PAPER I, PART 1

Taxonomy and Diversity of Life Forms (Units 1-2)

RPSC AP Zoology Paper 1 Notes · English Medium

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For the RPSC Assistant Professor (Zoology) examination, Paper I, and allied UGC-CSIR NET / Assistant Professor examinations

Contents

Chapter 1 Principles of Systematics and the Animal Body Plan 5
1.1 History and scope of animal systematics 5
1.2 Zoological nomenclature and the ICZN 5
1.3 Species, categories and the hierarchy 7
1.4 Schools of classification and tree reasoning 7
1.5 Molecular systematics 10
1.6 Animal body plans 11
1.7 The animal tree of life 13
1.8 Origin of Metazoa: Ediacaran to Cambrian 14
1.9 Animal diversity numbers and Indian taxonomic resources 15
Chapter 2 Porifera to Annelida: The Lower Invertebrates 17
2.1 Grades of organisation and the phyla covered 17
2.2 Phylum Porifera 17
2.3 Phylum Cnidaria 20
2.4 Phylum Ctenophora 23
2.5 Phylum Platyhelminthes 23
2.6 Phylum Nematoda 25
2.7 Minor pseudocoelomate phyla 27
2.8 Phylum Nemertea 28
2.9 Phylum Annelida 28
2.10 Comparative review: Porifera to Annelida</w:t><w:tab/><w:t>31
Chapter 3 Mollusca and Arthropoda 33
3.1 Phylum Mollusca 33
3.2 Class Gastropoda 34
3.3 Class Bivalvia (Pelecypoda, Lamellibranchia) 36
3.4 Class Cephalopoda 37
3.5 Pearl formation and Indian molluscan fisheries 38
3.6 Phylum Arthropoda 39
3.7 Subphylum Chelicerata 43
3.8 Subphylum Mandibulata 44
3.9 Comparison of the arthropod classes 46
Chapter 4 Echinodermata, Hemichordata and Comparative Invertebrate Biology 47
4.1 Phylum Echinodermata 47
4.2 Phylum Hemichordata 50
4.3 Phylum Chaetognatha 51
4.4 Lophophorate phyla 52
4.5 Comparative physiology of invertebrate phyla 52
4.6 Development patterns and larvae 54
4.7 Ecosystem services and economic importance of invertebrates 56
4.8 Invertebrate diversity in India 57
Chapter 5 Minor Phyla, Origins of Animals, Physical Biology and Model Invertebrates 58
5.1 The small phyla and enigmatic animal groups 58

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5.2 Life without oxygen and without water 59
5.3 Theories of the origin of Metazoa and Bilateria 60
5.4 Coral reefs: origin, calcification and heat stress</w:t><w:tab/><w:t>62
5.5 Physical biology of small animals 63
5.6 Hydrostatic skeletons and the geometry of body fibres 65
5.7 Invertebrate model organisms and classic experiments 66
5.8 Data interpretation and worked problems 67
Chapter 3 Protozoa, Arthropod Vectors and Major Parasitic Diseases 68
3.1 Protozoa: Biology and Classification</w:t><w:tab/><w:t>68
3.2 Intestinal, Urogenital and Free-living Protozoa 70
3.3 Kinetoplastid Parasites: Trypanosoma and Leishmania</w:t><w:tab/><w:t>71
3.4 Malaria 73
3.5 Arthropod Vectors 77
3.6 Transmission Dynamics: Vectorial Capacity and R0</w:t><w:tab/><w:t>78
3.7 Lymphatic Filariasis and Kala-azar Programmes in India 79
3.8 Vector Control, Surveillance and Diagnosis 79
Chapter 31 Classification up to Order: Survey of the Animal Phyla with Indian Examples 81
31.1 Ranks, grades and the key to the phyla 81
31.2 Nomenclature: worked problems beyond the basics</w:t><w:tab/><w:t>83
31.3 Protozoa, Porifera and Cnidaria to order 85
31.4 Flatworms, roundworms and annelids to order 87
31.5 Mollusca and Arthropoda to order 88
31.6 Echinodermata, Hemichordata and Chordata to order 90
31.7 The characters that define each rank 92
31.8 Inter-relationships of the phyla 93
31.9 Putting the survey to work 96
Chapter 32 Invertebrate Type Studies: Structure, Physiology, Reproduction and Economic Importance 98
32.1 Levels of organisation and the type-animal grid 98
32.2 Protozoan types 99
32.3 Sponge and cnidarian types 102
32.4 Helminth types: Fasciola, Taenia and Ascaris 104
32.5 Annelid types: Nereis, Pheretima and Hirudinaria 106
32.6 Molluscan types: Pila and Unio 107
32.7 Arthropod types: Palaemon and Periplaneta 108
32.8 Echinoderm type: Asterias (starfish) 108
32.9 Reproduction across the types 109
32.10 Economic importance: the ledger</w:t><w:tab/><w:t>111
32.11 Interpretation items 112
Chapter 14 Invertebrate Physiology, Larvae and Minor Phyla 113
14.1 Flagellar and ciliary movement 113
14.2 Locomotion in Protozoa, Coelenterata, Annelida and Echinodermata 115
14.3 Feeding and digestion patterns 116
14.4 Respiratory organs and pigments 118
14.5 Excretion and osmoregulation in lower and higher invertebrates 120
14.6 Nervous systems from primitive to advanced 122
14.7 Larval forms and their significance 123
14.8 Rotifera, Entoprocta, Phoronida and Ectoprocta 125
14.9 Coelom types and body-cavity organisation 127
14.10 Diagram-based problems and exam relevance 128
Chapter 22 Taxonomy in Practice, Indian Natural History and Ecology Problem Sets 129

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22.1 Taxonomy as a working procedure....129
22.2 Indian natural history....133
22.3 Seasonality and migration in the Indian region....137
22.4 Ecology problem sets with solutions....138
22.5 Indian ecosystems compared....142
22.6 Exam map for the thin parts of Units 8 and 9....143

Chapter 1 Principles of Systematics and the Animal Body Plan

Source: Zoology Master Notes, Unit 4, Chapter 1

1.1 History and scope of animal systematics

Systematics is the scientific study of the kinds and diversity of organisms and of all relationships among them (Simpson, 1961). **Taxonomy** is the theory and practice of describing, naming and classifying them; **nomenclature** is the naming part; **identification** assigns a specimen to an already described taxon. Turrill (1938) split taxonomic work into stages: **alpha** (descriptive, species-level), **beta** (arranging species in a natural system) and **gamma** (evolutionary and biological studies of populations). A **taxon** (pl. taxa) is a named group of organisms of any rank; a **category** (rank) is the level in the hierarchy.

1.1.1 From Aristotle to Linnaeus

Aristotle (384–322 BCE, Historia Animalium) grouped animals by structure and mode of reproduction, separating enaima (animals with red blood, roughly vertebrates) from anaima (without). The words "vertebrate" and "invertebrate" are not his; **Lamarck** (1801) established "animals without vertebrae" as a formal assemblage and recognised classes such as Mollusca, Crustacea and Arachnida. **John Ray** (1686–1704) gave an early working definition of the species as a lineage that breeds true.

Carl Linnaeus (1707–1778) fixed the method. Systema Naturae first appeared in 1735, but **the 10th edition (1758)** is the starting point of zoological nomenclature because it applied binomials consistently to animals (his plant equivalent is Species Plantarum, 1753). In 1758 the animal kingdom was divided into six classes: Mammalia, Aves, Amphibia, Pisces, Insecta and Vermes. Linnaeus's ranks were class, order, genus and species (plus variety); family and phylum were added later. His scheme was essentialist, based on a few easily seen characters, and non-evolutionary.

Cuvier (1812) used comparative anatomy and the "correlation of parts" to establish four embranchements: Vertebrata, Mollusca, Articulata and Radiata. (Von Baer, 1828, reached four types from embryology.) **Darwin** (1859) reinterpreted the hierarchy as the pattern of descent; **Haeckel** (1866) drew the first detailed phylogenetic trees, coined phylogeny, proposed the kingdom Protista and proposed that animals arose from a hollow-gut ancestor, the Gastraea (1874). **Hyman's** six-volume The Invertebrates (1940–1967) became the standard phylum-level synthesis; **Hennig** (1950, English edition 1966) founded phylogenetic systematics; **Sokal and Sneath** (1963) founded numerical taxonomy; and **Woese, Kandler and Wheelis** (1990) proposed the three domains (Bacteria, Archaea, Eukarya).

> **EXAMINER TRAP:** The domain level is **not** Linnaean; it was introduced in 1990. Linnaeus's top level was the kingdom (Animale, Vegetabile, Lapideum). The five-kingdom system is Whittaker (1969); the two-kingdom Plantae–Animalia system is older, and Haeckel (1866) added Protista.

1.2 Zoological nomenclature and the ICZN

Animal names are governed by the **International Code of Zoological Nomenclature (ICZN)**, administered by the **International Commission on Zoological Nomenclature** (founded 1895). The current **4th edition** was published in 1999 and has been in force since **1 January 2000**; it has since been amended (notably the 2012 amendment accepting electronic-only publication). The Code regulates names up to the family group; names above superfamily are not regulated, so Phylum names (e.g. Mollusca) are conventions. Other Codes cover plants, algae and fungi (ICN), prokaryotes (ICNP) and viruses (ICVCN); the same name may therefore legitimately exist in two kingdoms (a homonym between Codes is not invalid).

1.2.1 Principles

The Code rests on six working principles, each with a key article.

Principles of the ICZN and the commonly examined articles

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Principle (Article)	Content	Example
Binominal nomenclature (Art. 5)	A species name is a binomen: genus + specific name; subspecies trinomen	Panthera tigris tigris
Priority (Art. 23)	The oldest available name is the valid name; starting date 1 January 1758 (Art. 3)	Apatosaurus Marsh 1877 takes priority over Brontosaurus Marsh 1879 when both are treated as one genus
Homonymy (Art. 52)	Two taxa may not carry the same name; the junior homonym is rejected and replaced (a nomen novum, Art. 60)	Platypus Shaw 1799 preoccupied by a beetle (Herbst 1793); replaced by Ornithorhynchus Blumenbach 1800
Typification (Art. 61)	Every nominal taxon in the family, genus and species groups has a name-bearing type	Type specimen, type species, type genus
Coordination (Arts 36, 43, 46)	A name at one rank in a group is deemed established at all ranks of that group on the same date	Family Felidae = subfamily Felinae = superfamily Feloidea
First reviser (Art. 24)	Where names or spellings have equal status, the first author who chooses between them fixes precedence	Choice between simultaneously published synonyms

Reversal of precedence (Art. 23.9) protects stability: a senior synonym not used as valid after 1899 is set aside (nomen oblitum) if the junior name has been used in at least 25 works by at least 10 authors in the preceding 50 years, spanning at least 10 years (the junior is then a nomen protectum).

1.2.2 Availability and form of names

A name is **available** only if published after 1757 in a work meeting the Code's conditions: consistently binominal (Art. 11.4), Latin-alphabet, and, for names after 1930, accompanied by a description or definition, or a bibliographic reference to one (Art. 13). For new species-group names after 1999, the work must explicitly indicate the name is new and **fix a holotype or syntypes** (Art. 16). Since 2012 an electronic work must carry an ISSN/ISBN and be registered in **ZooBank** before publication. A name published without these is a nomen nudum and is unavailable. A **nomen dubium** is an available name of doubtful application, and a nomen novum is a replacement name.

The genus name is capitalised, the specific name is lower case, and both are italicised (underlined in manuscript). An author and year follow the name; the author's name is placed in **parentheses if the species was described in a different genus** from the one in which it now stands (Art. 51.3): the tiger is Panthera tigris (Linnaeus, 1758) because Linnaeus called it Felis tigris. Family-group names are formed from the stem of the type genus with fixed suffixes:

Ranks of the Linnaean hierarchy with zoological suffixes and two worked examples

Rank	ICZN suffix	Tiger	Eastern honey bee
Phylum	none (not regulated)	Chordata	Arthropoda
Class	none	Mammalia	Insecta
Order	none	Carnivora	Hymenoptera
Superfamily	-oidea	Feloidea	Apoidea
Family	-idae	Felidae	Apidae
Subfamily	-inae	Pantherinae	Apinae
Genus	–	Panthera	Apis
Species	–	Panthera tigris (Linnaeus, 1758)	Apis cerana Fabricius, 1793

1.2.3 Types

Name-bearing types fix the application of a name. In the species group they are the **holotype** (single specimen designated in the

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original description), **syntypes** (a series, when no holotype was designated), the **lectotype** (a syntype later chosen as the single bearer) and the **neotype** (designated when all original type material is lost, only under strict conditions). A **paratype**, **allotype** (opposite sex) or **topotype** (from the type locality) is **not** a name-bearing type. For a genus the type is a **type species**; for a family-group name it is a **type genus**. **Objective synonyms** share the same type; **subjective synonyms** have different types judged to belong to one taxon. When a species is moved the name stays with the type.

EXAMINER TRAP: Priority applies only to **available** names and only within the family, genus and species groups. It does not make an older name valid if it is a nomen nudum or if the taxon has been shown to be composite. Priority is also not unlimited: Art. 23.9 can override it.

1.3 Species, categories and the hierarchy

No single definition of species satisfies every group; more than twenty concepts have been listed. The important ones differ in the criterion they use.

Species concepts compared

Concept (author)	Defining criterion	Limitation
Typological/morphological	Constant diagnostic morphology (Linnaeus, Cuvier)	Polymorphism, sexual dimorphism, sibling species
Biological (Mayr, 1942)	Groups of actually or potentially interbreeding natural populations reproductively isolated from others	Not applicable to asexual taxa, fossils; ignores gene flow between good species
Evolutionary (Simpson, 1951; Wiley, 1978)	A single lineage with its own evolutionary role and tendencies	Hard to operationalise
Phylogenetic (Cracraft, 1983; Mishler & Theriot)	Smallest diagnosable cluster (Cracraft) or smallest monophyletic group	Splits populations heavily; many more "species"
Ecological (Van Valen, 1976)	A lineage occupying one adaptive zone (niche)	Niche boundaries vague
Recognition (Paterson, 1985)	Shared fertilisation/mate-recognition system	Needs knowledge of signals
General lineage (de Queiroz, 1998)	A separately evolving metapopulation lineage; other concepts are operational criteria	Conceptual rather than practical

Sibling (cryptic) species are morphologically near-identical but reproductively isolated: the malaria vector Anopheles culicifacies is a complex of five sibling species (A–E) with different vectorial capacity, distinguished by polytene-chromosome inversions and molecular markers. **Ring species** (the greenish warblers Phylloscopus trochiloides around the Tibetan Plateau is the standard example) are chains of interbreeding populations whose terminal members co-occur without interbreeding. **Subspecies** are geographic races, named by a trinomen, that are diagnosable but not reproductively isolated. **Allopatric**, **parapatric**, **peripatric** and **sympatric** speciation are treated in Unit 11.

1.3.1 The hierarchy

The mnemonic hierarchy is Domain, Kingdom, Phylum, Class, Order, Family, Genus, Species, with intermediate categories formed by the prefixes super-, sub- and infra-. Ranks are a human convention: a family of insects is not equivalent in age or diversity to a family of mammals, and ranks above species have no objective biological meaning. The **only natural unit** in the Linnaean scheme is the species (and, for cladists, the clade).

1.4 Schools of classification and tree reasoning

Three philosophies compete, differing in what a classification should reflect.

Phenetics, cladistics and evolutionary taxonomy

Feature	Phenetics (numerical taxonomy)	Cladistics (phylogenetic systematics)	Evolutionary taxonomy
Founders	Sokal & Sneath, 1963	Hennig, 1950/1966	Mayr, Simpson

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Feature	Phenetics (numerical taxonomy)	Cladistics (phylogenetic systematics)	Evolutionary taxonomy
Basis	Overall similarity, all characters equally weighted	Recency of common ancestry; shared **derived** characters	Descent plus degree of adaptive divergence
Output	Phenogram (UPGMA)	Cladogram	Phylogenetic tree with grades
Paraphyletic groups	Accepted if similar	Rejected	Accepted (e.g. Reptilia)
Weakness	Cannot separate homology from convergence	Ignores amount of divergence	Subjective ranking

1.4.1 Phenetics

Specimens are **OTUs** (operational taxonomic units) scored for many characters; a similarity or distance matrix is computed and clustered, classically by **UPGMA** (unweighted pair-group method with arithmetic mean; Sokal & Michener, 1958), which assumes a constant rate of change (a molecular clock) and yields a rooted ultrametric tree. Neighbour-joining (Saitou & Nei, 1987) relaxes the clock assumption.

WORKED EXAMPLE: UPGMA on OTUs A–D with distances AB = 2, AC = 7, AD = 11, BC = 9, BD = 11, CD = 6. Smallest distance = AB (2): join A and B at height 2/2 = 1 ; recompute d(AB,C) = (7 + 9)/2 = 8, d(AB,D) = (11 + 11)/2 = 11 ; the smallest distance is now CD (6): join C and D at height 3 ; d(AB,CD) = (7 + 9 + 11 + 11)/4 = 9.5 ; root at height 9.5/2 = 4.75. Result ((A,B),(C,D)).

1.4.2 Cladistics

Hennig's terms describe the **polarity** of character states (ancestral versus derived), established by **outgroup comparison**:

• **Plesiomorphy**: an ancestral state. Shared plesiomorphies (**symplesiomorphies**) do **not** define groups (e.g. a vertebral column unites no group of fishes to the exclusion of tetrapods).

• **Apomorphy**: a derived state. A shared apomorphy is a **synapomorphy** and defines a clade; a derived state unique to one terminal taxon is an **autapomorphy** (uninformative about grouping).

• **Homoplasy**: similarity not due to common ancestry, by convergence (wings of bats and birds are homologous as forelimbs but homoplastic as wings), parallelism, or reversal.

• **Homology** = similarity due to common ancestry; **analogy** = similar function without common origin.

Groups are classified by completeness of descent:

• **Monophyletic** (a clade): a common ancestor and **all** its descendants. Only these are valid in cladistics.

• **Paraphyletic**: includes the common ancestor but omits some descendants (Reptilia without birds; "fishes" without tetrapods; "invertebrates"; "Protozoa").

• **Polyphyletic**: its members' common ancestor is not included; the group is united by convergent traits ("warm-blooded animals"; "pseudocoelomates"; "worms", Vermes).

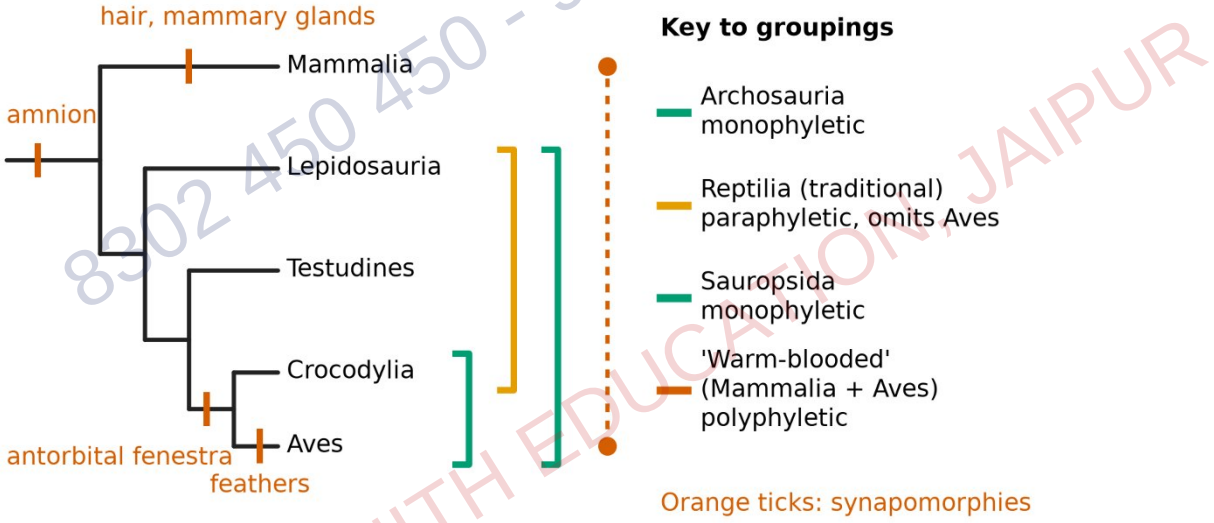


Figure 1. Cladogram of amniotes showing a monophyletic group (Archosauria, Sauropsida), a paraphyletic group (traditional

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Reptilia, omitting Aves) and a polyphyletic group (endothermic Mammalia plus Aves). Orange bars on branches are synapomorphies.

EXAMINER TRAP: Birds are not "polyphyletic" and they are not "reptiles' relatives": they are **nested inside Archosauria**, the sister group of Crocodylia. "Fishes" (Pisces) are a **paraphyletic**, not a polyphyletic, assemblage because the tetrapods descend from within the lobe-finned fishes.

1.4.3 Parsimony and tree choice

The **maximum parsimony** criterion (Fitch, 1971, for unordered states) selects the tree needing the fewest character-state changes (the shortest **tree length**). Only **parsimony-informative** sites (at least two states each occurring in at least two taxa) discriminate among trees. The number of possible bifurcating trees explodes with taxa: for n species the number of **rooted** trees is (2n−3)!! and of **unrooted** trees (2n−5)!!, where !! is the double factorial. Four taxa have 3 unrooted trees (15 rooted); ten taxa have 2,027,025 unrooted (34,459,425 rooted); twenty taxa have about 2.2×10^{20} unrooted trees, so heuristic searches are required.

WORKED EXAMPLE: Seven sites for taxa A–D (matrix in the figure). Sites 1–3 group AB|CD, sites 4–5 group AC|BD, site 6 groups AD|BC, site 7 is an autapomorphy of A. Length of tree AB|CD = 3 × 1 + 2 × 2 + 1 × 2 + 1 = 10 steps ; AC|BD = 3 × 2 + 2 × 1 + 1 × 2 + 1 = 11 ; AD|BC = 3 × 2 + 2 × 2 + 1 × 1 + 1 = 12. The shortest tree is AB|CD (10). Minimum conceivable steps m = 7 (one per variable site), so consistency index CI = m/s = 7/10 = 0.70.

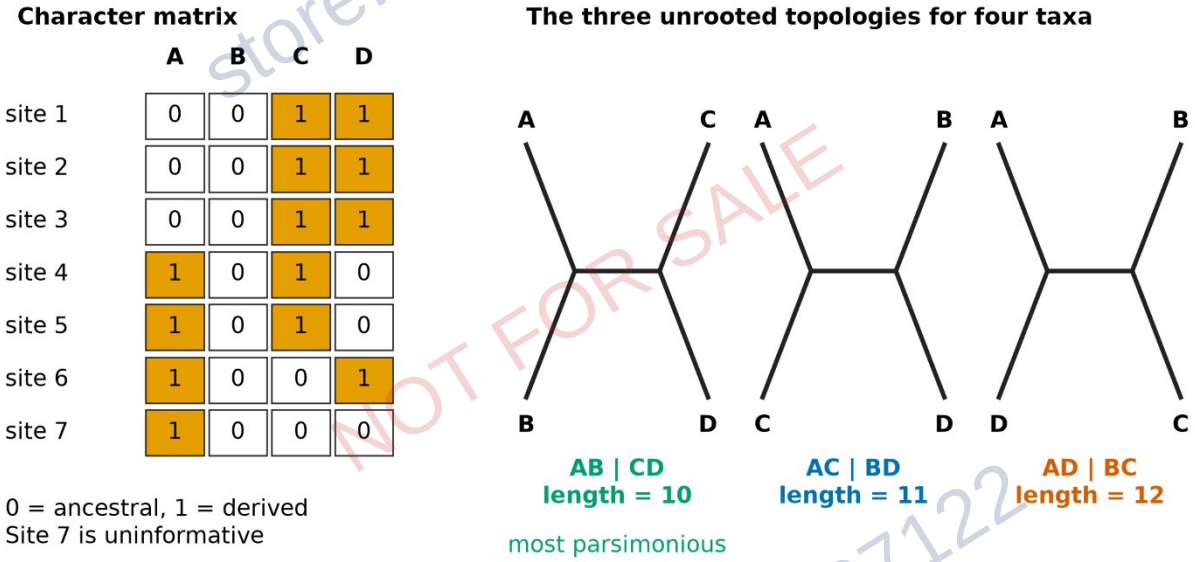


Figure 2. Parsimony for four taxa: a seven-site character matrix (orange = derived state) and the three possible unrooted trees with their lengths.

Parsimony fails when branches differ greatly in length (**long-branch attraction**; Felsenstein, 1978). **Maximum likelihood** and **Bayesian inference** use explicit substitution models and are now standard for molecular data. **Support** is measured by the **bootstrap** (Felsenstein, 1985; percentage of resampled datasets recovering a node), by Bayesian **posterior probability**, or by Bremer (decay) index. A **consensus tree** (strict, majority-rule) summarises several equally good trees. The **retention index** RI = (g − s)/(g − m) complements CI, where g is the maximum possible length.

NOTE: The **PhyloCode** (International Code of Phylogenetic Nomenclature, in its current form published 2020) proposes rank-free names tied to clades by node-, stem- or apomorphy-based definitions. It does not govern animal names; the ICZN remains in force.

1.5 Molecular systematics

Nucleotide and amino-acid sequences give thousands of characters, objective homology tests (alignment) and a measurable clock. Standard markers: **mitochondrial** DNA (COI, cyt b, 12S/16S; maternally inherited, fast; good for species and populations), **nuclear rRNA genes** (18S slow, for deep nodes; 28S; ITS fast, for species), single-copy nuclear genes, **ultra-conserved elements** and, increasingly, whole transcriptomes and genomes (**phylogenomics**, Dunn et al., 2008). Discordance between gene trees and the species tree arises from incomplete lineage sorting, hybridisation and paralogy; the **multispecies coalescent** reconciles them.

1.5.1 DNA barcoding

DNA barcoding (Hebert et al., 2003) identifies animal species with a 658-bp segment of the mitochondrial **cytochrome c oxidase**

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subunit I (COI) gene, matched against the reference library **BOLD** (Barcode of Life Data System), where sequences are clustered into **BINs** (Barcode Index Numbers). Barcoding relies on the **barcode gap**: the divergence within species is smaller than the divergence between species. It is used for species identification, detecting cryptic species, wildlife forensics, food authentication and metabarcoding of environmental DNA. Limitations: a single maternally inherited locus can be misled by **introgression**, Wolbachia-driven sweeps and nuclear mitochondrial pseudogenes (NUMTs); COI evolves too slowly in cnidarians and sponges to separate species; barcodes identify but do not by themselves define species. Plants use rbcL + matK, and fungi use ITS. **Integrative taxonomy** combines barcodes, morphology, ecology and behaviour. In India, institutions such as the ZSI and the ICAR–National Bureau of Fish Genetic Resources contribute barcode records to BOLD and GenBank.

1.5.2 Distances, models and clocks

The proportion of differing sites, p (the **p-distance**, or Hamming distance divided by length), underestimates true divergence because of multiple substitutions at one site. The **Jukes–Cantor (JC69)** correction assumes equal base frequencies and equal substitution rates:

$$d = -\tfrac{3}{4}\ln\left(1 - \tfrac{4}{3}p\right)$$

The **Kimura two-parameter (K2P)** model separates transitions (P) from transversions (Q): d = −½ ln(1 − 2P − Q) − ¼ ln(1 − 2Q).

WORKED EXAMPLE: Two sequences of 100 sites differ at 10 sites: p = 0.10 ; d(JC) = −0.75 ln(1 − 0.1333) = −0.75 × (−0.1431) = 0.107. At p = 0.30, d = −0.75 ln(0.600) = 0.383, showing that the correction grows rapidly; p cannot exceed 0.75 for random sequences (saturation). For K2P with P = 0.08 and Q = 0.04: d = −0.5 ln(1 − 0.16 − 0.04) − 0.25 ln(1 − 0.08) = 0.1116 + 0.0208 = 0.132.

The **molecular clock** (Zuckerkandl & Pauling, 1962) assumes substitutions accumulate roughly linearly with time, so divergence time T = d / 2r, where r is the rate per lineage (the factor 2 because both lineages evolve since the split). Rates need **calibration** with fossils or geological events; modern **relaxed-clock** Bayesian methods let rates vary among lineages.

WORKED EXAMPLE: A widely used arthropod mtDNA calibration (Brower, 1994) is about 2.3 % pairwise divergence per million years, i.e. r = 1.15 % per lineage per Myr. If two beetle populations show corrected COI distance d = 0.115, T = 0.115 / (2 × 0.0115) = 5 Myr.

1.6 Animal body plans

Animals (Metazoa) are multicellular, heterotrophic eukaryotes whose cells lack walls and are held by collagen-rich extracellular matrix and cell junctions. Their **body plan** is the combination of symmetry, tissue organisation, body cavity, segmentation and gut type; the first diagnostic split is between non-bilaterians and Bilateria.

1.6.1 Symmetry and tissue grade

• **Asymmetry**: most sponges and the placozoan Trichoplax. **Radial symmetry**: Cnidaria (adults), with **biradial** forms in ctenophores and anthozoans; adult echinoderms are secondarily pentaradial, derived from bilateral larvae. **Bilateral symmetry**: Bilateria, linked to directed locomotion and **cephalisation** (concentration of sense organs and ganglia at the anterior end).

• **Diploblastic** animals have ectoderm and endoderm separated by a non-cellular or sparsely cellular **mesoglea** (Cnidaria, Ctenophora; the muscle cells of ctenophores that lie in the mesoglea mean some authors call them triploblastic). **Triploblastic** animals have a third, cellular **mesoderm** between them (Bilateria). Sponges have cell layers but lack the organised tissues, nerves and muscles of eumetazoans (only homoscleromorphs have a basement membrane).

• Gut: absent (sponges); blind **gastrovascular** sac (cnidarians, flatworms); **complete** tube with mouth and anus (most Bilateria), allowing one-way flow and regional specialisation.

1.6.2 Body cavities

The mesoderm determines the type of cavity. In **acoelomates** (flatworms, nemerteans) solid mesodermal parenchyma fills the space between gut and body wall. In **pseudocoelomates** (nematodes, rotifers, gastrotrichs) the cavity is a persistent **blastocoel** lined by mesoderm only on the body-wall side, not around the gut. In **eucoelomates** the coelom is a **cavity entirely lined by mesodermal peritoneum**, which also forms the mesenteries that suspend the gut. In arthropods and most molluscs the coelom is reduced and the main cavity is a blood-filled **haemocoel**.

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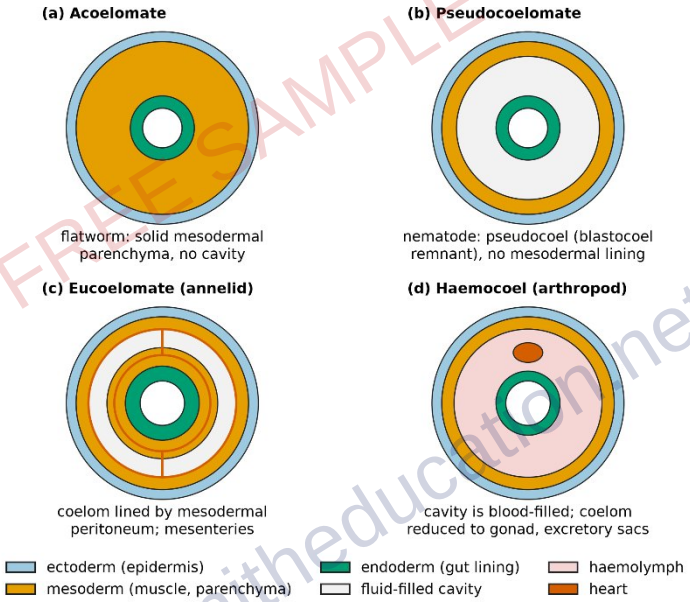


Figure 3. Transverse sections of four animal body plans: (a) acoelomate, (b) pseudocoelomate, (c) eucoelomate with peritoneum and mesenteries, (d) haemocoel. Colours: ectoderm blue, mesoderm orange, endoderm green.

The coelom forms in two ways: **schizocoely** (a solid mesodermal band splits; typical of annelids, molluscs, arthropods) and **enterocoely** (mesoderm pouches from the archenteron; echinoderms, hemichordates, cephalochordates). The detail of cleavage, blastopore fate and larval types is given in Chapter 4 of this unit. Coelom functions: hydrostatic skeleton (burrowing), freedom of gut movement, space for gonads and organs, transport, and storage.

EXAMINER TRAP: "Acoelomate–pseudocoelomate–coelomate" is a **grade** sequence, not a phylogeny. Molecular trees show that pseudocoelomate phyla are scattered (Ecdysozoa: nematodes; Spiralia: rotifers) and that acoelomate flatworms are nested within Spiralia. A body cavity can therefore be lost or reduced.

Body plans of major phyla

Phylum	Symmetry	Germ layers	Body cavity	Gut
Porifera	Asymmetrical or radial	Cell layers, no true tissues	None	None
Cnidaria	Radial	Diploblastic	None	Gastrovascular
Ctenophora	Biradial	Diploblastic*	None	Complete with anal pores
Platyhelminthes	Bilateral	Triploblastic	Acoelomate	Incomplete or absent
Nematoda	Bilateral	Triploblastic	Pseudocoelom	Complete
Annelida	Bilateral	Triploblastic	Schizocoelic coelom	Complete
Mollusca	Bilateral (torsion in gastropods)	Triploblastic	Reduced coelom, haemocoel	Complete
Arthropoda	Bilateral	Triploblastic	Haemocoel	Complete
Echinodermata	Pentaradial adult	Triploblastic	Enterocoelic	Complete (or blind in some)
Chordata	Bilateral	Triploblastic	Enterocoelic or by splitting	Complete

*See the note on mesoglea muscle above.

1.6.3 Segmentation

Metamerism is the serial repetition of body units, each with coelomic compartment, nerve ganglia, nephridia and muscle blocks; it is

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true in **Annelida**, **Arthropoda** (with tagmatisation: fusion of segments into head, thorax, abdomen) and **Chordata** (somites). Tapeworm strobilation is **pseudometamerism**, because only the reproductive units repeat. Serial repetition of gills and muscles in monoplacophorans is not considered true segmentation. Whether the segmentation of annelids, arthropods and chordates was inherited from a segmented bilaterian ancestor or evolved independently is unresolved.

1.7 The animal tree of life

Metazoa is monophyletic and its sister group is the unicellular **Choanoflagellata** (Choanozoa), with the Filasterea and Ichthyosporea more distant relatives, all grouped in the **Holozoa** within Opisthokonta. Animal synapomorphies include collagen IV and a basement membrane, specific cell-adhesion and signalling gene families, and sperm and egg produced in a multicellular body.

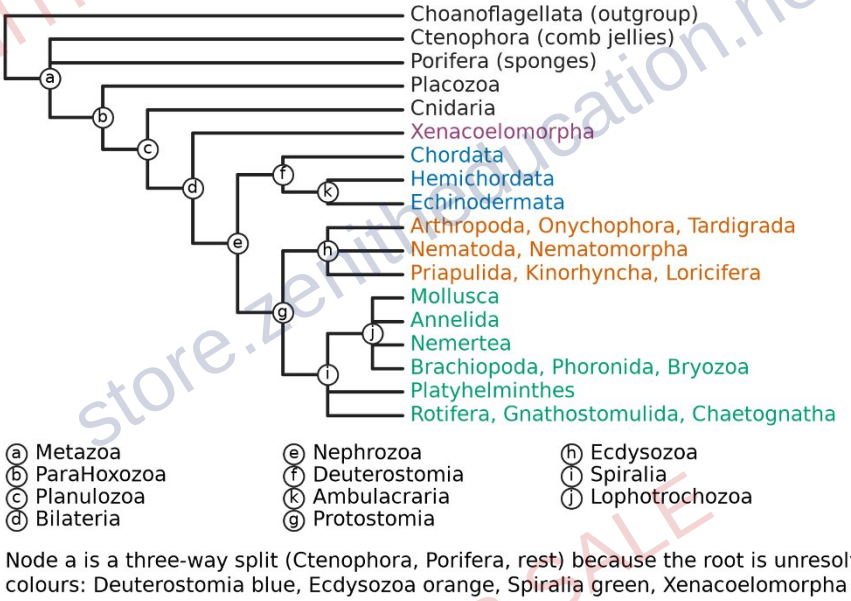


Figure 4. Consensus animal phylogeny. Lettered nodes are named in the key. Polytomies mark unresolved relationships (the root of animals; the arrangement within Ecdysozoa and Spiralia).

1.7.1 The root of the tree: Ctenophora-first or Porifera-first?

Which lineage branched first within Metazoa remains **unresolved**. Several analyses give Ctenophora as sister to all other animals (Dunn et al., 2008; Whelan et al., 2015; chromosome-scale gene-linkage evidence by Schultz et al., 2023), whereas others favour Porifera (Simion et al., 2017; Li et al., 2021). A 2025 Science paper reporting sponge-first was **retracted in February 2026** after the authors found errors in their pipeline, so the question stays open. The consequence is large: under ctenophore-first, the nervous system and muscles either arose twice or were lost in sponges and placozoans, and **Eumetazoa** (nerve cells, true tissues) is not monophyletic.

Other non-bilaterian points that are firmly supported: Placozoa, Cnidaria and Bilateria form **ParaHoxozoa** (they share ParaHox/Hox-type genes); Cnidaria + Bilateria form **Planulozoa**; and **Hox genes** are absent from sponges and ctenophores.

1.7.2 Bilateria

Bilateria comprises **Xenacoelomorpha** (acoels, nemertodermatids, Xenoturbella) and **Nephrozoa** (**Protostomia** + **Deuterostomia**). Xenacoelomorpha is placed either as sister to Nephrozoa (Cannon et al., 2016) or inside Deuterostomia as sister to Ambulacraria (Philippe et al., 2011, 2019); the question is unresolved, and a few analyses (Kapli et al., 2021) question the monophyly of Deuterostomia. Textbooks still use:

- **Deuterostomia**: Chordata, Hemichordata, Echinodermata (the last two form **Ambulacraria**).
- **Protostomia**, divided on molecular evidence into **Ecdysozoa** (moulting animals with a cuticle: Arthropoda, Onychophora, Tardigrada, Nematoda, Nematomorpha, Priapulida, Kinorhyncha, Loricifera) named by **Aguinaldo et al. (1997)** from 18S rDNA; and **Spiralia** (spiral cleavage), with **Lophotrochozoa** (named by Halanych et al., 1995; Mollusca, Annelida, Nemertea and the lophophorate phyla Brachiopoda, Phoronida, Bryozoa) plus Platyhelminthes and the **Gnathifera** (rotifers, gnathostomulids, micrognathozoans; chaetognaths are placed here by Marlétaz et al., 2019).

> **NOTE: Old versus new.** Indian textbooks traditionally teach Parazoa vs Eumetazoa, Radiata vs Bilateria, **Articulata** (annelids + arthropods, from segmentation), and Acoelomata, Pseudocoelomata, Coelomata. Molecular phylogenies reject Articulata: arthropods are **Ecdysozoa**, annelids **Lophotrochozoa**, so segmentation is convergent or ancestral-and-lost. The classical groups

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