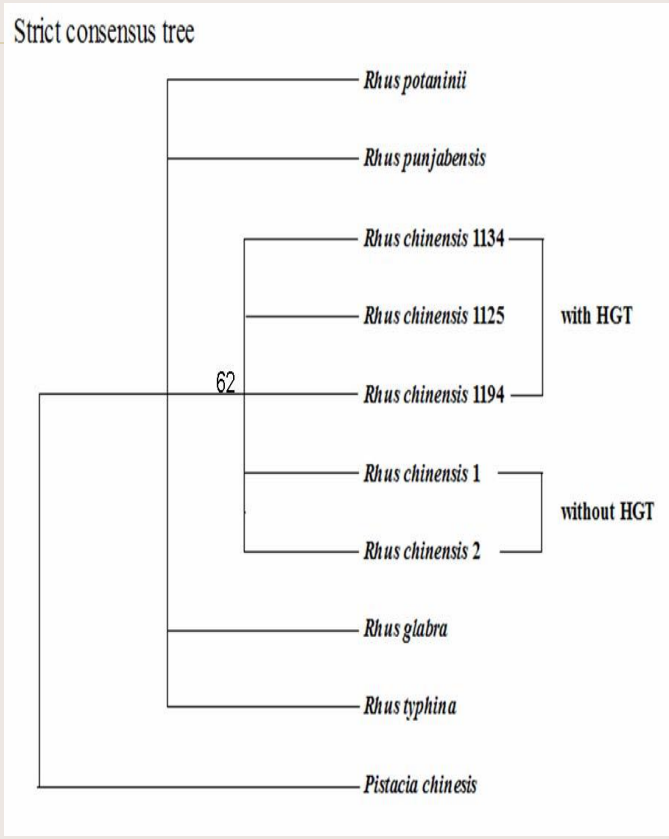
五倍子：一个植物与动物间的水平转移案例？！



倍蚜 / 盐肤木/
提灯藓 / 五倍子


1 11 21 31 41 51
Nurudea_shiraii ATTACAATAT TATTAACAGA CCGAAATCTA AATACATCTT TTTTTGATCC ATCAGGAGGA
Schlechtendalia_chinensis .... T.....CT.. .... T.....
Rhus_chinensis1194_HGT ---------- ---------- ---------- --..... ....
Rhus_chinensis1194 TCAT...CT. ...A.TGTTT TAAT..CGGC TCACGC.T.. ..AA.....T T.TTTAT..T
61 71 81 91 101 111
Nurudea_shiraii GGAGACCCTA TTTTATATCA ACATTTATTT TGATTTTTTG GACATCCTGA AGTATATATT
Schlechtendalia_chinensis .....T..A. .... .T.....A.. .....
Rhus_chinensis1194_HGT .....A. .....C.. ...C..T... ....C..... .....
Rhus_chinensis1194 TAT.C.GGCG A.GATAGGTG GATC.GG.AA .TGG.C.G.T CCG..T.... TAGG.GC.CC
121 131 141 151 161 171
Nurudea_shiraii TTAATTTTAC CAGGATTCGG CTTAATCTCA CATATTATTA GTCAAGAAAG AAATAAAAAT
Schlechtendalia_chinensis .... G.....T..T ..... .A..... T.....
Rhus_chinensis1194_HGT .... T..... ....
Rhus_chinensis1194 .G.CA.GGCA TTTCCACGAT TAA.TAA.AT TTC...C.GG T.GTT.CC.C C..GTCTCT.
181 191 201 211 221 231
Nurudea_shiraii GAAACATTCG GAAATATCAG AATAATTTAC GCAATATTAA CAATTGGATT ATTAGGATTT
Schlechtendalia_chinensis .....T. ..... T.....T ....T.. .....
Rhus_chinensis1194_HGT ....T.. .....
Rhus_chinensis1194 .CTC.TA.TA AGCTC.G.CT T.GT.GAAGT .GGTAGCGGC ACTGG.TGGA CGGTCT..CC
241 251 261 271 281 291
Nurudea_shiraii ATTGTATGAG CCCATCATAT ATTTACAATT GGAATAGATG TAGACACTCG AGCTTATTTT
Schlechtendalia_chinensis ..C..... .T..... .... .T..T..... .....
Rhus_chinensis1194_HGT ....C..... ....
Rhus_chinensis1194 GCCC.TAAGT GGT..T.CCA GCCATTCTGG A.G.GCAG.T G.TT..GCAA TTTC..G.C.
301 311 321 331 341 351
Nurudea_shiraii ACATCTGCTA CAATAATTAT TGCCATTCCA ACCGGAATTA AAATTTTCAG TTGACTTGCT
Schlechtendalia_chinensis .....A.... .T..... ....T..... .....T.. ...G.....A
Rhus_chinensis1194_HGT ....
Rhus_chinensis1194 T.....ATCT GGTGTT.C.. CCATT..AGG TT.TATCAAT TTTA.AA..A C.AT..CCAA
361 371 381 391 401 411
Nurudea_shiraii ACTATTTATG GATCAAAAAT TAATCTTTCT CCATCTACTA TTTGATCATT AGGATTTATT
Schlechtendalia_chinensis ....T.A..C ..C..A.T.. .....TA. ...T.....
Rhus_chinensis1194_HGT ....C... ....
Rhus_chinensis1194 CA.GCG.GGA CC.GG..TGA CT..GCA.AG ATCA.CT... ....TGTGG. CC.T.C..G.


Strict consensus tree
Meitanaphis elongallis
Nurudea yanoniella
Floraphis meitanensis
Floraphis choui
Schlechtendalia peitan
Melaphis rhois
Schlechtendalia chinensis
Nurudea ibofushi
1134 Rhus chinensis
Kaburagia rhusicola ovogalli
Kaburagia rhusicola
1194 Rhus chinensis
Kaburagia rhusicola ensigalli
Nurudea shiraii
Kaburagia rhusicola ovatirhus
Smynthurodes betae
Forda riccobonii
Pemphigus monophagu
1125 Rhus chinensis
Thecabius affinis
Prociphilus fraxinifol
Aphis spiraecola
Schizaphis graminum
Hormaphis cornu
Hormaphis similibetulae
Hamamelistes spinosus
Rhus-gall-aphids
Melaphidina
Fordini
Fordina
99
100
90
100
63
63
59
96
62
99
98
80
62
100
63


Strict consensus tree
Rhus potaninii
Rhus punjabensis
Rhus chinensis 1134
Rhus chinensis 1125
Rhus chinensis 1194
Rhus chinensis 1
Rhus chinensis 2
Rhus glabra
Rhus typhina
Pistacia chinesis
with HGT
without HGT
62

从猜测到验证

- 污染？ 重复/对照
- 群体？ 统计比例
- 遗传？ 种子检测
- 定位？ 两端序列
- ……

Exchange of Genetic Material Between Cells in Plant Tissue Grafts

Sandra Stegemann and Ralph Bock*

Tissue grafting includes applications ranging from plant breeding to animal organ transplantation. Donor and recipient are generally believed to maintain their genetic integrity, in that the grafted tissues are joined but their genetic materials do not mix. We grafted tobacco plants from two transgenic lines carrying different marker and reporter genes in different cellular compartments, the nucleus and the plastid. Analysis of the graft sites revealed the frequent occurrence of cells harboring both antibiotic resistances and both fluorescent reporters. Our data demonstrate that

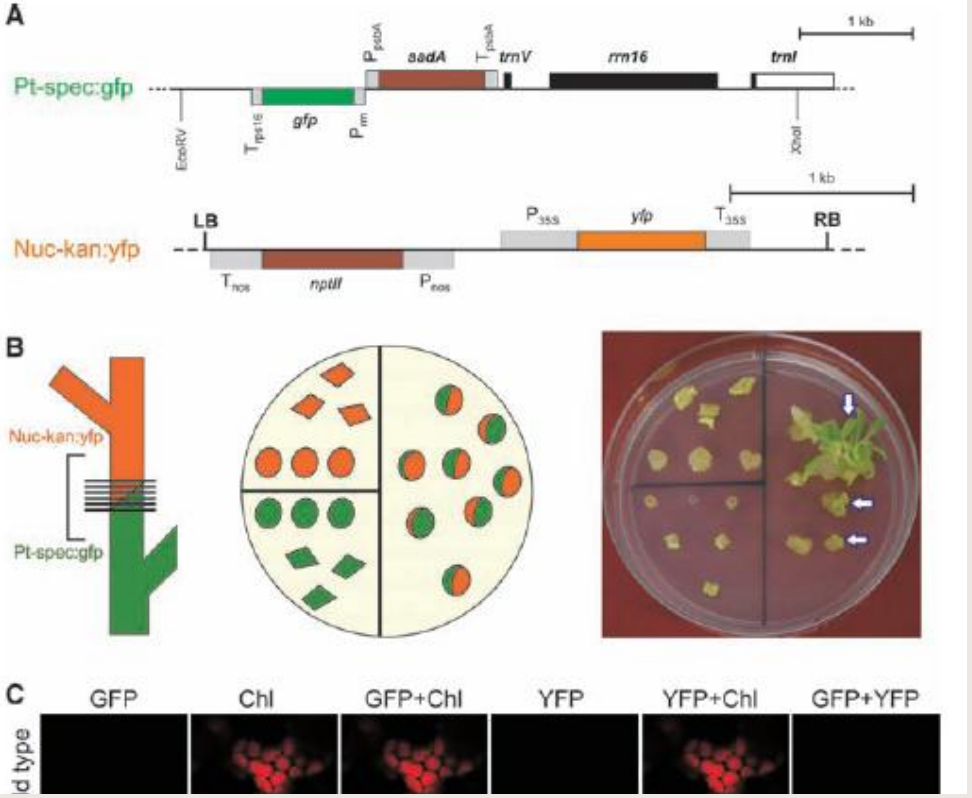


Fig. 1. Genetic screen for intercellular gene transfer. (**A**) Maps of the plastid genome in Pt-spec:gfp plants and the transgenic locus in Nuc-kan:yfp plants. P_{psbA} and T_{psbA}, promoter and terminator from the plastid *psbA* gene; P_{rrn}, promoter from the plastid rRNA operon; T_{rps16}, terminator from the plastid *rps16* gene; P_{nos} and T_{nos}, promoter and terminator from the nopaline synthase gene from *Agrobacterium tumefaciens*; P_{35S} and T_{35S}, promoter and terminator from the cauliflower mosaic virus 35S transcript; LB and RB, left and right borders of the T-DNA region; Eco RV and Xho I, restriction sites used for restriction fragment length polymorphism analysis (fig. S3). (**B**) Selection experiments. The grafted stem region was either sectioned (horizontal lines) or directly exposed to selection (bracket). The middle panel shows the arrangement of tissue explants, the right panel a selection plate (right half, stem sections from the graft site; upper left quarter, three stem sections and three leaf explants from Nuc-kan:yfp; lower left quarter, the corresponding explants from Pt-spec:gfp). After 4 weeks on medium with spectinomycin and kanamycin, some explants from the graft site developed growing callus tissue or regenerating shoots (arrows). (**C**) Expression and subcellular localization of the fluorescent reporters. The wild type, the two grafting partners, and a YG line were assayed for GFP, chlorophyll (Chl), and YFP fluorescence.

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