

**Chapter 1 : Systematics | ENT – General Entomology**

*This new text sets out to establish the key role played by systematics in deciphering patterns of evolution from the fossil record. It begins by considering the nature of the species in the fossil record and then outlines recent advances in the methodology used to establish phylogenetics.*

Loon - Systematics and Evolution - Fossil Record Fossil Record In prehistoric times, the loons had a more southerly distribution than today, and their fossils have been found in places such as California, Florida and Italy. The conflicting molecular data regarding their relationships is not much resolved by the fossil record; though they seem to have originated at the end of the Late Cretaceous like their presumed relatives, modern loons are only known with certainty since the Eocene. By that time almost all modern bird orders are at least strongly suspected to have existed – if not known from unequivocally identified specimens – anyway. Colymboides, the oldest unequivocal gaviiform genus known as of , is widely known from early Priabonian – about 37 million years ago Ma in the Late Eocene – to Early Miocene late Burdigalian, less than 20 Ma limnic and marine rocks of western Eurasia north of the Alpidic belt, between the Atlantic and the former Turgai Sea. It is usually placed in the Gaviidae already, but usually in a subfamily Colymboidinae, with the modern-type loons making up the Gaviinae. But the Colymboides material is generally quite distinct from modern loons, and may actually belong in a now-extinct family of primitive gaviiforms. Furthermore, the supposed genus could well be paraphyletic, so that for example Dyspetornis – which is now contained therein – might have to be separated again. A leg of an undescribed small diver was found in the Late Oligocene deposits at Enspel Germany ; it too may or may not belong to Colymboides. Of the crown genus Gavia , nearly ten prehistoric species have been named to date, and about as many undescribed ones await further study. The genus is known from the Early Miocene onwards, and the oldest members them are rather small some are smaller than the Red-throated Diver. List of fossil Gavia Gavia sp. Early Pliocene of Empoli, Italy Gavia sp. Early Pleistocene of Kairy, Ukraine Gavia cf. If so, it was from a bird slightly smaller than Common Loon. Older authors were quite sure the bone was indeed from a Gavia and even considered G. This is now regarded as rather unlikely due to the quite distinct range and age. The holotype vertebra may now be lost, which would make "G. In addition, there are some older fossils that are sometimes assigned to the Gaviiformes. From the Late Cretaceous, the genera Lonchodytes Lance Formation, Wyoming and Neogaeornis Quiniquina Formation, Chile have been described; both are usually allied with orders which are considered related to loons. In particular the latter is still sometimes explicitly proposed as a primitive loon as they both were initially, but other authors consider Neogaeornis a hesperornithiform; note however that neither Gaviiformes nor Hesperornithiformes are known from the Southern Hemisphere or anywhere near it. Of similarly doubtful validity and surrounded by considerable dispute is the supposed Late Cretaceous loon Polarornis Seymour Island, Antarctica. A piece of a carpometacarpus supposedly from Oligocene rocks near Lusk, Wyoming was described as Gaviella pusilla, but this handbone also shows some similarities to the plotopterids which were flightless wing-propelled divers and if these are apomorphic would make an unconvincing member of the Gaviidae though it still could be a small-winged gaviiform in an – as of yet undescribed – family "Gaviellidae": Parascaniornis, sometimes allied to the loons by early authors, was eventually determined to be a junior synonym of the hesperornithiform Baptonis. A supposed mid-Eocene diver fossil form Geiseltal Germany was erroneously assigned to Gavia. Read more about this topic: Loon , Systematics and Evolution Other articles related to "fossil record, fossil, fossils": As regards other material evidence, the undisputed fossil record of the hoatzins consists of a single backside of the cranium of a fossil hoatzin, specimen UCMP The fragmentary fossil Onychopteryx from the Eocene of Argentina and the quite complete but no less enigmatic Early-Middle Eocene Ypresian-Lutetian, some 48 million years ago Foro

**Chapter 2 : Bubalina - Wikipedia**

*Systematics and the Fossil Record* has 5 ratings and 0 reviews. This new text sets out to establish the key role played by systematics in deciphering patterns.

This section does not cite any sources. Please help improve this section by adding citations to reliable sources. Unsourced material may be challenged and removed. April See also: List of brood parasitic passerines The order is divided into three suborders, Tyranni suboscines , Passeri oscines , and the basal Acanthisitti [4]. Oscines have the best control of their syrinx muscles among birds, producing a wide range of songs and other vocalizations though some of them, such as the crows , do not sound musical to human beings ; some such as the lyrebird are accomplished imitators. The acanthisittids or New Zealand wrens are tiny birds restricted to New Zealand , at least in modern times; they were long placed in Passeri; their taxonomic position is uncertain, although they seem to be a distinct and very ancient group. Pterylosis or the feather tracts in a typical passerine Most passerines are smaller than typical members of other avian orders. The heaviest and altogether largest passerines are the thick-billed raven and the larger races of common raven , each exceeding 1. The superb lyrebird and some birds-of-paradise , due to very long tails or tail coverts, are longer overall. The smallest passerine is the short-tailed pygmy tyrant , at 6. Anatomy[ edit ] The foot of a passerine has three toes directed forward and one toe directed backward, called anisodactyl arrangement. This arrangement enables the passerine birds to perch upon vertical surfaces, such as trees and cliffs. The toes have no webbing or joining, but in some cotingas , the second and third toes are united at their basal third. The hind toe joins the leg at the same level as the front toes. The passeriformes have this toe arrangement in common with hunting birds like eagles and falcons. The leg arrangement of passerine birds contains a special adaptation for perching. A tendon in the rear of the leg running from the underside of the toes to the muscle behind the tibiotarsus will automatically be pulled and tighten when the leg bends, causing the foot to curl and become stiff when the bird lands on a branch. This enables passerines to sleep while perching without falling off. Some passerines, specifically in the family Ploceidae , are well known for their elaborate sexual ornaments, including extremely long tails. A well-known example is the long-tailed widowbird. Eggs and nests[ edit ] The chicks of passerines are altricial: Hence, the chicks require extensive parental care. Vinous-throated parrotbill has two egg colours, white and blue. This can prevent the brood parasitic Common cuckoo. Clutches vary considerably in size: Origin and evolution[ edit ] The evolutionary history of the passerine families and the relationships among them remained rather mysterious until the late 20th century. In many cases, passerine families were grouped together on the basis of morphological similarities that, it is now believed, are the result of convergent evolution , not a close genetic relationship. For example, the wrens of the Americas and Eurasia ; those of Australia ; and those of New Zealand look superficially similar and behave in similar ways, and yet belong to three far-flung branches of the passerine family tree; they are as unrelated as it is possible to be while remaining Passeriformes. The latter experienced a great radiation of forms out of the Australian continent. A major branch of the Passeri, parvorder Passerida , expanded deep into Eurasia and Africa, where a further explosive radiation of new lineages occurred. Extensive biogeographical mixing happens, with northern forms returning to the south, southern forms moving north, and so on. Earliest passerines[ edit ] Male superb lyrebird *Menura novaehollandiae*: This very primitive songbird shows strong sexual dimorphism , with a peculiarly apomorphic display of plumage in males. Perching bird osteology , especially of the limb bones, is rather diagnostic. Queensland Museum specimens F carpometacarpus and F tibiotarsus from Murgon, Queensland , are fossil bone fragments initially assigned to Passeriformes. From the Bathans Formation at the Manuherikia River in Otago , New Zealand, MNZ S a distal right tarsometatarsus of a tui -sized bird and several bones of at least one species of saddleback -sized bird have recently been described. The latter trait seems to have been lost and re-evolved multiple times in songbird evolution alone, judging from its distribution among the extant lineages. Sexual dichromatism is very rare among the basal lineages of Passerida, and probably their plesiomorphic condition. But among the youngest passerid clade, the Passeroidea , extremely colorful males and drab females are common, if not the rule. On the other hand,

among the basalmost Passeri a considerable number of strongly dimorphic lineages exist, too, such as the very ancient Menuridae, as well as many Meliphagoidea and Corvoidea. Sexual dimorphism is also not uncommon in the Acanthisittidae and prominent in some suboscines such as the Pipridae and Cotingidae. Early European passerines [edit] Wieslochia fossil In Europe, perching birds are not too uncommon in the fossil record from the Oligocene onward, but most are too fragmentary for a more definite placement: Early Oligocene of Luberon, France " suboscine or basal [17] Passeriformes gen. Late Oligocene of France " several suboscine and oscine taxa [18] Passeriformes gen. Middle Miocene of France and Germany " basal? Late Quaternary prehistoric birds In the Americas, the fossil record is more scant before the Pleistocene, from which several still-existing suboscine families are documented. Systematics and taxonomy [edit] Corvida and Passerida were classified as parvorders in the suborder Passeri; in accord with the usual taxonomic practice, they would probably be ranked as infraorders. As originally envisioned in the Sibley-Ahlquist taxonomy, they contained, respectively, the large superfamilies Corvoidea and Meliphagoidea, as well as minor lineages, and the superfamilies Sylvioidea, Muscicapoidea, and Passeroidea. The arrangement has been found to be oversimplified by more recent research. Since the mid-1990s, literally, dozens of studies are being published that try rather successfully to resolve the phylogeny of the passeriform radiation. The Passeri, though, can be made monophyletic by moving some families about, but the "clean" three-superfamily-arrangement has turned out to be far more complex and it is uncertain whether future authors will stick to it. Major "wastebin" families such as the Old World warblers and Old World babblers have turned out to be paraphyletic and are being rearranged. Several taxa turned out to represent highly distinct species-poor lineages, so new families had to be established, some of them " like the stitchbird of New Zealand and the Eurasian bearded reedling " monotypic with only one living species. For example, the kinglets constitute a single genus with less than 10 species today but seem to have been among the first perching bird lineages to diverge as the group spread across Eurasia. No particularly close relatives of them have been found among comprehensive studies of the living Passeri, though they might be fairly close to some little-studied tropical Asian groups. Treatment of the nuthatches, wrens, and their closest relatives as a distinct super-family Certhioidea is increasingly considered justified; the same might eventually apply to the tits and their closest relatives. This process is still continuing. Therefore, the arrangement as presented here is subject to change. However, it should take precedence over unreferenced conflicting treatments in family, genus, and species articles here. The Passerida subdivisions are updated as needed from the default sequence of the Handbook of the Birds of the World, [26] based on the most modern and comprehensive studies. Corvidae are placed last. This is because so many reallocations have taken place since about that a definite taxonomy has not been established yet, although the phylogeny is by and large resolved. The present sequence is an attempt to preserve as much of the traditional sequence while giving priority to adequately addressing the phylogenetic relationships between the families.

*Since the fossil record abounds with sampling and preservational biases it is emphasised that observed patterns can rarely be taken at face value. It is argued that evolutionary trees, constructed from combining phylogenetic and biostratigraphic data, provide the best approach for investigating patterns of evolution through geologic time.*

Ancestral state reconstruction of body size in the Caniformia Carnivora, Mammalia: The effects of incorporating data from the fossil record. Flynn , " To more rigorously reconstruct body sizes of ancestral forms within the Caniformia, body size and first appearance data were collected for extant and extinct taxa. Body sizes were reconstructed for four ancestral nodes using weighted squared-change parsimony on log-transformed body mass data. Reconstructions based on extant taxa alone favored large body sizes on the order of 10 to 50 kg for the last common ancestors of both the Caniformia and Arctoidea. When the temporal information associated with fossil data was discarded, body size reconstructions became ambiguous, demonstrating that incorporating both character state and temporal information from fossil taxa unambiguously supports a small ancestral body size, thereby falsifying hypotheses derived from extant taxa alone. Body size reconstructions for Caniformia, Arctoidea, and Musteloidea were not sensitive to potential errors introduced by uncertainty in the position of extinct lineages relative to the molecular topology, or to missing body size data for extinct members of an entire major clade the aquatic Pinnipedia. Incorporating character state observations and temporal information from the fossil record Show Context Citation Context

However, extant taxa represent only a subset of the total evolutionary diversity of any clade, and, therefore, any conclusion based Global climate change and the origin of modern benthic communities in Antarctica by Richard B. Blake - American Zoologist " Marine benthic communities living in shallow-water habitats , m depth in Antarctica possess characteristics reminiscent of Paleozoic marine communities and modern deep-sea communities. The absence of crabs and sharks, the limited diversity of teleosts and skates, the dominance of slow-moving invertebrates at higher trophic levels, and the occurrence of dense ophiuroid and crinoid populations indicate that skeleton-breaking predation is limited in Antarctica today, as it was worldwide during the Paleozoic and as it is in the deep sea today. The community structure of the antarctic benthos has its evolutionary roots in the Eocene. Data from fossil assemblages at Seymour Island, Antarctic Peninsula suggest that shallow-water communities were similar to communities at lower latitudes until they were affected by global cooling, which accelerated in the late Eocene to early Oligocene. That long-term cooling trend ultimately resulted in the polar climate and peculiar community structure found in Antarctica today. Declining temperatures beginning late in the Eocene are associated with the disappearance of crabs, sharks, and most teleosts. The sudden drop in predation pressure allowed dense ophiuroid and crinoid populations to appear and flourish. These late Eocene echinoderm populations exhibit low frequencies of sublethal damage regenerating arms , demonstrating that there was little or no predation from skeleton-breaking fish and decapods. Current scenarios of global climate change include predictions of increased upwelling and consequent cooling in temperate and subtropical upwelling zones. Limited ecological evidence suggests that such cooling could disrupt trophic relationships and favor retrograde community structures in those local areas. Opisthosomal fusion and phylogeny of Palaeozoic Xiphosura by Lyall I. Fusion of opisthosomal tergites to form a thoracetrone has previously been considered a characteristic of the xiphosuran superfamilies Euprooidea Eller , and Limuloidea Zittel, Results of a cladistic analysis of Palaeozoic xiphosuran genera indicate that Synziphosura - Unraveling the evolutionary radiation of the thoracican barnacles using molecular and morphological evidence: Crandall , " However, although the literature abounds with scenarios explaining the evolution of these barnacles, very few studies have attempted to test these hypotheses in a phylogenetic context. The few attempts at phylogenetic analyses have suffered from a lack of phylogenetic signal and small numbers of taxa. We collected DNA sequences from the nuclear 18S, 28S, and histone H3 genes and the mitochondrial 12S and 16S genes 4, bp

total and data for 37 adult and 53 larval morphological characters from 43 taxa representing all the extant thoracican suborders except the monospecific Brachylepadomorpha. The resulting phylogenetic trees answered key questions in barnacle evolution. The four-plated Iblomorpha were shown as the most primitive thoracican, and the plateless Heteralepadomorpha were placed as the sister group of the Lepadomorpha. These relationships suggest for the first time in an invertebrate that exoskeleton biomineralization may have evolved from phosphatic to calcitic. Sessilia Show Context Citation Context Hence, it seems more appropriate to constraint nodes to lie within some interval rather than fix them to a particular time Norell, The importance of even highly incomplete fossil taxa in reconstructing the phylogenetic relationships of the Tetraodontiformes Acanthomorpha by Francesco Santini, James C. The use of fossils in the phylogenetics of extant clades traditionally has been a contentious issue. Fossils usually are relatively incomplete, and their use commonly leads to an increase in the number of equally most parsimonious trees and a decrease in the resolution of phylogenies. Fossils alone, however, provide certain kinds of information about the biological history of a clade, and computer simulations have shown that even highly incomplete material can, under certain circumstances, increase the accuracy of a phylogeny, rather than decrease it. Because empirical data are still scarce on the effects of the inclusion of fossils on phylogenetic reconstructions, we attempted to investigate this problem by using a relatively well-known group of acanthomorph fishes, the Tetraodontiformes triggerfishes, pufferfishes, and ocean sunfishes, for which robust phylogenies using extant taxa already exist and that has a well-studied fossil record. Adding incomplete fossil taxa of tetraodontiforms usually increases the number of equally most parsimonious trees and often decreases the resolution of consensus trees. However, adding fossil taxa may help to correctly establish relationships among lineages that have experienced high degrees of morphological diversification by allowing for a reinterpretation of homologous and homoplastic features, increasing the resolution rather than decreasing it. Show Context Citation Context Most of the criticism connected with the inclusion of fossil taxa in phylogenetic inference is because fossils are to We use stratocladistics here to provide an overview of the phylogeny of the extinct echinoderm class Blastoidea. Both cladistic and stratocladistic methods evaluate al Both cladistic and stratocladistic methods evaluate alternative phylogenies by comparing the number of ad hoc hypotheses needed to reconcile each alternative to observed data. Minimization of ad hoc hypotheses selects the phylogeny best supported by data and enables phylogenetic analyses to incorporate data from different sources. Cladistics treats ad hoc hypotheses of homoplasy, whereas stratocladistics additionally considers ad hoc hypotheses of differential preservation probability of lineages in the stratigraphic record. The blastoid phylogeny derived using stratocladistics is more resolved than hypotheses selected by cladistics. Although the morphological characters are relatively homoplasious, in this instance the stratigraphic ordering of fossils provides both structure and altered polarity for the stratocladistic hypothesis. The stratocladistic phylogeny supports previous paleontological conclusions of convergence among blastoid lineages and facilitates evaluation of specific hypotheses of character transformation that are integral to recent systematic revisions. Additionally, consideration of temporal data makes some hypotheses of ancestor-descendant relationships more parsimonious than hypotheses of derivation from a common ancestor. The ability to recognize sequential members within single lineages allows more accurate estimation of faunal diversities and more specific reconstruction of evolutionary histories. Chief among possible confounding factors in stratocladistics are instances where preservation potential shows significant geographic variation, although problems of preservation are more tractable than the difficulties homoplasy presents for cladistic analysis. Scale and hierarchy must be incorporated into any conceptual framework for the study of macroevolution, i. Expansion of temporal and spatial scales reveals evolutionary patterns and processes that are virtually inaccessible to, and unpredictable from, s Expansion of temporal and spatial scales reveals evolutionary patterns and processes that are virtually inaccessible to, and unpredictable from, short-term, localized observations. These larger-scale phenomena range from evolutionary stasis at the species level and the mosaic assembly of complex morphologies in ancestral forms to the non-random distribution in time and space of the origin of major evolutionary novelties, as exemplified by the Cambrian explosion and post-extinction recoveries of metazoans, and the preferential origin of major marine groups in onshore environments and tropical waters.

Virtually all of these phenomena probably involve both ecological and developmental factors, but the integration of these com- The PhyloCode: Beating a dead horse? The concept of the PhyloCode has been evolving for some twenty years, and is supported by Lee and Skinner I argue against it here. PhyloCode names for taxa are by definition stable because they are established as labels for clades that are rigidly defined as geometric constructs. Phylogenetic relationships among all of the major decapod infraorders have never been estimated using molecular data, while morphological studies produce conflicting results. In the present study, the phylogenetic relationships among the decapod basal sub-order Dendrobranchiata and all of the current In the present study, the phylogenetic relationships among the decapod basal sub-order Dendrobranchiata and all of the currently recognized decapod infraorders within the suborder Pleocyemata Caridea, Stenopodidea, Achelata, Astacidea, Thalassinidea, Anomala, and Brachyura were inferred using 16S mtDNA, 18S and 28S rRNA, and the histone H3 gene. Phylogenies were reconstructed using the model-based methods of maximum likelihood and Bayesian methods coupled with Markov Chain Monte Carlo inference. The two suborders also were recovered as monophyletic, but with weaker support bp D 70; pP D 0. Newly developed multi-locus Bayesian and likelihood heuristic rate-smoothing methods to estimate divergence times were compared using eight fossil and geological calibrations. Estimated times revealed that the Decapoda originated earlier than MYA and that the radiation within the group occurred rapidly, with all of the major lineages present by MYA. Node time estimation under both approaches is severely affected by the number and phylogenetic distribution of the fossil calibrations chosen. For analyses incorporating fossils as fixed ages, more consistent results were Show Context Citation Context

**Chapter 4 : Evolution and Systematics, p. 4**

*This new text sets out to establish the key role played by systematics in deciphering patterns of evolution from the fossil record. It begins by considering the nature of the species in the fossil record and then outlines recent advances in the field.*

**Introduction to Systematics** By human standards, million years is a long, long time. Our human species is less than 2 million years old, birds and mammals have existed for no more than million years, dinosaurs first appeared million years ago, and the most primitive land plants arose about million years ago. But in order to observe the first arthropods, phylum Arthropoda we would have to travel back even further in time to a point nearly million years ago the Cambrian period of the Paleozoic era when bacteria and marine algae were the dominant forms of plant life, small invertebrate animals were abundant in warm, shallow seas, and land masses were still largely devoid of life. It seems incredible that we can even think of studying events that happened so long ago. But biologists and paleontologists have a wide array of tools and techniques that allow them to probe the world of today for clues that illuminate events of our distant past. Although most of our hypotheses about evolutionary beginnings are tentative and controversial, they provide a valuable framework in which to study similarities, differences, and relationships among all surviving taxa. Our understanding of each phylogenetic group is enhanced by learning how it has been shaped by the selective pressures of the past, and how it differs from its nearest relatives of the present.

**Tools and Techniques** The science of paleontology the study of prehistoric forms of life and the principles of systematics classification of organisms based on structural or evolutionary relationships are the traditional foundations of phylogenetic research. Both endeavors are based on two important assumptions: All forms of life share a similar DNA-based system of inheritance, and The process of natural selection has remained virtually unchanged throughout evolutionary time.

**Fossil Record** The fossil record is the pre-eminent database for phylogenetic research. Prehistoric arthropods were generally small and delicate. They did not preserve as well as larger animals with teeth, bones, or shells, but are more abundant as fossils than other soft-bodied invertebrates because their rigid exoskeleton maintained its shape and did not decay rapidly after death. Fossil arthropods can be found in sedimentary rock strata and in deposits of coal, shale, or volcanic ash throughout the world. Good fossil beds containing arthropods are relatively scarce, so the fossil record tends to be patchy. Many species are known to science by only a single specimen, while others are recognizable as species that still live today. Fossil insects can also be found in amber, the petrified resin sap of prehistoric trees. Once entangled in the sticky resin, captive insects were preserved in every detail as the viscous sap gradually hardened to glass-like consistency. Amber deposits, containing embedded insects from the early Cretaceous period through recent times, can be found in northern Europe around the shores of the Baltic Sea, in Asia etc. Until recently, scientists were forced to rely almost exclusively upon their own interpretations of the fossil record to reconstruct phylogenetic relationships. Many structural similarities between organisms are regarded as evidence of homology kinship, while many dissimilarities signify unrelatedness. Problems often arise because of differences in interpretation, absence of intermediate forms, loss of specialized adaptations reversion to more primitive conditions, and development of similar characteristics in unrelated groups convergent evolution. Classical taxonomists have always been constrained by the overwhelming volume of data and the subjectivity of the process. Within the past thirty years, however, exciting developments in chemistry, physics, and computer science have given evolutionary biologists a number of powerful new tools that furnish more precise and objective information about fossils and their relationship to extant life-forms.

**Radiometric dating** The approximate age of a fossil is vital information in assessing where it might fit into the family tree of its relatives. Fossils traditionally have been dated by the rock strata in which they occur. Relatively accurate ages of these strata can be inferred by measuring the concentration of a radioactive isotope such as carbon or by determining the ratio between a radioactive element uranium, thorium, or potassium and its spontaneous decay product. Plants and animals assimilate carbon from the atmosphere only while they are alive, so it is possible to determine approximate age of a fossil by measuring how much carbon has not yet decayed to nitrogen Carbon dating is reliable only

on specimens young enough to retain measurable amounts of carbon less than 50,000 years old. Older strata of rock that bear trace amounts of radioactivity may be dated by measuring the ratio between an unstable isotope such as uranium, thorium, or potassium and its stable decay product lead, lead, or argon respectively. The very long half-life of these isotopes from million to 14 billion years, makes them potentially useful for dating samples that range in age from , years to well before the beginning of prehistoric life. Numerical Taxonomy Digital computer technology provides a new and highly objective approach to evaluating similarities and differences among taxa. Statistical techniques, such as principal components analysis, cluster analysis, factor analysis, multidimensional scaling, and discriminant analysis can be applied methodically to large data sets containing morphological, behavioral, or biochemical information about taxonomic groups of interest. These statistical methods allow taxonomists to quantify the degree of overall similarity among groups of organisms. They may or may not depict true evolutionary relationships. Biochemistry Enzymes and metabolic pathways can reveal inherent patterns in nutrient processing, chemical defense, locomotion, intercellular and intracellular communication, or homeostatic mechanisms. The sudden appearance of a novel biochemical mutation may confer selective advantages and eventually lead to adaptive radiation of new species from a common ancestor. By assuming that mutation rates have been relatively constant throughout geological history, it is possible to estimate how long it has been since any two groups diverged from a common ancestor. Recently, biologists have even extracted and sequenced DNA from fossils. This amazing feat was accomplished by isolating fragments of DNA from insects termites and stingless bees preserved in amber. If these techniques prove applicable to a broad range of preserved specimens, they will allow us to study the genetic makeup of extinct organisms, and revolutionize our ability to explore relationships among the arthropods of today and their long-extinct ancestors.

**Chapter 5 : Passerine - Wikipedia**

*This new text sets out to establish the key role played by systematics in deciphering patterns of evolution from the fossil record. It begins by considering the nature of the species in the fossil record and then outlines recent advances in the methodology used to establish phylogenetic relationships, stressing why fossil evidence can be crucial.*

This is page 4 of a five-page document. Every new fossil discovered further supports this claim. Working through the dinosaur example above, I hope I have convinced you that systematics, as a method for inferring evolutionary relationships, can be applied to both living and fossil organisms. Does fossil data require any special consideration in systematic investigations? The evidence of evolution from the fossil record particularly relevant to systematics comes in three forms: Shape Perhaps the most valuable contribution that the fossil record provides is a tangible record of extinct fossil morphologies or character combinations that no longer coexist in organisms today. These unique character combinations are invaluable in piecing together relationships among living organisms that look quite different from one another birds and crocodiles, for example. However, fossil data comes almost exclusively in the form of morphology, usually skeletal morphology, which we must assume bears some interpretable relationship to the underlying genome, since the genome in fossils cannot be sampled directly. Aspects of morphology that are not mineralized are less likely to be preserved as fossils, although some soft tissues muscles, for example can leave an interpretable scar or mark on skeletal fossil material. Developmental or physiological processes of extinct organisms cannot be observed directly or experimented with. In this sense, fossils provide us with a much-reduced suite of characters for systematic analysis than do living organisms. Space Because of plate tectonics, the geography of the world today is different than it was in the past, and has changed continually over geologic time. Thus, we might find fossil organisms from different continents, or from sediments indicating different paleoclimatic conditions than where closely related living organisms are found today. Fossils can provide the only tangible record of ancient biogeographic ranges and can fill in important paleogeographic gaps between disjunct modern occurrences of closely related species. Paleobiogeographic data from fossils can thus be used to test hypotheses of phylogenetic relationship, and patterns of dispersal, among living taxa. Time The fossil record provides an ordered temporal record of the relative appearance of unique character combinations over millions of years of geologic time. What the fossil record lacks in direct evidence of development, genetics, physiology, behavior, and ecology, it provides in abundant sequential data on skeletal morphology that cannot be obtained from any other source. Characters hypothesized to exist in a common ancestor on the basis of their distribution among living taxa can be tested by their discovery at any of a number of stratigraphic levels, ordered in time. A relative temporal pattern implied by the internesting of clades one within another Figure 4 can be tested by its correspondence to the relative appearance of fossils, and the characters they possess, in a stratigraphic sequence Fisher, ; Huelsenbeck, ; Benton, ; Wagner, Hypotheses of character homology may also be tested for example, the evolution of the bones of the inner ear in amniotes. Some argue that character polarity can be read directly from the relative appearance of characters in the fossil record; character states that appear earlier are primitive, those that appear later are derived. Arguments about the incompleteness of the fossil record and nature of sampling from the fossil record are relevant to this issue, but are discussed in more detail in other chapters of this book and will not be revisited here. Examining the distribution of character states among living organisms in Species Y and extinct organisms in Fossil Species X, one could hypothesize a direct ancestor-descendant evolutionary relationship, diagrammed as an evolutionary tree Figure 9. The assumption that all or most ancestors of living taxa are preserved as actual fossils see Foote, is a difficult assumption for many phylogenetic systematists to accept. Why is this so? In addition to the completeness issues raised above, the following argument is relevant. If Fossil Species X is distinct enough in morphology to be given its own species name which is most often the case, then this indicates that some evolutionary change has occurred between X and its true ancestor, which is really the common ancestor of both X and Living Species Y Figure 9. Here, X is hypothesized to share common ancestry with Y, but is not necessarily considered to be the true ancestor of Y for the sole reason that it occurs earlier in time. The pattern of common

ancestry diagrammed in Figure 9. The fossil record can be viewed as a source of morphological characters that can better reveal patterns of common ancestry, and not only as a source of true ancestors. Classification refers to the ways that we organize organisms. Human beings name organisms and most other objects in the world. Names identify individuals uniquely; for example, Lou Gehrig was a particular baseball player. In the binomial system a name refers to both the particular individual and his or her family ancestry; Lou was a member of the Gehrig family. In some cultures, each person has a single unique name, like Confucius or Sacajawea. Just as we refer to each other by a given name and a surname, the international scientific community refers to organisms by a species name and a genus name, listing the genus name first. Consider the familiar dinosaur, *Triceratops horridus*. *Triceratops* is the genus name that means "having three horns"; *horridus* is the species name that means "projecting" or "standing on end" rather than horrid, as you might expect! By convention, genus and species names are always italicized or underlined. Scientific names often, but not always, refer to some feature or special characteristic of the organism that may help us remember what a given species looks like, and how it differs from other species. We need to agree on a set of rules for naming groups of species and groups of groups of species, to make it easier for us to talk about them. Classification refers to a system of organizing and naming living or once living things. What rules should we use for classifying organisms? For this reason, it is most informative to name groups of species on the basis of their phylogeny. Recall that phylogenies are hierarchical and clades are interested in Figure 4. Naming successively more inclusive clades, or groups of species that share common ancestry, reflects the process of descent with modification. Not all classifications are organized according to patterns of phylogenetic relationships, however. In fact, the system of classification that biologists and paleontologists use today was established before evolution was recognized as the process structuring patterns of phylogeny. See Hedegaard, this volume. Because evolutionary principles do not structure the Linnean system of classification, some, but not all named higher taxa are true clades. This can present a problem when higher taxa are treated uncritically as if they were clades. Phylogenetic systematists are working to identify the phylogenetic status of taxa named under the Linnean system. The grouping of genera into families, families into orders, and so on, are being revised to better reflect patterns of evolution. Some systematists have proposed a complete overhaul of the classification system itself so the principles governing the grouping of species into higher taxa are based fundamentally on evolution. de Queiroz and Gauthier, Perhaps by the next millennium, the ways in which systematists classify organisms will be based on truly evolutionary criteria.

### Chapter 6 : CiteSeerX – Citation Query Systematics and the fossil record

*Fossil Record. Lamprey fossils are rare because cartilage does not fossilize as readily as bone. The first fossil lampreys were originally found in Early Carboniferous limestones, marine sediments laid down more than million years ago in North America: *Mayomyzon pieckoensis* and *Hardistiella montanensis*, from the Mississippian Mazon Creek Lagerstätte and the Bear Gulch Limestone sequence.*

### Chapter 7 : Loon - Systematics and Evolution - Fossil Record | Technology Trends

*Systematics and the Fossil Record by Andrew B. Smith (author) and a great selection of similar Used, New and Collectible Books available now at [calendrierdelascience.com](http://calendrierdelascience.com)*

### Chapter 8 : In systematics and phylogeny, the fossil record is especially important because? | Yahoo Answers

*Mesozoic Fishes 2: Systematics and Fossil Record [Gloria ARRATIA, Hans-Peter SCHULTZE] on [calendrierdelascience.com](http://calendrierdelascience.com) \*FREE\* shipping on qualifying offers. The Mesozoic era was an important time in the evolution of chondrichthyan and actinopterygian fishes because it was then that most of the modern groups first entered the fossil record and began to radiate.*

Chapter 9 : Systematics and the Fossil Record: Documenting Evolutionary Patterns by Andrew B. Smith

*Tracking the Course of Evolution EVOLUTION AND SYSTEMATICS (cont.) by Sandra J. Carlson NOTE: This is page 4 of a five-page document. SYSTEMATICS AND THE FOSSIL RECORD Life on Earth in the past was different in many ways from life on Earth today.*