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BIO 306

SYSTEMATIC BIOLOGY

Course code: BIO 306

Course title: Systematic Biology

Course credit load: 2 Units

Series 1: Historical Foundations of Systematic Biology

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  - Sub Part 1.1.1: Definition and scope of systematics
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Introduction

Systematics is the scientific study of the diversity of life and the relationships among organisms. It provides the framework for naming, describing, and classifying all known organisms. Understanding how systematic biology developed historically, from the natural philosophy of ancient Greece through Linnaeus's binomial system to modern molecular phylogenetics, is essential for appreciating how and why classification is practised the way it is today.

This opening Series traces the history of systematic biology from pre-scientific classification through the three major eras: pre-Linnaean (before the mid-18th century), Linnaean (the period dominated by Linnaeus's methods), and Darwinian/post-Darwinian (from 1859 to the present). It establishes the conceptual and historical foundations on which all subsequent Series build.

Series Learning Outcomes

Upon completing this Series, you should be able to:

- **SLO 1.1** define systematics and distinguish it from taxonomy and classification (Linked to Part 1.1),
- **SLO 1.2** explain the importance of systematic biology in science and society (Linked to Part 1.1),
- **SLO 1.3** describe the contributions of pre-Linnaean naturalists to the development of systematic biology (Linked to Part 1.2),
- **SLO 1.4** describe Linnaeus's contributions to systematic biology and explain his sexual system and natural system (Linked to Part 1.3),
- **SLO 1.5** explain the impact of Darwinian evolutionary theory on systematics (Linked to Part 1.4), and
- **SLO 1.6** describe the New Systematics and modern developments in systematic biology (Linked to Part 1.4).

1.1 What is Systematic Biology?

1.1.1 Definition and scope of systematics

Systematics is the scientific study of the diversity of living organisms and their evolutionary relationships. It encompasses three interrelated activities: describing the diversity of life (taxonomy); organising that diversity into a hierarchical classification; and inferring evolutionary relationships among organisms (phylogenetics). Systematics is the broadest of these three: it integrates taxonomy, nomenclature, and phylogenetics into a unified science.

The scope of systematics includes: discovery and formal description of new species; identification of known specimens; construction of classifications that reflect evolutionary history; development and application of identification keys; curation of biological collections (herbaria, museums); study of patterns of biodiversity and biogeography; and provision of the nomenclatural framework that other biological sciences depend on. Every biological science from ecology to medicine ultimately depends on correctly identified and named organisms.

Fill in the blank: ________ is the scientific study of the diversity of living organisms and their evolutionary relationships; it encompasses taxonomy, nomenclature, and phylogenetics as a unified science.

1.1.2 Relationship between systematics, taxonomy, and classification

These terms are often used interchangeably but have distinct meanings. Taxonomy (from Greek taxis = arrangement, nomos = law) is the theoretical study of the principles, procedures, and rules underlying classification; it includes the practice of naming and describing organisms. Classification is the practical act of placing organisms into groups (taxa) based on their similarities or evolutionary relationships. Nomenclature is the system of rules for formally naming taxa.

Systematics is the broader science that includes all three plus the study of evolutionary relationships and patterns of biological diversity. A systematist identifies and describes organisms (taxonomy), assigns them to named groups (classification), and interprets their evolutionary history (phylogenetics). In practice, the terms taxonomy and systematics are often used synonymously, though systematics carries a stronger implication of the study of evolutionary relationships.

Fill in the blank: ________ is the practical act of placing organisms into named groups; taxonomy is the theoretical study of the principles and rules of classification; systematics is the broader science that includes both, plus the study of evolutionary relationships.

1.1.3 Importance of systematics

Systematics underpins all of biology. Without correctly identified and named organisms, no biological experiment can be reliably repeated by other scientists, no medical treatment can be safely based on a specific organism, and no conservation programme can target the right species. Systematics also provides the only comprehensive inventory of biodiversity, essential for monitoring species loss, prioritising conservation, and assessing ecosystem function.

Practical applications of systematics in Nigeria: identifying crop pests and the most effective biocontrol agents; correctly identifying medicinal plants (many Nigerian herbal medicines depend on specific plants that must be correctly identified to avoid toxic substitutions); identifying disease vectors (Anopheles mosquitoes, tsetse flies, blackflies causing river blindness); agricultural quarantine (identifying whether an intercepted pest is a known species or a new invasive); and support of traditional ecological knowledge systems that depend on reliable species names.

Fill in the blank: Systematics underpins all of biology because without correctly ________ and named organisms, no biological experiment can be reliably repeated and no conservation programme can target the right species.

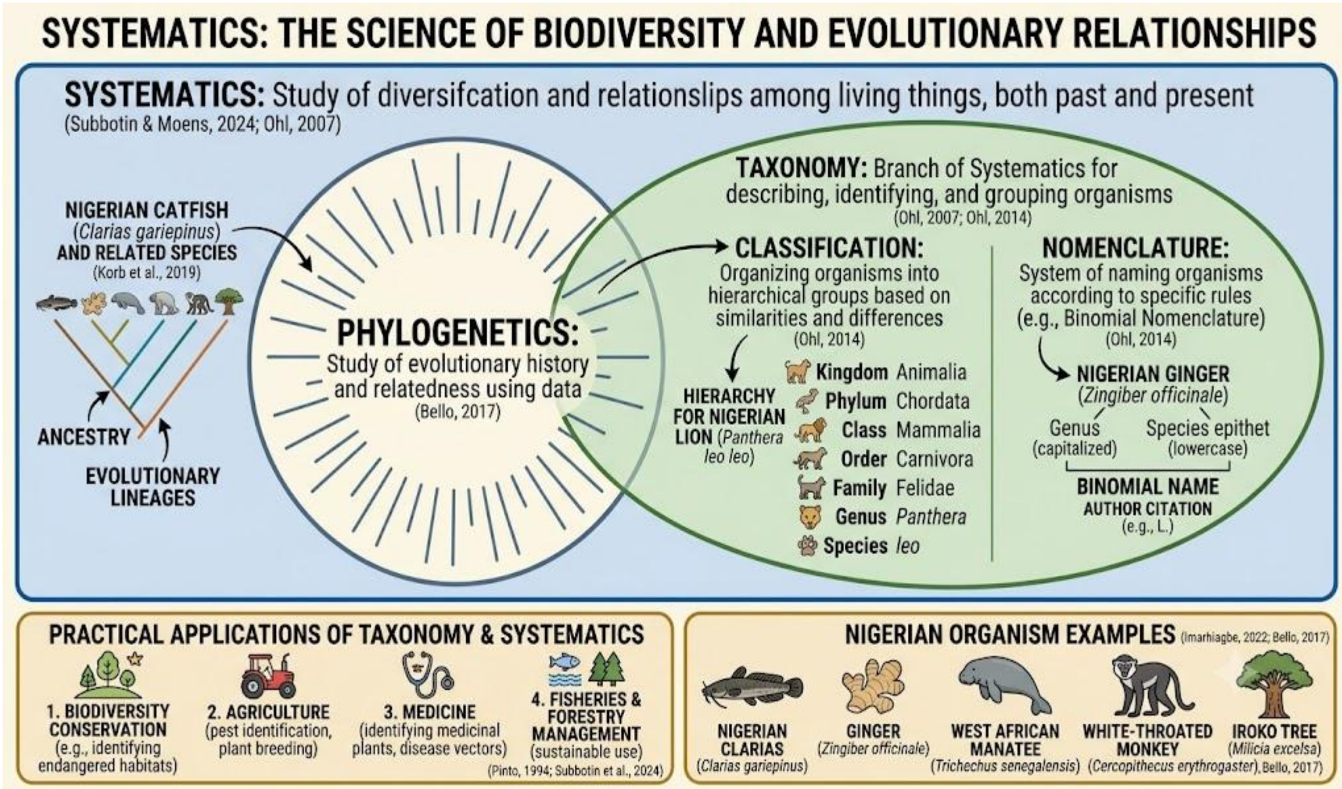


Figure 1.1: Diagram illustrating the relationship among systematics, taxonomy, classification, nomenclature, and phylogenetics

Pilot questions 1.1

1. Define systematics and state three activities it encompasses.
2. Distinguish between systematics, taxonomy, and classification.
3. State four practical applications of systematics in Nigeria.
4. Explain why systematics is described as underpinning all of biology.
5. Define nomenclature and explain its role within systematics.

1.2 Pre-Linnaean Systematics

1.2.1 Ancient Greek and Roman contributions

The systematic study of organisms began with ancient Greek natural philosophers. Aristotle (384-322 BC) made the most significant early contribution: he classified approximately 500 animal species based on structural and functional similarities, dividing them into Enaima (animals with blood; vertebrates) and Anaima (animals without blood; invertebrates); he described developmental patterns, habitats, and behaviour. His classification was not hierarchical in the modern sense but demonstrated the principle of grouping organisms by shared characters.

Theophrastus (371-287 BC), Aristotle's student and successor, applied similar methods to plants; he described approximately 500 plant species in Historia Plantarum and Causae Plantarum. He distinguished between trees, shrubs, undershrubs, and herbs (a classification still broadly useful today); he described plant morphology, ecology, and uses. Pliny the Elder (23-79 AD) compiled Naturalis Historia, a 37-volume encyclopaedia of natural history based largely on earlier sources; it was the primary reference for natural history in the Roman world.

Fill in the blank: ________ (384-322 BC) classified approximately 500 animal species, dividing them into Enaima (blood-bearing animals) and Anaima (bloodless animals); he is regarded as the founder of zoology and the first systematic biologist.

1.2.2 Medieval and Renaissance developments

During the medieval period in Europe, natural history largely stagnated; Latin translations of Aristotle and other classical texts were the main references. Islamic scholars, however, advanced botanical knowledge significantly: Ibn Sina (Avicenna; 980-1037) included descriptions of approximately 800 medicinal plants in his Canon of Medicine; Ibn al-Baitar (1197-1248) described over 1,400 plant species in Compendium on Simple Medicaments. Their work preserved and extended the Greek tradition through the medieval period.

The Renaissance (14th to 17th centuries) stimulated renewed interest in natural history through the recovery of classical texts, the invention of printing, and increased exploration. German

"Fathers of Botany": Otto Brunfels (1488-1534), Hieronymus Bock (1498-1554), and Leonhard Fuchs (1501-1566) produced illustrated herbals with first-hand plant observations; they began moving away from reliance on classical descriptions toward direct observation of specimens. Conrad Gessner (1516-1565) compiled Historia Animalium, an illustrated encyclopaedia covering all known animal groups.

Fill in the blank: During the Renaissance, the German "Fathers of Botany" (Brunfels, Bock, and Fuchs) produced illustrated ________ based on first-hand plant observations, moving away from the classical tradition of relying on ancient descriptions.

1.2.3 Immediate pre-Linnaean naturalists

Several naturalists in the late 16th and 17th centuries made critical advances immediately before Linnaeus. Andrea Cesalpino (1519-1603): the first to base plant classification on reproductive organs (fruits and seeds) rather than habit or use; he described approximately 1,500 plant species in De Plantis (1583). John Ray (1627-1705): English naturalist who introduced a more rigorous species concept based on common descent from the same parents; he classified approximately 18,600 plant species and used both vegetative and floral characters.

Caspar Bauhin (1560-1624): introduced the binomial (two-word) designation for species in his Pinax Theatri Botanici (1623), anticipating Linnaeus by over a century; he also distinguished synonyms (different names given to the same organism by different authors). Joseph Pitton de Tournefort (1656-1708): strengthened the genus concept and produced one of the clearest pre-Linnaean classifications of plants, recognising approximately 698 genera; his work directly influenced Linnaeus. These immediate pre-Linnaean naturalists provided the conceptual tools that Linnaeus systematised and reformed.

Fill in the blank: Caspar Bauhin (1560-1624) introduced the ________ (two-word) designation for species in his Pinax Theatri Botanici (1623), anticipating Linnaeus by over a century and also distinguishing synonyms for the same organism.

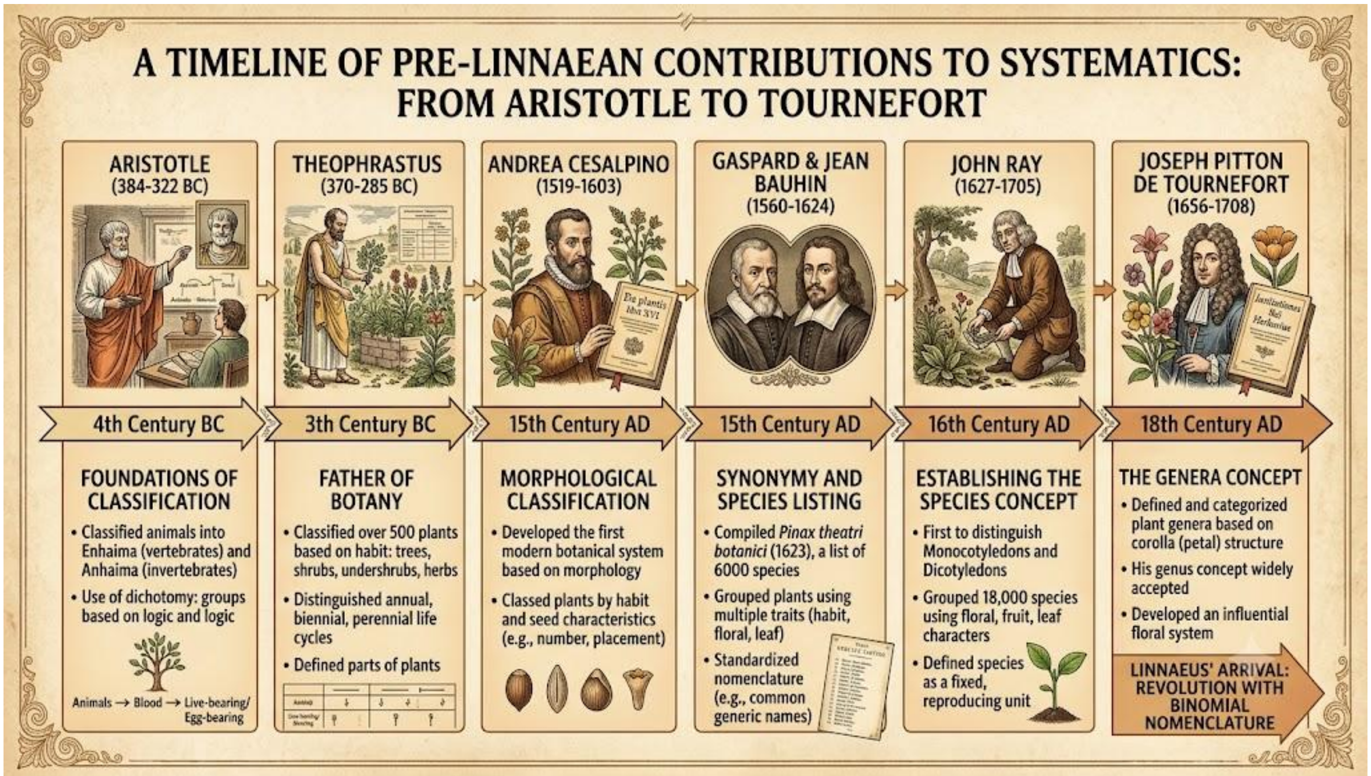


Figure 1.2: Timeline of pre-Linnaean contributions to systematics

Pilot questions 1.2

1. Describe Aristotle's contribution to systematic biology.
2. Describe Theophrastus's contribution to plant systematics.
3. Explain the contribution of Islamic scholars to the development of systematics.
4. Explain the significance of Caspar Bauhin's contribution to systematics.
5. Describe John Ray's contribution to the species concept.

1.3 Linnaean Systematics

1.3.1 Linnaeus and the reform of classification

Carl Linnaeus (1707-1778), a Swedish naturalist, transformed systematic biology through a series of major publications. Systema Naturae (1735, 1st edition; 1758, 10th edition; the 12th edition was the last during his lifetime): established the hierarchical classification of all organisms and introduced binomial nomenclature consistently; the 10th edition (1758) is the starting point for zoological nomenclature. Species Plantarum (1753): the starting point for botanical nomenclature; described approximately 7,700 plant species.

Linnaeus's reform addressed three problems that plagued pre-Linnaean systematics: (1) the lack of a stable naming system (pre-Linnaean names were often long polynomial phrases); (2) the absence of a universal hierarchical classification; (3) the proliferation of synonyms (multiple names for the same organism). By consistently applying binomial names (Genus + species epithet), a clear hierarchical system (class-order-genus-species), and the principle of priority (the earliest validly published name takes precedence), Linnaeus provided the foundation of modern systematics.

Fill in the blank: Linnaeus's Systema Naturae (10th edition, ________) is the starting point for zoological nomenclature; Species Plantarum (1753) is the starting point for botanical nomenclature.

1.3.2 Sexual system and natural system

Linnaeus's sexual system (artificial classification): he classified flowering plants primarily by the number and arrangement of stamens (male parts) and pistils (female parts). It was convenient, easily applied, and allowed rapid identification; it was not intended to reflect natural relationships. Class Monandria had one stamen; Diandria had two; and so forth. The sexual system was widely adopted because of its simplicity, not because it was believed to reflect true affinities.

Linnaeus himself acknowledged that the sexual system was artificial and sought to develop a natural system based on overall resemblance across many characters. He outlined his vision of a Methodus Naturalis but never completed it; he identified approximately 58 natural plant orders. The tension between artificial (convenient) and natural (reflective of true relationships) classification has recurred throughout the history of systematics and remains relevant in debates between phenetic and cladistic approaches today.

Fill in the blank: Linnaeus's ________ system classified plants by the number and arrangement of stamens and pistils; he acknowledged it was artificial and sought a natural system based on overall resemblance, but never completed his Methodus Naturalis.

1.3.3 Linnaeus's lasting contributions

Linnaeus's five lasting contributions to systematic biology: (1) Consistent application of binomial nomenclature to all organisms; (2) Clear hierarchical classification (class-order-genus-species); (3) The principle of priority for names; (4) Formal descriptions (diagnoses) for each taxon; (5) Type specimens: the designation of a single reference specimen (the type) to which the name of a species is permanently attached, ensuring stability of application. He also standardised the physical format of species descriptions.

Beyond these technical contributions, Linnaeus established the discipline of systematics as an empirical science with explicit rules and procedures. He trained approximately 23 apostles (students who travelled the world collecting specimens for him) and created the institutional model of a systematic botanist or zoologist who maintains a reference collection, publishes formal descriptions, and corresponds with a global network of collectors. The Uppsala University collection he built is still an important reference collection.

Fill in the blank: Linnaeus designated a single reference ________ specimen to which each species name is permanently attached; this innovation ensured the stable application of names and remains a foundation of modern nomenclature.

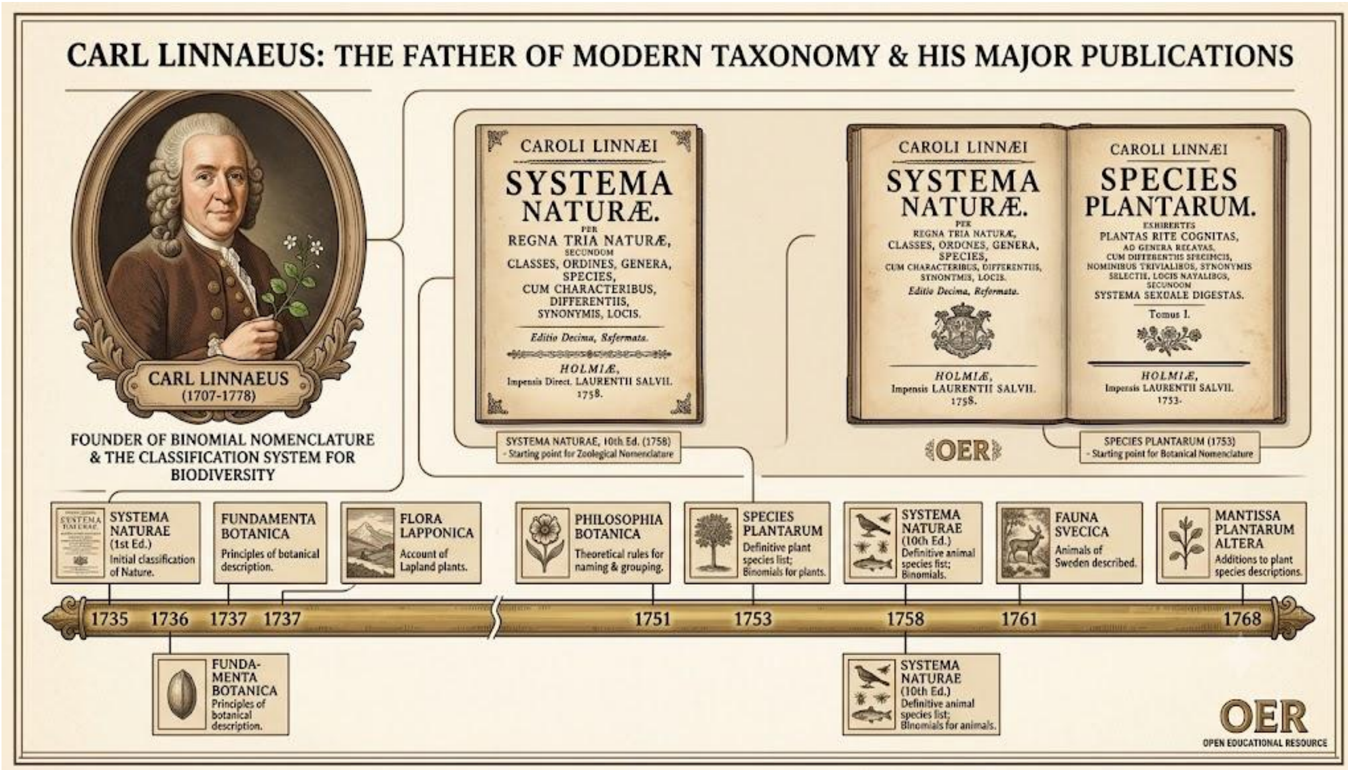


Figure 1.3: Portrait and key publications of Carl Linnaeus

Pilot questions 1.3

1. State the key publications of Linnaeus and their significance for nomenclature.
2. Describe Linnaeus's sexual system of classification and state one advantage and one limitation.
3. Explain the difference between an artificial and a natural classification.
4. State five lasting contributions of Linnaeus to systematic biology.
5. Explain the concept of the type specimen and its importance in nomenclature.

1.4 Darwinian and Post-Darwinian Systematics

1.4.1 Impact of evolutionary theory on systematics

Darwin's On the Origin of Species (1859) transformed systematics by providing an explanatory framework for the natural system that naturalists had sought since Linnaeus. If species are related by common descent, then a natural classification should reflect genealogy (ancestry).

Characters shared because of common descent (homologies) are the appropriate basis for classification; characters that evolved independently in unrelated lineages (analogies or convergences) should not be used to group organisms together.

The immediate post-Darwinian period produced the first explicitly phylogenetic classifications: Ernst Haeckel (1866) proposed the first phylogenetic tree diagrams and introduced the three-domain-level concept; systematic biologists began constructing classifications intended to reflect evolutionary trees rather than mere similarity. However, without the Modern Evolutionary Synthesis or molecular data, these phylogenies relied entirely on morphological characters and were often unreliable; the relationship between classifications and evolutionary trees remained disputed.

Fill in the blank: Darwin's theory of evolution by natural selection transformed systematics by explaining why a ________ classification exists: species related by common descent share characters inherited from their common ancestor, providing the scientific basis for grouping organisms by homology.

1.4.2 The New Systematics

The New Systematics is the term coined by Julian Huxley (1940) for the synthesis of genetics, cytology, ecology, and field natural history with classical Linnaean taxonomy. It arose from the Modern Evolutionary Synthesis of the 1930s and 1940s and recognised that populations, not just fixed species, are the units of evolution. Biosystematists used breeding experiments, chromosome studies, and population-level data to understand species boundaries, hybridisation, and subspecific variation.

Key contributions of the New Systematics: recognition of subspecies and polytypic species (species showing geographic variation); application of the Biological Species Concept (Ernst Mayr, 1942; species defined by reproductive isolation); use of statistical methods for analysing morphological variation; and the concept of the rassenkreis (circle of races). The New Systematics moved systematics from a purely descriptive discipline toward an experimental, biologically grounded science concerned with evolutionary process as well as pattern.

Fill in the blank: Julian ________ coined the term "New Systematics" in 1940 for the synthesis of genetics, population biology, and ecology with classical taxonomy; it recognised populations rather than fixed types as the units of evolution.

1.4.3 Modern developments in systematics

Modern systematics has been transformed by three developments: numerical taxonomy (phenetics; Sokal and Sneath, 1963): the application of multivariate statistical methods to classify organisms by overall similarity across many characters, without assumptions about evolutionary weighting; cladistics (Willi Hennig, 1950, 1966): classification strictly by shared derived characters (synapomorphies) reflecting common ancestry; and molecular systematics: use of DNA sequence data to infer phylogenies, which has revolutionised our understanding of relationships.

Molecular phylogenetics has overturned many traditional classifications, revealing convergent evolution in morphological characters previously used to define natural groups. The integration of molecular data with morphological characters and fossils has produced increasingly robust classifications (e.g. the APG classification of flowering plants; the NCBI taxonomy; the Open Tree of Life). Bioinformatics tools (BLAST, MEGA, MrBayes, PhyML) allow rapid phylogenetic analysis of genome-scale data. DNA barcoding (using short standardised DNA sequences, typically the CO1 gene) allows rapid identification of specimens.

Fill in the blank: ________ barcoding uses short standardised DNA sequences (typically the cytochrome oxidase I gene, CO1) to rapidly identify biological specimens; it is particularly useful for identifying cryptic species and for non-specialist identification of organisms.

Era	Key Period	Key Figures	Major Contributions	Species Concept Used
Pre-Linnaean	Antiquity to 1753	Aristotle, Theophrastus, Cesalpino, Ray,	Descriptions, herbals, first binomial designations, early species concept	Morphological (typological)

		Bauhin, Tournefort		
Linnaean	1753–1859	Carl Linnaeus	Binomial nomenclature, hierarchical classification, type specimens, principle of priority	Morphological (typological)
Darwinian & New Systematics	1859–1960s	Darwin, Haeckel, Mayr, Dobzhansky, Huxley	Phylogenetic classification, Biological Species Concept (BSC), polytypic species, population genetics	Biological Species Concept
Modern	1960s–present	Hennig, Sokal, Sneath, Woese, APG	Cladistics, phenetics, molecular phylogenetics, DNA barcoding	Phylogenetic, Biological, Ecological

Box 1.1: Summary of the three major eras of systematic biology

Pilot questions 1.4

1. Explain how Darwin's theory of evolution changed the goal of systematic classification.
2. Define the New Systematics and state two contributions it made to taxonomy.
3. Distinguish between phenetics (numerical taxonomy) and cladistics.
4. Explain how molecular systematics has transformed classification.
5. Explain what DNA barcoding is and state one application.

Series Summary

This Series covered the historical foundations of systematic biology. Systematics is the scientific study of the diversity of organisms and their evolutionary relationships; it encompasses taxonomy, classification, nomenclature, and phylogenetics. Pre-Linnaean: Aristotle classified approximately 500 animals (Enaima/Anaima); Theophrastus classified approximately 500 plants; medieval Islamic scholars (Ibn Sina, Ibn al-Baitar) preserved and extended classical knowledge; Renaissance herbalists (Brunfels, Bock, Fuchs) began first-hand observation; Cesalpino introduced classification by reproductive organs; Bauhin used binomial designations; John Ray introduced a species concept based on common descent; Tournefort developed the genus concept.

Linnaean: Linnaeus reformed systematics through Systema Naturae (starting point for zoological nomenclature, 10th edition 1758) and Species Plantarum (starting point for botanical nomenclature, 1753); introduced consistent binomial nomenclature, hierarchical classification, type specimens, formal diagnoses, and the priority principle; his sexual system (by stamen/pistil number) was artificial but convenient; he sought a natural system but never completed it. Darwinian: Darwin (1859) provided evolutionary explanation for natural classification; New Systematics (Huxley 1940) integrated genetics and population biology; modern systematics uses numerical taxonomy (Sokal/Sneath), cladistics (Hennig), and molecular phylogenetics (DNA sequences); DNA barcoding enables rapid species identification. By completing this Series, you should achieve all six SLOs (1.1 to 1.6).

Glossary of Terms

- **Analogy:** similarity between organisms resulting from convergent evolution rather than common ancestry; analogous characters should not be used to group organisms in natural classifications.
- **Binomial nomenclature:** the system of naming organisms with a two-part Latin name (Genus epithet + species epithet), introduced consistently by Linnaeus; each name is unique and internationally accepted.

- **Biosystematics:** the study of species boundaries and variation using experimental methods including breeding experiments, cytology, and population genetics; central to the New Systematics.
- **Cladistics:** the classification method that groups organisms strictly by shared derived characters (synapomorphies) reflecting common ancestry; developed by Willi Hennig.
- **Classification:** the practical act of placing organisms into named hierarchical groups (taxa) based on their similarities or evolutionary relationships.
- **DNA barcoding:** the use of a short, standardised DNA sequence (typically the cytochrome oxidase I gene, CO1 for animals; rbcL or matK for plants) to identify biological specimens.
- **Genus (plural: genera):** a taxonomic rank above species grouping related species that share a common ancestor and a set of diagnostic characters; the first part of a binomial name.
- **Herbarium:** a collection of dried, pressed, and labelled plant specimens mounted on sheets and stored systematically; a primary resource for systematic botany.
- **Homology:** similarity between organisms resulting from common ancestry (e.g. the forelimb of a horse and the wing of a bat are homologous); the basis for grouping organisms in natural classifications.
- **Methodus Naturalis:** Linnaeus's vision of a natural classification based on overall resemblance across many characters; he outlined it but never completed it; it foreshadowed post-Linnaean natural systems.
- **Natural classification:** a classification that reflects the true evolutionary relationships (genealogy) among organisms, based on homologous characters inherited from common ancestors.
- **New Systematics:** the term coined by Julian Huxley (1940) for the synthesis of genetics, population biology, cytology, and ecology with classical taxonomy.
- **Nomenclature:** the system of formal rules and procedures for naming taxa; governed internationally by the International Codes of Nomenclature for different groups of organisms.
- **Numerical taxonomy (phenetics):** the classification of organisms by overall similarity across many equally weighted characters, using multivariate statistical methods; developed by Sokal and Sneath.

- **Pinax Theatri Botanici:** the 1623 work of Caspar Bauhin that introduced binomial designations for plant species and distinguished synonyms; it influenced Linnaeus directly.
- **Priority (principle of):** the rule that the earliest validly published name for a taxon takes precedence over all later names (synonyms) for the same taxon.
- **Sexual system:** Linnaeus's artificial classification of flowering plants based on the number and arrangement of stamens and pistils; convenient but not reflective of natural relationships.
- **Species Plantarum:** Linnaeus's 1753 two-volume work describing all known plant species using binomial nomenclature; the starting point for botanical nomenclature.
- **Synapomorphy:** a shared derived character inherited from a common ancestor; the basis for defining clades in cladistic classification.
- **Systema Naturae:** Linnaeus's multi-edition work classifying all known animals, plants, and minerals; the 10th edition (1758) is the starting point for zoological nomenclature.
- **Systematics:** the scientific study of the diversity of living organisms and their evolutionary relationships; encompasses taxonomy, classification, nomenclature, and phylogenetics.
- **Taxonomy:** the theoretical study of the principles, rules, and procedures of naming and classifying organisms; includes the practice of describing and naming new species.
- **Type specimen:** the single reference specimen to which a species name is permanently attached; ensures the stable application of the name across time and by different workers.

Concept Check Questions [Series 1]

Objective Questions

1. ________ is the scientific study of the diversity of living organisms and their evolutionary relationships; it encompasses taxonomy, classification, nomenclature, and phylogenetics. (Linked to SLO 1.1)
2. ________ (384-322 BC) classified approximately 500 animal species and divided them into Enaima (blood-bearing) and Anaima (bloodless); he is regarded as the first systematic biologist. (Linked to SLO 1.3)
3. Caspar Bauhin introduced the ________ (two-word) designation for species in his Pinax Theatri Botanici (1623), anticipating Linnaeus by over a century. (Linked to SLO 1.3)
4. Linnaeus's Systema Naturae (10th edition, ________) is the internationally recognised starting point for zoological nomenclature. (Linked to SLO 1.4)
5. Julian ________ coined the term "New Systematics" in 1940 for the synthesis of genetics, population biology, and ecology with classical taxonomy. (Linked to SLO 1.6)

Short-Answer Questions

6. Distinguish between systematics, taxonomy, and classification. (Linked to SLO 1.1)
7. State three pre-Linnaean naturalists and one contribution of each. (Linked to SLO 1.3)
8. State three lasting contributions of Linnaeus to systematic biology. (Linked to SLO 1.4)
9. Explain the difference between Linnaeus's sexual system and his natural system. (Linked to SLO 1.4)
10. Explain how Darwin's theory changed the goal of systematic classification. (Linked to SLO 1.5)

Long-Answer Questions

11. Define systematics; distinguish it from taxonomy and classification; and explain its importance in biology and in Nigeria specifically. (Linked to SLOs 1.1, 1.2)
12. Describe the contributions of pre-Linnaean naturalists to systematics from Aristotle to Tournefort. (Linked to SLO 1.3)
13. Describe Linnaeus's contributions to systematic biology; explain his sexual and natural systems; and outline the development of the New Systematics and modern advances. (Linked to SLOs 1.4, 1.5, 1.6)

Answers to Concept Check Questions [Series 1]

Objective Questions

1. Systematics.
2. Aristotle.
3. Binomial.
4. 1758.
5. Huxley.

Short-Answer Questions

6. Systematics: the broad science studying diversity and evolutionary relationships, encompassing taxonomy, classification, nomenclature, and phylogenetics. Taxonomy: the theory and practice of naming and describing organisms. Classification: the practical act of placing organisms into named hierarchical groups.
7. Aristotle: classified approximately 500 animals; divided into Enaima and Anaima. Caspar Bauhin: introduced binomial designations and distinguished synonyms (Pinax, 1623). John Ray: introduced a species concept based on common descent and classified approximately 18,600 plants.
8. Consistent application of binomial nomenclature; hierarchical classification (class-order-genus-species); designation of type specimens to stabilise name application.
9. Sexual system: classified plants by stamen and pistil number; artificial but convenient. Natural system: sought to classify by overall resemblance reflecting true affinities; Linnaeus outlined it (Methodus Naturalis) but never completed it.
10. Darwin showed that species share characters because of common descent; therefore natural classification should reflect genealogy (ancestry); homologous characters (inherited from a common ancestor) became the proper basis for grouping organisms.

Long-Answer Questions

11. Systematics: scientific study of organic diversity and evolutionary relationships; encompasses taxonomy (naming and describing), classification (placing in groups), nomenclature (rules for naming), and phylogenetics (inferring relationships). Distinct from taxonomy (narrower; just naming/describing) and classification (just grouping). Importance: underpins all biology; no experiment is reproducible without correct identification; basis of conservation targeting; medical safety (Nigerian herbal medicine); pest and vector identification (Anopheles; tsetse; Striga); agricultural quarantine; biodiversity inventory.
12. Aristotle (384-322 BC): classified approximately 500 animals; Enaima vs Anaima; described development, habitat, behaviour; founder of zoology. Theophrastus (371-287 BC): classified approximately 500 plants; Historia Plantarum; trees, shrubs, undershrubs, herbs; founder of botany. Ibn Sina (980-1037): described approximately 800 medicinal plants; Canon of Medicine; preserved and extended Greek tradition. Renaissance herbalists (Brunfels, Bock, Fuchs, 1500s): first-hand observation; illustrated herbals. Cesalpino (1583): first classification by reproductive organs (fruits/seeds). Caspar Bauhin (1623): binomial designations; distinguished synonyms; Pinax Theatri Botanici. John Ray (1627-1705): species concept based on common descent; classified approximately 18,600 plants. Tournefort (1656-1708): strengthened genus concept; recognised approximately 698 genera.
13. Linnaeus reformed systematics through Systema Naturae (10th edition 1758; start of zoological nomenclature) and Species Plantarum (1753; start of botanical nomenclature). Five contributions: binomial nomenclature (Genus epithet consistently applied); hierarchical classification (class-order-genus-species); type specimens (name permanently attached to a reference specimen); formal diagnoses for each taxon; principle of priority (earliest valid name prevails). Sexual system: classified plants by stamen and pistil number; artificial but widely used for convenience; acknowledged by Linnaeus as not reflecting true relationships. Natural system: sought classification by overall resemblance; outlined Methodus Naturalis; never completed. New Systematics (Huxley 1940): synthesis of genetics, cytology, population biology; BSC (Mayr 1942); polytypic species; experimental methods. Modern: numerical taxonomy (Sokal/Sneath; overall similarity; multivariate statistics); cladistics (Hennig; synapomorphies; phylogenetic trees); molecular systematics (DNA sequences; overturned morphological classifications); DNA barcoding (CO1 gene; rapid identification; cryptic species).

Answers to Pilot Questions [Series 1]

Part 1.1

1. Systematics is the scientific study of the diversity of living organisms and their evolutionary relationships. Three activities: (1) taxonomy: naming and formally describing organisms; (2) classification: placing organisms into hierarchical named groups; (3) phylogenetics: inferring evolutionary relationships among organisms. Systematics is the broadest of these three and integrates all of them with the study of biodiversity patterns.
2. Systematics is the broadest science, studying organic diversity and evolutionary relationships, and it encompasses taxonomy, classification, nomenclature, and phylogenetics. Taxonomy is the theory and practice of naming and formally describing organisms and the taxa they belong to. Classification is the practical act of placing organisms into named hierarchical groups (taxa) based on their similarity or evolutionary relationships.
3. Four applications in Nigeria: (1) identifying crop pests (e.g. Striga hermonthica, witch weed on sorghum) and selecting effective biocontrol agents; (2) identifying medicinal plants to prevent toxic substitutions in Nigerian herbal medicine; (3) identifying disease vectors (Anopheles gambiae mosquitoes transmitting malaria; Glossina tsetse flies transmitting trypanosomiasis); (4) agricultural quarantine: determining whether an intercepted pest is a known species or a new invasive threat.
4. Systematics underpins all of biology because every biological science requires correctly identified and named organisms to function: a pharmacologist cannot develop a drug from an unnamed plant; an ecologist cannot publish repeatable results without correctly identified study organisms; a conservation biologist cannot target a specific threatened species without its correct name; a medical team cannot safely base a treatment on an organism identified only to generic level.
5. Nomenclature is the system of formal rules and procedures governing the naming of taxa; it specifies the grammatical form of names, which names are valid, how synonyms are handled, and how priority is determined. Its role within systematics: it ensures that each taxon has one universally accepted name, allowing scientists worldwide to communicate unambiguously about the same organism; without nomenclature, the same organism would accumulate different names in different countries and languages.

Part 1.2

1. Aristotle (384-322 BC) classified approximately 500 animal species using structural and functional criteria, dividing them into Enaima (animals with blood; roughly vertebrates) and Anaima (animals without blood; roughly invertebrates). He described developmental patterns, habitats, feeding behaviour, and reproductive modes. Although not hierarchical in the modern sense, his approach of grouping organisms by shared characters was the first systematic treatment of animal diversity and earned him the title of founder of zoology.
2. Theophrastus (371-287 BC) classified approximately 500 plant species in two major works: Historia Plantarum (Enquiry into Plants) and Causae Plantarum (The Causes of Plants). He divided plants into trees, shrubs, undershrubs, and herbs (a broadly useful classification). He described plant morphology, geographic distribution, ecology, and medicinal or agricultural uses. He is regarded as the father of botany, applying to plants the same observational approach Aristotle applied to animals.
3. Islamic scholars preserved and advanced the Greek botanical tradition during the European medieval period when natural history stagnated in Europe. Ibn Sina (Avicenna, 980-1037) described approximately 800 medicinal plants in the Canon of Medicine, a text that remained authoritative in European medicine until the 17th century. Ibn al-Baitar (1197-1248) described over 1,400 plant species in Compendium on Simple Medicaments, significantly expanding the known flora. Their work ensured the continuity of systematic knowledge across the medieval period.
4. Caspar Bauhin (1560-1624) made two key contributions that directly anticipated and influenced Linnaeus. First, he used a two-word (binomial) designation for species in his Pinax Theatri Botanici (1623), anticipating Linnaeus's systematic application of binomials by over 130 years; these designations were not yet consistently applied as a formal system but showed the value of concise two-word names. Second, he carefully identified and listed synonyms (different names given to the same plant by different earlier authors), reducing nomenclatural confusion and establishing the concept of synonymy that Linnaeus would formalise.
5. John Ray (1627-1705) proposed one of the most important pre-Linnaean species concepts: a species is a group of organisms that reproduce with each other and share a common origin from the same parents; offspring of the same parents always belong to the same species. This moved the species concept from pure morphological similarity toward biological reality. He classified approximately 18,600 plant species, using both vegetative and reproductive characters, and also described birds, fishes, and insects. His Historia Plantarum (1686-1704) was the most comprehensive botanical work before Linnaeus.

Part 1.3

1. Key publications: Systema Naturae (1735, first edition; 10th edition 1758 = starting point for zoological nomenclature; 12th edition 1768 final in his lifetime) classified animals, plants, and minerals in hierarchical categories. Species Plantarum (1753, two volumes) described approximately 7,700 plant species with consistent binomial names and is the starting point for botanical nomenclature. Genera Plantarum (1737) established the genus as the primary category. These publications provided the universal nomenclatural starting points that the international codes still reference.
2. Sexual system: classified flowering plants by the number and arrangement of stamens (male organs) and pistils (female organs); Class Monandria = one stamen; Diandria = two stamens; and so on. Advantage: easy to apply without specialist knowledge; allowed rapid identification from a single character set. Limitation: artificial (unrelated plants with the same stamen number were grouped together); did not reflect natural relationships. Natural system: aimed to group plants by overall resemblance across many characters reflecting true affinities; Linnaeus outlined it as Methodus Naturalis but never completed the work.
3. An artificial classification is based on one or a few arbitrarily chosen characters for convenience of identification (e.g. Linnaeus's sexual system grouping plants by stamen number); it does not aim to reflect natural relationships and may group unrelated organisms together. A natural classification groups organisms by their overall resemblance across many characters (phenetics) or by shared homologous characters reflecting common ancestry (cladistics); the goal is to produce groups that are predictive across many other characters and that reflect genuine biological relationships.
4. Five lasting contributions of Linnaeus: (1) Consistent application of binomial nomenclature: every known organism received a two-word Latin name (Genus epithet) used universally; (2) Hierarchical classification: a clear system of class-order-genus-species for all organisms; (3) Type specimens: each species name permanently attached to a reference specimen; (4) Formal diagnoses: standardised Latin descriptions defining each taxon; (5) Principle of priority: the earliest validly published name takes precedence, reducing the chaos of synonyms.
5. A type specimen is the single designated reference specimen to which a species name is permanently attached by the author who first described the species. When there is a dispute about what a species name refers to, the type specimen is the physical arbiter; the name applies to the

species to which the type specimen belongs, regardless of later disagreements about species boundaries. It ensures the stable application of names across time, across different workers, and across different taxonomic treatments, making it a cornerstone of nomenclatural stability.

Part 1.4

1. Before Darwin, the goal was to discover the "natural system" based on overall similarity, without understanding why such a system should exist. Darwin showed that organisms share characters because of common descent from shared ancestors; therefore a natural classification should reflect genealogy. Characters shared through common ancestry (homologies) became the correct basis for grouping; characters that evolved independently (analogies, convergences) should not group organisms. This changed the goal of classification from cataloguing similarity to reconstructing evolutionary history.
2. The New Systematics (Julian Huxley, 1940) was the synthesis of classical Linnaean taxonomy with genetics, cytology, population biology, and ecology. Two contributions: (1) it introduced the Biological Species Concept (Mayr, 1942; species defined by reproductive isolation), replacing the purely morphological species concept with a biologically meaningful criterion; (2) it recognised polytypic species and subspecies, acknowledging that species are not fixed types but variable populations showing geographic differentiation, which changed the way species boundaries were assessed and named.
3. Phenetics (numerical taxonomy; Sokal and Sneath, 1963): classifies organisms by overall similarity across many equally weighted characters using multivariate statistical methods; does not consider whether characters are ancestral or derived; produces phenograms; deliberately theory-free. Cladistics (Hennig, 1950/1966): classifies organisms strictly by shared derived characters (synapomorphies) inherited from common ancestors; explicitly reflects evolutionary history; only monophyletic groups (clades) are recognised as valid; produces cladograms; paraphyletic and polyphyletic groups are rejected.
4. Molecular systematics has transformed classification by providing an independent, objective data source (DNA sequences) that is not subject to the convergent evolution and morphological plasticity that misled morphological classifications. DNA comparisons have: revealed that many morphologically similar organisms are not closely related (cryptic diversity); shown that some morphologically disparate groups are closely related; overturned major traditional classifications

(e.g. the APG system of angiosperm classification, based on DNA, differs substantially from older morphological systems); and provided a molecular clock for estimating divergence times.

5. DNA barcoding uses a short standardised DNA sequence, most commonly the cytochrome oxidase subunit I (CO1) gene (~650 base pairs) for animals, or rbcL/matK for plants, to identify specimens by comparing their sequence to a reference library of known species. One application: rapid identification of insect pest species in agricultural quarantine, where morphological identification is difficult or requires specialist expertise; DNA barcoding allows a non-specialist to determine whether an intercepted insect is a known agricultural pest or a new invasive species within hours.

References and Attributions [Series 1]

Textual References (Books and External Sources)

- Judd, W. S., Campbell, C. S., Kellogg, E. A., Stevens, P. F., & Donoghue, M. J. (2008). Plant systematics: A phylogenetic approach (3rd ed.). Sinauer Associates.
- Stuessy, T. F. (2009). Plant taxonomy: The systematic evaluation of comparative data (2nd ed.). Columbia University Press.
- Mayr, E., & Ashlock, P. D. (1991). Principles of systematic zoology (2nd ed.). McGraw-Hill.
- FAO (Food and Agriculture Organization of the United Nations). (2025). Guidelines for sustainable agriculture. FAO.

Figures, Plates, Tables, and Boxes

- Figure 1.1: Relationships among systematics, taxonomy, classification, nomenclature, and phylogenetics Attribution: AI generated. Suggested OER search string: "systematics taxonomy classification nomenclature phylogenetics relationship diagram OER".
- Figure 1.2: Timeline of pre-Linnaean contributions to systematics Attribution: AI generated. Suggested OER search string: "pre-Linnaean systematics timeline Aristotle Theophrastus Cesalpino Bauhin John Ray Tournefort OER".

- Figure 1.3: Portrait and key publications of Carl Linnaeus Attribution: AI generated or open-access portraits. Suggested OER search string: "Carl Linnaeus portrait Systema Naturae Species Plantarum title page publications OER".
- Box 1.1: Summary table of the three major eras of systematic biology Attribution: AI generated. Suggested OER search string: "history systematics eras pre-Linnaean Linnaean Darwinian modern contributions table OER box".

Course code: BIO 306

Course title: Systematic Biology

Series 2: Taxonomic Hierarchies and Species Concepts

- **Part 2.1: The Taxonomic Hierarchy**
    - Sub Part 2.1.1: Major taxonomic categories
    - Sub Part 2.1.2: Categories above species
    - Sub Part 2.1.3: Categories below species
- **Part 2.2: The Species Concept**
    - Sub Part 2.2.1: The typological (morphological) species concept
    - Sub Part 2.2.2: The Biological Species Concept
    - Sub Part 2.2.3: Alternative species concepts
- **Part 2.3: Practical Application of the Hierarchy**
    - Sub Part 2.3.1: Placing organisms in the hierarchy
    - Sub Part 2.3.2: Characters used to define taxonomic categories
    - Sub Part 2.3.3: Monophyletic, paraphyletic, and polyphyletic groups
- **Part 2.4: Species in Practice**
    - Sub Part 2.4.1: Recognising and delimiting species
    - Sub Part 2.4.2: Cryptic species and species complexes
    - Sub Part 2.4.3: The species problem in Nigerian biodiversity

Introduction

The taxonomic hierarchy is the framework within which all organisms are organised, named, and communicated about. Understanding the ranks, their definitions, and the criteria used to assign organisms to them is fundamental to systematic biology. Equally important is understanding what a "species" means, since the species is the basic unit of classification and the level at which most biological work is conducted.

This Series covers the principal taxonomic categories from subspecies to domain, the major species concepts and their strengths and limitations, the practical application of hierarchical classification, and the real-world challenges of species delimitation in Nigeria. It builds directly on the historical foundations covered in Series 1 and prepares the ground for nomenclature (Series 3) and advanced systematics (Series 4).

Series Learning Outcomes

Upon completing this Series, you should be able to:

- **SLO 2.1** list and define the principal taxonomic categories from subspecies to domain and give examples (Linked to Part 2.1),
- **SLO 2.2** describe the categories above species (genus, family, order, class, phylum, kingdom, domain) and the criteria used to delimit them (Linked to Part 2.1),
- **SLO 2.3** describe the categories below species (subspecies, variety, form) and explain their significance (Linked to Part 2.1),
- **SLO 2.4** compare the major species concepts and evaluate their strengths and limitations (Linked to Part 2.2),
- **SLO 2.5** explain monophyletic, paraphyletic, and polyphyletic groups and state which is valid in cladistic classification (Linked to Part 2.3), and
- **SLO 2.6** describe the challenges of species delimitation in practice, including cryptic species (Linked to Part 2.4).

2.1 The Taxonomic Hierarchy

2.1.1 Major taxonomic categories

The taxonomic hierarchy organises all known organisms into a series of nested groups of increasing inclusiveness. The principal obligatory ranks are (from least to most inclusive): Species, Genus, Family, Order, Class, Phylum (Division in plants and fungi), Kingdom, and Domain. Each rank is defined by shared characters; all members of a taxon at a given rank share the characters that define that taxon, plus all characters shared at higher ranks.

The hierarchy is a natural consequence of the evolutionary process: species that share a more recent common ancestor share more characters and are grouped at a lower rank; species with a more distant common ancestor share fewer characters and are separated at a higher rank. Additional intermediate ranks (subgenus, subfamily, suborder, superorder, subclass, etc.) are used when the diversity within a rank is too great to be organised satisfactorily at the principal ranks alone.

Fill in the blank: The principal obligatory taxonomic ranks from least to most inclusive are: species, genus, family, order, class, ________, kingdom, and domain; additional intermediate ranks may be used when diversity within a rank is too great.

2.1.2 Categories above species

Genus (plural genera): groups closely related species sharing a common ancestor and a diagnostic character combination; the first part of the binomial name; e.g. Panthera (lions, leopards, tigers, jaguars). Family: groups related genera; name ends in -aceae (plants), -idae (animals), or -aceae (fungi); e.g. Fabaceae (legumes), Felidae (cats). Order: groups related families; e.g. Fabales (legumes and relatives), Carnivora (carnivores). Class: groups related orders; e.g. Mammalia, Magnoliopsida.

Phylum (Division in plants): groups related classes; e.g. Chordata (vertebrates and relatives), Magnoliophyta (angiosperms). Kingdom: traditionally five kingdoms (Monera, Protista, Fungi, Plantae, Animalia); replaced by the three-domain system in modern classification. Domain: the highest rank; three domains recognised (Bacteria, Archaea, Eukarya) based on ribosomal RNA analysis by Carl Woese (1977). The domain Eukarya includes Kingdoms Animalia, Plantae, Fungi, and Protista.

Fill in the blank: The three-domain system of Carl ________ (1977) is based on ribosomal RNA analysis; the three domains are Bacteria, Archaea, and Eukarya; Domain Eukarya includes Kingdoms Animalia, Plantae, Fungi, and Protista.

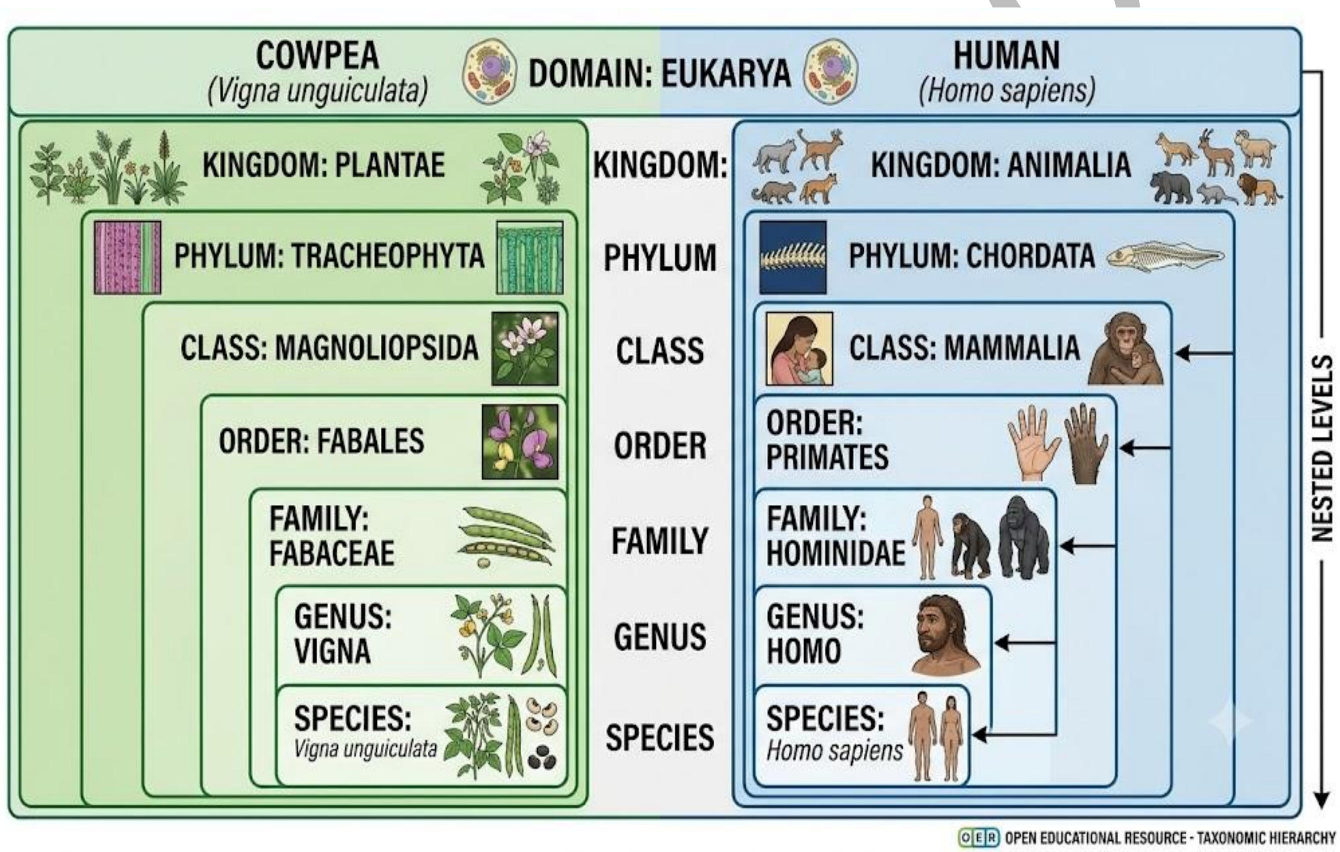


Figure 2.1: Diagram of the taxonomic hierarchy illustrated with a Nigerian organism

2.1.3 Categories below species

Subspecies: the principal infraspecific rank; a geographically defined population within a species that differs consistently in one or more characters from other populations of the same species; it has a trinomial name (Genus species subspecies); e.g. Pan troglodytes ellioti (Nigeria-Cameroon chimpanzee), a subspecies of the common chimpanzee Pan troglodytes. Subspecies intergrade with other subspecies where their ranges meet and can potentially interbreed.

Variety (varietas) and form (forma): botanical infraspecific ranks used below subspecies; variety refers to a population differing in one or a few characters, often within a continuous range; form is the lowest rank, referring to individual variants within a population (e.g. a colour form). In zoology, subspecies is the only formally recognised infraspecific rank; variety and form are not used. Cultivar: a cultivated variety maintained by human selection; not a formal botanical rank under the International Code but governed by the International Code of Nomenclature for Cultivated Plants.

Fill in the blank: A ________ is a geographically defined population within a species that differs consistently in one or more characters from other populations of the same species; it has a trinomial name and is the principal infraspecific rank in both botany and zoology.

Pilot questions 2.1

1. List the eight principal obligatory taxonomic ranks from least to most inclusive.
2. Define genus and family and give one Nigerian example of each.
3. State the three domains and explain the basis for the three-domain system.
4. Define subspecies and distinguish it from variety and form.
5. Give the full taxonomic classification of the cowpea (Vigna unguiculata) from species to domain.

2.2 The Species Concept

2.2.1 The typological (morphological) species concept

The typological or morphological species concept defines a species as a group of organisms that share a distinctive morphological appearance (the "type") and differ from other species by a diagnostic combination of morphological characters. It is the oldest species concept and the one applied by Linnaeus. It is still the most widely used in practice because: it can be applied to asexual organisms (bacteria, many protists); it is applicable to fossils; and it does not require knowledge of reproduction or genetics.

Limitations of the typological concept: (1) it is subjective (experts disagree on which characters are diagnostic and how much variation is tolerable within one species); (2) it misses cryptic species (morphologically identical but genetically and reproductively distinct species); (3) high intraspecific morphological variation (sexual dimorphism, polymorphism, age variation, geographic variation) can lead to splitting one biological species into multiple morphospecies; (4) convergent evolution can lead to grouping unrelated organisms as one morphospecies.

Fill in the blank: The ________ species concept defines a species by its diagnostic morphological appearance; it is the most widely used concept in practice because it can be applied to asexual organisms, fossils, and organisms for which reproductive data are unavailable.

2.2.2 The Biological Species Concept

The Biological Species Concept (BSC), proposed by Ernst Mayr in 1942, defines a species as a group of actually or potentially interbreeding natural populations that are reproductively isolated from other such groups. It emphasises reproductive compatibility and isolation as the defining criterion, providing a biological mechanism (gene pool integrity) for species distinctness. It is the most widely used concept in animal systematics and has strongly influenced speciation theory.

Strengths of the BSC: provides a clear, testable criterion (can two populations interbreed and produce fertile offspring?); explains the discreteness of species in sexually reproducing animals; links species concept to evolutionary mechanism (gene flow maintains cohesion; reproductive isolation allows divergence). Limitations: cannot be applied to asexual organisms, fossils, or purely allopatric populations that have never been tested; hybridisation between recognised species is common in plants, challenging the strict isolation criterion.

Fill in the blank: The Biological Species Concept (Mayr, 1942) defines a species as a group of interbreeding natural populations that are reproductively ________ from other such groups; its main limitation is that it cannot be applied to asexual organisms or fossils.

2.2.3 Alternative species concepts

Phylogenetic Species Concept (PSC; Cracraft, 1983): defines a species as the smallest monophyletic group of organisms diagnosable by at least one unique shared derived character (synapomorphy). It is widely used in modern molecular systematics because it provides an objective, operationalised criterion. A limitation: it tends to recognise more species than the BSC (fine-scale phylogenetic units may be recognised as species even if they interbreed with adjacent populations).

Ecological Species Concept (Van Valen, 1976): a species occupies a distinct adaptive zone (niche) and evolves separately from other species because of ecological differentiation. Cohesion Species Concept (Templeton, 1989): the most inclusive population sharing genetic and demographic cohesion. Recognition Species Concept (Paterson, 1985): species defined by a shared fertilisation system (specific mate recognition system, SMRS). In practice, taxonomists apply a pluralistic approach, choosing the concept most appropriate for the organisms and questions being addressed.

Fill in the blank: The ________ Species Concept (Cracraft, 1983) defines a species as the smallest monophyletic group diagnosable by at least one unique shared derived character; it tends to recognise more species than the Biological Species Concept.

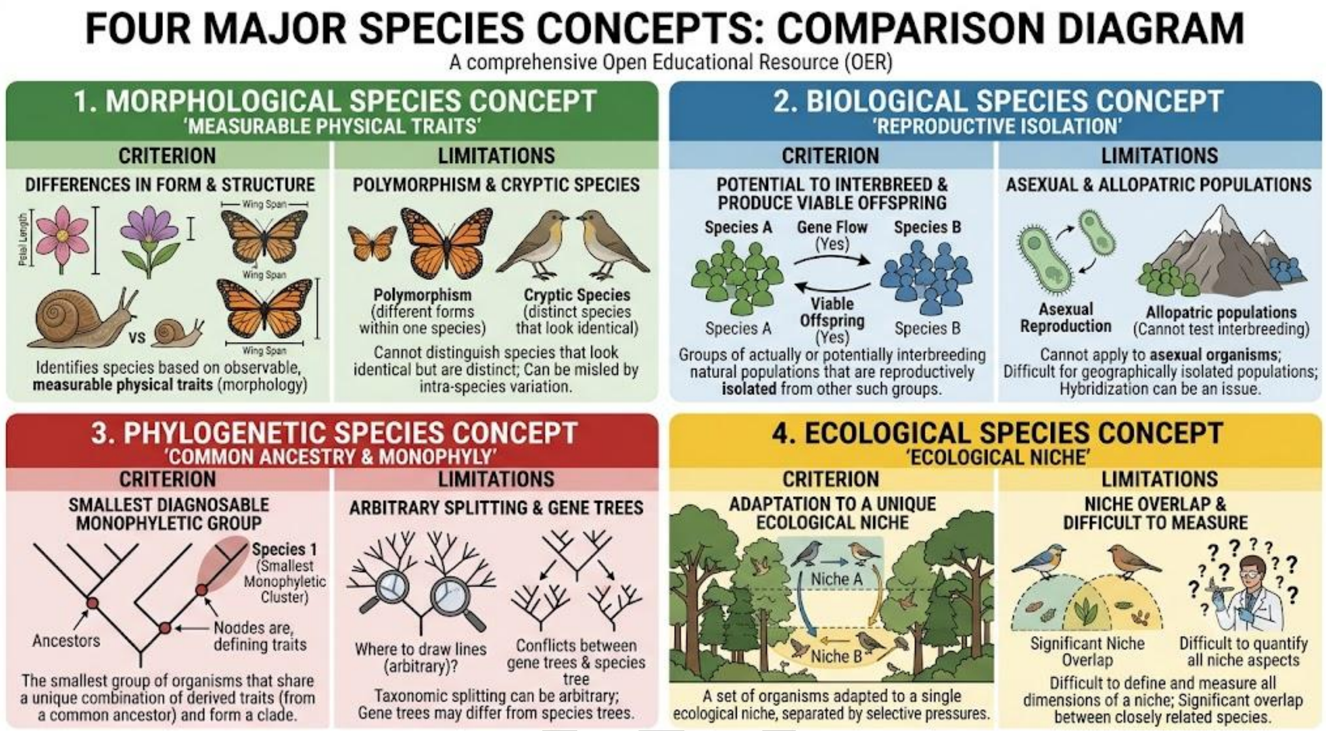


Figure 2.2: Diagram comparing four major species concepts

Pilot questions 2.2

1. Define the Typological Species Concept and state two limitations.
2. State the Biological Species Concept and give two strengths and two limitations.
3. Define the Phylogenetic Species Concept and explain how it differs from the BSC.
4. Explain why no single species concept is universally applicable.
5. Explain what is meant by a pluralistic approach to species concepts.

2.3 Practical Application of the Hierarchy

2.3.1 Placing organisms in the hierarchy

To place an organism in the taxonomic hierarchy, a taxonomist: (1) observes and describes the morphological, anatomical, and molecular characters of the specimen; (2) compares these characters with published descriptions of known taxa at each rank; (3) determines which existing taxon the specimen belongs to, or whether it represents a new taxon requiring description; (4) assigns the specimen to the appropriate rank at each level of the hierarchy. The hierarchy is applied top-down in identification: first determine kingdom, then phylum, then class, and so on down to species.

Herbaria and natural history museums are essential resources for this process: they hold type specimens and reference collections against which new specimens are compared. The Nigerian national herbarium (Federal Herbarium, Ibadan) and the University of Lagos and University of Ibadan herbaria hold important collections of Nigerian plant species. The Federal College of Forestry, Ibadan, and the Nigerian Institute for Oceanography and Marine Research (NIOMR) maintain collections of forestry specimens and marine organisms respectively.

Fill in the blank: Herbaria and natural history museums hold ________ specimens and reference collections that are essential for comparing new specimens and correctly placing them within the taxonomic hierarchy.

2.3.2 Characters used to define taxonomic categories

At the species level: morphological characters (size, shape, colour, texture, surface features); anatomical characters (internal structure, venation, cell shape); molecular characters (DNA sequences, allele frequencies); reproductive characters (pollen morphology, floral structure, mating behaviour). At genus level: combinations of morphological and anatomical characters shared by all members; typically the same type of characters used at species level but of broader diagnostic value.

At family level and above: major morphological innovations (e.g. the presence of latex in Euphorbiaceae; the characteristic inflorescence of Asteraceae); biochemical characters (alkaloid classes, secondary metabolite profiles); molecular phylogenetic data. At domain and kingdom level: fundamental cell organisation (prokaryote vs eukaryote; cell wall composition; ribosomal RNA structure). A general principle: the higher the rank, the more fundamental and deeply conserved the defining characters must be, reflecting shared ancestry at deeper nodes of the evolutionary tree.

Fill in the blank: The higher the taxonomic rank, the more fundamental and deeply ________ the defining characters must be, reflecting shared ancestry at progressively deeper nodes of the evolutionary tree.

2.3.3 Monophyletic, paraphyletic, and polyphyletic groups

A monophyletic group (clade) comprises an ancestor and all of its descendants; all members share a synapomorphy (shared derived character) inherited from their common ancestor. Example: Class Mammalia (all mammals and only mammals, descended from the last common mammalian ancestor). Monophyletic groups are the only valid groups in cladistic classification. Cladistic taxonomy requires that every formal taxon be monophyletic.

A paraphyletic group includes an ancestor and some but not all of its descendants; one or more descendant lineages are excluded. Example: "Reptilia" as traditionally defined excludes birds, which are also descendants of the reptilian ancestor; this makes traditional Reptilia paraphyletic. A polyphyletic group includes members that do not share their most recent common ancestor; the shared character arose by convergent evolution. Example: "warm-blooded vertebrates" grouping birds and mammals, which evolved endothermy independently. Both paraphyletic and polyphyletic groups are invalid in cladistic classification.

Fill in the blank: A ________ group comprises an ancestor and all of its descendants; it is the only type of group accepted as valid in cladistic classification; paraphyletic and polyphyletic groups are rejected because they do not accurately reflect evolutionary history.

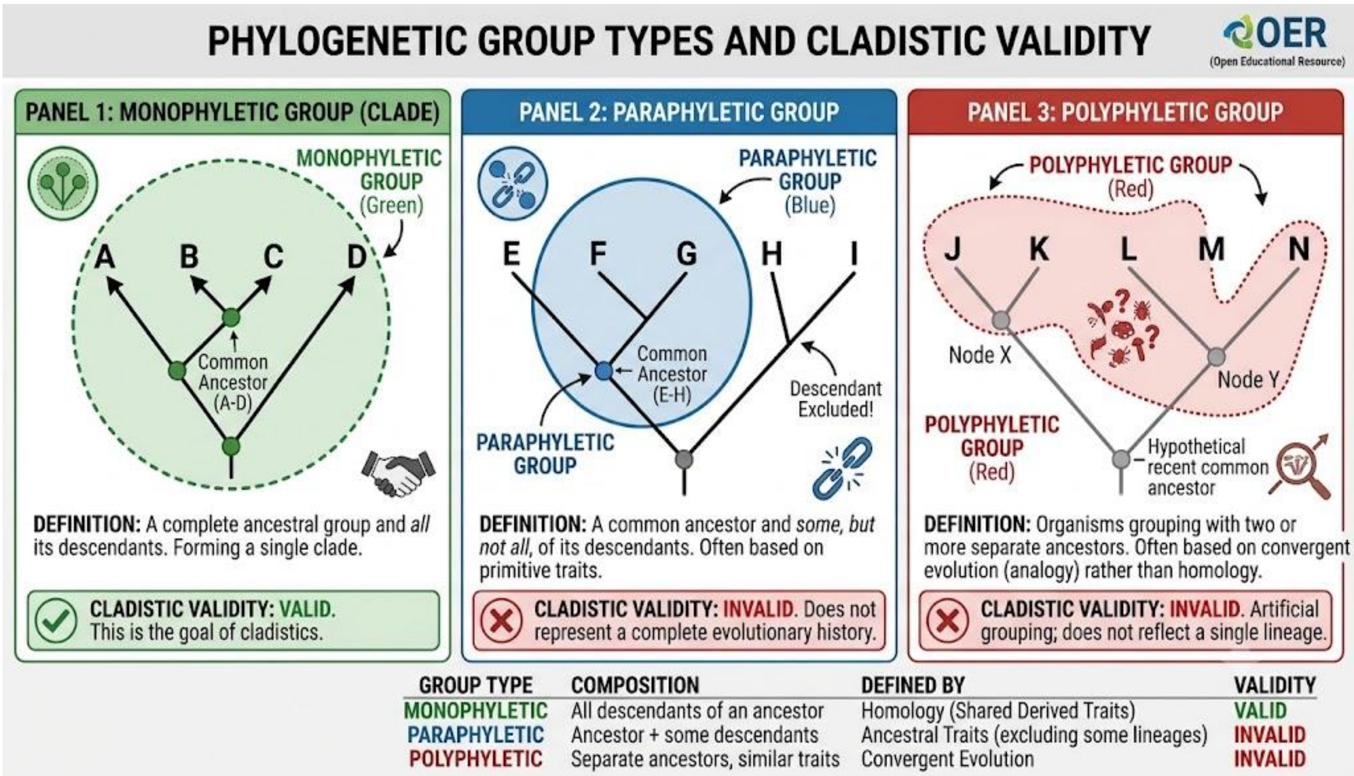


Figure 2.3: Cladogram illustrating monophyletic, paraphyletic, and polyphyletic groups

Pilot questions 2.3

1. Describe the procedure for placing an organism in the taxonomic hierarchy.
2. State four types of characters used to distinguish species.
3. Explain why characters used at higher taxonomic ranks must be more fundamental.
4. Define monophyletic group and explain why it is the only valid group in cladistics.
5. Distinguish between paraphyletic and polyphyletic groups with one example each.

2.4 Species in Practice

2.4.1 Recognising and delimiting species

Species delimitation is the process of determining the boundaries between species: deciding whether two populations represent one or two species. Three approaches are commonly used. Morphological approach: compare specimens against described species; if they fall outside the known range of variation of any described species, they may represent a new species. Biological approach: test whether two populations interbreed under natural conditions; reproductive isolation confirms species status under the BSC.

Molecular approach: compare DNA sequences (typically a molecular barcode or multi-locus dataset); populations separated by a threshold level of divergence (often 2-3% for CO1 in animals) and showing reciprocal monophyly in a gene tree may be recognised as distinct species. Integrative taxonomy: combines morphological, molecular, ecological, and behavioural data; this approach is now standard for formal species descriptions in leading journals. New species descriptions in Nigeria increasingly require both morphological and molecular evidence to be accepted for publication.

Fill in the blank: ________ taxonomy combines morphological, molecular, ecological, and behavioural data to delimit species; it is now the standard approach required by leading systematic journals for new species descriptions.

2.4.2 Cryptic species and species complexes

Cryptic species are two or more morphologically indistinguishable species that are genetically and reproductively distinct. They are discovered when molecular data reveal deep genetic divergence within what was considered a single species. Examples relevant to Nigeria: the Anopheles gambiae complex (at least seven morphologically identical mosquito species, some of which differ significantly in their capacity to transmit malaria); the Simulium damnosum complex (blackflies transmitting onchocerciasis/river blindness; multiple cryptic species with different vector competence).

A species complex is a group of closely related species that are difficult to distinguish morphologically and may hybridise; the boundaries between them are difficult to determine. Recognising cryptic species and species complexes has direct practical consequences in Nigeria: different cryptic species within the Anopheles gambiae complex have different insecticide resistance profiles and different abilities to transmit Plasmodium falciparum; treating them as a single species leads to ineffective malaria control strategies. Molecular identification tools (PCR-based assays, DNA barcoding) are now used to distinguish them in the field.

Fill in the blank: The Anopheles gambiae ________ comprises at least seven morphologically identical mosquito species with different abilities to transmit malaria; recognising these cryptic species is essential for effective malaria control in Nigeria.

2.4.3 The species problem in Nigerian biodiversity

Nigeria is estimated to support over 7,000 plant species, approximately 1,000 bird species, 274 mammal species, and thousands of invertebrate species, but large proportions remain poorly known. The "species problem" in Nigeria has several dimensions: (1) many species have not been formally described (especially invertebrates, fungi, microorganisms); (2) many existing species descriptions are outdated, based on inadequate material, or need revision using modern molecular methods; (3) taxonomic expertise is scarce and concentrated in a few universities and herbaria.

Under-description of Nigerian biodiversity has practical consequences: conservation assessments (IUCN Red List) cannot be made for undescribed species; ecosystem services cannot be attributed to unknown organisms; the full economic value of Nigeria's biodiversity (including potential pharmaceutical and agricultural resources) cannot be assessed. Investment in systematic biology, molecular facilities, and training of Nigerian taxonomists is therefore both a scientific and a development priority. Citizen science platforms (iNaturalist, GBIF) are increasingly used to generate occurrence records but require expert verification.

Fill in the blank: Nigeria's estimated 7,000+ plant species and thousands of invertebrate species are under-described; under-description means that ________ assessments (IUCN Red List) cannot be made for unknown species and ecosystem services cannot be attributed to organisms that have not been formally named.

Species Concept	**Defining Criterion**	**Applicability to Asexuals**	**Applicability to Fossils**	**Lump or Split Tendency**
Biological	Interbreeding populations	Not applicable	Not applicable (cannot test	Tends to lump

	reproductively isolated from others	(requires sexual reproduction)	reproductive isolation in fossils)	(focuses on reproductive cohesion)
Morphological/Typological	Shared physical traits and diagnostic morphology	Applicable (based on observable traits)	Applicable (fossil morphology)	Tends to lump if traits are broad, split if traits are narrowly defined
Phylogenetic	Smallest diagnosable monophyletic lineage	Applicable (DNA or morphology)	Applicable (fossil morphology, cladistics)	Tends to split (recognizes fine-scale lineages)
Ecological	Occupation of distinct ecological niche	Applicable (sexual and asexual)	Limited (hard to infer niche from fossils)	Variable, often splits based on niche differences
Cohesion	Genetic and ecological exchangeability	Applicable (sexual and asexual)	Limited (requires genetic/ecological data)	Tends to lump (emphasizes cohesion mechanisms)
Recognition	Shared mate recognition system	Not applicable to asexuals	Not applicable to fossils	Tends to lump (focuses on common

				recognition cues)

Box 2.1: Summary of major species concepts and their applicability

Pilot questions 2.4

1. Describe two approaches used to delimit species.
2. Define integrative taxonomy and explain why it is now the standard.
3. Define cryptic species and give one Nigerian example with its practical significance.
4. Explain what a species complex is and give one example.
5. Describe two consequences of under-description of Nigerian biodiversity.

Series Summary

This Series examined the hierarchical organisation of biological classification, tracing the eight obligatory taxonomic ranks from species through genus, family, order, class, phylum, kingdom, and domain, and exploring the categories recognised both above and below the species level. The three domains of life established by Woese in 1977 on the basis of ribosomal RNA sequencing were examined alongside traditional kingdom-level classification, and infraspecific categories including subspecies, variety, form, and cultivar were defined with attention to their differential use in zoological and botanical nomenclature.

The major species concepts were compared across their key criteria and limitations: the typological concept relies on diagnostic morphological characters but misses cryptic species; the biological concept of Mayr captures reproductive isolation but fails for asexual organisms and fossils; the phylogenetic concept of Cracraft is objective but tends to multiply species; and the ecological and recognition concepts offer complementary perspectives grounded in adaptive zone and mate recognition respectively. The distinction between monophyletic, paraphyletic, and polyphyletic groupings was established as the basis of valid cladistic classification, and the significance of cryptic species complexes including *Anopheles gambiae* and *Simulium* *damnosum* for vector control and insecticide resistance in Nigeria was used to illustrate the practical consequences of under-described biodiversity.

Glossary of Terms

- **Adaptive zone:** the ecological niche or range of resources and conditions that a species exploits; the basis of the Ecological Species Concept.
- **Biological Species Concept (BSC):** Mayr's (1942) definition of a species as a group of interbreeding natural populations reproductively isolated from other such groups.
- **Clade:** a monophyletic group comprising an ancestor and all of its descendants; the fundamental unit of cladistic classification.
- **Cryptic species:** two or more morphologically indistinguishable but genetically and reproductively distinct species, revealed by molecular or reproductive data.
- **Cultivar:** a cultivated variety of a plant maintained by human selection; governed by the International Code of Nomenclature for Cultivated Plants, not by the botanical code.
- **Division (Divisio):** the equivalent of Phylum in botanical and fungal classification; used instead of Phylum in the plant and fungal kingdoms.
- **Domain:** the highest rank in the taxonomic hierarchy; three domains are currently recognised (Bacteria, Archaea, Eukarya) based on ribosomal RNA data.
- **Ecological Species Concept:** Van Valen's (1976) concept defining a species as a lineage occupying a distinct adaptive zone and evolving separately from other lineages through ecological differentiation.
- **Family:** a taxonomic rank above genus and below order; animal family names end in -idae; plant family names end in -aceae.
- **Form (forma):** the lowest formal botanical rank below subspecies and variety; refers to individual variants within a population (e.g. a colour variant).

- **Herbarium:** a collection of preserved plant specimens used as reference material for taxonomic identification and comparison; the national herbarium of Nigeria is located in Ibadan.
- **Integrative taxonomy:** the combination of morphological, molecular, ecological, and behavioural data to delimit and describe species; now the standard approach in systematic biology.
- **Monophyletic group:** a group comprising an ancestor and all of its descendants; defined by one or more synapomorphies; the only type of group recognised as valid in cladistic classification.
- **Paraphyletic group:** a group that includes an ancestor and some but not all of its descendants; invalid in cladistic classification; e.g. traditional "Reptilia" excluding birds.
- **Phylum (plural: phyla):** a major taxonomic rank above class and below kingdom; in plants and fungi, the equivalent rank is called Division.
- **Phylogenetic Species Concept (PSC):** Cracraft's (1983) definition of a species as the smallest diagnosable monophyletic group of organisms sharing at least one unique synapomorphy.
- **Polyphyletic group:** a group whose members share a character that evolved independently (convergent evolution) rather than from a common ancestor; invalid in cladistic classification.
- **Species complex:** a group of closely related species with overlapping or difficult-to-distinguish morphologies, often partially interfertile; a challenge for species delimitation.
- **Species delimitation:** the process of determining the boundaries between species using morphological, molecular, reproductive, or ecological evidence.
- **Subspecies:** the principal infraspecific rank; a geographically defined population differing consistently in one or more characters from other populations of the same species; uses a trinomial name.

- **Synapomorphy:** a shared derived character inherited from a common ancestor; used to define monophyletic groups in cladistic classification.
- **Typological (Morphological) Species Concept:** the oldest species concept; defines a species by its diagnostic morphological appearance (the "type"); still the most widely used in practice.
- **Variety (varietas):** a botanical infraspecific rank below subspecies; refers to a population differing in a few characters, sometimes throughout the range of the species.

Concept Check Questions [Series 2]

Objective Questions

1. The three-domain system of Carl ________ (1977) is based on ribosomal RNA analysis; the three domains are Bacteria, Archaea, and Eukarya. (Linked to SLO 2.2)
2. A ________ is a geographically defined population within a species that differs consistently in one or more characters from other populations; it has a trinomial name. (Linked to SLO 2.3)
3. The Biological Species Concept (Mayr, 1942) defines a species as a group of interbreeding natural populations that are reproductively ________ from other such groups. (Linked to SLO 2.4)
4. A ________ group comprises an ancestor and all of its descendants; it is the only type of group accepted as valid in cladistic classification. (Linked to SLO 2.5)
5. The Anopheles gambiae ________ comprises at least seven cryptic mosquito species with different abilities to transmit malaria; recognising them is essential for effective malaria control. (Linked to SLO 2.6)

Short-Answer Questions

6. List the eight principal taxonomic ranks from species to domain. (Linked to SLO 2.1)
7. State two strengths and two limitations of the Biological Species Concept. (Linked to SLO 2.4)

8. Distinguish between paraphyletic and polyphyletic groups with one example each. (Linked to SLO 2.5)
9. Define cryptic species and explain their significance in malaria control in Nigeria. (Linked to SLO 2.6)
10. Define integrative taxonomy. (Linked to SLO 2.6)

Long-Answer Questions

11. Describe the taxonomic hierarchy from species to domain; define each principal rank; and give the complete classification of one Nigerian plant and one Nigerian animal. (Linked to SLOs 2.1, 2.2, 2.3)
12. Compare and contrast the Typological, Biological, and Phylogenetic Species Concepts, stating the defining criterion, strengths, and limitations of each. (Linked to SLO 2.4)
13. Explain monophyletic, paraphyletic, and polyphyletic groups; describe the challenges of species delimitation in Nigeria; and explain the significance of cryptic species for disease control. (Linked to SLOs 2.5, 2.6)

Answers to Concept Check Questions [Series 2]

Objective Questions

1. Woese.
2. Subspecies.
3. Isolated.
4. Monophyletic.
5. Complex.

Short-Answer Questions

6. Species, genus, family, order, class, phylum (division), kingdom, domain.
7. Strengths: provides a clear, testable criterion (interbreeding and reproductive isolation); explains the discreteness of animal species. Limitations: cannot apply to asexual organisms or fossils; hybridisation in plants makes strict reproductive isolation difficult to apply.
8. Paraphyletic: includes an ancestor and some but not all descendants; e.g. "Reptilia" excluding birds (invalid in cladistics). Polyphyletic: members share a convergent

character, not from the most recent common ancestor; e.g. "warm-blooded vertebrates" grouping birds and mammals (invalid).

9. Cryptic species are morphologically indistinguishable but genetically and reproductively distinct species. In Nigeria, the Anopheles gambiae complex contains multiple cryptic species with different insecticide resistance profiles and different capacities to transmit Plasmodium falciparum; treating them as one species leads to ineffective malaria control.
10. Integrative taxonomy combines morphological, molecular, ecological, and behavioural data to delimit and formally describe species; it is now the standard approach required by leading systematic journals.

Long-Answer Questions

11. Hierarchy (least to most inclusive): species (smallest obligatory rank; basic unit of classification); genus (groups related species sharing diagnostic characters and common ancestry; first part of binomial); family (groups related genera; -aceae in plants; -idae in animals); order (groups related families); class (groups related orders); phylum/division (groups related classes); kingdom (groups related phyla; traditionally five; now within three domains); domain (highest rank; Bacteria, Archaea, Eukarya; based on rRNA; Woese 1977). Nigerian plant example: cowpea (Domain Eukarya, Kingdom Plantae, Division Magnoliophyta, Class Magnoliopsida, Order Fabales, Family Fabaceae, Genus Vigna, Species Vigna unguiculata). Nigerian animal example: human (Domain Eukarya, Kingdom Animalia, Phylum Chordata, Class Mammalia, Order Primates, Family Hominidae, Genus Homo, Species Homo sapiens).
12. Typological/Morphological: criterion = diagnostic morphological appearance; strength = applicable to all organisms (asexual, fossils); limitation = subjective and misses cryptic species. Biological (Mayr 1942): criterion = reproductive isolation between natural populations; strength = objective biological criterion; reflects gene pool integrity; limitation = inapplicable to asexual organisms and fossils; fails where hybridisation is common (plants). Phylogenetic (Cracraft 1983): criterion = smallest diagnosable monophyletic unit with at least one synapomorphy; strength = objective; applicable to all organisms including asexual and fossil; limitation = tends to split species (recognises finer units than BSC), inflating species counts.

13. Monophyletic group: ancestor and all its descendants; defined by shared synapomorphies; only valid group in cladistic classification; e.g. Mammalia. Paraphyletic: ancestor and some descendants (others excluded); invalid in cladistics; e.g. traditional Reptilia excluding birds; Dicotyledonae excluding monocots. Polyphyletic: members share a convergent character not from the most recent common ancestor; invalid; e.g. warm-blooded vertebrates. Nigerian species delimitation challenges: approximately 7,000 plant species estimated but many undescribed; inadequate taxonomic expertise; outdated descriptions; need for molecular facilities. Cryptic species significance: Anopheles gambiae complex (seven+ cryptic species; different insecticide resistance; different Plasmodium transmission efficiency); Simulium damnosum complex (multiple blackfly species transmitting onchocerciasis); without correct identification, vector control programmes target the wrong species or use wrong insecticides, reducing effectiveness and wasting resources.

Answers to Pilot Questions [Series 2]

Part 2.1

1. Eight principal obligatory ranks, from least to most inclusive: (1) Species; (2) Genus; (3) Family; (4) Order; (5) Class; (6) Phylum (or Division in plants and fungi); (7) Kingdom; (8) Domain.
2. Genus: a taxonomic rank above species that groups related species sharing common ancestry and a diagnostic combination of characters; it is the first part of the binomial name. Nigerian example: Vigna (cowpea and related species). Family: a rank above genus grouping related genera; animal family names end in -idae; plant family names end in -aceae. Nigerian example: Fabaceae (legume family; includes cowpea, groundnut, soyabean).
3. The three domains are Bacteria (prokaryotes lacking a nuclear membrane; single circular chromosome; most known bacteria), Archaea (prokaryotes often found in extreme environments; different cell wall chemistry from Bacteria; more closely related to eukaryotes than to Bacteria), and Eukarya (organisms with a membrane-bound nucleus; includes all plants, animals, fungi, and protists). The system is based on Carl Woese's

(1977) analysis of 16S and 18S ribosomal RNA sequences, which showed that Archaea are as distinct from Bacteria as they are from Eukarya, warranting a rank above kingdom.

4. A subspecies is a geographically defined and genetically distinctive population within a species that differs consistently in one or more characters from other populations of the same species; it is named with a trinomial (three-word) name and can intergrade with other subspecies where ranges meet. Variety (varietas) is a botanical infraspecific rank used for populations differing in a few characters, sometimes scattered across the species range rather than geographically cohesive. Form (forma) is the lowest botanical rank, referring to individual variants within a population (e.g. a white-flowered individual in a normally purple-flowered species). Variety and form are not used in zoological nomenclature.
5. Cowpea full classification: Domain Eukarya; Kingdom Plantae; Division Magnoliophyta (flowering plants/angiosperms); Class Magnoliopsida (dicotyledons); Order Fabales; Family Fabaceae (legume family); Genus Vigna; Species Vigna unguiculata (L.) Walp.

Part 2.2

1. The Typological (Morphological) Species Concept defines a species as a group of organisms sharing a diagnostic morphological appearance that distinguishes them from all other species; species are identified by their match to a type specimen or published description. Two limitations: (1) it is subjective because different taxonomists may disagree on which morphological characters are diagnostic and how much variation is acceptable within a single species; (2) it misses cryptic species, which are morphologically indistinguishable but genetically and reproductively distinct, leading to under-recognition of true biodiversity.
2. BSC definition: a species is a group of actually or potentially interbreeding natural populations that are reproductively isolated from other such groups (Mayr, 1942). Two strengths: (1) provides a biologically meaningful, testable criterion based on gene flow and reproductive isolation; (2) explains why species appear as discrete units in nature (gene flow maintains cohesion within species; isolation allows divergence between

species). Two limitations: (1) cannot be applied to asexual organisms (bacteria, many protists, apomictic plants) or fossils because reproductive compatibility cannot be tested; (2) hybridisation between recognised species is common in plants and some animals, making clean reproductive isolation difficult to establish.

3. Phylogenetic Species Concept (PSC; Cracraft, 1983): defines a species as the smallest monophyletic group of organisms that is diagnosable by at least one unique shared derived character (synapomorphy). Differences from BSC: (1) the PSC can be applied to asexual organisms and fossils because it requires only shared derived characters, not reproductive compatibility; (2) the PSC tends to recognise finer units as species than the BSC, often splitting what the BSC would treat as one variable species into several phylogenetic species based on minor genetic or morphological differences; (3) the PSC does not require reproductive isolation as a criterion, only diagnosable monophyly.
4. No single species concept is universally applicable because different groups of organisms present different challenges: bacteria and other asexual organisms cannot be assessed using the BSC; fossils cannot be tested for reproductive compatibility under the BSC or for ecological differentiation under the Ecological Species Concept; plant hybridisation makes clean reproductive isolation rare; morphologically identical cryptic species require molecular or reproductive data to distinguish. Each concept was designed to address particular biological realities, so taxonomists use the concept most appropriate for the organisms and questions in hand.
5. A pluralistic approach to species concepts means that rather than insisting on one universally valid species concept, taxonomists select and apply the concept or combination of concepts most appropriate for the particular organisms, data, and questions being studied. A botanist working with polyploid plant complexes may use a combination of the Biological and Phylogenetic Species Concepts; a bacteriologist cannot apply the BSC and uses molecular criteria; a palaeontologist is restricted to morphological and phylogenetic criteria. Integrative taxonomy formalises the pluralistic approach by combining multiple data types to reach the best-supported species delimitation.

Part 2.3

1. Procedure for placing an organism in the hierarchy: (1) collect and preserve a specimen with associated data (locality, habitat, date, collector); (2) examine morphological, anatomical, and molecular characters of the specimen; (3) consult identification keys, monographs, regional floras or faunas, and herbarium/museum reference collections; (4) compare specimen characters with published descriptions and type specimens at each rank, starting from the highest rank (Kingdom/Domain) and proceeding downward to species; (5) determine whether the specimen matches a described taxon or represents a new species requiring formal description.
2. Four character types used at species level: (1) morphological characters (external size, shape, colour, surface texture); (2) anatomical characters (internal cell structure, venation, tissue arrangement); (3) molecular characters (DNA barcode sequences, allele frequencies, genome-level data); (4) reproductive characters (flower structure, pollen morphology, mating behaviour, ploidy level).
3. Characters used at higher ranks must be more fundamental because higher ranks group organisms that diverged from their common ancestor at a more distant point in the past; only characters that were present in that deeply ancestral lineage and have been retained in all descendant lineages are appropriate for defining such a broad group. At species level, minor morphological or molecular details may suffice; at phylum level, only fundamental cellular or body plan characters (e.g. the presence of a notochord in Phylum Chordata; the presence of a nuclear membrane in Domain Eukarya) are conserved across all members.
4. A monophyletic group (clade) consists of an ancestor and all of its descendants, defined by at least one shared derived character (synapomorphy) inherited from that ancestor. It is the only valid group in cladistic classification because: (1) it represents a complete and coherent evolutionary unit; (2) all members share the synapomorphy, making the group predictive (knowing a taxon belongs to the clade allows prediction of the presence of the synapomorphy); (3) paraphyletic and polyphyletic groups leave out some descendants or group unrelated taxa, making them misleading about evolutionary history.

5. Paraphyletic group: includes an ancestor and some but not all of its descendants; at least one descendant lineage is excluded. Example: "Dicotyledonae" as traditionally defined excludes monocotyledons, but monocots evolved from within the dicot grade, making traditional Dicotyledonae paraphyletic; invalid in cladistics. Polyphyletic group: members share a character that evolved independently (convergently) in two or more separate lineages; the group does not include the most recent common ancestor of all its members. Example: "algae" traditionally grouped all photosynthetic aquatic organisms regardless of their evolutionary origins; multiple independent lineages of photosynthetic organisms are included, making traditional "Algae" polyphyletic; invalid in cladistics.

Part 2.4

1. Two approaches to species delimitation: (1) Morphological approach: examine the specimen and compare its characters against published descriptions, type specimens, and identification keys; if the specimen falls outside the known range of variation of all described species, it may represent a new species; this approach is rapid and applicable without specialist equipment but is subjective and misses cryptic species. (2) Molecular approach: extract DNA from the specimen; sequence a standard barcode region (CO1 for animals; rbcL/matK for plants); compare the sequence against a reference library (BOLD, GenBank); populations that are reciprocally monophyletic and separated by a threshold divergence (typically 2-3% for CO1 in animals) may be recognised as distinct species.
2. Integrative taxonomy is the combination of multiple independent lines of evidence, including morphological, molecular, ecological, and behavioural data, to delimit and formally describe species. It is now the standard approach for two reasons: (1) no single data type is sufficient to detect all forms of species boundaries; morphological data alone misses cryptic species; molecular data alone may over-split or under-split without morphological corroboration; (2) leading systematic journals require multiple independent lines of evidence before accepting a new species description, reflecting the scientific consensus that integrative evidence produces more robust and stable species delimitations.

3. Cryptic species are two or more morphologically indistinguishable species that are genetically and reproductively distinct; they are detected using molecular, cytological, or reproductive data. Nigerian example with practical significance: the Anopheles gambiae complex, comprising at least seven morphologically identical mosquito species. Practical significance: different members of the complex have different insecticide resistance profiles and different efficiencies for transmitting Plasmodium falciparum malaria; vector control programmes that treat all members as a single species apply inappropriate insecticides or target the wrong species, reducing the effectiveness of malaria control in Nigeria.
4. A species complex is a group of closely related, recently diverged species that are difficult to distinguish morphologically, may be partially interfertile, and may have overlapping or uncertain species boundaries. Example: the Striga hermonthica complex in Nigeria; multiple closely related parasitic witch weed species infest sorghum, millet, and maize crops across different agroecological zones in Nigeria; distinguishing between them taxonomically is difficult because they share most morphological characters, but they differ in host specificity and geographic distribution, which affects the selection of resistant crop varieties for deployment.
5. Two consequences: (1) inability to make conservation assessments: the IUCN Red List requires a formally described species with a known distribution and population size estimate before a conservation status can be assigned; undescribed species cannot be assessed, meaning they cannot be prioritised for conservation and may go extinct before they are even known to science; Nigeria's invertebrate, fungal, and microbial diversity is especially under-described. (2) loss of potential pharmaceutical and agricultural resources: Nigeria's plants and microorganisms represent a vast unexplored reservoir of bioactive compounds; secondary metabolites used as medicines, pesticides, or food additives cannot be attributed to, patented, or sustainably harvested from organisms that have not been formally identified and named.

References and Attributions [Series 2]

Textual References (Books and External Sources)

- Mayr, E., & Ashlock, P. D. (1991). Principles of systematic zoology (2nd ed.). McGraw-Hill.
- Judd, W. S., Campbell, C. S., Kellogg, E. A., Stevens, P. F., & Donoghue, M. J. (2008). Plant systematics: A phylogenetic approach (3rd ed.). Sinauer Associates.
- Coyne, J. A., & Orr, H. A. (2004). Speciation. Sinauer Associates.
- FAO (Food and Agriculture Organization of the United Nations). (2025). Guidelines for sustainable agriculture. FAO.

Figures, Plates, Tables, and Boxes

- Figure 2.1: Taxonomic hierarchy diagram with classification of cowpea and human Attribution: AI generated. Suggested OER search string: "taxonomic hierarchy diagram cowpea Vigna unguiculata Homo sapiens domain kingdom phylum OER".
- Figure 2.2: Comparison of four major species concepts Attribution: AI generated. Suggested OER search string: "species concepts comparison diagram morphological biological phylogenetic ecological OER".
- Figure 2.3: Cladogram illustrating monophyletic, paraphyletic, and polyphyletic groups Attribution: AI generated. Suggested OER search string: "cladogram monophyletic paraphyletic polyphyletic diagram cladistics validity OER".
- Box 2.1: Summary comparison of major species concepts Attribution: AI generated. Suggested OER search string: "species concepts comparison table biological morphological phylogenetic ecological cohesion recognition OER box".

Course code: BIO 306

Course title: Systematic Biology

Course credit load: 2 Units

Series 3: Biological Nomenclature and Binomial System

- **Part 3.1: Principles of Biological Nomenclature**
  - Sub Part 3.1.1: Purpose and history of biological nomenclature
  - Sub Part 3.1.2: The International Codes of Nomenclature
  - Sub Part 3.1.3: Fundamental rules: priority, validity, and legitimacy
- **Part 3.2: The Binomial System**
  - Sub Part 3.2.1: Structure of a binomial name
  - Sub Part 3.2.2: Rules for writing scientific names
  - Sub Part 3.2.3: Author citations and date
- **Part 3.3: Type Specimens and the Type Concept**
  - Sub Part 3.3.1: Definition and purpose of type specimens
  - Sub Part 3.3.2: Categories of types
  - Sub Part 3.3.3: Designation and consultation of types
- **Part 3.4: Synonymy, Homonymy, and Name Changes**
  - Sub Part 3.4.1: Synonymy
  - Sub Part 3.4.2: Homonymy

- Sub Part 3.4.3: Why names change and how to handle name changes

Introduction

Biological nomenclature is the formal system of rules and procedures for naming organisms. It ensures that every species and higher taxon has a single, universally accepted scientific name that communicates unambiguously across all languages and disciplines. Without a stable and universally applied nomenclature, biological communication would be impossible: the same organism could have dozens of names in different countries, and the same name could refer to different organisms in different publications.

This Series covers the principles and history of nomenclature, the International Codes that govern naming in different groups of organisms, the binomial system introduced by Linnaeus and its current rules, the concept of the type specimen, and the common nomenclatural problems of synonymy and homonymy. These topics are essential for reading and using the systematic literature and for producing taxonomic publications.

Series Learning Outcomes

Upon completing this Series, you should be able to:

- **SLO 3.1** explain the purpose of biological nomenclature and describe the major International Codes (Linked to Part 3.1),
- **SLO 3.2** state and apply the fundamental rules of nomenclature: priority, validity, and legitimacy (Linked to Part 3.1),
- **SLO 3.3** explain the structure and rules of the binomial system and correctly write scientific names (Linked to Part 3.2),
- **SLO 3.4** explain author citations and the conventions for citing dates (Linked to Part 3.2),

- **SLO 3.5** define the type concept and distinguish among the main categories of type specimens (Linked to Part 3.3), and
- **SLO 3.6** define synonymy and homonymy and explain how name changes arise and are handled (Linked to Part 3.4).

3.1 Principles of Biological Nomenclature

3.1.1 Purpose and history of biological nomenclature

Biological nomenclature serves three principal purposes: (1) to provide each taxon with a unique, unambiguous, universally accepted name; (2) to ensure that names are stable over time (the same organism is always called by the same name); (3) to ensure that names are informative about the classification of the organism (the genus name indicates the group; family suffixes signal the rank). Pre-Linnaean names were polynomial phrases (e.g. Rosa sylvestris inodora seu canina, "wild odourless dog rose") that varied between authors.

Linnaeus solved the polynomial problem by consistently using a two-word name for each species (the binomial system), beginning with Systema Naturae (10th edition, 1758) for animals and Species Plantarum (1753) for plants. These dates are the starting points for nomenclature in their respective groups. After Linnaeus, the proliferation of new descriptions and synonyms made it clear that formal international rules were needed; the first international botanical nomenclature rules were agreed at the Paris Congress (1867); the first zoological code followed at the Berlin Congress (1901).

Fill in the blank: Linnaeus solved the pre-Linnaean polynomial naming problem by consistently applying a two-word (_________) name to each species; Species Plantarum (1753) and Systema Naturae (10th edition, 1758) are the respective starting points for botanical and zoological nomenclature.

3.1.2 The International Codes of Nomenclature

Because nomenclature was historically developed independently for different groups of organisms, multiple International Codes now govern naming in different kingdoms. International Code of Nomenclature for algae, fungi, and plants (ICN; formerly ICBN): governs naming of all plants, algae, and fungi; the current edition is the Shenzhen Code (2018). International Code of Zoological Nomenclature (ICZN; 4th edition, 1999): governs naming of all animals; maintained by the International Commission on Zoological Nomenclature.

International Code of Nomenclature of Prokaryotes (ICNP; formerly ICNB): governs naming of bacteria and archaea; uses different starting points and has some different rules from the other codes. International Code of Virus Classification and Nomenclature (ICVCN): governs viruses; uses English rather than Latin names. International Code of Nomenclature for Cultivated Plants (ICNCP): governs cultivar names. The ICN and ICZN are the two codes most relevant to biological students and share the core principles of priority, validity, and legitimacy but differ in several specific rules and starting dates.

Fill in the blank: The International Code of Nomenclature for algae, fungi, and plants (ICN) and the International Code of ________ Nomenclature (ICZN) are the two most relevant nomenclatural codes for biological students; both are based on the principles of priority, validity, and legitimacy.

3.1.3 Fundamental rules: priority, validity, and legitimacy

Priority: the principle that the earliest validly published name for a taxon takes precedence over all later names (synonyms) for the same taxon. "Earliest" is measured from the nomenclatural starting point for each group (1753 for plants; 1758 for animals). A name published after the starting point but before any other name for the same taxon has priority over all subsequent names. Priority ensures that a single, stable name is used for each taxon rather than whichever name a particular author prefers.

Validity: a name is validly published if it meets the formal requirements of the Code: published in a format accessible to the scientific community (in print or, since 2012 in botany, in an approved online publication); accompanied by a diagnosis or description of the taxon; and (in botany since 1935 and zoology since 1930) accompanied by designation of a type specimen.

Legitimacy: a validly published name is legitimate if it was not based on a type that is the type of an earlier legitimate name for the same taxon; an illegitimate name cannot take priority even if it was published first.

Fill in the blank: The principle of ________ states that the earliest validly published name for a taxon takes precedence over all later names (synonyms); for plants the starting point is 1753 (Species Plantarum); for animals it is 1758 (Systema Naturae, 10th edition).

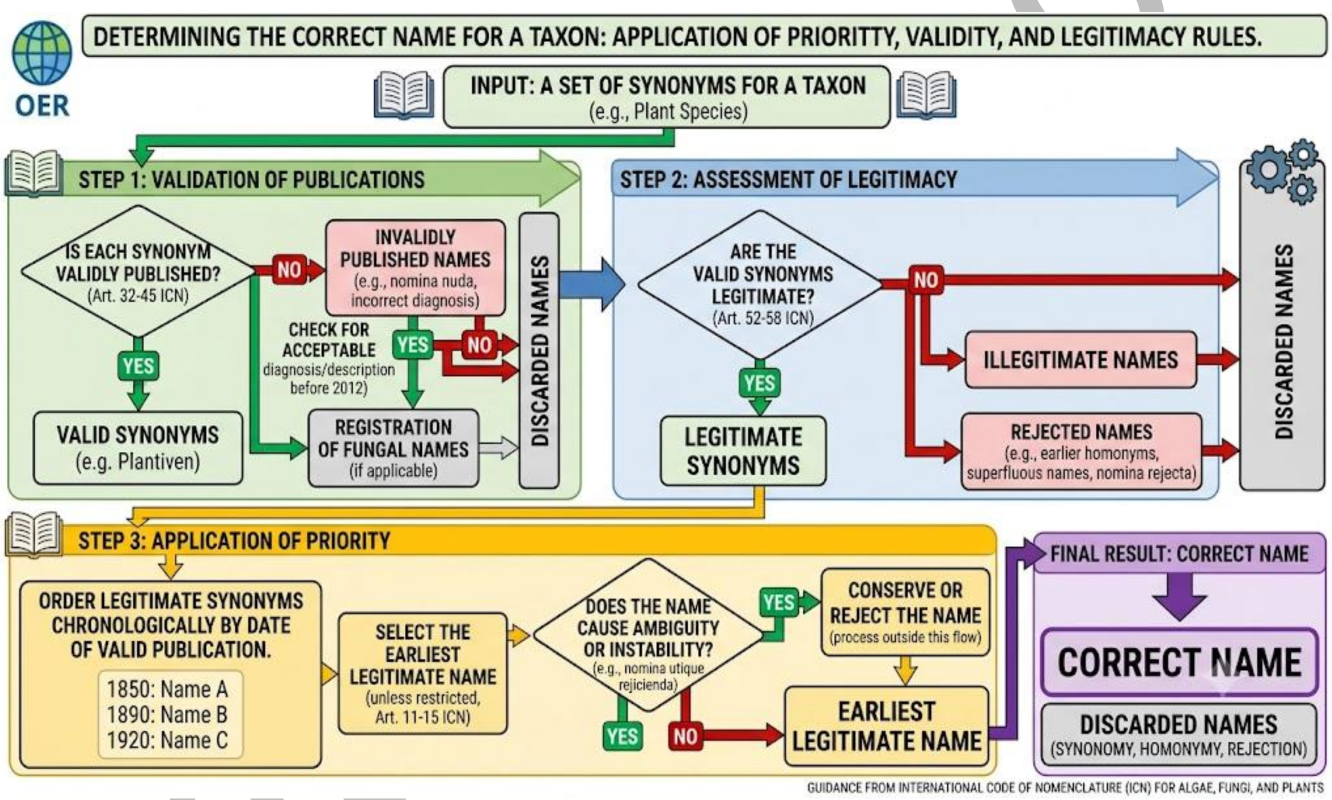


Figure 3.1: Diagram illustrating the principles of priority, validity, and legitimacy in nomenclature

Pilot questions 3.1

1. State the three principal purposes of biological nomenclature.
2. Name four International Codes of Nomenclature and state the group each governs.
3. Explain the principle of priority and state the starting points for botanical and zoological nomenclature.
4. Define validity as a requirement for a published name.

5. Distinguish between validity and legitimacy in nomenclature.

3.2 The Binomial System

3.2.1 Structure of a binomial name

A binomial name consists of two parts: the generic name (genus name) and the specific epithet (species epithet). The generic name is a noun (or adjective used as a noun) and must be unique within the Code (no two genera in animals, or in plants, can have the same name). The specific epithet is an adjective, noun, or participial adjective that qualifies the generic name; it need not be unique within the genus but is unique when combined with the generic name to form the complete binomial.

Examples: Vigna unguiculata (cowpea): generic name Vigna (a Latin noun); specific epithet unguiculata (Latin adjective meaning "small-clawed"). Homo sapiens (human): Homo (Latin noun; man); sapiens (Latin adjective; wise). Panthera leo (lion): Panthera (Latin noun; panther); leo (Latin noun; lion). A trinomial name for a subspecies adds a third word: Pan troglodytes ellioti (Nigeria-Cameroon chimpanzee). The complete binomial, together with the author citation, constitutes the full scientific name.

Fill in the blank: A binomial name consists of the ________ name (capitalised noun unique within the Code) and the specific epithet (lower case adjective or noun); together they form a unique combination that is the scientific name of the species.

3.2.2 Rules for writing scientific names

Rules for writing scientific names correctly: (1) The generic name begins with a capital letter; the specific epithet and all infraspecific epithets are in lower case (exception: in zoology, a specific epithet derived from a proper noun may be capitalised, though lower case is now generally preferred). (2) The binomial is always italicised in print; it is underlined when written or typed without italic capability. (3) After the full name has been written once in a document, the generic name may be abbreviated to its initial capital letter, e.g. V. unguiculata or H. sapiens.

(4) No part of the binomial name should be placed in quotation marks in normal use. (5) Family names and higher taxon names (above genus) are not italicised; they are written in Roman (upright) type and begin with a capital letter; e.g. Fabaceae, Mammalia, Chordata. (6) The specific epithet alone is never sufficient to refer to a species (because the same epithet may be used in different genera); always cite at least the abbreviated genus name with the epithet. (7) Common (vernacular) names are written in lower case without italics; e.g. cowpea, lion, Nigerian iroko.

Fill in the blank: In a correctly written scientific name, the generic name begins with a ________ letter and the specific epithet is in lower case; the entire binomial is italicised (or underlined when italic is not available).

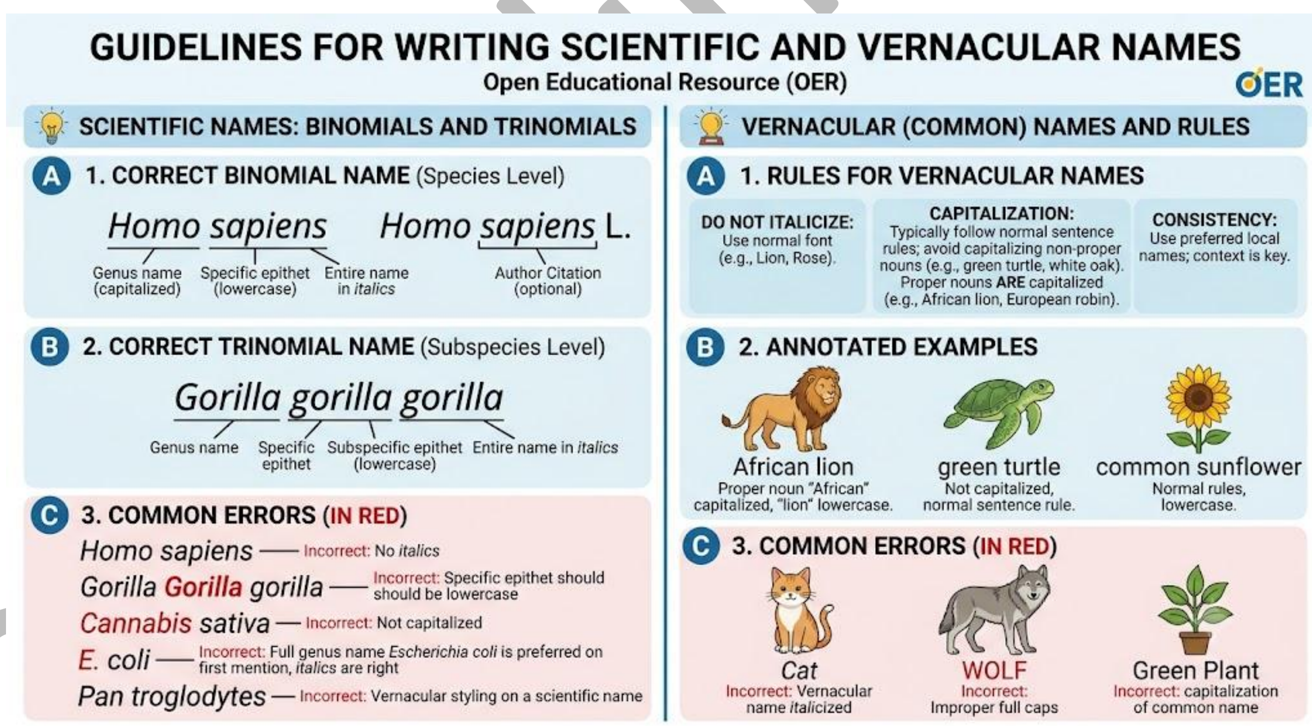


Figure 3.2: Annotated examples of correctly written scientific names

3.2.3 Author citations and date

Author citations identify who first validly published the name, providing a reference for the original description. In botany, the author's name is abbreviated following a standard list (Authors of Plant Names; Brummitt and Powell, 1992); e.g. L. = Linnaeus; R.Br. = Robert Brown; Hook.f. = Joseph Dalton Hooker filius (the son). In zoology, the author's name is usually written in full or abbreviated less formally; the year of publication is always cited after the author's name in zoology.

When a species is transferred to a different genus from the one in which it was originally described, the original author's name is placed in parentheses. Example: cowpea was originally described by Linnaeus as Phaseolus unguiculatus L.; when it was transferred to the genus Vigna, the name became Vigna unguiculata (L.) Walp. (Walpers is the author who made the new combination). The parenthetical author citation flags that the epithet was first used in a different genus, allowing readers to trace the nomenclatural history.

Fill in the blank: When a species is transferred to a different genus, the original author's name is placed in ________ ; e.g. Vigna unguiculata (L.) Walp. indicates that Linnaeus first described the species (in another genus) and Walpers made the new combination.

Pilot questions 3.2

1. State the two parts of a binomial name and define each.
2. State six rules for writing scientific names correctly.
3. Write the following names correctly: a) vigna unguiculata; b) Homo Sapiens; c) panthera LEO.
4. Explain what an author citation indicates and give one example.
5. Explain what parenthetical author citation means and give one example.

3.3 Type Specimens and the Type Concept

3.3.1 Definition and purpose of type specimens

A type specimen is the single physical specimen (or other element) to which a species name is permanently and irrevocably attached by the original author at the time of publication, or subsequently by lectotypification or neotypification. The type specimen is the permanent nomenclatural anchor of the name: it does not define the limits of the species (which may change as more specimens are studied) but determines which species the name belongs to in the event of any dispute.

Purpose of the type concept: (1) Stability: when taxonomists disagree about whether two populations represent one or two species, the type specimens are the physical reference points that determine which name applies to which entity; (2) Reproducibility: any scientist anywhere in the world can examine the type specimen and verify the application of the name; (3) Accountability: each name is traceable to a specific published description and a deposited, labelled specimen accessible in a public institution. Type specimens are usually deposited in major national or international herbaria or natural history museums.

Fill in the blank: A type specimen is the single physical specimen permanently attached to a species name; it does not define the ________ of the species but determines which species the name belongs to if there is a dispute about name application.

3.3.2 Categories of types

Holotype: the single specimen designated by the original author as the name-bearing type at the time of the original description; it is the primary type. Paratype: any specimen other than the holotype that was cited by the original author in the original description and is part of the type series; paratypes do not bear the name but document variation in the original concept of the species. Isotype (botany only): a duplicate of the holotype (a second collection made at the same time, from the same plant, by the same collector).

Lectotype: a specimen selected from the original type series (syntypes or paratypes) after the original publication to serve as the name-bearing type when no holotype was designated; lectotypification is done to stabilise the application of a name. Neotype: a specimen selected to serve as the name-bearing type when all of the original type material has been lost or destroyed; neotypification requires demonstration that no original material survives. Syntype: any specimen cited in the original description when no holotype was designated; the series of syntypes collectively bear the name until a lectotype is designated.

Fill in the blank: A ________ is selected from the original type series to serve as the name-bearing type when no holotype was designated; a neotype is selected when all original type material has been lost or destroyed.

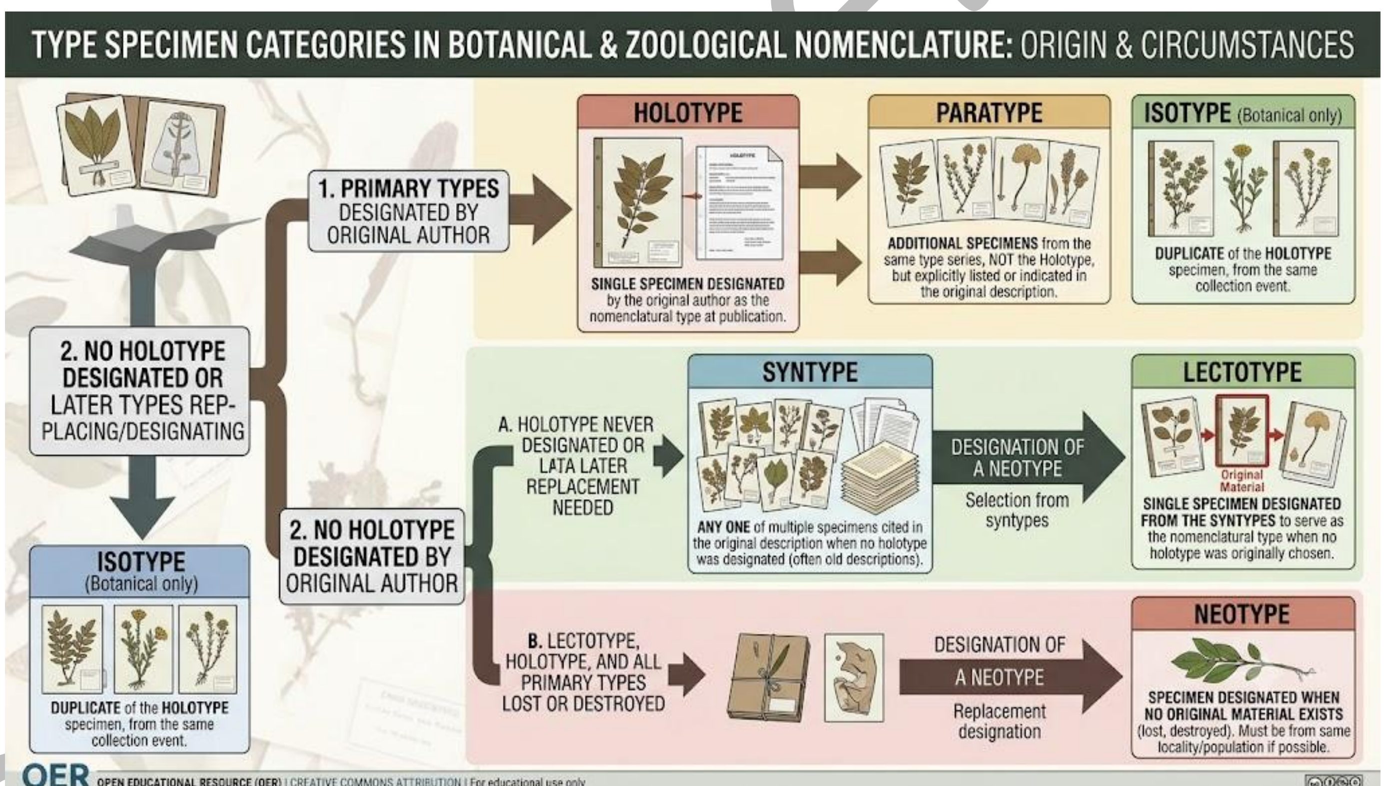


Figure 3.3: Diagram summarising the categories of type specimens and their relationships

3.3.3 Designation and consultation of types

Designation of a type: in the original description, the author designates one specimen as the holotype by explicit statement in the text (e.g. "Holotype: Nigeria, Lagos State, 15 June 2020, Adeyemi 1234, deposited at FHI [Federal Herbarium Ibadan]"). The type specimen must be deposited in a publicly accessible institution (herbarium or museum) where it can be examined by any scientist; it may not be in a private collection. Since 2007 (ICN), types of new species must be deposited in a recognised public herbarium.

Consulting a type: when revising a taxon, a taxonomist must examine the type specimen (or at least high-quality photographs or digital images if travel is impossible) to confirm the application of the name. Many types are housed in European institutions (Kew Herbarium, Natural History Museum London, Naturalis Leiden, Berlin Herbarium) because of the history of colonial botanical collection in Africa. The African Plants database and Global Plants initiative (JSTOR Global Plants) have digitised thousands of African plant type specimens, making them accessible online to Nigerian taxonomists.

Fill in the blank: Type specimens must be deposited in a publicly accessible ________ or natural history museum so that any scientist anywhere in the world can examine them to verify the application of a species name.

Pilot questions 3.3

1. Define a type specimen and state its purpose in nomenclature.
2. Distinguish between a holotype and a lectotype.
3. Define paratype, isotype, syntype, and neotype.
4. Explain why type specimens are important for Nigerian taxonomists.
5. Explain how the Global Plants initiative has improved access to types for African systematists.

3.4 Synonymy, Homonymy, and Name Changes

3.4.1 Synonymy

Synonyms are two or more different names applied to the same taxon. Objective synonyms (nomenclatural synonyms): names based on the same type specimen; regardless of how the taxon is circumscribed, these names always refer to the same entity; e.g. if Phaseolus unguiculatus L. and Vigna unguiculata (L.) Walp. are based on the same type, they are objective synonyms. Subjective synonyms (taxonomic synonyms): names based on different type specimens but which a particular taxonomist considers to refer to the same taxon; they depend on taxonomic judgement and may differ between authors.

Under the principle of priority, the earliest validly published synonym (the senior synonym) is the correct name; all later synonyms (junior synonyms) must be set aside. A complete synonymy lists all names ever applied to a taxon in chronological order, with the correct name first. Knowing the synonymy of a species is essential for searching the literature (older papers may use a junior synonym) and for determining the correct current name. Nigerian plants are particularly affected: many were described by European botanists in the 19th and early 20th centuries under names that have since been synonymised.

Fill in the blank: The ________ synonym is the earliest validly published name for a taxon; it takes priority over all later (junior) synonyms; when a species is synonymised, the senior synonym becomes the correct name.

3.4.2 Homonymy

Homonyms are the same name applied to two or more different taxa. Primary homonyms: two species in the same genus independently given the same specific epithet by different authors; both names may be validly published and legitimate, but one must be replaced. The later-published homonym (junior homonym) must be replaced with a new name (a nomen novum) because the same name cannot apply to two different species in the same genus. Secondary homonyms (in zoology): two originally described in different genera but subsequently placed in the same genus.

Generic homonyms: two genera in the same code independently given the same name; the junior homonym must be replaced. Note that an animal genus and a plant genus may bear the same name without conflict because animal and plant names are governed by different codes (ICZN and ICN respectively). The discovery of homonymy is one of the most common reasons for name changes in taxonomy; it requires the author of the junior homonym to publish a new replacement name (nomen novum) citing the homonymy as the reason.

Fill in the blank: ________ are the same name applied to two different taxa; the later-published homonym (junior homonym) must be replaced with a new name (nomen novum) because the same name cannot refer to two different taxa within the same nomenclatural code.

3.4.3 Why names change and how to handle name changes

Names change for several legitimate reasons: (1) Priority: an earlier validly published name is discovered; the later (currently used) name must be replaced by the earlier one; (2) Homonymy: the currently used name is found to be a junior homonym and must be replaced by a nomen novum; (3) Synonymy: two previously separate species are found to be the same species; the junior synonym is suppressed and the senior synonym becomes correct; (4) New combination: a species is moved to a different genus, requiring a new binomial while retaining the specific epithet.

Handling name changes in practice: always cite the full synonymy when describing or revising a taxon; use the most recent authoritative treatment (monograph, flora, or checklist) for the currently accepted name; consult databases such as The Plant List, Plants of the World Online, Catalogue of Life, and GBIF for verified current names. In Nigeria, the Flora of West Tropical Africa (Hutchinson and Dalziel; 3 volumes) remains the primary reference for plant identifications though many names have since changed; the Flora of Nigeria and state-level checklists provide more current information.

Fill in the blank: When a species is transferred to a different genus, a new ________ is made: the specific epithet is retained but combined with the new genus name; the original author is placed in parentheses and the combining author is added.

Term	**Definition**	**Example**
Synonym	Different names referring to the same taxon	*Panthera leo* vs. *Leo africanus*

Senior Synonym	The earliest published valid name among synonyms	*Panthera leo* (1758) is senior to *Leo africanus* (1827)
Junior Synonym	Later-published name for the same taxon, superseded by senior synonym	*Leo africanus* is junior synonym of *Panthera leo*
Homonym	Same name used for different taxa	*Aotus* (owl monkey genus) vs. *Aotus* (plant genus)
Nomen Novum	A new replacement name for a taxon when the old name is invalid	*Aotus* (plant genus) renamed *Aotus* → *Pseudanthus*
Combination	New genus-species pairing when species is moved	*Agaricus campestris* → *Psalliota campestris*
Lectotype	A specimen later chosen as the name-bearing type when original holotype was not designated	A single herbarium sheet designated as lectotype for *Vitellaria paradoxa*
Neotype	A specimen selected as type when original type is lost or destroyed	A new specimen designated as neotype for *Gulo gulo* after holotype loss

Box 3.1: Summary of nomenclatural terms and common causes of name changes

Pilot questions 3.4

1. Define synonymy and distinguish between objective and subjective synonyms.
2. Explain the principle of priority as it applies to synonyms.
3. Define homonymy and explain what action is required when a junior homonym is discovered.
4. State four reasons why a scientific name may change.
5. Name two databases used to find currently accepted names for Nigerian plants.

Series Summary

This Series covered biological nomenclature, the formal system of rules that governs how organisms are named. The purpose of nomenclature is to give every species a unique, stable, and universally accepted name that means the same thing to scientists everywhere, regardless of language. Different international codes govern different groups of organisms: the ICN covers plants, algae, and fungi; the ICZN covers animals; the ICNP covers prokaryotes; and the ICNCP covers cultivated plants. Three fundamental rules underpin all codes: the principle of priority (the earliest validly published name takes precedence, with starting points of 1753 for plants and 1758 for animals); validity (a name must be published in an accessible format with a description and a designated type specimen); and legitimacy (a name cannot be based on a type already used for a different taxon). The binomial system, introduced by Linnaeus, gives each species a two-part name consisting of a capitalised generic name and a lower-case specific epithet, written in italics and followed by the author citation.

Type specimens are the permanent nomenclatural anchors of species names: the holotype is the single specimen designated by the original author as the definitive reference for a name, while paratypes, isotypes, syntypes, lectotypes, and neotypes serve as additional or replacement anchors under specific circumstances. Many African plant type specimens are held at Kew and the Natural History Museum in London and are accessible through JSTOR Global Plants. Name changes arise when the rules of priority, homonymy, or synonymy are applied: when two names refer to the same taxon, the earlier (senior) synonym is correct and the later (junior) synonym is set aside; when the same name has been applied to two different taxa, the junior homonym must be replaced. Key references for Nigerian taxonomy include the Flora of West Tropical Africa, Plants of the World Online, and GBIF.

Glossary of Terms

- **Author citation:** the name of the author(s) who first validly published a scientific name, appended after the binomial; in botany abbreviated by a standard list; in zoology followed by the year.

- **Binomial name:** the two-part scientific name of a species, consisting of the generic name (capitalised) and the specific epithet (lower case), both italicised.
- **Combination (comb. nov.):** a new binomial formed by transferring a species epithet from one genus to another; the original author is placed in parentheses and the new combination's author is added after.
- **Diagnosis:** a formal Latin description of the characters that distinguish a new taxon from all related taxa; required for valid publication under the ICN (or, in botany since 2012, a description in English).
- **Generic name:** the first part of a binomial; a capitalised noun (or noun equivalent) that is unique within the relevant nomenclatural code; designates the genus.
- **Holotype:** the single specimen designated by the original author as the name-bearing type at the time of original description; the primary type; can only be changed by lectotypification or neotypification.
- **Homonym:** the same name given independently to two different taxa; the earlier-published name is the senior homonym; the later-published is the junior homonym, which must be replaced by a nomen novum.
- **ICN (International Code of Nomenclature for algae, fungi, and plants):** the nomenclatural code governing the naming of all plants, algae, and fungi; the current edition is the Shenzhen Code (2018).
- **ICZN (International Code of Zoological Nomenclature):** the nomenclatural code governing the naming of all animals; the current edition is the 4th edition (1999).
- **Illegitimate name:** a validly published name that is not legitimate because it was based on a type already used for another taxon (a superfluous name) or because the name itself had already been validly published for a different taxon (a homonym).
- **Isotype:** a duplicate specimen of the holotype collected at the same time, from the same individual, by the same collector; used in botany only; has secondary nomenclatural importance.

- **Junior homonym:** the later-published of two identical names applied to different taxa; must be replaced by a nomen novum.
- **Junior synonym:** a later-published name for the same taxon as the senior synonym; set aside under the principle of priority.
- **Lectotype:** a specimen selected from the original type series (syntypes or paratypes) to serve as the name-bearing type after original publication, when no holotype was designated.
- **Legitimacy:** the quality of a validly published name that was not based on a type already used for another name; a legitimate name can compete for priority.
- **Neotype:** a specimen designated to serve as the name-bearing type when all original type material has been lost or destroyed; requires formal evidence that no original material survives.
- **Nomen novum (nom. nov.):** a new replacement name published specifically to replace a junior homonym; it is based on the same type as the replaced name.
- **Nomenclatural starting point:** the publication date from which names must be validly published to compete for priority; 1753 (Species Plantarum) for plants; 1758 (Systema Naturae, 10th edition) for animals.
- **Objective synonym:** a synonym based on the same type specimen as another name for the same taxon; objective synonyms always refer to the same entity regardless of taxonomic opinion.
- **Paratype:** a specimen, other than the holotype, cited by the original author in the original description; documents the variation included in the original species concept.
- **Priority:** the nomenclatural principle that the earliest validly published name for a taxon takes precedence over all later names; the foundation of nomenclatural stability.
- **Senior synonym:** the earliest validly published name for a taxon; the correct name under the principle of priority.

- **Specific epithet:** the second part of a binomial name; a lower-case adjective, noun, or participial adjective that qualifies the generic name.
- **Subjective synonym:** a synonym based on a different type specimen from another name but considered by a taxonomist to refer to the same taxon; depends on taxonomic judgement and may differ between authorities.
- **Synonym:** any name other than the currently accepted name that has been applied to the same taxon; may be a senior or junior synonym depending on the date of publication.
- **Syntype:** any specimen cited in the original description when no single holotype was designated; collectively the syntypes bear the name until a lectotype is chosen from among them.
- **Trinomial name:** a three-part name used for a subspecies: Genus species subspecies; all three parts italicised.
- **Type concept:** the nomenclatural principle that every species name is permanently attached to a single physical type specimen (or element) that serves as the reference point for the application of the name.
- **Validity:** the property of a name that meets all formal requirements of the relevant Code: published in an accessible format, accompanied by a description or diagnosis, and with a type designation.

Concept Check Questions [Series 3]

Objective Questions

1. Linnaeus's ________ (1753) and Systema Naturae (10th edition, 1758) are the nomenclatural starting points for botanical and zoological nomenclature respectively. (Linked to SLO 3.1)
2. The principle of ________ states that the earliest validly published name for a taxon takes precedence over all later names for the same taxon. (Linked to SLO 3.2)

3. In a binomial name, the generic name begins with a ________ letter and the specific epithet is in lower case; both parts are italicised in print. (Linked to SLO 3.3)
4. The single specimen designated by the original author as the name-bearing type is called the ________ ; it is the primary type and the permanent nomenclatural anchor of the name. (Linked to SLO 3.5)
5. A ________ is the same name applied to two different taxa; the later-published (junior) homonym must be replaced by a new name (nomen novum). (Linked to SLO 3.6)

Short-Answer Questions

- State the three fundamental principles of nomenclature. (Linked to SLO 3.2)
- State six rules for writing scientific names correctly. (Linked to SLO 3.3)
- Explain what a parenthetical author citation indicates and give one example. (Linked to SLO 3.4)
- Distinguish between objective and subjective synonyms. (Linked to SLO 3.6)
- Define lectotype and neotype and state when each is designated. (Linked to SLO 3.5)

Long-Answer Questions

1. Explain the purpose and history of biological nomenclature; describe the main International Codes; and state and explain the three fundamental principles of nomenclature. (Linked to SLOs 3.1, 3.2)
2. Explain the binomial system: describe the structure of a binomial name; state the rules for writing names correctly; and explain author citations including parenthetical author citations. (Linked to SLOs 3.3, 3.4)
3. Explain the type concept; describe the main categories of type specimens; and define synonymy and homonymy, explaining how they lead to name changes. (Linked to SLOs 3.5, 3.6)

Answers to Concept Check Questions [Series 3]

Objective Questions

6. Species Plantarum.
7. Priority.
8. Capital.
9. Holotype.
10. Homonym.

Short-Answer Questions

11. Priority (earliest valid name prevails); validity (published in accessible format with description/diagnosis and type); legitimacy (not based on a type already used for another taxon).
12. (1) Generic name capitalised; specific epithet lower case; (2) binomial italicised or underlined; (3) genus may be abbreviated after first mention (e.g. V. unguiculata); (4) family and higher names in Roman type, not italicised; (5) specific epithet alone insufficient (always include at least abbreviated genus); (6) common names lower case and not italicised.
13. Parenthetical author citation means the species was originally described in a different genus; the original author is placed in parentheses and the combining author follows. Example: Vigna unguiculata (L.) Walp. means Linnaeus first described the species (as Phaseolus unguiculatus) and Walpers transferred it to Vigna.
14. Objective synonyms share the same type specimen; they always refer to the same entity regardless of taxonomic opinion. Subjective synonyms have different types but are judged by a taxonomist to be the same species; they depend on taxonomic opinion and may differ between authorities.
15. Lectotype: designated from the original type series when no holotype was originally named; chosen to stabilise the application of the name. Neotype: designated when all

original type material is lost or destroyed; requires proof that no original material survives.

Long-Answer Questions

1. Purpose of nomenclature: unique, unambiguous, and stable names for all taxa; communication across languages and disciplines. History: pre-Linnaean polynomial names were unstable; Linnaeus introduced consistent binomials (Species Plantarum 1753; Systema Naturae 10th edition 1758); first international rules (Paris 1867 botany; Berlin 1901 zoology). International Codes: ICN (algae, fungi, plants; Shenzhen Code 2018); ICZN (animals; 4th edition 1999); ICNP (prokaryotes); ICVCN (viruses); ICNCP (cultivated plants). Three fundamental principles: priority (earliest valid name prevails; plants from 1753; animals from 1758); validity (published in accessible format; accompanied by description/diagnosis; with type designation since 1930s/1935); legitimacy (not based on a type already used for another taxon; illegitimate names cannot compete for priority).
2. Binomial structure: generic name (capitalised noun, unique within code, first part of name) + specific epithet (lower case adjective or noun, qualifies genus name). Rules: generic name capitalised; epithet lower case; italicised in print (underlined in handwriting); genus may be abbreviated after first use; family names and above in Roman type; epithet never used alone; common names lower case Roman. Author citations: appended after binomial; in botany abbreviated by standard list (L. = Linnaeus; Hook.f. = Hooker filius); in zoology author name followed by year. Parenthetical citation: when a species is transferred to a new genus, the original author goes in parentheses; the author making the new combination is added outside parentheses; e.g. Vigna unguiculata (L.) Walp. (original in Phaseolus by L.; transferred to Vigna by Walpers).
3. Type concept: every species name permanently attached to a single physical type specimen; the type determines which species the name belongs to in a dispute; does not define species limits but anchors the name. Type categories: holotype (single specimen designated by original author; primary type); paratype (other specimens in original

description; documents variation); isotype (duplicate of holotype; botany only); syntype (any specimen when no holotype designated; collectively bear name until lectotype chosen); lectotype (chosen from syntypes to stabilise a name when no holotype exists); neotype (designated when all original material is lost). Synonymy: two or more names for the same taxon; senior synonym (earliest; correct under priority); junior synonym (later; set aside); objective synonymy (same type); subjective synonymy (different types; same taxon by taxonomic judgement). Homonymy: same name for different taxa; junior homonym must be replaced by nomen novum. Other causes of name change: new combination (transfer to new genus); discovery of earlier valid name; reclassification. Databases for Nigeria: Plants of the World Online; Flora of West Tropical Africa; GBIF; Catalogue of Life.

Answers to Pilot Questions [Series 3]

Part 3.1

6. Three principal purposes: (1) to provide each taxon with a unique, unambiguous, and universally accepted name that communicates the same organism to scientists regardless of their language or country; (2) to ensure stability of names over time so that the same organism is always referred to by the same name and historical literature remains interpretable; (3) to ensure that names are informative about the hierarchical classification of the organism through their grammatical form (genus name; family suffix; rank indicator).
7. Four International Codes: (1) ICN (International Code of Nomenclature for algae, fungi, and plants): governs all plants, algae, and fungi; current edition is the Shenzhen Code (2018). (2) ICZN (International Code of Zoological Nomenclature): governs all animals; current 4th edition (1999). (3) ICNP (International Code of Nomenclature of Prokaryotes): governs bacteria and archaea; uses different starting points from ICN and

ICZN. (4) ICNCP (International Code of Nomenclature for Cultivated Plants): governs cultivar names; uses fancy epithets in single quotes rather than Latin binomials.

8. The principle of priority states that the correct name for a taxon is the earliest name that was validly published for it after the nomenclatural starting point. For plants: the starting point is 1 May 1753 (the date of publication of Linnaeus's Species Plantarum); any name published for a plant before this date is not considered. For animals: the starting point is 1 January 1758 (the date of publication of the 10th edition of Linnaeus's Systema Naturae). If a species has been given two or more valid names by different authors, the earliest one is the correct name; all later names are junior synonyms that must be set aside.
9. A name is validly published if it meets three formal requirements of the relevant Code: (1) it must be published in a format accessible to the scientific community (a printed scientific publication, or since 2012 in botany, a registered electronic publication in an approved journal); (2) it must be accompanied by a diagnosis (Latin description distinguishing the new taxon from related taxa) or, in botany since 2012, a description in English; (3) it must be accompanied by designation of a type specimen deposited in a publicly accessible institution (required in botany since 1935 and in zoology since 1930).
10. Validity refers to whether a name meets all formal publication requirements of the Code (accessible publication, description/diagnosis, type designation); a validly published name has been formally introduced into nomenclature. Legitimacy refers to whether a validly published name can compete for priority; a name is illegitimate if it was based on a type already serving as the type of an earlier legitimate name for the same taxon (a superfluous name), or if the name itself was already validly published for a different taxon (a homonym). An illegitimate name has been validly published but cannot be used as the correct name even if it would otherwise have priority.

Part 3.2

11. Two parts of a binomial name: (1) The generic name (genus name): the first part; a noun (or noun equivalent) in the nominative singular; always written with a capital initial letter; unique within the relevant nomenclatural code (no two genera of animals, and no

two genera of plants, can have the same name); it designates the genus to which the species belongs. (2) The specific epithet: the second part; a lower-case adjective agreeing in gender with the generic name, or a noun in apposition, or a genitive noun; it qualifies the generic name and is unique only in combination with the generic name (the same epithet may be used in different genera).

12. Six rules for writing scientific names correctly: (1) The generic name always begins with a capital letter; (2) the specific epithet is always in lower case (zoological exception: epithets derived from proper nouns may be capitalised but lower case is now generally preferred); (3) the entire binomial (and trinomial) is italicised in print or underlined in handwriting when italics are not available; (4) after the full name has been stated once, the generic name may be abbreviated to its initial capital letter with a full stop (e.g. V. unguiculata; H. sapiens); (5) family names and higher taxon names are written in Roman (non-italic) type with a capital initial letter; (6) the specific epithet must never be cited alone without at least the abbreviated generic name.
13. Correct forms: a) Vigna unguiculata (generic name capitalised; epithet lower case; italicised); b) Homo sapiens (not "Homo Sapiens"; specific epithet must be lower case; italicised); c) Panthera leo (not "panthera LEO"; generic name capitalised; epithet lower case; italicised).
14. An author citation identifies the person who first validly published the scientific name, enabling readers to trace the original description. Example: Vigna unguiculata (L.) Walp. here L. = Linnaeus, who published the original name, and Walp. = Walpers, who made the new combination; the citation tells readers exactly where to find the original description and the new combination.
15. A parenthetical author citation indicates that the species was originally described in a different genus from the one in which it is currently placed; the original author's name is enclosed in parentheses, and the author who made the new combination is placed outside the parentheses. Example: Vigna unguiculata (L.) Walp.: Linnaeus first described the cowpea as Phaseolus unguiculatus; Walpers transferred it to the genus Vigna, creating the new combination Vigna unguiculata; the parentheses around L. signal that the species was not originally placed in Vigna, allowing taxonomic historians to trace the nomenclatural history.

Part 3.3

1. A type specimen is the single physical specimen (or other nomenclatural element) to which a species name is permanently and irrevocably attached by the original author at the time of the original description, or subsequently by formal lectotypification or neotypification. Purpose in nomenclature: it provides a permanent physical reference point for the application of the name; when taxonomists dispute whether two populations are separate species, the type specimens are the physical arbiters determining which name applies to which entity; the type does not define the limits of the species (which may change with new knowledge) but anchors the name.
2. Holotype: the single specimen explicitly designated by the original author as the name-bearing type at the time of original description; the primary type; there can be only one holotype for each name. Lectotype: a specimen subsequently selected from the original type series (syntypes or paratypes) to serve as the name-bearing type, designated after the original description because no holotype was originally designated; lectotypification is performed to stabilise the application of a name when there is ambiguity among the syntypes.
3. Paratype: any specimen, other than the holotype, cited by the original author in the original description; paratypes do not bear the name but document the variation in the original species concept and allow subsequent researchers to understand the range of material the author considered. Isotype (botany only): a duplicate specimen of the holotype, collected at the same time from the same individual by the same collector; has secondary nomenclatural importance when the holotype is lost. Syntype: any specimen cited in the original description when no holotype was designated; the syntypes collectively bear the name until one is selected as lectotype. Neotype: a specimen designated to serve as the name-bearing type when it is established that all of the original type material (holotype, lectotype, syntypes, isotypes) has been irretrievably lost or destroyed.
4. Type specimens are important for Nigerian taxonomists for two reasons: (1) Many species described from Nigeria or West Africa in the 19th and early 20th centuries were described by European botanists and zoologists who deposited type specimens in

European institutions (Kew Herbarium, Natural History Museum London, Berlin Herbarium); Nigerian taxonomists working on Nigerian flora and fauna must examine or access these types to confirm name applications when revising Nigerian taxa. (2) The JSTOR Global Plants initiative and similar digitisation projects have produced high-resolution images of type specimens held in European collections; while this reduces but does not eliminate the need for physical examination, it has greatly increased access for Nigerian systematists who cannot always travel abroad.

5. The Global Plants initiative (hosted on JSTOR and collaborating with Kew, NHM London, and dozens of other herbaria worldwide) has digitised and made freely available high-resolution images of type specimens for hundreds of thousands of plant species, including many African plant types. For Nigerian systematists, this means: (1) type specimens previously accessible only by expensive overseas travel can now be examined online from a university computer in Nigeria; (2) comparison of Nigerian material with European-held types is now routine rather than exceptional; (3) lectotypification of older names that lack holotypes can be performed more confidently using images of the full syntype series rather than relying on a single institutional visit.

Part 3.4

1. Synonymy is the situation where two or more different validly published names have been applied to the same taxon. Objective synonyms (nomenclatural synonyms): based on the same type specimen; they always refer to the same entity regardless of how broadly or narrowly the species is circumscribed; e.g. if the same individual plant was the type of two separately published names, those names are objective synonyms. Subjective synonyms (taxonomic synonyms): based on different type specimens but judged by a particular taxonomist to belong to the same species; they depend on taxonomic opinion and two taxonomists may disagree about whether the types represent one or two species.
2. The principle of priority requires that among all valid names for the same taxon, the earliest validly published one (the senior synonym) is the correct and accepted name; all later-published names for the same taxon are junior synonyms and must be set aside.

Example: if Species A was validly described in 1820 and Species B was separately described in 1875 for what is now considered the same taxon, the 1820 name has priority and is the correct name; the 1875 name is a junior synonym that appears in the synonymy list but is not used as the accepted name.

3. Homonymy is the situation where the same name has been independently applied to two different taxa. When a junior homonym is discovered, the author who discovers it must publish a new replacement name (nomen novum; abbreviated nom. nov.) for the junior homonym; the nomen novum is based on the same type as the replaced junior homonym; the reason for the new name is stated explicitly in the publication citing the homonymy. Example: if two authors independently named two different species "Vigna nigerica", the later-published one must be replaced with a new name; the name "Vigna nigerica" can only apply to the earlier-described species.
4. Four reasons why a scientific name may change: (1) Priority: an earlier validly published name is discovered that has precedence over the currently used name; (2) Homonymy: the currently used name is found to be a junior homonym and must be replaced by a nomen novum; (3) Synonymy: two previously separate species are considered the same species; the junior synonym is suppressed; (4) New combination: a species is transferred to a different genus, requiring a new binomial with a parenthetical author citation; the specific epithet is retained but combined with the new genus name.
5. Two databases for currently accepted names of Nigerian plants: (1) Plants of the World Online (POWO; https://powo.science.kew.org): maintained by the Royal Botanic Gardens, Kew; provides accepted names, synonymy, distribution maps, and images for all vascular plant species; frequently updated; most comprehensive current reference. (2) GBIF (Global Biodiversity Information Facility; https://www.gbif.org): aggregates biodiversity occurrence records from institutions worldwide; provides accepted names following Catalogue of Life backbone taxonomy; includes occurrence records from Nigerian herbarium specimens; useful for distributions in addition to names.

References and Attributions [Series 3]

Textual References (Books and External Sources)

1. International Code of Nomenclature for algae, fungi, and plants (Shenzhen Code). (2018). Regnum Vegetabile 159. Koeltz Botanical Books.
2. International Code of Zoological Nomenclature. (1999). 4th ed. International Trust for Zoological Nomenclature.
3. Stuessy, T. F. (2009). Plant taxonomy: The systematic evaluation of comparative data (2nd ed.). Columbia University Press.
4. FAO (Food and Agriculture Organization of the United Nations). (2025). Guidelines for sustainable agriculture. FAO.

Figures, Plates, Tables, and Boxes

1. Figure 3.1: Priority, validity, and legitimacy flowchart Attribution: AI generated. Suggested OER search string: "nomenclature priority validity legitimacy flowchart synonyms correct name OER".
2. Figure 3.2: Annotated examples of correctly written scientific names Attribution: AI generated. Suggested OER search string: "binomial name scientific name format rules italics capital letter author citation annotation OER".
3. Figure 3.3: Type specimen categories diagram Attribution: AI generated. Suggested OER search string: "type specimens categories holotype paratype isotype lectotype neotype syntype diagram OER".
4. Box 3.1: Summary of nomenclatural terms and common causes of name changes Attribution: AI generated. Suggested OER search string: "nomenclature terms synonyms homonyms nomen novum combination lectotype neotype table OER box".

Course code: BIO 306

Course title: Systematic Biology

Series 4: Advances in Systematics and Numerical Taxonomy

- **Part 4.1: Numerical Taxonomy (Phenetics)**
  - Sub Part 4.1.1: Origins and principles of numerical taxonomy
  - Sub Part 4.1.2: Operational Taxonomic Units and character scoring
  - Sub Part 4.1.3: Similarity coefficients and clustering methods
- **Part 4.2: Cladistics (Phylogenetic Systematics)**
  - Sub Part 4.2.1: Principles of cladistics
  - Sub Part 4.2.2: Types of characters: plesiomorphies, apomorphies, and synapomorphies
  - Sub Part 4.2.3: Constructing and interpreting cladograms
- **Part 4.3: Molecular Systematics**
  - Sub Part 4.3.1: Molecular markers used in systematics
  - Sub Part 4.3.2: Methods of phylogenetic analysis
  - Sub Part 4.3.3: Applications of molecular systematics
- **Part 4.4: Integrating Approaches: Modern Systematic Practice**
  - Sub Part 4.4.1: Comparing phenetics, cladistics, and molecular systematics
  - Sub Part 4.4.2: Integrative taxonomy in practice

- Sub Part 4.4.3: Systematics and biodiversity informatics

Introduction

The second half of the 20th century saw three transformative advances in systematic methodology: numerical taxonomy (the application of multivariate statistics to classification), cladistics (the strict use of shared derived characters to reconstruct evolutionary trees), and molecular systematics (the use of DNA and protein sequences to infer phylogenies). These approaches are not mutually exclusive and modern systematists increasingly integrate them into a unified framework.

This Series covers the principles and methods of numerical taxonomy, cladistics, and molecular systematics; compares these approaches; and examines how they are integrated in modern practice. It also introduces biodiversity informatics tools that are transforming the way systematic data are collected, curated, and used. Understanding these advances is essential for reading modern systematic literature and for contributing to the description of Nigeria's biodiversity.

Series Learning Outcomes

Upon completing this Series, you should be able to:

- **SLO 4.1** explain the principles of numerical taxonomy and describe OTUs, character scoring, similarity coefficients, and clustering methods (Linked to Part 4.1),
- **SLO 4.2** explain the principles of cladistics and distinguish between plesiomorphies, apomorphies, and synapomorphies (Linked to Part 4.2),
- **SLO 4.3** construct and interpret a simple cladogram (Linked to Part 4.2),
- **SLO 4.4** describe the main molecular markers used in systematics and the methods of phylogenetic analysis (Linked to Part 4.3),
- **SLO 4.5** compare phenetics, cladistics, and molecular systematics in terms of their principles, outputs, and limitations (Linked to Part 4.4), and

- **SLO 4.6** describe the role of biodiversity informatics and databases in modern systematics (Linked to Part 4.4).

4.1 Numerical Taxonomy (Phenetics)

4.1.1 Origins and principles of numerical taxonomy

Numerical taxonomy (also called phenetics) was developed by Peter Sneath and Robert Sokal (Principles of Numerical Taxonomy, 1963) as a reaction to what they perceived as the subjectivity of traditional taxonomy. The core philosophy is that classification should be based on overall similarity across as many equally weighted characters as possible, without any prior assumptions about evolutionary relationships or the relative importance of characters. The approach is explicitly atheoretical: characters are not weighted by their presumed evolutionary significance.

Five principles of numerical taxonomy (Sokal and Sneath): (1) the greater the content of information in a classification, the better; (2) every character is of equal weight (equal weighting principle); (3) overall similarity should be based on as many characters as possible; (4) distinct taxa can be recognised from the pattern of overall similarity; (5) taxonomy is a strictly empirical science; phylogenetic speculation is excluded. Phenetics produces phenograms (branching diagrams based on overall similarity) not phylogenetic trees (which represent evolutionary history).

Fill in the blank: Numerical taxonomy (phenetics) was developed by Sneath and ________ (1963); its core principle is that classification should be based on overall similarity across many equally weighted characters, without assumptions about evolutionary relationships.

4.1.2 Operational Taxonomic Units and character scoring

An Operational Taxonomic Unit (OTU) is the basic unit used in numerical taxonomic analysis; it may be an individual specimen, a species, a population, or any other consistently defined entity being compared. OTUs are scored for a set of characters; each character is recorded as a state for each OTU. Characters used in phenetic studies include: morphological (presence/absence of structures; size measurements); anatomical (cell dimensions, pore size, wall thickness); biochemical (presence of specific compounds); molecular (restriction fragment lengths, allele presence/absence).

Character states may be: binary (0 or 1; present or absent); multistate qualitative (coded as 0, 1, 2 for different states of the same character, e.g. leaf margin: entire = 0, serrate = 1, dentate = 2); quantitative (continuous measurements standardised before analysis). The data for all OTUs and all characters are assembled into a data matrix (a table with OTUs as rows and characters as columns); each cell contains the character state of that OTU for that character. Typically 50 to 100 or more characters are used to ensure that the similarity estimate is stable and not dominated by any one feature.

Fill in the blank: An ________ (OTU) is the basic unit of numerical taxonomic analysis; it may be a specimen, a species, or any consistently defined entity; the data for all OTUs and characters are assembled into a data matrix with OTUs as rows and characters as columns.

4.1.3 Similarity coefficients and clustering methods

After scoring the data matrix, similarity between each pair of OTUs is calculated using a similarity coefficient. The simple matching coefficient (SSM) counts the proportion of characters for which two OTUs share the same state (whether present or absent). The Jaccard coefficient (SJ) counts only matches where the character is present in both OTUs, excluding shared absences; this is preferred when shared absences are uninformative. Correlation coefficients and Euclidean distances are used for quantitative characters.

The similarity coefficients form a similarity matrix (an OTU x OTU table of pairwise similarities). Clustering methods organise OTUs into groups (clusters) based on their pairwise similarities. UPGMA (Unweighted Pair Group Method with Arithmetic Mean): the most common method; links the two most similar OTUs first, then progressively adds the next most similar; produces a phenogram. The result is a dendrogram (branching tree diagram) in which branch lengths are proportional to similarity; groups at the same branch level represent phenons (groups defined by a chosen similarity threshold).

Fill in the blank: ________ (Unweighted Pair Group Method with Arithmetic Mean) is the most common clustering method in numerical taxonomy; it links the two most similar OTUs first and progressively adds the next most similar to produce a phenogram.

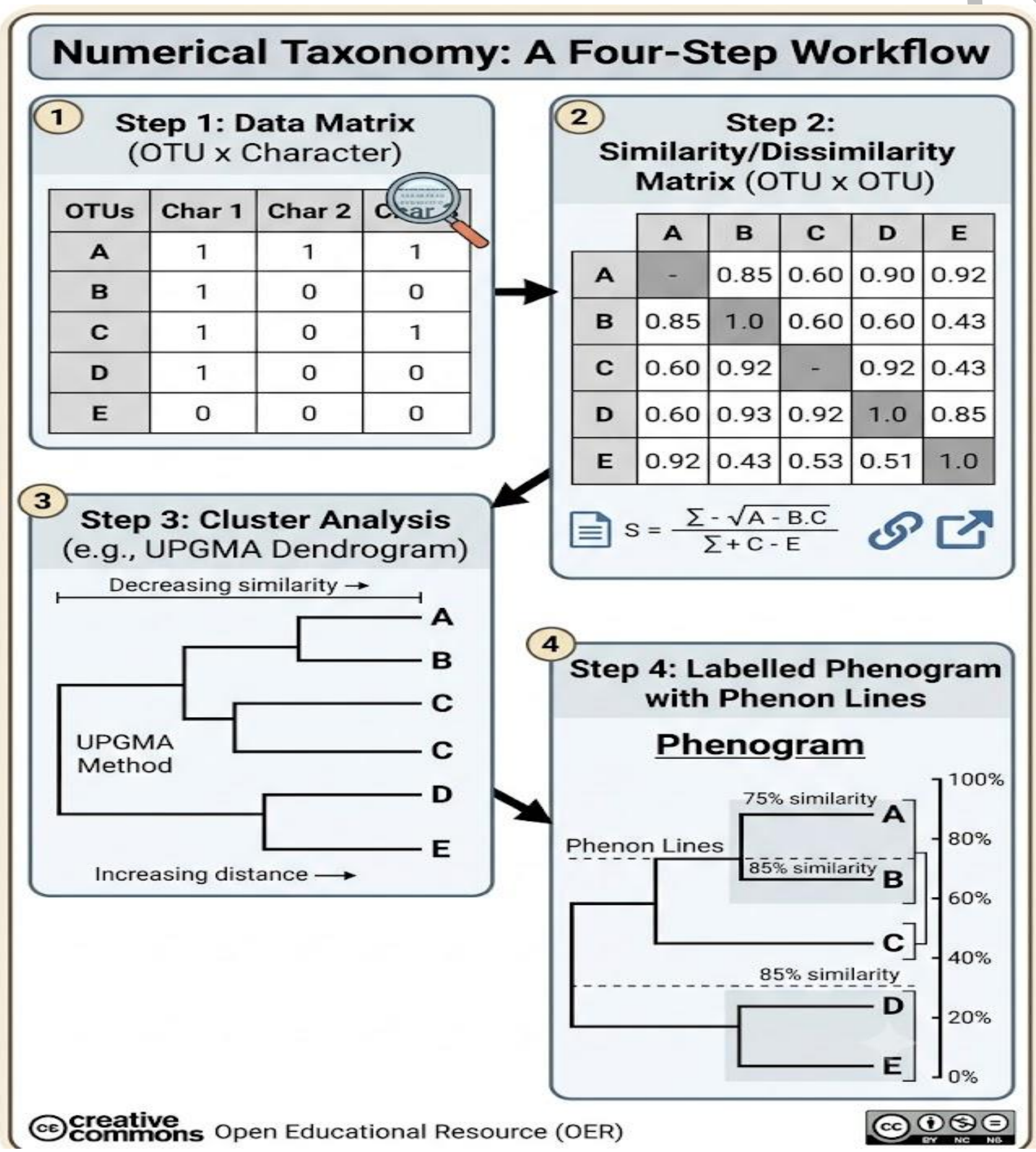


Figure 4.1: Numerical taxonomy workflow from data matrix to phenogram

Pilot questions 4.1

- State five principles of numerical taxonomy.
- Define OTU and describe the structure of a data matrix in numerical taxonomy.
- Distinguish between the simple matching coefficient and the Jaccard coefficient.
- Explain the UPGMA clustering method.
- State two advantages and two limitations of numerical taxonomy.

4.2 Cladistics (Phylogenetic Systematics)

4.2.1 Principles of cladistics

Cladistics (phylogenetic systematics) was developed by the German entomologist Willi Hennig in Grundzuge einer Theorie der Phylogenetischen Systematik (1950) and its English translation Phylogenetic Systematics (1966). The central principle is that classification must reflect evolutionary history (phylogeny) and that only monophyletic groups (clades) are valid taxonomic entities. Cladistics rejects paraphyletic and polyphyletic groups as artificial because they do not represent complete evolutionary lineages.

Three fundamental concepts in cladistics: (1) only shared derived characters (synapomorphies) reflect common ancestry and are the valid basis for grouping organisms; (2) shared ancestral characters (symplesiomorphies) are uninformative for grouping because they may be retained from a distant common ancestor shared with many other groups; (3) the most parsimonious cladogram (the one requiring the fewest evolutionary changes to explain the observed character distribution) is preferred as the best hypothesis of evolutionary relationships (parsimony criterion).

Fill in the blank: Cladistics was developed by Willi ________ (1950/1966); it classifies organisms strictly by shared derived characters (synapomorphies) reflecting common ancestry; only monophyletic groups are considered valid taxa.

4.2.2 Types of characters: plesiomorphies, apomorphies, and synapomorphies

Characters in cladistic analysis are classified relative to the evolutionary tree being studied. Plesiomorphy (ancestral character state): a character state inherited from a distant ancestor and retained in many lineages; it is shared broadly and therefore uninformative for identifying close relationships within the group being studied. Example: the presence of a vertebral column is a plesiomorphy for mammals (shared with all vertebrates) and is useless for distinguishing relationships among mammals.

Apomorphy (derived character state): a character state that is evolutionarily new (derived) relative to the ancestral state; it arose in one lineage and may or may not be shared among descendants. Synapomorphy: a shared derived character state inherited from a common ancestor by two or more taxa; it is the evidence for a clade. Example: the presence of hair is a synapomorphy of all mammals, defining the clade Mammalia. Autapomorphy: a derived character found only in one taxon; it diagnoses that taxon but does not provide evidence for relationships with other taxa.

Fill in the blank: A ________ is a shared derived character state inherited from a common ancestor by two or more taxa; it is the key evidence used in cladistics to identify clades and define monophyletic groups.

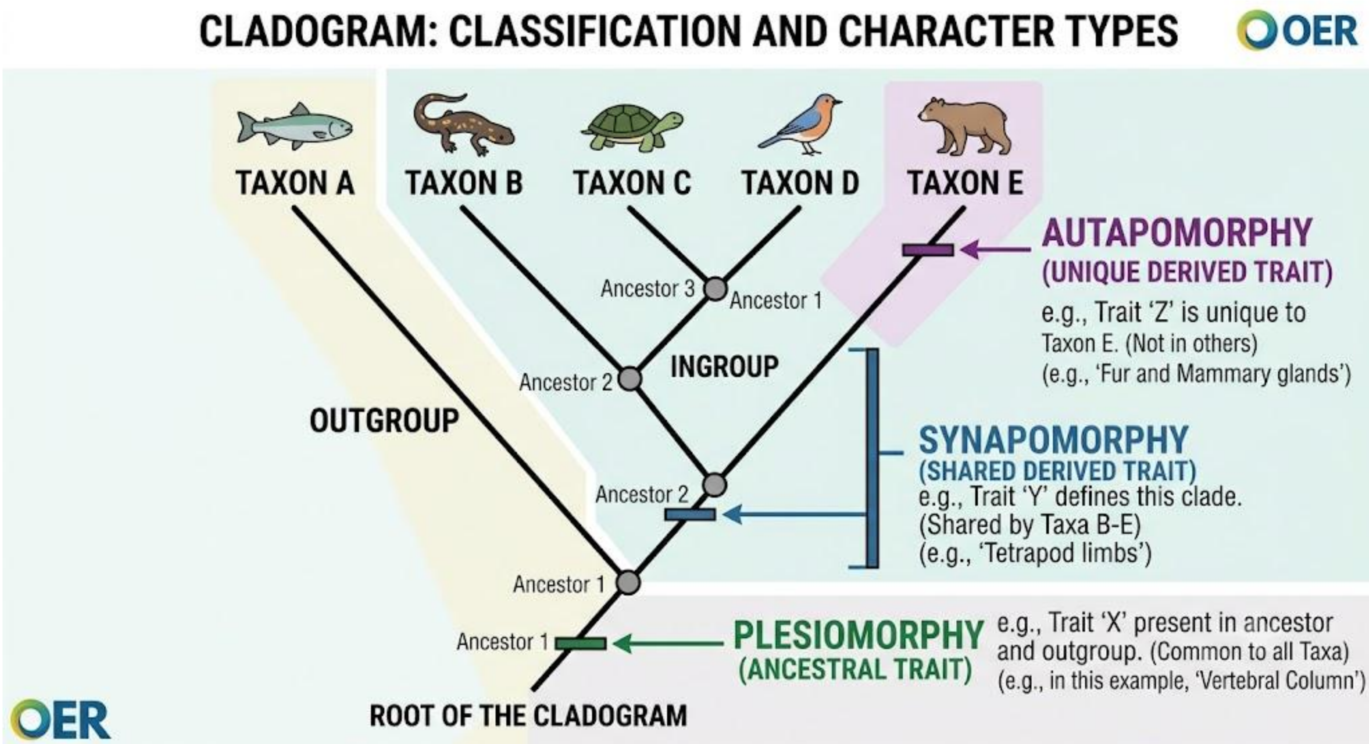


Figure 4.2: Cladogram illustrating plesiomorphies, synapomorphies, and autapomorphies

4.2.3 Constructing and interpreting cladograms

Steps in constructing a cladogram by hand (parsimony): (1) select taxa (ingroup) and an outgroup (a closely related taxon used to determine which character states are ancestral); (2) score each taxon for each character; (3) determine the polarity of each character (which state is ancestral, which is derived) by outgroup comparison: the state shared with the outgroup is plesiomorphic; the state not found in the outgroup is apomorphic; (4) group taxa that share apomorphies; (5) choose the topology requiring the fewest character state changes (most parsimonious cladogram).

Interpreting a cladogram: each internal node represents a hypothetical common ancestor; the branch pattern (topology) represents the hierarchical pattern of descent; branch length may or may not represent amount of change depending on the software; sister groups are the taxa that share an immediate common ancestor; the outgroup is the most distantly related taxon used to root the tree. Homoplasy is the occurrence of the same character state in two or more taxa not because of common ancestry but because of convergent evolution; it reduces parsimony and weakens the support for clades that depend on that character.

Fill in the blank: ________ comparison is used in cladistics to determine character polarity: the character state shared with the outgroup is plesiomorphic (ancestral); the state not found in the outgroup is apomorphic (derived).

Pilot questions 4.2

- State the three fundamental concepts of cladistics.
- Distinguish between plesiomorphy, synapomorphy, and autapomorphy.
- Explain why symplesiomorphies are uninformative in cladistic analysis.
- Explain the parsimony criterion in cladistics.
- Define homoplasy and explain its effect on cladistic analysis.

4.3 Molecular Systematics

4.3.1 Molecular markers used in systematics

Molecular systematics uses nucleotide sequences (DNA or RNA) or amino acid sequences (proteins) to infer phylogenetic relationships. Commonly used markers are chosen to match the evolutionary depth being studied. For deep-level phylogenetics (relationships among phyla, classes, or orders): ribosomal RNA genes (18S rDNA for eukaryotes; 16S rDNA for prokaryotes) and large subunit rRNA (28S); highly conserved across all life. For family-to-genus-level relationships: the chloroplast genes rbcL and matK (plants); cytochrome b (animals); nuclear ribosomal ITS (Internal Transcribed Spacer; plants and fungi).

For species-level and population-level studies: mitochondrial cytochrome oxidase I (CO1; the standard animal barcode); rbcL + matK (plant barcodes); ITS2; microsatellites (highly variable repetitive sequences; used for population genetics and species delimitation). For genomics-scale phylogenetics: genome-scale data including hundreds or thousands of single-copy nuclear genes (phylogenomics); RADseq and whole-genome sequencing. The choice of marker depends on the taxonomic level being studied: a marker that evolves too slowly will show no variation at species level; one that evolves too fast will show no signal at order level.

Fill in the blank: The mitochondrial cytochrome oxidase I (CO1) gene is the standard ________ marker for animals; for plants the standard barcode combination is rbcL + matK; these short DNA sequences allow rapid identification of specimens against a reference library.

4.3.2 Methods of phylogenetic analysis

Distance methods: molecular distances (pairwise sequence divergences) are calculated and clustered by UPGMA or neighbour-joining (NJ) to produce a tree; fast and computationally simple; NJ is particularly popular because it does not assume constant evolutionary rate (no molecular clock assumption) and handles unequal branch lengths well. Maximum parsimony (MP): finds the tree topology that requires the fewest nucleotide changes to explain the observed sequence data; computationally expensive for large datasets; may be misleading when evolutionary rates vary greatly among lineages (long-branch attraction).

Maximum likelihood (ML): evaluates all possible trees and selects the one with the highest probability of producing the observed data, given an explicit model of sequence evolution (e.g. GTR + gamma model); statistically rigorous; accounts for rate heterogeneity. Bayesian inference (BI): uses Bayesian statistics to calculate the posterior probability of each tree topology and branch length given the sequence data and a prior model; results expressed as posterior probability support values; implemented in MrBayes and BEAST. ML and BI are now the standard methods for robust phylogenetic analysis.

Fill in the blank: ________ inference uses Bayesian statistics to calculate the probability of each tree topology given the sequence data and a prior model of evolution; it provides posterior probability support values and is one of the two standard methods for robust phylogenetic analysis.

4.3.3 Applications of molecular systematics

Major applications of molecular systematics: (1) Phylogenetic classification: constructing phylogenies that serve as the basis for natural classification; the APG (Angiosperm Phylogeny Group) classification of flowering plants, based on chloroplast and nuclear DNA, has replaced earlier morphological systems and is the global standard. (2) Species delimitation: identifying cryptic species and resolving species boundaries using multi-locus data; essential for the Anopheles gambiae complex and other cryptic Nigerian pest and disease vector complexes.

(3) Molecular clock analysis: using calibrated substitution rates to estimate when lineages diverged; e.g. estimating when the West African and Central African populations of gorilla diverged to justify recognising them as distinct subspecies. (4) Biogeography: reconstructing the geographic origins and dispersal history of lineages; e.g. reconstructing the colonisation history of West Africa by plant families. (5) DNA barcoding: rapid species identification of specimens against a reference library (BOLD Systems); particularly valuable for identifying Nigerian insect pests, plant material at customs, and fish sold in markets.

Fill in the blank: The APG (Angiosperm Phylogeny Group) classification of flowering plants is based on ________ and nuclear DNA sequence data; it has replaced earlier morphological systems and is now the globally accepted standard classification for angiosperms.

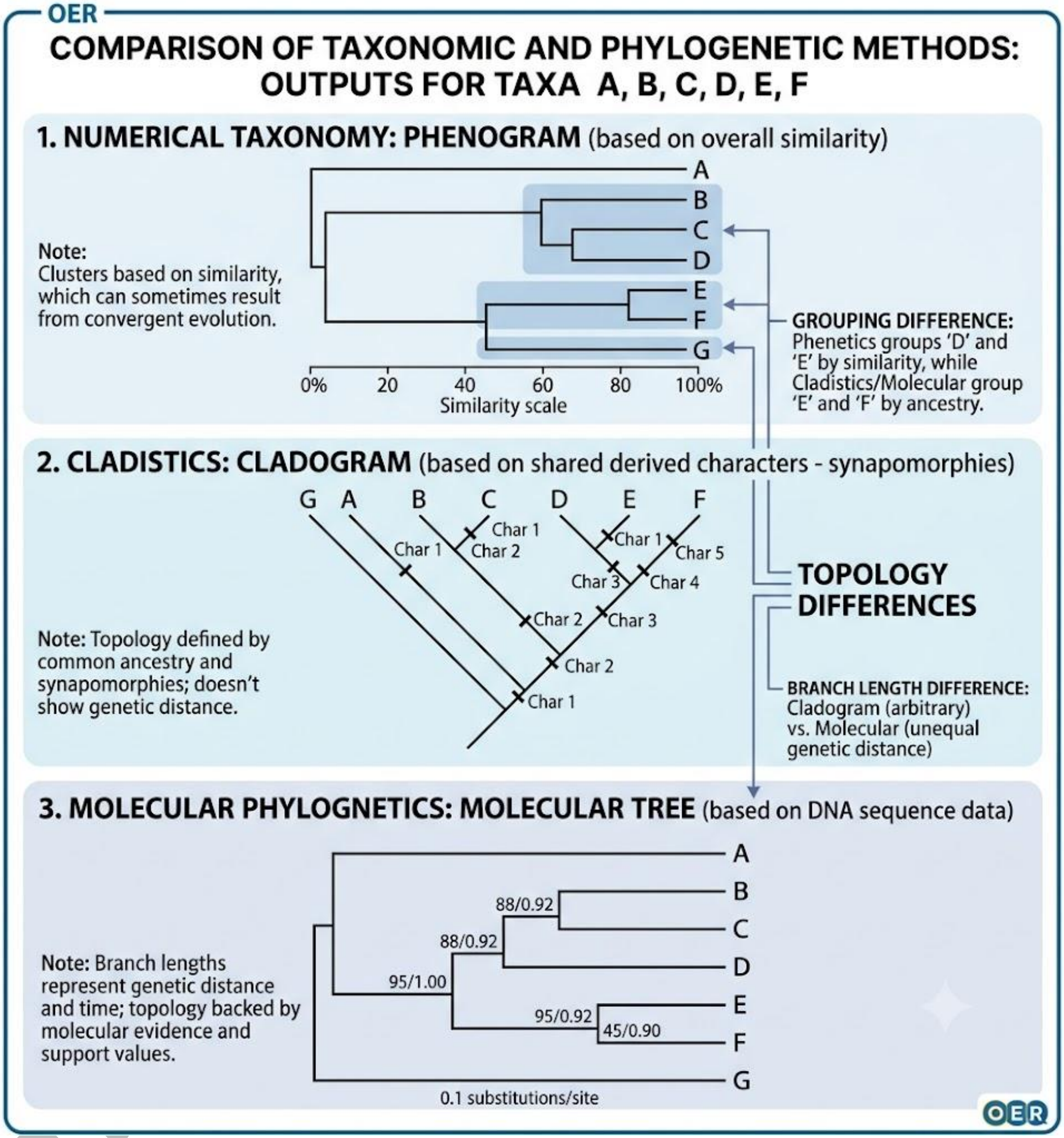


Figure 4.3: Comparison of phenogram, cladogram, and molecular phylogenetic tree for the same set of taxa

Pilot questions 4.3

1. Name four molecular markers used in systematics and state the taxonomic level each is best suited for.
2. Distinguish between maximum parsimony and maximum likelihood methods of phylogenetic analysis.
3. Explain what the Angiosperm Phylogeny Group (APG) classification is and on what data it is based.
4. Explain how molecular systematics is used to delimit cryptic species.
5. Explain what DNA barcoding is and describe one application in Nigeria.

4.4 Integrating Approaches: Modern Systematic Practice

4.4.1 Comparing phenetics, cladistics, and molecular systematics

Phenetics, cladistics, and molecular systematics differ in their theoretical basis, the characters they use, and their outputs. Phenetics: theory-free; uses all characters equally weighted; output is a phenogram based on overall similarity; does not distinguish ancestral from derived characters; does not explicitly reflect evolutionary history; produces stable, repeatable classifications but classifications may not be natural (may include paraphyletic groups). Cladistics: theory-explicit (descent with modification); uses only shared derived characters; output is a cladogram representing phylogenetic relationships; only monophyletic groups valid; may produce classifications with many unnamed ranks.

Molecular systematics: uses DNA/protein sequence data rather than morphological characters; avoids problems of convergent morphological evolution; provides quantitative branch lengths and statistical support values; has transformed our understanding of relationships; but: sequences also suffer from convergent evolution (homoplasy at the molecular level); the results depend on the model of sequence evolution chosen; and interpretation still requires integration with morphological, fossil, and ecological data. Modern systematics regards molecular and morphological evidence as complementary, not competing.

Fill in the blank: Modern systematics regards molecular and ________ evidence as complementary; molecular data avoid morphological convergence but require model assumptions; morphological data provide interpretable characters but suffer from convergent evolution.

4.4.2 Integrative taxonomy in practice

Integrative taxonomy combines morphological, molecular, ecological, acoustic, and behavioural data to produce the best-supported species delimitations and classifications. The workflow for describing a new species using an integrative approach: (1) collect and preserve specimens with full locality and ecological data; (2) obtain morphological measurements and descriptions; (3) extract DNA and sequence one or more markers; (4) analyse molecular data to determine whether the specimen is genetically distinct from known species; (5) compare morphological characters with type specimens; (6) if genetic and morphological distinctness are both confirmed, prepare a formal description.

Integrative taxonomy has been applied to several Nigerian taxa. The Cross River gorilla (Gorilla gorilla diehli) was distinguished from the Western Lowland gorilla (Gorilla gorilla gorilla) partly on the basis of morphometric and molecular data. Nigerian forest tree species in families such as Meliaceae (mahogany family) and Leguminosae that were previously poorly known are being revised using combined morphological and molecular approaches. Ecological niche modelling can also be integrated, using distribution data from GBIF to predict suitable habitat and identify geographically separate populations as candidates for species status.

Fill in the blank: ________ taxonomy combines morphological, molecular, ecological, and behavioural data to delimit and describe species; it is now the standard approach for new species descriptions and is being applied to revise poorly known Nigerian taxa.

4.4.3 Systematics and biodiversity informatics

Biodiversity informatics is the application of information technology to the collection, management, and analysis of biodiversity data. Major global databases: GBIF (Global Biodiversity Information Facility; www.gbif.org): aggregates occurrence records from hundreds of institutions worldwide; over 2 billion occurrence records; includes Nigerian specimen data from major herbaria. Plants of the World Online (POWO; Kew): authoritative current names and synonymy for all vascular plants; distribution maps. Catalogue of Life: comprehensive taxonomy covering all life; used as the backbone by GBIF.

iNaturalist (www.inaturalist.org): a citizen science platform for recording biodiversity observations with georeferenced photographs; used by nature watchers and researchers; identifications made by the community; records contribute to GBIF. Barcode of Life Data Systems (BOLD; www.boldsystems.org): the reference library for DNA barcodes; used for rapid molecular identification. African Plants Database (Geneva); JSTOR Global Plants (type images). For Nigeria, developing the capacity to contribute to and use these databases is a priority: systematic data curated in Nigeria should be shared with global platforms to maximise its value for conservation and research.

Fill in the blank: ________ (Global Biodiversity Information Facility) aggregates over 2 billion biodiversity occurrence records from institutions worldwide; it includes Nigerian specimen data and is the primary global platform for accessing biodiversity occurrence information.

Approach	**Theoretical Basis**	**Characters Used**	**Output**	**Valid Groups**	**Character Weighting**	**Limitations**	**Key References**
Phenetics	Overall similarity (numerical taxonomy)	Morphological, physiological, biochemical	Dendrograms (phenograms)	Any groupings based on similarity	Equal weighting of all characters	Ignores evolutionary history; convergent traits can mislead	Sokal & Sneath (1963)
Cladistics	Shared derived	Morphological,	Cladograms	Only monophy	Emphasis on	Sensitive to	Hennig (1966)

	characters (synapomorphies)	molecular, behavioral	(branching diagrams)	letic groups valid	derived characters	character selection; homoplasy complicates analysis	
Molecular Systematics	Genetic sequence comparison, molecular phylogenetics	DNA, RNA, protein sequences	Phylogenetic trees	Monophyletic groups supported by molecular data	Weighting by substitution models, gene regions	Requires advanced technology; incomplete lineage sorting; horizontal gene transfer	Woese (1977), APG (1998–present)

Box 4.1: Comparison of phenetics, cladistics, and molecular systematics

Pilot questions 4.4

1. Distinguish between the outputs of phenetics and cladistics.
2. Explain why modern systematics regards molecular and morphological data as complementary.
3. Describe the workflow for describing a new species using integrative taxonomy.
4. Name four biodiversity informatics databases and state the type of data each holds.
5. Explain why contributing Nigerian biodiversity data to global databases is a priority.

Series Summary

This Series covered major advances in systematics and numerical taxonomy. Numerical taxonomy, or phenetics, developed by Sneath and Sokal in 1963, classifies organisms using overall similarity, equal character weighting, OTUs, data matrices, similarity coefficients such as simple matching and Jaccard, and UPGMA clustering to produce phenograms. Its strengths are objectivity and repeatability, while its weaknesses include ignoring evolutionary direction and sometimes producing unnatural groups. Cladistics, introduced by Hennig, recognises only monophyletic groups and distinguishes plesiomorphies, synapomorphies, and autapomorphies. Outgroup comparison is used to determine character polarity, parsimony selects the tree with the fewest evolutionary changes, and homoplasy may weaken clade support.

Molecular systematics uses markers suited to different taxonomic levels, including 18S and 16S rDNA, rbcL, matK, ITS, CO1, and microsatellites. Its major methods include UPGMA, neighbour joining, maximum parsimony, maximum likelihood, and Bayesian inference using tools such as MrBayes and BEAST. Applications include APG angiosperm classification, cryptic species identification, molecular clocks, biogeography, and DNA barcoding through BOLD. Integrative taxonomy combines morphological, molecular, and ecological evidence and is now widely used in modern species descriptions, including studies of the Cross River gorilla and Nigerian forest trees. Biodiversity informatics resources covered include GBIF, POWO, Catalogue of Life, iNaturalist, BOLD, and JSTOR Global Plants. By completing this Series, students should achieve SLOs 4.1 to 4.6.

Glossary of Terms

1. **Apomorphy:** a derived (evolutionarily new) character state that arose in one lineage; may be shared (synapomorphy) or unique to one taxon (autapomorphy).
2. **Autapomorphy:** a derived character state found only in one taxon; it diagnoses that taxon but provides no evidence for its relationships with other taxa.

3. **Bayesian inference (BI):** a method of phylogenetic analysis that uses Bayesian statistics to calculate posterior probability support values for tree topologies, given sequence data and a prior model of evolution.
4. **Cladogram:** a branching diagram produced by cladistic analysis showing the hypothetical evolutionary relationships among taxa, based on the distribution of synapomorphies.
5. **Data matrix:** in numerical taxonomy, a table with OTUs as rows and characters as columns; each cell contains the character state of that OTU for that character.
6. **GBIF (Global Biodiversity Information Facility):** an international open-access database aggregating biodiversity occurrence records from institutions worldwide; accessible at www.gbif.org.
7. **Homoplasy:** the occurrence of the same character state in two or more taxa not because of common ancestry but because of convergent evolution, parallelism, or reversal; it reduces the support for clades in both morphological and molecular phylogenetics.
8. **Jaccard coefficient:** a similarity coefficient used in numerical taxonomy that considers only shared presences (shared absences excluded); preferred when shared absences are uninformative.
9. **Maximum likelihood (ML):** a method of phylogenetic analysis that selects the tree topology with the highest probability of producing the observed data under an explicit model of sequence evolution; standard method for robust analysis.
10. **Maximum parsimony (MP):** a method of phylogenetic analysis that selects the tree requiring the fewest evolutionary changes to explain the observed character data; computationally expensive for large datasets.
11. **Molecular clock:** the approximately constant rate of molecular sequence change over time; used to estimate divergence dates between lineages when calibrated against fossil dates.

12. **Neighbour-joining (NJ):** a distance-based tree-building method that groups taxa by minimising total branch length; does not assume a molecular clock; fast and widely used for large datasets.
13. **Numerical taxonomy:** the classification of organisms by overall similarity across many equally weighted characters, using multivariate statistical methods; also called phenetics; developed by Sokal and Sneath (1963).
14. **OTU (Operational Taxonomic Unit):** the basic unit of comparison in numerical taxonomy; may be a specimen, a species, a population, or any consistently defined entity.
15. **Outgroup:** a taxon related to but outside the ingroup, used in cladistic analysis to determine the polarity of characters (which state is ancestral).
16. **Parsimony criterion:** the principle that the most parsimonious cladogram (requiring the fewest evolutionary changes) is preferred as the best hypothesis of evolutionary relationships.
17. **Phenetics:** see Numerical taxonomy.
18. **Phenogram:** a branching diagram produced by numerical taxonomy (phenetics), showing overall similarity among OTUs; branch lengths are proportional to phenetic similarity.
19. **Plesiomorphy:** an ancestral character state retained from a distant common ancestor; shared broadly across lineages; uninformative for identifying close relationships within the group being studied.
20. **Polarity:** the evolutionary direction of a character state; determining polarity (which state is ancestral, which derived) requires outgroup comparison.
21. **Posterior probability:** in Bayesian inference, the probability assigned to each tree topology or clade after incorporating the sequence data and the prior model; expressed as a value from 0 to 1.

22. **Simple matching coefficient (SSM):** a similarity coefficient in numerical taxonomy that counts the proportion of characters for which two OTUs share the same state, including shared absences.
23. **Symplesiomorphy:** a shared ancestral character state; uninformative in cladistics because it may be retained from a distant ancestor shared with many other groups.
24. **Synapomorphy:** a shared derived character state inherited from a common ancestor by two or more taxa; the key evidence for a clade in cladistic analysis.
25. **UPGMA (Unweighted Pair Group Method with Arithmetic Mean):** the most common clustering method in numerical taxonomy; links the two most similar OTUs first and progressively adds others to build a phenogram.

Concept Check Questions [Series 4]

Objective Questions

1. Numerical taxonomy (phenetics) was developed by Sneath and ________ (1963); its core principle is equal weighting of all characters and classification by overall similarity. (Linked to SLO 4.1)
2. Cladistics was developed by Willi ________ (1950/1966); it classifies organisms strictly by shared derived characters (synapomorphies) and recognises only monophyletic groups as valid. (Linked to SLO 4.2)
3. A ________ is a shared derived character state inherited from a common ancestor; it is the key evidence for a clade in cladistic analysis. (Linked to SLO 4.2)
4. The mitochondrial cytochrome oxidase I (CO1) gene is the standard animal ________ marker; for plants the standard combination is rbcL + matK. (Linked to SLO 4.4)
5. ________ (Global Biodiversity Information Facility) aggregates over 2 billion occurrence records from institutions worldwide, including Nigerian specimen data. (Linked to SLO 4.6)

Short-Answer Questions

- State five principles of numerical taxonomy. (Linked to SLO 4.1)
- Distinguish between a synapomorphy and a plesiomorphy and explain why only synapomorphies are informative in cladistics. (Linked to SLO 4.2)
- Distinguish between maximum parsimony and Bayesian inference as phylogenetic methods. (Linked to SLO 4.4)
- State three differences between phenetics and cladistics. (Linked to SLO 4.5)
- Name four biodiversity informatics databases and state the type of data each holds. (Linked to SLO 4.6)

Long-Answer Questions

1. Explain the principles of numerical taxonomy; describe OTUs, data matrices, similarity coefficients, and UPGMA clustering; and state two advantages and two limitations of the approach. (Linked to SLO 4.1)
2. Explain the principles of cladistics; distinguish between plesiomorphies, synapomorphies, and autapomorphies; and describe how a cladogram is constructed and interpreted. (Linked to SLOs 4.2, 4.3)
3. Describe the main molecular markers used in systematics; compare distance, parsimony, maximum likelihood, and Bayesian methods; and explain how molecular systematics, cladistics, and phenetics are integrated in modern systematic practice. (Linked to SLOs 4.4, 4.5)

Answers to Concept Check Questions [Series 4]

Objective Questions

6. Sokal.
7. Hennig.
8. Synapomorphy.
9. Barcode.
10. GBIF.

Short-Answer Questions

11. (1) Greater information content = better classification; (2) equal weighting of all characters; (3) overall similarity based on as many characters as possible; (4) distinct taxa recognised from the pattern of overall similarity; (5) taxonomy is strictly empirical; phylogenetic speculation excluded.
12. Synapomorphy: a shared derived character state inherited from a common ancestor; it is evidence for a clade because all members of the clade share it by descent. Plesiomorphy: an ancestral character state retained from a distant ancestor; uninformative because it may be shared by many distantly related groups and does not indicate close relationship.
13. Maximum parsimony: selects the tree requiring the fewest evolutionary changes; computationally expensive; may be misled by unequal rates (long-branch attraction). Bayesian inference: calculates posterior probability of each tree given sequence data and a prior model; provides statistical support values; standard for modern robust analysis.
14. (1) Theoretical basis: phenetics is atheoretical (overall similarity); cladistics is explicitly evolutionary (only shared derived characters). (2) Output: phenogram vs cladogram. (3) Valid groups: phenetics accepts any phenetically cohesive group; cladistics accepts only monophyletic groups.
15. GBIF (georeferenced occurrence records); Plants of the World Online/POWO (accepted plant names and synonymy); BOLD Systems (DNA barcode sequences for identification); JSTOR Global Plants (high-resolution images of herbarium type specimens).

Long-Answer Questions

1. Numerical taxonomy (Sokal and Sneath 1963): five principles (high information content; equal weighting; many characters; distinct taxa from overall similarity; strictly empirical). OTU: the basic unit of comparison (specimen, species, or population). Data matrix: rows = OTUs; columns = characters; cells = character states (binary 0/1 or multistate). Similarity coefficients: simple matching coefficient (counts shared states including shared absences); Jaccard coefficient (shared presences only; excludes shared absences). UPGMA: links the two most similar OTUs first; progressively builds a phenogram; branch lengths proportional to similarity. Two advantages: objective and repeatable (same data give same result regardless of the taxonomist); uses many characters simultaneously, reducing the influence of any single character. Two limitations: may produce non-natural (paraphyletic) groups because it ignores evolutionary direction; phenetic similarity may reflect convergent evolution rather than common ancestry, grouping distantly related look-alikes together.
2. Cladistics (Hennig 1950/1966): three fundamental concepts: only synapomorphies (shared derived characters) reflect common ancestry and are valid for grouping; symplesiomorphies (shared ancestral characters) are uninformative; the most parsimonious tree is the best hypothesis. Character types: plesiomorphy (ancestral state shared with distant relatives; uninformative for close grouping; e.g. vertebral column in mammals); synapomorphy (shared derived state from a common ancestor; evidence for a clade; e.g. hair defining Mammalia); autapomorphy (derived state unique to one taxon; diagnoses that taxon but provides no relationship evidence). Outgroup comparison determines polarity: character state shared with the outgroup is plesiomorphic; state absent in outgroup is apomorphic. Constructing a cladogram: select ingroup and outgroup; score characters; determine polarity; group taxa sharing apomorphies; choose most parsimonious topology. Interpreting: nodes = hypothetical common ancestors; topology = nested pattern of descent; sister groups share an immediate common ancestor; homoplasy = same state arising independently, weakening clade support.
3. Molecular markers: 18S/16S rDNA (deep levels: phyla, classes); rbcL + matK (family-genus in plants); ITS (plant and fungal genera and species); CO1 (animal species

barcoding); microsatellites (population level). Methods: distance (UPGMA, NJ: fast; pairwise distances clustered; NJ handles unequal rates); maximum parsimony (fewest changes; computationally slow; long-branch attraction problem); maximum likelihood (best-fit tree under explicit sequence evolution model; statistically rigorous; accounts for rate heterogeneity); Bayesian inference (posterior probability support; model-based; MrBayes, BEAST; ML and BI are now the standard). Integration: phenetics outputs phenograms (overall similarity; good for rapid grouping; may include paraphyletic groups; atheoretical); cladistics outputs cladograms (phylogenetic relationships; only monophyletic groups; theory-explicit; morphological convergence a problem); molecular systematics provides quantitative branch lengths and statistical support but depends on model choice; modern practice (integrative taxonomy) uses all three types of evidence to produce the most robustly supported classification; morphological data remain essential for fossil taxa, identification, and understanding adaptations; molecular data resolve relationships that morphology cannot.

Answers to Pilot Questions [Series 4]

Part 4.1

6. Five principles of numerical taxonomy (Sokal and Sneath, 1963): (1) A classification with greater information content is better than one with less; (2) every character is of equal a priori weight (equal weighting principle); (3) overall similarity should be assessed using as many characters as possible; (4) distinct taxa can be recognised from the pattern of overall similarity; (5) taxonomy is a strictly empirical science from which phylogenetic speculation is excluded.
7. An OTU (Operational Taxonomic Unit) is the basic unit used in a numerical taxonomic analysis; it is any consistently defined entity being compared and may be a specimen, a species, a population, or a higher taxon. The data matrix is a rectangular table with OTUs as rows and characters as columns; each cell contains the character state of that OTU for that character; binary states are coded as 0 (absent) or 1 (present); multistate characters

are coded as 0, 1, 2, etc.; quantitative characters are standardised before inclusion. A matrix of 20 OTUs and 60 characters produces a 20 x 60 table with 1,200 cells.

8. The simple matching coefficient (SSM) calculates the proportion of characters for which two OTUs have the same state, including both shared presences (1-1 matches) and shared absences (0-0 matches): SSM = (a + d) / (a + b + c + d), where a = both present, d = both absent, b and c = mismatches. The Jaccard coefficient (SJ) considers only shared presences: SJ = a / (a + b + c); it excludes shared absences on the grounds that two organisms sharing the absence of a character may do so for entirely different reasons, making the shared absence uninformative about their relationship; the Jaccard coefficient is preferred when shared absences are large and likely uninformative.
9. UPGMA (Unweighted Pair Group Method with Arithmetic Mean) is an agglomerative hierarchical clustering method used to build a phenogram from a similarity matrix. Step 1: find the pair of OTUs with the highest pairwise similarity; link them at that similarity level to form the first cluster. Step 2: recalculate the average similarity between the new cluster and all remaining OTUs by averaging all pairwise similarities. Step 3: find the next most similar pair (which may be two OTUs or an OTU and a cluster) and link them at their average similarity level. Steps 2-3 are repeated until all OTUs are incorporated into a single branching tree. The result is a phenogram in which the height of each node represents the similarity level at which the taxa were linked.
10. Two advantages: (1) Objectivity and reproducibility: the same data matrix processed by the same method will always produce the same result, regardless of who performs the analysis; numerical taxonomy removes the subjective bias of individual taxonomists. (2) Multi-character basis: using 50-100 or more characters simultaneously produces a more stable and robust similarity estimate than judgements based on a few chosen characters; no single character can dominate the result. Two limitations: (1) May produce non-natural (paraphyletic) groups: because overall similarity is used without reference to evolutionary direction, organisms that have independently evolved similar appearances may be grouped together (convergent evolution misleads the analysis). (2) Ignores evolutionary direction: by treating all characters as equally weighted and ancestral vs derived states as irrelevant, phenetics may produce classifications that do not reflect the true evolutionary history of the organisms.

Part 4.2

11. Three fundamental concepts of cladistics: (1) Only shared derived characters (synapomorphies), inherited from a common ancestor, provide valid evidence for grouping organisms together in a clade; (2) Shared ancestral characters (symplesiomorphies) are uninformative for identifying close relationships within the group being studied because they may be retained from a distant ancestor shared with many other groups; (3) The most parsimonious cladogram, the one requiring the fewest total evolutionary changes (character state transitions) to explain the observed character distribution, is the preferred hypothesis of evolutionary relationships.
12. Plesiomorphy (ancestral character state): a character state inherited from a distant ancestor and retained broadly across many lineages; it is uninformative for close grouping within the group being studied; e.g. the presence of a backbone is a plesiomorphy shared by all vertebrates and useless for distinguishing among mammals. Synapomorphy (shared derived character state): a derived character state shared by two or more taxa by inheritance from their common ancestor; it is the evidence for the clade; e.g. the presence of hair is a synapomorphy uniting all mammals. Autapomorphy (unique derived character state): a derived character found only in one taxon; it diagnoses that taxon uniquely but provides no information about its relationships with other taxa.
13. Symplesiomorphies (shared ancestral characters) are uninformative in cladistic analysis because they are retained from an ancestor common to many lineages, not just the ones being compared. If both a fish and a mammal have a backbone, this shared character does not indicate that fish and mammals are sister groups; the backbone was present in the ancestor of all vertebrates and is retained by all descendants. Using a symplesiomorphy to group taxa would incorrectly unite all organisms that share it regardless of their actual evolutionary proximity; it would produce an artificial group based on shared retention of an ancestral feature rather than evidence of a recent exclusive common ancestor.
14. The parsimony criterion in cladistics states that among all possible cladogram topologies that could explain the distribution of characters among the taxa being studied, the most parsimonious one, requiring the smallest total number of evolutionary changes (character

state transitions), is preferred as the best hypothesis of evolutionary relationships. The rationale is Occam's razor: the simplest explanation (fewest assumptions of independent evolutionary events) is preferred over more complex ones. In practice, for a dataset with n taxa and m characters, many different tree topologies are possible, and parsimony analysis searches through these to find the tree or trees with the minimum number of steps; each additional independent origin of the same character on the tree adds to the total step count and reduces parsimony.

15. Homoplasy is the occurrence of the same character state in two or more taxa not because they inherited it from their most recent common ancestor but because it evolved independently (convergent evolution), arose in parallel in two lineages, or was lost and then regained (reversal). In morphological cladistics, homoplasy reduces the support for clades that are defined by homoplastic characters because the shared character no longer provides reliable evidence of common ancestry. When a character is mapped onto the most parsimonious tree and found to have arisen more than once, it contributes to a measure of tree quality called the consistency index (CI); a CI of 1 means no homoplasy; a CI approaching 0 means extensive homoplasy. High homoplasy makes it difficult to determine which characters truly reflect common ancestry and weakens confidence in the resulting cladogram.

Part 4.3

1. Four molecular markers and their levels: (1) 18S rDNA (eukaryote small subunit ribosomal RNA): deep-level phylogenetics; relationships among phyla, kingdoms, and domains; evolves very slowly; conserved across all eukaryotes. (2) Chloroplast rbcL gene (large subunit of RuBisCO): plant systematics at family-to-order level; moderate rate of evolution; part of the standard plant barcode. (3) Mitochondrial cytochrome oxidase I (CO1): the standard animal DNA barcode; species-level identification; evolves fast enough to distinguish closely related species. (4) Nuclear ITS (Internal Transcribed Spacer): widely used for species and genus-level phylogenetics in plants, fungi, and some animals; highly variable; can distinguish closely related species and populations.

2. Maximum parsimony (MP): evaluates possible tree topologies and selects the one requiring the fewest total nucleotide changes to explain the observed sequence data; does not use an explicit model of sequence evolution; computationally expensive for large datasets because the number of possible topologies grows exponentially with the number of taxa; can be misled by long-branch attraction (when two lineages with high substitution rates are incorrectly grouped together because they independently acquire similar derived states). Maximum likelihood (ML): uses an explicit statistical model of sequence evolution (e.g. the GTR + gamma model, which accounts for different rates of change between nucleotide pairs and rate heterogeneity across sites); selects the tree topology with the highest likelihood of producing the observed data under this model; statistically rigorous; accounts for rate heterogeneity; computationally intensive but feasible with RAxML and IQ-TREE software.
3. The Angiosperm Phylogeny Group (APG) classification is a series of published classifications of flowering plants (angiosperms) produced by an international collaborative group of plant systematists. The first APG classification (APG I, 1998) was based on two chloroplast genes (rbcL and atpB); subsequent versions (APG II 2003, APG III 2009, APG IV 2016) added more molecular data and refined the classification. The APG system has replaced the older morphological classifications (e.g. Cronquist, Takhtajan, Dahlgren) as the global standard for angiosperm families and orders; it has significantly changed the placement of many families and merged or split others based on molecular evidence; all major plant databases (POWO, GBIF) and Nigerian flora treatments are now updated to APG IV.
4. Molecular systematics is used to delimit cryptic species through multi-locus sequencing and phylogenetic analysis. When morphologically indistinguishable populations show reciprocal monophyly (each population forms a distinct clade in a gene tree with no shared haplotypes), genetic divergence above a threshold (often 2-3% for CO1 in animals), and consistent differences at several independent loci, this provides molecular evidence that they are genetically isolated and may be distinct species. In the Anopheles gambiae complex, molecular studies using multiple nuclear and mitochondrial loci first revealed that what was considered a single species comprised seven reproductively isolated species with distinct geographic distributions and ecological preferences; this

was later confirmed by evidence from crossing experiments, cytogenetics (different chromosomal inversions), and ecological data.

5. DNA barcoding is the use of a short, standardised DNA sequence, typically the mitochondrial cytochrome oxidase subunit I (CO1) gene (~650 bp) for animals or the rbcL + matK combination for plants, to identify biological specimens by comparing their sequence against a reference library of sequences from known species (BOLD Systems or GenBank). One application in Nigeria: rapid identification of fish species sold in Nigerian markets. Many commercially important fish species in the Niger Delta and Atlantic coastal fisheries are morphologically similar as juveniles or when filleted; DNA barcoding allows the correct species to be identified from a small tissue sample, enabling market monitoring, detection of mislabelled fish, management of targeted species, and documentation of which species are being harvested at different seasons.

Part 4.4

1. Phenetics output: a phenogram (dendrogram) in which branch lengths represent degrees of overall phenetic similarity; groups (phenons) are defined by choosing a similarity threshold; no evolutionary direction is implied; any phenetically cohesive group may be recognised regardless of whether it is monophyletic. Cladistics output: a cladogram in which the topology represents the hierarchical pattern of shared derived characters; each node represents a hypothetical common ancestor; only monophyletic groups (clades) are recognised as valid taxa; the tree is rooted and directional; branch lengths in a strict cladogram do not necessarily represent amount of change but only the sequence of branching events.
2. Molecular and morphological evidence are complementary because each type of evidence has strengths where the other has weaknesses. Molecular data avoid the convergent morphological evolution that misleads morphological analyses (organisms with similar body shapes due to similar selective pressures, e.g. sharks and dolphins, are correctly separated by molecular data because their DNA sequences clearly differ); but molecular analyses can be misled by molecular homoplasy (convergent nucleotide substitutions), require explicit model assumptions, and cannot be applied to extinct taxa without preserved DNA. Morphological data provide interpretable characters whose biological

meaning is understood (they can be linked to function and ecology), are applicable to fossils, and are necessary for identification; but they are prone to convergent evolution. Using both together provides cross-validation and a more complete picture.

3. Integrative taxonomy workflow for a new species: (1) Collect and preserve multiple specimens with full locality, habitat, and ecological data; deposit voucher specimens in a recognised public herbarium or natural history museum. (2) Prepare morphological descriptions: take measurements of all relevant characters; photograph key diagnostic features; compare with type specimens of related species. (3) Extract DNA from fresh or silica-dried tissue and sequence one or more markers (e.g. CO1 and ITS for a plant; rbcL + matK + ITS2 for a plant species); submit sequences to GenBank. (4) Perform phylogenetic analysis (ML or Bayesian) to determine whether the new specimen forms a distinct clade relative to known species. (5) If molecular distinctness is confirmed, confirm morphological distinctness from the types of related species. (6) Prepare a formal description following the requirements of the relevant Code (ICN or ICZN): provide a Latin or English diagnosis; designate a holotype; publish in a peer-reviewed journal.
4. Four biodiversity informatics databases: (1) GBIF (Global Biodiversity Information Facility; www.gbif.org): geographically referenced occurrence records for all living organisms aggregated from hundreds of institutions; over 2 billion records; used for distribution mapping and species discovery. (2) Plants of the World Online (POWO; www.plantsoftheworldonline.org; maintained by Kew): authoritative current accepted names and synonymy for all vascular plants, with distribution maps and images. (3) BOLD Systems (Barcode of Life Data Systems; www.boldsystems.org): the reference library for DNA barcode sequences (CO1 for animals; rbcL/matK for plants); used for rapid molecular identification of unknown specimens. (4) JSTOR Global Plants (www.plants.jstor.org): high-resolution images of herbarium type specimens from institutions worldwide; essential for Nigerian taxonomists needing to consult types held in overseas herbaria.
5. Contributing Nigerian biodiversity data to global databases is a priority for five reasons: (1) Nigerian specimens in national herbaria, universities, and research institutes represent irreplaceable knowledge about Nigeria's biodiversity that is currently not accessible to global researchers unless digitised and shared; (2) global assessments of species

distributions, IUCN Red List evaluations, and biogeographic analyses are biased when African data are underrepresented; contributing Nigerian records improves their accuracy and relevance to the African region; (3) shared data can be used for environmental impact assessments and land-use planning in Nigeria itself, by making occurrence data available to government planners via GBIF; (4) sharing data builds Nigerian systematic capacity by creating networks with international collaborators and identifying gaps in Nigerian collections; (5) digital sharing multiplies the use and impact of Nigerian taxonomic work, increasing citations, collaborations, and funding opportunities for Nigerian systematists.

References and Attributions [Series 4]

Textual References (Books and External Sources)

1. Sokal, R. R., & Sneath, P. H. A. (1963). Principles of numerical taxonomy. W.H. Freeman.
2. Hennig, W. (1966). Phylogenetic systematics. University of Illinois Press.
3. Judd, W. S., Campbell, C. S., Kellogg, E. A., Stevens, P. F., & Donoghue, M. J. (2008). Plant systematics: A phylogenetic approach (3rd ed.). Sinauer Associates.
4. FAO (Food and Agriculture Organization of the United Nations). (2025). Guidelines for sustainable agriculture. FAO.

Figures, Plates, Tables, and Boxes

1. Figure 4.1: Numerical taxonomy workflow from data matrix to phenogram Attribution: AI generated. Suggested OER search string: "numerical taxonomy workflow data matrix similarity matrix UPGMA dendrogram phenogram OER".
2. Figure 4.2: Cladogram illustrating plesiomorphies, synapomorphies, and autapomorphies Attribution: AI generated. Suggested OER search string: "cladogram plesiomorphy synapomorphy autapomorphy character types diagram OER".

3. Figure 4.3: Comparison of phenogram, cladogram, and molecular phylogenetic tree Attribution: AI generated. Suggested OER search string: "phenogram cladogram molecular phylogenetic tree comparison diagram OER".
4. Box 4.1: Comparison of phenetics, cladistics, and molecular systematics Attribution: AI generated. Suggested OER search string: "phenetics cladistics molecular systematics comparison table OER box".

Course code: BIO 306

Course title: Systematic Biology

Course credit load: 2 Units

Series 5: Keys, Keying, and Practical Applications

- **Part 5.1: Identification Keys: Types and Principles**
  - Sub Part 5.1.1: Purpose and types of identification keys
  - Sub Part 5.1.2: The dichotomous key
  - Sub Part 5.1.3: Multi-access (polyclave) and synoptic keys
- **Part 5.2: Constructing Dichotomous Keys**
  - Sub Part 5.2.1: Principles of key construction
  - Sub Part 5.2.2: Choosing and phrasing characters
  - Sub Part 5.2.3: Worked example: constructing a key to Nigerian legume genera
- **Part 5.3: Using Keys in Practice**
  - Sub Part 5.3.1: Procedure for keying out a specimen
  - Sub Part 5.3.2: Common problems and how to handle them
  - Sub Part 5.3.3: Verification of an identification
- **Part 5.4: Practical Applications of Systematics**
  - Sub Part 5.4.1: Systematics and agriculture in Nigeria
  - Sub Part 5.4.2: Systematics and medicine and public health
  - Sub Part 5.4.3: Systematics and conservation

Introduction

Identification is the everyday practical application of systematic biology. Before any organism can be named, studied, or managed, it must be identified correctly. Identification keys are the primary tools for this task: they allow a non-specialist to identify an unknown specimen by following a structured sequence of choices based on observable characters.

This final Series covers the types of identification keys, their construction and use, common problems encountered when keying out specimens, and the practical applications of systematic biology in Nigerian agriculture, medicine, public health, and conservation. These topics tie together the theoretical foundations of the previous four Series into a practical, applied framework.

Series Learning Outcomes

Upon completing this Series, you should be able to:

- **SLO 5.1** describe the main types of identification keys and state the purpose of each (Linked to Part 5.1),
- **SLO 5.2** explain the structure and principles of a dichotomous key (Linked to Part 5.1),
- **SLO 5.3** construct a simple dichotomous key for a set of organisms (Linked to Part 5.2),
- **SLO 5.4** use a dichotomous key to identify an unknown specimen and verify the identification (Linked to Part 5.3),
- **SLO 5.5** describe common problems encountered when using keys and explain how to handle them (Linked to Part 5.3), and
- **SLO 5.6** describe the practical applications of systematic biology in Nigerian agriculture, medicine, and conservation (Linked to Part 5.4).

5.1 Identification Keys: Types and Principles

5.1.1 Purpose and types of identification keys

An identification key is a structured tool that allows a user to determine the identity of an unknown organism by making a series of choices based on observable characters. Keys are the principal practical tool of taxonomy: they convert the technical knowledge of a specialist into a form usable by a non-specialist. A well-constructed key should work for any specimen belonging to the group it covers, regardless of whether the specimen was available when the key was written.

Main types of identification keys: (1) Dichotomous key: the most common type; presents the user with a series of pairs (couplets) of mutually exclusive statements at each step; the user selects the matching statement and is directed to the next couplet or to an identification. (2) Multi-access (polyclave) key: allows the user to choose any character to start with and to use characters in any order; useful when specimens are incomplete; typically computer-implemented. (3) Synoptic key: presents a table or matrix of diagnostic characters; the user reads across rows or down columns to find the taxon whose character combination matches the specimen.

Fill in the blank: A ________ key is the most common type; it presents the user with pairs of mutually exclusive statements (couplets) at each step; the user selects the matching statement and is directed to the next couplet or to a final identification.

5.1.2 The dichotomous key

A dichotomous key is structured as a series of numbered couplets. Each couplet presents two contrasting statements (leads) labelled a and b (or 1a and 1b); the user reads both and selects the one that matches the specimen; that lead directs the user either to the next couplet number or to the name of the taxon. The key terminates when the user arrives at an identification. The term "dichotomous" means "branching into two"; each couplet splits the group of possible taxa into two subgroups.

Two formats are used. Indented (yoked) format: the matching lead at each couplet is indented progressively, showing the branching structure visually; the two leads of each couplet are adjacent. Bracketed (numbered) format: all couplets are numbered sequentially from 1 to n regardless of level; the two leads of a couplet have the same number (e.g. 1a and 1b) but may be separated in the text; at the end of each lead, the user is directed to a couplet number or a name. The bracketed format is used by most floras and faunas (e.g. Flora of West Tropical Africa).

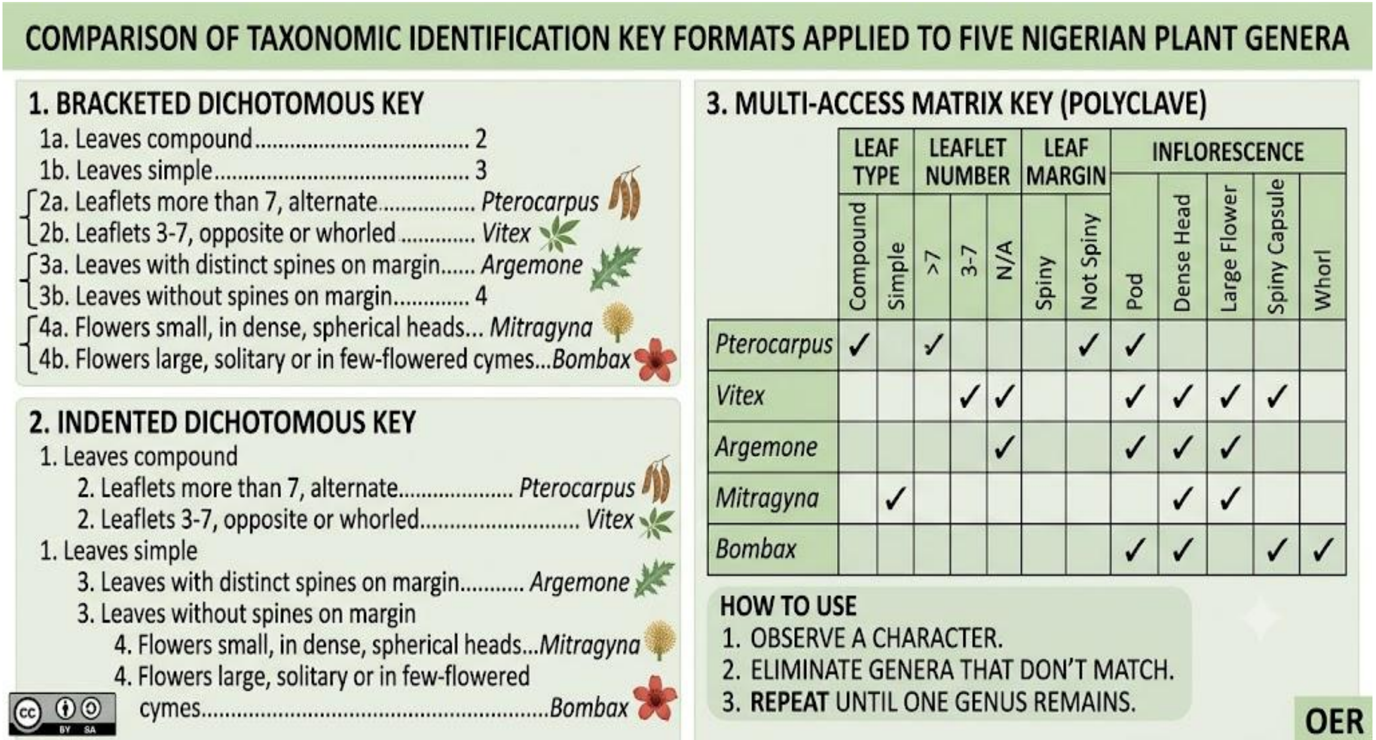
Fill in the blank: The ________ (numbered) format of a dichotomous key numbers all couplets sequentially; the two leads of each couplet carry the same number (e.g. 5a and 5b) and the user is directed to a higher couplet number or to an identification at the end of each lead.

5.1.3 Multi-access (polyclave) and synoptic keys

A multi-access key (polyclave) lists all characters for all taxa in a matrix format; the user may choose any character and in any order; taxa that do not match the chosen character state are progressively eliminated until only one taxon remains. Advantages: incomplete specimens can still be keyed (missing characters can be skipped); characters can be chosen in the order easiest to observe; more robust than a dichotomous key to damaged or unusual specimens.

Synoptic keys (diagnostic keys or character tables): present characters as a grid with taxa as rows and characters as columns; each cell shows the character state; the user scans across columns to find the row that matches all observed character states. Synoptic keys are useful for teaching and for specialists familiar with the group. Computer-assisted identification: interactive keys implemented in software (e.g. Lucid, Intkey, or online tools like iKey) are multi-access keys with a graphical interface; they are increasingly replacing printed keys for groups with many taxa.

Fill in the blank: A ________ key allows the user to choose characters in any order and is useful when specimens are incomplete; taxa that do not match a chosen character state are progressively eliminated until only one taxon remains.



	LEAF TYPE		LEAFLET NUMBER			LEAF MARGIN		INFLORESCENCE				
	Compound	Simple	>7	3-7	N/A	Spiny	Not Spiny	Pod	Dense Head	Large Flower	Spiny Capsule	Whorl
Pterocarpus	✓		✓				✓	✓				
Vitex				✓	✓			✓	✓	✓	✓	
Argemone					✓			✓	✓	✓		
Mitragyna		✓							✓	✓		
Bombax								✓	✓		✓	✓

Figure 5.1: Comparison of dichotomous (bracketed and indented) and multi-access key formats

Pilot questions 5.1

- Define an identification key and state its purpose.
- Distinguish between bracketed and indented formats of a dichotomous key.
- State two advantages of a multi-access key over a dichotomous key.
- Explain what a synoptic key is.
- Explain what computer-assisted identification is and name one software platform.

5.2 Constructing Dichotomous Keys

5.2.1 Principles of key construction

A well-constructed dichotomous key must meet six requirements. (1) Each couplet presents exactly two contrasting statements (not three or more). (2) The two leads of each couplet are mutually exclusive: no specimen can match both simultaneously. (3) Each lead should begin with the same noun or phrase as the opposing lead, so that the contrast is immediately obvious. (4) Characters used should be stable, observable without specialist equipment, and constant within the taxon (not seasonal or variable). (5) Characters should be stated positively wherever possible (avoid "not having"); negative statements are harder to verify.

(6) Key characters should be chosen in sequence to divide the remaining taxa as evenly as possible at each step; a character that divides 10 taxa into two groups of 5 is more efficient than one that separates 1 from 9. (7) The first couplet should use the most broadly informative character available. (8) Important or diagnostic characters should appear early in the key; trivial or variable characters should be reserved for final separations. (9) Each taxon should appear only once (at a terminal lead). (10) The key should cover all taxa in the group for which it is designed.

Fill in the blank: In a dichotomous key, the two leads of each couplet must be mutually ________ so that no specimen can match both simultaneously; characters should be stable and observable without specialist equipment.

5.2.2 Choosing and phrasing characters

Characters suitable for keys: morphological characters that are visible to the eye or with a hand lens (10x); present year-round (not just in flower or fruit if possible); not variable within the taxon (size ranges should be given for quantitative characters). Avoid: characters that require microscopy or chemical tests for non-specialist keys; characters that vary with age, sex, or season; characters requiring comparison with reference material; vague terms (large, small) without quantification.

Phrasing leads correctly: begin each lead with the subject of the couplet (e.g. "Leaves" for a couplet about leaf characters); give quantitative values as ranges (e.g. "lamina 3-8 cm long"); parallel the two leads using the same grammatical structure and the same starting word; make the contrast explicit (e.g. "Leaves opposite" vs "Leaves alternate"); avoid double negatives; use standard morphological terminology defined in a glossary if needed.

Fill in the blank: In phrasing key leads, each lead in a couplet should begin with the same ________ word or phrase so that the contrast between the two alternatives is immediately apparent to the user.

5.2.3 Worked example: constructing a key to Nigerian legume genera

Five common Nigerian legume genera: Vigna (cowpea; annual herb; leaves trifoliate; flowers papilionaceous; pods linear, 8-20 cm; seeds kidney-shaped); Cajanus (pigeon pea; shrub; leaves trifoliate; pods 4-9 cm; seeds spherical to ovoid); Arachis (groundnut; annual herb; leaves paripinnate with 4 leaflets; geocarpic: pods develop underground); Parkia (dawadawa; tree; leaves bipinnate; flowers in globose heads; pods 30-45 cm; seeds in orange pulp); Acacia (mimosa; tree or shrub; leaves bipinnate or reduced to phyllodes; stipular spines; flowers small in heads or spikes).

Key to five Nigerian legume genera: 1a. Trees or shrubs ... 2. 1b. Herbs ... 3. 2a. Leaves bipinnate; flowers in globose heads; pods 30-45 cm; seeds in orange pulp ... Parkia. 2b. Leaves bipinnate or reduced; stipular spines present; flowers in heads or spikes; pods 5-15 cm ... Acacia. 3a. Leaves paripinnate (4 leaflets); pods developing underground (geocarpic) ... Arachis. 3b. Leaves trifoliate ... 4. 4a. Shrubs; pods 4-9 cm; seeds spherical to ovoid ... Cajanus. 4b. Annual herbs; pods 8-20 cm; seeds kidney-shaped ... Vigna.

Fill in the blank: In the key above, couplet 1 uses ________ habit (tree or shrub vs herb) as the first character to divide the five genera into two groups; habit is chosen first because it is the most broadly informative character and is always observable.

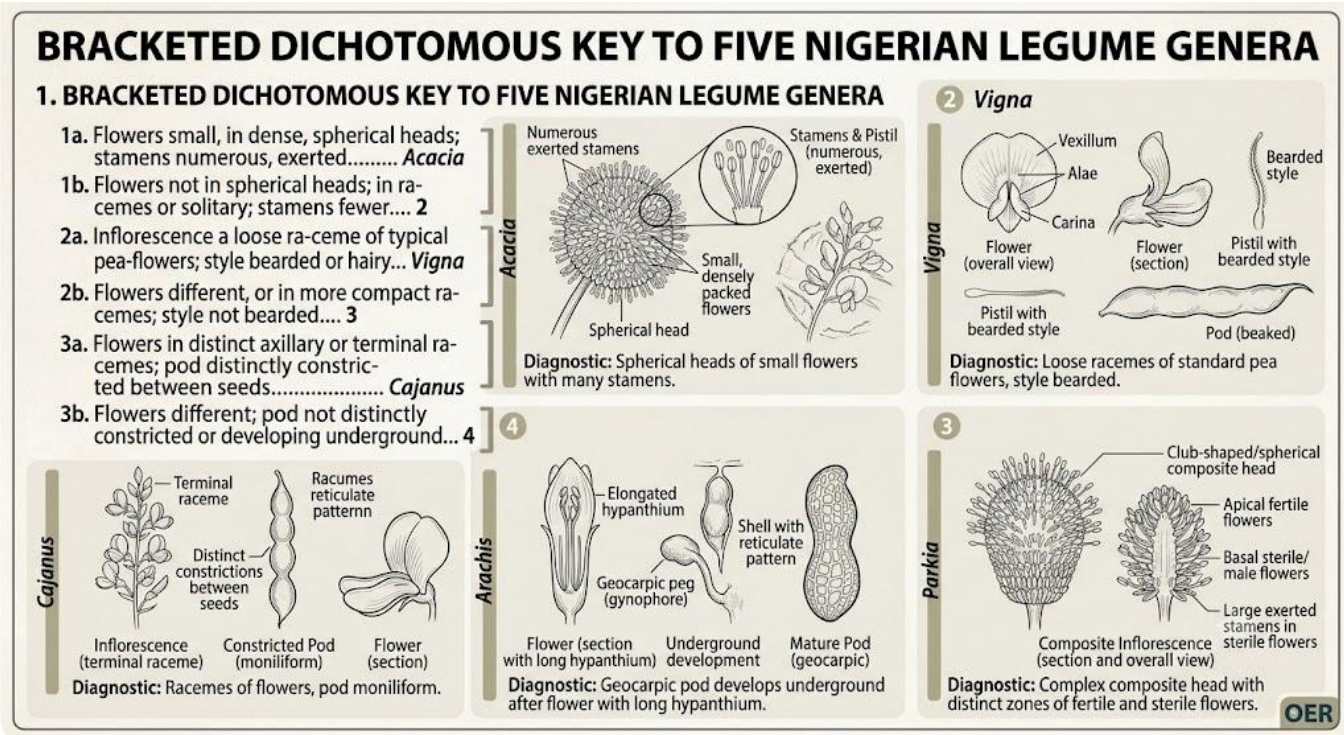


Figure 5.2: Dichotomous key to five Nigerian legume genera in bracketed format with diagnostic illustrations

Pilot questions 5.2

- State five principles of good key construction.
- State four types of character that should be avoided in keys.
- Explain how to phrase the two leads of a couplet correctly.
- Explain why the first couplet of a key should use the most broadly informative character.
- In the worked example key, explain why "tree or shrub vs herb" was chosen for couplet 1.

5.3 Using Keys in Practice

5.3.1 Procedure for keying out a specimen

Step-by-step procedure for using a dichotomous key: (1) Examine the specimen thoroughly before beginning: note habit (tree, shrub, herb, grass), stem, leaves, flowers, and fruit; use a hand lens for details; collect additional material if missing structures are required by the key. (2) Start at couplet 1 of the key; read both leads carefully before making a choice; do not choose on the basis of the first lead alone. (3) Select the lead that best matches the specimen and note the number or name it directs you to.

(4) Proceed to the indicated couplet and repeat the process; do not skip couplets. (5) Continue until a taxon name is reached. (6) Verify the identification (see 5.3.3). Always use the key appropriate to the geographic region and the group being identified; a key written for European plants will not work reliably for Nigerian specimens. Always use good material: wilted, juvenile, or incomplete specimens are harder to key; flowering and fruiting material gives the best results.

Fill in the blank: Before beginning to use a dichotomous key, the user should examine the specimen ________ and note all observable characters (habit, stem, leaves, flowers, fruit); read both leads of couplet 1 before making a choice.

5.3.2 Common problems and how to handle them

Common problems when keying: (1) Missing characters: the specimen lacks the structure referred to in a couplet (e.g. no flowers when the key requires floral characters); solution: try to locate material with the missing part; if impossible, try both leads and check both resulting identifications against reference descriptions. (2) Intermediate specimens: the specimen does not clearly match either lead (e.g. leaves that are neither clearly "alternate" nor clearly "opposite" because of unusual variation); solution: try both leads and compare resulting identifications.

(3) Key errors: the key may be incorrectly written or based on characters that vary more than expected; solution: if the identification cannot be confirmed against a reference description, consult a specialist or a second key. (4) Immature or damaged material: immature fruits or absent flowers may make key characters inaccessible; solution: collect complete material or revisit the plant at a different season. (5) Geographic scope: using a key outside its intended geographic range; solution: always use a key written for the relevant region (e.g. Flora of Nigeria for Nigerian specimens).

Fill in the blank: When a key specimen lacks a character required at a couplet, the user should try ________ leads of the couplet and compare both resulting identifications against reference descriptions before deciding.

5.3.3 Verification of an identification

An identification obtained from a key should always be verified before it is accepted. Verification steps: (1) Compare the specimen against a full published description or diagnosis of the taxon identified; the description should match in all key characters and most other characters. (2) Examine type specimen images (via JSTOR Global Plants or other databases) for the identified species; the specimen should match the type. (3) Compare the specimen with authenticated herbarium material of the identified species in a reference collection.

(4) Consult a regional flora or monograph to confirm that the identified species occurs in the geographic area where the specimen was collected; if it does not, the identification is likely wrong. (5) For critical identifications (e.g. for publication, for medical or agricultural decisions), submit the specimen to a specialist for confirmation. A correctly identified voucher specimen should be deposited in a recognised herbarium with full collection data, even for teaching collections, as it provides a permanent record of the identification.

Fill in the blank: After obtaining an identification from a key, it must be ________ by comparing the specimen against a published description, examining type specimen images, and confirming that the species occurs in the geographic region of collection.

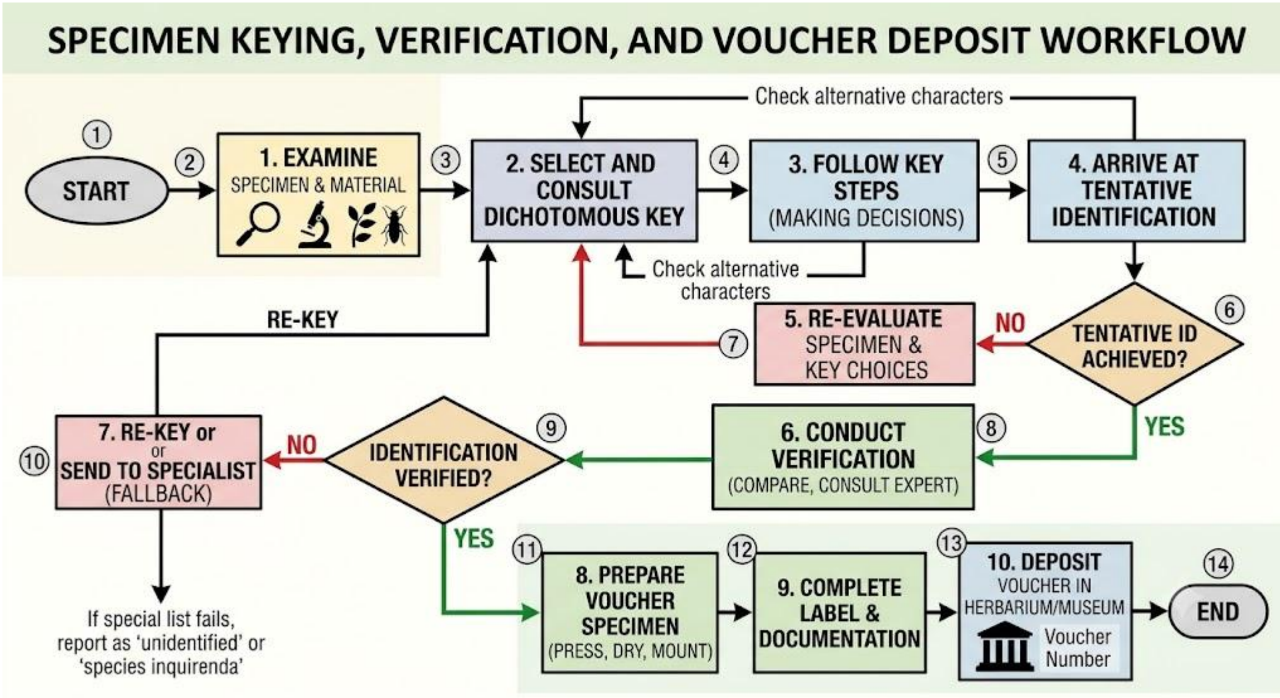


Figure 5.3: Flowchart of the procedure for keying out and verifying an identification

Pilot questions 5.3

1. List the steps for using a dichotomous key to identify a specimen.
2. Explain how to handle a specimen that lacks the character required at a couplet.
3. Explain why an identification from a key must be verified.
4. State three ways of verifying an identification.
5. Explain why a key written for European plants may not work for Nigerian specimens.

5.4 Practical Applications of Systematics

5.4.1 Systematics and agriculture in Nigeria

Systematic biology underpins Nigerian agriculture in several ways. Crop identification and improvement: correct identification of cultivated plants and their wild relatives is essential for plant breeding; wild relatives of Nigerian crops (cowpea, sorghum, yam, cassava) are an important source of disease resistance and stress tolerance genes; they can only be found and used if correctly identified to species. Pest and disease identification: correct identification of crop pests (insects, nematodes, pathogens) and weeds is the first requirement for effective management.

Striga (witch weed) identification: Nigeria has several species of Striga (Striga hermonthica, Striga asiatica, Striga aspera, Striga gesnerioides) with different host ranges and different responses to control measures; correct identification is essential for selecting the right control strategy. Biological control: any biological control programme requires precise identification of both the pest and the proposed control agent to ensure host specificity and prevent non-target effects. Quarantine: identifying whether an intercepted organism is a known species or a new invasive is a systematic task with major economic implications.

Fill in the blank: Nigeria has several species of ________ (witch weed) with different host ranges; correct systematic identification is essential for selecting the right control strategy for each crop-parasite combination.

5.4.2 Systematics and medicine and public health

Medicinal plant identification: Nigeria has a rich tradition of herbal medicine; many medicinal plants are routinely sold in markets under vernacular names that may be applied to several morphologically similar species; incorrect identification can result in the use of a toxic substitute; systematic biology is essential for quality control in herbal medicine and for developing standardised remedies. The National Agency for Food and Drug Administration and Control (NAFDAC) requires botanical voucher specimens for all registered herbal products.

Disease vector identification: correct identification of disease vectors is essential for public health interventions; examples include: Anopheles gambiae complex mosquitoes (malaria vectors; seven cryptic species with different insecticide resistances and transmission efficiencies); Simulium damnosum complex (vectors of onchocerciasis/river blindness; multiple species with different distribution and vector competence); Glossina (tsetse flies; vectors of African trypanosomiasis; multiple species with different geographic distributions requiring different control approaches). Systematic errors in vector identification directly compromise the effectiveness of disease control programmes.

Fill in the blank: The National Agency for Food and Drug Administration and Control (________) requires botanical voucher specimens for all registered herbal products in Nigeria; this ensures that the plant used in registered medicines is correctly identified and traceable.

5.4.3 Systematics and conservation

Conservation decisions require accurate knowledge of species identity and distribution. A species cannot be protected if it is not described and named; its conservation status cannot be assessed if its distribution is not known. Nigeria has a significant number of endemic and threatened species: examples include the Cross River gorilla (Gorilla gorilla diehli), the Nigeria-Cameroon chimpanzee (Pan troglodytes ellioti), the drill (Mandrillus leucophaeus), the Preuss's red colobus (Piliocolobus preussi), and numerous endemic plant species in the Cameroon Highlands and Niger Delta.

Systematic biology supports conservation through: (1) species discovery and description (new species found in poorly sampled areas of Nigeria, especially in invertebrates, plants, and microorganisms); (2) taxonomic revision (clarifying which populations represent distinct species meriting separate conservation management); (3) IUCN Red List assessments (requiring correctly identified species with known distributions); (4) systematic surveys of target habitats (Cross River, Omo, Okumu forest reserves) to inventory taxa that may be threatened; (5) genetic data to define management units for ex-situ conservation breeding programmes.

Fill in the blank: IUCN Red List assessments require correctly identified species with known ________ ; without systematic biological knowledge, threatened species cannot be identified, assessed, or prioritised for conservation.

Field	Application	Nigerian Example	Impact
Agriculture	Identification of crop pests and beneficial organisms	Biological control of maize pests using entomopathogenic nematodes (EPNs) and parasitoids	Reduces pesticide use, improves yields, enhances food security

Medicine	Classification of medicinal plants and discovery of active compounds	Use of *Azadirachta indica* (neem) and *Morinda lucida* in traditional medicine	Provides pharmacological leads for malaria and fever treatment
Public Health	Vector identification and control strategies	Integrated Vector Management (IVM) for malaria vectors (*Anopheles gambiae*)	Reduces malaria transmission, improves community health
Conservation	Species inventory and biodiversity monitoring	Hadejia-Nguru Wetlands (RAMSAR site) protecting migratory waterbirds	Guides habitat protection, supports international conservation commitments
Agriculture & Public Health Link	Managing vector-borne diseases in irrigation schemes	Control of schistosomiasis and malaria in Nigerian irrigation zones	Improves agricultural productivity and reduces disease burden

Box 5.1: Summary of practical applications of systematic biology in Nigeria

Pilot questions 5.4

1. State three ways in which systematics supports agriculture in Nigeria.
2. Explain the importance of correct species identification for vector control in Nigeria.
3. Explain why NAFDAC requires voucher specimens for herbal products.
4. State three ways in which systematics supports conservation in Nigeria.
5. Name four threatened Nigerian species and state the systematic evidence that distinguishes each as a distinct taxon.

Series Summary

This final Series covered identification keys, key construction, and practical applications of systematic biology. The main key types are dichotomous keys, which use paired mutually exclusive statements in bracketed or indented formats; multi-access or polyclave keys, which allow users to select characters in any order and are useful for incomplete specimens; and synoptic keys, which present character states in a matrix. Good keys should contain exactly two contrasting leads per couplet, use positive and mutually exclusive statements, rely on stable and observable characters, begin with the most informative character, and divide taxa as evenly as possible. Suitable characters should be morphological, available throughout the year, and minimally variable, while seasonal, vague, or microscopy-dependent features should generally be avoided.

During keying, the specimen should be examined carefully, both leads in each couplet should be read before a choice is made, and the user should follow the indicated sequence until an identification is reached. The result should then be confirmed using published descriptions, type images, geographic distribution, and reference collections. Missing or intermediate characters may require testing both leads, while suspected key errors should be checked with another key or a specialist. In Nigeria, systematic biology is applied in agriculture for identifying crop wild relatives, *Striga* species, pests, and quarantine organisms; in medicine for medicinal plant identification and NAFDAC voucher requirements; in public health for identifying vectors such as the *Anopheles gambiae*, *Simulium damnosum*, and *Glossina* complexes; and in conservation for describing endemic species, conducting IUCN assessments, and defining management units. Completing this Series should enable students to achieve SLOs 5.1–5.6 and all BIO306 course outcomes.

Glossary of Terms

1. **Autapomorphy:** (see Series 4); a derived character unique to one taxon; used in key construction to diagnose terminal taxa.

2. **Bracketed (numbered) format:** a dichotomous key layout in which all couplets are numbered sequentially; the two leads of each couplet carry the same number (e.g. 3a and 3b) and may be separated in the printed text.
3. **Computer-assisted identification:** the use of software (e.g. Lucid, Intkey) to implement a multi-access key with a graphical interface; allows characters to be entered in any order and taxa to be eliminated progressively.
4. **Couplet:** a pair of contrasting statements in a dichotomous key; the user selects the matching statement and is directed to the next couplet or to an identification.
5. **Diagnostic key (synoptic key):** a tabular or matrix key in which characters are listed as columns and taxa as rows; the user identifies the taxon by matching all observed characters to a row.
6. **Dichotomous key:** an identification key structured as a series of couplets of mutually exclusive statements; at each couplet the user selects one of two alternatives and proceeds until an identification is reached.
7. **Flora:** a systematic catalogue of the plant species of a defined geographic area, including descriptions and identification keys; e.g. Flora of West Tropical Africa (Hutchinson and Dalziel).
8. **Indented (yoked) format:** a dichotomous key layout in which the matching lead at each couplet is progressively indented, visually showing the branching structure.
9. **Lead:** one of the two contrasting statements in a couplet of a dichotomous key; choosing the correct lead directs the user to the next step.
10. **Multi-access key (polyclave):** an identification key in which the user may choose characters in any order; useful for incomplete specimens; taxa are eliminated as characters are entered.
11. **NAFDAC:** National Agency for Food and Drug Administration and Control; the Nigerian federal agency responsible for regulating herbal medicines; requires authenticated botanical voucher specimens for registered herbal products.

12. **Striga:** a genus of parasitic flowering plants (witch weeds; Orobanchaceae) that attach to the roots of cereal crops; multiple species occur in Nigeria with different host ranges and control requirements.

13. **Synoptic key:** see Diagnostic key.

14. **Verification:** the process of confirming an identification obtained from a key by comparing the specimen against a published description, type specimen images, reference material, and geographic range data.

15. **Voucher specimen:** a herbarium or museum specimen preserved as permanent physical evidence of an identification or a biological study; deposited in a recognised institution accessible to future researchers.

Concept Check Questions [Series 5]

Objective Questions

1. A ________ key is the most common type of identification key; it presents users with pairs of mutually exclusive statements (couplets) and directs them to the next step or to an identification. (Linked to SLO 5.1)
2. In a dichotomous key, the two leads of each couplet must be mutually ________ so that no specimen can match both simultaneously. (Linked to SLO 5.2)
3. A ________ key allows the user to choose characters in any order and is particularly useful for keying incomplete specimens. (Linked to SLO 5.1)
4. Nigeria has several species of ________ (witch weed), each with a different host range; correct systematic identification is required to select the right control strategy. (Linked to SLO 5.6)
5. ________ (National Agency for Food and Drug Administration and Control) requires botanical voucher specimens for all registered herbal products in Nigeria. (Linked to SLO 5.6)

Short-Answer Questions

- Distinguish between bracketed and indented formats of a dichotomous key. (Linked to SLO 5.2)
- State four principles of good dichotomous key construction. (Linked to SLO 5.3)
- State four types of character that should be avoided when constructing keys. (Linked to SLO 5.3)
- Describe two common problems encountered when using a key and state how each is handled. (Linked to SLO 5.5)
- State three ways in which systematic biology supports conservation in Nigeria. (Linked to SLO 5.6)

Long-Answer Questions

1. Describe the main types of identification keys; explain the structure of a dichotomous key in both bracketed and indented formats; and explain what a multi-access key is and when it is preferred. (Linked to SLOs 5.1, 5.2)
2. Explain the principles of constructing a dichotomous key; describe how to choose and phrase characters; and construct a simple key to four Nigerian plants or animals of your choice. (Linked to SLO 5.3)
3. Describe the procedure for using a key and verifying an identification; describe common problems and their solutions; and explain the practical applications of systematic biology in Nigerian agriculture, medicine, and conservation. (Linked to SLOs 5.4, 5.5, 5.6)

Answers to Concept Check Questions [Series 5]

Objective Questions

6. Dichotomous.
7. Exclusive.
8. Multi-access (polyclave).
9. Striga.
10. NAFDAC.

Short-Answer Questions

11. Bracketed: all couplets numbered sequentially; the two leads carry the same number (e.g. 3a/3b); may be separated in the text; standard in most floras. Indented: matching lead progressively indented to show branching; the two leads of each couplet are adjacent.
12. (1) Exactly two mutually exclusive leads per couplet; (2) both leads begin with the same subject word; (3) characters must be stable and observable without specialist equipment;

(4) the most broadly informative character is used at couplet 1 to divide taxa as evenly as possible.

13. Avoid: characters requiring microscopy; characters variable with age, sex, or season; vague quantitative terms without ranges; characters present in only one of the two groups at a couplet (non-contrasting).
14. Missing characters: try both leads of the couplet and compare both resulting identifications against descriptions. Intermediate specimens: try both leads; compare both identifications; consult a second key or specialist if neither matches well.
15. (1) Species discovery and description of unknown taxa; (2) IUCN Red List assessments requiring correct species identification and distribution data; (3) defining management units using morphological and genetic data (e.g. separating Cross River gorilla from Western Lowland gorilla).

Long-Answer Questions

1. Types of keys: dichotomous (pairs of mutually exclusive couplets; most common; bracketed or indented format); multi-access/polyclave (any character order; robust for incomplete specimens; computer-implemented); synoptic (matrix grid; specialist use). Dichotomous structure: bracketed format (sequential couplet numbers; leads e.g. 3a/3b; lead directs to next number or name; standard in Flora of West Tropical Africa); indented format (progressive indentation shows branching; both leads adjacent; easier to see structure). Multi-access key: user selects characters in any order; taxa not matching are eliminated; preferred when specimens are incomplete or character sequence is uncertain.
2. Key construction principles: exactly two leads per couplet; mutually exclusive; same subject word to start each lead; stable, observable characters; most informative character first; even division of taxa at each step. Character selection: choose morphological, year-round, non-variable characters; give quantitative ranges; avoid microscopy-required, seasonal, or vague characters. Simple key to four Nigerian plants (example: Vigna, Cajanus, Parkia, Acacia): 1a. Tree or shrub...2. 1b. Herb...3. 2a. Leaves bipinnate; pods large (30-45 cm); seeds in orange pulp...Parkia. 2b. Stipular spines; flowers small in

heads or spikes...Acacia. 3a. Leaves trifoliate; pods 8-20 cm; seeds kidney-shaped...Vigna. 3b. Leaves trifoliate; shrubby herb; pods 4-9 cm...Cajanus.

3. Keying procedure: examine specimen before starting; start at couplet 1; read both leads; select matching lead; proceed to indicated couplet; repeat until identification reached. Verification: compare with published description; examine type specimen images (JSTOR Global Plants); confirm species occurs in the collection area; deposit voucher. Common problems: missing characters (try both leads; compare both results); intermediate specimens (try both leads; check descriptions); key errors (consult second key; contact specialist). Agricultural applications: identifying crop wild relatives for breeding; identifying Striga species for correct control; pest and quarantine identification. Medical/public health: medicinal plant identification (NAFDAC voucher requirement; preventing toxic substitutions); vector identification (Anopheles gambiae complex; Simulium damnosum; Glossina). Conservation: species discovery and description; IUCN Red List assessments; management unit definition using morphological and genetic data.

Answers to Pilot Questions [Series 5]

Part 5.1

6. An identification key is a structured tool that allows a user to determine the identity of an unknown organism by making a series of choices based on observable characters. Its purpose is to convert specialist systematic knowledge into a form usable by non-specialists, allowing rapid and consistent identification of organisms without requiring a trained taxonomist for every identification.
7. Bracketed format: couplets numbered sequentially from 1 to n; the two leads of each couplet carry the same number (e.g. 5a and 5b); a lead directs the user either to a higher couplet number or to a name; standard format used in most regional floras including the Flora of West Tropical Africa. Indented format: the matching lead at each step is progressively indented, displaying the branching structure visually; both leads of each

couplet appear adjacent on the page; useful for teaching the structure of a key but impractical for keys covering many taxa because deep indentation compresses the text.

8. Two advantages: (1) allows the user to choose characters in any order, making it possible to key incomplete specimens by skipping characters of missing structures; in a dichotomous key, if the required character is absent, the key cannot proceed. (2) more robust to unusual or aberrant specimens because the user can start with the characters most clearly observable on the particular specimen rather than being forced to address a predetermined first character.
9. A synoptic key is a tabular or matrix identification tool that presents taxa as rows and diagnostic characters as columns (or vice versa); each cell shows the character state of that taxon for that character. To identify an unknown specimen, the user reads across the row (or down the column) matching the character states of the specimen until only one taxon matches all observed states. It is useful for specialists already familiar with the characters of the group but less accessible to beginners than a dichotomous key.
10. Computer-assisted identification is the use of software to implement a multi-access key with a graphical interface; the user selects characters and their states by clicking on images or menus; the software eliminates taxa that do not match and narrows the list until one taxon remains. One software platform: Lucid (developed at the University of Queensland; widely used for plant, insect, and pest identification; available as a desktop program and a web-based platform).

Part 5.2

11. Five principles: (1) each couplet presents exactly two contrasting statements, not three or more; (2) the two leads are mutually exclusive so no specimen can match both; (3) both leads begin with the same subject word or phrase for clear contrast; (4) characters must be stable, observable without specialist equipment, and constant within the taxon; (5) the first couplet uses the most broadly informative character to divide the full group as evenly as possible.

12. Four character types to avoid: (1) characters requiring microscopy or chemical tests (inaccessible to non-specialists in the field); (2) characters that vary with age, sex, or season (unreliable because the relevant state may not be present at the time of identification); (3) vague quantitative terms without numerical ranges (e.g. "large leaves" without specifying measurements); (4) characters present in only one of the two groups at a couplet (non-contrasting characters cannot discriminate between the two leads).
13. Each lead should begin with the same subject noun (e.g. "Leaves..." for both leads of a leaf-character couplet) so the contrast is immediately apparent. Quantitative characters should give ranges (e.g. "lamina 3-8 cm long" vs "lamina 12-25 cm long"). State the character positively wherever possible (e.g. "leaves alternate" rather than "leaves not opposite"). Use parallel grammatical structure in both leads. Avoid double negatives and technical jargon without a glossary.
14. The first couplet divides the whole group of taxa to be identified; if the first character divides 10 taxa into two unequal groups of 9 and 1, then the 9 must all be separated in subsequent couplets (increasing key length and difficulty) while the group of 1 is immediately identified. A character that divides 10 taxa into two groups of 5 halves the identification problem at each step, minimising the number of subsequent couplets needed and making the key shorter, faster, and more efficient.
15. In the worked key, couplet 1 uses "tree or shrub vs herb" because this character: (1) is always observable regardless of season or maturity of the specimen; (2) divides the five genera into two nearly equal groups (2 woody vs 3 herbaceous) which is close to the ideal even split; (3) is the most obvious and easily determined character before examining leaves, flowers, or fruits in detail; using a floral character first would require the specimen to be in flower.

Part 5.3

1. Steps for using a dichotomous key: (1) Examine the specimen fully before starting; note habit, leaves, flowers, and fruit; use a hand lens for details. (2) Start at couplet 1; read both leads completely before deciding. (3) Select the matching lead and note the number

or name it directs to. (4) Proceed to the indicated couplet; read both leads again. (5) Repeat until a taxon name is reached. (6) Verify the identification against a published description and type images.

2. When a specimen lacks a required character, try both leads of that couplet and follow each through the key to an identification; then compare both proposed identifications against published descriptions to determine which one matches the rest of the specimen's features. If neither matches well, collect additional material with the missing structure, consult a second key, or submit the specimen to a specialist.
3. An identification from a key is only a hypothesis; keys can contain errors; character states can overlap between taxa; and the key may not have been designed with the particular specimen in mind. Verification confirms that the proposed identification is correct by checking the specimen against independent evidence (full description, type specimen, reference collection, distribution data) before the name is relied upon for scientific, agricultural, or medical purposes.
4. Three verification methods: (1) compare the specimen against the full published description or diagnosis of the identified taxon in a flora, monograph, or species account; all key characters and most other characters should match; (2) examine type specimen images via JSTOR Global Plants or other digitised herbarium databases to compare with the name-bearing type of the identified species; (3) confirm that the identified species is recorded from the geographic area of collection using a regional flora, checklist, or GBIF occurrence data.
5. A key written for European plants is based on the species that occur in Europe; Nigerian plants are different species (and often different genera or families) that were not included when the key was constructed; the leads in such a key were written to distinguish European taxa from each other, not Nigerian taxa; a Nigerian specimen will frequently fail to match either lead correctly because neither lead describes it accurately, leading to a wrong identification or an inability to proceed.

Part 5.4

1. Three ways: (1) Identification of wild crop relatives: Nigeria's wild Vigna, Sorghum, and Dioscorea species are potential sources of disease resistance and stress tolerance genes for crop improvement; they can only be collected, characterised, and used in breeding programmes if correctly identified to species by a botanist. (2) Pest and weed identification: correct species identification is the first step in pest management; different Striga species have different host ranges and respond differently to control methods, so misidentification leads to ineffective management. (3) Quarantine: systematic examination of intercepted plant material at ports of entry identifies potential invasive species before they establish, preventing economic damage.
2. Most disease vectors in Nigeria occur as complexes of morphologically identical cryptic species with different characteristics. In the Anopheles gambiae complex, the seven sibling species differ in insecticide resistance profiles (e.g. Anopheles gambiae s.s. vs Anopheles arabiensis differ in kdr resistance allele frequency) and in competence as malaria vectors; applying the same insecticide to all populations treats them as a single species and fails where resistance is present in only some members of the complex. Similarly, the Simulium damnosum complex contains species that are primary vectors of Onchocerca volvulus in different river systems; targeting the wrong species with larviciding operations wastes resources and fails to control river blindness transmission.
3. NAFDAC requires voucher specimens to ensure that each registered herbal product can be traced to a correctly identified plant species; a voucher specimen deposited at a recognised herbarium provides permanent, verifiable evidence of the plant used, allowing future users (pharmacists, regulators, researchers) to confirm the identity of the plant material if any question arises about efficacy or safety. Without a voucher, it is impossible to verify retrospectively whether the correct plant was used or whether a toxic substitute was included; the voucher requirement prevents accidental or fraudulent substitution of one species for another.
4. Three ways: (1) Species discovery and description: many Nigerian endemic species remain undescribed; systematic surveys and publication of new species descriptions create the formal names that trigger IUCN assessment and legal protection. (2) IUCN

Red List assessments: every IUCN assessment requires correct species identification, synonymy resolution, and a known geographic distribution; systematic taxonomy provides all three. (3) Defining conservation management units: morphological and molecular systematic data determine whether geographically separate populations represent distinct subspecies or species that need separate conservation strategies; e.g. the Cross River gorilla and Western Lowland gorilla are managed separately because systematic data confirm they are distinct subspecies.

5. Cross River gorilla (Gorilla gorilla diehli): distinguished from the Western Lowland gorilla (Gorilla gorilla gorilla) by morphometric analysis of skulls and facial structures and by molecular data (microsatellite and mitochondrial DNA); the approximately 200-300 individuals in Cross River and Benue States form a genetically distinctive subspecies. Nigeria-Cameroon chimpanzee (Pan troglodytes ellioti): distinguished from other chimpanzee subspecies by both molecular (mitochondrial and nuclear DNA) and morphological characters; restricted to forested areas of Cross River State and south-west Cameroon. Drill (Mandrillus leucophaeus): distinguished from the closely related mandrill (Mandrillus sphinx) by morphological characters (coat colour, facial markings) and geographic range; listed as Endangered on the IUCN Red List. Preuss's red colobus (Piliocolobus preussi): distinguished from other West African red colobus species by coat colour, morphometric characters, and molecular data; Critically Endangered.

References and Attributions [Series 5]

Textual References (Books and External Sources)

1. Hutchinson, J., & Dalziel, J. M. (1954-1972). Flora of West Tropical Africa (2nd ed., 3 vols., revised by Keay and Hepper). Crown Agents.
2. Stuessy, T. F. (2009). Plant taxonomy: The systematic evaluation of comparative data (2nd ed.). Columbia University Press.
3. Judd, W. S., Campbell, C. S., Kellogg, E. A., Stevens, P. F., & Donoghue, M. J. (2008). Plant systematics: A phylogenetic approach (3rd ed.). Sinauer Associates.

4. FAO (Food and Agriculture Organization of the United Nations). (2025). Guidelines for sustainable agriculture. FAO.

Figures, Plates, Tables, and Boxes

1. Figure 5.1: Comparison of dichotomous and multi-access key formats Attribution: AI generated. Suggested OER search string: "dichotomous key bracketed indented format multi-access polyclave matrix comparison OER".
2. Figure 5.2: Dichotomous key to five Nigerian legume genera with illustrations Attribution: AI generated. Suggested OER search string: "dichotomous key Nigerian legume genera Vigna Cajanus Arachis Parkia Acacia bracketed format OER".
3. Figure 5.3: Flowchart for keying out and verifying an identification Attribution: AI generated. Suggested OER search string: "keying out specimen flowchart verification voucher herbarium deposit OER".
4. Box 5.1: Practical applications of systematic biology in Nigeria Attribution: AI generated. Suggested OER search string: "systematic biology practical applications Nigeria agriculture medicine conservation vector control OER box".