INTERNATIONAL JOURNAL OF ZOOLOGICAL SCIENCES
(ISSN: 2693-3624)
VOL.06 ISSUE01 (2026)

Research Article

Integrative Taxonomy and Species Delimitation in the Era of Molecular Ecology: Theoretical Foundations, Methodological Convergence, and Implications for Biodiversity Science

Dr. Alejandro M. Ríos [1]

[1]Department of Biological Sciences, Universidad Nacional de Córdoba, Argentina

Received: 12 November 2025
Revised: 2 December 2025
Accepted: 20 December 2025
Published: 01 January 2025

Abstract

Biodiversity science is fundamentally structured around the concept of species, yet the definition, delimitation, and recognition of species remain among the most contested issues in biology. Over recent decades, advances in molecular biology, phylogenetics, ecology, and computational modeling have profoundly reshaped taxonomic practice, giving rise to integrative taxonomy as a dominant paradigm. This article presents a comprehensive and theoretically grounded examination of integrative taxonomy and species delimitation, synthesizing insights from molecular systematics, morphological analysis, ecological differentiation, biogeography, and scenario-based biodiversity modeling. Drawing exclusively on established literature, this study explores how different species concepts influence biodiversity assessments, how molecular techniques have transformed evolutionary inference, and how integrative approaches mitigate the limitations of single-data frameworks. Particular emphasis is placed on plant, fungal, algal, cyanobacterial, and animal case studies that demonstrate the practical consequences of species delimitation choices for conservation planning, ecosystem service modeling, and global biodiversity assessments. The article further interrogates the epistemological status of species as hypotheses, the role of coalescent theory and multilocus data in resolving complex evolutionary histories, and the implications of taxonomic uncertainty for large-scale biodiversity scenarios such as those developed by IPBES. By providing an exhaustive theoretical elaboration and critical analysis, this work positions integrative taxonomy not merely as a methodological toolkit but as a conceptual synthesis essential for robust biodiversity science in the Anthropocene.

Keywords: Integrative taxonomy, species delimitation, molecular systematics, biodiversity modeling, evolutionary theory, conservation biology

INTRODUCTION

The concept of species lies at the very heart of biological science, serving as the primary unit for classification, evolutionary inference, ecological analysis, and conservation policy. Despite this centrality, the definition and delimitation of species remain deeply contentious, shaped by philosophical debates, methodological innovations, and practical constraints. Traditional taxonomy relied heavily on morphological traits and expert judgment, often assuming that species boundaries were discrete, stable, and objectively identifiable. However, accumulating evidence from molecular biology, population genetics, and ecology has revealed that biological diversity is frequently structured as continua rather than neatly bounded units. This realization has profound implications for biodiversity research, as species counts underpin estimates of extinction rates, ecosystem resilience, and the distribution of ecosystem services.

The emergence of molecular techniques in the late twentieth and early twenty-first centuries marked a turning point in systematics. DNA sequencing enabled researchers to detect cryptic diversity, reconstruct evolutionary histories with unprecedented resolution, and test long-standing taxonomic hypotheses. Studies on fungi, for example, demonstrated that molecular data could radically alter understanding of evolutionary relationships within major clades, revealing deep divergences masked by morphological conservatism (Yang, 2011). Similar revelations have occurred across plants, animals, algae, and microorganisms, challenging the sufficiency of morphology-based taxonomy and exposing the limitations of single-character approaches.

At the same time, the proliferation of species concepts—biological, phylogenetic, ecological, and others—has complicated rather than resolved debates about species delimitation. Each concept emphasizes different criteria, such as reproductive isolation, monophyly, or niche differentiation, leading to divergent taxonomic outcomes when applied to the same organisms. The impact of these conceptual differences extends beyond academic discourse; biodiversity inventories, conservation priorities, and environmental policy decisions are all sensitive to how species are defined (Agapow et al., 2004). As a result, species delimitation is no longer viewed as a purely descriptive exercise but as a hypothesis-driven scientific process with far-reaching consequences.

Integrative taxonomy has emerged as a response to these challenges. Rather than privileging a single data type or species concept, integrative taxonomy advocates the explicit combination of multiple lines of evidence, including morphology, molecular phylogenetics, population genetics, ecology, biogeography, and even functional traits. The central premise is that congruence among independent datasets provides stronger support for species hypotheses than any single source of evidence alone. This approach has been successfully applied across diverse taxa, from vascular plants and diatoms to insects and mammals, revealing both hidden diversity and instances where apparent differentiation does not warrant species recognition (Cardoso et al., 2009; Pinheiro et al., 2018).

Beyond its taxonomic implications, integrative taxonomy plays a critical role in broader biodiversity science. Global initiatives such as the Intergovernmental Platform on Biodiversity and Ecosystem Services rely on species-level data to model future scenarios of biodiversity change and ecosystem service provision (Ferrier et al., 2016). Taxonomic uncertainty can propagate through these models, affecting projections and policy recommendations. Consequently, improving the robustness and transparency of species delimitation is essential not only for systematics but also for conservation planning and sustainable development.

Despite significant advances, integrative taxonomy faces methodological, theoretical, and practical challenges. Integrating heterogeneous data types raises questions about weighting, congruence, and conflict resolution. Molecular datasets may reveal deep genetic structure without corresponding ecological or morphological differentiation, while ecological divergence may occur rapidly with minimal genetic change. Moreover, the application of coalescent-based species delimitation models introduces assumptions about population history and gene flow that may not hold universally (Carstens and Dewey, 2010). Addressing these challenges requires not only technical expertise but also a clear understanding of the philosophical foundations of species concepts and the epistemological status of taxonomic decisions.

This article aims to provide a comprehensive and theoretically rich examination of integrative taxonomy and species delimitation, grounded exclusively in established literature. By synthesizing conceptual debates, methodological developments, and empirical case studies, it seeks to elucidate how integrative approaches enhance our understanding of biological diversity and why they are indispensable for contemporary biodiversity science. In doing so, it highlights the dynamic and hypothesis-driven nature of taxonomy and underscores its relevance for addressing global environmental challenges.

METHODOLOGY

The methodological framework of this research is entirely qualitative and theoretical, grounded in an exhaustive synthesis of peer-reviewed literature spanning systematics, molecular ecology, evolutionary biology, and biodiversity assessment. Rather than generating new empirical data, the study adopts a critical integrative approach, systematically analyzing how different methodological traditions contribute to species delimitation and how their integration resolves or reframes long-standing taxonomic problems. This approach aligns with the epistemological understanding of species as hypotheses, subject to testing and revision as new evidence emerges (Pante et al., 2015).

The first methodological pillar involves conceptual analysis of species concepts and their implications for biodiversity studies. Foundational discussions on the impact of species concepts were examined to understand how theoretical commitments influence empirical outcomes and conservation metrics (Agapow et al., 2004). This analysis provides a lens through which subsequent methodological choices are evaluated, emphasizing that no method operates independently of conceptual assumptions.

The second pillar focuses on molecular systematics, including DNA barcoding, multilocus phylogenetics, and coalescent-based species delimitation. Studies demonstrating the utility and limitations of single-locus markers, particularly mitochondrial DNA, were analyzed to assess their role in associating life stages, detecting cryptic species, and informing taxonomic decisions (Ahrens et al., 2007; Carew et al., 2005). Multilocus approaches were examined in detail to understand how gene tree discordance arises and how statistical frameworks, such as Bayesian concordance analysis, address this complexity (Ane et al., 2007; Belfiore et al., 2008).

The third methodological pillar involves morphological and ecological data integration. Case studies where morphological variation was reassessed in light of molecular evidence were analyzed to demonstrate how traditional characters can regain significance when interpreted within an evolutionary framework (Baker and DeSalle, 1997). Ecological differentiation, including habitat specificity and niche divergence, was considered as an independent axis of evidence supporting species hypotheses, particularly in plant and microbial taxa where morphology alone is often insufficient (Cheng et al., 2021; Maltsev et al., 2021).

The fourth pillar examines integrative taxonomic workflows applied to diverse taxa. Detailed analyses of studies describing new species using combined molecular, morphological, and ecological data were undertaken to identify common methodological patterns and best practices (Erst et al., 2020; Maltseva et al., 2022; Banaev et al., 2023). These case studies were not treated as isolated examples but as empirical tests of integrative taxonomy as a coherent scientific approach.

Finally, the methodology incorporates a synthesis of biodiversity modeling and scenario assessment literature, particularly work associated with IPBES. This component examines how species-level taxonomic decisions influence large-scale assessments of biodiversity change and ecosystem services, highlighting the downstream consequences of taxonomic uncertainty (Ferrier et al., 2016).

Throughout the analysis, emphasis is placed on theoretical coherence, methodological transparency, and critical evaluation. Conflicting results and alternative interpretations are explicitly discussed, reflecting the understanding that integrative taxonomy is not a mechanistic procedure but an iterative, interpretive process. By weaving together conceptual, methodological, and applied perspectives, this methodological approach aims to produce a comprehensive and publication-ready synthesis of integrative taxonomy in contemporary biodiversity science.

RESULTS

The synthesis of literature reveals several consistent patterns that emerge across taxonomic groups and methodological approaches. First, reliance on single data sources, whether morphological or molecular, frequently leads to incomplete or misleading species delimitations. Molecular studies consistently demonstrate that morphologically defined species may encompass multiple deeply divergent lineages, as seen in fungi, diatoms, and vascular plants (Yang, 2011; Maltsev et al., 2021). Conversely, apparent genetic differentiation does not always correspond to ecologically or evolutionarily independent units, underscoring the need for integrative evaluation.

Second, multilocus molecular approaches provide a more nuanced understanding of evolutionary history than single-locus analyses. Gene tree discordance is shown to be pervasive, particularly in rapidly radiating lineages and species complexes, reflecting processes such as incomplete lineage sorting and historical gene flow (Belfiore et al., 2008). Bayesian and coalescent-based frameworks help reconcile these discrepancies but also introduce model-dependent assumptions that must be critically assessed (Ane et al., 2007; Carstens and Dewey, 2010).

Third, integrative taxonomy consistently leads to either the recognition of previously unrecognized species or the synonymization of taxa that lack sufficient evidence for distinctiveness. In plants, integrative studies of species complexes reveal that morphological plasticity and environmental variation can obscure true evolutionary relationships, while combined datasets clarify speciation patterns and historical biogeography (Pinheiro et al., 2018; Cheng et al., 2021). Similar patterns are observed in algae and cyanobacteria, where integrative approaches uncover both cryptic diversity and instances of morphological convergence (Kulikovskiy et al., 2022; Gaysina et al., 2022).

Fourth, species delimitation outcomes have direct implications for biodiversity assessment and conservation modeling. Studies of endemic floras and regional biodiversity hotspots demonstrate that integrative taxonomy often increases recognized diversity, thereby altering estimates of endemism and conservation priority (Erst et al., 2022). These findings underscore the sensitivity of biodiversity metrics to taxonomic resolution and methodological rigor.

Collectively, the results indicate that integrative taxonomy enhances both the accuracy and explanatory power of species delimitation. By triangulating evidence from multiple independent sources, it reduces the risk of both over-splitting and under-recognition of biodiversity. At the same time, the results highlight that integration does not eliminate uncertainty but rather makes it explicit and scientifically tractable.

DISCUSSION

The findings synthesized in this article reinforce the view that species are best understood as testable hypotheses rather than immutable entities. This perspective has profound implications for taxonomy, evolutionary biology, and conservation science. Integrative taxonomy operationalizes this view by treating different data types as independent tests of species hypotheses, thereby aligning taxonomic practice with the broader scientific method (Pante et al., 2015).

One of the most significant theoretical implications concerns the relationship between species concepts and methodological choices. The diversity of species concepts reflects different emphases on evolutionary processes, yet integrative taxonomy demonstrates that these concepts need not be mutually exclusive. Instead, they can be viewed as complementary lenses through which biological diversity is examined. For example, phylogenetic monophyly, ecological distinctiveness, and morphological diagnosability often converge in well-supported species, while discordance among these criteria highlights areas where evolutionary processes are ongoing or complex (Agapow et al., 2004).

Despite its strengths, integrative taxonomy faces notable challenges. Integrating heterogeneous datasets raises questions about how to resolve conflicts among lines of evidence. Molecular divergence without ecological differentiation may reflect historical isolation followed by secondary contact, while ecological divergence without genetic differentiation may indicate recent or rapid adaptation. Deciding whether such patterns warrant species recognition requires informed judgment rather than algorithmic solutions. Furthermore, coalescent-based models, while powerful, rely on assumptions about population structure and gene flow that may not hold across all taxa or spatial scales (Carstens and Dewey, 2010).

Another limitation concerns data availability and expertise. Integrative taxonomy is resource-intensive, requiring access to molecular laboratories, ecological data, and taxonomic expertise. This can create disparities in taxonomic knowledge across regions and taxa, potentially biasing global biodiversity assessments. Addressing these challenges will require investment in capacity building, data sharing, and methodological standardization.

From an applied perspective, the integration of robust taxonomy into biodiversity modeling frameworks is essential. Scenario-based assessments of biodiversity and ecosystem services, such as those conducted by IPBES, depend on accurate species-level data to inform projections and policy decisions (Ferrier et al., 2016). Taxonomic uncertainty can propagate through these models, affecting estimates of vulnerability, resilience, and ecosystem function. Integrative taxonomy, by clarifying species boundaries and making uncertainty explicit, enhances the reliability of such assessments.

Future research should focus on developing transparent frameworks for data integration, refining models that accommodate complex evolutionary histories, and expanding integrative approaches to under-studied taxa and regions. Advances in genomic technologies, ecological modeling, and bioinformatics offer unprecedented opportunities to deepen integration, but they must be coupled with rigorous conceptual foundations to avoid replacing one form of reductionism with another.

CONCLUSION

Integrative taxonomy represents a transformative approach to understanding biological diversity, uniting conceptual clarity with methodological pluralism. By synthesizing molecular, morphological, ecological, and biogeographical evidence, it provides a robust framework for species delimitation that acknowledges complexity rather than obscuring it. The evidence reviewed in this article demonstrates that integrative approaches not only improve taxonomic accuracy but also enhance the relevance of taxonomy for biodiversity assessment, conservation planning, and ecosystem service modeling.

In an era of rapid environmental change and biodiversity loss, the stakes of taxonomic decisions have never been higher. Species counts inform global indicators, guide conservation investments, and shape our understanding of life's evolutionary history. Integrative taxonomy, grounded in the view of species as hypotheses, offers a scientifically rigorous and adaptable pathway forward. By embracing uncertainty, fostering methodological integration, and maintaining theoretical rigor, biodiversity science can better meet the challenges of the Anthropocene.

REFERENCES

1. Agapow, P.M.; Bininda-Emonds, O.R.P.; Crandall, K.A.; Gittleman, J.L.; Mace, G.M.; Marshall, J.C.; Purvis, A. The impact of species concept on biodiversity studies. Quarterly Review of Biology 2004, 79, 161–179.
2. Ahrens, D.; Monaghan, M.T.; Vogler, A.P. DNA-based taxonomy for associating adults and larvae in multi-species assemblages of chafers. Molecular Phylogenetics and Evolution 2007, 44, 436–449.
3. Ane, C.; Larget, B.; Baum, D.A.; Smith, S.D.; Rokas, A. Bayesian estimation of concordance among gene trees. Molecular Biology and Evolution 2007, 24, 412–426.
4. Baker, R.H.; DeSalle, R. Multiple sources of character information and the phylogeny of Hawaiian Drosophilids. Systematic Biology 1997, 46, 654–673.
5. Banaev, E.V.; Tomoshevich, M.A.; Khozyaykina, S.A.; Erst, A.A.; Erst, A.S. Integrative taxonomy of Nitraria, description of a new enigmatic species and key to all currently known species. Plants 2023, 12, 593.
6. Belfiore, N.M.; Liu, L.; Moritz, C. Multilocus phylogenetics of a rapid radiation in the genus Thomomys. Systematic Biology 2008, 57, 294–310.
7. Cardoso, A.; Serrano, A.; Vogler, A.P. Morphological and molecular variation in tiger beetles of the Cicindela hybrida complex. Molecular Ecology 2009, 18, 648–664.
8. Carew, M.E.; Pettigrove, V.; Hoffman, A.A. The utility of DNA markers in classical taxonomy. Annals of the Entomological Society of America 2005, 98, 587–594.

9. Carstens, B.C.; Dewey, T.A. Species delimitation using a combined coalescent and information-theoretic approach. Systematic Biology 2010, 59, 400–414.

10. Cheng, S.; Zeng, W.; Wang, J.; Liu, L.; Liang, H.; Kou, Y.; Wang, H.; Fan, D.; Zhang, Z. Species delimitation of Asteropyrum based on morphological, molecular, and ecological variation. Frontiers in Plant Science 2021, 12, 681864.

11. Erst, A.S.; Sukhorukov, A.P.; Mitrenina, E.Y.; Skaptsov, M.V.; Kostikova, V.A.; Chernisheva, O.A.; Troshkina, V.; Kushunina, M.; Krivenko, D.A.; Ikeda, H. An integrative taxonomic approach reveals a new species of Eranthis in North Asia. PhytoKeys 2020, 140, 75–100.

12. Erst, A.S.; Nikulin, A.Y.; Nikulin, V.Y.; Ebel, A.L.; Zibzeev, E.V.; Sharples, M.T.; Baasanmunkh, S.; Choi, H.J.; Olonova, M.V.; Pyak, A.I. Distribution analysis and DNA barcodes of the endemic vascular flora of the Altai mountains. Systematic Biodiversity 2022, 20, 1–30.

13. Ferrier, S.; Ninan, K.N.; Leadley, P.; Alkemade, R.; Acosta, L.A.; Akçakaya, H.R.; Brotons, L.; Cheung, W.; Christensen, V.; Harhash, K.A. IPBES Methodological Assessment of Scenarios and Models of Biodiversity and Ecosystem Services. IPBES Secretariat, Bonn, 2016.

14. Gaysina, L.A.; Johansen, J.R.; Saraf, A.; Allaguvatova, R.Z.; Pal, S.; Singh, P. Roholtiella volcanica, a new species of Cyanobacteria from volcanic soils. Diversity 2022, 14, 620.

15. Kulikovskiy, M.; Genkal, S.; Maltsev, Y.; Glushchenko, A.; Kuznetsova, I.; Kapustin, D.; Gusev, E.; Martynenko, N.; Kociolek, J.P. Resurrection of the diatom genus Stephanocyclus based on an integrated molecular and morphological approach. Fottea 2022, 22, 181–191.

16. Maltsev, Y.; Maltseva, S.; Kociolek, J.P.; Jahn, R.; Kulikovskiy, M. Biogeography of the cosmopolitan diatom Hantzschia amphioxys sensu lato. Scientific Reports 2021, 11, 4266.

17. Maltseva, S.; Bachura, Y.; Erst, T.; Kulikovskiy, M.; Maltsev, Y. Description of Desmonostoc caucasicum using an integrative taxonomic approach. Phycologia 2022, 61, 514–527.

18. Pante, E.; Puillandre, N.; Viricel, A.; Arnaud-Haond, S.; Aurelle, D.; Castelin, M.; Chenuil, A.; Destombe, C.; Forcioli, D.; Valero, M. Species are hypotheses. Molecular Ecology 2015, 24, 525–544.

19. Pinheiro, F.; Dantas-Queiroz, M.V.; Palma-Silva, C. Plant species complexes as models to understand speciation and evolution. Critical Reviews in Plant Sciences 2018, 37, 54–80.

20. Yang, Z.L. Molecular techniques revolutionize knowledge of basidiomycete evolution. Fungal Diversity 2011, 50, 47–58.