
The family Theridiidae is one of the most diverse assemblages of spiders, from both a morphological and ecological point of view. The family includes some of the very few cases of sociality reported in spiders, in addition to bizarre foraging behaviors such as kleptoparasitism and araneophagy, and highly diverse web architecture. Theridiids are one of the seven largest families in the Araneae, with about 2200 species described. However, this species diversity is currently grouped in half the number of genera described for other spider families of similar species richness. Recent cladistic analyses of morphological data have provided an undeniable advance in identifying the closest relatives of the theridiids as well as establishing the family’s monophyly. Nevertheless, the comb-footed spiders remain an assemblage of poorly defined genera, among which hypothesized relationships have yet to be examined thoroughly. Providing a robust cladistic structure for the Theridiidae is an essential step towards the clarification of the taxonomy of the group and the interpretation of the evolution of the diverse traits found in the family. Here we present results of a molecular phylogenetic analysis of a broad taxonomic sample of the family (40 taxa in 33 of the 79 currently recognized genera) and representatives of nine additional araneid families, using approximately 2.5 kb corresponding to fragments of three nuclear genes (Histone 3, 18SrDNA, and 28SrDNA) and two mitochondrial genes (16SrDNA and CoI). Several methods for incorporating indel information into the phylogenetic analysis are explored, and partition support for the different clades and sensitivity of the results to different assumptions of the analysis are examined as well. Our results marginally support theridiid monophyly, although the phylogenetic structure of the outgroup is unstable and largely contradicts current phylogenetic hypotheses based on morphological data. Several groups of theridiids receive strong support in most of the analyses: latrodectines, argyrodesines, hadrotarsines, a revised version of spintharines and two clades including all theridiids without trace of a colulus and those without colular setae. However, the interrelationships of these clades are sensitive to data perturbations and changes in the analysis assumptions.

The wrens (Aves: Troglodytidae) are a group of primarily New World insectivorous birds, the monophyly of which has long been recognized, but whose intergeneric relationships are essentially unknown. In order to test the monophyly of the group, and to attempt to resolve relationships among genera within it, sequences from the mitochondrial cytochrome b gene and the fourth intron of the nuclear [beta]-fibrinogen gene were obtained from nearly all genera of wrens, from their relatives as suggested by traditional taxonomy and DNA-DNA hybridization analyses, and from additional passerines. Maximum likelihood analysis of the two data sets yielded maximal congruence between independently derived estimates of relationship, outperforming a variety of weighted parsimony methods. Hierarchical likelihood ratio tests indicated that the two gene regions differed significantly in every estimated parameter of sequence evolution, and combined analysis of the two data sets was accomplished using a heterogeneous-model Bayesian approach. Independent and simultaneous analyses of both data sets supported monophyly of the wrens (excluding one recently added member, the monotypic genus Donacobius) and a sister-group relationship between wrens and the gnatcatchers (Polioptila). Additionally, strong support was found for paraphyly of the genus Thryothorus, and for a sister-group relationship between the genera Cistothorus and Troglodytes. Analyses of these data failed to resolve basal relationships within wrens, possibly due to ambiguity in rooting with a distant, species-poor outgroup. Analysis of the combined data for wrens alone yielded results which were largely congruent with relationships inferred using the complete data set, with the benefit of stronger support for relationships within the group. However, alternative rootings of this ingroup tree were weakly supported by nucleotide substitution data. Insertion-deletion events suggest that the genus Salpinctes may be sister to all other wrens.


http://www.sciencedirect.com/science/article/B6WNH-4D2WMC3-4/2/68117290843c09cfb228e5e217634af

Nucleotide sequences of the mitochondrial cytochrome b gene are reported from bats of the genus Myotis including species of the endemic southern African subgenus Cistugo, Myotis (Cistugo) sebrai and Myotis (Cistugo) lesueuri. We also examined Myotis annectans from Southeast Asia, and Myotis macropus from Australia. The two species of Cistugo and Myotis annectans represent the only species of Myotis to differ in chromosome number from the common 2n = 44 found in >40 species. Our results show that the two species of Cistugo are more divergent from the other species of Myotis than several other well-recognized genera and we recommend elevating Cistugo to full generic rank. Myotis annectans groups well within Myotis, clustering with other Southeast Asian and Japanese species, and thus represents the only species of Myotis known to have diverged from the common 2n = 44 karyotype. Myotis macropus clusters within a clade that includes Southeast Asian species.


http://www.sciencedirect.com/science/article/B6WNH-49S7XSK-2/2/282c38530dc3d082751bc69ab73bac42

To reconstruct the phylogenetic position of the extinct cave lion (Panthera leo spelaea), we sequenced 1 kb of the mitochondrial cytochrome b gene from two Pleistocene cave lion DNA samples (47 and 32 ky B.P.). Phylogenetic analysis shows that the ancient sequences form a clade that is most closely related to the extant lions from Africa and Asia; at the same time, cave
lions appear to be highly distinct from their living relatives. Our data show that these cave lion sequences represent lineages that were isolated from lions in Africa and Asia since their dispersal over Europe about 600 ky B.P., as they are not found among our sample of extant populations. The cave lion lineages presented here went extinct without mitochondrial descendants on other continents. The high sequence divergence in the cytochrome b gene between cave and modern lions is notable.


Suprafamilial relationships among characiform fishes and implications for the taxonomy and biogeographic history of the Characiformes were investigated by parsimony analysis of four nuclear and two mitochondrial genes across 124 ingroup and 11 outgroup taxa. Simultaneous analysis of 3660 aligned base pairs from the mitochondrial 16S and cytochrome b genes and the nuclear recombination activating gene (RAG2), seven in absentia (sia), forkhead (fkh), and [alpha]-tropomyosin (trop) gene loci confirmed the non-monophyly of the African and Neotropical assemblages and corroborated many suprafamilial groups proposed previously on the basis of morphological features. The African distichodontids plus citharinids were strongly supported as a monophyletic Citharinoidei that is the sistergroup to all other characiforms, which form a monophyletic Characoidei composed of two large clades. The first represents an assemblage of both African and Neotropical taxa, wherein a monophyletic African Alestidae is sister to a smaller clade comprised of the Neotropical families Ctenolucidae, Lebiasinidae, and the African Hepsetidae, with that assemblage sister to a strictly Neotropical clade comprised of the Crenuchidae and Erythrinidae. The second clade within the Characoidei is strictly Neotropical and includes all other Characiformes grouped into two well supported major clades. The first, corresponding to a traditional definition of the Characidae, is congruent with some groupings previously supported by morphological evidence. The second clade comprises a monophyletic Anostomoidea that is sister to a clade formed by the families Hemiodontidae, Parodontidae, and Serrasalmidae, with that assemblage, in turn, the sistergroup of the Cynodontidae.

Serrasalmidae, traditionally regarded as a subfamily of Characidae, was recovered as the sistergroup of (Anostomoidea (Parodontidae + Hemiodontidae)) and the family Cynodontidae was recovered with strong support as the sistergroup to this assemblage. Our results reveal three instances of trans-continental sistergroup relationships and, in light of the fossil evidence, suggest that marine dispersal cannot be ruled out a priori and that a simple model of vicariance does not readily explain the biogeographic history of the characiform fishes.


http://www.sciencedirect.com/science/article/B6WNH-48KFF3P-2/2/47bc8c274a60106c3da8f8504a28f5f

Previous molecular phylogenetic studies have examined the taxonomic relationships among a number of typical emberizid sparrow genera. To help clarify these relationships, we sequenced a 1673 base pair fragment for the complete sequence of three mitochondrial genes: adenosine triphosphatase (Atp8 and Atp6) and cytochrome oxidase subunit III (COIII) for 38 sparrow species, along with Passerina amoena (Cardinalidae) and Piranga ludoviciana (Thraupidae) which were selected as the outgroups. Our analysis confirms the monophyly of traditional genera such as Junco, Melospiza, and Zonotrichia. Although Calcarius and Plectrophenax are often thought to be putative emberizids, all our analyses placed these genera basal to all other
sparrows examined. As observed with Calcarius, Spizella did not form a monophyletic group, with S. arborea being the sister-taxon to Passerella iliaca. Our analyses also suggest that Aimophila ruficeps is probably more closely related to the "brown towhees" (Pipilo aberti, P. crissalis, and P. fuscus) than its putative congeners. The genus Ammodramus was also not monophyletic, since it appears that Passerculus sandwichensis is more closely related to A. henslowii and A. leconteii then either one is related to its congener A. savannarum. Finally, our analyses exhibited other unsuspected associations, such as the sister-taxon relationships between Amphispiza bilineata and the Chondestes grammacus/Calamospiza melanocorys clade, and Amphispiza belli and Pooecetes gramineus.

http://www.sciencedirect.com/science/article/B6WNH-4FMBK98-4/2/dd9ecca5ecd445b7ad6894c87e554024

Here we apply a combination of phylogeographic and historical demographic analyses to the study of mtDNA sequence variation within the Blue-crowned Manakin (Lepidothrix coronata), a widespread Neotropical bird. A high degree of phylogeographic structure allowed us to demonstrate that several vicariant events, including Andean uplift, the formation of riverine barriers, and climatically induced vegetational shifts, as well as a non-vicariant process, range expansion, have all acted, at varying spatial and temporal scales, to influence genetic structure within L. coronata, suggesting that current historical hypotheses of the origin of Neotropical avian diversity that focus on single vicariant mechanisms may be overly simplistic. Our data also support an origin (>2 mybp) that is substantially older than the late Pleistocene for the genetic structure within this species and indicate that phylogeographic patterns within the species are not concordant with plumage-based subspecific taxonomy. These data add to a growing body of evidence suggesting that the origin of several Neotropical avian species may have occurred in the mid-Pliocene, thus, geological arguments surrounding putative Pleistocene vicariant events, while interesting in their own right, may have little relevance to Neotropical avian diversification at the species level.

http://www.sciencedirect.com/science/article/B6WNH-4783K6K-1/2/047833090815bf05218ec4905e7105c8

http://www.sciencedirect.com/science/article/B6WNH-47TNSB8-2/2/67e6e755288629e3e6ff2e3d9290e75a

Inferring phylogenetic relationships among closely related plant species is often difficult due to the lack of molecular markers exhibiting enough nucleotide variability at this taxonomic level. Moreover, gene tree does not necessarily represent the true species tree because of random sorting of polymorphic alleles in different lineages. A solution to these problems is to use many
amplified fragment length polymorphisms (AFLP) distributed throughout the whole genome, to infer cladistic and phenetic among-species relationships. Phylogenetic relationships among interfertile species of Trollius L. (Ranunculaceae) were investigated using nuclear DNA (ITS1 + 5.8S rRNA + ITS2) and chloroplast DNA (trnL intron and trnL-trnF intergene spacer) sequences, and AFLP markers. ITS sequences were not informative at the intrageneric level, but confirmed the sister relationship between Trollius and Adonis genera, and provided new information on the phylogenetic relationships among five Ranunculaceae genera. Chloroplast DNA was more informative among Trollius species, but not consistent with the sections previously described. AFLP proved to be a powerful tool to resolve the complex genetic relationships between the morphological entities constituting the genus Trollius. Although as much as 76.1% of the total AFLP variability was found within a priori defined morphological groups, the remaining 23.9% variability differentiating groups was sufficient to generate congruent and robust cladistic and phenetic trees. Several morphological traits, independent from those used to define groups, were mapped onto the molecular phylogeny, and their evolution discussed in relation to the absence/presence of pollinator-seed parasite Chiastocheta flies.


Genetic data were used to identify Recent species of free-living bryozoans (Cupuladriidae) from both sides of the Isthmus of Panama, and to examine their phylogenetic relationships, species richness, and population structures. An approximately 480 bp fragment of the 16S mitochondrial rRNA gene was sequenced from 182 individuals from Panama, the Gulf of Mexico, and El Salvador. Ten haplotype groups (Cupuladria 4, 5, and 6; Discoporella 1, 2, 3A, 3B, 3C, 7, and 8) were identified. Genetic distances between haplotype groups (3.2-26.5%; K2P + [Gamma]) were 1-2 orders of magnitude greater than within groups (0.1-1.4%). Seven of the haplotype groups represent morphologically distinct species; Discoporellas 3A-C appear to be cryptic species. Phylogenetic analyses identified two pairs of transisthmian sister clades. An average divergence rate derived from other taxa suggests that Cupuladrias 4 and 5 diverged [ap]7 Ma, a Discoporella 7 clade diverged from a 3A-C clade [ap]11 Ma, and the 3A-C clade radiated [ap]6-4 Ma; these events all predated final closure of the isthmus 3 Ma. The Caribbean side of the isthmus, with 5 species, is only marginally richer in cupuladriids than the Pacific side, with 4, but has greater phylogenetic depth. The Caribbean retains lineages stemming from a New World Miocene radiation that are not represented in the eastern Pacific; extant eastern Pacific cupuladriids share most recent common ancestry with only two of the Caribbean lineages. Species in the eastern Pacific tend to show shallow population structures, with high levels of gene flow between geographically separate populations, whereas Caribbean species tend to show deeper populations structures, with indications of restricted gene flow between Bocas del Toro/Gulf of Mosquitos and Costa Arriba/San Blas. The population structures derive from Pleistocene histories and may be of limited value in interpreting the macroevolutionary pattern, as our results provide no evidence of speciation on either side of the isthmus following closure in the late Pliocene.


Studies of Neotropical birds, and their distributions and areas of endemism, in particular, have
been central in the formulation of hypotheses proposed to explain the high species diversity in the Neotropics. We used mtDNA sequence data (ATPase 6 and 8, COI, and cyt b) to reconstruct the species-level phylogenies for two genera, Pionopsitta (Aves: Psittacidae) and Pteroglossus (Aves: Ramphastidae), compare our results with previous morphology-based phylogenetic analyses, and estimate the absolute timing of lineage and biogeographic divergences. Both the Pionopsitta and Pteroglossus phylogenies support a hypothesis of area relationships in which a divergence of the Serra do Mar (Atlantic Forest, Brazil) region of endemism is followed by the divergence of cis- and trans-Andean regions, then a split between the upper and lower Amazon basin, next the divergence of the Guyana area, and finally diversification of taxa in the upper Amazon basin's areas of endemism. Phylogenies of both genera support a hypothesis of area relationships that is similar to that proposed by Prum [XIX International Ornithological Congress (1988), 2562] for high-vagility species, but while they agree on the relative timing of area divergence (vicariance) events, they yield different absolute time estimates for those divergences when the typical avian mtDNA clock calibration is used. Taken at face value, the time estimates indicate that both genera began to diversify before the start of the Pleistocene, and that climatic and habitat shifts alone do not account for the diversification of these taxa.


http://www.sciencedirect.com/science/article/B6WNH-4DXK9Y9-4/2/8c14e9413b8620da324e88fa78947692

Variation in a 252-nucleotide segment of the cytochrome b gene from 26 gibbons is described. DNA was extracted from hair, amplified, and directly sequenced. These sequences represent seven of the nine nominal species and three of the four hylobatid subgenera. Variation was observed at 55 sites, 42 of which are phylogenetically informative. Levels of transitional and transversional divergence between the taxa are similar to those reported for homologous mtDNA sequences in other mammals. Parsimony, maximum likelihood, and bootstrap analyses (1) support some traditional phylogenetic hypotheses (monophyly of the concolor gibbons), (2) suggest previously unrecognized affinities between the lar species group and Hylobates klossi and between H. lar and H. agijs unko, and (3) show that this segment does not contain information sufficient for completely resolving gibbon relationships at the subgeneric level. The study demonstrates the great potential of noninvasive DNA sampling for phylogenetic analyses of mammals.


http://www.sciencedirect.com/science/article/B6WNH-4FFH20D-2/2/f8d7492acf2a57c846109cc68cb80970

The epichloe endophytes are systemic, constitutive, and often vertically transmitted fungal symbionts of grass species in subfamily Pooideae. Prior studies indicate that several asexual epichloe endophytes (Neotyphodium species) have evolved directly from sexual (Epichloe) species, whereas others evolved by hybridization between two or more endophyte species. In this paper, we investigate the phylogenies of 27 Neotyphodium spp. isolates from 10 native grass species (in 4 tribes) in 22 populations throughout Argentina. Relationships among these fungi and a worldwide collection of epichloe endophytes were estimated by phylogenetic analysis of sequences from variable portions (mainly introns) of genes for [beta]-tubulin (tub2) and translation elongation factor 1-[alpha] (tefl). Most of the Argentine endophyte isolates were interspecific hybrids of Epichloe festucae and E. typhina. Only one isolate was a hybrid of a different ancestry,
and three isolates were apparently non-hybrid endophytes. These results indicate that interspecific hybridization, which promotes genetic variation, was common during the evolution of the endophytes of Argentine grasses.


http://www.sciencedirect.com/science/article/B6WNH-4C2NKD5-1/2/91844db8219e55d1830a8d405d8525e0

In recent years we have investigated the evolution of the Holarctic leaf-beetle genus Timarcha using molecular approaches, but to date several important questions remained unanswered, including its systematic arrangement in a temporal context, or the phylogenetic placement of the Nearctic taxa. Here I present a reanalysis of available genetic data together with newly generated data for key taxa (markers 16S rDNA, CO2, ITS-2, and 18S rDNA), including the Nearctic species (subgenus Americanotimarcha), using direct optimization-based phylogenetic reconstructions. Lineage ages are estimated using maximum likelihood branch-length estimates and the molecular clock calibration derived from several presumed vicariance events in the Mediterranean. Phylogenetic analyses and 18S rDNA divergences suggest the ancient divergence of the Nearctic and Palaeartic lineages, related to the North Atlantic opening in the middle Eocene. The diversification of the Palaeartic Timarcha seems closely related to the geological evolution of the Mediterranean area during the Tertiary, with Pleistocenic climate changes affecting species ranges and lineage extinction, but not resulting in extensive speciation.


http://www.sciencedirect.com/science/article/B6WNH-48Y069B-1/2/2e37be624691a1f854385553d1a4aa1d

Tuatara (two species of Sphenodon) are the last representatives of a branch of an ancient reptilian lineage, Sphenodontia, that have been isolated on the New Zealand landmass for 82 million years. We present analyses of geographic variation in allozymes, mitochondrial DNA, nuclear DNA sequences, and one-way albumin immunological comparisons. These all confirm a surprisingly low level of genetic diversity within Sphenodon for such an ancient lineage. We hypothesise a recent extended population bottleneck, probably during the Pliocene/Pleistocene glaciation cycles, to explain the current paucity of variation. All data sets reveal clear genetic differentiation between the northern populations and those in Cook Strait, but offer conflicting views of the history and taxonomic relationships of the Cook Strait population on North Brother Island, currently recognised as Sphenodon guntheri. Allozymes show this population to be the most divergent of all tuatara populations, but preliminary mitochondrial DNA data indicate few differences between S. guntheri and Cook Strait Sphenodon punctatus. Interpretation of the trees is confounded by the lack of a suitable outgroup. As in other cases of conflicting nuclear and mitochondrial data sets, the different data sets likely reveal different aspects of the animals’ evolutionary history, and introgression is not uncommon between species pairs.

Hyvonen, J., S. Koskinen, et al. (2004). "Phylogeny of the Polytrichales (Bryophyta) based on
Phylogenetic analyses of Polytrichales were conducted using morphology and sequence data from the chloroplast genes rbcL and rps4 plus the trnL-F gene region, part of the mitochondrial nad5 and the nuclear-encoded 18S rDNA. Our analyses included 46 species representing all genera of Polytrichales. Phylogenetic trees were constructed with simultaneous parsimony analyses of all sequences plus morphology and separate combinations of sequence data only. Results lend support for recognition of Polytrichales as a monophyletic entity. Oedipodium griffithianum appears as a sister taxon to Polytrichales or as a sister taxon of all mosses excluding Sphagnales and Andreaeales. Within Polytrichales, Alophosia and Atrichopsis, species without the adaxial lamellae (in Atrichopsis present but poorly developed on male gametophyte) otherwise typical of the group are sister to the remaining species followed by a clade including Bartramiopsis and Lyellia, species with adaxial lamellae covering only the central portion of the leaves. Six taxa with an exclusively Southern Hemisphere distribution form a grade between the basal lineages and a clade including genera that are mostly confined to the Northern Hemisphere.


http://www.sciencedirect.com/science/article/B6WNH-49CN2XB-5/2/49a692ddb4c88198c0a1971fa9dd4aa

A phylogeny of 19 of the 22 currently recognized species of Myiarchus tyrant-flycatchers is presented. It is based on 842 bp of mitochondrial DNA (mtDNA) sequences from the ATPase subunit 8 and ATPase subunit 6 genes. Except for the morphologically distinct M. semirufus, mtDNAs of the remaining 18 species fall into either of two clades. One comprises predominantly Caribbean and Central and North American taxa (Clade I), and the other is of predominantly South American taxa (Clade II). The phylogeny is only very broadly concordant with some vocal characters and also with the limited morphological diversity for which the group is well known. Paraphyly in several species (M. swainsoni, M. tuberculifer, M. ferox, M. phaeocephalus, M. sagrae, M. stolidus) suggests that morphological evolution, albeit resulting in limited morphological diversity, has been more rapid than that of mtDNA, or that current taxonomy is faulty, or both. A South American origin for Myiarchus is likely. Dispersal and vicariance both appear to have been involved in generating the present-day distribution of some species. Relatively recent dispersal events out of South America are inferred to have brought species of Clades I and II into broad sympatry. Jamaica has been colonized independently at least twice by members of Clades I and II. The phylogeny brings a historical perspective that in turn suggests that ecological study of closely related species from within each major clade where they are sympatric will be especially rewarding.


http://www.sciencedirect.com/science/article/B6WNH-4CHRY76-1/2/6e102df9ebc94bffc074ddbf3d459d03
Nucleotide sequences of mitochondrial genes (ND1, ND2, COI, and tRNAs) were determined for 38 samples representing 15 taxa of tropidurid lizards from the Galapagos Islands and mainland South America. Phylogenetically informative characters (759 of 1956) were analyzed under Bayesian, maximum likelihood, and parsimony frameworks. This study supports the hypothesis that tropidurid lizards dispersed to the Galapagos on at least two separate occasions. One dispersal event involved an eastern Galapagos clade (Microlophus habelii and M. bivittatus, on Marchena and San Cristobal islands, respectively) the sister taxon of which is M. occipitalis from coastal Ecuador and Peru; the closest mainland relative of the western Galapagos clade was not unambiguously identified. The wide-ranging M. albemarlensis is revealed to be a complex of weakly divergent lineages that is paraphyletic with respect to the insular species M. duncanensis, M. grayii, and M. pacificus.


http://www.sciencedirect.com/science/article/B6WNH-4CPVM0R-1/2/ceac61e394db4e7fae7f4c459ec66f4a

Fishes of the Superorder Osteoglossomorpha (the "bonytongues") constitute a morphologically heterogeneous group of basal teleosts, including highly derived subgroups such as African electric fishes, the African butterfly fish, and Old World knifefishes. Lack of consensus among hypotheses of osteoglossomorph relationships advanced during the past 30 years may be due in part to the difficulty of identifying shared derived characters among the morphologically differentiated extant families of this group. In this study, we present a novel phylogenetic hypothesis for this group, based on the analysis of more than 4000 characters from five molecular markers (the mitochondrial cytochrome b, 12S and 16S rRNA genes, and the nuclear genes RAG2 and MLL). Our taxonomic sampling includes one representative of each extant non-mormyrid osteoglossomorph genus, one representative for the monophyletic family Mormyridae, and four outgroup taxa within the basal Teleostei. Maximum parsimony analysis of combined and equally weighted characters from the five molecular markers and Bayesian analysis provide a single, well-supported, hypothesis of osteoglossomorph interrelationships and show the group to be monophyletic. The tree topology is the following: (Hiodon alosoides, (Pantodon buchholzi, (((Osteoglossum bicirrhosum, Scleropages sp.), (Arapaima gigas, Heterotis niloticus)), ((Gymnarchus niloticus, Ivindomyrus opdenboschi), ((Notopterus notopterus, Chitala ornata), (Xenomystus nigri, Papyrocranus afer))))))). We compare our results with previously published phylogenetic hypotheses based on morpho-anatomical data. Additionally, we explore the consequences of the long terminal branch length for the taxon Pantodon buchholzi in our phylogenetic reconstruction and we use the obtained phylogenetic tree to reconstruct the evolutionary history of electroreception in the Notopteroidei.


http://www.sciencedirect.com/science/article/B6WNH-4DYVPKS-6/2/d24d2bdff5b50478cb857053f28947e5d

We examine the complete nucleotide sequences of the mitochondrial cytochrome oxidase II gene of 13 species of insects, representing 10 orders. The genes range from 673 to 690 by in length, encoding 226 to 229 amino acids. Several insertion or deletion events, each involving one or two codons, can be observed. The 3' end of the gene is extremely variable in both length and sequence, making alignment of the ends unreliable. Using the first 639 nucleotide positions, for
which unambiguous alignments could be obtained, we examine the neighbor-joining trees based on nucleotide divergences and based on conserved subsets of that data, including transversion and amino acid and second codon position divergences. Each of these subsets produces different trees, none of which can be easily reconciled with trees constructed using morphology and the fossil record. Bootstrap analysis using second codon positions strongly supports affinities between the order Blatteria (cockroaches) and the order Isoptera (termites) and between a wasp and the published honeybee sequence (Order Hymenoptera). The divergence of insect orders is very ancient and may have occurred too rapidly for easy resolution using mitochondrial protein sequences. Unambiguous resolution of insect orders will probably require analysis of many additional taxa, using the COII gene and other conserved sequences.


Oriental voles of the genus Eothenomys are predominantly distributed along the Southeastern shoulder of the Qinghai-Tibetan Plateau. Based on phylogenetic analyses of the mitochondrial cytochrome b gene (1143 bp) obtained from 23 specimens (eight species) of Oriental voles collected from this area, together with nucleotide sequences from six specimens (two species) of Japanese red-backed voles (Eothenomys andersoni and Eothenomys smithii) and five species of the closely related genus Clethrionomys, we revised the systematic status of Eothenomys. We also tested if vicariance could explain the observed high species diversity in this area by correlating estimated divergence times to species distribution patterns and corresponding paleogeographic events. Our results suggest that: (1) the eight species of Oriental voles form a monophyletic group with two distinct clades, and that these two clades should be considered as valid subgenera—Eothenomys and Anteliomys; (2) Eothenomys eleusis and Eothenomys miletus are not independent species; (3) Japanese red-backed voles are more closely related to the genus Clethrionomys than to continental Asian Eothenomys taxa; and (4) the genus Clethrionomys, as presently defined, is paraphyletic. In addition, the process of speciation of Oriental voles appears to be related to the Trans-Himalayan formation via three recent uplift events of the Qinghai-Tibetan Plateau within the last 3.6 million years, as well as to the effects of the mid-Quaternary ice age.


To better understand the evolutionary history of the genus Centaurium and its relationship to other genera of the subtribe Chironiinae (Chironieae: Gentianaceae), molecular analyses were performed using 80 nuclear ribosomal ITS and 76 chloroplast trnLF (both the trnL UAA intron and the trnL-F spacer) sequences. In addition, morphological, palynological, and phytochemical characters were included to a combined data matrix to detect possible non-molecular synapomorphies. Phylogenetic reconstructions support the monophyly of the Chironiinae and an age estimate of ca. 22 million years for the subtribe. Conversely, both molecular data sets reveal a polyphyletic Centaurium, with four well-supported main clades hereafter treated as separate genera. The primarily Mediterranean Centaurium s.s. is closely related to southern African endemics Chironia and Orphium, and to the Chilean species Centaurium cachanlahuen. The
resurrected Mexican and Central American genus Gyrandra is closely related to Sabatia (from eastern North America). Lastly, the monospecific genus Exaculum (Mediterranean) forms a monophyletic group together with the two new genera: Schenkia (Mediterranean and Australian species) and Zeltnera (all other indigenous American centauries). Several biogeographical patterns can be inferred for this group, supporting a Mediterranean origin followed by dispersals to (1) North America, Central America, and South America, (2) southern Africa (including the Cape region), and (3) Australia and Pacific Islands.


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http://www.sciencedirect.com/science/article/B6WNH-4698TKT-G/2/0fb9bf50aed09e6c4f9518016b4fb7e0


http://www.sciencedirect.com/science/article/B6WNH-4894317-1/2/14a8677a2ae2e3967cd007c7f17b3092

The phylogenetic relationships of the members of the phylum Sipuncula are investigated by means of DNA sequence data from three nuclear markers, two ribosomal genes (18S rRNA and the D3 expansion fragment of 28S rRNA), and one protein-coding gene, histone H3. Phylogenetic analysis via direct optimization of DNA sequence data using parsimony as optimality criterion is executed for 12 combinations of parameter sets accounting for different indel costs and transversion/transition cost ratios in a sensitivity analysis framework. Alternative outgroup analyses are also performed to test whether they affected rooting of the sipunculan topology. Nodal support is measured by parsimony jackknifing and Bremer support values. Results from the different partitions are highly congruent, and the combined analysis for the parameter set that minimizes overall incongruence supports monophyly of Sipuncula, but nonmonophyly of several higher taxa recognized for the phylum. Mostly responsible for this is the split of the family Sipunculidae in three main lineages, with the genus Sipunculus being the sister group to the remaining sipunculans, the genus Phascolopsis nesting within the Golfingiiformes, and the genus Siphonosoma being associated to the Phascolosomatidea. Other interesting results are the position of Phascolion within Golfingiidae and the position of Antillesoma within Aspidosiphonidae. These results are not affected by the loci selected or by the outgroup chosen. The position of Apionsoma is discussed, although more data would be needed to better ascertain its phylogenetic affinities. Monophyly of the genera with multiple representatives (Themiste, Aspidosiphon, and Phascolosoma) is well supported, but not the monophyly of the genera
Nephasoma or Golfingia. Interesting phylogeographic questions arise from analysis of multiple representatives of a few species.


http://www.sciencedirect.com/science/article/B6WNH-470M3Y9-1/2/79ecefc87b39a47604f03bfa1025d1fb

The species of thrips found on Acacia constitute a major component of the Australian thrips fauna, with at least 235 species in more than 30 genera, many of these being in the process of description as new. These thrips exhibit social behaviours, ranging from solitary and colonial species to a variety of more complex social organisations. Furthermore, the domiciliary habits of these species include domicile construction, gall induction, and opportunistic use of abandoned galls and domiciles. This suite of thrips also includes a variety of inquiline and kleptoparasitic taxa. To understand how these various traits have evolved and interact in this diverse group, we have reconstructed a phylogeny for 42 species of thrips associated with Acacia around Australia. We obtained DNA sequence data from two nuclear genes (Elongation Factor-1[alpha] and wingless) and one mitochondrial gene (cytochrome oxidase I) and analysed these using maximum parsimony and maximum likelihood methods. A phylogeny resulting from such analysis allows inference of evolutionary transitions in domiciliary habits, social organisations, and parasitic behaviours. Gall induction and parasitic behaviour are postulated to each have a single origin, with no losses of either trait. Once parasitism evolved a remarkable radiation followed that allowed exploitation of very diverse hosts. Our data do not allow hypotheses of single versus multiple origins of domicile building to be resolved while opportunistic gall use appears to have arisen several times.


http://www.sciencedirect.com/science/article/B6WNH-49CN2XB-2/2/d5feac373ac0f96efc1b2459d5287e21

A common challenge in reconstructing phylogenies involves a high frequency of short internal branches, which makes basal relationships difficult to resolve. Often it is not clear whether this pattern results from insufficient or inappropriate data, versus from a rapid evolutionary radiation. The snapping shrimp genus Synalpheus, which contains in excess of 100 species and is a prominent component of coral-reef faunas worldwide, provides an example. Its taxonomy has long been problematic due to the subtlety of diagnostic characters and apparently widespread variability within species. Here we use partial mt COI and 16S rRNA sequences and morphological characters to reconstruct relationships among 31 species in the morphologically well-defined gambarelloides species group, a putative clade of obligate sponge associates that is mostly endemic to the Caribbean and contains the only known eusocial marine animals. Analysis of the combined data produced a single tree with good support for many terminal clades and for relationships with outgroups, but poor support for branches near the base of the gambarelloides group. Most basal branches are extremely short and terminal branches are long, suggesting a relatively ancient, but rapid radiation of the gambarelloides group. This hypothesis is supported by significant departure from a null model of temporally random cladogenesis. Calibration of divergence times among gambrelloides-group species using data from three geminate pairs of Synalpheus species separated by the isthmus of Panama suggests a major radiation between ~5 and 7 Mya, a few My before final closure of the Panamanian seaway during a period of spreading
carbonate environments in the Caribbean; a second, smaller radiation occurred ~4 Mya. This molecular evidence for a rapid radiation among Caribbean marine organisms in the late Miocene/early Pliocene is strikingly similar to patterns documented from fossil data for several other Caribbean reef-associated invertebrate taxa. The similar patterns and timing of cladogenesis evidenced by molecular and fossil data for different Caribbean and East Pacific taxa suggests that the radiation involved a wide range of organisms, and strengthens the case that poor basal resolution in the gambarelloides group of Synalpheus reflects a real evolutionary phenomenon. The rapid radiation also helps explain the historical difficulty of diagnosing species in Synalpheus.


We sequenced nearly the entire carbomoyl phosphate synthase (CPS) domain of CAD, or rudimentary, (ca. 4 kb) from 29 species of flies representing all major clades within Eremoneura, or higher flies, and several orthorrhaphous brachyceran outgroups. We compared these sequences with orthologs from Anopheles gambiae and Drosophila melanogaster to assess structure, compositional bias, and phylogenetic utility. CAD is large (6.6+ kb), complex (comprised of three major and myriad minor functional domains) and relatively free of introns, extreme nucleotide bias (except third codon positions), and large hypervariable regions. The CPS domain possesses moderate levels of nonsynonymous divergence among taxa of intermediate evolutionary age and conveys considerable phylogenetic signal. Phylogenetic analysis of CPS sequences under varying methods and assumptions resulted in well-resolved, strongly supported trees concordant with many traditional ideas about higher dipteran phylogeny and with prior inferences from 28S rDNA. The most robustly supported major eremoneuran clades were Cyclorrhapha, Platypezoidea, Eumuscomorpha, Empidoidea, Atelestidae, Empidoidea exclusive of Atelestidae, Hybotidae s.l., Microphoridae + Dolichopodidae, and Empididae s. str. Because CAD is ubiquitous, apparently single copy (at least within holometabolous insects), readily obtained from several insect orders using primers described herein, and exhibits considerable phylogenetic utility, it should have wide applicability in insect molecular systematics.


Large subunit ribosomal DNA (LSU rDNA) sequence data from 120 taxa and cytochrome oxidase subunit 1 (COI) sequence data from 27 taxa are analyzed separately and together to estimate the internal phylogeny of the class Demospongiae and to evaluate how consistent these data are with pre-existing hypotheses of relationship concerning order-level monophyly and relationships. The monophyly of Porifera is only slightly inconsistent with LSU data, which do not support the monophyly of the class Demospongiae regardless of the inclusion or exclusion of Homoscleromorpha (this result is likely due to the placement of a single hexactinellid taxon within the Demospongiae), however, no LSU support is found for the monophyly of Silicea (Demospongiae + Hexactinellida) unless homoscleromorphs are excluded. Neither the subclasses Ceractinomorpha and Tetractinomorpha, nor the orders Halichondrida, Hadromerida,
and Haplosclerida are supported as monophyletic under any data partition. The haplosclerid suborders Haplosclerina and Petrosina are supported as monophyletic to the exclusion of the suborder Spongillina, and the orders Dictyoceratida, Verongida, Poecilosclerida, Astrophorida, Spirophorida, Homosclerophorida, and Agelasida are largely reconstructed as monophyletic, with the exception of few anomalously placed taxa. Few inter-order relationships are strongly supported by any data partition, but there is moderate support for a verongid + chondrosid clade and a tetractinellid + halichondrid clade. Furthermore, LSU data strongly support the existence of two novel clades that do not correspond to the existing classification and that show no morphological uniformity. Finally, every data partition supports the monophyly of a clade that includes the order Agelasida, some members of the genus Axinella, and two taxa tentatively identified as belonging to the orders Hadromerida and Halichondrida.


http://www.sciencedirect.com/science/article/B6WNH-48GF21T-K/2/a44881d415a6bb4987ee8aa137a63be8

A homeotic gene, LEAFY, has been suggested to be a single-copy gene in diploid angiosperms. Nucleotide sequences of the second intron of this gene, along with those of several regions of the chloroplast genome (tmL-tmF, tmD-tmY-tmE-tmT, and matK-tmK) and nuclear ribosomal ITS, were obtained from the species of Neillia and Stephanandra to examine the phylogenetic utility of the intron and to elucidate the phylogenetic relationships among species of the two genera. PCR amplification of the second intron of LEAFY using universal degenerate primers produced PCR products in sufficient quantity for successful direct sequencing. The length of the intron ranged from 591 to 622 base pairs (bp) in Neillia and Stephanandra, except in N. thibetica (ca. 1370 bp), and sequence analysis of this region from multiple accessions revealed low levels of infraspecific variation. Comparison of the LEAFY data with ITS and cpDNA data demonstrated that the LEAFY intron was the most variable and useful for phylogenetic analysis at the species level, providing many more phylogenetically informative characters per 100 bp (7.4) than either ITS (3.2) or cpDNA (0.7). Phylogenetic analyses of LEAFY data using both maximum parsimony and likelihood methods generated well supported and highly resolved gene trees with few homoplasies (CI=0.97). Stephanandra is monophyletic and is nested within Neillia in both LEAFY and cpDNA trees, while the relationship is poorly resolved by ITS data. LEAFY and cpDNA data, however, strongly conflicted with respect to the position of Stephanandra: LEAFY trees placed Stephanandra as sister to the ((N. affinis, N. gracilis), N. thyrsiflora) clade whereas cpDNA data suggested Stephanandra is sister to N. uekii. Both gene trees, however, are nearly identical to each other when Stephanandra is excluded. A hybrid origin of Stephanandra is suggested as a plausible hypothesis to explain the incongruence between LEAFY and cpDNA data sets, though gene duplication/loss and lineage sorting events cannot be ruled out as possibilities.


http://www.sciencedirect.com/science/article/B6WNH-46RD1H5-1/2/4bf7fbe07bc70e7c2c0724472c26ff56

We constructed phylogenetic hypotheses for Mesoamerican Rhamdia, the only genus of primary freshwater fish represented by sympatric species across Central America. Phylogenetic relationships were inferred from analysis of 1990 base pairs (bp) of mitochondrial DNA (mtDNA),
represented by the complete nucleotide sequences of the cytochrome b (cyt b) and the ATP synthase 8 and 6 (ATPase 8/6) genes. We sequenced 120 individuals from 53 drainages to provide a comprehensive geographic picture of Central American Rhamdia systematics and phylogeography. Phylogeographic analysis distinguished multiple Rhamdia mtDNA lineages, and the geographic congruence across evolutionarily independent Rhamdia clades indicated that vicariance has played a strong role in the Mesoamerican diversification of this genus. Phylogenetic analyses of species-level relationships provide strong support for the monophyly of a trans-Andean clade of three evolutionarily equivalent Rhamdia taxa: R. guatemalensis, R. laticauda, and R. cinerascens. Application of fish-based mitochondrial DNA clocks ticking at 1.3-1.5% sequence divergence per million years (Ma), suggests that the split between cis- and trans-Andean Rhamdia extends back about 8 Ma, and the three distinct trans-Andean Rhamdia clades split about 6 Ma ago. Thus the mtDNA divergence observed between cis- and trans-Andean Rhamdia species is too low to support an ancient colonization of Central America in the Late Cretaceous or Paleocene as had been hypothesized in one colonization model for Mesoamerican fishes. Rather the mtDNA data indicate that Rhamdia most likely colonized Central America in the late Miocene or Pliocene, promoting a strong role for the Isthmus of Panama in the Mesoamerican expansion of this genus. Basal polytomies suggest that both the R. laticauda and R. guatemalensis clades spread rapidly across the Central American landscape, but differences in the average mtDNA genetic distances among clades comprising the two species, indicate that the R. laticauda spread and diversified across Mesoamerica about 1 million years before R. guatemalensis.


http://www.sciencedirect.com/science/article/B6WNH-4C5HRR5-1/2/3e347039028d538cfe2b3153047698e0

This paper focuses on the phylogenetic relationships of eight North American caenophidian snake species (Carphophis amoena, Contia tenuis, Diadophis punctatus, Farancia abacura, Farancia erythrogramma, Heterodon nasicus, Heterodon platyrhinos, and Heterodon simus) whose phylogenetic relationships remain controversial. Past studies have referred to these “relict” North American snakes either as colubrid, or as Neotropical dipsadids and/or xenodontids. Based on mitochondrial DNA ribosomal gene sequences and a likelihood-based Bayesian analysis, our study suggests that these North American snakes are not monophyletic and are nested within a group (Dipsadoidea) that contains the Dipsadidae, Xenodontidae, and Natricidae. In addition, we use the relationships proposed here to highlight putative examples of parallel evolution of hemipenial morphology among snake clades.


http://www.sciencedirect.com/science/article/B6WNH-49M0ND6-1/2/87fb955d1c9b8609a6d0f53dcc32b97a

Plant resistance to many types of pathogens and pests can be achieved by the presence of disease resistance (R) genes. The nucleotide binding site-leucine rich repeat (NBS-LRR) class of R-genes is the most commonly isolated class of R-genes and makes up a super-family, which is often arranged in the genome as large multi-gene clusters. The NBS domain of these genes can be targeted by polymerase chain reaction (PCR) amplification using degenerate primers.
Previous studies have used PCR derived NBS sequences to investigate both ancient R-gene evolution and recent evolution within specific plant families. However, comparative studies with the Asteraceae family have largely been ignored. In this study, we address recent evolution of NBS sequences within the Asteraceae and extend the comparison to the Arabidopsis thaliana genome. Using multiple sets of primers, NBS fragments were amplified from genomic DNA of three species from the family Asteraceae: Helianthus annuus (sunflower), Lactuca sativa (lettuce), and Cichorium intybus (chicory). Analysis suggests that Asteraceae species share distinct families of R-genes, composed of genes related to both coiled-coil (CC) and toll-interleukin-receptor homology (TIR) domain containing NBS-LRR R-genes. Between the most closely related species, (lettuce and chicory) a striking similarity of CC subfamily composition was identified, while sunflower showed less similarity in structure. These sequences were also compared to the A. thaliana genome. Asteraceae NBS gene subfamilies appear to be distinct from Arabidopsis gene clades. These data suggest that NBS families in the Asteraceae family are ancient, but also that gene duplication and gene loss events occur and change the composition of these gene subfamilies over time.


http://www.sciencedirect.com/science/article/B6WNH-4CJ46KB-1/2/c3fb43da1314a188e6d1e66fcdabaaf2

In order to delimit and understand the evolution of the Meteoriaceae, we provide phylogenetic analyses using the internal transcribed spacer 2 (ITS2) of nuclear ribosomal DNA in combination with two plastid markers, trnL-F and psbT-H. In contrast to the widely used trnL-F region, the psbT-H gene cluster, coding for proteins of photosystem II, has been rarely used to address systematic questions among the different land plant lineages. To overcome the problem of potential ambiguous alignments of non-coding DNA regions, the data were independently analyzed using direct optimization. The comparison and evaluation of the obtained results showed that the inferred cladograms based on the different phylogenetic approaches are very similar, with only minor differences. In combination with morphological characters, generic relationships as well as taxonomic and nomenclatural problems, especially regarding the key genera Meteorium and Papillaria are discussed in detail. New insights into generic relationships of the Meteoriaceae are provided, such as the exclusion of the monospecific southern South American genera Ancistrodes and Cryphaeophilum, which are subsequently transferred to the Hookeriaceae and Cryphaeaceae, respectively. Phylogenetic reconstructions using maximum likelihood as well as parsimony approaches reveal that at the familial level the Meteoriaceae s. l. are polyphyletic, if the formerly recognized "Trachypodaceae" are considered as a separate family. Based on our results we favor the synonym of the Trachypodaceae with the Meteoriaceae.


http://www.sciencedirect.com/science/article/B6WNH-49M0ND6-2/2/16716c181922f3479428cedc5bde9ece

Damselfishes in the family Pomacentridae represent one of the few families of reef fishes found on coral reefs irrespective of location. At a local scale, damselfishes are often the most abundant coral reef fish, and their study has provided much of our current understanding of the ecology of tropical reef animals. The study of phylogenetic relationships among the Pomacentridae has lagged ecological investigation of the group, thus limiting historical perspective on the remarkable
species richness of the family. In this study, we used 1989 bp of DNA sequence representing three mitochondrial genes and 1500 bp of the single copy nuclear RAG1 region to infer hypotheses of relationship for the group. Our analysis includes 103 Pomacentridae species in 18 genera, and three of the four named subfamilies: Amphiprioninae, Chromisinae, and Pomacentrinae. The Bayesian method of phylogenetic reconstruction was applied to the data, because even with a large number of sequences it is an efficient means of analysis that provides intuitive measures of support for tree topologies and for the parameters of the nucleotide substitution model. Four Pomacentridae clades were identified with high statistical support whether the data were analyzed from a mtDNA, RAG1 or combined perspective, and in all analyses the current subfamilial classification of the Pomacentridae was rejected. At the genus level, Amphiprion, Chromis, and Chrysiptera were also rejected as natural groups. Abudefduf, Amblyglyphidodon, Dascyllus, Neoglyphidodon, Neopomacentrus, and Pomacentrus were each strongly supported as monophyletic genera but the support for monophyly is nonetheless compromised by sample size, except in the case of Dascyllus and Abudefduf for which we have sampled almost all of the described species.


The role of natural hybridization and introgression as part of the evolutionary process is of increasing interest to zoologists, particularly as more examples of gene exchange among species are identified. We present mitochondrial and nuclear sequence data for Hyalomma dromedarii, Hyalomma truncatum, and Hyalomma marginatum rufipes (Acari: Ixodidae) collected from one-humped camels in Ethiopia. These species are well differentiated morphologically and genetically; sequence data from the mitochondrial DNA (mtDNA) cytochrome oxidase I gene indicates 10-14% divergence between the species. However, incongruence between morphology and the mtDNA phylogeny was observed, with multiple individuals of H. dromedarii and H. truncatum present on the same mtDNA lineage as H. marginatum rufipes. Thus, individuals with morphology of H. dromedarii and H. truncatum are indistinguishable from H. marginatum rufipes on the basis of mtDNA. Multiple copies of ITS-2 were subsequently cloned and sequenced for a subset of individuals from the mtDNA phylogeny, representing both 'normal' and 'putative hybrid' individuals. Very low sequence divergence (0.3%) was observed within 'normal' individuals of both H. dromedarii and H. truncatum relative to the 'putative hybrid' individuals (6 and 2.7%, respectively). The pattern of intra-individual variation in ITS-2 within 'putative hybrid' individuals, particularly in H. dromedarii, strongly suggests that gene flow has occurred among these Hyalomma species, but no indication of this is given by the morphology of the individuals.


Ants are one of the most ecologically and numerically dominant families of organisms in almost every terrestrial habitat throughout the world, though they include only about 1% of all described insect species. The development of eusociality is thought to have been a driving force in the striking diversification and dominance of this group, yet we know little about the evolution of the major lineages of ants and have been unable to clearly determine their primitive characteristics.
Ants within the subfamily Amblyoponinae are specialized arthropod predators, possess many anatomically and behaviorally primitive characters and have been proposed as a possible basal lineage within the ants. We investigate the phylogenetic relationships among the members of the subfamily, using nuclear 28S rDNA sequence data. Outgroups for the analysis include members of the poneromorph and leptanillomorph (Apomyrma, Leptanilla) ant subfamilies, as well as three wasp families. Parsimony, maximum likelihood, and Bayesian analyses provide strong support for the monophyly of a clade containing the two genera Apomyrma + Mystrium (100% bpp; 97% ML bs; and 97% MP bs), and moderate support for the monophyly of the Amblyoponinae as long as Apomyrma (Apomyrminae) is included (87% bpp; 57% ML bs; and 76% MP bs). Analyses did not recover evidence of monophyly of the Amblyopone genus, while the monophyly of the other genera in the subfamily is supported. Based on these results we provide a morphological diagnosis of the Amblyoponinae that includes Apomyrma. Among the outgroup taxa, Typhlomyrmex grouped consistently with Ectatomma, supporting the recent placement of Typhlomyrmex in the Ectatomminae. The results of this present study place the included ant subfamilies into roughly two clades with the basal placement of Leptanilla unclear. One clade contains all the Amblyoponinae (including Apomyrma), Ponerinae, and Proceratiinae (Poneroid clade). The other clade contains members from subfamilies Cerapachyinae, Dolichoderinae, Ectatomminae, Formicinae, Myrmeciinae, and Myrmicinae (Formicoid clade).


Mycetomal organs attached to the esophagus of hematophagous leeches which are known to harbor endosymbiotic bacteria were removed from three species in the leech family Glossiphoniidae. Anatomical observations indicated that placobdellid mycetomes are paired and caecate, inserting into the esophagus posterior to the proboscis. Light and electron microscopy demonstrated that there is a single layer of mycetome epithelial cells harboring Gram-negative rods and that these epithelial cells are ultrastructurally distinct from neighboring esophageal epithelial cells. Fluorescent in situ hybridization with eubacterial and alphaproteobacterial probes localized the bacteria solely to the mycetomes both in adult and in unfed juvenile leeches whereas a gammaproteobacterial probe did not yield a bound fluorescent signal. DNA was isolated from these tissues and subjected to PCR amplification using bacteria-specific primers for 16S and 23S rDNA. Results from sequencing the amplification products and phylogenetic analysis with other Alphaproteobacteria revealed that the bacteria resident in these organs comprise a new genus of Alphaproteobacteria, Reichenowia n. gen., closely related to the nitrogen-fixing, nodule-forming Rhizobiaceae. The three bacterial strains, though different from each other were each other's closest relatives, suggesting a history of close coevolution with their leech hosts.


http://www.sciencedirect.com/science/article/B6WNH-47HK3HT-5/2/7c38c4e76fafa0797640536304f7b10

The Platyrhini, or New World monkeys, are an infraorder of Primates comprised of 16 genera. Molecular phylogenetic analyses have consistently sorted these genera into three groups: the Pitheciidae (e.g., saki and titi monkeys), Atelidae (e.g., spider and howler monkeys), and Cebidae
(e.g., night monkeys, squirrel monkeys, and tamarins). No consensus has emerged on the relationships among the three groups or within the Cebidae. Here, ~0.8 kb of newly generated intronic DNA sequence data from the X-linked glucose-6-phosphate dehydrogenase (G6PD) locus have been collected from nine New World monkey taxa to examine these relationships. These data are added to 1.3 kb of previously generated G6PD intronic DNA sequence data [Mol. Phylogenet. Evol. 11 (1999) 459]. Using distance and parsimony-based techniques, G6PD sequences provide support for an initial bifurcation between the Pitheciidae and the remaining platyrrhines, linking Atelidae and Cebidae as sister taxa. Bayesian methods provided a conflicting phylogeny with Atelidae as outgroup. Within the Cebidae, a sister relation between Aotus and the Cebus/Saimiri clade is favored by parsimony analysis, but not by other analyses. Potential reasons for the difficulty in resolving family level New World monkey phylogenetics are discussed.


http://www.sciencedirect.com/science/article/B6WNH-4967F2T-2/2/48f4439f6e122d16606e39f6dfdd9ed0f

Although the family Sciuridae is large and well known, phylogenetic analyses are scarce. We report on a comprehensive molecular phylogeny for the family. Two nuclear genes (c-myc and RAG1) comprising approximately 4500 bp of data (most in exons) are applied for the first time to rodent phylogenetics. Parsimony, likelihood, and Bayesian analyses of the separate gene regions and combined data reveal five major lineages and refute the conventional elevation of the flying squirrels (Pteromyinae) to subfamily status. Instead, flying squirrels are derived from one of the tree squirrel lineages. C-myc indels corroborate the sequence-based topologies. The common ancestor of extant squirrels appears to have been arboreal, confirming the fossil evidence. The results also reveal an unexpected clade of mostly terrestrial squirrels with African and Holarctic centers of diversity. We present a revised classification of squirrels. Our results demonstrate the phylogenetic utility of relatively slowly evolving nuclear exonic data even for relatively recent clades.


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http://www.sciencedirect.com/science/article/B6WNH-47S6M2C-2/2/e7535d0f07bc07da50e3c06f69281281

The phylogeny of groups within Gobioidei is examined with molecular sequence data. Gobioidei is a speciose, morphologically diverse group of teleost fishes, most of which are small, benthic, and marine. Efforts to hypothesize relationships among the gobiod group have been hampered by the prevalence of reductive evolution among goby species; such reduction can make identification of informative morphological characters particularly difficult. Gobies have been
variously grouped into two to nine families, several with included subfamilies, but most existing
taxonomies are not phylogenetic and few cladistic hypotheses of relationships among goby
groups have been advanced. In this study, representatives of eight of the nine gobioi families
(Eleotridae, Odontobutidae, Xenisthmidae, Gobiidae, Kraemeriidae, Schindleriidae,
Microdesmidae, and Ptereleotridae), selected to sample broadly from the range of goby diversity,
were examined. Complete sequence from the mitochondrial ND1, ND2, and COI genes (3573 bp)
was used in a cladistic parsimony analysis to hypothesize relationships among the gobioi
groups. A single most parsimonious topology was obtained, with decay indices indicating strong
support for most nodes. Major phylogenetic conclusions include that Xenisthmidae is part of
Eleotridae, and Eleotridae is paraphyletic with respect to a clade composed of Gobiidae,
Microdesmidae, Ptereleotridae, Kraemeriidae, and Schindleriidae. Within this five-family clade,
two clades are recovered. One includes Gobionellinae, which is paraphyletic with respect to
Kraemeriidae, Sicydiinae, Oxudercinae, and Amblyopinae. The other contains Gobiinae, also
paraphyletic, and including Microdesmidae, Ptereleotridae, and Schindleriidae. Previous
morphological evidence for goby groupings is discussed; the phylogenetic hypothesis indicates
that the morphological reduction observed in many goby species has been derived several times
independently.

reveals a diversity of co-infecting Wolbachia strains in Acromyrmex leafcutter ants." Molecular

http://www.sciencedirect.com/science/article/B6WNH-475B9D7-3/2/0bbab6a302941e820c97890b65266546

reconstruction of recently diverged lineages in Mitthyridium (Muscic: Calymperaceae)." Molecular

http://www.sciencedirect.com/science/article/B6WNH-46WNYGM-3/2/daef3b413ab5e1d0d2843c69bb6296dd

A portion of the nuclear gene glyceraldehyde 3-phosphate dehydrogenase (gpd) was sequenced
in 26 representatives of the paleotropical moss, Mitthyridium, and a group of 20 outgroup taxa to
assess its utility for phylogenetic reconstruction compared with the better understood chloroplast
markers, rps4 and trnL. Primers based on plant and fungal sequences were designed to amplify
gpd in plants universally with the exclusion of fungal contaminants. The piece amplified spanned
4 introns and 3 of 9 exons, based on comparisons with complete sequence from Arabidopsis.
Size variation in gpd ranged from 891 to 1007 bp, in part attributable to 6 indels of variable length
found within the introns. Intron 6 contributed most of the length variation and contained a variable
purine-repeat motif of possible use as a microsatellite. Phylogenetic analyses of the full gpd
amplicon yielded well-resolved trees that were in nearly full accord with the trees derived from the
cpDNA partitions for analyses of both the ingroup and ingroup + outgroup taxon sets. Pairwise
nucleotide substitution rates of gpd were as much as 2.2 times higher than those in rps4 and 2.8
times higher than in trnL. Excision of the introns left suitable numbers of parsimony informative
characters and demonstrated that the full gpd amplicon could be compartmentalized to provide
resolution for both shallow and deep phylogenetic branches. Exons of gpd were found to behave
in a clock-like fashion for the 26 ingroup taxa and select outgroups. In general, gpd was found to
hold great promise not only for improving resolution of chloroplast-derived phylogenies, but also
for phylogenetic reconstruction of recent, diversifying lineages.
Sigmodontine rodents are the most diverse family-level mammalian clade in the Neotropical region, with about 70 genera and 320 recognized species. Partial sequences (1266 bp) from the first exon of the nuclear gene encoding the Interphotoreceptor Retinoid Binding Protein (IRBP) were used to infer the phylogenetic relationships among 44 species representing all 16 currently recognized genera of the largest sigmodontine tribe, the Oryzomyini. Monophyly of the tribe was assessed relative to 15 non-oryzomyine sigmodontine taxa representing all major sigmodontine lineages. Twelve taxa from seven muroid subfamilies were used as outgroups. The resulting matrix included 71 taxa and 386 parsimony-informative characters. Phylogenetic analysis of this matrix resulted in 16 equally parsimonious cladograms, which contained the following well-supported groups: (i) a monophyletic Oryzomyini, (ii) a clade containing all oryzomyines except Scolomys and Zygodontomys, (iii) a clade containing Oecomys, Handleymys, and several species of forest-dwelling Oryzomys, and (iv) a clade containing the remaining oryzomyine taxa. The last clade is composed of two large subclades, each with lower nodal support, containing the following taxa: (i) Microryzomys, Oligoryzomys, Neacomys, and Oryzomys balneator; (ii) Holochilus, Lundomys, Pseudoryzomys, Nectomys, Amphinectomys, Sigmodontomys, and several species of open-vegetation or semiaquatic Oryzomys. Regarding relationships among non-oryzomyine taxa, sigmodontines, neotomines, and tylomyines do not form a monophyletic group; a clade containing Rheomys and Sigmodon is basal relative to all other sigmodontines; and the remaining sigmodontines are grouped in three clades: the first containing Thomasomyni, Akodontini, and Reithrodon; the second containing Abrothrichini, and Phyllotini, plus Wiedomys, Juliomys, Irenomys, and Delomys; and the third containing the oryzomyines. No conflict is observed between IRBP results and previous robust hypotheses from mitochondrial data, while a single case of incongruence is present between the IRBP topology and robust hypothesis from morphological studies.

http://www.sciencedirect.com/science/article/B6WNH-48FK4VN-1/2/b9140e4a7cf75e4f5c9a8d95913e23c6

A molecular phylogeny is presented for the subfamily Littorininae (including representatives of all subgeneric taxa and all members of a group of southern-temperate species formerly classified as 'Nodilittorina'), based on sequence data from two nuclear (18S rRNA, 28S rRNA) and two mitochondrial (12S rRNA, CO1) genes. The phylogeny shows considerable disagreement with earlier hypotheses derived from morphological data. In particular, 'Nodilittorina' is polyphyletic and is here divided into four genera (Echinolittorina, Austrolittorina, Afrolittorina new genus, and the monotypic Nodilittorina s.s.). The phylogenetic relationships of 'Littorina' striata have been controversial and it is here transferred to the genus Tectarius, a surprising relationship for which there is little morphological support. The relationships of the enigmatic Mainwaringia remain poorly resolved, but it is not a basal member of the subfamily. The two living species of Mainwaringia are remarkable for a greatly elevated rate of evolution in all four genes examined; it is suggested that this may be connected with their protandrous hermaphroditism, which is unique in the family. The molecular phylogeny provides a new framework for the adaptive radiation of the Littorininae, showing more frequent shifts between habitats and climatic regimes than previously suspected, and striking parallelism of morphological characters. The fossil record of littorinids is poor, but ages of clades are estimated using a calibration based on a Lower Eocene age of the genus Littoraria. Using these estimates, the antitropical distribution of Littorina and Afrolittorina is an ancient pattern of possibly Cretaceous age. The five members of Austrolittorina show a Gondwanan distribution in Australia, New Zealand, and South America. Based on the morphological uniformity within this clade, relatively recent (Plio-Pleistocene) trans-Pacific dispersal events seemed a likely explanation, as proposed for numerous other congeneric marine taxa. However, molecular estimation of ages of divergence suggest an initial vicariance between Australian and South American lineages at 40-73 Ma, contemporary with the later stages of fragmentation of the Gondwanan supercontinent, followed by more recent (but still mid-Cenozoic) dispersal events across the Tasman Sea and the Pacific Ocean. Afrolittorina is another Cretaceous clade, now restricted to southern Africa and southern Australia, but divergence between these lineages (29-55 Ma) post-dates Gondwanan fragmentation. Within both Austrolittorina and Afrolittorina all sister-species divergences are estimated to fall in the range 10-47 Ma, so that there is no evidence for speciation events in the Plio-Pleistocene.


http://www.sciencedirect.com/science/article/B6WNH-4CT5YFS-4/2/87b46543eff7302df012b11c010371d0

DNA sequencing studies of the granule-bound starch synthase gene (GBSSI) indicate the presence of two loci in Viburnum. Gene trees from separate and combined phylogenetic analyses of the GBSSI paralogues are generally congruent with each other and with trees from previous analyses, especially those of Donoghue et al. [Syst. Bot. 29 (2004) 188] based on nuclear ribosomal ITS and chloroplast trnK intron DNA sequences. Specifically, our GBSSI trees confirm (i) the monophyly of some and non-monophyly of other traditionally recognized taxonomic sections, (ii) the presence of three major supra-sectional lineages within Viburnum, and (iii) the resolution of many species relationships within the section-level clades. Analyses of GBSSI also provide greater resolution of relationships within the largest supra-sectional lineage. Relationships at the base of the Viburnum phylogeny remain uncertain; in particular, the position of the root, relationships among the supra-sectional clades, and the exact placement of several
smaller groups (e.g., Viburnum clemensiae, Viburnum urceolatum, and section Pseudotinus). In two lineages each GBSSI paralogue is represented by two distinct sequences. The presence of additional copies appears to be correlated with polyploidy in these clades. Placement of the homoeologues in our gene trees suggests the possibility of a hybrid origin for these polyploids.


http://www.sciencedirect.com/science/article/B6WNH-49H1KWC-1/2/deae7d1c950b45c0a903f2f56914abad

Nucleotide sequences of the spacer region of the histone gene H2A-H2B from 36 species of Drosophila melanogaster species group were determined. The phylogenetic trees were reconstructed with maximum parsimony, maximum likelihood, and Bayesian methods by using Drosophila pseudoobscura as the out group. Our results show that the melanogaster species group clustered in three main lineages: (1) montium subgroup; (2) ananassae subgroup; and (3) the seven oriental subgroups, among which the montium subgroup diverged first. In the third main lineage, suzukii and takahashii subgroups formed a clade, while eugracilis, melanogaster, elegans, ficusphila, and rhopaloa subgroups formed another clade. The bootstrap values at subgroup levels are high. The phylogenetic relationships of these species subgroups derived from our data are very different from those based on some other DNA data and morphology data.