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Species Delimitation in Environmental Philosophy: Ontological, Epistemological, and Axiological Reflections from Mitochondrial Markers to Machine Learning

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ABSTRACT

Species delimitation is not only a technical problem in systematics but also a central concern in environmental philosophy and biodiversity ethics, raising ontological, epistemological, and axiological questions about how we conceive and value the living world. Building on a rapidly expanding body of empirical and theoretical work across reptiles, amphibians, fishes, plants, fungi, and diverse invertebrates, this review reassesses species delimitation in the genomic and machine-learning era through the lens of environmental philosophy. Recent studies reveal ubiquitous cryptic diversity, reticulate evolutionary histories, mitonuclear discordance, polyploidy, and complex biogeographic structure that challenge simple, morphology-based taxonomies and naive assumptions about species as sharply bounded natural kinds (e.g., Burbrink et al., 2022; Serrano & Ortiz, 2023; Sklenář et al., 2022). Coalescent-based models, phylogenetic networks, speciation-based delimitation frameworks, and unsupervised machine learning now provide powerful tools for diagnosing independently evolving lineages and interrogating the "gray zone" of speciation under gene flow (e.g., Barley et al., 2024; Chan et al., 2023; Pyron, 2023). Ontologically, these developments force us to clarify what species are in a world of continua, reticulation, and arrested speciation (de Queiroz, 2025; Burbrink et al., 2023). Epistemologically, they expose how inferences about species boundaries depend on model choice, marker selection, data integration, and uncertainty quantification, including the persistent dominance and limitations of mitochondrial DNA (Wüster, 2025). Axiologically, decisions to split or lump lineages reshape conservation priorities, legal protection, and the distribution of moral concern, with direct implications for biodiversity hotspots and environmental justice. We synthesize best practices for integrative species delimitation and argue that explicit attention to ontological coherence, epistemic robustness, and axiological transparency is essential for a philosophically informed and ethically responsible taxonomy.

Keywords: *species delimitation; environmental philosophy; ontological and epistemological perspectives; axiology and biodiversity ethics; integrative taxonomy;*

phylogenomics and machine learning; speciation continuum

INTRODUCTION

Species are the fundamental units of biodiversity assessment, conservation planning, and evolutionary analysis. Yet they are simultaneously central objects of environmental philosophy, because any proposal about how many species exist and where they occur presupposes answers to questions about what species are (ontology), how we can know and justify their boundaries (epistemology), and why they matter morally and politically (axiology).

Classical taxonomy treated species as relatively discrete morphological units. Molecular systematics and phylogeography overturned this simple picture by revealing extensive geographic structure, cryptic diversity, and complex histories of gene flow and hybridization across many clades (e.g., Burbrink, 2022; Guillory et al., 2024; MacGuigan et al., 2023). Phylogeographically structured lineages and "gray zones" of speciation are now recognized in taxa as diverse as salamanders, lizards, frogs, freshwater fishes, and alpine plants (e.g., Kuchta et al., 2024; Barley et al., 2024; MacGuigan et al., 2023; Serrano & Ortiz, 2023).

In parallel, conceptual work has argued for a unified species concept that treats species as separately evolving metapopulation lineages, without requiring any single diagnostic property—such as reproductive isolation or monophyly—as necessary or sufficient (de Queiroz, 2025). This lineage ontology anchors much of the recent debate about how to interpret genomic structure, hybrid zones, and the speciation continuum (Burbrink et al., 2024; Sánchez et al., 2023).

At the methodological level, species delimitation has progressed from single-locus mitochondrial trees to multilocus coalescent models, demographic inference, speciation-based delimitation frameworks, and increasingly, to machine learning that integrates genetics, geography, phenotype, and environment (Hillis et al., 2021; Pyron, 2023; Salles et al., 2025; Parsons et al., 2024). These developments expand the epistemic toolkit but also raise new philosophical questions about evidence, model dependence, and uncertainty.

For environmental philosophy and biodiversity ethics, these changes are not merely technical. The way we delimit species affects which lineages receive names, legal recognition, and conservation resources; how we prioritize hotspots; and how we conceptualize responsibilities to nonhuman beings and ecosystems. Splitting a complex into multiple species can elevate the perceived rarity of some lineages; lumping can obscure localized endemism and vulnerability (e.g., Sklenář et al., 2022; Serrano & Ortiz, 2023; Wüster et al., 2024).

In this review, we:

1. Clarify the ontological status of species in the lineage framework and its alternatives.
2. Examine epistemological challenges in delimiting species across diverse empirical systems.
3. Explore the axiological implications of species delimitation for conservation and biodiversity ethics.
4. Highlight how genomic and machine-learning approaches reshape these debates.
5. Propose best practices for an integrative, philosophically explicit, and ethically reflective species taxonomy.

We draw on recent literature across animals, plants, and fungi—including reptiles and amphibians (e.g., Barley et al., 2024; Burbrink & Myers, 2025; Wüster, 2025), freshwater fishes (MacGuigan et al., 2023), plants (Serrano & Ortiz, 2023; Soares et al., 2024), fungi (Sklenář et al., 2022), and taxonomic critiques (Wüster et al., 2024; Burbrink et al., 2022)—to illustrate how philosophical and ethical questions are entangled with empirical practice.

MATERIALS & METHODS

Study Design

This work is a narrative literature review and philosophical synthesis, not an empirical experimental study. It synthesizes conceptual and empirical literature on species delimitation, environmental philosophy, and biodiversity ethics from the late 20th century to 2025.

Literature Sources and Selection

The corpus of references and abstracts used here was drawn from:

- An existing literature review draft on species delimitation and environmental philosophy, including its curated reference list.
- A corresponding RIS file of recent empirical and conceptual studies on species delimitation across taxa provided by the authors.

Only peer-reviewed articles and book chapters were considered. No additional references were introduced beyond those contained in the authors extracted corpus, in accordance with the project's constraints.

Analytical Approach

The literature was organized into thematic clusters:

1. Ontological debates about species (lineage ontology, subspecies).
2. Epistemological tools (mtDNA, coalescent models, networks, ML).
3. Empirical case studies across major organismal groups.
4. Axiological and ethical implications for conservation, environmental justice, and biodiversity values.

RESULTS

Ontology of Species: Lineages, Kinds, and Environmental Philosophy

From essentialist kinds to lineage individuals

Historically, species were frequently conceived as essentialist kinds, defined by shared intrinsic properties. Environmental philosophers have criticized this view for its poor fit with evolutionary theory and for encouraging a static picture of nature (de Queiroz, 2025). In evolutionary biology, the move to lineage-based ontologies reframes species as spatiotemporally extended individuals: systems of populations connected by gene flow and descent rather than by an immutable essence (Hillis et al., 2021).

The unified species concept articulates this view explicitly: species are separately evolving metapopulation lineages, and widely used properties (reproductive isolation, monophyly, ecological distinctness) are contingent outcomes of divergence, not defining criteria (de Queiroz, 2025). Ontologically, this shift has several implications relevant to environmental philosophy:

- It highlights that species have histories and trajectories, not just static trait profiles.
- It supports the idea that species themselves, not only organisms, can be bearers of moral concern, as historical achievements of evolution.
- It reframes extinction and conservation as the loss or preservation of these extended individuals, not merely the disappearance of a set of traits.

Ontology in the gray zone of speciation

The gray zone of speciation—where lineages are partially isolated, hybridizing, and structured across geography and environment—poses challenges for lineage ontology (Burbrink et al., 2024; Sánchez et al., 2023). Empirical studies show that many clades occupy intermediate positions along a speciation continuum:

- In spotted whiptail lizards (Aspidoscelis gularis complex), dense genomic sampling reveals continuous gene flow and hybrid speciation; nonetheless, a two-species arrangement best reflects deeply differentiated lineages across environmental gradients (Barley et al., 2024).
- The Wehrle's salamander complex exhibits multiple genetic clusters; some are strongly supported as species by coalescent methods, while others show shallow divergence (Kuchta et al., 2024).

- Patagonian Liolaemus (L. kingii clade) inhabit a gray zone where model-based delimitation uncovers complex diversification with incomplete lineage sorting and ongoing gene flow (Sánchez et al., 2023).

Mangrove pit vipers demonstrate how gene flow and reticulation can create artefactual basal branches and non-monophyly if ignored in phylogenetic analyses (Chan et al., 2023).

These systems stress-test lineage ontology by forcing the question: how much independence is required for a lineage to count as a species? Environmental philosophy must grapple with the possibility that species boundaries are inherently fuzzy, and that any sharp taxonomy involves degrees of idealization and convention.

Subspecies, ontology, and ethical tension

The persistence of the subspecies rank exemplifies the intersection of ontology and ethics. Burbrink et al. (2022) argue that subspecies are ontologically unstable: either they are separately evolving lineages and thus species, or they are arbitrary geographic variants lacking clear evolutionary meaning. Reliance on subspecies and non-evolutionary criteria (e.g., partial reproductive isolation) can disconnect taxonomy from lineage ontology and from the genealogical relationships that ground individuality.

This ambiguity has ethical consequences. If conservation policies treat subspecies as less important than species, ontologically incoherent categories can result in uneven protection for lineages that are, in fact, distinct evolutionary entities (Burbrink et al., 2022). A lineage-based ontology pushes toward taxonomies that avoid pseudo-hierarchies of value and instead recognize a spectrum of evolutionary individuality with explicit thresholds tied to specific purposes (e.g., legal listing vs. ecological monitoring).

Epistemology of Species Delimitation in the Genomic Era

Markers, models, and the dominance of mitochondrial DNA

The epistemology of species delimitation concerns how we justify claims that particular lineages are independently evolving. Molecular data have transformed this landscape, but they come with important limitations. A central issue is the over-reliance on mitochondrial DNA (mtDNA).

Wüster (2025) surveyed non-avian reptile taxonomy and found that mtDNA remains dominant: it appears in 84% of species-level descriptions and delimitation studies and is the sole marker in 44%. This is epistemically problematic because mtDNA is a single, maternally inherited locus; it is particularly prone to introgression, selective sweeps, and incomplete lineage sorting (Wüster, 2025).

Controversies over anaconda taxonomy illustrate this danger: taxonomic proposals based heavily on mtDNA, with sparse nuclear data and weak morphological support, led to unstable species hypotheses and high-profile public confusion (Wüster et al., 2024). Similar patterns appear in whiptail lizards and Patagonian lizards, where mitonuclear discordance reveals past mitochondrial capture and introgression (de Medeiros Magalhães et al., 2025; Sánchez et al., 2023).

Studies that integrate nuclear genomic data and explicit demographic models provide more robust epistemic access to lineage independence. For example:

- In North American racers (Coluber constrictor), isolation–migration models and tests of locus–environment associations reveal two unrecognized species maintained by selection across subtropical–temperate ecoregions despite gene flow (Burbrink & Myers, 2025).
- In the Ameivula ocellifera complex, ultraconserved elements (UCEs) and mitogenomic data reveal reticulate evolution and mitochondrial capture,

demonstrating that mtDNA alone would misrepresent species boundaries (de Medeiros Magalhães et al., 2025).

- In the Etheostoma nigrum fish complex, ddRAD data and phylogenomics resolve multiple evolutionary lineages previously hidden under a single name (MacGuigan et al., 2023).

These examples show that epistemic reliability in delimitation depends on marker choice, sampling design, and joint analysis of genomic and environmental data.

Coalescent-based models and genealogical divergence

Multispecies coalescent (MSC) models—as implemented in tools like BPP and STACEY—have become central in species delimitation, treating species as coalescent units and estimating divergence and gene-tree discordance (Hillis et al., 2021; Sklenář et al., 2022). Yet MSC outputs require careful interpretation; they cannot be treated as oracles.

In Aspergillus series Versicolores, Sklenář et al. (2022) combined multilocus phylogenies and MSC models with single-locus delimitation approaches (GMYC, PTP, ABGD). Despite a previous taxonomy recognizing 17 species, most methods supported only four species, and morphology and physiology showed high within-species variation and overlap. This case shows how integrative evidence can support lumping in a clade of environmental and medical significance.

In the Plethodon wehrlei salamander complex, BPP supports multiple candidate species; however, the genealogical divergence index (gdi) indicates that only some lineages are clearly distinct species, illustrating the need to combine MSC support with quantitative divergence metrics and biological reasoning (Kuchta et al., 2024).

Epistemologically, MSC models provide probabilistic evidence about lineage structure but depend on priors, model assumptions, and sampling. Environmental philosophy reminds us that delimitation thresholds inevitably reflect values and pragmatic aims (e.g., conservation, nomenclatural stability), not just data.

Networks, reticulation, and speciation-based delimitation

Because many lineages have reticulated histories, tree-based methods may misrepresent their diversification. Phylogenetic networks and speciation-based delimitation models explicitly incorporating gene flow provide a more realistic epistemic framework.

Chan et al. (2023) used genomic data and delineate, a speciation-based model, to delimit species in the mangrove pit viper complex. They showed that failure to account for admixture created an artefactual basal "ladder" of admixed populations; once gene flow was incorporated, a different, biologically plausible delimitation emerged.

Barley et al. (2024) integrated phylogenetic and coalescent tools to clarify species boundaries in spotted whiptail lizards, showing how gene flow across the speciation continuum shapes the patterns we interpret as species limits. Other studies in Malagasy snakes and Sulawesi lizards similarly highlight widespread reticulation in adaptive radiations, challenging strictly bifurcating tree models (DeBaun et al., 2023; McGuire et al., 2023; Reilly et al., 2022, 2023; Burbrink et al., 2023).

These approaches deepen the epistemology of species delimitation by asking not only whether lineages exceed some divergence threshold but also whether they represent outcomes of speciation processes with stable hybrid zones, ecological differentiation, and limited gene flow.

Machine learning as an epistemic tool

Machine learning is increasingly used to integrate high-dimensional datasets for species delimitation and biodiversity assessment:

- Pyron (2023) introduced unsupervised Self-Organizing Maps (SOMs) and SuperSOMs integrating genetic, geographic, environmental, and

phenotypic data, providing clusters that can be interpreted as species hypotheses without assuming a parametric model for each data type.
- Parsons et al. (2024) used predictive ML models trained on climatic and life-history traits to predict hidden genetic diversity in salamanders, identifying environmental variables that best forecast cryptic structure.
- Salles and Domingos (2025) reviewed a range of ML applications, emphasizing both opportunities and limitations, including sensitivity to training data quality and taxonomic coverage.

From an environmental-philosophical perspective, ML-based delimitation raises new epistemic and ethical questions:
- How should algorithmically derived clusters be interpreted ontologically—as species, populations, or intermediate entities?
- How can we guard against bias amplification, where ML models reproduce and intensify sampling inequities?
- To what extent should ML outputs influence conservation prioritization in data-poor regions?

These questions underscore that epistemic tools are never neutral; their design and deployment embody tacit assumptions and values.

Empirical Landscapes: Herpetofauna, Fishes, Plants, and Fungi

To ground the philosophical discussion, this section summarizes key empirical systems that illustrate ontological, epistemological, and axiological issues in species delimitation.

Reptiles and amphibians: hotspots of cryptic diversity

Reptiles and amphibians have been central in recent species-delimitation research:
- North American racers (Coluber constrictor): Burbrink and Myers (2025) used genome-wide SNP data and isolation–migration models to show that selection maintains species boundaries at subtropical–temperate ecoregion interfaces despite gene flow, revealing two previously unrecognized species and highlighting the role of environmental transitions.
- Wehrle's salamander complex and Plethodon kentucki: Kuchta et al. (2024) and Watts et al. (2024) used anchored hybrid enrichment and MSC analyses to delimit species in complexes shaped by gradual range fragmentation. They identified multiple candidate species and deep structure within nominal taxa.
- Patagonian Liolaemus (L. kingii clade): Sánchez et al. (2023) applied coalescent-based, model-driven delimitation to a lizard clade in the speciation gray zone, highlighting how partial isolation and complex demographic histories challenge binary species decisions.
- Sulawesi flying lizards (Draco lineatus group) and southern Wallacean Cyrtodactylus geckos: McGuire et al. (2023) and Reilly et al. (2023) combined phylogenomics and biogeography to show that current taxonomy drastically underestimates diversity, with evidence for ancient hybridization, cryptic lineages, and arrested speciation.
- Bufo japonicus and Bufo bufo–B. verrucosissimus: studies in Japan and Türkiye used population genetics and hybrid-zone analyses to clarify range limits and potential contact zones, illustrating how amphibian delimitations inform monitoring of climate-sensitive hybrid zones (Fukutani et al., 2023; Dursun et al., 2023).

These cases are especially relevant for biodiversity ethics because they occur in recognized hotspots (e.g., Sulawesi, Madagascar, South American Dry Diagonal) where species limits strongly influence conservation assessments and land-use decisions (Guillory et al., 2024; DeBaun et al., 2023).

Table 1. Representative genomic species-delimitation studies in herpetofauna and fishes

Taxon / Complex	Region / System	Main Data Types	Key Delimitation / Modelling Frameworks	Main Outcome for Species Limits	Ref.
Coluber constrictor racers	Subtropical–temperate ecoregions, USA	Genome-scale SNPs, environment	Isolation–migration models; locus–environment tests	Two unrecognized species maintained by selection despite gene flow	Burbrink & Myers, 2025
Plethodon wehrlei complex	Eastern North America	Anchored hybrid enrichment	STRUCTURE; MSC (BPP); gdi	Multiple candidate species; mixed support for several lineages	Kuchta et al., 2024
Plethodon kentucki	Cumberland Plateau, USA	Genomic SNPs	Population structure; MSC	Deep structure suggests cryptic lineages within a nominal species	Watts et al., 2024
Aspidoscelis gularis complex	North America	Reduced-representation genomics	Coalescent tools; reticulation modelling	Two-species arrangement best reflects speciation continuum	Barley et al., 2024
Etheostoma nigrum complex	Eastern North American rivers	ddRAD; phylogenomics	Population genomics; phylogenetics	Multiple evolutionary lineages delimited as species	MacGuigan et al., 2023
Mangrove pit vipers	SE Asian mangrove systems	Genomic SNPs	Speciation-based model (Delineate); gene flow modelling	New species recognized after accounting for phylogenetic conflict and gene flow	Chan et al., 2023
Draco lineatus group	Sulawesi and nearby islands	mtDNA, SNPs, exon capture	Phylogeography; clustering; demographic models	≥15 species, including cryptic species and cases of arrested speciation	McGuire et al., 2023
Cyrtodactylus (southern Wallacea)	Southern Wallacea archipelagos	>1,100 nuclear loci	Phylogenomics; clustering; biogeographic modelling	Up to 25 candidate species vs. 8 currently described; multiple dispersal waves	Reilly et al., 2023

Plants: polyploidy, cryptic lineages, and environmental gradients

Plant species delimitation is often complicated by polyploidy, hybridization, and subtle morphological variation:

- In Iberian Jasione (Campanulaceae), Serrano and Ortiz (2023) combined phylogenetics, GMYC and ASAP delimitation, morphology, cytology, and ploidy to untangle a complex group. They identified cryptic species and showed that biogeographical regionalization (chorological subprovinces) aligns with evolutionary units.
- In Petunia species from South American river systems, low-coverage genomic sequencing and demographic models revealed multiple lineages and showed that rivers act as strong phylogeographic barriers despite limited morphological differentiation (Freitas et al., 2024).
- Highland Solanaceae in South American grasslands exhibit hidden speciation revealed by genomic and demographic analyses, with several lineages

embedded within nominal species (Soares et al., 2024).

These examples show how integrative approaches are crucial for accurately assessing plant biodiversity and identifying environmentally coherent units relevant for conservation planning.

Fungi: collapsing over-split taxonomies

Fungal systematics illustrates the opposite problem: over-splitting. In Aspergillus series Versicolores, Sklenář et al. (2022) analyzed 518 strains using multilocus phylogenies (benA, CaM, RPB2, Mcm7, Tsr1), multiple single-locus and multi-locus delimitation methods, and morphological and physiological data. Most methods converged on a four-species concept, in stark contrast to earlier schemes with 17 species. Phenotypic characters were highly variable and overlapping, and single-gene trees yielded inconsistent identifications.

From an axiological standpoint, both splitting and lumping have consequences: over-splitting can distort risk assessments in medical and environmental contexts, whereas excessive lumping can obscure distinct ecological roles and responses to environmental change.

Table 2. Plant and fungal case studies illustrating cryptic diversity, polyploidy, and taxonomic revision

Group / Complex	Region / Habitat	Data Types	Main Methods	Key Species-Delimitation Insights	Ref.
Jasione sessiliflora group	Western Mediterranean, Iberian basin	Phylogenetics; GMYC; ASAP; ploidy; morph.	Phylogenetic delimitation; cytology	Cryptic species revealed; biogeographic subprovinces match evolutionary units	Serrano & Ortiz, 2023
Petunia guarapuavensis–scheideana	South American riverine landscapes	Low-coverage genome sequencing	Population genomics; demographic models	River barriers and rapid divergence yield multiple lineages despite subtle morphology	Freitas et al., 2024
Highland Solanaceae	Southern South American grasslands	Genome sequencing; demography	Population genomic & demographic models	Hidden speciation and multiple lineages within nominal species	Soares et al., 2024
Aspergillus series Versicolores	Global, various substrates	Multilocus phylogeny; morphology; physio.	MSC (STACEY); GMYC; ABGD; PTP	Taxa reduced from 17 to 4 species; high intraspecific phenotypic variability	Sklenář et al., 2022

The Gray Zone, Subspecies, and Philosophical Frictions

The speciation continuum and phylogeographic lineages

The idea of a speciation continuum—spanning weakly structured populations to fully isolated species—is central to modern delimitation (Burbrink et al., 2024; Sánchez et al., 2023). Phylogeographic lineages revealed by genomic data occupy various positions along this continuum.

Burbrink et al. (2024) propose a set of tests linking species limits to speciation processes, emphasizing that lineages maintained across environmental transitions with stable hybrid zones and non-introgressing genomic regions should count as species in an ontological sense. Similarly, in the Etheostoma nigrum complex, riverine history, glacial cycles, and low dispersal yield lineages that differ in age and degrees of gene flow, requiring nuanced taxonomic judgments (MacGuigan et al., 2023). Salamander complexes show that gradual fragmentation produces multiple levels of divergence, challenging binary population/species categorizations (Kuchta et al., 2024; Watts et al., 2024).

From an environmental-philosophical standpoint, if species form a continuum, then any strict "cut" reflects pragmatic and axiological choices—about legal recognition, communication needs, and conservation priorities—rather than purely metaphysical truths.

Critiquing the subspecies rank

The subspecies debate captures tensions between ontology, epistemology, and axiology. Burbrink et al. (2022) criticize subspecies as often lacking clear evolutionary meaning and resting on weak evidence. Yet, in some regional contexts, careful integrative analyses of contact zones and hybridization—such as in *Bufo japonicus* or between *Bufo bufo* and *B. verrucosissimus*—are crucial for understanding environmental drivers of divergence and forecasting shifts under climate change (Fukutani et al., 2023; Dursun et al., 2023).

A philosophically informed taxonomy should either abandon subspecies or restrict it to well-defined operational roles, making explicit the evolutionary evidence and ethical stakes of labeling lineages as "subspecific."

Axiology and Biodiversity Ethics: Why Species Boundaries Matter

Splitting, lumping, and conservation triage

From a biodiversity ethics perspective, species boundaries are normatively loaded. Conservation law, Red List assessments, and funding schemes treat species as core units. Taxonomic splits can elevate threat categories by revealing narrow-range endemics, while taxonomic lumps can depress perceived risk (Sklenář et al., 2022; Serrano & Ortiz, 2023; Soares et al., 2024). Examples include:

- Recognition of new species in Coluber and Plethodon complexes highlights localized endemics with distinct conservation needs (Burbrink & Myers, 2025; Kuchta et al., 2024; Watts et al., 2024).
- Underestimation of diversity in southern Wallacea and Sulawesi lizards may obscure cryptic island endemism, with implications for development, mining, and infrastructure planning (McGuire et al., 2023; Reilly et al., 2023).
- Over-splitting in Aspergillus Versicolores would inflate the number of medically and environmentally relevant taxa, potentially confusing risk assessments and regulatory frameworks (Sklenář et al., 2022).

Thus, environmental philosophy and biodiversity ethics demand transparency about how delimitation decisions redistribute conservation resources and moral attention.

Table 3. Axiological and conservation implications of species-delimitation decisions

System / Region	Delimitation Outcome	Key Ethical / Conservation Implication	Ref.
Coluber constrictor (USA)	Two unrecognized species identified	Reveals hidden biodiversity and adaptive boundaries at ecoregion interfaces	Burbrink & Myers, 2025
Plethodon wehrlei complex	Multiple lineages of varying status	Requires nuanced listing and management of partially isolated taxa	Kuchta et al., 2024
Etheostoma nigrum complex	Several new species delimited	Highlights localized endemics; informs fine-scale river management	MacGuigan et al., 2023
South American Dry Diagonal biota	Complex phylogeographic patterns	Conservation planning must integrate historical geoclimatic drivers	Guillory et al., 2024
Aspergillus Versicolores	Reduction from 17 to 4 species	Avoids artificial inflation of risk categories and diagnostic confusion	Sklenář et al., 2022
Sulawesi / Wallacea lizard radiations	Substantial underestimation of species	Development must account for cryptic island endemism and unique lineages	McGuire et al., 2023; Reilly et al., 2023

Environmental justice and taxonomic bias

Species delimitation is shaped by geopolitical and taxonomic biases. Genomic and ML-based studies often focus on charismatic taxa or well-funded regions, whereas other clades and regions remain under-studied (Guillory et al., 2024; Maritz et al., 2021). This raises concerns about environmental justice: unnamed or unstudied lineages may be more readily sacrificed to development, and their extinctions may pass unrecorded.

ML models trained on biased data risk reinforcing these patterns (Parsons et al., 2024). A justice-aware biodiversity ethics advocates targeted taxonomic and genomic work in underrepresented regions and clades, open data infrastructures (e.g., phylogatR; Burbrink, 2022), and frameworks that explicitly consider how epistemic inequities translate into differential vulnerability.

Beyond species: valuing lineages, populations, and ecosystems

Environmental philosophy has long argued that value in nature is not restricted to species. Populations, communities, and ecosystems can also be morally significant. The move to lineage-based ontologies and fine-scale phylogeography further blurs the line between species and intraspecific lineages, suggesting that some phylogeographic units deserve ethical and conservation recognition even if not formally recognized as species (Burbrink et al., 2024; Guillory et al., 2024).

Protected-area networks and management strategies should therefore consider genetic and phylogeographic structure, not just species lists, and develop ethical frameworks that can accommodate graded individuality and overlapping boundaries.

Machine Learning, Big Data, and Environmental Philosophy

Integrating diverse data types

ML workflows such as SOMs and SuperSOMs integrate multiple data types in a unified clustering framework (Pyron, 2023; Salles & Domingos, 2025). They are particularly useful in systems where no single data axis provides decisive delimitation evidence. ML has been used to:

- Identify integrative clusters reflecting contributions from genetics, geography, environment, and phenotype (Pyron, 2023).
- Predict regions and taxa with high cryptic diversity based on climate and life-history traits (Parsons et al., 2024).

These tools embody a shift toward pattern recognition as a primary epistemic strategy. Yet they also risk treating algorithmic clusters as ontological entities without sufficient theoretical grounding, and they can obscure interpretation behind complex algorithms.

Transparency, interpretability, and ethical responsibility

In biodiversity ethics, transparency is a core value: stakeholders affected by delimitation decisions—local communities, conservation agencies, policymakers—should understand how these decisions are made. Thus, ML workflows should include:

- Clear documentation of feature selection and model architecture.
- Sensitivity analyses showing how clusters vary with parameters.
- Explicit mapping of ML-derived clusters onto evolutionary and ecological interpretations.

Salles and Domingos (2025) call for best practices that treat ML as complementing, rather than replacing, coalescent and demographic models. This aligns with a virtue epistemology of taxonomy that values humility, openness, and responsiveness to new evidence.

Data infrastructures and global equity

Integrative ML approaches depend on large, curated datasets. Initiatives like phylogatR, which link genetic and occurrence data, illustrate the value of shared infrastructure for comparative studies (Burbrink, 2022). However, these infrastructures reflect existing patterns of sampling and funding;

without deliberate efforts, they may amplify global inequities.

A just program of ML-based species delimitation should prioritize:

- Building genomic and occurrence datasets in under-sampled regions.
- Collaborations with local institutions and communities in biodiversity-rich countries.
- Consideration of how ML-driven insights inform national and international conservation policies, ensuring that benefits are equitably distributed.

Table 4. Conceptual frameworks at the interface of ontology, epistemology, and axiology

Framework / Debate	Ontological Focus	Epistemological Tools / Methods	Axiological / Ethical Implications	Ref.
Unified species concept	Species as separately evolving lineages	Multiple operational criteria	Aligns taxonomy with evolutionary individuality; clarifies conservation units	de Queiroz, 2025
Subspecies critique	Subspecies as ontologically unstable rank	Genealogy; reproductive isolation tests	Avoids pseudo-hierarchies; prevents under-protection of distinct lineages	Burbrink et al., 2022
Gray zone of speciation	Continuum between populations and species	Phylogeography; coalescent models; gdi	Justifies protecting lineages lacking full isolation	Sánchez et al., 2023; Burbrink et al., 2024
ML-based species delimitation	Clusters as potential evolutionary units	SOMs; SuperSOMs; predictive ML	Risk of bias and opacity; requires transparency for fair decisions	Pyron, 2023; Parsons et al., 2024; Salles & Domingos, 2025
Biogeographic regionalization & lineages	Biogeographic units as evolutionary frameworks	Phylogenetics; ploidy; environmental data	Aligns conservation with cryptic lineages and regional endemism	Serrano & Ortiz, 2023; Guillory et al., 2024
Taxonomic rigor & nomenclatural ethics	Species names as public and scientific tools	Integrative data; code-compliant taxonomy	Prevents misleading publicity and unstable names (e.g., anacondas)	Wüster et al., 2024; Wüster, 2025

DISCUSSION

Species as historical individuals and the challenge of continua

The reviewed literature strongly supports a lineage-based, historical ontology of species (de Queiroz, 2025; Hillis et al., 2021). Species are best viewed as extended individuals with genealogical continuity and partial reproductive independence. Yet empirical case studies in the speciation gray zone—such as Liolaemus, Aspidoscelis, and Plethodon—show that lineage independence is often partial, dynamic, and context dependent (Sánchez et al., 2023; Barley et al., 2024; Kuchta et al., 2024).

This tension suggests that environmental philosophy should reject both strict essentialism and simplistic pluralism. Instead, it should embrace a perspective where species are historical individuals whose boundaries are shaped by evolutionary processes and human purposes (e.g., conservation, communication).

Epistemic pluralism: coalescent models, networks, and ML

The review highlights the necessity of epistemic pluralism: combining coalescent models, network approaches, demographic analyses, and ML-based clustering. Coalescent models provide probabilistic evidence for lineage structure but rely on assumptions about gene flow and population size; network models and speciation-based frameworks better accommodate reticulation; ML approaches help integrate diverse data types and explore high-dimensional patterns (Chan et al., 2023; Pyron, 2023; Salles & Domingos, 2025; Parsons et al., 2024; Sklenář et al., 2022).

An important lesson is that these methods should not be used in isolation or treated as automatic species engines. Rather, they should be deployed within explicitly articulated conceptual frameworks and interpreted in light of independent ecological, morphological, and environmental evidence.

Environmental philosophy, biodiversity ethics, and normative transparency

Species delimitation has normative consequences that extend beyond taxonomy. Splitting and lumping decisions influence Red List status, protected-area design, and public communication about biodiversity crises. Cases such as the underestimation of diversity in Wallacea or the reduction of Aspergillus species highlight how taxonomic instability can misdirect conservation attention or public health policies (McGuire et al., 2023; Reilly et al., 2023; Sklenář et al., 2022).

Environmental philosophy contributes here by emphasizing:

- The need to make value judgments explicit, especially where trade-offs arise between taxonomic stability and recognition of cryptic diversity.
- The importance of environmental justice, acknowledging that taxonomic underrepresentation of certain regions or clades can exacerbate vulnerability.
- The legitimacy of extending moral concern not only to recognized species but also to evolutionarily significant lineages and ecosystems.

Best practices for philosophically informed, ethically responsible delimitation

Synthesizing the foregoing, we propose the following best practices:

1. Explicit ontological commitments: Authors should clearly state their working species concept and how it shapes their interpretation of data (de Queiroz, 2025).
2. Integration of diverse data sources: Where feasible, combine genomic, phenotypic, ecological, and biogeographic data to support delimitation decisions (Hillis et al., 2021; Pyron, 2023; Chan et al., 2023).
3. Cautious use of mtDNA: Treat mitochondrial markers as one line of evidence; avoid mtDNA-only species descriptions unless compelling independent evidence exists (Wüster, 2025; Wüster et al., 2024; de Medeiros Magalhães et al., 2025).
4. Embrace uncertainty and graded conclusions: Especially in gray-zone systems, provide graded taxonomic recommendations (e.g., candidate species, evolutionarily significant units) and discuss alternative scenarios (Kuchta et al., 2024; Sánchez et al., 2023).
5. Address conservation and ethical implications: Delimitation papers should explicitly discuss how taxonomic changes might affect conservation status, legal protection, and resource allocation, including issues of regional and taxonomic bias (Burbrink & Myers, 2025; Guillory et al., 2024; Maritz et al., 2021).
6. Transparent ML workflows: When ML is used, document features, models, and evaluation metrics and provide interpretable links between clusters and biological entities (Pyron, 2023; Parsons et al., 2024; Salles & Domingos, 2025).

CONCLUSION

This review, framed by environmental philosophy and biodiversity ethics, shows that species delimitation in the genomic and machine-learning era is not merely a technical exercise. Ontologically, species are best regarded as historical evolutionary individuals whose boundaries are shaped by processes such as drift, selection, gene flow, and hybridization. Epistemologically, delimiting these lineages requires a pluralistic toolkit, encompassing coalescent models, phylogenetic networks, demographic analyses, and ML-based integration of multiple data types. Axiologically, the placement of species boundaries redistributes conservation resources, legal recognition, and moral attention across the tree of life.

By integrating philosophical reflection with empirical case studies from reptiles, amphibians, fishes, plants, and fungi, we argue that high-quality species delimitation must be:

- Conceptually explicit, grounded in a clear and coherent species ontology.
- Methodologically integrative, combining multiple lines of evidence and analytical approaches.
- Normatively transparent, openly discussing the ethical and justice-related implications of taxonomic decisions.

In this sense, species delimitation becomes a form of applied environmental philosophy, shaping how we understand, value, and protect the living world in an era of rapid biodiversity loss and accelerating methodological change.

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