

Molecular Phylogeny And Homology Debates

Compiled By Paul Nethercott

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**Amphibians
Birds
Bivalves
Cephalopods
Crustaceans
Echinoderms And Crinoids
Eukaryotes And Protozoa
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Amphibians

Amphibians

1. The Appendicular Skeleton, By Kat Pawley

There has been much **debate** over the last two decades involving temnospondyls, concerning the origin of terrestrial vertebrates (summarized in Clack, 2002), the phylogenetic relationships of early tetrapods, and the origin of modern liss amphibians and amniotes. Page 561

2. Origin And Early Evolution Of The Amniotes, By David S Berman

Cladistic analyses of Paleozoic tetrapod relationships have yielded dramatically contradictory results (Gauthier et al., 1988; Carroll, 1995; Laurin and Reisz, 1995, 1997; Laurin, 1998), despite the use of similar computerized algorithms and extremely large data sets. Major sources of this problem, according to Carroll (1995), can be attributed to: 1) the lack of at least some data from all known taxa and 2) the lack of more information of more plesiomorphic members of recognized clades that are not known from their presumably earlier fossil record. Thus, if any of the recent cladistic analyses of late Paleozoic tetrapod relationships are used to construct a morphological series that traces the early evolutionary changes of a particular region of the tetrapod skeleton to its culmination in the amniote condition, the result is often, predictably, questionable. Page 938

Potentially important to the controversy of the phylogenetic position of the baphetids is the recent description by Lombard and Bolt (1995) of the Lower Carboniferous amphibian *Whatcheeria*, which in their phylogenetic scheme was placed tentatively as the first outgroup of the anthracosaurs. Page 952

With the additional consideration of the diadectomorphs, his phylogeny encountered further problems, and he was unable to resolve the relationships between the three taxa. The final solution was an unresolved trichotomy. Page 953

3. The Origin Of Terrestrial Vertebrates, By Robert L. Carroll

These events serve as informative models for the study of other major transitions and large scale radiations, but they also point to the problems of the incomplete nature of the fossil record and the difficulties of establishing relationships. It is especially difficult to classify early tetrapods because their origin and early radiation occurred within several distinct environments, having different likelihoods of preservation in the sedimentary record. Page 1202

Most Paleozoic labyrinthodonts belong to the Temnospondyli (Holmes, 2000). They appear to be monophyletic in origin, but their specific relationships to Upper Devonian or other Carboniferous labyrinthodonts remain uncertain. Page 1207

4. Phylogeny of Rhacophoridae, By Guohua Yu

The phylogenetic relationships among rhacophorid frogs are under dispute. Page 571

Although many studies of phylogeny based on morphological or molecular datasets have been reported for this rich and diverse group, and previous molecular studies have provided compelling evidence in support of the Buergeriinae–Rhacophorinae dichotomy among Rhacophoridae, the phylogenetic placement and taxonomy of some genera and species of Rhacophoridae are still under **debate**. Page 571

Additionally, these differences in the phylogenetic placement and validity of Feihyla make the phylogenetic placement of *Chiromantis* ambiguous. Page 571

Controversies on the phylogenetic placement of *Aquixalus odontotarsus* and the validity of genus *Aquixalus* are ongoing. Page 571

5. Australian Frog Genera *Crinia*, By Kathryn Read

This group has been the subject of a number of long-standing taxonomic and phylogenetic **debates**. Page 294
The biogeographic and taxonomic **debates** have been so protracted largely due to the lack of a robust phylogeny covering all species able to test alternative taxonomic scenarios. Page 295

6. Origin of extant amphibians, By Diego San Mauro

One of the most hotly **debated** topics in vertebrate evolution is the origin of extant amphibians (Lissamphibia). The recent contribution of molecular data is shedding new light on this **debate**, but many important questions still remain unresolved. Page 554

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There are over 6500 species of extant amphibians distributed in all continents except Antarctica (AmphibiaWeb, 2010; Frost, 2009), and their origin and phylogenetic relationships (particularly those among the three orders) have long been hotly **debated** (Carroll, 2009; Schoch and Milner, 2004). Page 554

Much has been written recently about the origin and possible ancestry of extant amphibians (Anderson et al., 2008; Carroll, 2007, 2009; Marjanovic and Laurin, 2008a, 2009; Ruta and Coates, 2007; Schoch and Milner, 2004; Vallin and Laurin, 2004), and this is still an ongoing **debate**. Page 558

All this may simply reflect the ongoing **debate** on the performance of relaxed clock molecular dating methods (Welch and Bromham, 2005), and how their estimates are affected by the different assumptions they make about rate change. Page 558

The Temnospondyli hypothesis has received the wider acceptance so far, but support for each of the three hypotheses differs greatly from study to study, and the issue is still hotly **debated**. Page 559

Three main competing hypotheses have been proposed regarding the most plausible 'candidate' ancestor group of the extant amphibians. The first hypothesis suggests that the Temnospondyli are the closest relatives of the extant amphibians (Benton, 1990; Bolt, 1991; Milner, 1988; Panchen and Smithson, 1987; Ruta et al., 2003; Trueb and Cloutier, 1991a). A second hypothesis suggests instead that the Lepospondyli are the closest relatives of extant amphibians (Laurin, 1998; Laurin and Reisz, 1997; Marjanovic and Laurin, 2008a, 2009; Vallin and Laurin, 2004). The third hypothesis proposes a polyphyletic nature of extant amphibians (with respect to major Paleozoic amphibian lineages), with frogs and salamanders arising among temnospondyls and caecilians among lepospondyls (Anderson, 2008; Anderson et al., 2008; Carroll, 2001, 2007; Carroll et al., 2004). The Temnospondyli hypothesis has received the wider acceptance so far, but support for each of the three hypotheses differs greatly from study to study, and the issue is still hotly **debated**. Page 559

7. A mitogenomic perspective, By Peng Zhang

For example, the largest family of caecilians, the Caeciliidae, which includes 101 of the 176 currently recognized species (AmphibiaWeb, 2009), is probably paraphyletic with respect to the Typhlonectidae and possibly the Scolecomorphidae and the interrelationships of its constituent genera are still under **debate** (Wilkinson et al., 2003; Wake et al., 2005; Frost et al., 2006; Roelants et al., 2007; Loader et al., 2007, and see below). More uncertain is the position of the Scolecomorphidae, which might be either the sister group of Caeciliidae plus Typhlonectidae (Wilkinson and Nussbaum, 1996; Roelants et al., 2007) or within Caeciliidae (Wilkinson et al., 2003; Frost et al., 2006). Page 480

8. Gene and species trees, By Tuliana O. Brunes

Mitochondrial and nuclear DNA phylogenies were not completely concordant. Page 1125

Phylogenetic analyses of mtDNA ND2 showed five main clades with high support but with their relationships unresolved. Page 1126

This would also explain the lack of resolution to infer phylogenetic relationships among these three species. Page 1128

9. Higher-level salamander relationships, By Peng Zhang

Phylogenetic relationships among the salamander families have been difficult to resolve, largely because the window of time in which major lineages diverged was very short relative to the subsequently long evolutionary history of each family. Page 492

There is a lack of consensus regarding family-level phylogenetic relationships for living salamanders. Page 492

10. DNA markers in midwife toads, By H. Goncalves

One case that exemplifies this problem is the long-standing **debate** on the phylogeny of midwife toads. Page 494

11. Phylogenetic relationships of Pelobatoidea, By Mario Garcia-Paris

Elucidating the phylogenetic relationships of basal anurans has proved difficult using either morphological or molecular data sets (Ford and Cannatella, 1993; Hay et al., 1995). The most recent morphological (Ford and

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Cannatella, 1993; Gao and Wang, 2001) and molecular (Hay et al., 1995; Ruvinsky and Maxon, 1996) hypotheses of relationships for the Anura deeply disagree in the position of Pelobatidae. Page 12

Both rooting strategies allowed the positions of the other outgroup species, particularly *Xenopus*, to remain free with respect to the ingroup, since the interrelationships among Pelobatoidea and Pipoidea are subject of **debate** (Ford and Cannatella, 1993; Gao and Wang, 2001; Hay et al., 1995; Roček, 1980). Page 13

Relationships among species of Pelobates have been extensively **debated** (Barbadillo et al., 1997; Busack et al., 1985; Cannatella, 1985; Estes, 1970; Gislén, 1936; Lathrop, 1997). None of these hypotheses was fully resolved, except that of Barbadillo et al. (1997), which used osteological characters and genetic data. Page 19

12. Malagasy poison frog, By Atsushi Kurabayashi

The phylogenetic relationships within the family Mantellidae have been a subject of **debate** for the past few decades with all genera recently allocated to this family often considered members of the family Ranidae (true frogs) or Rhacophoridae (Asian tree frogs) (reviewed by Vences and Glaw, 2001). The phylogenetic affinity of the genera *Mantella* and *Mantidactylus* with ranids or rhacophorids is also controversial due to their unique combination of morphological characters; for example, the femoral gland in *Mantella* and *Mantidactylus* is also sometimes found in some ranids, while some features of the tarsal elements are also found in both ranids and rhacophorids (e.g., Wilkinson et al., 2002). Page 230

13. Molecular clocks, By Michael S. Y. Lee

However, the more precise affinities of lissamphibians remain contentious. The three hypotheses with most current support (reviewed in detail by Schoch and Milner, 2004) are discussed below, along with their implications for divergence dates. Page 635

14. Stream-dwelling frog, By Ivan C. Phillipsen

The ability of NCPA to uncover true evolutionary patterns has been **debated** recently (Knowles, 2008; Templeton, 2009). The main argument against NCPA is that in simulation studies a high proportion of NCPA inferences are actually “false positives” (Knowles, 2008). Page 157

Given the ongoing **debate** over NCPA, we include it here not as a stand-alone analysis, but to provide additional support for inferences made using phylogenetic and population genetic analyses. Page 157

15. High Andean tree frog, By Carlos E. Guarnizo

It still under **debate**, however, exactly when most of the tremendous diversification of the Northern Andes occurred (Roy et al., 1997; García-Moreno et al., 1999; Chesser, 2000; Kosciński et al., 2008; Rull, 2006). Page 89

16. Amazonian poison frogs, By R. Symula

The Refuge Hypothesis has been investigated by a number of researchers and has been the focus of considerable **debate** (Brown, 1982; Froehlich et al., 1991; Nores, 1999; Prance, 1982; Prance, 1973; Rasanen et al., 1991; Vanzolini, 1970). Page 455

17. Evolution of bell frogs, By Emma L. Burns

The time of divergence of the eastern and western bell frog groups has been a matter for **debate**. Page 577

18. Hox genes in amphibians, By An Mannaert

At present, the origin of these clusters, either by whole-genome duplications or by cluster duplications, is still the subject of **debate** (reviewed by Wolfe, 2001). Page 449, 450

19. Peruvian poison frogs, By Jennifer L. Roberts

The Amazon basin is a region of unparalleled biodiversity, the origin of which has been a subject of continuing **debate**. Page 149

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Birds

1. The vertebrate fossil record, By Johannes Muller

The use of this date, however, has not been free of controversy, which recently culminated in an open **debate** involving both paleontologists and molecular biologists. Page 1069

However, from a strictly paleontological perspective, the mammal–bird split is problematic because: (a) there are not enough fossil localities from the early Late Carboniferous that predate the earliest known evidence of the split, (b) the same is true for the number of fossil localities immediately after the first appearance of amniotes and (c) there are still several long ghost lineages in the phylogeny of early amniotes and their sister taxa. Page 1074

2. Early origins of modern birds, By Michael J. Benton

Two major current phylogenetic questions are hotly **debated**, however: the origins of Metazoa (multi celled animals), and the origins of modern bird and mammal groups. In both cases, molecular evidence suggests that the point of origin is twice as old as the oldest known fossils. This implies either that half the fossil record of animals, and of modern birds and mammals, is cryptic, or that the molecular conclusions are flawed. Either way, there is a strong challenge to the integrity of molecular phylogenetic analytical techniques, or to claims by palaeontologists that the history of life can be divined from the fossil record. The question of metazoan origins has been **debated** already in BioEssays. Page 1043

These dramatic claims are one of many challenges to “traditional” morphology-based views. Past experience does not indicate which way the **debate** will go, whether the molecular challenge, or the status quo, will be upheld. Nonetheless, **debates** such as these have often been heated, and it is worth reviewing the current position. Page 1044

In cases of conflict and error, molecular trees suffer many of the same methodological problems as morphological, for example the choice of taxa in the in group, the choice of out group taxa, the choice and definition of characters, and the choice of algorithm. Results obtained using either technique may be confused by problems of convergence, long branch attraction, and rapid splitting of lineages (star phylogenies). In addition, special features of molecular phylogeny reconstruction cause problems: variable rates of substitution at different sites, differential rates of transitions and transversions, and multiple substitutions at sites. Page 1044

The postulation of rare or cryptic ancestors does not really resolve anything, and is just a restatement of the problem; there is no independent evidence for the proposal that ancestors were cryptic other than the assumption that such ancestors were there and yet have not been found. The proposal fails absolutely on a probability argument: why should some 20–30 lineages, the modern bird and mammal orders reputed to have existed undetected through most of the Cretaceous, all uniformly have remained cryptic until they blossomed forth in abundance and with autapomorphies in place and fully displayed between 70 and 55 million years ago? Page 1047

There are numerous other substantial problems to be considered before accepting date estimates founded on molecular data. As Bromham and colleagues point out, current estimates of specific dates of divergence between various clades of mammals vary enormously, and sometimes by as much as 100%. Page 1049

However, from a strictly paleontological perspective, the mammal–bird split is problematic because: (a) there are not enough fossil localities from the early Late Carboniferous that predate the earliest known evidence of the split, (b) the same is true for the number of fossil localities immediately after the first appearance of amniotes and (c) there are still several long ghost lineages in the phylogeny of early amniotes and their sister taxa. Page 1074

3. Molecular phylogeny of songbirds, By Greg S. Spicer

Relationships among the families of passerine birds have been the subject of many **debates** over the years (Sibley and Ahlquist, 1990). With the development of new molecular systematic techniques, the **debate** over relationships within the passerines has become even more heated. Page 325

However, despite the attention to this phylogenetic problem, many familial relationships within the Passeriformes remain unresolved. Page 325

Molecular phylogenetic results have been fraught with a lack of resolution, as well, due to the lack of phylogenetic signal in the genes chosen for the studies. Page 326

4. Phylogeny of the avian genus, By John P. Dumbacher

For the phylogenetic analyses, gaps were simply coded as missing data. Although gaps certainly contain additional information, exactly how to code and model the evolution of insertions and deletions is less straight forward and subject to some **debate**. Page 777

5. Multi-locus phylogeny, By Silke Fregin

The relationships among the genera in Acrocephalidae sensu Johansson et al. (2008) and their relationships to other taxa have long been **debated** based on morphology and zoology. Page 866

6. Mitochondrial marker sequences, By Martin J. Riesing

So far, classification is based on osteological and other morphological traits, but the phylogenetic information of those characters may be blurred by convergence. Page 328

Phylogenetic relationships between Buteo and related genera are also not well understood. Page 328, 329

7. Phylogeny of “core Gruiformes”, By Matthew G. Fain

Opinions on the systematic relationships of birds in the avian order Gruiformes have been as diverse as the families included within it. Despite ongoing **debate** over monophyly of the order and relationships among its various members, recent opinion has converged on the monophyly of a “core” group of five families classified as the suborder Grues. Page 515

For well over a century, avian systematists have **debated** their phylogenetic relationships and even whether they constitute a monophyletic assemblage. Page 515

8. Phylogeny of Paroaria, By Liliana M. Dávalos

The phylogenetic position of the genus has been controversial, and Paroaria has been assigned to various tribes within the family Fringillidae. Page 234

9. Phylogeny of long-tailed tits, By Martin Päckert

To date there is a lively **debate** on the species status of some narrowly distributed SE Asian taxa as well as on their phylogenetic relationships to other congeners. Page 953

10. A phylogeny of the megapodes, By Sharon M. Birks

Here, we use maximum-likelihood analyses of RDP1 and ND2 to construct our primary hypotheses for megapode phylogeny, but we also take advantage of having two independent estimates of phylogeny to further explore differences in evolutionary dynamics between nuclear and mitochondrial sequences as well as the effects of weighting in parsimony analyses—a topic of ongoing **debate**. Page 409

11. Phylogeny of swiftlets, By Henri A. Thomassen

Due to a lack of distinctive morphological characters, swift taxonomy and phylogeny has always been an area of disagreement. Page 86

12. Specific chicken repeat, By Simone Treplin

While the monophyly of the order Passeriformes as well as its suborders suboscines (Tyranni) and oscines (Passeri) is well established, both on morphological and molecular grounds, lower phylogenetic relationships have been a continuous matter of **debate**, especially within oscines. This is particularly true for the rock fowls (genus Picathartes), which phylogenetic classification has been an ongoing puzzle. Sequence-based molecular studies failed in deriving unambiguously resolved and supported hypotheses. Page 328

However, as most of the evolutionary lineages originated through a rapid radiation during the early Tertiary, phylogenetic relationships within the group have been a continuous matter of **debate**. Page 328

Due to their unique suit of morphological traits, the phylogenetic position of these species within Passeriformes has been the object of extensive **debate** and still remains a puzzle. Page 328

13. Phylogeny of the snubnose darters, By Tamra C. Mendelson

Phylogenetic relationships among snubnose species have been a challenge to resolve at all levels of divergence, from the monophyly of species to deeper relationships among subgenera. Page 1253

At deeper levels, relationships among Ulocentra and closely related subgenera also have generated **debate**. In particular, relationships among Ulocentra and its two closest relatives, subgenera Etheostoma and Nanostoma, have been difficult to resolve. Page 1253

Relationships among species within Ulocentra, however, were not fully resolved in the mtDNA analysis, with multiple cases of species-level paraphyly. Therefore, the monophyly of species, relationships among species, and relationships among subgenera remain an open question. Page 1253

14. Phylogeny of the NewWorld Orioles, By Kevin E. Omland

Unfortunately, phylogenetic relationships within the genus are poorly known, with only a few previous studies providing testable phylogenetic hypotheses. Beecher (1950) studied skull characteristics and nest shape and concluded that there were two distinct lineages of orioles, each of which had evolved independently from different *Agelaius*-like ancestors. Page 224

15. Molecular systematics, By Leo Joseph

Debate concerning their circumscription has most recently centered on the position of four genera, Neophema, Neopsephotus, Pezoporus and Psittacella, the last two having never been adequately included in sequence-based analyses. Page 675

While recognizing current **debate** over the calibration of rates of molecular evolution (e.g., Lovette, 2004; Ho, 2007), we note that the conventional calibration for mtDNA evolution of 2% per million years (Tarr and Fleischer, 1993) would suggest that the split between *Pe. Occidentalis* and *Pe. wallicus/Pe. flaviventris* likely occurred about 3.3 mya, certainly before the Pleistocene. Page 681

16. Phylogenetic relationships, By J. M. Pons

The relationships among gulls are still the focus of controversial **debates**. Page 686

The skuasalcids clade is sister to a clade including larids, terns, and skimmers, but relationships between these three latter groups remain uncertain. Page 686

Nevertheless, the main source of uncertainty over the timing of gull evolution is the calibration of the tree. Page 696

This situation of multiple incongruence between morphological characters and phylogeny in gulls contrast with the good agreement between plumage patterns and phylogeny in terns. Page 696

17. The evolutionary history of cockatoos, By Nicole E. White

Waterhouse (2006) stated the need for additional Cretaceous fossils before any certainty can be brought to the **debate**. Page 617

However, dating Cacatuidae using 40 mtDNA genomes and well-accepted fossil calibrations also provided insights into the broader **debate** regarding evolution of the Psittaciformes. Page 618

18. Calibration of a molecular clock, By Martin Packert

The ongoing **debate** on the reliability of avian molecular clocks is actually based on only a small number of calibrations carried out under different assumptions with respect to the choice and constraints of calibration points or to the use of substitution model. Page 1

However, the fossil record is poor in many, especially younger avian lineages, and thus fossil dating is almost limited to avian orders and families but fails for clock calibration at the genus, species, or subspecies level. Page 2

19. Phylogeography of giant petrels *Macronectes*, By N. M. S. M. Techow

There has been much **debate** recently on the suitability of mitochondrial DNA (mtDNA) phylogenies for discerning avian taxonomy, as there is no theoretical basis for associating gene trees with population lineages (Avice, 2000). Page 472

20. The continuum of pigeon evolution, By Gillian C. Gibb

Even the large avian study (169 taxa, 32 kb of nuclear sequence) of Hackett et al. (2008) has not resolved the relationship of pigeons. Page 699

Among the Neoaves just what is the closest relative of pigeons has been an unresolved **debate** for decades. Page 699

21. Phylogeny of the Charadriiform birds, By Tara A. Paton

Because of the difficulties of constructing a robust phylogeny for Charadriiform birds using morphological characters, recent studies have turned to DNA sequences to resolve the systematic uncertainties of family-level relationships in this group. However, trees constructed using nuclear genes or the mitochondrial Cytochrome b gene suggest deep-level relationships of shorebirds that differ from previous studies based on morphology or DNA–DNA hybridization distances. Page 657

The phylogenetic relationships within shorebirds (Aves: Charadriiformes) continue to be a fascinating problem to systematists because hypotheses generated by morphological and biochemical methods are vastly different. Page 657

22. Divergence among neognath birds, By Alison L. Chubb

To date, there is little consensus concerning the phylogenetic relationships among neognath orders, which include all extant birds except ratites and tinamous. Different data sets, both molecular and morphologic, have yielded radically different and often unresolved ordinal topologies, especially within the neoaves clade. This lack of resolution and ongoing conflict indicates a need for additional phylogenetic characters to be applied to the question of higher-level avian phylogeny. Page 140

Higher-level phylogenies of modern birds (subclass Neornithes) have been plagued by lack of resolution and disagreement among different data sets, both morphologic and molecular (reviewed in Cracraft and Clarke, 2001). Page 140

The ZENK tree provides another data set to fuel this unresolved **debate**. Despite growing clarity about relationships at the base of the avian tree (Paleognathae vs. Neognathae and Galloanserae vs. Neoaves) and the potential for an alliance between flamingos and grebes, relationships among most other major lineages of modern birds remain largely uncertain. Page 148

23. New World suboscine birds, By R. Terry Chesser

Species composition of families in the Furnarii (sensu Ames, 1971 and Raikow, 1987), in contrast, has with few exceptions been well defined, but the monophyly and relationships of specific families have been a matter of **debate**. Page 12

24. Molecular evolution in space, By Rauri C.K. Bowie

This split remains controversial and is exemplified by the **debate** over the taxonomic assignment of Olive Sunbirds on Zanzibar Island off the east coast of Africa. Page 70

25. The Five-lined skink, By Briar J. Howes

The hypothesis that Pleistocene refugial dynamics have played a disproportionate role in generating current diversity in North America has proven controversial (Arbogast and Slowinski, 1998; Avise et al., 1998; Klicka and Zink, 1997; Zink and Slowinski, 1995). For example, dates of divergence of many species of birds appear to predate the latter half of the Pleistocene (Klicka and Zink, 1997), a period during which glacial expansion and recession was proposed to have fragmented the range of many ancestral species (Mengel, 1964). Recent evidence suggests that this **debate** over the importance of Pleistocene dynamics is somewhat misdirected. Page 183

26. Analysis of the “true thrushes”, By John Klicka

Although the “true thrushes” (Turdinae, sensu Sibley and Monroe, 1990) are one of the most widespread and well-known “families” of birds in the world, their taxonomic affiliations with other lineages, and relationships among constituent genera have long confounded taxonomists. Page 486

27. East Asian Erithacus robin, By Shin-Ichi Seki

The phylogenetic relationship among the Erithacus robins, however, is still a question under **debate** (Kajita, 1999; Ornithological Society of Japan, 2000). Page 899

28. Genetic homogeneity in rosy-finches, By Sergei V. Drovetski

The southern part of the range is inhabited by the three currently recognized species, which have fueled past taxonomic **debates**. Page 442

29. Diversification of the blue tits, By L. Kvist

The definition of taxonomic units is problematic and has been under strong **debate** for decades. Page 509

30. The Greenside Darter, By Amanda E. Haponski

The question of whether or not to elevate taxa and which species concept to use has been **debated** and reviewed extensively in the literature (see Zink and McKittrick, 1995; Mayden, 1997; Coyne and Orr, 2004). Page 80

31. Phylogenetic relationships of Finches, By M. A. A. Van der Meij

The fringillids can be divided into two groups, the Fringilla species and the cardueline Wnches (Sibley and Ahlquist, 1990; Stempel, 1987), but there have been many **debates** about the relationship of the genus Fringilla. Page 97

32. White-chinned and Spectacled Petrels, By N. M. S. Mareile Techow

There has been much **debate** about the definition of a species (e.g. Helbig et al., 2002; Avise, 2004). Page 30

33. Relationships between Clerodendrum, By Dorothy A. Steane

The position of Kalaharia relative to Clerodendrum has long been a source of **debate**. Page 44

34. Evolution of Modern Birds, By M. Andreina Pacheco

This places mitogenomic studies in birds at the core of intense **debates** in avian evolutionary biology. Page 1927

Debates about the origin of the parrots and cockatoos reflect those of the Neornithes in general, with some studies suggesting that they originated in Gondwana during the Cretaceous. Page 1939

35. Molecular Phylogeny of the Parrots, By Timothy F. Wright

The question of when modern birds (Neornithes) first diversified has generated much **debate** among avian systematists. Page 2141

The timing of the diversification of modern birds (Neornithes) is one of the most contentious issues in avian systematics. At the heart of the **debate** is a mismatch between the fossil record, which includes few modern forms prior to the Cretaceous/Tertiary (K/T) boundary. Page 2141

Debates about the origin of the parrots and cockatoos (Order Psittaciformes, hereafter “parrots” or “psittaciforms”) mirror those of the Neornithes in general, with some workers suggesting that they originated in Gondwana during the Cretaceous (Cracraft 1973; Forshaw 1989), whereas others, citing fossil evidence of stem group parrots from Tertiary deposits in Europe. Page 2141

36. Resolving Deep Neoaves Phylogeny, By Renae C. Pratt

Clearly, the root of Neoaves is still under **debate**; however, we now have a number of possibilities to be tested by future analyses. Page 322

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Bivalves

Bivalves

1. Early Cretaceous Bivalvia, By James S. Crampton

Despite this, taxonomic and phylogenetic relationships within the family are relatively poorly resolved because of widespread homoplasy, commonly high levels of intraspecific morphological variability, and the paucity of useful morphological characters. Page 89

In other cases, however, they obscure taxonomic and phylogenetic relationships and distort estimates of standing diversity and taxic rates. These problems may be acute in fossil groups such as the inoceramids that have rich and well-studied fossil records and experienced apparently rapid, phyletic evolution. Page 92

The problem is further complicated by taxonomic uncertainties involving some key ammonite lineages (e.g., Amedro, 1992). Page 97

2. Late Triassic Bivalvia, By Christopher A. Mc Roberts

The origin of Halobia from Daonella, Apaimella, or other posidoniid is unclear. Early workers who have considered the question (e.g., Bronn, 1830; Smith, 1927; Encheva, 1978) support a monophyletic origin of Halobia derived directly from Daonella. Other authors, most notably Ichikawa (1958), Gruber (1976) and Polubotko (1984) have suggested that Halobia s.l. was polyphyletic with members evolving directly from some combination of one or more Daonella and/or Peribositria lineages. Page 624

3. Resolution of the family Dreissenidae, By Thomas W. Therriault

Considerable uncertainty exists in determination of the phylogeny among extant members of the Dreissenidae, especially those inhabiting the Ponto-Caspian basin, as multiple systematic revisions based on morphological characteristics have failed to resolve relationships within this group of bivalves. Page 479

These analyses have resulted in confusion regarding phylogenetic relationships within the family. Page 479

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Cephalopods

1. Cephalopods From The Upper Cretaceous, By Dirk Fuchs

Although the “Vampyropoda-hypothesis” has been largely supported (Engeser and Bandel, 1988; Engeser, 1988; Haas, 2002; Donovan et al., 2003; Klug et al., 2005; Fuchs, 2006a, 2006b; Fuchs et al., 2007b), the systematic position of the Prototeuthidina remains a source of considerable **debate** (Donovan and Toll, 1988; Young et al., 1998; Vecchione et al., 1999; Bizikov, 2008). Page 234

Although the phylogenetic value is still poorly known (even in living taxa), the cephalic cartilage morphology of *Dorateuthis* also indicates closer affinities with vampyropods than with teuthids (compare Nixon, 1998, fig. 3). Page 245

The phylogenetic origin of the Prototeuthidina within the vampyropods is still unsolved. Page 246

Despite this incomplete knowledge related to the direct origin of the Prototeuthidina, polarization of some character states can be ascertained. Page 247

2. Ontogeny And Heterochrony In Ammonoids, By Daniel A. Stephen

One reason for this dearth of study is that most extant cephalopods are coleoids, which lack shells, and therefore, have a meager fossil record. Consequently, the phylogeny of the Coleoidea is not known in detail, and analysis of ancestor-descendant taxa is essentially impossible at this time. Page 818

In contrast to the situation with modern cephalopods, there are numerous papers on heterochrony in ammonoids. Indeed, ammonoids have been a favorite battleground for **debate** since the time of Hyatt and the infancy of heterochronic research. Examples have come from both the Mesozoic and the Paleozoic. Page 818

3. Cephalopod origin and evolution, By Bjorn Kroger

Different paleontological hypotheses have been proposed for the origin of cephalopods among fossil Cambrian monoplacophoran-like molluscs and other forms. Page 605

The now classical, but **debated**, hypothesis of cephalopod ancestry is that *Plectronoceras* derived from the tall, conical, bottom-living (benthic) mollusc *Knighthoconus* which has walls in the shell (septa) that separate multiple chambers. Page 605

The reconstruction of the phylogeny of fossil coleoids is complicated by the rarity of fossils and often times incomplete preservation. The existence of Paleozoic representatives of the ten armed squids (Decabrachia) is currently under discussion. Page 609

Similarly, the origin of the eight-armed vampyropods is still **debated**. Page 609

4. Phylogeny of coleoid cephalopods, By Jan Strugnell

The resolution of higher level phylogeny of the coleoid cephalopods (octopuses, squids, and cuttlefishes) has been hindered by homoplasy among morphological characters in conjunction with a very poor fossil record. Initial molecular studies, based primarily on small fragments of single mitochondrial genes, have produced little resolution of the deep relationships amongst coleoid cephalopod families. Page 426

However, phylogenetic relationships between the nine Incirrata families (Supplementary Appendix 1) are less clear and have been **debated** extensively in the literature (Naef, 1921–1923; Robson, 1929, 1931; Voight, 1997; Voss, 1977; Young and Vecchione, 1996). Page 427

Although each of these families and suborders are understood to form monophyletic groups, there is much **debate** concerning the validity of the ordinal level of classification (Berthold and Engeser, 1987; Naef, 1921–1923; Voss, 1977; Young and Vecchione, 1996). Page 427

(COI), were sequenced (Supplementary Appendix 1). The most appropriate method for analysing multiple genes in phylogenetic analyses is an issue of some **debate** (DeBry, 2003; Huelsenbeck et al., 1996). Page 428

5. Divergence time of Spirulida and Sepiida, By Kerstin Martina Warnke

Cephalopods

The phylogenetic position of the mesopelagic decabrachian cephalopod *Spirula* is still a matter of **debate**. Page 390

Molecular characters also yield contradictory indications as to the position of *Spirula* (for discussion see Warnke and Keupp, 2005). These differ depending on the gene(s) and the methods of analyses used (Bonnaud et al., 1994; Carlini et al., 2000; Warnke et al., 2003). Fossil records of coleoids are generally scarce. Widely accepted is *Ceratisepia* (70 mya) as the stem group of the Sepiida and *Groenlandibelus* (100 mya) as the stem group of the Spirulida (Benton, 1993; Hewitt and Jagt, 1999, Keupp pers. comm.). Older fossil records remain ambiguous as it is still unknown whether the late Carboniferous *Shimanskya* (Doguzhaeva et al., 1999) belongs to the spirulids (Hewitt and Jagt, 1999; Keupp pers. comm.). Thus the age in which Spirulida originated is still unclear. Page 390

Thus the origin is still uncertain and does not agree with fossil records. Page 390

Whether *Shimanskaya* is a member of the Spirulida is still a matter of **debate** (Doguzhaeva et al., 1999; Hewitt and Jagt, 1999). Page 393

6. Mitochondrial genome structure, By Shin-ichi Yokobori

There are several important issues concerning coleoid phylogeny which are still under **debate**, including (1) relationships between octopuses, vampire squids, and decapods. Page 899

7. Relationships among cirrate octopods, By Stuart B. Piertney

There has been considerable **debate** (O_Shea, 1999; Robson, 1932; Villanueva et al., in press; Voss, 1988a,b) about which morphological characters should be used to define cirrate phylogeny. Page 352

8. Evaluation of the squid genus *Illex*, By David B. Carlini

Validity of *I. oxygonius* as a separate species has been a matter of considerable **debate** (Roper et al., 1998). Page 496

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Crustaceans

1. Dikelocephalid Trilobites, By Seung-Bae Lee

However, it is **difficult to evaluate their relationship** due to uncertain generic concepts of some Laurentian dikelocephalids (Raasch, 1951; Robison and Pantoja-Alor, 1968; Taylor and Halley, 1974; Ludvigsen and Westrop, 1983; Fortey, 1994). Page 282

2. Lichidae Trilobita, By H. B. Whittington

They are present in the earliest Ordovician strata, and range into the Devonian, but their origins remain a **mystery**. Page 306

Until more and particularly entire exoskeletons, is known of these species, it will be **difficult** to discern lichid origins. Page 306

An issue in **debate** is whether to place the Lichidae in a separate higher taxon, ranging from Superfamily to Order (Moore, 1959; Hupe, 1953, 1955; Bergstrom, 1973), or to ally them in an Order with the Odontopleuroidea (Henningsmoen, 1951; Thomas and Holloway, 1988; Fortey, 1990; *in* Kaesler et al., 1997). Page 314

Firstly, that the origin of lichids, of their ancestry in pre-Tremadoc strata, remains **unknown**. Secondly, that there is a great gap in our knowledge of how and where the early diversification and migrations of species occurred, in the time between early Tremadoc and late Arenig. Page 315

3. Epipunctae And Phosphatized Setae, By Jisuo Jin

[The precise position of the Agnostida within or outside of this clade of trilobites is still the subject of **debate** (e.g., Fortey and Whittington, 1989; Fortey, 1990; Ramskold and Edgecombe, 1991; Shergold, 1991; Bergstrom, 1992; Babcock, 1994; Fortey and Theron, 1994; Fortey and Owens, 1997; and Edgecombe and Ramskold, 1999).] Page 692

The timing of the Cambrian radiation is a topic that has been extensively **debated** (see Gould, 1989; Signor and Lipps, 1992; Fortey et al., 1996; Knoll, 1996; Raff, 1996; and Lieberman, 1999b). Some have argued that the Cambrian radiation significantly predates the Neoproterozoic-Cambrian boundary (e.g., Darwin, 1859; Davidson et al., 1995; Fortey et al., 1996; Fortey and Owens, 1997; Wray et al., 1996; Ayala et al., 1998; Xiao et al., 1998; Fortey, 2001) whereas others have suggested that the radiation occurred just before the start of the Cambrian (McNamara, 1986; Gould, 1989; Hughes, 1991; Valentine et al., 1994). Page 696

4. Paleozoic Beyrichioidean Ostracodes, By Ewa Olempska

There is also some **debate** concerning relationships of the late Paleozoic ostracodes with cruminate dimorphism, especially paraparchitids, recently incorporated into the Palaeocopida (Jones, 2004; Liebau, 2005), Leiocopida (Whatley et al., 1993; Olempska, 1999; Watabe and Kaesler, 2004; Hoare and Merrill, 2004; Williams et al., 2005), and Podocopida (Becker, 2000). Page 717

The placement of several mid and late-Paleozoic genera with cruminate dimorphism (e.g., the Late Devonian *Bouckaertites* Tschigova, 1977, *Zaninaella* Tschigova, 1977, and the Early Carboniferous “*Bernix*” Jones, 1885, *Pseudoleperditia* Schneider, 1956, *Copelandella* Bless and Jordan, 1971, *Armenites* Tschigova, 1977, *Malnina* Jones, 1989, and several others) is the subject of a **debate** (e.g., Robinson, 1969; Bless and Jordan, 1971; Sohn, 1979; Jones, 1989; Abushik, 1990; Tibert and Scott, 1999). Page 717

There are several lineages within the mid and late-Paleozoic beyrichioideans, and the precise phylogenetic relationships in these species are still far from being clear. Page 726

5. Affinities Of Illaenidae, By Harry B. Whittington

It is used as a division of equal rank in Fortey's (1990, fig. 19; Fortey and Owens *in* Kaesler, 1997, fig. 196) diagram, however, for a division that includes a heterogeneous assemblage of portions of groups of known ancestry and groups of uncertain ancestry. Page 879

6. Cladistic Analysis Of Early Trilobites , By Frederick A. Sundberg

In contrast, using the different species of *Schistometopus* would have created **problems** in a noncladistic phylogenetic analysis or cladistic analyses using representative species or “generic” character states. Page 928

Determining the phylogenetic relationships among these ptychopariids is also **hindered** by the lack of information about the different sclerites for several taxa. Page 929

7. The Decapoda, By Rodney M. Feldmann

Recent attempts to place decapods in a phylogenetic context have yielded widely divergent patterns and, to date, **nothing resembling consensus** has been reached. This is not to say that progress has not been made. Page 1021

The **debate** goes on (Guinot and Tavares, 2001). Thus, it is clear that the arrangement and relationships of the so-called “primitive” crabs is anything but clear. Page 1023, 1024

8. Trilobite Systematics, By Richard A. Fortey

Different approaches to phylogenetics have influenced the way trilobites have been classified. Classical evolutionary taxonomy, the stratigraphical approach, and cladistics have all contributed in different ways to the current classification, which has evolved piecemeal, **and is still unsatisfactory** in some ways. Nonetheless, progress towards a phylogenetic classification has been made, especially as the result of information from ontogenies provided. Page 1141

Many of the outstanding high-level **systematic problems** boil down to understanding and identifying Cambrian sister taxa of known clades, or in some cases challenging the homogeneity of clades once the appropriate relationships are resolved. Ontogenies of Cambrian trilobites are likely to be crucial in this quest. Page 1148

There still seem to me to be some **problems** in the objective appraisal of relationships because the former study only used type species (often imperfectly known) as its basis, and olenelloids are allegedly very plastic in morphology—how do we know that the original basis of these genera was appropriate? Page 1148

9. Early Ordovician Ostracods, By Maria Jose Salas

However, it is clear that without new detailed information from soft anatomy, the relationships between the Ostracoda and Bradoriida remain hypothetical. This phylogenetic hypothesis can only truly be tested when more evidence from fossilized soft tissues becomes available in lowermost Ordovician ostracods and Cambrian bradoriids (other than kunmingellids). Page 1394

10. Development and phylogeny of arthropods, By Pat Simpson

It addressed ways to resolve the still uncertain relationships between the different groups of arthropods and featured talks discussing phylogeny and comparative developmental biology. There seems to be a general consensus that insects and crustaceans are probably sister groups and there is a suggestion that myriapods (millipedes and centipedes) are related to insects and crustaceans. However, the position of the Chelicerates (spiders, scorpions, horseshoe crabs) is still under **debate**. Page 223

11. Arthropod Evolution, By D. Osorio

Insect and crustacean lineages diverged over 500 Myr ago, and there are continuing uncertainties about whether they evolved from a common arthropod ancestor or, alternatively, they evolved independently from annelid worms. Page 419

The evolutionary origins and diversification of the Arthropoda are the subject of continued **debate**, recently enlivened by studies of the arthropod radiation during the mid-Cambrian period. Arguments about evolutionary relationships between the main arthropod groups, and whether the Palaeozoic lineages that survived and prospered were fundamentally fitter than those that perished, have not been resolved by palaeontology or by classical comparative anatomy and embryology. Page 419

12. Coral-inhabiting barnacles, By N. Simon-Blecher

It has been difficult to establish the phylogenetic relationships among Pyrgomatidae because of the apparent convergence of morphological characteristics, and due to the use of non-cladistic systematics, which emphasize ancestor-descendant relationships rather than sister-clade relationships. Page 1333

The phylogenetic relationships among Pyrgomatidae have been difficult to establish due to the use of non-cladistic systematics, which emphasize ancestor-descendant relationships and not sister-clade relationships, and because of the apparent convergence of morphological characteristics, e.g., fusion of opercular plates and wall-plates occurred several times during Pyrgomatidae evolution. Page 1333, 1334

The phylogenetic affinities of these subfamilies have not yet been unequivocally demonstrated. Page 1334

Because the monophyly of Pyrgomatidae is not fully accepted, its phylogenetic position among Balanomorpha has never been resolved. Page 1334

Despite the considerable **debate** concerning phylogenetic relationships of Pyrgomatidae, a molecular based phylogenetic analysis of these organisms has never been conducted. Page 1335

13. Phylogeny of the squat lobsters, By K. E. Schnabel

It aims to consolidate recent hypotheses into a single framework addressing commonalities and discrepancies in the ongoing and vigorous **debate** over internal anomuran relationships with a specific focus on the status and position of Galatheaidea. Page 158

14. Phylogeny of Paramysis, By Asta Audzijonyte

Finally, the genus Paramysis also contains seven more species from the Mediterranean Sea and Northeast Atlantic, and the phylogenetic relationship of these truly marine species to the Ponto-Caspian taxa has been a matter of continued **debate** (Czerniavsky, 1882; Sars, 1907; Derzhavin, 1939). Page 739

The origin of endemic diversity in ancient lakes is a question related to several contentious topics in evolutionary biology, including the importance of sympatric speciation and the roles of long-term environmental stability versus instability in promoting diversification. Page 738

15. Branchiopod crustaceans, By Jeremy R. deWaard

While this provides a unique setting to investigate the exploration of phenotypic space, our understanding of the origin and evolution of these morphological reconfigurations is inhibited by our lack of a robust phylogeny for the group. Page 491

These studies, a diverse assemblage in themselves, have failed to achieve the Holy Grail: a consensus on branchiopod relationships. Page 491

Although the phylogeny of the branchiopods has been redrawn on numerous occasions, many details remain incomplete (Fig. 1). Page 492

How best to approach data collection for phylogenetic estimation remains a contentious issue, and incomplete taxon sampling is often cited as a major source of error in phylogenetic studies. Page 499

In the present study, we naturally do not know the 'true phylogeny' with which to determine with certainty the superior strategy. Page 499

16. 37 more arthropods, By Jon Mallatt

Also **debated** is the position of pycnogonids; that is, whether sea spiders are the sister group to chelicerates (Waloszek and Dunlop, 2002), or are the sister group of all other extant arthropods, which have been termed Cormogonida. Page 785

The relations within Pancrustacea, especially among the major groups of crustaceans, have prompted a century and-a-half of **debate** among morphological taxonomists. Page 786

Much interest and **debate** center around which arthropod group is the nearest relative of hexapods, with recent discussion focusing on whether it is Malacostraca. Page 787

The relations among the entognath groups—collembolans, proturans, and diplurans—are much **debated**. This problem was recently reviewed by several authors. Page 788

Relations among the holometabolan orders are **debated**, but one group that seems firmly established is Trichoptera. Page 789

17. The disunity of Crustacea, By Kenneth Meland

Historically, conflicting ideas on Malacostraca phylogeny have often involved issues concerning monophyly of Mysidacea and Peracarida. Page 1084

18. Phylogenetics of the brachyuran crabs, By Shane T. Ah Yong

Since then, **debate** has continued over the status of Podotremata, Heterotremata and Thoracotremata (Tavares, 2003). Page 581

Interrelationships of the eubrachyurans are largely unresolved, though the majoids and Dorippoides lie outside of the remaining eubrachyurans. Page 581

19. Phylogenetic relationships within the Mysidae, By T. Remerie

Mysid phylogeny is poorly understood and few attempts were made over the last decades to revise the earlier established systematic relationships between higher taxonomic levels within the Mysida. Page 770

These studies gave more insight in the evolutionary link between the formerly accepted suborders Lophogastrida and Mysida within the order Mysidacea, which now can be considered different orders while the “old” Mysidacea disappears. However, this ongoing **debate** does not discuss the status of lower taxonomic levels within the order Mysida (families, subfamilies, tribes, and genera). Page 770

Relationships within the Mysini are much less straightforward, since two clades are resolved in the analyses. Page 775

20. Rapid radiation and cryptic speciation, By Annie Machordom

Despite their ecological importance and high diversity, many aspects of the biology of squat lobsters are poorly understood, and there is still much **debate** regarding their systematic and phylogenetic history (McLaughlin and Lemaitre, 1997; Schram, 2001). Page 259

Aside from their taxonomy, the phylogenetic affinities among the squat lobsters are **poorly understood**. The systematics of the group has not been fully resolved, and current taxonomic treatments divide genera into several large groups based on the number of male pleopods, general spinulation and the shape of the carapace and abdomen (Baba, 1988; Baba and de Saint Laurent, 1996; Macpherson and Machordom, 2001). Page 260

Moreover, given there is **no fossil record** to clarify the time of divergence of the different groups, nor are there any clear marine barriers that could justify the isolation of the ancestors of these species, we did not undertake molecular clock calibration of the divergences found. Page 274

21. Testing the new animal phylogeny, By Sarah J. Bourlat

The interrelationships among living phyla of metazoans have been the subject of controversy for a century, and represent a challenge in both morphological and molecular terms. Page 23

The phylogenetic position of the pycnogonids leads to **debate** concerning the origin of arthropod head appendages. The **debate** centres around the suggested homology of pycnogonid chelifores to the protocerebral ‘great appendages’ of certain Cambrian stem-group arthropods rather than to the deutocerebral chelicerae of spiders (Maxmen et al., 2005). If true, this would support the idea of the pycnogonids as a basal branch of the arthropods (Budd and Telford, 2005). Page 26

22. Estimation of decapod phylogeny, By Megan L. Porter

Phylogenetic relationships among all of the major decapod infraorders have never been estimated using molecular data, while morphological studies produce conflicting results. Page 355

Unfortunately, there are as many hypotheses of decapods phylogenetic relationships as there are experts with opinions (Schram, 2001), with no consensus in sight (Fig. 1). Page 356

Even with a large number of conflicting hypotheses regarding decapod phylogenetic relationships, there appears to be general agreement on the monophyly of the suborder Pleocyemata and the informal ‘Reptantia.’ Page 357

However, it is not the final answer to the long **debate** regarding decapod relationships; indeed, it appears to add yet another scheme to the already large set of hypotheses concerning decapod phylogenetic relationships. Page 365

23. Molecular phylogeny of the Calanoida, By Leocadio Blanco-Bercial

The order Calanoida includes some of the most successful planktonic groups in both marine and freshwater environments. Due to the morphological complexity of the taxonomic characters in this group, subdivision and phylogenies have been complex and problematic. Page 103

Our understanding of the evolutionary history of the calanoid copepods has been markedly limited by the lack of a fossil record and the complex effects of environmental variation over the geological history of the oceans. Page 103

Although the reliability of phylogenies based on nuclear ribosomal RNA genes is still in **debate** (von Reumont et al., 2009; Wägele and Mayer, 2007), these genes have been widely used to resolve phylogenetic relationships among many taxa as single-gene analyses. Page 110

24. Erratic rates of molecular evolution, By Oive Tinn

Dating evolutionary origins of taxa is essential for understanding rates and timing of evolutionary events, often inciting intense **debate** when molecular estimates differ from first fossil appearances. For numerous reasons, ostracods present a challenging case study of rates of evolution and congruence of fossil and molecular divergence time estimates. On the one hand, ostracods have one of the densest fossil records of any metazoan group. Page 157

We also report multiple cases of significant incongruence between fossil and molecular estimates of divergence times in Ostracoda. Page 157

As a result, the two primary estimation methodologies are often **debated**. The classical paleontological method uses first fossil appearance as an estimate for the evolutionary origin of a taxon. Critics argue these estimates may be unreliable because they require fossil preservation of taxonomically important characteristics, reliable phylogenetic placement, and accurate stratigraphic dating. Furthermore, true first fossil appearances should systematically underestimate actual origins of taxa (Smith and Peterson, 2002). Page 157

Despite their voluminous fossil record, estimating divergence times in Ostracoda may be difficult for at least two reasons. First, ostracod taxonomy is controversial (Horne et al., 2005; Martin and Davis, 2001; Schram, 1986). Page 158

Low preservational potential of myodocopes is further supported by the rarity of sub-fossil carapaces in habitats where living individuals are known (Eagar, 1995) and by a low total number of myodocope fossils compared to podocopes and may explain the completely missing fossil record of the myodocope families. Page 166

Instead, we view fossil taxonomy as a difficult problem in Ostracoda that probably contributed to the observed incongruence. Page 166

25. Relationships among the sea spiders, By Susan E. Masta

Pycnogonids, or sea spiders, are an enigmatic group of arthropods. Their unique anatomical features have made them difficult to place within the broader group Arthropoda. Page 59

Pycnogonida, or sea spiders, are arthropods with anatomical features so unique that their relationships to other members of Arthropoda have been enigmatic. Page 59

More data, including data from different sources, is necessary to resolve the placement of Pycnogonida within Arthropoda. Pycnogonids typically possess anterior appendages termed chelifores, and the lack of clear homology of these appendages with other arthropod appendages has fueled **debate** over the closest relatives of pycnogonids. Page 59

26. Relationships in the crayfish genus, By Peter Trontelj

Despite these research efforts relationships and biogeography of the eastern populations of *A. pallipes* remain uncertain, as do nearly all systematic questions concerning *A. torrentium*. Page 213

Thus, apart from a taxonomic revision, a re-evaluation of biogeographic data is needed to reach consistent phylogeographic and systematic conclusions. Page 213

27. The branchiopod *Artemia*, By Ilias Kappas

The significance of natural hybridization has been among the most heated **debates** in evolutionary research. Primarily sparked by the opposing views of prominent zoologists and botanists (Mayr, 1963; Lewontin and Birch, 1966; Arnold, 1997; Rieseberg, 1997), the controversy over the frequency and role of hybridization in evolutionary change still remains unsettled to a large extent. Page 192

28. Uroptychus naso complex, By Gary C. B. Poore

Despite the considerable **debate** related to the exact position and origins of the biogeographic breaks mentioned, it is unquestionable that the composition and geographical patterns of marine and terrestrial biota are influenced by the complicated geological history of the zone. Page 168

29. Austropotamobius italicus, By Carlos Pedraza-Lara

The **debate** is therefore still open, and more exhaustive studies and robust databases are needed to provide convincing explanations for the phylogeographic structure and history of *A. italicus*. Page 328

30. The giant freshwater prawn, By Mark de Bruyn

Much **debate** has surrounded the systematic relationships of many species within this group (e.g., Holthuis, 1950, 1995; Johnson, 1973; Pereira, 1997), which has until recently been based exclusively on comparisons of external morphological characteristics. Page 251

31. Afrotropical Freshwater crab, By Savel R. Daniels

Consequently, phylogenetic and biogeographic affinities among invertebrates that also appear to have undergone a radiation on Madagascar remain enigmatic and the subject of vigorous **debate** (Bott, 1955, 1965; Ng et al., 1995; Ortmann, 1902; Rodriguez, 1986; Von Sternberg et al., 1999). Page 228

Noticeably, several taxonomic authorities have questioned the validity of the superfamilies and their stability (Cumberlidge, 1999; Holthuis, 1979; Ng, 2004; Ng and Sket, 1996; Ng and Tan, 1998; Von Sternberg et al., 1999) further fueling the biogeographic **debate** over freshwater crab origins. Page 228

32. Phylogeography of the common shrimp, By Joana Campos

Frequent recombination would need to be invoked, but the evidence for recombination in animal mitochondria is still under **debate** (see Barr et al., 2005 for a review). Page 1020, 1021

33. Divergence within Crustacea, By T. Lefébure

Nevertheless, almost all **debate**s were developed on theoretical grounds while utility and consequences of the use of DNA in taxonomy have not been tested on broad datasets. Page 435

34. Relationships within the Phyllopoda, By Anke Braband

The phylogenetic relationships within the Phyllopoda are nevertheless a matter of **debate**.

35. Relationships within the Phyllopoda, By Anke Braband

The phylogenetic relationships within the Phyllopoda are nevertheless a matter of **debate**. Page 229

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Echinoderms And Crinoids

1. Solving The Mystery Of Crinoid Ancestry, By Thomas E. Guensburg

Occasionally a new fossil emerges that challenges our understanding of the origin and early phylogeny of a major taxon. The single specimen reported here represents such a find. Its unusual arm morphology has provided provocative evidence in the ongoing **debate** over crinoid ancestry (Paul and Smith, 1984; Ausich, 1998; Mooi et al., 1994; Guensburg and Sprinkle, 2001, 2003; Rozhnov, 2002, 2007), but the phylogenetic importance of this discovery was diminished by a lack of diagnostic information. Is this fossil unequivocally a crinoid, and if so, where does it reside in the crinoid tree? Page 350

2. Analysis Of Blastoid Phylogeny, By Abrian E. Bodenbender

However, despite this attention and extensive monographic work, their phylogenetic history is still incompletely known. Page 351

Unlike Wagner's (1995) method of confidence interval sieving, stratocladistics does not treat discordance between phylogenetic hypotheses and the stratigraphic record [even if it is "significant" relative to a model of confidence intervals on stratigraphic ranges (Marshall, 1990, 1994)] as grounds for dismissing phylogenetic hypotheses without further evaluation. Page 354

The effect of this is to shift most of the burden for explaining incongruence between phylogenetic hypotheses and the stratigraphic record to ad hoc proposals of unequal preservation probabilities. Page 354

Despite the concerns addressed here, the stratocladistic analysis of blastoids demonstrates that the additional data recorded in the stratigraphic record lead to enhanced resolution of problems that are intractable, or nearly so, with morphological data alone. Page 367

Geographically variable preservation probabilities can potentially compromise one of the basic assumptions of stratocladistics and represent a problem for which there is presently no simple solution other than reducing the number of stratigraphic levels or adjusting stratigraphic parsimony debt on a tree by tree basis (Fisher, 1992). Page 367

3. Recognition Of The Echinodermata, By Daniel B. Blake

Phylogenetic back ground. The peculiar morphology of the Brisingida suggests a derived position (Mah, 2000) whereas the phylogenetic position of the Paxillosida has been much **debated**. Page 366

Much **debate** centered on the position of the Paxillosida. Page 366

Much **debate** centered on the position of the Paxillosida. Bather (1921) and Mortensen (1921) thought that the paxillosidans were primitive [discussed in Blake (1989) and Blake, Janies, and Mooi (2000)]. Fell (e.g., 1963) argued that *Luidia* and *Astropecten* represent the first two steps beyond a somasteroid ancestry, and Gale (1987) and Lafay et al. (1995) subsequently favored a basal position for paxillosidans among crown-group asteroids. Alternatively, MacBride (1921), Blake (1987, 1988), Knott and Wray (2000), and Blake and Hagdorn (2003) rejected a primitive or basal position for paxillosidans. Page 366

4. Evaluating Internal Versus External Characters, By Lindsey R. Leighton

ABSTRACT—Evolutionary relationships between the Echinoconchidae, Productidae, Buxtoniinae, and Juresaniinae (Phylum Brachiopoda, Order Productida) have been the subject of **debate** for the better part of a century. Page 659

Third, the recent revision of the Brachiopod Volume of the *Treatise on Invertebrate Paleontology* (Brunton et al., 2000), proposes a different classification of the Productida from the classification of the original *Treatise* (Muir-Wood and Williams, 1965), which once again raises the **debate** over the placement of these three higher taxa relative to each other. The original *Treatise* (Muir-Wood and Williams, 1965), which emphasized internal characters as diagnostic, placed the Juresaniinae within the Buxtoniidae, and suggested that the Buxtoniidae and Echinoconchidae were closely related. In contrast, the revised *Treatise* (Brunton et al., 2000) placed the Juresaniinae within the Echinoconchidae, and put the Buxtoniinae (reduced to a subfamily) in an entirely different superfamily, primarily on the basis of external features and shell shape (Brunton et al., 1995). Page 659

5. Plate Homology And Phylogeny, By David Ware

However, comparison of plate patterns in boot shaped cornutes also suggests that the precise phylogenetic position of scotiaecystids is still uncertain, depending on whether the absence of Mc is original. Page 785

6. The Study Of Crinoids During The 20th Century, By William I. Ausich

Development of a phylogenetic classification has been a primary pursuit of crinoid paleontologists during the 20th century. Wachsmuth and Springer and Bather vigorously **debate**d crinoid classification during the waning years of the 19th century, and although tremendous progress has been made a comprehensive phylogenetic classification is still the primary objective for crinoid research during the early 21st century. Page 1161

A continuing theme in crinoid systematics has been the struggle to create classification schemes based on presumed phylogenetic criteria as opposed to those merely phenetic. At the turn of the last century the phylogenetic content of classification schemes was being **debate**d, as it is when we enter the 21st century. Page 1161

The Crinoidea as a whole is regarded as monophyletic, but from whence this clade was derived and where it fits within the Echinodermata are matters of **debate**. Page 1165

The *Treatise* classification left those expecting a phylogenetic classification puzzled in many instances. Four examples illustrate this point. Page 1165

The immediate challenge for the study of crinoids is to establish a phylogenetic classification for the entire class. Page 1167

Both discovery of new faunas in critical intervals and uniform application of various phylogenetic techniques will be needed to sort out the pressing issues and to develop a working consensus. Especially important concerns are homology of aboral cup plates, origination of the Crinoidea, early morphologic diversification, phylogeny of the cladids, and definition and early phylogeny of the Articulata. Molecular techniques should be able to help resolve phylogenetic questions within the articulata, but most major phylogenetic questions are among various Paleozoic groups for which little help can be expected from molecular information. Page 1167

7. Distinguishing heat from light, By Philip C. J. Donoghue

It is unfortunate, therefore, that the fossil taxa that are deemed to be of greatest import, such as entirely soft-bodied organisms from Cambrian and Precambrian Lagerstätten, are among the most hotly **debate**d. Page 179

The example of carpoids demonstrates that fossil organisms can be difficult to interpret because no simple comparative model exists; consensus over carpoids remained out of reach because an organism that shared chordate and echinoderm like characters did not fit deuterostome phylogeny. Metazoan phylogeny remains poorly resolved and we have no idea of the homologies shared by most clades of phyla. It should come as no surprise that interpretations of fossil organisms such as Odontogriphus, the halkieriids, wiwaxiids, and other halwaxiids, remain so hotly **debate**d. Page 182

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Eukaryotes And Protozoa

1. Phylogenomics, By Danielle Gadelle

We have not rooted the trees of Fig. 5 since phylogenetic relationships between the three domains of life are still highly **debated**. Page 241

2. A kingdom's progress, By Patrick J. Keeling

Although they lack classical mitochondria, the Parabasalia do contain a double membrane-bound metabolic organelle called the hydrogenosome whose origin has been the source of some **debate**. Page 90

3. The eukaryotic nucleus, By David Moreira

The origin of eukaryotes remains a hotly **debated** issue. Various models have been suggested, generally explaining only partially how one or more properties of the eukaryotic cell might have arisen from simpler ancestors. However, none of them explains satisfactorily the origin of one of the most crucial eukaryotic features: the nuclear compartment. In particular, no convincing selective forces have been proposed for its formation from nucleus-lacking ancestors, and a definite explanation that satisfies cell biologists is still missing. Page 525

4. The origin of eukaryotes, By Anthony M. Poole

To our knowledge, the only proposed phylogenetic result suggesting eukaryotes group within archaea is the eocyte tree, which instead groups eukaryotes with crenarchaea, not euryarchaeota. The eocyte tree is a source of ongoing **debate** and, rightly or wrongly, the prevailing consensus is that archaea and eukaryotes are sister groups. Page 79

5. Nucleomorph genomes, By John M. Archibald

The exact number of secondary endosymbioses that have occurred during eukaryotic evolution is hotly **debated**, although a minimum of two (and probably three) events are required to account for the known spectrum of secondary plastid-containing organisms. Page 393

6. Events in plastid evolution, By Debashish Bhattacharya

Over time, the prokaryotic endosymbiont surrendered its autonomy and became the light-harvesting, carbon dioxidefixing, oxygen-producing organelle present in modern-day eukaryotic photosynthesizers. The number of times this occurred is actively **debated**. Page 1240

But it is not known with certainty whether the plastids in these groups evolved once or multiple times. The answer to this question has a fundamental impact on our understanding of eukaryotic evolution. Page 1240

7. The origin of eukaryotes, By Yaacov Davidov

The identity of the primordial protomitochondrion host and how the association between the two evolved are still hotly **debated**. Page 748

The exact origin of the archaeal signal is **debated**, as some analyses suggest that it forms a sister group to the Crenarchaeota, while others propose that it originated from within the Euryarchaeota, or from an ancient, unknown archaeal lineage. Page 750

The origin of the eukaryotic cell is one of the most **debated** and enigmatic issues in evolutionary biology. This **debate** includes many cycles of discarded and subsequently rediscovered hypotheses. Here, we have addressed a few central questions concerning the different eukaryogenesis models in the light of the recently published literature. Page 755

8. The origin of Metazoa, By Kirill V. Mikhailov

The origin of multi cellular animals and the nature of their ancestor are long-**debated** and challenging questions in both classical and modern biology. Page 758

9. The cytoplasmic structure, By David S. Thaler

Fundamental questions in evolution concern deep divisions in the living world and vertical versus horizontal information transfer. Two contrasting views are: (1) three super kingdoms Archaea, Eubacteria, and Eukarya

based on vertical inheritance of genes encoding ribosomes; versus (2) a prokaryotic/eukaryotic dichotomy with unconstrained horizontal gene transfer (HGT) among prokaryotes. Page 774

The present article asserts that sequence analysis alone is not able to solve the most important evolutionary problems it has framed (because the distinction between “vertical” and “horizontal” evolution becomes ambiguous) and that “bench experiments” – which have so far not played a role in this **debate** – have the potential to break the conceptual logjam. Page 778

10. A whole-genome phylogeny, By Maria Pia Di Bonaventura

High levels of topological incongruence are not unusual in genomic datasets. For instance, Rokas et al. (2003) presented evidence from yeast genomes in which 45 of the 106 gene partitions conflicted with the concatenated hypothesis. Page 955

11. Phylogeny of calcareous dinoflagellates, By Marc Gottschling

The systematic position of Thoracosphaera and its putative phylogenetic affinity to Calciodinellaceae have been discussed controversially. Page 445

12. Salmonella enterica strains, By Eric W. Brown

Horizontal transfer has played an active role in structuring several regions of the Salmonella genome, though its evolutionary impact on the entire chromosome remains a matter of **debate** (Groisman et al., 1992; Ochman et al., 2000). Page 103

13. Evolution of arginine deiminase, By Manuel Zuniga

These incongruities have been previously observed for a large number of proteins (see, for example, Brown and Doolittle, 1997) and have led to a lively **debate** among researchers favoring a view in which horizontal gene transfer has played a major, continued role in evolution (Doolittle, 1999; Jain et al., 1999) and others who consider that unrecognized paralogy explains many of these anomalous phylogenies (Forterre and Philippe, 1999; Glansdorff, 2000). Page 440

14. Chagas' disease parasite, By E. Pfeiler

Although considered valid species in the present study, the taxonomic status of members of the phyllosoma complex has been the subject of **debate** for many years. Page 218

15. GC/AT distribution patterns, By Elisa Calistri

The origin and fixation of isochores has been the object of a long lasting **debate** between the supporters of neutral and selectionist models. Page 229

16. Microsatellite Variation, By M. Imwong

The unusual patterns of variation in the *P. falciparum* genome have generated a lively **debate** about parasite origins and evolutionary history (Su, Mu, and Joy 2003; Hartl 2004). Recent studies have also revealed conflicting views on the ancestry of the related parasite *Plasmodium vivax*. Page 1016

17. Complex Spliceosomal Organization, By Lesley Collins

A number of trees representing eukaryotic evolution (Embley and Hirt 1998; Dacks and Doolittle 2001; Simpson and Roger 2002) have been published, but there is still **debate** as to the placement of many lineages on these trees. This is expected because there are inherent problems associated with reconstructing the deeply diverging lineages. Page 1054

18. Networks of Gene Sharing, By Thorsten Kloesges

A hefty **debate** is currently ablaze about the utility and meaning of the “tree of life” (see Doolittle and Baptiste 2007 vs. Galtier and Daubin 2008 cf. Baptiste et al. 2009), particularly in the context of the overall evolutionary history of prokaryotes. One could argue that the **debate** boils down to the difference between attempts to reconstruct the whole of the evolutionary process and attempts at organismal classification (Doolittle 1999). Page 1063

19. Lateral Transfer of Genes, By Martin G. Klotz

Only recently, with the flood of available whole genome sequence data and a renewed intensity of the **debate** about the universal tree of life, a very few reports on lateral gene transfer (LGT) from prokaryotes into the Eukaryota have been published. Page 1098

20. Grouping of Plant and Animal, By Gayle K. Philip

Despite substantial work, the phylogeny of malaria parasites remains **debated**. Page 1192

Appropriate molecular markers and methods for reconstruction of Plasmodium phylogeny have long been subjects of **debate**. Page 1192

In particular, the evolutionary position of the most virulent human parasite Plasmodium falciparum and the closely related chimpanzee parasite Plasmodium reichenowi has been the subject of **debate**. Page 1192

21. Plastid-Derived Genes, By Claudio H. Slamovits

Details of this complex evolution are still **debated**, and one major problem in resolving several of these **debates** lays in the accurate determination of the distribution of plastids. Page 1297

Ever since the discovery of the apicoplast, its possible relationship to dinoflagellate plastids has been **debated**, and this question is intimately tied to the larger hypothesis that all eukaryotes with secondary plastids derived from red algae acquired them in a single event, the so called chromalveolate hypothesis (Cavalier-Smith 1999). Page 1304

22. Phylogeny of Lobose Amoebae, By Jose F. Fahrni

Furthermore, the position of pelobionts—the free-living amitochondriate amoebae—is **debated**. Page 1881

23. The Protein Import Channel, By Michael J. Dagley

The identification of mitosomes in Giardia generated significant **debate** on the evolutionary origin of these organelles, whether they were highly reduced mitochondria or the product of a unique endosymbiotic event in an amitochondrial organism. Page 1941

24. Archaeal Roots of Eukaryotes, By Natalya Yutin

The emergence of eukaryotes is one of the central, and hotly **debated**, themes in evolutionary biology. These **debates** have led to multiple, competing hypotheses that present drastically different scenarios for the origin of the complex eukaryotic cell (Martin and Muller 1998; Embley and Martin 2006; Kurland et al. 2006; Martin and Koonin 2006; Dagan and Martin 2007; Poole and Penny 2007b). Page 1619

Because the position of the root of the eukaryotic tree is still subject to **debate** (see e.g., Stechmann and Cavalier-Smith 2002), the trees are presented in an unrooted format, with a basal trifurcation. Page 1883

25. Evolutionary History of Gene Duplication, By Shehre-Banoo Malik

However, the evolutionary relationships among these genes are unclear, with some **debate** as to whether eukaryotic homologs originated by lateral gene transfer. Page 2827

26. Closest Relatives of Animals, By Guiling Sun

These notions have constantly been under **debate** (Stiller and Hall 1997; Stiller et al. 2001; Nozaki et al. 2003; Nozaki 2005; Sanchez-Puerta and Delwiche 2008; Bodyl et al. 2009), and recent studies have painted a more complex picture of the evolutionary history of photosynthesis in eukaryotes. Page 2887

27. The Evolution of SMC Proteins, By Neville Cobbe

Consequently, it is not clear from the codon usage data in which direction this transfer event occurred, whether from archaea to cyanobacteria or vice versa, and there is still **debate** as to which is actually the older group of prokaryotes (Hedges et al. 2001; Cavalier-Smith 2002). Page 338

28. Eukaryotic Marine Green Alga, By Nigel Grimsley

Understandably, the frontiers of the species concept is still a matter of **debate** in single-cell organisms (Schlegel and Meisterfeld 2003), and the “pragmatic” definition of species can either rely on morphological observation “morphospecies” or on molecular markers “operational taxonomic units” (Weisse 2008). Page 52

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Fish

1. Fossil Ceratioid Anglerfishes , By Giorgio Carnevale

Although the usual biological features and bizarreness of these fishes have stimulated intense **debate** and discussion, attracting the curiosity of many ichthyologists during the last century (see, e.g., Regan, 1926; Regan and Trewavas, 1932; Beebe and Crane, 1947; Waterman, 1948; Bertelsen, 1951; Maul, 1961; Pietsch and Orr, 2007), their evolutionary history remains elusive, mostly because they are nearly unrepresented in the fossil record. Page 996

Unfortunately, lack of resolution, for the most part due to a lack of salient morphological data (certainly caused by the strongly reductive trends in skeletal architecture), resulted in the origin of polytomies at the basal and derived positions of the phylogenetic tree. Moreover, because of their virtual absence in the fossil record, ceratioids cannot be used to define the exact sequence of events in the phylogeny of such a group. Page 1004

2. A New Actinopterygian From Greenland, By Matt Friedman

Although there are some areas of agreement between their phylogenies, such as the basal or near-basal position of *Cheirolepis*, a consensus remains elusive. Studies with broader taxonomic and character samples also fail to retrieve consistent patterns of interrelationships. Page 1193

Given the uncertainties regarding the phylogenetic position of *Dialipina*, we have decided to carry out our analysis in two parts. Page 1194

The relationships among the major sarcopterygian clades were left free to vary, thereby accommodating a wide range of conflicting phylogenetic hypotheses (Cloutier and Ahlberg, 1996; Chang and Yu, 1997; Zhu and Schultze, 2001). As our study does not include non-osteichthyans, it is impossible for us to address the position of *Dialipina* within Osteichthyes. Page 1194

Unfortunately, the limited taxonomic and morphological scope of our study does not permit us to make any further contributions to the **debate** on the phylogenetic position of *Dialipina* and other putative early actinopterygians. Page 1198

The environmental context for the origins and evolution of early vertebrates has been a subject of considerable interest and **debate** (Romer and Grove, 1935; Thomson, 1980; Halstead, 1985). Page 1198

3. Relationships of the Coelacanth, By Rafael Zardoya

Yet, despite many studies that are based on either morphology or molecules, the phylogenetic relationships among tetrapods and the other two living groups of lobe-finned fishes, the coelacanth and the lungfishes, are still unresolved and **debate**d. Page 5449

4. Hagfish embryos, By Nicholas D. Holland

The corrected version of neural crest origin in hagfishes, although important in itself, takes on a broader significance for questions about the phylogeny of vertebrates (a term used inclusively here to include jawless forms lacking vertebrae). It is still unsettled whether the most-basal group of living vertebrates consists of the hagfishes alone or comprises a clade including lampreys along with hagfishes (this latter arrangement is the cyclostome hypothesis). Page 835

This is unfortunate, because the nature of the head mesoderm in basal vertebrates is central to the old **debate** between segmentalists and anti-segmentalists. Segmentalists presume that the protochordate ancestor of the vertebrates (being rather like an amphioxus) had a head region including muscular somites that, during early vertebrate evolution, became the segmented head mesoderm. In contrast, the anti-segmentalists are of two main sorts. The more extreme view is that the protochordate ancestor of the vertebrates (being rather like the tadpole larva of an ascidian tunicate) lacked muscular somites of any kind anteriorly. Page 835

5. Ribosomal RNA genes, By Jon Mallatt

The relationships among the three subgroups of sarcopterygians— lungfishes, coelacanth, and tetrapods—have generated much **debate** (reviewed by Meyer and Zardoya, 2003). Obviously, we cannot resolve this **debate**, because we did not even recover a monophyletic Sarcopterygii. Page 1017

6. Phylogeny of the Gasterosteidae, By Michelle Y. Mattern

Using five mitochondrial genes produced a topology that is not significantly different from the phylogenetic tree based upon morphology and behavior. However, those two topologies do produce different pictures of character evolution in the gasterosteids. Page 375

In order to resolve this problem, additional data need to be incorporated into the dataset. The behavioral and morphological data are currently being revised and combined with the molecular characters to produce a total evidence study for the family. Hopefully that analysis will resolve the issue of two statistically equivalent, yet topologically different, trees. Page 375

7. Shark tales, By Ximena Vélez-Zuazo

However, despite a long evolutionary history, commercial, and conservation importance, phylogenetic relationships within the sharks are poorly understood. Page 207

Other issues of **debate** are the relative position of Squatiniformes, Squaliformes, and Pristiophoriformes within Squalimorphii, and those of Carcharhiniformes, Orectolobiformes, and Lamniformes within Galeomorphii. Early morphological data placed Squaliformes sister to Pristiophoriformes. Page 208

At the family level, there is even less agreement among studies. The monophyly and placement of many, perhaps most, families are still in **debate**. Page 208, 209

Both the lack of clear phylogenetic understanding at the higher level, as well as the absence of species-level phylogenies are a hindrance for making other evolutionary inferences, for example, studying character evolution, the rate of molecular evolution and approximate time of appearances. Page 209, 210

The monophyly and position of the family Odontaspidae are unresolved in our phylogeny. Page 212

In sum, our results are incongruent with a large number of taxonomical groups, especially at the family and genus level. Given that many prior phylogenetic studies also conflict with taxonomy, it seems that existing taxonomy will require careful revision. Our results should provide a guide to where further effort in phylogenetic knowledge is most needed so as to satisfactorily resolve shark phylogeny and taxonomy. Page 216

8. North American minnows, By G. R. Moyer

Although much is known about the taxonomy, biology, and life history of Hybognathus species, their phylogenetic relations with each other remain unclear. Page 514

The phylogenetic relations among members of this clade were left unresolved by morphological data; likewise, due to incongruence in mtDNA and nuclear datasets, phylogenetic relationships among these closely related taxa remain unclear. Phylogenetic placement of *H. regius* and *H. hankinsoni* also were unresolved using morphological data; however, molecular data resolved them as sister taxa. Page 523

9. Phylogeny and biogeography, By John S. Sparks

Relationships among constituent taxa remain, for the most part, unresolved. Page 720

10. Molecular phylogeny of damsel fishes, By Nian-Hong Jang-Liaw

However, there is some **debate** over the monophyly of this suborder. Based on morphological characters, these four families form a monophyletic group (Kaufman and Liem, 1982; Stiassny and Jensen, 1987). Page 445

11. Major groups of catfishes, By John P. Sullivan

Deep within Siluroidei are 12 large, strongly supported groups with poorly resolved interrelationships. Page 636

Despite such recent progress, relationships among catfish families, genera and most species are not sufficiently resolved to craft a comprehensive classification, or to allow precise higher level biogeographic analyses or character mapping (e.g. Diogo, 2004a). The many conflicting or incompletely resolved hypotheses of relationships based on morphology or molecules need testing with additional characters and species. Page 637

12. Diversification of rockfishes, By John R. Hyde

Phylogenetic lineage reconstruction is often obscured or poorly supported due to saturation and back mutation at informative genetic loci while paleo-geographic landmarks are often so distant they do not provide good mileposts for estimating the timing of speciation events. Page 791

The phylogeny and evolution of the group has been the subject of much **debate** and has resulted in a great deal of confusion (see Kendall, 2000; for a comprehensive and entertaining review). Page 791

13. Evolutionary affinity of bill fishes, By A. G. Little

These attributes, combined with analyses of other morphological and molecular data, have led to a general perception that tunas and billfishes are close relatives, though this hypothesis has been vigorously **debated**. Page 897

At the center of **debate** surrounding scombroid phylogeny are the billfishes, comprised of the monotypic Xiphiidae and the monophyletic Istiophoridae (Collette et al., 2006). The phylogenetic relationships of billfishes have been explored in numerous morphological and molecular studies with resulting phylogenetic hypotheses differing dramatically, but more recently edging toward classifying billfishes in their own suborder, Xiphoidei. Page 897

These similarities have led to a general perception that tunas and billfishes are close relatives, though the “closeness” has been vigorously **debated**. Page 900

14. Molecular Phylogeny of the Prickly Shark, By Giacomo Bernardi

The relationships between the squalomorphs and other superorders of sharks and the relationships between the different orders within the squalomorphs are a matter of **debate**. Page 161

The classification of the cartilaginous fishes, and of the sharks in particular, is still under **debate**. The phylogeny of the sharks proposed by Compagno (1977) leaves many uncertainties that have not been clarified. Page 161

15. Phylogeny of elasmobranchs, By Christopher J. Winchell

The interrelationships of the extant elasmobranchs (neoselachians), a group that evidently originated in the Early Triassic (Cuny and Benton, 1999; Thies, 1982), are subject to **debate**. Page 214

The taxonomic positions of *Heterodontus* and *Chlamydoselachus* are controversial. Page 221

The positions were so unstable that we cannot disprove the idea that *Heterodontus* is in a monophyletic. Page 221

However, because relationships among the rajid skates, some guitarfish genera, and stingrays are uncertain (McEachran et al., 1996), our trees placing *Raja* basally and *Rhinobatos* closer to the myliobatiforms (*Potamotrygon*, *Urobatis*) could be informative. Page 222

Outstanding problems to be addressed by future gene-based studies are: (1) relations of *Heterodontus* and hexanchiforms to other sharks; (2) relations among lamniforms, carcharhiniforms, and orectolobiforms; and (3) batoid interrelationships. Page 222

16. Gene tree parsimony, By James A. Cotton

There is no doubt that lizards and snakes form part of a monophyletic radiation of diapsid reptiles, although there has been some **debate** about the exact relationships between the different extant lineages within this radiation, as discussed above. Similarly, there has been **debate** about the exact relationships between hagfish, lampreys and gnathostomes (Delarbre et al., 2002; Janvier, 1996), but the only hypotheses supported by recent work are that lampreys and hagfish form a monophyletic cyclostomes group, or that hagfish are the most basal vertebrates, with lampreys a sister-group to the gnathostomes. Page 306

17. A problematic group of fishes, By Katriina L. Ilves

Relationships among the species of Northern Hemisphere smelts (family Osmeridae) have long been **debated** in the fish systematics literature. Eight independent studies based on morphological characters failed to reach any consensus on osmerid interrelationships. Page 163

However monumental, McAllister's (1963) study did not quell the **debate** about osmerid interrelationships, as the uncertainty surrounding the phylogenetic placement and biogeography of this group continues to the present day. Page 163

Eight morphology-based hypotheses of systematic relationships among osmerid genera. Page 164

18. The Dalmatian genus Phoxinellus, By Jörg Freyhof

The phylogenetic structure of this family is still under **debate**, but several subfamilies are widely accepted and seem to form strongly supported monophyletic clades (Chen et al., 1984; Howes, 1991; Liu et al., 2002). Page 416

19. Paleoclimatic history, By Tine Huysse

The systematic relationships of the sand gobies with other gobioids remains unclear from morphology but the most likely sister group to the sand gobies has to be looked for in the Indo-Pacific region (Mckay and Miller, 1997). Page 325

In conclusion, there are presently two scenarios on the origin of the freshwater lifestyle in the sand gobies. Page 333

20. The gonorynchiform fishes, By Sébastien Lavoué

Recurrent **debates** concern the relative position of the paedomorphic fishes *Cromeria* and *Grasseichthys* (some of the smallest vertebrates) (Grande, 1994; Howes, 1985; Lenglet, 1974), and the relative positions of *Chanos* and *Gonorynchus* as the most basal group (Fink and Fink, 1981, 1996; Gayet, 1993; Grande and Poyato-Ariza, 1999; Greenwood et al., 1966; Patterson, 1984) (Figs. 2A–E). Page 167

The respective advantages of various methods of phylogenetic inference have also been largely **debated**, with sometimes conflicting conclusions reached. Page 174

In part because their paedomorphic features makes it difficult to establish their phylogenetic affinities, the systematic of *Cromeria* and *Grasseichthys* have been **debated** for a long time, and their phylogenetic placement is still uncertain. Page 174

21. Phylogenetic structure of *Zacco platypus*, By A. Perdices

The phylogenetic relationships of the genus *Zacco* are under **debate** and then, the selection of the closest outgroup is not straightforward. Page 194

22. Biogeography of the cyprinid tribe, By Lei Yang

Here, we do not intend to involve in the **debate** over the definitions over convergence and parallelism, and believe those three criteria also work for the detection of parallelism. Page 264

23. *Lepidogalaxias salamandroides*, By Jun Li

Fig. 1. Six recent major hypotheses for phylogenetic relationships of lower euteleostean fishes based on morphology (a–b) and molecules (c–f). Asterisk (*) indicates the new erected order in this study (for details see the section of Section 4). Page 933

24. Divergence times of Lizard Fishes, By Matthew P. Davis

There has been much **debate** on the taxonomy and phylogenetic interrelationships among members of the *Dercetidae* (e.g., Chalifa 1989a; Taverne 1987, 1991, 2005; Gallo et al. 2005). Page 1196

25. DNA in Dalmatian cyprinids, By Jorg Freyhof

The phylogenetic structure of the fish family *Cyprinidae* is still under **debate**, but several subfamilies are widely accepted forming well supported monophyletic units (Chen et al., 1984; Howes, 1991). Page 351

26. Evolution of the Metazoan PHD, By Kalle T. Rytkonen

Our results are more equivocal about the relationships among the HIF-3 alpha genes in cartilaginous fishes, teleosts, and mammals, which is currently a matter of some **debate** (Law et al. 2006; Richards 2009). Page 1921

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Invertebrates

1. Generic Concepts, By William I. Ausich

The position of *Dizygocrinus* is problematic. Page 40

2. A New Arthropod From The Early Cambrian, By Dongjing Fu

The accurate phylogenetic assessment will remain the subject of **debate** until more information becomes available. Page 567

3. Small Shelly Fauna From North-East Greenland, By Christian B. Skovsted

Thus, an arthropodan origin remains uncertain. Page 1088

Furthermore, at least 24 taxa, whose relationship to extant groups is uncertain, have also been recovered. Page 1089

These triangular fossils are always broken, and their affinity to other fossil remains from the Early Cambrian is uncertain. Page 1107

4. Relationships And Classification Of Scleractinia, By Jaroslaw Stolarski

There are no clear cut arguments that would support one of these hypotheses; however, the traditional paradigm that microstructures are the most conservative and thus the most useful characters in higher-rank classification supports the hypothesis of a polyphyletic origin of traditional guyniids. Because most of the traditional guyniids are living taxa, molecular studies or other biologically oriented approaches could provide new input to this **debate**. Page 1101

Despite the fact that this new area of research wrestles with very basic interpretative problems, one hopes that a new generation of molecular paleobiologists will solve most of these initial difficulties and will provide reliable cross-checking tools, independent of typical biological-based and purely geometrical microstructural approaches. Page 1106

5. Conodonts: Past, Present, Future, By Walter C. Sweet

Consequently, combined with their rich fossil record, conodonts can now make a significant contribution to the **debate** about the relative importance of stratigraphic and morphologic data in phylogenetic reconstruction (e.g., Smith, 1998, 2000). Page 1182

6. Eggs and embryos, By Simon Conway Morris

At the heart of this **debate** concerning the phylogenetic importance of metazoan larva is the problem of how best to interpret their anatomy. Page 679

This is certainly what happens in living larva, but how relevant are such observations to unravelling metazoan phylogeny? The battle-lines are now being drawn. Page 680

7. It's a long way from amphioxus, By Jordi Garcia-Fernandez

Initial molecular analyses of the Hox cluster and other regulatory genes in amphioxus, together with the first synteny analyses of the human genome, excitingly generated the modern 2R hypothesis, with two full polyploidisation events from invertebrates to mammals. For years, '2R or not 2R' has been a subject of hot **debate**. Page 671

8. Complete nucleotide sequences, By Shin-ichi Yokobori

Morphological studies have aroused controversy on the phylogenetic relationship of entoprocts to other metazoan taxa. Page 613

The relationships among the lophotrochozoan phyla are still under **debate**. Page 623

9. Ribosomal RNA genes, By Jon Mallatt

However, the relative positions of Ophiuroidea (brittle stars) and Asterozoa (sea stars) within Eleutherozoa are **debated**. The most extensive morphological and molecular-phylogenetic studies have had difficulty distinguishing between two preferred arrangements. Page 1015

10. Phylogenetic analysis with multiple markers, By Annette F. Govindarajan

Much of the **debate** between these hypotheses centers on the nature of the *Obelia* medusa. Page 821

Future research on the genetic mechanisms of medusa development will be helpful in evaluating the evolutionary relationship between these morphologies. One missing piece of information concerns the phylogenetic placement of *Hartlaubella*, a monotypic genus which could not be obtained for this study. Page 832

11. Nearly complete rRNA genes, By Jon Mallatt

Acoelomorpha, consisting of acoels and nemertodermatids, is a controversial group. Debate has raged over whether the Acoelomorpha are the most basally arising Bilateria, and whether they are diphyletic. Page 14

The tree calculated from all 197 taxa (Fig. 2) recovers many accepted clades but fails to show key groups of the new animal phylogeny. Page 14

12. Symbiodinium-like dinoflagellates, By Mauricio Rodriguez-Lanetty

To date, there is still a **debate** upon which circumstances either sexuality or asexuality is favored by natural selection. Page 166

13. Relationships among sea anemones, By M. Daly

The phylogenetic position of the athenarian family Edwardsiidae has long been the subject of **debate** (see Daly et al., 2002), and it remains unclear. Page 299

14. Phylogenomic Taxon Sampling, By K.S. Pick

A recent phylogenomic analysis adds further controversy to this **debate** (Dunn et al. 2008) (c.f., Hejnol et al. 2009). Page 1983

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14. Phylogenomic Taxon Sampling, By K.S. Pick, *Molecular Biology And Evolution*, 2010, Volume 27, Number 9, Pages 1983–1987 Page 100

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Insects

1. Segments and parasegments, By Jean S. Deutsch

The monophyly of the Arthropoda is at present generally admitted. Extant arthropods comprise four main groups, Chelicerata, Crustacea, Hexapoda and Myriapoda. The phylogenetic relationships between these groups have recently been reconsidered, and are still **debated**. Page 1117

The monophyly of the 'Myriapoda' (millipedes and centipedes and their kin) is still **debated**. Page 1119

2. The centipede *Strigamia maritima*, By Wallace Arthur

The order contains many extant families. The internal phylogeny of the order is poorly understood, but some recent studies have made a start on addressing this problem. Page 654

There has been much **debate** over the evolutionary importance of this phenomenon, but this **debate** has been hindered by a lack of information on the mechanisms underlying apparent instances of constraint/bias. Page 655

3. Development and phylogeny of arthropods, By Pat Simpson

It addressed ways to resolve the still uncertain relationships between the different groups of arthropods and featured talks discussing phylogeny and comparative developmental biology. There seems to be a general consensus that insects and crustaceans are probably sister groups and there is a suggestion that myriapods (millipedes and centipedes) are related to insects and crustaceans. However, the position of the Chelicerates (spiders, scorpions, horseshoe crabs) is still under **debate**. Page 223

4. Stalk-eyed flies, By Ian Warren

The phylogenetic subgroups of the Brachycera have been much **debated** but there is general agreement that the Cyclorhaphora, flies that develop from a pupa enclosed in a modified form of the last larval cuticle or puparium form a monophyletic group with its origins in the late Triassic. Page 300, 301

5. Spider models, By Alistair P. McGregor

Phylogenetic relationships of selected extant arthropod taxa. Note that the higher order relationships of the arthropod classes are **debated**. Page 488

6. Arthropod Evolution, By D. Osorio

Insect and crustacean lineages diverged over 500 Myr ago, and there are continuing uncertainties about whether they evolved from a common arthropod ancestor or, alternatively, they evolved independently from annelid worms. Page 419

The evolutionary origins and diversification of the Arthropoda are the subject of continued **debate**, recently enlivened by studies of the arthropod radiation during the mid-Cambrian period. Arguments about evolutionary relationships between the main arthropod groups, and whether the Palaeozoic lineages that survived and prospered were fundamentally fitter than those that perished, have not been resolved by palaeontology or by classical comparative anatomy and embryology. Page 419

7. Molecular phylogeny, By Jerome Albre

In this genus, composed of around 100 mountain species, the *Erebia tyndarus* complex has certainly been a major source of **debate** for more than a century. Page 196

The status of sibling species among the Lepidoptera is actually matter of **debate**, some authors advocating an important reduction of so-called "good species." Page 196

8. Isolation and phylogeny, By Tim Verslycke

The relative positioning of the ecdysozoans (e.g., insects) and lophotrochozoans (e.g., bivalves) within metazoan phylogeny remains the subject of active **debate**, both based on molecular and morphological approaches (Glennier et al., 2004). Page 769

9. Phylogeny of acariform mites, By Mirosława Dabert

Despite their importance, it is still not clear if this marvellous acarine diversity derives from a single ancestor or if “a mite-style” body plan originated independently from two or more arachnid ancestors (for review see Dunlop and Alberti, 2008). Page 222

The phylogenetic affinities among these lineages and their taxonomic consequences, especially the origin of the vast cohort Astigmata, are a subject of widespread and unfinished **debate**. Page 223

Sparse molecular phylogenetic reconstructions of relationships among main groups of Acariformes have given surprisingly contradictory results. Page 223

10. Molecular phylogeny and diversification, By Marco Trizzino

However, and despite their obvious relevance, our understanding of the phylogeny and biogeography of many of the large groups that could be considered most representative of the evolutionary processes leading to the current diversity is very incomplete. Page 1

11. Phylogeny of the Genus *Rhagoletis*, By James J. Smith

Despite a considerable literature describing the biology of flies in the tephritid genus *Rhagoletis*, the phylogenetic relationships of the more than 60 species classified within the genus are not well resolved. Knowledge of these relationships is important, not only in terms of obtaining information that will be useful for the control of *Rhagoletis* where it is an agricultural pest, but also in determining what role host plant shifts have played in the generation of *Rhagoletis* species diversity, a focal point in **debate** over the role of sympatric speciation in the evolutionary process. Page 33

12. The phylogeny of acorn weevils, By Joseph Hughes

In general, phylogeny reconstruction is faced with the difficulty of how to combine multiple data. Page 612

13. Mesozoic-aged Eremoneuran Diptera, By John K. Moulton

Mesozoic-aged divergences (65–250 mya) are a major hurdle for molecular systematists inferring arthropod relationships because few currently available markers adequately track these events (Friedlander et al., 1992, 1994; Hillis and Dixon, 1991; Wiegmann et al., 2000). This is particularly true if the divergences occurred in rapid succession, i.e., as an explosive radiation (Fishbein et al., 2001). Page 363

14. The phylogeny of flies, By John K. Moulton

The greatest degree of concordance among the competing classifications/phylogenies exists between those of Chvala (1983) and Moulton and Wiegmann (2004). Moulton and Wiegmann (2004) recovered trees largely concordant with Chvala's (1983) empidoidean classification, with the exception being that Chvala inferred Atelestidae to be the sister group to Cyclorrhapha. Page 702

15. Earth-boring dung beetles, By Regina L. Cunha

Phylogenetic relationships within the family are based exclusively on morphology and remain controversial. Page 578

Although earth-boring dung beetles are fairly represented in the fossil record (Krell, 2007) there is no information regarding lineage-splitting events within the family that lead to current species diversity. Page 578

Few studies have focused on Geotrupidae, and phylogenetic relationships among earth-boring dung beetles remain poorly understood. Thus far, phylogenetic studies on Geotrupidae have been mostly based on morphological data, and rendered poorly resolved or even contradictory results. Page 579

Phylogenetic relationships within Geotrupidae have been a long-standing **debate** encouraged by the wealth of conflicting evolutionary proposals based on morphological studies. Page 581

16. North American admiral butterflies, By Sean P. Mullen

Within North America, the Viceroy (*L. archippus*) is the basal lineage while the relationships among the remaining species are not well resolved. Page 747

Unfortunately, the utility of this group of butterflies as a subject of speciation research has been limited by the lack of a well-supported phylogenetic hypothesis. Page 748

However, without knowledge of the phylogenetic relationships between the two continental faunas of these butterflies, it is difficult to assess this hypothesis. Page 749

Given the widespread confusion regarding phylogenetic relationships among species and genera within the subtribe Limenitidini, it is clear that there is a need for further revisionary taxonomic work of the Palearctic members of the genus *Limenitis* and other closely related groups. Page 757

17. African *Dacus*, By M. Virgilio

Regardless these efforts, the phylogenetic relationships among *Dacus* species remained largely unresolved mainly because of the difficulties in assigning homologous character states. Page 531

The comparisons between the molecular phylogeny and the morphological classification revealed a number of discrepancies and, in the vast majority of cases, the molecular data were not compatible with the monophyly of the currently recognised subgenera. Page 531

Conversely, disagreement between molecular phylogeny and morphospecies taxonomy could provide the starting point of a **debate** towards a more consistent classification. Page 532

18. A phylogenetic revision of the *Glaucopsyche*, By L. V. Ugelvig

Despite much research on the socially parasitic large blue butterflies (genus *Maculinea*) in the past 40 years, their relationship to their closest relatives, *Phengaris*, is controversial and the relationships among the remaining genera in the *Glaucopsyche* section are largely unresolved. Page 237

The relationships between these genera are poorly known, and were not well resolved in a previous molecular phylogeny that included representatives of ten of the genera (Als et al., 2004). Page 238

19. Hennig's orphans revisited, By Isaac S. Winkler

The composition of this group and relationships among included families have been controversial. Page 746

Determining phylogenetic relationships among families in this assemblage is arguably the most difficult problem in the systematic of Diptera (McAlpine, 1989), and a consensus classification has not yet been achieved. Page 746

The limits, composition and phylogenetic relationships of the remaining superfamilies have been historically more problematic. Page 746

Relationships among "acalyprate" flies are notably difficult because of their large diversity and the high level of homoplasy observed in most studied character systems. DNA sequence data have proven to be no exception to this latter difficulty. Page 756

Because both molecular and previous morphological hypotheses are subject to this random error and generally poorly supported, it is difficult to evaluate the accuracy of many relationships presented here. Page 757

20. Placement of *Conopidae*, By Joel F. Gibson

The question of how *Conopidae* is related to the remaining schizophoran families, however, has been the source of some **debate**. Page 91

21. Gall-forming aphids, By M. Inbar

One of the most striking characteristics of gall-forming insects is the variability in gall position, morphology, and complexity. Our knowledge of the driving forces behind the evolutionary divergence of gall types is limited. Page 504

Finally, an alternative scenario proposes that gall morphologies radiated with no adaptive value for the insects. Page 505

22. Phylogeny of the higher *Libelluloidea*, By Jessica Ware

Although libelluloid dragonflies are diverse, numerous, and commonly observed and studied, their phylogenetic history is uncertain. Page 289

While it is clear that a well-supported phylogenetic hypothesis is needed in order to reach an understanding of the evolution of these traits, phylogenetic relationships among libelluloid families remain highly contentious, with numerous hypotheses proposed (Fig. 1 and Table 1). Page 290

23. Phylogeny of the orchid bees, By Alice Michel-Salzat

Despite previous phylogenetic studies of on morphological characters, the relationships among the five euglossine genera remain under **debate**. Page 309

Without fossils, this remains speculative. Page 320

24. Phylogeny and Bayesian divergence, By Shaun L. Winterton

The lack of external corroborative evidence from fossils for Cretaceous-aged divergences weakens our hypothesis of relationships and ages for weakly supported nodes at the base of Panopinae and Acrocerinae (partim). For improved estimates of phylogeny and divergence times in acrocerids it is equally important to both increase the taxon sampling for DNA sequence data in these clades, and to discover intermediate aged fossils of Acroceridae to provide corroborative evidence of ages. Page 830

25. Ribosomal protein genes, By Stuart J. Longhorn

The phylogenetic relationships among holometabolan insect orders remain poorly known, despite a wealth of previous studies. In particular, past attempts to clarify the sister-group of the enigmatic order Strepsiptera with rRNA genes have led to intense **debate** about long-branch attraction (the ‘Strepsiptera problem’), without resolving the taxonomic question at hand. Page 846

There is little consensus on the phylogenetic relationships among holometabolan orders from morphological data (Kristensen, 1991, 1999) (Fig. 1A and B). Page 846

Hypothetical relationships of holometabolan insect orders from various types of data. Page 847

26. Microgastrine wasp genera, By Jonathan C. Banks

Uncertainty in phylogenetic estimation at higher taxonomic levels is inevitable, due to the confounding effects of factors that may indicate alternative patterns. Page 690

27. Primate sucking lice, By Jessica E. Light

Oftentimes, host data (e.g., molecular, morphological, or fossil data) are insufficient to resolve certain aspects of host history and in these cases data from a cospeciating parasite may provide vital information that can be used to infer events in host evolutionary history. Page 376

28. Molecular phylogenetics of the spider family, By Michael G. Rix

The spider family Micropholcommatidae is an enigmatic taxon of uncertain limits and uncertain affinities. Various phylogenetic hypotheses have been proposed for the family, but these hypotheses have never been tested with a robust phylogenetic analysis. The existence of similar Australasian and New World taxa, the possibility of morphological convergence associated with extreme ‘smallness’, and the apparent paucity of synapomorphic morphological characters, have all clouded generic relationships in this group. Page 1031

Alternative hypotheses proposed for the phylogenetic position of the Micropholcommatidae. Page 1033

Methodological comparisons are central to systematic biology, and have traditionally generated much **debate** and little consensus. Parsimony, likelihood and Bayesian methods each bring a set of assumptions, benefits and recognised problems to the issue of phylogenetic inference. Page 1045

29. Phylogenetic multi-locus codon, By James S. Patterson

The **debate** over the monophyly of triatomine bugs and the temporal origin of triatomine bugs are linked and could be used to assess the vicariance of Gondwanaland breakup, or test whether the date of the molecular clock is accurate. Page 609

The genetic and morphological similarity between the Reduviinae and Triatominae, around which the monophyly **debate** rests, raises an important evolutionary question: why was haematophagous behaviour unable to evolve prior to the formation of South America in comparison to their immediate ancestors such as *Opisthacidus* spp. and *Zelurus* sp.? Page 620

30. Domestication of olive fly, By F. Nardi

The origin and ancient history of the olive tree is still matter of **debate**, but its basal diversification occurred most likely following the aridification of African midlands at the beginning of the Pliocene. Page 678

Mitochondrial sequences have been exploited extensively to study evolutionary processes at the species level (Avice, 2000; Zink and Barrowclough, 2008 for a recent **debate**). Page 679

31. Family level relationships of tarantulas, By Nadia A. Ayoub

Although gaps have been shown to be phylogenetically informative (e.g., Johnson and Soltis, 1995; Baldwin and Markos, 1998; Giribet and Wheeler, 1999), there is **debate** over the best method for including gaps in phylogenetic inference. Page 398

32. Dragonfly Genera Libellula, By Thomas Artiss

Considerable **debate** exists over several relationships within Libellula, as well over the status of two putative genera often placed as subgenera within Libellula: Ladona and Plathemis. Page 348

33. Relationships among the Braconidae, By Kevin M. Pitz

Phylogenetic relationships among the Braconidae have been a source of contention, **debate**, and uncertainty for many years. This uncertainty has been evident in the conflicting relationships and lack of resolution obtained from various morphological (van Achterberg, 1984; Quicke and van Achterberg, 1990; Wharton et al., 1992) and molecular datasets (Dowton et al., 1998; Belshaw et al., 1998; Dowton et al., 2002). Page 338

34. Insect Order Hymenoptera, By James N. Derr

The parasitoids belong to at least nine currently recognized superfamilies whose relationships and composition are the subject of some **debate** (Konigsmann, 1978a; Rasnitsyn, 1980, 1988; Naumann and Masner, 1985; Gibson, 1986; Gauld and Bolton, 1988). Page 136, 137

35. Polyphyly of the Zaprionus, By Amir Yassin

This issue is still under **debate** among world Drosophila researchers (e.g., McEvey et al., 2008; O'Grady et al., 2008; Prigent, 2008; Yassin, 2008; Dalton, 2009) and consideration of the Commission. Page 338

36. Southern Appalachian opilionid, By Steven M. Thomas

Although the inter-relationships and monophyly of certain opilion subgroups is an area of **debate** and active research, Laniatores monophyly is universally accepted (reviewed in Giribet and Kury, 2007). Page 646

37. Relationships among Bactrocera, By Paul T. Smith

The issue of whether to combine data sets in phylogenetic analysis is a subject of much **debate** (e.g., Bull et al., 1993; De Queiroz, 1993; De Queiroz et al., 1995; Huelsenbeck et al., 1996; Nixon and Carpenter, 1996), and no clear consensus has emerged. Page 13

38. Libelluloid dragonflies, By Jessica L. Ware

The two topologies differ in their placement of Corduliidae and Macromiidae, whose mutual relationships with Libellulidae were unresolved in a previous analysis by Ware et al. (2007) and have been the subject of considerable **debate** (see Ware et al., 2007 for a detailed review). Page 428

39. The genus Drosophila, By Amir Yassin

Deciding where to draw the line in species diagnosis and delimitation is akin to the "lumping and splitting" **debate** that continues to frustrate traditional taxonomists. Page 510

40. Rocky Mountain grasshopper, By W. Chapco

This viewpoint has subsequently led to some heated **debate** concerning the species status of *M. spretus* and the species-defining value of genitalic characters (Cohn, 1994; Lockwood, 1996). Page 810

41. The Chagas disease vector, By Fernando A. Monteiro

However, while contingency table analysis is statistically robust, the accuracy of the conclusions drawn using the inference key is still subject to **debate** (Knowles and Maddison, 2002). Page 54

42. Queens of the Little Fire Ant, By Olivier Rey

However, the short-term advantages of sexual reproduction remain a matter of **debate**, and asexuality appears to emerge easily and independently from sexual lineages (Simon et al. 2003). Page 2591

43. Regulatory Regions of Drosophila Genes, By Michael H. Kohn

The role that natural selection may play in shaping patterns of polymorphism and divergence of protein encoding sequences has been a long-standing issue of **debate** (Kimura 1968; King and Jukes 1969; Ohta 1973; Nei 1987). Page 374

44. Support for the Ecdysozoa Hypothesis, By Lars Podsiadlowski

The ongoing Articulata/Ecdysozoa **debate** is in need of additional ground pattern characters for Panarthropoda (Arthropoda, Tardigrada, and Onychophora). Page 42

Here, we compare the onychophoran mitochondrial gene order with that in other Bilateria and perform a sequence-based phylogenetic analysis, which contributes to the ongoing Articulata/Ecdysozoa **debate**. Page 42

45. Genome of the House Centipede, By Enrico Negrisolo

Although there is almost unanimous consensus on the monophyly of the phylum (Giribet and Ribera 2000), there is also hot **debate** about the phylogenetic relationships among the four main arthropodan lineages: chelicerates, myriapods, crustaceans, and hexapods. Page 770

46. History of Drosophila buzzatii, By Hafid Laayouni

There is, however, little consensus about the extent or importance of genetic interactions in the evolutionary process after more than half a century of **debate** (Whitlock et al. 1995). Page 931

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Introns

1. The Mediterranean Fruit Fly, By Jan Kwiatowski

The origin and evolution of introns have been the subjects of much **debate**. Page 77

2. Evolutionary Dynamics of Introns, By Malay Kumar Basu

Origin and evolution of introns are often considered within the context of the **debate** between the introns-early and introns-late concepts, a conundrum that emerged shortly after the discovery of the exon–intron organization of eukaryotic genes. Page 111

3. Two Distinct Globin Families, By Anja Roesner

Intron positions are considered as valuable clues for gene evolution, but the antiquity of introns within globin genes and their positional stability have been a matter of **debate**. Page 18

4. Unique Intron Positions, By Scott William Roy

The timing, causes, and mechanisms of intron origin have long been matters of **debate** (e.g., Hickey and Benkel 1986; Stoltzfus 1994; Elder 1991, 2000; Giroux et al. 1994; Poole et al. 1998; Venkatesh et al. 1999; Lynch 2002; Fedorov et al. 2003; Mourier and Jeffares 2003; de Roos 2004; Fedorov and Fedorova 2004; Roy 2004; Sverdlov, Babenko, et al. 2004; Collins and Penny 2005; Niu et al. 2005; Lin and Zhong 2005; Perumal et al. 2005; Fedorov and Fedorova 2006; Knowles and McLysaght 2006; Logsdon 1991). Page 1447

These results have important implications for the ongoing **debate** on the relative importance of intron gain and loss (Rogozin et al. 2003, 2005; Babenko et al. 2004; Qiu et al. 2004; Csuro's et al. 2005; Nguyen et al. 2005; Roy and Gilbert 2005a, 2005b), and support the notion that early eukaryotic ancestors were very intron rich, with intron losses outnumbering intron gains through subsequent evolution over a wide variety of eukaryotic lineages (Roy and Gilbert 2005a, 2005b). Page 1448

These data inform the more general **debate** about the incidence of parallel intron insertion (Tarrío et al. 2003; Qiu et al. 2004; Sadusky et al. 2004; Stoltzfus 2004; Csuro's 2005; Nguyen et al. 2005; Sverdlov et al. 2005). Page 1451

5. Intracellular Life Stages, By Erin E. Gill

Within most eukaryotes, these core characteristics are generally shared by most genes, and although spliceosomal introns are variable in density between genomes, overall they are very common (although there is a long-standing **debate** about their origin, potential functions, and evolutionary significance) (Collins and Penny 2005; Rogozin et al. 2005; Koonin 2006). Page 1579

6. Intron Loss and Gain in Plants, By Scott William Roy

Despite ongoing **debate** (Fedorov et al. 2001; Roy et al. 2001; Kaessmann et al. 2002; Roy et al. 2002; de Souza 2003; Fedorov et al. 2003; Roy 2003; Vibranovski et al. 2005), momentum has shifted in recent years toward the perspective that introns were absent in the common ancestor of prokaryotes (which lack spliceosomal introns) and eukaryotes and have arisen during the course of intron evolution (e.g., Cavalier-Smith 1985, 1991; Stoltzfus et al. 1994; Logsdon 1998; Ruvinsky et al. 2005; Ruvinsky and Ward 2006; Whamond and Thornton 2006). Page 171

7. Absence Polymorphisms in Daphnia, By Angela R. Omilian

Since the discovery of spliceosomal introns (Berget et al. 1977; Chow et al. 1977; Evans et al. 1977; Goldberg et al. 1977), their origins and evolutionary roles have been **debated** (reviewed in Roy and Gilbert 2006; Lynch 2007). Page 2129

Our findings are relevant to another idea at the heart of the introns-early versus introns-late **debate**—the preferential insertion of new introns at proto-splice sites. Page 2136

8. Relationship of Intron Positions, By Danny W. De Kee

Claims of intron-structure correlations have played a major role in **debates** surrounding split gene origins. Page 2158

9. Smoke Without Fire, By Scott William Roy

Identification of recently gained spliceosomal introns would provide crucial evidence in the continuing **debate** concerning the age and evolutionary significance of introns. Page 2259

10. Initial Stage of Domain Shuffling, By Kazuhiko Ohshima

However, vigorous **debate** continues about the timing, mechanisms, and causes of spliceosomal intron evolution (Roy and Gilbert 2006; De Kee et al. 2007). Page 2522

11. Loss and Gain of Introns, By Yong-Hwee Loh

Ever since the discovery of spliceosomal introns about 30 years ago, the evolutionary origin and significance of spliceosomal introns have been the subject of a lively **debate** (Jeffares et al. 2006; Roy and Gilbert 2006). Page 526

12. Deletion Bias in Avian Introns, By Kevin P. Johnson

The role of selection on intron size is a matter of **debate** (Clark, Leicht, and Muse 1996; Carvalho and Clark 1999; Comeron and Kreitman 2000; Duret 2001; Lynch 2002; Waltari and Edwards 2002). Page 599

Resolving this **debate** will require an understanding of the underlying mutation rates and substitution properties of insertion and deletion events (indels) in introns. Page 599

13. Extremely Intron-Rich Genes, By Miklos Csuros

For the last 30 years, the study of intron evolution had been coached, primarily, as a **debate** between the so-called introns-early and introns-late concepts. Page 903

14. A Sequence-Based Model, By Danny W. De Kee

Claims of intron-structure correlations have played a major role in **debates** surrounding split gene origins. Page 2158

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Introns

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Mammals

1. When Clocks Collide, By Christopher A. Brochu

The outcome of this particular conflict colored the nature of the **debate** for many years. New fossil discoveries eventually put the human-chimp split much closer to the molecular estimate (Fleagle, 1998). Page 1

2. Late Neogene Dwarf Tapir, By Richard C. Hulbert Jr.

Because of these limitations, the phylogenetic affiliation and chronologic range of “*T.*” *polkensis* have remained **enigmatic**. Page 238

There had been considerable previous **debate** about whether the fossil vertebrates found in the phosphate mines consisted of one or two faunas, and how this fauna (or faunas) correlated with those from the central and western United States and Europe. Page 238

3. Ancestor Of Wild Dogs, By Adam Hartstone-Rose

The evolutionary origin of *L. pictus* **is poorly understood**. Despite numerous morphological (Tedford et al., 1995; Van Valkenburgh and Koepfli, 1993; Zrzavy and Ricankova, 2004) and molecular studies (Bardeleben et al., 2005; Lindblad-Toh et al., 2005; Zrzavy and Ricankova, 2004), its phylogenetic relationship to other canids, especially the genera *Canis* (Linnaeus, 1758; wolf-like dogs) and *Cuon* (Hodgson, 1838; the Asiatic dhole), has remained controversial (see also nomenclatural note in Material and Methods, below). The phylogenetic uncertainty of the lineage is heightened by the extremely sparse record of fossil African canids, which means that the evolutionary path leading to *L. pictus* is poorly known. Page 299

4. Metaphiomys (Rodentia: Phiomysidae), By Nancy J. Stevens

The evolutionary history of the living African rodent families is a topic of considerable **debate**, yet it is generally agreed that the modern cane rats (*Thryonomys* Fitzinger, 1867) and dassie rats (*Petromus* Smith, 1831) have an evolutionary history within the infraorder Phiomorpha (e.g., Wood, 1968). Page 407

5. Super Family Of Marsupial, By Jeanette Muirhead

Relationships among peramelemorphians (commonly called bandicoots) and their relationships to other marsupials **are contentious**. Page 512

6. Windows On The Evolution Of Picrodus, By Craig S. Scott

By contrast, the position of picrodontids within plesiadapiforms has not been easily resolved and at present no consensus concerning this important issue has emerged. Page 656

7. Evaluating Internal Versus External Characters, By Lindsey R. Leighton

Debate over the relative phylogenetic value of internal vs. external characters is roughly analogous to the **debate** in mammalian systematics over the value of dental, cranial, and post-cranial characters (Szalay, 1985; Van Valen, 1993; Sanchez-Villagra and Williams, 1998). Page 659

8. Implications For Mammalian Paleobiogeography, By Pieter Missiaen

Uncertainties about the ancestor of Eotitanops and the exact phylogenetic relations of the species included in the genus, together with the apparently frequent intercontinental dispersal of brontotheres (Mihlbachler, 2008), still prevent us from providing a conclusive answer to the geographic origin of brontotheres. Page 675

9. The Phylogeny Of Bunodont Marsupials, By Robin M. D. Beck

The complex combination of plesiomorphies, apomorphies related to bunodonty, and striking autapomorphies present in *Numbigilga* n. gen. render its phylogenetic **affinities obscure**. Page 758

10. Identification Of A New Species, By G. D. Wesley

The relationships among the earliest carnivorans or carnivoramorphans (“miacoids,” Flynn and Galiano, 1982; Hunt and Tedford, 1993; Wyss and Flynn, 1993; Flynn, 1998), especially regarding their position relative to the crown clade Carnivora, are still unclear. One reason for this uncertainty is the scarcity of relatively complete fossil material for most early taxa. This is certainly true for *Tapocyon*. Page 769

11. The Oldest Skull Of The Order Carnivora, By T. J. Meehan

There are several hypotheses on the systematic of early carnivorans, including recognition of a third family (Didymictidae; Flynn and Galiano, 1982), and there has been uncertainty about the relationship of each family in relation to one another and to the Suborders Feliformia and Caniformia. Page 1091

The oldest known carnivoran, *Ravenictis*, is of earliest Paleocene age (Puercan) and has been assigned to Miacoidea with uncertain familial affinities (Fox and Youzwyshyn, 1994). Page 1091

12. Early Mammalian Radiations, By Richard L. Cifelli

For organizational purposes, it is convenient to follow some broad systematic framework for mammals, notwithstanding the fact that placement of several major groups is unsettled and the subject of intense **debate**. Page 1214

This morphological transition remains unchallenged, and molar pattern justifiably continues to figure prominently in **debate** about the relationships of early mammals. Page 1218

All workers since Ride (1964) have recognized the enormity of marsupial diversity by placing them in multiple orders, though relationships remain **debate**d in many cases. Page 1220

13. The late Oligocene of Eritrea, By Jeheskel Shoshani

In addition, the phylogenetic connections of elephantimorphs to more archaic taxa were uncertain and subject to considerable **debate** (2, 8, 16–17). Page 17296

14. The vertebrate fossil record, By Johannes Muller

The use of this date, however, has not been free of controversy, which recently culminated in an open **debate** involving both paleontologists and molecular biologists. Page 1069

15. Early origins of modern birds, By Michael J. Benton

Two major current phylogenetic questions are hotly **debated**, however: the origins of Metazoa (multi celled animals), and the origins of modern bird and mammal groups. In both cases, molecular evidence suggests that the point of origin is twice as old as the oldest known fossils. This implies either that half the fossil record of animals, and of modern birds and mammals, is cryptic, or that the molecular conclusions are flawed. Either way, there is a strong challenge to the integrity of molecular phylogenetic analytical techniques, or to claims by palaeontologists that the history of life can be divined from the fossil record. The question of metazoan origins has been **debate**d already in BioEssays. Page 1043

These dramatic claims are one of many challenges to “traditional” morphology-based views. Past experience does not indicate which way the **debate** will go, whether the molecular challenge, or the status quo, will be upheld. Nonetheless, **debates** such as these have often been heated, and it is worth reviewing the current position. Page 1044

In cases of conflict and error, molecular trees suffer many of the same methodological problems as morphological, for example the choice of taxa in the in group, the choice of out group taxa, the choice and definition of characters, and the choice of algorithm. Results obtained using either technique may be confused by problems of convergence, long branch attraction, and rapid splitting of lineages (star phylogenies). In addition, special features of molecular phylogeny reconstruction cause problems: variable rates of substitution at different sites, differential rates of transitions and transversions, and multiple substitutions at sites. Page 1044

The postulation of rare or cryptic ancestors does not really resolve anything, and is just a restatement of the problem; there is no independent evidence for the proposal that ancestors were cryptic other than the assumption that such ancestors were there and yet have not been found. The proposal fails absolutely on a probability argument: why should some 20–30 lineages, the modern bird and mammal orders reputed to have existed undetected through most of the Cretaceous, all uniformly have remained cryptic until they blossomed forth in abundance and with autapomorphies in place and fully displayed between 70 and 55 million years ago? Page 1047

There are numerous other substantial problems to be considered before accepting date estimates founded on molecular data. As Bromham and colleagues point out, current estimates of specific dates of divergence between various clades of mammals vary enormously, and sometimes by as much as 100%. Page 1049

However, from a strictly paleontological perspective, the mammal–bird split is problematic because: (a) there are not enough fossil localities from the early Late Carboniferous that predate the earliest known evidence of the split, (b) the same is true for the number of fossil localities immediately after the first appearance of amniotes and (c) there are still several long ghost lineages in the phylogeny of early amniotes and their sister taxa. Page 1074

16. Human Evolution, By Bernard Wood

It is the extent to which those regional characteristics are continued within the regional populations that succeeded them that lies at the root of ongoing **debate** about the origin of anatomically modern humans. Page 952

17. Phylogeny of Old World monkeys, By Jinchuan Xing

Branching order within the Asian lineage is one of the more hotly **debated** areas in Old World monkey phylogeny. One view, based on fossil and morphology studies, indicates that *Nasalis* was the Wrst to diverge from the rest of the group (Peng et al., 1993). On the other hand, karyotypic studies indicate that the *Pygathrix* was the Wrst to diverge and a relatively close relationship between *Nasalis* and *Trachypithecus* exists (Bigoni et al., 2003, 2004). Page 876

Using a consensus approach, Disotell (2003) was unable to resolve the relationships between many of these genera. The *Alu* insertion data presented here are useful in resolving some of these problematic relationships. Page 876

18. Phylogeny of the bears, By Li Yu

The taxonomic classification and phylogenetic relationships within the bear family remain argumentative subjects in recent years. Page 480

19. Phylogeny of musk deer, By Saurav Guha

The phylogenetic status of the infra order Pecora is controversial, even though it is supported by paleontological, morphological, and molecular evidence. Page 585

However, the relationship among the pecoran families remains open for some **debate**, as the phylogenetic analyses have been complicated by numerous cases of morphological convergence among the pecoran families. Page 586

20. Mitochondrial DNA coding, By Corey S. Davis

Despite extensive interest in the systematics of Pinnipedia, questions remain concerning phylogenetic relationships within the Phocidae or “true” seals. Page 363

Although the arctoid (bear-like) affinities of all pinnipeds are readily accepted, there has been significant **debate** over whether the pinnipeds originated from one (monophyletic) or two (diphyletic) ancestral stock(s) (Mitchell and Tedford, 1973). Related to this **debate** is the question of which specific group of terrestrial carnivores gave rise to the pinnipeds (Flynn, 1988). Page 363

Monophyly of the Phocinae has not been questioned since King (1966), yet considerable **debate** exists over relationships within the group. Page 364

In contrast to the lack of study focusing on the relationships of the major caniform lineages is the substantial attention given to resolution of the **debate** over a monophyletic versus diphyletic origin of the pinnipeds, the identification of the sister group of the pinnipeds (if monophyletic), and the related **debate** concerning the relationships among the three pinniped families, Phocidae, Odobenidae, and Otariidae. Page 372

In the context of an increasing acceptance of the monophyletic origin of the pinnipeds, considerable **debate** still exists concerning their affinities. Page 372

21. Phylogeny of Oriental voles, By Jing Luo

A comprehensive phylogeny based on unambiguous characters and appropriate phylogenetic reconstruction methods is still required to shed light on the classification and evolutionary history of this group. Page 351

22. The effect of branch lengths, By Austin L. Hughes

The relationships among the orders of eutherian (placental) mammals represents an unresolved phylogenetic question to which issues of both taxon sampling and LBA are relevant. Page 82

Because only three mammalian species were involved, the present analyses cannot resolve the controversial question of the branching order of the major lineages of placental mammals. Page 87

23. Phylogeny of old world deer, By Christian Pitra

Despite the continuous accumulation of palaeontological, morphological, karyological, and behavioural data, the evolution of this group of deer has been a matter of much speculation and **debate**, as is reflected in uncertainties about evolutionary relationships at different taxonomic levels (Table 1). Page 880

24. Phylogeny of the squirrels, By Scott J. Steppan

However, the utility of this body of knowledge is compromised by an incomplete understanding of their phylogenetic relationships. Page 703

25. Bat Phylogeny, By Francois-Joseph Lapointe

This **debate** is an epistemological as well as a methodological one. Page 55

For all these reasons, we believe that the answer to the matter which is at issue in the **debate** will come through a global approach involving total evidence as well as consensus. Page 55

This last combination illustrates the implications of our distance-based approach to the total evidence versus consensus **debate**. Page 58

26. A complete species-level phylogeny, By Zoltan Takacs

The Hylobatidae (gibbons) are among the most endangered primates and their evolutionary history and systematics remain largely unresolved. Page 456

While gibbons represent one of the three major adaptive radiations of anthropoid primates in Southeast Asia, and despite several revisions of gibbon systematic (e.g. Geissmann, 1995; Groves, 1972; Marshall and Sugardjito, 1986; Pocock, 1927) and various scenarios proposed to explain the radiation of this group (e.g., Chivers, 1977; Groves, 1993; HaimoV et al., 1982), their evolutionary history and systematics remain largely unresolved. Phylogenetic relationships, even among the main divisions of the Hylobatidae family are unclear, and the total number of species is contested. Page 456, 457

Fossil evidence applicable to gibbon evolution is very limited and its interpretation is considered problematic (Fleagle, 1984, 1999). Earlier studies applying morphological, behavioral or vocal characters to address the evolutionary relationships among gibbons have produced inconsistent results (Creel and Preuschoft, 1984; Geissmann, 1993, 2002a; Groves, 1972; HaimoV et al., 1982). Page 457

Fig. 2. Published representations of the phylogenetic relationships among gibbon taxa. (A) Groves (1972); (B) Chivers (1977); (C) HaimoV et al. (1982); (D) Creel and Preuschoft (1984); (E) Garza and WoodruV (1992); (F) Hayashi et al. (1995); (G) Purvis (1995); (H) Zhang (1997); (I) Zehr (1999); (J) Roos and Geissmann (2001); and (K) Geissmann (2002b, vocal data). Page 458

However, we recognize, that assigning generic-level status to these four clades remains open to **debate**. Page 464

27. Phylogeny of mysticete whales, By Amanda L. Rychel

By combining data into a single analysis, a better estimate of the true phylogeny may be obtained and/or overall clade support may be improved. However, this is based on the assumption that the several data partitions are not strongly incongruent. In the **debate** over whether to combine data or not, both possibilities have been shown to occur. Page 899

Even though combining data will continue to be a contentious issue, an argument for combining data, even between data sets with different phylogenetic histories can be made (Wiens, 1998). Page 899

28. Evolution of RNases, By Lin Xu

In this short communication, we reanalyzed a recent study (Zhang, 2006) and demonstrated that the uncertainty of inferred phylogeny may lead to different conclusions about parallel evolution of DNA substitutions. Page 397

29. Evolution of South American rats, By Yuri L.R. Leite

The phylogenetic relationships between capromyids, Myocastor, and other echimyids have long been a matter of **debate**. Page 460

30. Living squirrel monkeys, By Kenneth L. Chiou

In the absence of fossil data, molecular phylogenies offer the opportunity to evaluate the tempo and mode of speciation in extant taxa (Moritz et al., 2000). Page 737

31. Toothed whale monophyly, By Masato Nikaido

However, research published in the last several years has made the issue of the monophyly or paraphyly of toothed whales a subject of **debate**. Page 216

Despite extensive **debate** for more than ten years, the phylogenetic position of sperm whales has not been definitively determined with strong bootstrap probability (Milinkovitch et al., 1994; Adachi and Hasegawa, 1995; Milinkovitch, 1995; Arnason and Gullberg, 1996; Smith et al., 1996; Cerchio and Tucker, 1998). Page 216

Although the position of beaked whales has been the subject of **debate** too, we focus on the three lineages of dolphins, sperm whales and baleen whales in order to simplify the problem. Page 219

32. The red panda's ancestry, By Jun J. Sato

Few species have been of more disputed affinities than the red or lesser panda (*Ailurus fulgens*), an endangered endemic Southeast Asian vegetarian member of the placental mammalian order Carnivora. This peculiar carnivoran has mostly been classified with raccoons (Procyonidae) or bears (Ursidae), grouped with the giant panda (*Ailuropoda melanoleuca*) in their own family, or considered a separate lineage of equivocal ancestry. Page 907

Even though the bear nature of the giant panda was convincingly demonstrated almost half a century ago (Davis, 1964) and the perception of this species as part of a sister lineage to all other living ursids has become ultimately widespread (O'Brien et al., 1985; Bininda-Emonds et al., 1999; Bininda-Emonds, 2004), the relationships of the red panda have remained puzzling and highly controversial despite a variety of data classes examined. Only over the last two decades, attempts to decipher the enigma of the red panda's affinities, whether based on morphologic or genetic grounds or both, have resulted in an impressively broad range of hypothesized relationships. Page 908

For a discussion of the limitations of these two measures of phylogenetic confidence and an ongoing **debate** on their interrelationship, see Suzuki et al. (2002), Wilcox et al. (2002), Alfaro et al. (2003), Cummings et al. (2003), Douady et al. (2003), Erixon et al. (2003), Huelsenbeck and Rannala (2004), Simmons et al. (2004), Zander (2004), Pickett and Randle (2005), Yang and Rannala (2005), Alfaro and Holder (2006), Simon et al. (2006), Svennblad et al. (2006), Wheeler and Pickett (2008), and references cited therein. Page 909

33. Chacoan peccaries, By Jaime Gongora

There is ongoing paleontological, cytogenetic, and molecular **debate** about phylogenetic relationships among them. Page 181

There are two hypotheses about the location in the New World of the divergence of the tayassuids. Page 181

Whichever hypothesis is true, at the present the oldest known Tayassuidae family fossil found in North America has been dated at about 33–36 MYBP. Page 182

The divergence time estimates from this study should be viewed with caution as there is incomplete information on fossil dating and history of New World peccaries as well as ambiguity of extinct and extant New World peccary relationships based on fossil and morphological data. Page 186

34. Phylogenetic studies of pantherine cats, By Li Yu

The pantherine lineage, as the most recently evolved (within 1–8 MYA; Janczewski et al., 1995; Pecon Slattery et al., 1994) and largest felid group (around 20 cat species; Janczewski et al., 1995) has demonstrated great confusion in their taxonomy and phylogeny. Page 483

They had been disputably assigned to 2–13 genera under various classification schemes in past studies (Ewer, 1973; Hemmer, 1978; Leyhausen, 1979; Nowak, 1999) and moreover, phylogenetic relationships among these pantherine species have also been controversial. Page 483

Our results demonstrate that individual genes, including the six previously published gene data (tree not shown), and the combined nuclear dataset, fail to recover a satisfying phylogeny. This lack of resolution is largely due to insufficient phylogenetic information in individual loci. Page 493

35. The Praomys group, By E. Lecompte

The basal relationships within the Praomys group are poorly resolved, suggesting a rapid radiation at about 7–9 million years ago based on genetic divergence rates calibrated from the fossil record. Discrepancies between molecular and morphological results probably reflect of numerous convergences as well as variations in the rates of morphological evolution among lineages. Page 899

The systematics of the group long has been and remains a matter of **debate** (for review, see Lecompte et al., 2002b). This is partly due to the low level of morphological differentiation among the species as well as between the genera, making it difficult to find phylogenetically informative characters (but see Lecompte et al., 2002a, however). Page 899, 900

The conflict between morphological and molecular trees is presented in Figure 6. Page 910

The conflict between morphological and molecular data shows important discrepancies between them, probably resulting from numerous morphological convergences in relation with the habitat type occupied (“savannah” or “forest”). Page 916

36. Unraveling ancient segmental duplication, By Amir Ali Abbasi

This contention famously known as 2R hypothesis has been the subject of intense **debate** over the past couple of decades (Skrabaneck and Wolfe, 1998; Martin, 1999, 2001; Hughes and Friedman, 2003; Furlong and Holland, 2004; Donoghue and Purnell, 2005; Kasahara, 2007; Abbasi, 2008, 2010; Abbasi et al., 2009; Furlong and Holland, 2002). Page 836

37. Haemadipsoid leeches, By Elizabeth Borda

Few deep historical biogeographic studies exist for soft bodied invertebrates that leave no fossil trace. Our robust phylogeny for the terrestrial blood feeding leeches, leaving perhaps as many questions unanswered as answered, beckons more extensive consideration of these notorious annelids. Page 153

The phylogenetic relationships between recent Elephantidae (Proboscidea, Mammalia), that is to say extant elephants (Asian and African) and extinct woolly mammoth, have remained unclear to date. The prevailing morphological scheme (mammoth grouped with Asian elephant) is either supported or questioned by the molecular results. Recently, the monophyly of woolly mammoths on mitochondrial grounds has been demonstrated (Thomas et al., 2000), but it conflicts with previous studies (Barriel et al., 1999; Derenko et al., 1997). Page 421

Yet, some of them, as the large dorsal parietal bulges and concave fronto-parietal region, although evolving in parallel are already more comparable in early Mammuthus and Elephas species, known so far. Yet, because the skulls of earliest African mammoths such as Mammuthus subplanifrons and Mammuthus africanavus are still poorly known, the **debate** is not closed. Page 431, 432

38. A newly discovered baleen whale, By Takeshi Sasaki

Molecular systematists have invested much effort to elucidate the evolutionary history of balaenopterids and their relatives. Nevertheless, the phylogenetic relationships among the species of the monophyletic clade comprising the families Balaenopteridae and Eschrichtiidae have been difficult to resolve (Adegoke et al., 1993; Arnason et al., 1993; Arnason and Gullberg, 1994; Rychel et al., 2004). Page 40

Moreover, molecular phylogenetic studies that are based on the traditional view of the genus Balaenoptera (such as Wada et al., 2003) may be insufficient to definitively establish the complete evolutionary history of these

species given our current knowledge of the phylogenetic relationships among the species of the Balaenopteridae+Eschrichtiidae clade, which cross conventional taxonomic ranks (Arnason et al., 1993; Arnason and Gullberg, 1994; Nikaido et al., 2006; Rychel et al., 2004; Sasaki et al., 2005). Page 41, 42

The number of possible trees was 105. Page 45

39. A phylogeny of Diprotodontia, By Robert W. Meredith

Even though the marsupial order Diprotodontia is one of the most heavily studied groups of Australasian marsupials, phylogenetic relationships within this group remain contentious. Page 554

Much of the **debate** has focused on relationships among the families of possums and whether possums are monophyletic or paraphyletic. Page 554

Resolving higher-level relationships within Diprotodontia has proved difficult. Page 555

We recognize that the interpretation of these fossils as crown-group metatherians is not agreed on by all workers (e.g. the cladistic analysis of Sánchez-Villagra et al., 2007). Page 558

The inclusion of fossil taxa (if they existed for these nodes) would help resolve these issues in that they could be transitional forms. Page 569

40. Inference of whale phylogeny, By Laura May-Collado

Several issues of Cetacean phylogenetics have been intensely **debated**, as a result of independent datasets (morphology, nuclear DNA, and mitochondrial DNA) suggesting conflicting hypotheses. These **debates** include the phylogenetic placement of Cetacea as sister to Artiodactyla. Page 344

41. Phylogeny of muroid rodents, By Sharon A. Jansa

One of the outstanding **debates** in muroid systematic is whether the burrowing muroids form a monophyletic group, or whether the morphological adaptations associated with underground life (reduced eyes and pinnae, reduced limbs, well-developed fore claws, fusiform body shape; Stein, 2000) have evolved independently. Page 267

The pattern of relationships among these lineages is still an open question, and we refrain from naming them pending further morphological and molecular studies of these taxa. Page 272

42. Improved resolution of Cetartiodactyla, By Xuming Zhou

However, phylogenetic relationships within Cetartiodactyla remain controversial. For example, the root of Cetartiodactyla has proven to be elusive (Gatesy et al., 2002; Ursing et al., 2000), and three hypotheses have been postulated: a basal position for Tylopoda (Gatesy et al., 1999) or Suina (Matthee et al., 2001) or a monophyletic clade containing Tylopoda and Suina (Arnason et al., 2000) as a sister group to Cetruminantia (Cetacea + Hippopotamidae + Ruminantia). Page 1

Although great advances have been made in advancing our understanding of cetacean phylogenetics, these studies have also created some new controversies (Kingston et al., 2009). For example, the monophyly of Odontoceti has been challenged previously and sperm whales were placed in many positions according to different molecular studies (Arnason and Gullberg, 1994; Milinkovitch et al., 1994). Additionally, the phylogenetic relationships among river dolphins (Inia, Pontoporia, Platanista, and Lipotes) have also been **debated** (Cassens et al., 2000; Nikaido et al., 2001b; McGowen et al., 2009; Xiong et al., 2009), but the positions of Platanista and Lipotes have been difficult to resolve even with complete mitogenomes or concatenations of several nuclear genes (McGowen et al., 2009; Xiong et al., 2009). Another contentious issue is the relationships among the superfamily Delphinoidea, which contains three families, Monodontidae (beluga and narwhal), Phocoenidae (porpoises), and Delphinidae (dolphins). Page 2

43. Perspective on Mammalian Evolution, By Michael J. Stanhope

The evolutionary relationships of the various orders of placental mammals remain an issue of uncertainty and controversy. Page 148

At present there is no single hypothesis of eutherian ordinal relationships that is widely accepted. One area of considerable **debate** has been the proposed superorder Archonta, a grouping of Primates, Scandentia (tree shrews), Dermoptera (flying lemurs), and Chiroptera (bats). Page 148

Many issues in mammalian phylogeny have in all likelihood remained intractable and controversial because of evolutionary splitting events that were close enough in time and in character that they represent a considerable challenge for phylogenetic analysis. Page 148

44. *Lepus* in Eastern Asia, By Chunhua Wu

In spite of several classification attempts among taxa of the genus *Lepus*, phylogenetic relationships still remain poorly understood. Page 45

45. Nuclear gene sequences, By Emma C. Teeling

Molecular and morphological hypotheses disagree on the phylogenetic position of New Zealand's short-tailed bat *Mystacina tuberculata*. Most morphological analyses place *Mystacina* in the superfamily Vespertilionoidea, whereas molecular studies unite *Mystacina* with the Neotropical noctilionoids and imply a shared Gondwanan history. To date, competing hypotheses for the placement of *Mystacina* have not been addressed with a large concatenation of nuclear protein sequences. Page 308

Although the mystacinid lineage is too young to have originated in New Zealand before it split from the other Gondwanan landmasses (80 mya), the exact geographic origin of these lineages is still uncertain and will not be answered until more fossils are found. Page 308

46. The genus *Artibeus*, By Rodrigo A.F. Redondo

Although *Artibeus* in the broad sense (including the *Dermanura* and *Koopmania* subgenera) is widely accepted as monophyletic (Simmons, 2005), the relationships among the species inside both subgenera (or genera) is a matter of intense **debate** (Van den Bussche et al., 1998; Lim et al., 2004; Guerrero et al., 2004; Guerrero et al., 2003; Marques-Aguiar, 1994; Owen, 1987, 1991; Handley, 1987). Page 44

Although *A. obscurus* is easily distinguishable from other large *Artibeus*, the phylogenetic relationship of this species is poorly resolved in morphological analysis (Marques-Aguiar, 1994). Page 54

47. The prehistory of Central Africa, By Chiara Batini

The origin of *L1c* and the processes leading to its present distribution are still a matter of **debate**, due both to lack of data concerning some crucial areas and to the low level of resolution used in most studies. Page 636

Any attempt to shed light on the peopling of Central Africa is made difficult by the incompleteness of the data accumulated so far and the limited value of some more indirect lines of evidence. Page 642

48. Rare endemic Malagasy lemur, By I. B. Ravaoarimanana

We are aware of that species recognition under different species concepts is a continuous matter of controversial **debate** among evolutionary biologists and taxonomists (Avice and Wollenberg, 1997; Cracraft, 1989; O'Brien and Mayr, 1991; Zink and McKittrick, 1995). Page 445

49. African Hominoid Trichotomy, By Wendy J. Bailey

However, the question of whether gorillas, chimpanzees, and humans separated ancestrally from one another in a simultaneous three-way split or in two well-demarcated speciation events has not been decisively answered despite three decades of research and **debate** (Goodman, 1962, 1963, 1976; Sarich and Wilson, 1967; Dene et al., 1976; Sarich and Cronin, 1976; Groves, 1986; Andrews, 1987; Andrews and Martin, 1987; Holmquist et al., 1988; Miyamoto and Goodman, 1990). Page 97

50. Oligocene to Miocene diversification, By Cynthia Steiner

Contradicting ideas about didelphid phylogenetic affinities result from the use of different approaches for the analysis of morphological characters, chromosomes, allozymes, and more recently DNA sequences (for a summary, see Jansa and Voss, 2000). Debates are principally focused around the phylogeny of mouse-sized opossums and the position of *Monodelphis* and *Metachirus* within Didelphinae. Page 364

51. Letter to the Editor, By Zhixi Su

At any rate, all of us (Zhang, 2009; Xu et al., 2009) agree that new experimental data from more leaf monkeys are crucial to resolve the disagreements. Page 610

52. A Phylogenetic Study of the Gibbons, By J. Carlos Garza

Advances in our understanding of gibbon phylogeny may resolve **debate**s about the evolution and adaptive significance of other variable traits, such as pelage and vocalizations. Page 209

53. Molecular systematics of Vampyressine bats, By Steven R. Hofer

Relationships among vampyressine bats continue to be **debated** and have proven difficult to resolve with either morphological or molecular data (e.g., Owen, 1987; Porter and Baker, 2004; Wetterer et al., 2000), perhaps reflecting a rapid and contemporaneous radiation among these fruit-eating specialists. Most of the **debate** seems rooted in “molecules versus morphology,” and centers around two entangled issues about monophyly and rank status of Vampyressa and Vampyriscus, and their relationships with Chiroderma, Ectophylla, and Mesophylla. Page 424

Rank status of Vampyriscus (*bidens*, *brocki*, and *nymphaea*) and whether or not its species and those of Vampyressa (*melissa*, *pusilla*, and *thyone*) shared a most recent common ancestry has been **debated** extensively. Page 432

Affinities of the monotypic genera Ectophylla (*E. alba*) and Mesophylla (*M. macconnelli*) have been the source of **debate** since the 1960s, which mostly is the result of incongruence between morphological and other types of data (“molecules versus morphology”). Page 433

54. Intraordinal phylogenetics of treeshrews, By Link E. Olson

While the monophyly of Scandentia is well-supported, the supraordinal relationships of this group have been a matter of great **debate** (see review in Sargis, 2002a). Page 657

Compared to the few **debates** regarding the basal relationships among treeshrews, those concerning generic distinction have been more controversial (see Olson et al., 2004a for review). Page 658

55. In Memoriam, By Derek E. Wildman

This again proves the point, in my view, that consideration of the place of humans within the natural world will always be **debated**. Page 2

56. Phylogeography of the armadillo, By Sebastián Poljak

It is important to note that the **debate** about the statistical validation of the inferences of NCA became stronger in the past 2 years (see Knowles, 2008 and Templeton, 2009a,b). Page 40

57. Phylogenetic position of Rhagomys, By Guillermo D’Elía

Therefore, a taxon-dense phylogenetic analysis including all species of both tribes is needed to optimize the geographic location of the sigmodontine common ancestor, which is one of the main points of the **debate** in sigmodontine historical biogeography (reviewed in D’Elía, 2000 and Pardiñas et al., 2002). Page 563

58. Nuclear gene sequences, By Heather Amrine-Madsen

Expanded concatenations of DNA sequences, improved models of sequence evolution, and other types of molecular data, including indels and SINEs, may help to resolve this **debate**. Page 194

59. Phylogenetics of red-backed voles, By Joseph A. Cook

The phylogenetic relationships and geographic limits of North American species of *Clethrionomys* have long been **debated** (e.g., Bee and Hall, 1956). Page 774

60. Rhabdomys pumilio subspecies, By Ramugondo V. Rambau

In spite of the **debate** on the accuracy of molecular clocks (Avice, 1994; Gillespie, 1986; Martin and Palumbi, 1993; Rambaut and Bromham, 1998) they have nonetheless proved useful for dating cladogenic events in rodents (e.g., Ducroz et al., 2001; Jolley et al., 2000; Smith and Patton, 1999). Page 572

61. The Sorex araneus group, By G. Yannic

Therefore, investigation of genomic regions with different inheritance patterns, coalescence time and mutation rates is warranted in order to obtain an accurate picture of the species’ evolutionary history (e.g., Leache, 2010) (but see the recent **debate** on the use of mtDNA versus nuclear DNA in avian phylogeography; Barrowclough and Zink, 2009; Edwards and Bensch, 2009; Zink and Barrowclough, 2008). Page 1062

62. Divisions among Collared peccaries, By Jaime Gongora

Genetic analysis of the Collared peccary can elucidate ongoing **debate** about taxonomy and differentiation. Page 2

63. History of the genus *Sus*, By Stefano Mona

The systematic status of species belonging to the genus *Sus* has been a matter of **debate** for decades (Groves, 1981). Page 757

64. Phylogenetics of the Diprotodontia, By M. J. Osborne

The affinities of the Burramyidae have also been **debated** with Szalay (1994) including this group within the Petauridae on the basis of pedal anatomy. Page 220

65. A novel family of tRNA, By Jurgen Schmitz

While all these studies contribute to a better understanding of the superordinal clustering of mammalian orders, the evolutionary affiliations among the members constituting the four major eutherian groups emerging from these studies are still a matter of scientific **debate**. Page 341

66. Description of Mitochondrial DNA, By Louis G. Kessler

The empirical and conceptual issues raised by these findings are highly analogous to those in the long-standing **debate** about rates of molecular evolution and times of separation of ancestral hominids from African apes. Page 109

Alternatively, if we question the reliability of the fossil assignments for waterfowl, a scenario arises that is analogous to the current **debate** over the divergence time of ancestral humans from African apes. Page 122

67. Support Patterns from Different Outgroups, By Adrian Schneider

The very early divergences of the eutherian mammals into Afrotheria, Xenarthra, and Boreoeutheria (consisting of Euarchontoglires and Laurasiatheria) are still **debated**. Page 1265

The branching order of Primates, Rodentia, and Laurasiatheria (e.g., Carnivora and Artiodactyla) is also subject to **debate**. Page 1266

The position of Lagomorpha (here represented by rabbit and pika) has been long **debated** with the main hypotheses focusing on the relative positions of Lagomorpha, Rodentia and Primates. Page 1267

68. Evolution of the Metazoan PHD, By Kalle T. Ryttonen

Our results are more equivocal about the relationships among the HIF-3 alpha genes in cartilaginous fishes, teleosts, and mammals, which is currently a matter of some **debate** (Law et al. 2006; Richards 2009). Page 1921

69. Philippine Mitochondrial DNA, By Kristina A. Tabbada

Their origins have been the subject of scientific inquiry and discussion for over two centuries, and the study of the region's prehistory has played a key role in the broader **debates** over the first dispersals of humans out of Africa as well as the influence of agriculture and the role of demographic expansions in recent human evolution. Page 21

70. Quantifying the Phylodynamic Forces, By Marc Gottschling

The felid phylogeny has long been a matter of **debate**, and the molecular tree of the felid hosts provided by (Rector et al. 2007) neither agrees with a comprehensive molecular phylogeny of cats (Johnson et al. 2006) nor with the phylogeny obtained in this study. The internal phylogeny of Pi-PVs is also not entirely congruent to the rodent host tree topology (Schulz et al. 2009). A solid case of cophylogenetic relationships between PVs and their mammalian hosts supported by identical tree topologies, even on a local scale, is thus still wanting. Page 2110

71. Testing for Ancient Admixture, By Eric Y. Durand

Among anthropologists, there is a long-standing **debate** on the relationships between modern humans and different groups of archaic humans such as Neandertals. Page 2239

72. The Primates' Gliding Sister?, By Jurgen Schmitz

Although a general agreement on the major groups of eutherian orders and their phylogenetic affiliations is emerging, the evolutionary affiliations among the members constituting these groups are still subject to **debate**. Page 2308

Early primate evolution between the late Cretaceous and the end of the Eocene continues to be an issue of lively **debate**. Of particular interest are the interrelationships between extant and fossil primates and other eutherians, where questions of phylogeny still largely remain unresolved. Page 2308

For the part of nuclear DNA-based evidence, this could provide a final settlement for the **debate** of primate origins. Page 2311

73. Early Y Chromosome Lineages, By Chiara Batini

Finally, our study contributes to the **debate** on the geographical origin of Homo sapiens in sub-Saharan Africa, providing evidence for the retention of early Y chromosome lineages in East and Central but not in Southern Africa. However, we note that the current absence of significant palaeo-anthropological investigation, together with the possibility of different fossil preservation conditions in central Africa, makes the extremely long human fossil record in eastern Africa inconclusive in solving this issue. Page 2611

74. Diversity in Rhesus Monkeys, By Don J. Melnick

Reconstructions of the human-African great ape phylogeny by using mitochondrial DNA (mtDNA) have been subject to considerable **debate**. Page 282

75. Large-Scale mtDNA Screening, By Qing-Peng Kong

Hitherto, **debate** on whether the earlier hominid populations had been “completely” replaced by modern humans continues, especially for East Asia where abundant and successive hominid fossil records have been discovered and continuity of the morphological characters between Homo erectus and modern East Asians has been proposed (Wu 2005, 2006). Page 513

76. Representation for Convergent Evolution, By Yasuhiro Kitazoe

The evolutionary history of placental mammals is also in **debate** (Easteal 1999; Benton and Ayala 2003). Page 705

77. Divergences of Human Gene Trees, By Michael G. B. Blum

Two competing hypotheses are at the forefront of the **debate** on modern human origins. Page 889

The process by which modern humans arose has been the subject of much **debate** in paleoanthropology (Stringer 2002). Especially the extent of admixture between anatomically modern humans and archaic populations of Homo has been vigorously **debated** (Wolpoff et al. 2000; Templeton 2002; Garrigan and Hammer 2006; Plagnol and Wall 2006; Fagundes et al. 2007). Page 889

78. Nucleotide Compositional Plasticity, By Jurgen Schmitz

The phylogenetic relationship of tarsiers to other primates has been a source of **debate** for many decades. Page 544

79. Philippine Mitochondrial DNA, By Kristina A. Tabada

Their origins have been the subject of scientific inquiry and discussion for over two centuries, and the study of the region’s prehistory has played a key role in the broader **debates** over the first dispersals of humans out of Africa as well as the influence of agriculture and the role of demographic expansions in recent human evolution. Page 21

80. The Role of Landscape Barriers, By Gyaneshwer Chaubey

Moreover, the southeast Asian populations have been underrepresented in all previous studies, and furthermore, no high-resolution autosomal evidence has been considered in these **debates**. Therefore, the genetic origins of Austroasiatic-speaking populations remain largely controversial. Page 1016

81. History of Niger-Congo Groups, By Cesare de Filippo

Yet, because the results of such estimates depend to a large extent on the mutation rates used, which are very variable and subject to considerable **debate** (Zhitovovskiy et al. 2004), age estimations should be considered with due caution. Page 1260

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Methodology

1. When Clocks Collide, By Christopher A. Brochu

The conflict is a matter of interpretation, and as long as competing hypotheses are not completely understood, the magnitude of the “conflict” will be exaggerated. As seen in the papers in this issue, we still have a long way to go to resolve some of the inconsistencies between sources of information—but an integrative approach holds the greatest promise in achieving the one goal of understanding the history of life as thoroughly as possible. Page 1.

2. Missing Links, By Kevin Padian

This brings us to a very important distinction in tracing lineages. The title of this book is *Missing Links*. I have seldom, if ever, heard a professional paleontologist refer to any specimen as a “missing link.” In most respects, paleontology largely gave up the literal search for “missing links” decades ago. (Here, by “missing links” I mean transitional forms, direct ancestors, specific critters that fill gaps in lineages.) So, in a book intended for students who don’t know much about the subject, why focus on an outmoded concept? Page 620

3. Origin And Early Evolution Of The Amniotes, By David S Berman

Cladistic analyses of Paleozoic tetrapod relationships have yielded dramatically contradictory results (Gauthier et al., 1988; Carroll, 1995; Laurin and Reisz, 1995, 1997; Laurin, 1998), despite the use of similar computerized algorithms and extremely large data sets. Major sources of this problem, according to Carroll (1995), can be attributed to: 1) the lack of at least some data from all known taxa and 2) the lack of more information of more plesiomorphic members of recognized clades that are not known from their presumably earlier fossil record. Thus, if any of the recent cladistic analyses of late Paleozoic tetrapod relationships are used to construct a morphological series that traces the early evolutionary changes of a particular region of the tetrapod skeleton to its culmination in the amniote condition, the result is often, predictably, questionable. Page 938

Potentially important to the controversy of the phylogenetic position of the baphetids is the recent description by Lombard and Bolt (1995) of the Lower Carboniferous amphibian *Whatcheeria*, which in their phylogenetic scheme was placed tentatively as the first outgroup of the anthracosaurs. Page 952

With the additional consideration of the diadectomorphs, his phylogeny encountered further problems, and he was unable to resolve the relationships between the three taxa. The final solution was an unresolved trichotomy. Page 953

4. Systematic Paleontology, By Jonathan M. Adrain

How do we generate phylogenies? Debate, of course, rages on this issue. Page 1056

Resolution of the **debate** over whether phylogeny should be read from the rocks is central to the future development of paleontological systematics. Page 1057

5. Evidence for Punctuated Gradualism, By Bjorn A. Malmgren

One of the fundamental problems in this **debate** is the lack of well-conceived studies employing detailed morphologic measurement and a rigorous biometric testing strategy. We believe that much more time should be devoted to generating real data on real evolutionary lineages than to endless theoretical discussions on hypothetical evolutionary models. Thus, instead of forcing our data to fit preconceived models, we would prefer to formulate the models from real- world paleontologic data. Page 377

6. Extinction, By Andy Purvis

The **debate** continues, with key points of contention including (1) the rate at which non-deleterious mutations arise, (2) the extent to which “deleterious” mutations provide evolutionary potential in changing environments, and (3) how conservative to be when faced with such uncertainties. Page 1125

7. The shape of life, By Matthew A. Wills

Whether this disparity was generated in the time permitted by a literal reading of the body fossil record, or over a more protracted period extending far back into the Precambrian is still hotly **debated**. Page 1150

8. Phylogeny of g-proteobacteria, By James R. Brown

Because of HGT, there are intense **debates** in the evolutionary biology community as to whether or not the faithful reconstruction of the universal tree of life is possible. Page 464

9. From 2R to 3R, By Axel Meyer

However, the relative importance of both gene duplication and divergent transcriptional regulation in explaining the evolution of biological complexity remains a subject of vigorous **debate**. Page 937

10. Effects of sequence alignment, By Nick Goldman

There has been much **debate** about the best procedures for molecular phylogenetic inference, that is, estimation of evolutionary relationships from genetic sequence data. These discussions have been predominantly based on comparisons of different methods for estimating evolutionary trees from aligned DNA, RNA, or amino acid sequences. Page 287

Perhaps because of longstanding **debate**s regarding phylogeny estimation methodology, variation in the results of this final stage of analyses has received by far the most attention. Page 288

11. Molecular Evolution, By Ross J. MacIntyre

Since then, the clock's existence has been the subject of considerable analysis and **debate**. Page 700

12. Reproductive mode and speciation, By David W. Zeh

How new species arise during evolution is one of the most fundamental but highly contentious issues in biology. Speciation occurs when populations diverge sufficiently to become reproductively isolated; but is this isolation initiated by pre-fertilization barriers to gene flow or by postzygotic genetic incompatibility? There is currently little consensus regarding the answer to this question, and much **debate** over the relative importance of mutation accumulation, sexual selection, selfish genetic elements and intergenomic conflict in the speciation process. Page 938

13. Reconstructing evolutionary relationships, By Carlos Briones

Nonetheless, these analyses have also resulted in major, ongoing, taxonomic **debates** (Bromham and Penny, 2003; Doolittle, 1999; Huynen et al., 1999; Mayr, 1998; Woese, 2000; Wolf et al., 2002). At the base of the controversy lies the fact that tree reconstruction is affected by horizontal gene transfer, which is currently acknowledged as a driving force of prokaryotic evolution (Clarke et al., 2002; Kurland et al., 2003; Nesbo et al., 2001; Ochman et al., 2000) and may even involve lateral transfer of rRNA operons (Perez-Luz et al., 1998; Yap et al., 1999). Other discrepancies are related to the constancy of the rate of the molecular clock among different genes and organisms, and to the influences that population size and fixation of mutations with a selective effect have on the divergence of sequences (Bromham and Penny, 2003). Moreover, the release of complete genome sequences from over 200 organisms has fueled this **debate** by showing that phylogenies constructed with many universally distributed genes may exhibit important differences with the rRNA-based universal tree. Page 372

14. Evolution of a complex minisatellite, By Paula Barros

The reconstruction of the phylogenetic history of a microsatellite locus is a very challenging task. Currently, we do not know the nature of the substitution process that might operate at these loci, or how insertion and deletions arise in each case, and therefore, statements of homology—the alignment—are very uncertain. Page 493

In this case we are not confident enough in our estimate to enter into this **debate**, as the estimation of allelic phylogenies from microsatellite loci is still a very difficult undertaking. The analysis of the homology between the great apes and humans revealed that the highest homology in the organization of MsH43 was between orang-utan and humans. This result does not agree with the standard phylogeny of primates. Page 493

15. Lusitania revisited, By Graham Rowe

However, interesting questions still await resolution. Lusitanian distributions of fauna and flora in western Europe, for example, have puzzled biogeographers for more than 150 years. Lusitanian species have highly disjunct distributions in Ireland and in Iberia, often with few or no other populations inbetween. Despite much **debate**, no agreed explanation for Lusitanian distributions has yet emerged. Page 335

16. Gene tree parsimony, By James A. Cotton

Of the few remaining criticisms, most are reflections of a wider **debate**, that between consensus and “total-evidence” methods for using multiple sources of evidence in phylogenetic reconstruction. We revisit this **debate** briefly, to suggest that these criticisms are not decisive in deciding between gene tree parsimony and uninode coding methods. A further subset of the criticisms are aimed at only a particular implementation of the gene tree parsimony method—that of the program GENETREE (Page, 1998), and overlook a number of recent algorithmic developments. Page 298, 299

The **debate** over whether to combine data from multiple different sources of evidence in a single data matrix for phylogenetic analysis has been on-going for over a decade (for reviews see de Queiroz et al., 1995; Huelsenbeck and Bull, 1996). Three different opinions have been reflected in the literature. Page 300

There has been a long **debate** between proponents of these methods for dealing with multiple data sources in systematics. Page 300

In the sense that one uses the sequence data directly and the other considers tree from the separate data partitions, gene tree parsimony and uninode coding represent alternative sides of the **debate** over combined analysis vs. Consensus methods. Simmons and Freudenstein's criticisms #4 and #5 reflect this **debate**—a **debate** that is still active (Levausser and Lapointe, 2001) and can hardly be considered a decisive criticism of gene tree parsimony. Page 301

17. Tempo of speciation, By Hendrik-Jan Megens

Molecular systematics is frequently beset with phylogenetic results that are not fully resolved. Researchers either state that the absence of resolution is due to character conflict, explosive speciation, or some combination of the two, but seldom do they carefully examine their data to distinguish between these causes. Page 1181

Despite careful phylogenetic analysis using multiple gene regions and thousands of base pairs, the historical relationships of many groups of organisms remain unresolved (e.g., Arnaiz-Villena et al., 1999; Lessa and Cook, 1998; Waits et al., 1999). These enigmatic cases have led researchers to postulate rapid radiation events, where the lack of characters supporting an internal node is explained by insufficient time for substitutions to occur (Mardulyn and Whitfield, 1999; Waits et al., 1999). Page 1182

18. Why weight?, By Karl M. Kjer

Philosophical issues aside, the **debate** over phylogenetic methods could be considered a **debate** over the best treatment of homoplastic data, since non-homoplastic data are likely to reveal phylogenetic patterns accurately by most reasonable methods (Hillis et al., 1994; Simon et al., 1994). Page 999

19. Letter to the Editor, By Tan Siew Hoong Denise

Most biologists agree that species occupy “a pivotal position in all aspects of biology” (Cracraft, 2000), but despite decades of **debate** it appears unlikely that biologists will ever settle on a single species concept (Wheeler and Meier, 2000). Page 688

Given that a resolution of the species concept **debate** is not in sight, we thus urge all authors who propose new species to be explicit about which species concept they use. Page 689

20. Implications for Character Weighting, By Gerhard Haszprunar

Throughout a long-lasting history of **debate** (as reviewed by Boyden, 1943; Remane, 1989; Rieppel, 1988, 1994; Panchen, 1992) most biologists agree that it is essential for phylogenetics to analyze similarities in order to distinguish homologies from analogies (or homoplasies in general). There is, however, no general agreement about the optimal method of inference of homology. Page 333

21. Recovery of fusion genomes, By C. Donovan Bailey

Current **debate** surrounding the origin of this complex assemblage of genes focuses on the competing causal mechanisms (e.g., Spring, 2003). Page 264

22. Falsifications and corroborations, By Kevin G. Helfenbein

Though there has been much **debate** regarding the nature of the relationship between Darwinian evolutionary theory and systematics, particularly as to whether one justifies the other (see, for example, Brower, 2000), there is no denying a relationship. Page 275

23. Analysis of the *Bufo gargarizans*, By Jinzhong Fu

Although what constitutes a species is a subject of intense **debate**, there is a general agreement that species are segments of evolutionary lineages (deQueiroz, 1998). Page 211

24. mtDNA and microsatellite loci, By Nicolás M. Suárez

The definition of taxonomic units has been under **debate** for Decades. Page 562

25. 10 years after Avise, By M. J. Hickerson

While such simulation testing of NCPA has provoked **debate** (Beaumont, 2008b; Garrick et al., 2008; Knowles, 2008; Templeton, 2004, 2009a,b), it is also a sign that the field is becoming a more statistically rigorous endeavor and that empiricists are coming to recognize that equating genealogical pattern with demographic and evolutionary processes can lead to over interpretation when ignoring coalescent stochasticity in the data. Page 293

26. Vicariance or parapatry?, By Florence Tellier

The role of demographic history versus selection for creating these patterns has always puzzled evolutionists and the **debate** about sympatric and allopatric speciation remains controversial (Bolnick and Fitzpatrick, 2007; Fitzpatrick et al., 2008). Page 679

27. Implications for DNA barcoding, By Amanda D. Roe

Using only mitochondrial characters has always been controversial (Dunn, 2003; Lipscomb et al., 2003; Seberg et al., 2003; Tautz et al., 2003), and recent **debates** have been particularly heated (Moritz and Cicero, 2004; Ebach and Holdrege, 2005; Hebert and Gregory, 2005; Meyer and Paulay, 2005; Will et al., 2005) in light of the increasing popularity of projects such as the Consortium for the Barcode of Life (<http://barcoding.si.edu/>). Page 325

28. DNA sequence library, By Torbjørn Ekrem

Many of the central issues in antagonist **debates** about the ‘‘promise and perils’’ of DNA barcoding (Besansky et al., 2003; Blaxter, 2004; Hebert and Gregory, 2005; Lorenz et al., 2005; Moritz and Cicero, 2004; Wheeler, 2005; Will and Rubinoff, 2004; Will et al., 2005) are essentially rooted in phylogenetics. Page 540

29. Letter to the editor, By John S. Sparks

It is obvious from this symposium volume and the studies cited within, that the methods for DNA taxonomy alone, or its integration into taxonomy as a whole, are still a topic of considerable **debate**. Page 901

30. Base Compositions of Genes Encoding, By Rachael A. Ream

There is a long-standing **debate** in molecular evolution concerning the putative importance of GC content in adapting the thermal stabilities of DNA and RNA. Page 105

31. Caenorhabditis elegans Genome, By Asher D. Cutter

However, much **debate** exists about whether natural selection mediates such redundancy (Lynch and Conery 2000; Kondrashov et al. 2002; Wagner 2002), and it has been argued that this could result from many duplicates actually representing pseudogenes (Reece-Hoyes et al. 2007). Page 1206

32. Evolutionary Divergence, By Fabia U. Battistuzzi

Molecular and nonmolecular time estimates do not always agree, and their differences have fuelled **debates** on possible biases inherent in both types of data and the methods of analyses (Ayala 1999; Smith and Peterson 2002; Graur and Martin 2004; Hedges and Kumar 2004; Reisz and Muller 2004; Blair and Hedges 2005; Pulquerio and Nichols 2007; Peterson et al. 2008). Page 1289

33. More Genes or More Taxa?, By Antonis Rokas

The relative contribution of taxon number and gene number to accuracy in phylogenetic inference is a major issue in phylogenetics and of central importance to the choice of experimental strategies for the successful reconstruction of a broad sketch of the tree of life. Maximization of the number of taxa sampled is the strategy favored by most phylogeneticists, although its necessity remains the subject of **debate**. Page 1337

34. Evolution of Proteins, By Bernardo Lemos

However, the relationship between evolutionary variation in gene expression and protein sequence is controversial. Page 1345

35. Human and Mouse Malaria, By Cristian I. Castillo-Davis

Although there is still much **debate** concerning the process by which initially identical duplicate genes come to diverge in sequence and function, it is certain that after duplication, the resulting genes are subject to either one of two fates: silencing of one copy by degenerative mutations or preservation of both copies via natural selection. Page 1424

36. Gene Regulatory Network, By Rory Johnson

Consequently, **debate** continues as to the relative contributions to evolution from regulatory versus coding DNA mutation (Hoekstra and Coyne 2007). Page 1491

37. Tropomyosin Genes in Metazoans, By Manuel Irimia

Much of the **debate** about the emergence of new functions has focused on two possibilities: changes in gene expression patterns across environmental conditions, developmental stages, tissues, or subcellular locations; or emergence of new genic products, primarily by genomic duplication and/or alternative splicing (AS). Page 1504 Whether morphological innovation arises mainly through the recruitment of nearly unchanged proteins and functional gene networks or through changes in protein functions is the subject of a hot **debate** (Wagner and Lynch 2008), and only few examples of protein neofunctionalization were reported in recent literature. Page 1515

38. Toll-Like Receptor Multigene, By Miguel Alcaide

However, the ability of MHC diversity to explain the entirety of wildlife immunogenetics has been the subject of **debate**, and investigation of other candidate genes for immunoeology has been encouraged (Acevedo-Whitehouse and Cunningham 2006; Radwan et al. 2009). Page 1713

39. Programmed Genetic Instability, By Yongzhong Zhao

A longstanding **debate** in evolutionary biology concerns how species of increasing structural complexity maintain their capacity for genetic variation—and, hence, adaptation and divergence—despite a predictably increasing need for genetic fidelity (Gulick 1893; Gould JL and Gould CG 1997). Page 1737

40. Gene Family Size, By Feng-Chi Chen

The evolution of duplicate genes, however, is an issue of **debate**. Page 1750

41. The Impact of Fossils, By Laura A. Hug

In any case, the relative validity of fossil versus molecular divergence date estimation continues to be **debated**. Page 1889

The positive impact of increased taxon sampling on phylogeny determination has often been posited (Delsuc, Brinkmann and Philippe 2005), although there has been considerable **debate** over the relative impacts of taxon versus site inclusion (Hedtke, Townsend and Hillis 2006). Page 1890

This indicates that the **debate** surrounding the method of constraining fossils in molecular clock analysis (Graur and Martin 2004; Hedges and Kumar 2004; Reisz and Muller 2004; Blair and Hedges 2005; Glazko, Koonin and Rogozin 2005) is justified; molecular clock studies would benefit from greater caution taken when implementing these constraints. Page 1893

Considerable **debate** has surrounded the use of single versus multiple fossil constraints on molecular dating analyses (e.g. see Graur and Martin 2004; Hedges and Kumar 2004). Page 1893

42. Domesticated Transposase Genes, By Rebecca K. Cowan

While transposons have traditionally been viewed as genomic parasites or ‘‘junk DNA,’’ the discovery of transposon-derived host genes has fueled an ongoing **debate** over the evolutionary role of transposons. Page 2084

43. Evidence from Published Sequences, By Emmanuel D. Ladoukakis

The question of whether animal mitochondrial DNA (mtDNA) undergoes recombination has recently been the subject of intense **debate**. Page 2127

44. Estimation of Phylogenetic Inconsistencies, By Victor Soria-Carrasco

Whereas gene transfer within the same species or between closely related species is well-known and cellular mechanisms to favor it have been described, the evolutionary significance of the transfer of genes between distant species is a matter of controversy, and there is an active **debate** about whether the latter type of transfer is quantitatively anecdotal (Glansdorff 2000; Kurland 2005) or reflects a paradigm shift in prokaryotic evolution (Gogarten et al. 2002; Baptiste et al. 2005). Page 2319

45. Evolution of Transcription Factors, By Richard Jovelin

Whether phenotypic evolution proceeds predominantly through changes in regulatory sequences or changes in protein sequences has ignited an intense **debate**, with the argument in favor of the cis-regulatory hypothesis focusing on the prediction of strong conservation of TF function (Carroll 2005, 2008; Hoekstra and Coyne 2007; Wray 2007; Stern and Orgogozo 2008). Page 2373

46. Determinants of Protein Evolution, By Eric A. Franzosa

The effect of protein-core size on protein evolution has been studied by multiple groups, resulting in **debate** as to its mechanisms and significance (Bloom et al. 2006; Lin et al. 2007; Zhou et al. 2008). Page 2392

47. 16 Yeast Genomic Variables, By Fabian J. Theis

There has been much **debate** as to whether proteins involved in many interactions evolve more slowly, with some studies confirming this trend (Fraser et al. 2002), whereas others rejecting it (Batada et al. 2006). Page 2506

48. Hot Spots in the Human Genome, By Mikael Brandstrom

The study of the relationship between microsatellite polymorphism and recombination is relevant to this **debate** because if recombination drives microsatellite evolution through a mutagenic effect, recombination rate should be correlated with microsatellite variability. Page 2579

49. Histories of Dioxygen Reductases, By Celine Brochier-Armanet

Understanding the origin and evolution of cellular processes is fundamental to understand how biological activity has shaped the history of our planet. Among these, aerobic respiration is probably one of the most **debated**. Page 285

Our study of O2Red is a good example and allowed bringing an updated insight on a long-standing **debate** around the origin and evolution of enzymes involved in a fundamental energy conversion process such as aerobic respiration. Page 295

50. Genes Involved in HIV Pathogenesis, By Millan Ortiz

There is **debate** about the best handling of short deletions or insertions in the analysis of sequence evolution (Loytynoja and Goldman 2008). Page 2867

51. Large-Scale mtDNA Screening, By Qing-Peng Kong

However, it has to be pointed out that although there are some **debates** on the accuracy of molecular dating with the rho statistic (Cox 2008), the estimated ages of the basal lineages only provide a rough time range when they began to differentiate and may serve as some kind of circumstantial evidence in support of their long-time existence in the region. Page 519

52. Faster-Z Evolution, By Judith E. Mank

These studies provide a broad consensus for Faster-X Evolution; however, the underlying evolutionary mechanism remains a subject of **debate**. Page 661

53. Multiple Evolutionary Rate Classes, By Christopher Oldmeadow

The proportion of functional sequence in the human genome is currently a subject of **debate**. Page 942

Despite the vast amount of analysis of the human genome, it is unclear what proportion is functional. Page 942

54. Accuracy in AFLP Data Sets, By Maria Jesus Garcia-Pereira

Although it is generally accepted that AFLPs may not provide an accurate estimate of species phylogeny when genetic divergence is too high, it is still a matter of **debate** where this limit is (Meudt and Clarke 2007). Page 989

55. Microsatellites Within Genes, By You-Chun Li

Debates over whether SSRs play any functional role in organism development, adaptation, survival, and evolution are never-ending. Page 991

56. Animal Mitochondrial DNA, By Emmanuel D. Ladoukakis

The question of whether animal mitochondrial DNA (mtDNA) undergoes recombination has recently been the subject of intense **debate**. Page 2127

57. American Arabis divaricarpa, By Marcus A. Koch

Although molecular clock hypotheses are still under **debate**, for ITS a substitution rate of approximately 0.5% to 2.5% nucleotide divergence per 1 million years can be assumed. Page 347

58. Splicing in Phylum Rotifera, By Natalia N. Pouchkina-Stantcheva

The lack of sequence conservation and the apparently sporadic occurrence of trans-splicing among different phyla have prompted **debate** about its evolutionary origin. Page 1482

59. Evidence to Date the Tree of Life, By Michael J. Benton

Current **debate**s about which are the “best” fossil dates for calibration move to consideration of the most appropriate constraints on the ages of tree nodes. Page 26

This date was based on the age of the oldest members of the synapsid and diapsid clades (Benton 1990), and yet these basal fossils have been **debated**, as has the dating of the rocks from which they come. Page 26

So, **debates** about the superiority of one “calibration” date or another are irrelevant in the context of a search for the most appropriate distribution of dates and minimum and maximum constraints—the only bad dates are those that predate the evolutionary event upon which they are supposed to provide a minimum constraint. Page 26

It is still **debated** whether an analysis based on many genes and few dates or few genes and many dates is preferable. Page 26

However, the phylogenetic position of the plesiadapiforms is **debated**—they were probably close relatives of primates, but not primates proper (Bloch and Boyer 2002). Page 32

The age of these deposits has been much **debated** (Dyke and Van Tuinen 2004), and they fall either below or above the KT boundary (65.5 MYA 6 0.3 Myr). Page 37

The topology of the basal region of the cladogram around the split of Archosauromorpha and Lepidosauromorpha has been agreed (although some higher parts of the cladogram are still much **debated**, especially the placement of Sauropterygia and Ichthyosauria). Page 38

The most ancient lepidosauromorph is **debated**—Benton (1993, p. 688) indicated that Saurosternon bainii, sole representative of the Saurosternidae, may be the oldest, but he was uncertain. Page 38

The age of the Joggins Formation has been much **debated**, and figures in the range from 320 to 305 MYA have been cited recently. Page 39

Dating the earliest record of successive sister taxa is complicated by long-standing **debate** over the relative phylogenetic position and monophyly of the various groups. Page 44

60. Evolutionary and Functional Relationships, By Gipsi Lima-Mendez

These showed that similar morphology does not imply genetic similarity or vice versa, raising serious **debate** on the validity of the ICTV taxonomy (Hendrix et al. 2000; Brussow and Hendrix 2002; Lawrence et al. 2002; Nelson 2004). Page 762

61. Programmed Genetic Instability, By Yongzhong Zhao

A longstanding **debate** in evolutionary biology concerns how species of increasing structural complexity maintain their capacity for genetic variation—and, hence, adaptation and divergence—despite a predictably increasing need for genetic fidelity (Gulick 1893; Gould JL and Gould CG 1997). Page 1737

62. Evolution of Transcription Factors, By Richard Jovelin

Whether phenotypic evolution proceeds predominantly through changes in regulatory sequences or changes in protein sequences has ignited an intense **debate**, with the argument in favor of the cis-regulatory hypothesis focusing on the prediction of strong conservation of TF function (Carroll 2005, 2008; Hoekstra and Coyne 2007; Wray 2007; Stern and Orgogozo 2008). Page 2373

Methodology

63. Supermatrix Rooted Triples, By Michael DeGiorgio

Though statistical power generally increases with the size of a data set, the accuracy of concatenation is currently under **debate**. Page 552

64. Tropomyosin Genes in Metazoans, By Manuel Irimia

Much of the **debate** about the emergence of new functions has focused on two possibilities: changes in gene expression patterns across environmental conditions, developmental stages, tissues, or subcellular locations; or emergence of new genic products, primarily by genomic duplication and/or alternative splicing (AS). Page 1504 Whether morphological innovation arises mainly through the recruitment of nearly unchanged proteins and functional gene networks or through changes in protein functions is the subject of a hot **debate** (Wagner and Lynch 2008), and only few examples of protein neofunctionalization were reported in recent literature. Page 1515

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Molluscs

1. Paleozoic Problematic Fossils, By Ben Waggoner

The Cambrian genus *Scenella*, known from the Burgess Shale and similar Lagerstätte, has been the subject of **debate**; at least some specimens assigned to *Scenella* are more likely to be cap-shaped shells (Landing and Narbonne, 1992). Other proposed Paleozoic ‘chondrophorines’ have also been reinterpreted as mollusc or brachiopod shells, trace fossils, or rotational sweep marks (e.g., Horny, 1985; Kase, 1988; Jensen et al., 2001). Page 53

2. Gastropoda, Neritidae; Late Cretaceous, By John W. M. Jagt

The origin and relationships within the Neritoidea are still under **debate** (Beck, 1992; Saul and Squires, 1997; Bandel and Fryda, 1999; Bandel, 2001; Kano et al., 2002). Page 201

3. The Late Paleozoic Gastropoda, By A. Nutzel

Subulitids have long been an enigmatic group of Paleozoic gastropods: their origins have been obscure, their phylogenetic relationships perplexing and their relationships to post-Paleozoic gastropods unclear. Page 575

Such subulitid like shells may occur in the subclasses Caenogastropoda and Heterostropha, but since subulitoids normally have a smooth shell and thus comparatively few shell characters, their classification and systematic placement is particularly difficult. As a consequence, statements about their occurrence and their phylogeny are vague. Thus, even the impact of the end-Permian mass extinction on the phylogeny and diversity of this group is largely unknown. Page 575

4. A Primitive Halobia, By Christopher A. Mc Roberts

Debate continues regarding the origin and phylogeny of *Halobia*. Several workers suggest that *Halobia* is polyphyletic, having arisen from several *Posidonia* and *Daonella* ancestors (e.g., Gruber, 1976; Polubotko, 1988). Page 602

5. Paleobiogeographic Constraints, By Purbasha Rudra

Three of Kitchin’s (1903) trigoniid species, *Trigonia trapeziformis*, *T. spissicostata*, and *T. cardiniiformis*, have been frequently examined taxonomically, but their phylogenetic relationships remain uncertain. Taxonomic designations have ranged from grouping them within a single subgenus to separating them into different subfamilies. Page 1066

6. Gastropod Phylogenetics, By Peter J. Wagner

However, paleontologists usually study only adult shells (teleoconchs), and many malacologists maintain that teleoconch characters reflect phylogeny poorly if at all. Page 1128

Euomphaloids diverged from the likely ancestors of vetigastropods, caenogastropods, etc., in the late Cambrian and high uncertainty about phylogenetic relationships is consistent with early divergences. Page 1131

7. Late Paleozoic Evolution, By Alexander Nutzel

Possible phylogenetic relationships of the largely smooth ‘subulitoid’ gastropods and similar Mesozoic forms are difficult to substantiate because there are few discrete shell characters available. Page 1187

The phylogenetic relationships of the Imoglobidae are still obscure but they are probably descendants of the Early and Middle Paleozoic Perunelomorpha (family Cuchlinidae). However, it is unclear whether this group has any Mesozoic descendants. Page 1187

8. The Cambrian Explosion, By Richard A. Fortey

The evolutionary relationships between high-level taxa classes and phyla of living organisms have frequently been the subject of controversy. Page 429

The relationship of Ediacaran animals to the known phyla, with the possible exception of Cnidaria, was the subject of **debate** from the outset. The controversy continues, with some authorities claiming affinities with living animals, while others, no less vigorously, declare that the Ediacaran animals are a ‘side branch’ in the story of metazoan evolution, if relevant at all. Whatever the ultimate outcome of these **debates**, it is certainly true that the Ediacaran animals are not, in any simple sense, obvious ‘ancestors’ of those that came later. Page 429

Likewise among molluscs, the most primitive are the aplacophorans, minute forms lacking shells, whose detailed relationships with the rest of the molluscs is still under **debate**. Page 433

9. Phylogeny of nutmeg shells, By Maria Vittoria Modica

The relationships of the Cancellariidae to other Caenogastropoda have been the subject of **debate** for a long time. Page 685

10. Phylogeny of the family Pectinidae, By Marco Barucca

Despite these very different life strategies, pectinid shells are highly conservative in shape and offer few clues for the unravelling of phylogenetic issues. Consequently, phylogenetic studies based on morphological features have not yielded conclusive results. Page 89

Their morphological features, though useful for classification at the species level, provide scarce phylogenetic information. Indeed, the attribution of several species at both the genus and the subfamily level within the current morphology-based systems is far from being univocal, as different authors give different degrees of importance to morphological features. Page 89

11. Molecular phylogeny of Mollusks, By Federico Plazzi

Despite huge fossil, morphological and molecular data, bivalves' early evolutionary history is still a matter of **debate**: recently, established phylogeny has been mostly challenged by DNA studies, and little agreement has been reached in literature, because of a substantial lack of widely-accepted methodological approaches to retrieve and analyze bivalves' molecular data. Page 641

Bivalve taxonomy and phylogeny are long-**debated** issues, and a complete agreement has not been reached yet, even if this class is well known and huge fossil records are available. In fact, bivalves' considerable morphological dataset has neither led to a stable phylogeny, nor to a truly widely accepted higher-level taxonomy. As soon as they became available, molecular data gave significant contributions to bivalve taxonomy and phylogenetics, but little consensus has been reached in literature because of a substantial lack of shared methodological approaches to retrieve and analyze bivalves' molecular data. Page 641

12. The long way to diversity, By Angela Dinapoli

Many questions regarding gastropod phylogeny have not yet been answered. One major question is the molecular confirmation of the Heterobranchia concept based upon morphological studies conducted by Haszprunar (1985a, 1988). This diverse taxon comprises the Euthyneura (with the Opisthobranchia and Pulmonata), and the "Lower Heterobranchia" (with several "primitive" or "basal" members such as Valvatoidea, Architectonicoidea, Omalogyroidea, Rissoelloidea and Pyramidelloidea). Page 60

13. Crassostrea mitogenomes, By Xiangyun Wu

However, inconsistent or conflicting conclusions can be drawn when different DNA sequences are used for phylogenetic analyses (e.g., Zhang et al., 2005; Reece et al., 2008). Page 448

14. The Adriatic Flexopecten complex, By J. M. Pujolar

Despite including some of the most important species from the point of view of fisheries and aquaculture, the systematics and evolution of the family Pectinidae is a matter of continuing **debate**, mostly due to the demonstrated phenotypic plasticity in bivalve shell morphologies on which most of the taxonomies are based on. Page 942

Determining whether a group of organisms constitutes a species, a sub-species or a population has been a topic of **debate** among evolutionary biologists. Page 944

15. Building Gene Sets in Molluscs, By Daniel J. Jackson

Although deep-level relationships between major molluscan clades remain the topic of long-standing **debate** and current research, monophyly for the major extant groups (Monoplacophora, Polyplacophora, Gastropoda, Bivalvia, Cephalopoda, and Scaphopoda) is generally accepted and supported by morphological and molecular data (Sigwart and Sutton 2007; Wilson et al. 2009). Page 592

Molecular and morphological analyses of extant groups often yield conflicting phylogenetic topologies generating much **debate** concerning sister-group relationships within the Mollusca (Ponder and Lindberg 2008); however, larger molecular data sets that include difficult to sample early branching taxa are yielding

increasingly resolved topologies (Wilson et al. 2009). Until these phylogenetic issues are resolved, a complete understanding of the evolutionary origins of nacre will remain obscure. Page 605

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15. Building Gene Sets in Molluscs, By Daniel J. Jackson, *Molecular Biology And Evolution*, 2010, Volume 27, Number 3, Pages 591–608 Page 102

Plants

1. When Clocks Collide, By Christopher A. Brochu

Other conflicts have received less attention but remain no less perplexing, such as the origin of angiosperms (Doyle, 1998; Wikstrom et al., 2001) and gaviaoid crocodylians (Brochu, 1997; Harshman et al., 2003). These have remained robust to improved data sets and techniques—the more we look at fossils, molecules, or algorithms, the stronger the disparity seems to grow. Page 1.

2. Morphologic Evolution, By Michael Knappertsbusch

After splitting events there is a considerable amount of gradual change involved in the evolution of *C. leptoporus* morphotypes, which suggests a more complex phylogenetic model than punctuated equilibrium or phyletic gradualism alone. Page 725

3. Photosynthetic evolution, By Ralph A. Bungard

After all, the chloroplast itself is an ancient remnant of once free living cyano bacteria whose structure, function and genome has been winnowed down and modified to such an extent that its precise phylogenetic origins are still under **debate**. Page 235

4. Classification of *Frullania Raddi*, By Jörn Hentschel

Whereas the general circumscription of *Frullania* is without controversy, the position of a few species with aberrant morphology is subject to **debate**. Page 148

5. Macaronesian endemics, By Ruth Jaén-Molina

Our molecular data allowed us to assess some taxonomic treatments of the Macaronesian taxa based on morphological features alone that have stirred **debate**. Page 979

6. *Eucalyptus* (Myrtaceae), By Dorothy A. Steane

As a result of these factors, reconstructing the phylogenetic history of *Eucalyptus* species has been problematic for systematists, even with the application of molecular techniques. *Eucalypt* researchers have tested a range of molecular techniques (see below), but none has proven to be suitable for resolving relationships among closely related species within sections or between closely related sections. Page 206

There has been considerable **debate** about how well single-gene phylogenies reflect species phylogenies (see Liu et al. (2009) and references therein) and researchers have often lamented the lack of an efficient method of whole-genome phylogeny reconstruction. Page 218

7. Diversification of mangrove fauna, By D. G. Reid

For mangrove littorinids the fossil record is equally old, but there is conflicting phylogenetic evidence for an ancestral habitat on either rocky shores or mangroves. Page 186

8. Fast evolution, By Jin-Hua Ran

However, in recent years, extraordinarily high substitution rates have been documented from mtDNA of several angiosperm genera, such as *Pelargonium* (Palmer et al., 2000; Parkinson et al., 2005; Bakker et al., 2006), *Plantago* (Cho et al., 2004; Bakker et al., 2006), *Silene* (Städler and Delph, 2002; Houliston and Olson, 2006; Barr et al., 2007; Mower et al., 2007; McCauley and Ellis, 2008; Sloan et al., 2008), and *Acorus* (Mower et al., 2007), intensifying the **debate** on the evolution of plant mtDNA. Page 136

However, the monophyly of conifers is still controversial due to the conflicting results among various molecular studies, especially with regard to the relationship between Pinaceae and Gnetales. Page 146

9. Phylogeny of the Polytrichales, By Jaakko Hyvoonen

At the moment it seems that none of the morphological characters is a very good indicator of phylogeny, since all of them show considerable homoplasy. Page 924

10. Major clades of parmelioid lichens, By Oscar Blanco

The phylogeny and classification of parmelioid lichens has been a matter of **debate** for several decades. Page 52

The morphology and physiological effects of these pores have been studied intensely during the last decades (Beltman, 1978; Green et al., 1981, 1985; Hale, 1973, 1981; Lumbsch and Kothe, 1992; Sancho et al., 2000; Yoshimura and Hurutani, 1987), but their evolutionary history is currently poorly understood. Page 52

11. Major clades of the Asteraceae, By Jose L. Panero

Most of the studies listed above have been unable for the most part to clarify the phylogenetic positions of anomalous or transitional genera. Page 758

If the evolutionary histories of the nuclear and chloroplast compartments in Asteraceae truly differ so extensively at the tribal relationships it would be remarkable, and could suggest an even greater role of hybridization in generating Asteraceae diversity. However, this interpretation of the incongruence between these nuclear and plastome topologies is confounded by other factors that can lead to conflicting phylogenetic signal, namely sampling error and homoplasy arising from the assessment of sequence orthology as well as nucleotide substitution saturation. Page 774

However, the position of Stifftioideae is still equivocal and the phylogenetic relationships among the three main lineages of the Cichorioideae are still problematic. Page 775

12. Carnivorous plant genus *Genlisea*, By Andreas Fleischmann

So far, reliable relaxed-clock estimates for the age of Lentibulariaceae have been hampered by both the absence of useful fossil calibration points and the uncertainty with respect to the phylogenetic position of the family within Lamiales. Page 780

13. Origin of Macaronesian *Sideritis*, By Janet C. Barber

Numerous hypotheses of taxonomic relationships in *Sideritis* have been proposed over the years, including a variety of sectional and subgeneric circumscriptions and even the segregation of the Macaronesian taxa as a separate genus, *Leucophaea* (Kunkel, 1973; Webb and Berthelot, 1845). Page 295

Few clear-cut morphological characters delimit subgenera and sections and there has been particular disagreement over sectional circumscription of the relatively few annual species. Page 295

Explanations for the woody nature of oceanic island plants have differed. Page 303

14. Ancient extant seed plant *Cycas*, By Long-Qian Xiao

An important and often **debated** issue is the effect of ITS pseudogenes on phylogenetic inferences. Page 169

Although the evolutionary relationships among these are **debated**, cycads are likely the earliest diverged gymnosperm lineage (e.g. Chaw et al., 2000), because their mature pollen has multi-ciliate sperms and their ovules are borne on the margins of leaf-like megasporophylls (Stevenson, 1990). Page 169

This suggests that the phylogenetic analysis can provide some insights into the evolution in *Cycas*. However, the currently **debated** evolutionary relationships and delimitations of intra-generic taxonomic units cannot be addressed here, because a too small sample size (only 6 out of about 90 species) was sampled. Page 176

15. The sectional level in *Eucalyptus*, By Fiona S. Poke

Understanding evolutionary relationships among eucalypts is difficult because of the diversity of the genus (includes approximately 700 species) and the propensity for inter specific hybridisation (Griffin et al., 1988). As a result, there has been much **debate** about the taxonomy and phylogeny of the genus. Page 160

In conclusion, phylogenetic analysis using a single copy nuclear gene, CCR, was unable to resolve three sections of *Eucalyptus* into monophyletic groups, similar to previous studies using nrDNA. Page 169

16. Origins of vivipary and salt secretion, By Suhua Shi

The most remarkable morphological specializations of mangroves are vivipary, salt secretion, and aerial roots. There has been a long **debate** on whether the complex traits vivipary and secreters have a single origin, the answer to which has profound implications for the mechanism of evolution in mangroves. Page 159

Although we are in favor of the multiple origin hypothesis for both vivipary and salt secretion based on our analysis, we realize the final conclusion will depend much on the knowledge about the rate of loss and gain of these characters, which cannot be resolved by the sequence data presented in this study. Unfortunately such information is scarce either from molecular biology or plant physiology. Page 164

17. Phylogeographic patterns, By Heidi M. Meudt

Despite recent systematic studies, many important questions remain regarding taxonomy, biogeographic patterns, and character evolution within the Hebe complex. Page 320

18. Relationships within Cornales, By Qiu-Yun Xiang

Cornales traditionally represented one of the systematically most problematic groups of flowering plants. The systematic **debate** largely centered on the circumscription and relationships of the core member, Cornaceae (for reviews see Eyde, 1988; Xiang and Soltis, 1998; Xiang et al., 1993). Page 36

This lack of strong support for basal nodes of the phylogenetic trees (or relationships among major lineages) suggests either conflict in characters or insufficient information in the sequence data to solve deep relationships within the Cornales. Page 54

19. Phylogenetic relationships of Ruteae, By Gabriele Salvo

The different types of datasets were partly incongruent with each other. The discordant phylogenetic patterns between the phytochemical and molecular trees might be best explained in terms of convergence in secondary chemical compounds. Page 736

More generally, the choice of characters for phylogenetic analysis has been a crucial and controversial issue in systematics (e.g., Hart et al., 2004; Stace, 2005) and the relative role of molecular and morphological data in reconstructing phylogenies has been extensively **debated** (Hillis, 1987; Patterson, 1988; Sytsma, 1990; Donoghue and Sanderson, 1992; Novacek, 1994; Baker et al., 1998; Wahlberg and Nylin, 2003; Wortley and Scotland, 2006). Directly linked to character choice is the controversy about combined versus separate analyses of different datasets (Bull et al., 1993; de Queiroz et al., 1995). Page 736

20. Sorting wheat from chaff, By M. Virginia Sanchez-Puerta

Studies of molecular data have partially clarified the pattern of plastid acquisition and transfer; complete plastid genomes provide support for some clades, although resolution of other phylogenetic questions is less clear, and different studies have at times reached conflicting conclusions. As with any comparison of phylogenetic analyses, such conflict may represent a biological phenomenon or an analytical artifact. Page 885

In addition, a heated **debate** exists regarding the relative importance of taxon sampling and site sampling in phylogenetic analyses, while limited resources force compromises between the number of genes and taxa included in any analysis (Graybeal, 1998; Rokas and Carroll, 2005; Rosenberg and Kumar, 2001; Soltis et al., 2004). Page 892

21. Diversification in the Andes, By Federico Luebert

However, both the timing of the major stages of the Andean uplift and the onset of aridity in western South America remain controversial. Page 90

Fossil evidence encompassing the relevant periods across the western flank of the Andes is scarce. Estimation of divergence ages onto plant molecular phylogenies (Renner, 2005) has the potential to contribute to this **debate** and to provide feedback in reconstructing the history of the earth and its biota. Page 91

22. The Qinghai-Tibetan Plateau, By Jian-Quan Liu

Senecioneae, the largest tribe in the Asteraceae with 3200 species and 120 genera (Bremer, 1994), has been the subject of much **debate** with regard to its phylogenetic composition. Page 32

23. North American Psoraleaceae, By Ashley N. Egan

However, the relative utility of gap characters has been a matter of **debate**. Page 540

24. Hawaiian Dryopteris, By J. M. O. Geiger

There has been much **debate** and confusion regarding specific and subspecific classifications and in the understanding of the evolutionary relationships among the taxa, especially for the Hawaiian species (Fraser-Jenkins, 1986, 1994; Herat, 1979; Palmer, 2003; Wagner, 1993, 1995; Wagner et al., 1999a). There have also been conflicting views regarding the historical biogeography of these taxa and their origins in the Islands. Page 393

25. The red algal tribe, By Lynne McIvor

All our analyses show *Aglaothamnion* to be paraphyletic. Whether this genus is justifiable has previously caused fierce **debate** amongst algal taxonomists. Page 441

In the light of our phylogenetic analyses, the **debate** concerning whether *Aglaothamnion* and *Callithamnion* should be recognized as separate genera has been shown to be well-founded: there is no simple answer to the question. Page 443

26. Early-diverging eudicots, By Sangtae Kim

There has been considerable **debate** concerning the primitive or ancestral habit in the angiosperms, woody vs. herbaceous. Authors of modern classifications (e.g., Cronquist, 1981; Takhtajan, 1997) favored a woody ancestral condition. Page 17

27. Rates of synonymous substitutions, By Guy Drouin

The later is a significant advantage because estimating the divergence times of seed plant species is complex and still the subject of much **debate** (Soltis et al., 2002; Magallon and Sanderson, 2005). Page 827

28. Pestalotiopsis and allied genera, By Rajesh Jeewon

The taxonomic history and complexity of *Pestalotiopsis* and its allies have been **debated** for over half a century (Arx, 1981; Guba, 1955; Roberts and Swart, 1980; Steyeart, 1949; Sutton, 1969, 1980) and more recently by Nag Rag (1993). Page 379

29. Pestalotiopsis taxonomy, By Ai-Rong Liu

Morphological based classification of *Pestalotiopsis* species has always been a taxonomic **debate** over the last five decades. Page 533

30. Divergence in *Dyosma versipellis*, By Ying-Xiong Qiu

The origin of greater species diversity of vascular plant genera in eastern Asian temperate forests when compared with their sister taxa in eastern North America has been the subject of much recent **debate** (Qian and Ricklefs, 2000, 2001; Harrison et al., 2001). Page 281

31. Polarity of Gene Fusion, By Yoji Nakamura

Determining the state of fusion or fission of the gene pairs identified here in the suspectedly basal angiosperm *Amborella*, for example, where a raging **debate** exists regarding its evolutionary position because large sequence data sets give conflicting results with strong support (Goremykin et al. 2004; Lockhart and Penny 2005), may shed further light on this and other currently difficult phylogenetic issues. Page 120 **Page 65**

32. Grouping of Plant and Animal, By Gayle K. Philip

Another major **debate** concerns the relationships of three eukaryotic Kingdoms (Animalia, Plantae, and Fungi) to each other. Page 1175

33. Differentiated Sunflower Species, By Jared L. Strasburg

Interest in documenting positive selection within species and adaptive divergence between species is motivated not only by the ongoing **debate** about the relative roles of neutral and selective processes in evolution but also by the promise that identifying genes under divergent selection between species can help us to understand both gene function and the nature of adaptive phenotypic differences (Steiner et al. 2007; Barrett et al. 2008). Page 1341

34. Phylogeny of Extant Seed Plants, By Chung-Shien Wu

In the past decade, molecular data have been widely used to reexamine the traditional evolutionary schemes of seed plants but have generated an even more diverse set of phylogenetic hypotheses, especially about relationships among the 4 surviving groups of gymnosperms and the angiosperms (see also review by Burleigh and Mathews 2004). Page 1366

35. Glyceraldehyde-3-Phosphate, By James T. Harper

There are contrasting views as to whether the two green plastid lineages are related (Cavalier-Smith 1999; Archibald and Keeling 2002), and the **debate** over the origin of red plastids is thornier still. Page 1730

36. Evolutionary Innovation of Angiosperms, By Judith Nardmann

Plants

The evolutionary relationship between higher land plants, gymnosperms and angiosperms, jointly seed plants, is still a matter of **debate**. Page 1745

37. Plastid Genome Sequence, By Hameed Khan

Biochemical and molecular data indicate that cryptophyte plastids are derived from red algae, yet the question of whether or not cryptophytes acquired their red algal plastids independent of those in heterokont, haptophyte, and dinoflagellate algae is of long-standing **debate**. Page 1832

38. Alphabets for Phylogenetic Inference, By Edward Susko

Years of controversy have surrounded the identity of the basal-most node in the angiosperm phylogeny. For instance, the placement of Amborella within the radiation of angiosperms has evoked a **debate** about the basal node in angiosperm phylogeny (Goremykin et al. 2003, 2004; Soltis et al. 2004; Lockhart and Penny 2005; Martin et al. 2005). Page 2146

This would usually be considered the correct relationship, although there has been considerable **debate**. Page 2147

39. Distance Method Adjustments, By Jihua Wu

This placement has been the source of considerable **debate** (Goremykin et al. 2003, 2004; Soltis et al. 2004; Lockhart and Penny 2005; Martin et al. 2005; Jansen et al. 2007; Moore et al. 2007). Page 2694

40. Covarion-like Evolution in Protein Sequences, By Huai-Chun Wang

For instance, the place of Amborella within the radiation of angiosperms has evoked a **debate** about the basal node in angiosperm phylogeny (Goremykin et al. 2003, 2004; Soltis et al. 2004; Lockhart and Penny 2005; Martin et al. 2005). Page 302

41. Genomes of the Green Algae, By Monique Turmel

In this context, it is worth mentioning that the nature of the progenitor of all green plants has generated intense **debate** and is still controversial (Melkonian 1984; O'Kelly 1992; Sym and Pienaar 1993). A better understanding of the relationships among prasinophyte lineages will be required before one can infer with confidence evolutionary scenarios of cellular changes. Page 644

42. The Placement of Mesostigma, By Naiara Rodriguez-Ezpeleta

The scaly green flagellate *Mesostigma viride* has an important place in the **debate** on the origin of green plants. Page 723

43. Stability and Oligomycin Resistance, By Marie Lapaille

In Chlorophyta, aside from the well-accepted basal position of Prasinophyceae, the relative branching order of Chlorophyceae, Trebouxiophyceae, and Ulvophyceae is still a matter of **debate**, which led us to consider three different subtrees (Pombert et al. 2004, 2005; Rodriguez-Ezpeleta et al. 2007). Similarly, unresolved relationships within Chlorophyceae (e.g., Lewis and McCourt 2004) entail three variants of each subtree, thus amounting to nine possible evolutionary scenarios. Page 1636

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Reptiles

1. Patterns Of Calibration, By Christopher A. Brochu

Slightly older fossils from the Hell Creek Formation (Lancian) of Montana might represent a caiman (Bryant, 1989), but the phylogenetic placement of this form **is unclear**; although it is not directly considered in this study, some of the range extensions applied in our analysis would approximate an alligatorine-caimanine split based on it. Calibration within *Crocodylus* is difficult, both because of the **unclear relationships** among living species and **the uncertain affinities** of many fossils assigned to the group. Page 10

The continental record in South America, where caimans spent much of their history, is sporadic. Many fossils relevant to **the problem of caiman phylogeny** have not yet been analyzed phylogenetically. Caimans have an imperfectly known record, and range extensions further back into the Neogene are not unreasonable. Page 24

But in some cases, these oldest estimates may be much older than the fossil record would suggest, and if older fossils are unavailable for physical reasons (e.g., relevant units were never exposed and cannot be sampled), we may never be able to test these hypotheses, rendering them functionally unfalsifiable. **Debates** over the origins of mammalian and avian orders have been mired in such issues for many years, and without major new discoveries, they are likely to continue into the future. Page 25

The solution lies not only in the continued search for robust phylogenetic hypotheses of fossils, but in the development of better molecular analytical methods. Page 28

2. End-Permian Tetrapod Extinctions, By Kenneth D. Angielczyk

Although these patterns have played a prominent role in **debate** about the taxonomy and phylogenetic relationships of Triassic dicynodont anomodonts, they have received little attention in the wider paleontological literature. Page 528

Although the phylogenetic relationships of anomodonts have been the subject of much scrutiny (e.g., Cluver and King, 1983; King, 1988; Cox, 1998; Modesto et al., 1999, 2003; Modesto and Rychczynski, 2000; Rychczynski, 2000; Angielczyk, 2001, 2002, 2004, 2007; Angielczyk and Kurkin, 2003; Maisch, 2001, 2002; Surkov and Benton, 2004; Vega-Dias et al., 2004; Maisch and Gebauer, 2005; Surkov et al., 2005; Ray, 2006; Frobisch, 2007), a general consensus has yet to be reached and no recent analysis has included a large sample of both Permian and Triassic taxa. Page 535

3. Fossil Snakes, By Olivier Rieppel

The presence of well developed hind limbs in *Pachyrhachis* and *Haasiophis* also creates methodological **problems** for the cladistic analysis of the phylogenetic relationships of these fossil snakes. Scenarios of snake origins are reviewed and found to be deficient in the absence of a well corroborated hypothesis of snake relationships within Squamata. Page 536

The current **debate** on snake relationships and origins has resulted in such a flurry of papers that it is no longer easy for readers, not closely involved in the argument, to follow the details. Page 536

The origin of snakes, as well as the reconstruction of phylogenetic interrelationships among basal snakes, has been **a long standing problem** in herpetology and paleo-herpetology (Rieppel, 1988), but one that has seen an important recent resurgence of interest. Page 536

Scenarios on the origin and early evolution of snakes necessarily remained linked to the search for the “ancestor,” or sister-group, of snakes, but a consensus **failed** to emerge. Page 537

Haas’ descriptions of *Pachyrhachis* and *Estesius* highlight the **problem** of character conflicts that rendered it difficult for him to assess unequivocally the relationships of these fossils. Page 537

Looking back on this **debate** on the origin of snakes and snake interrelationships, several core issues can be identified. These include issues of taxon sampling (Rieppel and Zaher, 2000a; Coates and Ruta, 2000), ambiguities in the diagnosis, or in the use, of higher taxa (Rieppel and Zaher, 2001; Rieppel et al., 2002) and, most importantly, disagreements about character delimitations (Rieppel and Zaher, 2000a, 2000b; Rieppel and Kearney, 2001, 2002). Page 538

With *Haasiophis*, *Pachyrhachis*, and *Podophis* representing macrostomatan snakes, the question of the sister-group relationships of snakes within Squamata, or of snake “origins,” **remains unresolved**. Page 554

Evidently, the ecology of snake origins must remain an open question until their sister-group relationships within Squamata have been determined. Until such time, we would like to close on a cautionary note, once again drawing attention to the fact that the fossil record of snakes is very incomplete (Rage, 1984), for which reason our knowledge of the evolution of limblessness in snakes remains **very incomplete** as well. Page 555

4. The Lower Permian Of Germany, By Johannes Muller

The first taxon described from this locality was *Thuringothyris mahlendorffae* Boy and Martens, 1991, a small eureptile of **uncertain phylogenetic** affinities. Page 726

On the basis of the phylogenetic position, short **ghost lineage**, and plesiomorphic anatomy, it is reasonable to use *Thuringothyris* as a starting point for interpretations on the morphological evolution of early captorhinids. Page 737

5. An Early Polycotyloid Plesiosaur, By Tamaki Sato

The Plesiosauria is a clade of Mesozoic marine reptiles known from the Late Triassic to the very end of the Cretaceous. In spite of their widespread occurrence, however, plesiosaurian phylogeny, especially that of Cretaceous forms, is still under **debate**. Page 907

6. The Affinities Of Mosasaurs And Snakes, By Michael S. Y. Lee

Apart from mosasaurs and aigialosaurs, all the marine pythonomorphs are very imperfectly known. For instance, dolichosaurs, *Adriosaurus*, and *Aphanizocnemus* can be coded for less than 35 percent of characters. Such an amount of missing information means that support for their phylogenetic positions **is not very robust**, as indicated by low bootstrap and Bremer support (Fig. 8). Missing information also reduces support throughout the tree, as the poorly-known taxa can fit into many different places with only slight loss in parsimony. Additionally, most of the characters that unite dolichosaurs, *Aphanizocnemus*, and *Adriosaurus* with snakes, to the exclusion of mosasaurs and aigialosaurs, are correlates of body elongation and limb reduction. Thus, the evidence that these taxa are more closely related to snakes than to mosasaurs and aigialosaurs is relatively weak. Page 927

7. Phylogenetically Defined Clade Names, By Walter G. Joyce

This type of definition is especially useful for defining the names of node-based phylo-taxa with **uncertain** internal relationships; that is to say, name application would be fixed by composition regardless of ideas regarding in group relationships. Page 995

The origin of turtles has been hotly **debated** for more than a century, and a consensus is still lacking. The precise composition of *Pantestudines* thus remains unclear. It is now generally agreed that turtles are not sister to a *mammalian* 1 *saurian* (s. Gauthier et al., 1988a) clade within *Amniota* (s. Gauthier, 1984), as was once thought (e.g., Gaffney, 1980). Some paleontologists placed turtles as sister to captorhinids (Gaffney and McKenna, 1979; Gaffney and Meylan, 1988; Gauthier et al., 1988b), but that relationship has been rejected in favor of hypotheses placing turtles as sister to *Sauria* within *Reptilia* (s. Gauthier et al., 1988a, 1988b; Gauthier, 1994), although the exact relationships are still in dispute [i.e., procolophonids (Reisz and Laurin, 1991; Laurin and Reisz, 1995) or pareiasaurs (Lee, 1995, 1997)]. Still other paleontologists take a more divergent view in which turtles are regarded as the sister to *Lepidosauria* (Rieppel and DeBraga, 1996; DeBraga and Rieppel, 1997; Rieppel and Reisz, 1999), and thus within the clade *Sauria* rather than among more basal *amniotes*. Page 996

In addition to its principal crown groups, *Trionychia* and *Kinosternoidea* (see below), *Trionychoidea* is currently thought to include a series of basal turtles from the Early Cretaceous of uncertain phylogenetic relations, making it difficult to fix the ages of its basal divergences. Page 1001

Because the placement of *Platysternon megacephalum* **remains uncertain** to date (see above), we purposefully define *Chelydridae* independent of the phylogenetic placement of *Platysternon megacephalum*. Page 1004

8. A New Genus And Species Of Sea Turtle , By Thomas M. Lehman

Recognition of this new species further increases the known diversity of Cretaceous sea turtles, and is of interest in examining the phylogeny of sea turtles. *T. fischbecki* is likely a primitive protostegid but has several features

generally thought to be synapomorphic for more derived lineages, making its systematic placement uncertain. Page 1163

However, in having somewhat uncertain affinities it is certainly not alone among sea turtles. There has long been disagreement over the placement of some taxa (e.g., *Allopleuron*, *Desmatochelys*, *Notochelone*) and with the recent descriptions of basal representatives of each sea turtle lineage, the morphological boundaries between the three traditional clades have become less distinct. Page 1176

9. Archosaur Phylogenetics, By Christopher A. Brochu

A few extinct groups remain controversial, such as the pterosaurs, and **debate** persists over the phylogenetic relationships among extant bird lineages, which have proved difficult to resolve, and divergence timing estimates within Aves and Crocodylia remain the source of contention. Page 1185

We also encounter interesting conflicts between fossil and molecular data sets regarding lineage divergence timing within both birds and crocodylians, and at least some sequence-based analyses argue that turtles belong within Archosauria. These challenges lie at the interface between paleontology and neontology. Page 1185

The only pseudosuchian lineage to survive the Triassic is Crocodylomorpha, which includes an assemblage of gracile “sphenosuchians” (the monophyly of which is **debated**, e.g., Benton and Clark, 1988; Walker, 1990; Sereno and Wild, 1992; Wu and Chatterjee, 1993; Clark et al., 2000) and crocodyliforms. Page 1187

Because we cannot actually *know* the true phylogeny, deciding between these scenarios will be difficult. Page 1193

Other interesting fossils, when considered in a phylogenetic framework, imply even more ghost lineages in the Cretaceous (Hope, 1998; Stidham, 1998a), though the identifications are not always accepted (Dyke and Mayr, 1999). Page 1195

10. Basal Sauropodomorphs, By T. S. Kuttly

At present, the relationships of basal sauropodomorphs and the origins of sauropods represent two of the more confused and controversial aspects of dinosaur phylogeny (see Yates, 2003a; Wilson, 2005). Page 1236

11. Distinguishing heat from light, By Philip C. J. Donoghue

Debate over the affinity of chaetognaths, sea spiders, Xenoturbella and even familiar organisms such as snakes and turtles, is testament to the endurance of this problem: the identification of homology requires, among other criteria, an a priori hypothesis of grouping at some level before the process of comparative anatomical interpretation can proceed. Page 180

12. Ribosomal RNA genes, By Jon Mallatt

The position of turtles in amniotes, however, is **debated**. Page 1017

Turtles. There has been much **debate** over whether turtles are primitively ‘anapsids’ (with no temporal opening in the skull) or whether their anapsid condition was secondarily derived from a diapsid ancestor. Page 1017

13. Horned lizard phylogeny, By Wendy L. Hodges

By fully exploring the data and with all available analytical techniques, it became evident that certain patterns are present in the data, yet the data were insufficient in their power to resolve the basal relationships in Phrynosoma. Although progress has been made in our analyses, additional data are needed to tease apart basal relationships within this genus. Some of these data sources could be found in additional molecular sequences (perhaps nuclear genes), fossil data, or more detailed morphological analyses. Page 969

14. South African limbless lizard, By Savel R. Daniels

Although monophyly of the Acontinae is well supported (Greer, 1970), phylogenetic relationships among the three genera within this subfamily have been the subject of considerable **debate** (Branch, 1998; Broadley, 1968; Rieppel, 1982). Page 315

In the absence of fossil data for this group with which to test biogeographic hypotheses, it is difficult to calibrate rates of molecular evolution. Page 322

15. Low genetic divergence, By Jennifer M. Hay

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. Page 1

Interpretation of tuatara phylogenetic trees is confounded by the absence of an appropriate outgroup, so the trees are unrooted and directionality of nucleotide substitutions cannot be determined. Page 13

16. The Phylogeny of Xantusiid Lizards, By Brian I. Crother

The search for the best estimate of phylogenetic relationships among taxa is the ultimate goal in the reconstruction of the pattern of evolutionary history. The appropriate methods to achieve that goal have been and remain the subject of much **debate** (e.g., this paper and a plethora of others), but studies such as Hillis et al. (1992) may help identify the most reliable methods for reconstructing evolutionary history. Even though **debate** exists, most of the methods favored by “phylogeneticists” are those to which at least some of the basic tenets and philosophy can be traced back to Hennig (1966). Page 292

17. Molecular phylogeny of *Vipera*, By Thomas Garrigues

No molecular phylogeny of *V. aspis* subspecies has yet been published, although studies based on morphology have generated considerable **debate** (Nauulleau, 1997; Saint Girons, 1978; ZuY, 2002). Page 36

18. Phylogeny for Marine Turtles, By Peter H. Dutton

However, **debate** continues over the phylogenetic relationships within the Cheloniidae, with uncertainties existing at almost all taxonomic levels. Pages 511–521

19. The phylogeny of tortoises, By James F. Parham

Despite boasting a rich fossil record (AuVenberg, 1974) and diverse living members (Ernst and Barbour, 1989), the evolutionary relationships of tortoises remain poorly known. Sadly, the uncertainties about the history of tortoises are matched by uncertainties about their future. Page 51

However, the underlying mechanisms responsible for associated rates of molecular and morphological evolution remain unclear, and such correlations are still **debate**d (e.g., Bromham et al., 2002; Marko and Moran, 2002). Page 58

20. A puzzling phylogenetic problem, By Saverio Vicario

Because phylogenetic relations within Xantusiidae could be affected by alternative outgroup topologies, which are themselves the subjects of **debate**, we also explicitly tested the effects of topological uncertainties among potential outgroups on ingroup phylogeny. Page 245

21. Phrynosomatine sand lizards, By James A. Schulte

The phrynosomatine sand lizards are a well-studied clade of squamate reptiles for which several alternative phylogenetic hypotheses have been proposed. Page 700

22. The phylogeny of pit vipers, By Todd A. Castoe

The deepest phylogenetic divergences among pit vipers have yet to be resolved with strong support. Page 92

Currently, there are twelve genera of New World pit vipers recognized (Campbell and Lamar, 2004) and the relationships among these remain poorly understood and inconsistent across studies. Page 92

Despite the efforts of numerous authors, phylogenetic relationships within the subfamily Crotalinae remain controversial, particularly at the intergeneric level (e.g., Gutberlet and Harvey, 2004; Malhotra and Thorpe, 2004; Parkinson et al., 2002). Three issues have likely played major roles in the generation of inconsistent conclusions or poor resolution across studies. Page 92

23. A nesting of vipers, By Wolfgang Wüster

Despite their medical interest, the phylogeny of the snake family Viperidae remains inadequately understood. Page 445

Colubroidea: the age of the basal divergence of the Colubroidea (i.e., between the vipers and their sister clade in the context of this study) remains subject to considerable **debate**. Page 451

24. The turtle family Geoemydidae, By Phillip Q. Spinks

The turtle family Geoemydidae represents the largest, most diverse, and most poorly understood family of turtles. Little is known about this group, including intrafamilial systematics. The only complete phylogenetic hypothesis for this family positions geoemydids as paraphyletic with respect to tortoises, but this arrangement has not been accepted by many workers. Page 164

In spite of these analyses, phylogenetic relationships and the taxonomy derived from those relationships within the Geoemydidae remain uncertain. The widespread confusion regarding the phylogenetic content and relationships of the Geoemydidae stems from at least three issues. Page 167

25. Gene tree parsimony, By James A. Cotton

The trees also all **fail** to resolve relationships within the reptiles, or present a somewhat unusual phylogeny within this group. Page 306

There is no doubt that lizards and snakes form part of a monophyletic radiation of diapsid reptiles, although there has been some **debate** about the exact relationships between the different extant lineages within this radiation, as discussed above. Similarly, there has been **debate** about the exact relationships between hagfish, lampreys and gnathostomes (Delarbre et al., 2002; Janvier, 1996), but the only hypotheses supported by recent work are that lampreys and hagfish form a monophyletic cyclostomes group, or that hagfish are the most basal vertebrates, with lampreys a sister-group to the gnathostomes. Page 306

26. Phylogeography of endemic toads, By Maria Tereza C. Thomé

However, genetic diversity within and among morphospecies is **unknown**, and their phylogenetic relationships have not been established. Page 1020

Although these four clades are well-supported and largely uncontested, the relationships among them have been the subject of considerable **debate** (reviewed by Wilgenbusch and de Queiroz, 2000). Page 700

27. Chinese toad-headed lizards, By Xianguang Guo

The toad-headed lizards of genus Phrynocephalus are distributed from northwestern China to Turkey and are one of the major components of the central Asian desert fauna. To date, published morphological and molecular phylogenetic hypotheses of Phrynocephalus are only partially congruent, and the relationships within the genus are still far from clear. Page 643

Despite considerable previous morphological, allozyme, karyological, osteological, and ethological work, the phylogenetic and taxonomic relationships within the toadheaded lizards remain controversial and largely unresolved (e.g., Arnold, 1999; Dunayev, 1996; Golubev, 1993; Macey et al., 1993, and references therein), especially those among the approximately 18 Chinese species (Zhao and Alder, 1993; Pang et al., 2003). Page 644

28. History of the snake-eyed lizards, By P. Kyriazi

The snake-eyed lizards of the genus Ophisops (Lacertidae) have been through a series of taxonomical revisions, but still their phylogenetic relationships remain uncertain. Page 795

29. Indian Ocean tortoises, By Eric P. Palkovacs

The evolution and pattern of island colonization of Dipsochelys have remained a topic of much **debate**. Page 217

30. Early history of snakes, By Nicolas Vidal

This last point has important bearing on the origin of snakes, one of the most controversial fields in vertebrate evolution since the 19th century. The **debate** has been recently fuelled by the discovery of fossils of three marine snake species (“pachyophiids”) with small but welldeveloped hindlimbs (genera Pachyrhachis, Haasiophis, and Eupodophis) (Caldwell and Lee, 1997; Rage and Escuillie, 2000; Rieppel et al., 2003; Tchernov et al., 2000). Page 786

31. Distribution in night snakes, By Daniel G. Mulcahy

However, the timing of events is **debated**. Page 537

Currently, there is **debate** in the geological literature regarding the exact timing of the Cape separation from mainland Mexico: 7.5-8.2 mya (Oskin and Stock, 2003) versus 12-14 mya (Ferrari, 1995; see also Henry and Aranda-Gomez, 2000). Page 542

32. Phylogeography of the spotted skink, By Stephanie N. J. Greaves

The relative impacts of these processes on biogeographic patterns in New Zealand taxa has long been a subject of **debate**. Page 730

However, the taxonomic status of southern populations as a separate species has been **debated**. Page 734

33. Caribbean Rock Iguana, By Catherine L. Malone

Unfortunately, the geological history of this area is unclear and the origin of its biota is a subject of intense **debate** (Crother and Guyer, 1996; Hedges, 1996a; Hedges et al., 1992, 1994; Kluge, 1988; Williams, 1989). The controversy centers on the relative importance of vicariance versus dispersal in shaping the distribution of the founding Caribbean biota. Page 270

34. The false gharial, By Ray E. Willis

The morphological versus molecular **debate** continues because both sets of data appear to be robust; albeit deriving totally different conclusions. Page 793

35. Lizard Anolis Carolinensis, By Peter A. Novick

The respective importance of these different factors is unclear and remains a matter of **debate** (Eickbush and Furano 2002; Furano et al. 2004; Neafsey et al. 2004; Kordis et al. 2006; Song and Boissinot 2007). Page 1812

36. DNA Sequences of the Green Turtle, By Yoshinori Kumazawa

Turtles have highly specialized morphological characteristics, and their phylogenetic position has been under intensive **debate**. Page 784

Recent intensive **debate** on the phylogenetic position of turtles has raised the more general and fundamental question of how evolutionary processes of morphologically specialized organisms like turtles can best be understood (see, e.g., Rieppel and deBraga 1996). Page 791

37. Origin and Evolution of the Snake Venom, By B. G. Fry

The evolution of the venomous function of snakes and the diversification of their toxins has been of tremendous research interest and considerable **debate**. Page 870

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Sponges

Sponges

1. A History Of Phylogenetic Interpretation, By Stephen M. Rowland

Archaeocyaths are calcareous, conical, Cambrian fossils with a long history of phylogenetic uncertainty and changing interpretations. The history of phylogenetic interpretation of archaeocyaths reveals five distinct schools of thought: the coelenterate school, the sponge school, the algae school, the Phylum Archaeocyatha school, and the Kingdom Archaeata school. Page 1065

Throughout the history of **debate** concerning archaeocyathan phylogeny, relatively little attention had been paid to how the organisms had actually lived. Page 1074, 1075

The isolation in which many paleontologists worked prior to the 1980s almost certainly contributed to the variety of phylogenetic interpretations concerning archaeocyaths. Page 1076

2. An evaluation of support, By Scott A. Nichols

Due to morphological character conflict and simplicity, the relationships between major demosponge lineages remain incompletely resolved and the monophyly of most higher-taxa within the class Demospongiae remains suspect. Page 82

Due to morphological character conflict and simplicity, the relationships between major demosponge lineages remain incompletely resolved and the monophyly of most higher-taxa within the class Demospongiae remains suspect. Page 91

3. Analysis of freshwater sponges, By Martin J. Meixner

The exact position of several sponge taxa and the monophyly of the phylum Porifera is a matter of **debate** (Adams et al., 1999; Borchellini et al., 2004,2001; Cavalier-Smith et al., 1996; Collins, 1998; Medina et al., 2001). Page 882

4. Demosponge EST Sequencing, By Matija Hrcet

There is an ongoing **debate** on the molecular phylogeny aspects of basal metazoans (Dohrmann et al. 2008; Srivastava et al. 2008; Philippe et al. 2009; Sperling et al. 2009), and although we did not address this issue directly, we hope that the data provided in this paper will provide further evidence for understanding the complex relations between Porifera, Placozoa, and Eumetazoa. Page 2754

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4. Demosponge EST Sequencing, By Matija Hrcet, Molecular Biology And Evolution, 2010, Volume 27, Number 12, Pages 2747–2756

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Tunicates

Tunicates

1. Ascidian molecular phylogeny, By Xavier Turon

The position of the Appendicularia remains controversial (Swalla et al., 2000), although a recent study suggests that they are the sister group to the aplousobranch ascidians (Stach and Turbeville, 2002). Page 309

1933; Monniot et al., 1991; Van Name, 1945). The relationships between the members of Aplousobranchiata are unclear (Kott, 1990), a fact that is reflected in the poor agreement in its internal classification. Page 310

2. Erosion of phylogenetic signal, By Thomas Stach

The molecular phylogenetic position of Tunicata and internal interrelationship of higher tunicate taxa is controversial. High substitution rates and extreme gene order variability hamper phylogenetic analyses. Page 860

Textbooks classify Tunicata into the subtaxa Ascidiacea, Thaliacea and Appendicularia, but phylogenetic relationships of these subtaxa is under **debate**. Page 861

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2. Erosion of phylogenetic signal, By Thomas Stach, Molecular Phylogenetics and Evolution, 2010, Volume 55, Pages 860–870

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Vertebrates

1. Organizing chordates, By Jordi Garcia-Fernandez

Understanding how the chordate body plan originated and evolved is still controversial. Page 619

However, whether the vertebrate organizer was primitively present in early chordates or was acquired at the origin of vertebrates was unclear and a subject of **debate**. Page 619

2. Vertebrate neural crest, By Gerhard Schlosser

However, two conflicting models have been put forward to explain how contiguous domains of neural crest and paraxial primordium are established at the neural plate border and these different models suggest a common or independent evolutionary origin of neural crest and placodes, respectively. Page 660

At present, we do not have sufficient evidence either from developmental studies in vertebrates or from comparative and paleontological studies to conclusively decide between these two scenarios. Page 661

3. The odontode explosion, By Gareth J. Fraser

How and when tooth-like units (odontodes) originated during vertebrate evolution continues to cause a stir among palaeontologists and evolutionary developmental biologists. Page 808

Two main theories polarise the field: the traditional view, that skin denticle competent ectodermal-epithelium folded and integrated into the mouth to provide the inductive capacity for teeth – the ‘outside-in theory’ – is contested by the ‘inside-out theory’ that teeth, born from endoderm, originated in the posterior pharynx of jawless vertebrates with dental potential co-opted anteriorly to oral jaws during gnathostome evolution. Page 809

Debate about the appearance and evolution of odontodes during early vertebrate evolution is firmly rooted in the classic problem of anatomical homology. Page 809

4. The Endothelin System, By Ingo Braasch

Several models have been proposed to explain the emergence of the neural crest in vertebrates and its evolutionary origin is matter of an ongoing **debate** (reviewed in Donoghue et al. 2008). Page 784

5. Context-Dependent Mutation Rates, By Ryan D. Hernandez

Isochores appear to have entered vertebrate genomes; 310–350 MYA (Bernardi et al. 1997), but there is still considerable **debate** regarding their formation and which evolutionary forces are acting to maintain them (Bernardi 2000; Fryxell and Zuckerkandl 2000; Meunier and Duret 2004). Page 2196

6. 500-Myr-Old Syntenic Block, By Wei Wang

The nature of the last common ancestor of vertebrates is of enormous research interest. This area of interest has been rigorously researched in the past and present. Knowledge in this area has increased steadily, which, in the not too distant time, we hope to understand in the evolution process. Page 784

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Whales

1. Molecular Clock Divergence, By Jessica M. Theodor

ABSTRACT—Molecular clock estimates of divergence times for artiodactyls and whales **vary widely** in their agreement with the fossil record. Recent estimates indicate that the divergence of whales from artiodactyls occurred 60 Ma, a date which compares well with the first appearances of fossil whales around 53.5 Ma, and artiodactyls at 55 Ma. Other estimates imply significant gaps in the fossil record. A date of 65 Ma for the divergence of Suidae and Ruminantia predates the appearance of Ruminantia by over 10 million years, and an estimate of 58 Ma for the divergence of Suidae from Cetacea implies a gap of over 20 million years. Further, although a molecular clock estimate has not been reported, the hypothesis that hippos are the closest living relatives of the whales implies a potential **ghost lineage** for hippos of over 40 million years. There are only two living species of hippos, and their fossil record is sparse, while cetaceans and other artiodactyls are speciose and have rich fossil records. A **40-million-year gap** in the fossil record of hippos could be explained by several possibilities: inadequate biogeographic sampling, taphonomic biases, or undifferentiated primitive morphology. Similarly, a number of possible problems may exist in the molecular data: rate variation in the genes sampled, the low numbers of genes examined, and insufficient age calibrations. In addition, there are potential problems in molecular phylogeny estimation, such as long branch attraction and inappropriate taxonomic sampling. Additional estimates of divergence times among living taxa should provide a broader framework for comparison with the fossil record and provide information to help identify which of these factors are **causing conflict**. Page 39.

2. Molecular tree of extant cetaceans, By Michael R. McGowen

Cetaceans are remarkable among mammals for their numerous adaptations to an entirely aquatic existence, yet many aspects of their phylogeny remain **unresolved**. Page 891

The secondarily aquatic nature of whales and dolphins has inspired numerous phylogenetic studies and prompted **debate** concerning their origins among terrestrial mammals (reviewed in Gatesy and O’Leary, 2001; O’Leary and Gatesy, 2008). No less attention has been given to elucidating relationships among the major groups of cetaceans. Page 891

However, many relationships within Cetacea **remain less certain**, despite multiple efforts to resolve discrete portions of the phylogeny using a diverse array of systematic markers (mitochondrial [mt] DNA [Árnason et al., 1991a, 2000, 2004; Árnason and Gullberg, 1993, 1994, 1996; Milinkovitch et al., 1993, 1994, 1996; Rosel et al., 1995; Montgelard et al., 1997; LeDuc et al., 1999; Cassens et al., 2000; Hamilton et al., 2001; Dalebout et al., 2002, 2003, 2004; Rychel et al., 2004; Sasaki et al., 2005, 2006; Yan et al., 2005; Caballero et al., 2007; McGowen et al., 2008; Xiong et al., 2009], exons, introns, pseudogenes [references in Table 1], transposons [Nikaido et al. 2001a, 2001b, 2006, 2007], and morphology [Heyning, 1997; Messenger and McGuire, 1998; Geisler and Sanders, 2003; Deméré et al., 2008]). Page 891, 892

In addition to this conflict, previous **phylogenetic hypotheses disagree** concerning the branching sequence of the three most basal odontocete clades (Physeteroidea, Ziphiidae, Platanistidae), the exact position of the now extinct Chinese river dolphin *Lipotes vexillifer*, and the relationships of species within the delphinid, ziphiid, and balaenopteroid radiations. Page 892

In the **absence** of a cohesive species-level phylogeny, there is also a lack of divergence estimates for most cetacean speciation events Page 892

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2. Molecular tree of extant cetaceans, By Michael R. McGowen, Molecular Phylogenetics and Evolution, 2009, Volume 53, Pages 891–906

Worms

1. Early Jurassic Hydrothermal Vent Community, By Crispin T. S. Little

The presence of vestimentiferan tube worm fossils in the Figueroa deposit is at odds with the supposed time of origin of the modern vestimentiferans (=100 Ma), based on molecular data. Page 542

2. Parallel evolution of segmentation, By Ariel D. Chipman

I start by presenting and discussing the data that have led many researchers to suggest a common origin for segmentation, and follow this with a discussion of the data that make this scenario unlikely. There are problems with many of the arguments in both directions, and I also discuss these. Page 61

The third super phylum Lophotrochozoa, which includes the segmented annelids, has a much poorer fossil record than Deuterostomia or Ecdysozoa, and the interpretation and affinity of early lophotrochozoans is hotly **debated**. Page 64

While the **debate** about the interpretation of the phylogenetic relationships of these fossils is bound to continue (and has only been reviewed briefly here), it is generally accepted by most of the authors cited above that already in the Cambrian, segmentation was a trait distinguishing annelids from other lophotrochozoans. Page 64, 65

3. Looks can deceive, By Elizabeth M. Perkins

The morphological based taxonomy of highly derived parasite groups is likely to poorly reflect their evolutionary relationships. Page 705

Consequently the current morphological classification shows little correspondence with the phylogenetic relationships within the family. Page 705

This is not an uncommon dilemma and there has been much **debate** in the literature about how to combine traditional taxonomy with phylogenetic relationships. Page 713

4. Syndermatan phylogeny, By Holger Herlyn

Apart from the phylogeny within the Acanthocephala, the acanthocephalan sistergroup still remains unresolved. Page 155

5. Haemadipsoid leeches, By Elizabeth Borda

A scourge of tropical and subtropical jungles, blood feeding terrestrial leeches of Haemadipsidae have long confused systematists and defied sensible biogeographic interpretation. The family Haemadipsidae usually includes problematic taxa that neither fit the typical Indo Pacific distribution of the group, nor properly match diagnostic characters used to define the family. Page 142

6. Character loss in orbiniid phylogeny, By Christoph Bleidorn

Orbiniid phylogeny is matter of **debate** and incongruence between hypothesis based on molecules and morphology has been repeatedly reported. Moreover, the phylogenetic position of the “oligochaetoid polychaetes” of the taxon *Questa* varies between morphological and molecular cladistic analyses. Page 57

The position of orbiniids within Annelida is disputed. Whereas the cladistic analysis of morphological data by Rouse and Fauchald (1997) favors a close relationship to Paraonidae, molecular analyses recovered Parergodrilidae as their sister group (e.g., Bleidorn, 2005; Struck et al., 2008). Based on chaetal arrangement, Hoffmann and Hausen (2007) propose a closer relationship to Spionidae. Struck et al. (2007) discuss a possible position within the acicula-bearing errant polychaete taxa (Phyllodocida and Eunicida). Relationships within Orbiniidae are also under discussion. Page 57

7. New insights into polychaete phylogeny, By Christoph Bleidorn

Annelid systematics and the ingroup relationships of polychaete annelids are matter of ongoing **debate** in recent analyses. Page 279

Worms

The phylogenetic relationships of these polychaete taxa are matter of ongoing **debate** in recent papers on annelid morphology (Bartolomaeus, 1998; Hausen, 2001; Hausen and Bartolomaeus, 1998; Meyer and Bartolomaeus, 1996; Purschke, 1997; Rouse and Fauchald, 1997, 1998; Westheide, 1997; Westheide et al., 1999). Page 279

8. Phylogenetic assessment of the earthworm, By Marcos Pérez-Losada

These four taxa are morphologically very similar and difficult to differentiate because of their morphological variability. Consequently, their taxonomic status and their phylogenetic relationships have been a matter of discussion for more than a century. Page 293

9. Evolutionary origins of nematodes, By Neil B. Chilton

The evolutionary relationships of the different suborders and superfamilies within the Strongylida, based on morphological characters, have also been the subject of considerable **debate** (Skrjabin et al., 1952). Page 120

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