1. Encyclopedia of Insects (Academic Press, 2003)

Thompson, F. C. (2003). Nomenclature and Classification, Principles of. In Resh, V. H. & Cardé, R. T. (Eds.), Encyclopedia of Insects (pp. 798-807). Academic Press.

Overview

Thompson's chapter provides a comprehensive introduction to the principles of biological nomenclature and classification, written from the perspective of a practicing entomologist. The work serves as both a primer for non-specialists and a thoughtful reflection on the philosophical and practical challenges inherent in biological systematics. As a U.S. government employee, Thompson's contribution is in the public domain, making it freely accessible to a wide audience.

Key Contributions

1. Distinction Between Classification and Nomenclature

Thompson clearly differentiates between classification as the arrangement of organisms into hierarchical groups and nomenclature as the system of names and rules governing those names. This fundamental distinction is crucial for understanding how biological information is organized and communicated.

2. The Dual-Key Concept

A particularly valuable contribution is Thompson's proposal that nomenclature should support two unique keys:

- The valid name (the correct name within a classification)
- The original name (the name as first proposed, which remains invariant across classifications)

This dual-key system allows for information retrieval across multiple, sometimes conflicting classifications while preserving the predictive power of valid names as phylogenetic hypotheses.

3. Scientific Names as Hypotheses

Thompson emphasizes that scientific names are not merely labels but represent testable hypotheses about relationships, characters, and taxa. This philosophical position acknowledges that classifications are provisional and subject to change as knowledge improves—a point that has significant implications for both scientific communication and legal contexts (as elaborated in the legal review below).

4. Paradigms and Classification Approaches

The chapter reviews three major paradigms in systematics:

- Phenetics (overall similarity)
- Evolutionary systematics (phylogeny with consideration of degree of divergence)
- Cladistics (strict monophyly)

Thompson concludes that cladistic classifications are mandatory for predictive, maximally informative systems, though he acknowledges the practical challenges of translating phylogenetic trees into ranked classifications.

5. Practical Guidelines for Classification

Thompson offers four pragmatic guidelines:

1. Only monophyletic taxa should be recognized
2. Subordination or sequencing should be used appropriately
3. "Empty" taxa should not be named
4. Traditional groups and ranks should be preserved where possible

Critical Assessment

Strengths:

- Accessible writing style suitable for non-specialists
- Clear exposition of complex concepts
- Historical perspective on the development of the International Code of Zoological Nomenclature
- Practical recommendations grounded in real-world taxonomic practice

Limitations:

- Limited discussion of molecular phylogenetic methods, which were already becoming prominent at the time of writing (2003)
- Brief treatment of the PhyloCode controversy, though Thompson clearly favors traditional Linnaean ranks
- Strong advocacy for cladistics may not fully represent the diversity of legitimate approaches in modern systematics

Relevance:
Thompson's chapter remains valuable as an introduction to systematic principles, though subsequent developments in molecular phylogenetics and the ongoing debate over rank-based versus rank-free nomenclature warrant updating. The

discussion of the dual-key concept is particularly prescient in the context of biodiversity informatics and the challenges of integrating data across multiple classifications.

2. PLoS ONE (Public Library of Science, 2015)

Ruggiero, M. A., Gordon, D. P., Orrell, T. M., Bailly, N., Bourgoin, T., Brusca, R. C., et al. (2015). A Higher Level Classification of All Living Organisms. PLoS ONE, 10(4), e0119248.

Overview

Ruggiero et al. present a consensus higher-level classification of all living organisms, designed to serve as the taxonomic backbone for the Catalogue of Life (CoL) and the Integrated Taxonomic Information System (ITIS). The work represents an unprecedented collaborative effort involving more than 3,000 taxonomists and 140 taxonomic databases, synthesizing diverse expert opinions into a unified, ranked hierarchy from superkingdom to order.

Key Contributions

1. A Practical, Consensus-Based Framework

The authors explicitly state their goal is pragmatic rather than purely phylogenetic: to provide a coherent framework for data integration in biodiversity databases. The classification is "neither phylogenetic nor evolutionary but instead represents a consensus view that accommodates taxonomic choices and practical compromises." This honest acknowledgment of the classification's purpose is refreshing and appropriately sets expectations for users.

2. Seven-Kingdom System

The proposed classification uses two superkingdoms (Prokaryota and Eukaryota) and seven kingdoms:

- Archaea (Archaeobacteria)
- Bacteria (Eubacteria)
- Protozoa
- Chromista
- Fungi
- Plantae
- Animalia

This schema extends Cavalier-Smith's six-kingdom system, reflecting advances in understanding of eukaryotic diversity.

3. Retention of Paraphyletic Groups Where Practical

The authors explicitly reject the strict cladistic position that paraphyletic groups should never be recognized, instead evaluating each case on its practicability and usage. This pragmatic approach allows retention of well-known and useful groups such as:

- Prokaryota
- Protozoa
- Crustacea
- Sarcopterygii
- Reptilia

This is a significant departure from the cladistic orthodoxy advocated by Thompson and reflects the practical needs of the biodiversity informatics community.

4. Treatment of Problematic Groups

The paper addresses several contentious taxonomic issues:

- Porifera: Retained as a single phylum with four classes, pending resolution of questions about monophyly
- Myxozoa: Classified as a subphylum of Cnidaria
- Gnathifera: Four phyla recognized (Acanthocephala, Gnathostomulida, Micrognathozoa, Rotifera) despite molecular evidence suggesting closer relationships
- Chordata: Traditional three subphyla retained (Cephalochordata, Urochordata, Vertebrata)

5. Explicit Acknowledgment of Tentative Nature

The authors repeatedly emphasize that their classification is interim and subject to change. They establish a five-year review cycle to incorporate advances in phylogenetic knowledge, recognizing that "classifications are syntheses of biological knowledge that must be regularly updated."

Critical Assessment

Strengths:

- Unprecedented scope and scale of expert consultation
- Explicitly pragmatic approach that acknowledges the limitations of purely phylogenetic classifications for database integration
- Transparent discussion of compromises and unresolved issues
- Comprehensive table (extending 60 pages in the supplemental materials) provides practical reference for biodiversity informatics

- Open access publication ensures wide availability

Limitations:

- The classification's compromise nature may satisfy no one completely
- Retaining paraphyletic groups while claiming to use "monophyletic origin" as a criterion creates conceptual inconsistency
- The decision to list taxa alphabetically below infrakingdom for easier searching sacrifices phylogenetic information for convenience
- Some decisions (e.g., recognition of 96 phyla) appear influenced more by historical tradition than by evolutionary divergence
- The classification lacks the detailed justification for many rank assignments, making it difficult for users to understand the rationale behind specific choices

Relevance:
This classification has become the de facto standard for many biodiversity databases and has been widely adopted as a reference framework. The paper's explicit acknowledgment of the practical compromises necessary for data integration makes it a valuable touchstone for discussions about the role of classification in biodiversity informatics

3. Biotechnology Law Report (Mary Ann Liebert, 2025)

Jacobs, N. (2025). Clades, classifications, and claims: Patent strategies for organism-centered inventions in an evolving world. Biotechnology Law Report.

Overview

Jacobs addresses the intersection of evolutionary biology, systematics, and patent law, specifically examining how the evolutionary nature of organisms and changing taxonomic classifications create challenges for patentees. The work, informed by the author's dual background in virology and patent law, provides practical recommendations for drafting patent specifications to address the uncertainties posed by biological evolution and changing nomenclature.

Key Contributions

1. The "Species Problem" in Patent Context

Jacobs identifies the controversy over species concepts in bacteriology and virology as a source of uncertainty in claim construction. Because patent claims often refer to bacterial or viral species, and because these concepts are contested even within the scientific community, courts may rely on extrinsic evidence (expert testimony, dictionaries) that introduces unpredictability. The author recommends that patentees provide controlling definitions grounded in the relevant literature to mitigate this uncertainty.

2. Nomenclatural Changes Over a Patent Term

The paper provides a compelling case study of how bacterial strain designations can change multiple times during a 20-year patent term. Strain H2_18, isolated in 2014, was successively classified as:

- *Clostridium* sp. (2014-2019)
- *Faecalicatena* sp001487105 (2019-2020)
- *Mediterraneibacter massiliensis* (2020-2021)
- Either *F. acetigenes* or *M. massiliensis* depending on the classification framework

This instability poses challenges for infringement analysis and can lead to disputes over whether an accused product falls within claim scope.

3. Evolution of Viral Nomenclature

Jacobs reviews the nomenclature of influenza viruses, noting:

- Subtype designations (e.g., H1N1, H3N2) remain stable despite ongoing antigenic drift
- The 2009 pandemic necessitated the new designation "A(H1N1)pdm09" to distinguish a novel lineage
- Clade designations within subtypes are frequently updated

The author argues that claiming by subtype alone may be too broad for enablement, while claiming by specific isolate is too narrow for commercial relevance.

4. Relationship Between Taxonomy and Claim Support

Drawing on cases such as *Amgen v. Sanofi*, *Juno v. Kite*, *BASF Plant Science*, and *Plant Genetic Systems*, Jacobs demonstrates how:

- Functional genus claims (antibodies defined by binding properties) face enablement challenges
- Genus claims lacking structural characterization face written description challenges
- Intermediate taxa (genera, families) may offer a middle ground between overly broad and overly narrow claims

5. Practical Recommendations for Patent Drafting

The author offers several specific recommendations:

1. Define key terms: Provide controlling definitions of taxonomic categories based on relevant literature

2. Describe methods of identification: Outline steps for determining whether an organism falls within the claimed category
3. Link principles to conservation depth: Explain the biological principle underlying the invention and the taxonomic level at which relevant features are conserved
4. Enumerate diversity: Provide examples representing the diversity within claimed taxa
5. Account for temporal change: Describe historical and anticipated diversity, particularly for evolving populations like influenza viruses

Critical Assessment

Strengths:

- Expert integration of biological and legal perspectives
- Concrete case studies grounded in real-world examples
- Practical, actionable recommendations for patent practitioners
- Sophisticated understanding of systematic biology
- Recognition that "evolution poses problems for patentees" and that systematics offers solutions

Limitations:

- Focused primarily on bacteria and viruses; applicability to eukaryotes is acknowledged but not fully explored
- Does not address the special challenges posed by horizontal gene transfer in bacteria, which complicates phylogenetic inferences and species concepts
- The recommendation to "describe the historical and present diversity within relevant taxa" may be burdensome in practice
- Does not engage with the philosophical question of whether living organisms are patentable at all
- The paper's reliance on genus-level claims may be challenged by the Federal Circuit's "war on genus claims"

Relevance:
Jacobs' paper addresses a significant and growing tension in biotechnology patent law. As evolutionary biology increasingly reveals the dynamic, contingent nature of biological entities, patent law's reliance on fixed descriptions and stable categories becomes increasingly strained. The author's recommendations offer a constructive path forward that embraces rather than ignores biological complexity.

Comparative Analysis

Thematic Integration

These three papers, spanning a 22-year period (2003-2025), address the same fundamental questions from different perspectives:

Theme	Thompson (2003)	Ruggiero et al. (2015)	Jacobs (2025)
Purpose of classification	Scientific communication and hypothesis testing	Data integration and practical utility	Legal certainty and claim support
Approach to paraphyly	Reject; monophyly mandatory	Accept where practical and useful	Acknowledge but focus on legal implications
Primary audience	Entomologists and biology students	Biodiversity informatics community	Patent attorneys and biotechnology professionals
Stance on ranks	Traditional Linnaean ranks essential	Retains ranks for practical reasons	Describes legal implications of ranks

Treatment of uncertainty	Acknowledges but downplays	Explicitly embraced as inevitable	Central concern requiring mitigation

Points of Tension

1. Monophyly vs. Practicality

Thompson's insistence on monophyly contrasts sharply with Ruggiero et al.'s pragmatic retention of paraphyletic groups. Jacobs, writing from a legal perspective, acknowledges that paraphyletic groups may be more useful for patent law if they circumscribe organisms sharing practical characteristics (e.g., pathogenic potential, metabolic capacity).

2. Rank vs. Rank-Free Classification

Thompson and Ruggiero et al. both defend Linnaean ranks, though for different reasons (predictive power vs. data integration). Jacobs' paper, while not directly engaging with the PhyloCode debate, implicitly supports ranked classification because ranks provide defined categories that can be referenced in claims.

3. The Role of Phylogenetics

Thompson's cladistic position holds that classifications should reflect phylogenetic hypotheses as accurately as possible. Ruggiero et al. acknowledge phylogeny as a basis but prioritize practical utility. Jacobs focuses on how phylogenetic understanding can be leveraged to support legal arguments about written description and enablement.

4. Stability vs. Progress

Thompson acknowledges that scientific progress requires taxonomic change but emphasizes stability in nomenclature. Ruggiero et al. explicitly anticipate updates every five years. Jacobs' legal perspective highlights the tension between fixed patent language and evolving biological knowledge.

Recommendations for Future Research

1. Empirical Studies of Taxonomic Instability

Quantitative analysis of how frequently taxonomic names change across different groups and how these changes affect legal disputes would provide valuable evidence to support or challenge Jacobs' recommendations.

2. Comparative Studies of Classification Use

Research on how different user communities (ecologists, conservation biologists, patent attorneys, public health officials) actually use classifications would inform debates about the appropriate trade-offs between phylogenetic accuracy and practical utility.

3. The PhyloCode and Patent Law

Analysis of how rank-free nomenclature would affect patent claims, including the challenges of referencing clades defined by phylogenetic methods (node-based, stem-based, or apomorphy-based definitions).

4. Legal Status of Biological Deposits

Clarification of how biological deposits under the Budapest Treaty interact with patent claim construction, particularly when deposited strains are later reclassified.

5. Interdisciplinary Dialogue

The apparent disconnect between biological systematics and patent law warrants greater interdisciplinary engagement. Systematists would benefit from understanding how their classifications are used in legal contexts, while patent practitioners would benefit from deeper understanding of systematic principles.

Conclusion

These three papers represent distinct but complementary approaches to the challenges of biological classification and nomenclature. Thompson's chapter provides a foundational introduction to systematic principles, emphasizing the predictive power of cladistic classifications. Ruggiero et al.'s consensus classification demonstrates the practical compromises required for biodiversity data integration, sacrificing phylogenetic purity for utility at scale. Jacobs' legal analysis highlights the concrete consequences of taxonomic uncertainty in patent law, offering practical strategies for navigating the intersection of evolution and intellectual property.

Together, these works illustrate that biological classification serves multiple, sometimes conflicting, purposes. No single classification can fully satisfy scientific, informatic, and legal needs simultaneously. The ongoing challenge—for systematists, database managers, and legal practitioners alike—is to develop frameworks that acknowledge this multiplicity while still providing the stability and utility that diverse users require.