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Revising Insect Species Boundaries Without Destabilizing Taxonomy Requires Governance of Conflict Rather Than Resistance to Change

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ABSTRACT

Species boundaries in insects are increasingly revised as genomic, morphological, ecological, geographic, behavioural, and life-stage evidence are combined at finer resolution. Such revisions are often portrayed as a conflict between taxonomic accuracy and nomenclatural stability. That framing is incomplete because instability can arise not from revision itself but from poorly governed transitions between observation, species-level interpretation, and nomenclatural action. This perspective develops a framework for analysing revision decisions under evidential discordance. It distinguishes evidence signals from taxonomic conclusions, identifies recurrent sources of conflict among mitochondrial, nuclear, morphological, geographic, ecological, and model-based evidence, and separates biological discordance from technical artefact. Contrasting insect cases show that additional evidence may justify either splitting or synonymizing, whereas algorithmic or marker-specific partitions should not be treated as automatic species decisions. The article therefore argues that stable taxonomy does not require resistance to change. It requires transparent rules for recording why boundaries are revised, which evidence was decisive, which alternatives remain plausible, and how decisions may be revisited. Nomenclatural continuity and biological accuracy are treated as distinct objectives that can sometimes converge but should not be conflated. The framework proposed here is conceptual rather than prospectively validated and does not prescribe universal genetic, morphological, geographic, or reproductive thresholds. Its purpose is to make conflict explicit and taxonomic change reconstructable.

Keywords: Species delimitation, Integrative taxonomy, Nomenclatural stability, Taxonomic governance, Evidential discordance, Insect systematics

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Introduction

Insect taxonomy is repeatedly asked to perform two functions that are related but not identical: represent biologically defensible species boundaries and maintain names stable enough for communication, regulation, conservation, agriculture, and cumulative research. Integrative taxonomy has shown why the first function cannot be fulfilled by freezing inherited classifications. In tephritid fruit flies, combinations of morphological, molecular, behavioural, and ecological evidence have altered interpretations of long-standing species complexes in more than one direction, including both recognition of previously obscured diversity and consolidation of taxa [1]. Revision is therefore not synonymous with taxonomic inflation. It is a response to changing evidential resolution.

The difficulty is that different evidence systems can produce different partitions of the same organisms. In butterflies, reconciliation of classical taxonomy with multispecies-coalescent analyses showed that model-derived

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lineage structure and historically recognized species need not map one-to-one [2]. In another butterfly system, extreme mitochondrial variation did not correspond straightforwardly to nuclear genomic species structure [3]. These examples make a central distinction unavoidable: a gene tree, barcode cluster, genomic component, morphological discontinuity, ecological association, or geographic break is an observation or inference about one dimension of variation; it is not, by itself, the taxonomic conclusion.

The prevailing debate is consequently mis-specified when it is reduced to "stability versus change." Resistance to revision can preserve familiar names while preserving an inaccurate boundary, whereas rapid revision can improve biological representation yet obscure how competing evidence was weighed. This article advances a proposed alternative: govern the conflict that precedes taxonomic action. The argument is not that disagreement can be eliminated, nor that one evidence class should dominate. Instead, revision decisions should expose the path from evidence to interpretation to nomenclatural consequence, including uncertainty, plausible alternatives, and the conditions under which the decision should be reconsidered.

Materials and Methods

This article uses a conceptual analysis rather than a new delimitation dataset. The analytical unit is the revision decision: the sequence by which observations are converted into a species hypothesis and then into an action affecting names. The approach first separates evidence acquisition from species-level inference. That separation is necessary because the multispecies coalescent may delimit population structure under some conditions rather than completed species, so an inferred partition cannot automatically be equated with taxonomic rank [4]. The conceptual analysis therefore treats outputs from delimitation procedures as evidence-bearing propositions whose interpretation depends on the biological process represented by the model and on independent information.

Three recurrent contextual dimensions are then used to interrogate revision claims. First, geography matters because the same magnitude or pattern of differentiation has different implications under sympatry, parapatry, or allopatry; spatial separation may generate structure without establishing species-level independence [5]. Second, sampling design and dataset composition affect the behaviour of molecular delimitation methods. Comparative work in Chrysomelidae shows that agreement among methods and with existing taxonomy varies with sampling and taxonomic properties, making family-specific performance estimates unsuitable as universal decision thresholds [6]. Third, delimitation can be strengthened conceptually by representing speciation as a process rather than treating every structured lineage as an equivalent endpoint [7].

On this basis, the analysis asks four questions of each type of revision evidence: what was directly observed; what biological interpretation was inferred; what alternative explanation remains plausible; and what nomenclatural action, if any, follows. No universal weighting scheme is assumed. The purpose is instead to identify where inferential steps require explicit justification, especially when evidence classes disagree or when the consequence of revision extends beyond the focal systematic study.

Results and Discussion

The selected insect cases show that species boundaries change for at least three analytically distinct reasons: previously hidden lineage structure becomes diagnosable, formerly recognized divisions lose evidential support, or the interpretation of a given signal changes when a broader evidence class is added. These routes have different taxonomic directions but a common logic: the accepted boundary is conditional on the evidence available and the inference made from it.

Phylogenomics in the *Temnothorax salvini* group illustrates revision toward greater recognized diversity. Integrative use of ultraconserved elements, morphology, and geographic information supported a substantially more differentiated species treatment than the earlier classification [8]. By contrast, analysis of the balsam woolly adelgid complex supported consolidation of a historically unstable multi-species arrangement toward fewer species, showing that additional evidence can justify synonymizing as well as splitting [9]. The relevant contrast is not "progressive splitting" against "conservative lumping," but whether the revised boundary better accommodates the total evidence and its uncertainties.

Independent corroboration can also transform the interpretation of initially ambiguous signals. In skipper butterflies, nuclear genomic data supported cryptic species hypotheses that had been suggested by DNA barcodes and ecology, demonstrating the value of confirmation across partly independent evidence classes [10]. UCE

phylogenomics similarly resolved a recent radiation in fungus-farming ants in which morphology alone provided limited separation among lineages [11]. In the endangered weevil *Pachyrhynchus sonani*, geographic isolation, genomic differentiation, and phenotypic information—including sex-related morphological complexity—had to be interpreted jointly when evaluating island species limits and their conservation implications [12]. None of these cases establishes a rule that genomic evidence should always dominate morphology or geography. They show instead that a boundary becomes more defensible when distinct observations converge on the same lineage interpretation and known sources of non-independence are considered.

Species boundaries also change because analytical methods partition variation differently. In Xenidae, several molecular delimitation approaches returned markedly different numbers of putative species even though all indicated substantial cryptic diversity [13]. Such variation matters because candidate lineages generated by an algorithm are not nomenclatural acts. A method may identify structure worth explaining without determining where formal species boundaries must be placed. The taxonomic problem is therefore not solved by selecting the highest, lowest, or most familiar candidate count. It requires an evidential argument for why a particular partition merits species status in that biological system.

Sources of evidential conflict

Evidential discordance is not a single phenomenon. It can arise from real evolutionary history, from the properties of the organisms being compared, from the markers chosen, from sampling design, or from technical error. Treating all disagreement as equivalent is especially hazardous because superficially similar conflicts may require different responses.

Nearctic ambush bugs provide an example in which molecular, geometric-morphometric, and ecological evidence had to be reconciled against complications that include sexual dimorphism, polymorphism, and historical processes capable of producing marker discordance [14]. Such a pattern does not identify its own mechanism. By contrast, work on *Empria* sawflies demonstrated that cross-contamination could coexist with strong mitonuclear discordance, making technical quality control a prerequisite before biological explanations are assigned [15]. A disagreement between mitochondrial and nuclear partitions therefore cannot safely be labelled introgression, incomplete lineage sorting, hybridization, contamination, or taxonomic error without evidence discriminating among those alternatives.

“Molecular evidence” is likewise too broad to function as a single vote. UCE datasets resolved long-standing systematic problems in Central European bee complexes where mitochondrial and barcode histories were problematic, showing the value of dense independent nuclear evidence in some settings [16]. Yet nuclear markers are not inherently immune to interpretive failure. In parasitoid wasps, intragenomic variation in ITS2 was large enough to complicate species delimitation and phylogenetic interpretation [17]. The relevant question is consequently not whether a datum is molecular, but what inheritance pattern, copy behaviour, sampling process, and analytical assumptions govern the signal.

Conflict between morphology and molecular evidence is also directionally inconsistent. Genome-wide RADseq data in the *Melanoplus scudderi* complex supported morphologically recognized species despite earlier mitochondrial paraphyly [18]. Conversely, multilocus analyses in *Phoebis* butterflies produced alternative delimitation hypotheses that required reconciliation with morphology and barcode information rather than automatic adoption of a single model output [19]. These cases undermine both morphology-first and genomics-first hierarchies. Evidence classes differ in relevance, independence, and susceptibility to particular failure modes; their value is conditional on the question and the taxon's history.

For revision governance, the key implication is that discordance should be triaged before it is adjudicated. A conflict may be evidentially informative because independent signals reflect different histories, or it may be artifactual because the signal is technically compromised. It may also be expected under geographic structure or incomplete lineage sorting without implying species-level separation. The taxonomic decision becomes defensible only after these possibilities are made explicit.

Nomenclatural stability versus biological accuracy

Nomenclatural stability is valuable because names are infrastructure: they connect specimens, databases, ecological records, regulatory lists, conservation assessments, and prior literature. But stability becomes scientifically hazardous when it is treated as evidence for the underlying species boundary. The history of the *Bactrocera dorsalis* complex illustrates a different problem: an integrative, peer-reviewed taxonomic treatment

may itself become destabilized when subsequent authority claims reverse or challenge it without commensurate evidential scrutiny [20]. Peer review does not make a taxonomic conclusion permanent or infallible, but it provides a visible arena in which evidence, methods, and counterarguments can be assessed.

The converse risk is to control instability by constraining taxonomic science. Arguments developed in the context of taxonomy and conservation emphasize that scientific taxonomy must retain independence from systems that would prescribe preferred classifications for administrative convenience [21]. The appropriate distinction is therefore between governance of nomenclatural consequences and control of scientific conclusions. A governance process may require disclosure, evidence traceability, archived versions, and explicit reasons for change without predetermining which species hypothesis must prevail.

This article accordingly proposes two non-equivalent forms of stability. Name continuity is the persistence of a familiar nomenclatural arrangement through time. Decision continuity is the ability to reconstruct why a boundary was accepted, revised, retained, or challenged even when names change. Name continuity can be lost while decision continuity is preserved; conversely, names can remain unchanged while the evidential basis becomes opaque or obsolete. Biological accuracy is also not a binary property available for direct measurement in every revision. It is better treated as the degree to which a species hypothesis remains congruent with the strongest relevant evidence while surviving plausible alternative explanations.

The practical tension is therefore not resolved by maximizing either change or continuity. A stable but weakly supported boundary and a rapidly revised but poorly documented boundary are both governance failures of different kinds. Because prose can obscure when the same stable or changed name reflects biologically different evidential states, **Table 1** separates name continuity, decision continuity, and evidential adequacy without converting them into a score.

Table 1. Decision states separating nomenclatural continuity from evidential adequacy in insect species-boundary revision

Species-boundary history		**Revision audit**	
Boundary condition	**Taxonomic history**	**Concordance ledger**	**Governance record**
		Continuity states	
Familiar boundary with current concordance	Existing treatment remains consistent with the relevant morphology, genomic evidence, geography, ecology, behaviour, or other applicable data	No materially conflicting independent evidence has emerged. Absence of detected conflict does not establish that unsampled populations, stages, sexes, or evidence classes are irrelevant	Retaining the name is compatible with both name continuity and the current evidential interpretation. Continue taxon-appropriate sampling and preserve the provenance of identifications. Evidence-supported state.
Familiar boundary under unresolved discordance	Existing name persists while relevant evidence classes disagree	Conflicting marker, morphological, geographic, ecological, or model-derived signals remain unexplained. Discordance may reflect structure, introgression, lineage sorting, technical artefact, marker behaviour, or inadequate sampling	Retention avoids premature nomenclatural action but does not validate the inherited biological boundary. Resolve the source of discordance before interpreting retention as biological confirmation. Proposed governance interpretation.
		Active revision states	
Revised boundary with convergent support	A changed treatment is supported by partly independent evidence classes	Concordant genomic, phenotypic, geographic, ecological, behavioural, or life-history evidence after recognizable artefacts are considered. Concordance remains taxon-, sampling-, and history-dependent and is not equivalent to absolute certainty	Loss of name continuity may accompany a better-supported species interpretation. Test whether diagnoses and lineage interpretations persist across relevant ranges, stages, sexes, and populations. Evidence-supported pattern; governance interpretation proposed.
Revised boundary dominated by one model or marker system	Species-level action follows a strong analytical partition with limited independent corroboration	A delimitation model, clustering result, barcode partition, or marker genealogy provides most of the separation. Population structure, marker-specific history, geography, and model assumptions may resemble species separation	Nomenclatural action may outrun the demonstrated biological interpretation of the partition. Seek independent evidence and test sensitivity to sampling, geography, marker choice, and alternative models. Evidence-supported risk pattern.

		Decision-history states	
Reversal without reconstructable evidential comparison	A previous treatment is displaced or challenged without transparent comparison of evidence and methods	The nomenclatural or authority change is visible but its evidential relationship to the previous treatment is incomplete. Subsequent workers may confuse disagreement about evidence with disagreement about authority or naming	Instability increases because users cannot determine what changed scientifically and what merely changed nomenclaturally. Require explicit comparison with prior evidence, methods, alternatives, and decision history. Evidence-supported governance concern.
Stable name with obsolete or opaque evidential basis	Nomenclature remains unchanged even though provenance is unavailable or materially different evidence has accumulated	Continuity of usage exceeds continuity of the documented evidential basis. Long persistence, widespread use, or administrative convenience does not independently corroborate species status	Apparent stability can conceal unresolved uncertainty about the biological boundary. Reassess when new evidence materially alters the inferential basis while preserving a traceable history of the prior treatment. Proposed governance state.

Governance principles for revision

Governance should begin where evidence is translated into a taxonomic act, not where evidence is collected. A governance system therefore need not dictate whether morphology, genomics, ecology, behaviour, geography, or reproductive information is intrinsically superior. Its task is to make the translation from these signals to a species decision visible, challengeable, and revisable. Governance principles developed for authoritative species lists provide a useful precedent: transparent criteria, separation between scientific judgement and list administration, archived versions, explicit documentation of change, and traceable responsibility can preserve scientific freedom while making downstream use more stable [22]. These principles do not demonstrate that any particular governance system will reduce taxonomic instability in insects, but they establish that stability and scientific revisability need not be opposites.

This article therefore proposes a discordance-triage architecture with four governance functions. First, evidence provenance should be recorded before conflict is interpreted. Second, discordance should be classified as potentially biological, methodological, technical, or unresolved rather than being forced into a single explanation. Third, the taxonomic action should be separated from the evidential state: splitting, synonymizing, or retaining a name is a decision made under evidence, not an observation. Fourth, each decision should carry a revision pathway specifying what new evidence would justify reopening it. The architecture deliberately allows an unresolved state because forcing every conflict into immediate taxonomic change can be as misleading as prohibiting change.

The architecture also distinguishes scientific disagreement from governance failure. Two analyses may legitimately favour different species hypotheses because they use different models, geographic samples, or evidence classes. Governance failure arises when those differences cannot be reconstructed, when alternatives are omitted, or when nomenclatural implementation obscures what changed scientifically. Accordingly, dissent should be preserved as part of the revision record rather than erased once a preferred treatment is adopted.

Because this distinction is difficult to recover from prose alone, **Figure 1** compresses the proposed triage logic while keeping observed evidence, interpretation, taxonomic action, uncertainty, and later revision visually separate.

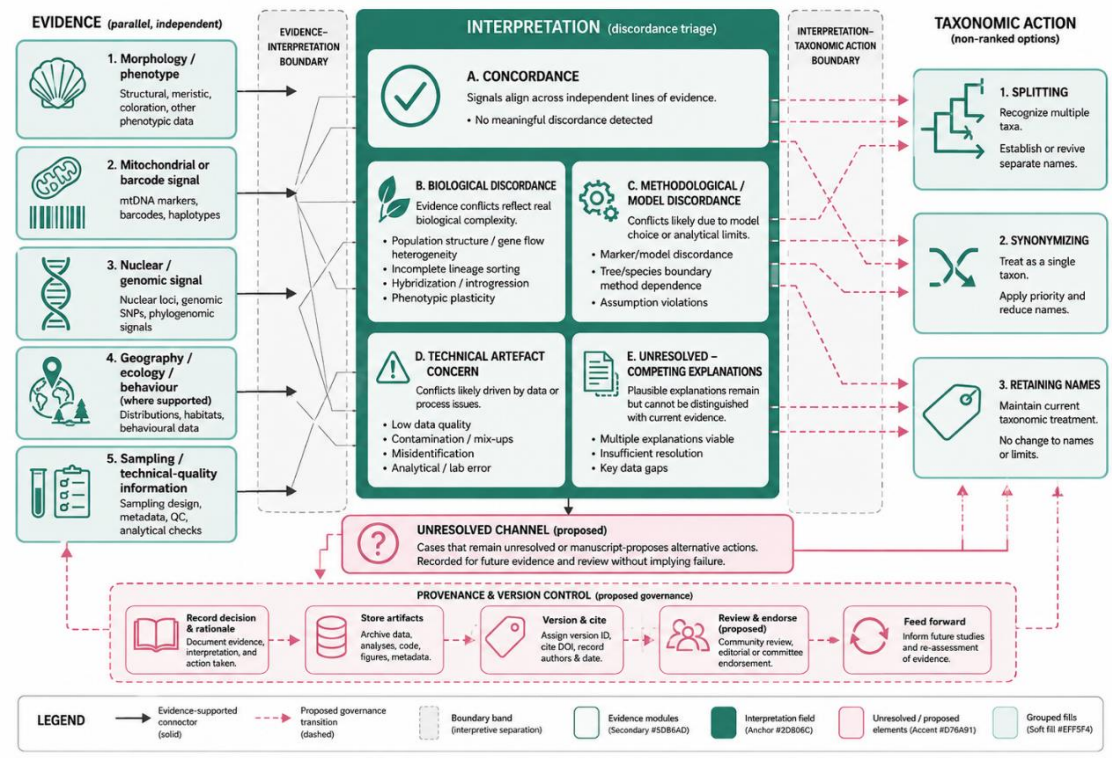


Figure 1. Discordance triage at the evidence–interpretation boundary of insect species revision

Thresholds for splitting, synonymizing, and retaining names

Taxonomic action requires evidential adequacy, but adequacy is not equivalent to a universal quantitative cutoff. Arguments against highly accelerated species descriptions emphasize that efficiency cannot justify omission of critical comparative information needed to establish what is being diagnosed and how it differs from known taxa [23]. This supports a requirement for defensible comparison, not a rule that every insect revision must use the same data modality.

The proposed decision logic therefore treats splitting, synonymizing, and retaining as different questions. Splitting asks whether an observed partition is sufficiently independent, diagnosable, and robust to plausible alternatives to justify recognizing more than one species. Synonymizing asks whether previously named units remain independently supported once broader evidence and historical explanations are considered. Retaining asks whether current evidence is insufficient to justify a nomenclatural change, not whether the inherited boundary has been biologically confirmed. Contrasting insect cases demonstrate why direction cannot be prescribed in advance: integrative evidence has supported additional species, consolidation, and independent corroboration of cryptic diversity [8–10].

No action should be triggered solely because one algorithm yields a particular number of lineages, one marker is deeply divergent, or an existing name is widely used. Evidence should instead be tested for independence, geographic and sampling dependence, technical vulnerability, and compatibility with plausible evolutionary histories. When conflict remains unresolved, retention can function as a provisional governance state, but the unresolved evidence and conditions for reassessment should remain visible.

Table 2 is needed because these three actions can share the same evidence classes yet require different inferential questions; the register separates those questions without turning them into a numerical score.

Table 2. Context–mechanism–outcome register for deciding whether insect names should be split, synonymized, or provisionally retained

Action candidate		Action control		
Nomenclatural action	**Evidence configuration**	**What the action changes**	**Failure hazard**	**Documentation and reopening rule**
Split candidate	Concordant genomic, morphological,	Previously broad taxon contains recurring, partly independent	Population structure, sampling gaps,	Test diagnosability and robustness across relevant

	ecological, behavioural, geographic, or life-history evidence	lineage differences. Additional species recognition may be justified	introgression, marker history, and incomplete lineage sorting may mimic separation	populations, sexes, stages, and methods. Proposed decision rule.
Synonymy candidate	Shared genomic structure, weak or non-independent diagnoses, historical admixture, or revised interpretation of earlier characters	Named units lose independent support when broader evidence is examined. Fewer species may better represent the available evidence	Recent divergence or ongoing gene flow can obscure real differences; absence of one diagnostic class is not decisive	Reassess original diagnoses and alternative historical explanations before nomenclatural consolidation. Proposed decision rule.
Provisional retention	Discordant markers, model-sensitive partitions, inadequate geography, uncertain technical quality, or sparse sampling	Evidence conflicts or is insufficient to discriminate among plausible species hypotheses. Existing nomenclature is retained temporarily without being treated as biologically validated	Administrative continuity may be mistaken for evidential support	Record unresolved conflict and specify evidence capable of reopening the decision. Proposed governance state.
Strong single-source partition	Deep barcode split, clustering solution, or model-delimited lineage with limited independent corroboration	One marker, algorithm, or evidence class dominates the inferred boundary. Signals a hypothesis requiring corroboration rather than automatic taxonomic action	Marker inheritance, structure, geography, and model assumptions may drive the partition	Add independent evidence and sensitivity analyses before formal action. Evidence-supported risk pattern.
Cross-evidence convergence	Agreement across appropriately sampled genomic and non-genomic evidence	Independent evidence classes support the same lineage interpretation. Confidence in the species hypothesis increases	Concordance can still share hidden dependencies or incomplete geographic coverage	Test boundary persistence where contact, life-stage variation, or unsampled populations could challenge it. Evidence-supported pattern; decision implication proposed.
Reversal request	New data or reinterpretation directly contradicts the evidential basis of the previous decision	A prior split, synonymy, or retained treatment is challenged by new evidence. Revision can be legitimate without being destabilizing if the evidential comparison is explicit	Authority, familiarity, or policy consequence can be confused with scientific support	Compare new and previous evidence symmetrically and preserve both decision histories. Proposed governance rule.

Documentation and version control

Taxonomic decisions remain useful only if later researchers can determine which concept of a name was applied. Explicit citation of taxonomic and identification sources is therefore part of evidential provenance, not merely bibliography, because it helps reconstruct what taxon concept underlay a record [24]. Provenance also extends beyond adult morphology. NGS barcode matching has shown that adult and larval material can be linked at useful scale, improving the ability to associate life stages that would otherwise remain taxonomically disconnected [25]. Such linkage remains dependent on reference coverage and successful matching; it does not make characters from one stage automatically diagnostic in another.

Version control should consequently preserve four items: the accepted species hypothesis, the evidence classes used, material uncertainties or dissent, and the reason for any later change. This article proposes that a revision record should remain cumulative rather than overwriting prior states. Large molecular datasets do not remove the need for that discipline. Data-driven insect phylogeny has expanded resolution while retaining uneven sampling and unresolved nodes, illustrating that increased data volume and increased certainty are not synonymous [26]. A nomenclatural system that records only the current name but not the evidential history therefore loses scientifically relevant information.

The central implication is that revision and stability are not opposites. Integrative insect studies have supported splitting, synonymizing, and corroboration of cryptic species hypotheses [8–10]. A governance system should

therefore be direction-neutral: it should ask whether the inferential path is defensible, not whether the outcome preserves or multiplies names.

This requirement becomes more important when discordance is heterogeneous. Ambush bugs, sawflies, and bees demonstrate that similar-looking conflicts can involve biological history, technical contamination, or marker-specific limitations [14–16]. Additional cases show that intragenomic variation, geographic structure, model behaviour, and morphology–genome disagreement can alter interpretation without supplying a universal hierarchy among evidence classes. The proposed triage architecture addresses this by separating observation, explanation, and action.

The framework has important limits. It has not been prospectively tested, and the literature considered here spans different insect orders, sampling designs, marker systems, and historical questions. Rules appropriate to island weevils, recent ant radiations, parasitoid wasps, or economically important fruit flies cannot simply be transferred to all insects. Nor does governance resolve philosophical disagreement about species concepts. Its narrower purpose is to prevent that disagreement from becoming opaque nomenclatural change. A second limit concerns downstream systems. Regulatory, conservation, ecological, and biodiversity databases may differ in how rapidly they can absorb a revised species treatment. The proposed framework therefore does not imply that one implementation timetable is appropriate for every user. Governance should preserve the scientific decision and its date while allowing downstream systems to document when and why they adopt, defer, or reinterpret that treatment. This implementation distinction also requires future evaluation rather than assumption.

Evaluation should therefore focus on reconstructability rather than on claiming that governance produces "correct" taxonomy. Useful tests would ask whether independent researchers can recover why a boundary changed, identify which evidence remained unresolved, reproduce the comparison between competing hypotheses, and determine what evidence would trigger reconsideration. Taxonomic communities could also examine whether versioned decision records reduce ambiguity in ecological databases, conservation assessments, biosecurity systems, and subsequent systematic work. Those are validation priorities, not demonstrated outcomes.

The proposed distinction between name continuity and decision continuity is especially important. A name may change while the evidential history remains fully traceable; conversely, a stable name can mask decades of shifting concepts. Treating the latter as stability confuses nomenclatural persistence with scientific continuity. Governance of conflict therefore offers a way to accommodate revision without celebrating change for its own sake.

Conclusion

Revising insect species boundaries need not destabilize taxonomy if change is made reconstructable. The critical requirement is not resistance to splitting, synonymizing, or reinterpretation, but governance of the evidential conflict that precedes those actions. Molecular, morphological, ecological, geographic, behavioural, and model-based signals should remain distinguishable from the species conclusions they inform, and unresolved alternatives should remain visible rather than being forced into premature certainty. The framework advanced here is a proposed conceptual architecture, not a validated decision algorithm and not a universal species criterion. Its value lies in separating evidence, interpretation, nomenclatural action, uncertainty, and revision history. Taxonomic stability is thereby reframed as continuity of justified decisions rather than immobility of names.

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