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Taxonomic Revision in the Genomic Era Requires Reproducible Treatment of Species Concepts, Synonymy, and Changing Evidence

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ABSTRACT

Genomic datasets have transformed insect systematics by increasing the resolution with which population structure, lineage divergence, introgression, discordance and cryptic diversity can be detected. Yet greater analytical resolution does not by itself make taxonomic revision more reproducible. Species boundaries remain interpretive conclusions formed from evidence under an explicit or implicit species concept, while synonymy and splitting additionally require historical names, type-associated information, geography, morphology and other evidence to be reconciled with contemporary molecular results. This perspective argues that revision reproducibility therefore depends on preserving the inferential path between observation and nomenclatural action rather than merely preserving sequence data or executable analyses. We develop a proposed Revision-Provenance Framework that separates evidence classes, analytical outputs, species criteria, taxonomic interpretations, historical name application and subsequent evidence updates. Published insect revisions show why these distinctions matter: genome-scale analyses can support synonymy, reveal previously unrecognized species, expose conflicts with mitochondrial diagnostics, or alter higher-level classification, and the direction of change is strongly dependent on taxon, geography, sampling and analytical assumptions. Historical names constitute a separate evidential problem because genomic lineages cannot be assigned nomenclatural identity without traceable connections to specimens, types and prior usage. The framework consequently treats revision as a versioned scientific decision whose rationale should remain reconstructable when evidence changes. It is proposed as an auditable organizational architecture, not as a validated algorithm for discovering objectively correct species boundaries.

Keywords: Species delimitation, Integrative taxonomy, Phylogenomics, Synonymy, Taxonomic provenance, Nomenclatural revision

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Introduction

Genomic systematics has greatly expanded the amount and resolution of evidence available for delimiting biological lineages, but it has not removed the conceptual decisions that connect genetic differentiation to

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taxonomic recognition. Contemporary integrative taxonomy still confronts heterogeneous species concepts, unequal evidence classes and non-standardized ways of combining molecular, morphological, ecological and computational information [1]. Genomic data can clarify lineage history, admixture and population structure, yet their taxonomic meaning remains dependent on the criterion used to recognize species and on the geographic context in which divergence is observed [2]. The reproducibility problem is therefore not simply whether another investigator can rerun a bioinformatic pipeline. It is whether that investigator can reconstruct why a particular analytical result was considered sufficient for synonymy, splitting or retention of an existing treatment.

This problem becomes clearer when species are treated as revisable scientific hypotheses rather than immutable outputs of a delimitation algorithm. A heuristic view of species permits recognition to depend on congruent properties produced by lineage-specific evolutionary and ecological processes while acknowledging that the available evidence may be incomplete [3]. Large-scale integrative taxonomy similarly distinguishes preliminary operational units from subsequent validation, demonstrating the practical value of keeping discovery and taxonomic confirmation analytically separate [4]. For taxonomic revision, that separation is consequential: a barcode cluster, a multispecies-coalescent partition, a morphologically diagnosable form and a nomenclaturally valid species name are not interchangeable entities.

Genome-scale inference can also create an appearance of precision that exceeds what a species-level conclusion warrants. Multispecies-coalescent analyses can delimit population structure even when that structure should not automatically be interpreted as a species boundary [5]. Under particular demographic and sampling conditions, increasingly informative multilocus data may intensify support for population subdivision and thereby contribute to over-splitting if the operational output is equated directly with species status [6]. Conversely, genome-wide evidence can collapse previously recognized species hypotheses, as demonstrated outside insects in an Antarctic radiation where phylogenomic reassessment substantially reduced accepted diversity [7]. Genomics therefore has no intrinsic directional tendency toward either splitting or lumping. Even the label “cryptic species” can obscure different evolutionary processes when genetic differentiation, phenotypic similarity and reproductive or ecological independence are not distinguished explicitly [8].

The central argument developed here is that genomic-era revision requires a reproducible record of the transition from evidence to inference and from inference to nomenclatural action. That record must preserve what was observed, how the evidence was analysed, which species criterion governed interpretation, how discordant evidence was treated, how historical names were connected to inferred entities and what later information would justify reassessment. We term this organizational architecture the proposed Revision-Provenance Framework. It is not intended to impose one universal species concept. Its purpose is to make competing taxonomic conclusions inspectable and comparable even when researchers legitimately differ in concept, evidence weighting or interpretation.

Materials and Methods

The framework was constructed through a structured conceptual synthesis of methodological work on species delimitation, model adequacy and geographic structure; governance work on taxonomic traceability; and recent integrative insect revisions involving synonymy, splitting, historical name reconciliation and genomic reassessment. Evidence was organized according to the inferential role it can legitimately perform rather than according to molecular versus non-molecular provenance alone. The resulting architecture distinguishes direct observations, analytical outputs, species-level interpretation, nomenclatural assignment and subsequent revision. It also treats model assumptions, sampling geography and evidence discordance as provenance information rather than as secondary methodological detail.

The first requirement is to record assumptions that can change the biological interpretation of genomic structure. Species delimitation under gene flow is particularly informative because migration and lineage independence need not be mutually exclusive; inference therefore depends on how migration is represented rather than on a simple presence-versus-absence rule [9]. A revision that reports genomic partitions without recording whether its analytical model assumes no migration can conceal an important condition of the resulting boundary. Likewise, biologically plausible violations of a multispecies-coalescent model can alter inferred species limits, and model-checking approaches show that adequacy should be evaluated rather than assumed [10]. The proposed framework consequently separates the data-generating evidence from the assumptions of the model used to transform those data into lineage hypotheses.

Geography forms a second provenance layer. Isolation by distance and discontinuous sampling may yield patterns that resemble independently evolving units, whereas sympatric or geographically connected structure may have different implications [11]. Geographic configuration is therefore not a descriptive annotation added after delimitation; it constrains the interpretation of genetic discontinuity. The framework requires the geographic sampling design and the relationship between candidate units to remain visible when a species-level decision is reconstructed.

A third requirement is to preserve independent evidence classes instead of combining them into an opaque declaration of "integrative support." Empirical delimitation has shown that phylogenomic and high-resolution phenotypic information can converge on species hypotheses, but the significance of that convergence derives precisely from the relative independence of the underlying observations [12]. In the proposed framework, morphology, nuclear genomic structure, mitochondrial genealogy, ecology, reproductive evidence, behaviour, geography and other relevant classes remain separately identifiable until the interpretive step. Discordance is retained rather than averaged away.

Finally, taxonomic decisions require explicit archival and governance logic. Principles proposed for authoritative species lists emphasize transparency, traceability, documentation of alternative treatments and preservation of prior versions [13]. We extend that logic from downstream lists to the revision itself. A reproducible revision should preserve not only the accepted outcome but also the evidence state and inferential reasoning that produced it. This does not convert taxonomy into a mechanical procedure. Instead, it permits later investigators to distinguish a disagreement about data from a disagreement about models, species criteria, evidence weighting or nomenclatural interpretation.

Results and Discussion

Under the proposed framework, reproducibility begins by declaring what kind of entity a delimitation analysis is intended to recover. This requirement is necessary because taxonomic discovery units and formally recognized species can otherwise become conflated. DNA barcodes are highly useful for specimen association and preliminary lineage discovery, but barcode clusters alone are insufficient grounds for a complete species description when diagnostic, comparative and nomenclatural evidence has not been addressed [14]. The important distinction is not molecular versus morphological taxonomy. It is discovery evidence versus taxonomic inference. Operational algorithms likewise cannot substitute for a declared species criterion. In a large chrysomelid benchmark, the apparent efficiency of single-marker delimitation methods changed with sampling and taxonomic characteristics, including properties of the underlying sequence data and difficulty of identification [15]. Method performance was therefore conditional rather than universal. An algorithmic partition should consequently be recorded as an analytical output whose relevance to a species concept still has to be stated.

More elaborate genomic procedures do not remove this interpretive requirement. Hierarchical multispecies-coalescent delimitation incorporating migration can reduce some forms of over-splitting under tested conditions, but its decisions remain dependent on model structure and operational criteria [16]. The framework therefore distinguishes species concept, operational criterion and analytical implementation. A researcher may, for example, adopt an evolutionary-lineage interpretation, specify an operational criterion concerning sustained lineage independence, and then use genomic analyses to evaluate relevant evidence. Recording only the software output would erase two of the three inferential levels.

Allopatry further demonstrates why these levels matter. Across selected Lepidoptera, nuclear differentiation among geographically separated populations varied substantially, and correspondence between mitochondrial and nuclear patterns was incomplete [17]. Allopatric differentiation can reflect long-term lineage separation, geographic structure, demographic history or combinations of these processes. Neither low nor high genomic differentiation has a taxonomically invariant meaning outside its biological and geographic context. Explicit species concepts therefore improve reproducibility not by forcing agreement, but by revealing where alternative taxonomic judgments originate.

Evidence for synonymy

Synonymy is sometimes treated as a conservative taxonomic outcome, yet genomic evidence shows that it can require as much inferential justification as splitting. In the *Bactrocera frauenfeldi* complex, phylogenomic analysis integrated with morphology and biogeography supported synonymizing *B. albistrigata* with *B.*

frauenfeldi, while mitochondrial COI alone provided unreliable separation across much of the complex [18]. The relevant conclusion was not that genomic evidence automatically overrides morphology or mitochondrial evidence. Rather, multiple evidence classes failed to support independent species status for a historically named morphotype.

The *Stylops* case illustrates a more complex form of revision. Whole-genome data supported several synonymies while simultaneously identifying previously undescribed diversity, and species counts produced by one delimitation procedure were sensitive to the number of loci analysed [19]. This is important because a changing algorithmic partition must not be confused with a biological increase or decrease in the number of species. The proposed provenance approach instead records the evidence update, the altered analytical result and the separate taxonomic interpretation.

Historical taxonomic impasses may similarly produce mixed actions rather than a simple lumping outcome. Integrative analysis of Epyrinae combined extensive morphological and molecular information to reassess placements, revalidate taxa and establish synonymies within a broader phylogenetic context [20]. In *Chanohirata*, multiple molecular delimitation approaches combined with morphology supported both synonymic treatment and recognition of new species within the same revision [21]. These cases undermine any attempt to classify methods or investigators as intrinsically "splitter" or "lumper." The direction of a revision is an outcome of case-specific evidence, concept and nomenclatural history.

For reproducibility, evidence for synonymy should therefore specify which previously recognized entities are being compared, whether their diagnoses remain independent, how their genomic variation is distributed geographically and whether conflicting evidence is retained in the record. A synonymic act may be well supported even when some differentiation persists, but the reasoning that distinguishes intraspecific structure from independently evolving lineages must remain explicit.

Evidence for splitting

The complementary problem is determining when existing taxonomy masks independently supported lineages. Integrative reassessment of the previously monotypic butterfly genera *Agraulis* and *Dryas* demonstrated that combined morphological, molecular and geographic evidence could reveal additional species-level diversity within an apparently simple historical treatment [22]. The strength of such splitting does not derive from novelty itself; it derives from correspondence among evidence classes that are relevant to the stated species criterion.

Genome-scale evidence may be especially informative when an established diagnostic marker has limited resolution. In the *Bactrocera dorsalis* complex, genomic analyses revealed additional species-level diversity while also demonstrating limits to mitochondrial barcode diagnosis [23]. This does not establish a general hierarchy in which nuclear genomic evidence is intrinsically superior to mitochondrial data. Mitochondrial loci may remain highly informative for identification in many groups. The case instead shows that a marker can fail to track the lineage boundaries relevant to a particular revision.

Other genomic differences require still more caution. Whole-genome sequencing in the *Valenzuela flavidus* complex indicated differences in ploidy among lineages associated with a taxonomically difficult reproductive system [24]. Ploidy is a biologically important distinction and may provide evidence of evolutionary independence, but a ploidy difference is not itself a universal species criterion. The taxonomic conclusion must remain separable from the observation.

The same safeguard applies across taxonomic ranks. Phylogenomics of Noctuoidea supported substantial higher-level classificatory change while retaining uncertainty in some deep relationships depending on dataset and analytical treatment [25]. Such results demonstrate the resolving power of genomic evidence, but they also illustrate a level-of-analysis boundary: support for a deep clade and recognition of a family-level lineage cannot be converted into a rule for delimiting species. The proposed framework therefore requires each revision to state the taxonomic rank and biological inference to which a particular evidence class is being applied.

Splitting should consequently be documented as an evidential transition rather than as a count of newly recognized species. The reproducible question is whether the prior species hypothesis has become inadequate under newly available, independently interpretable evidence, and whether that evidence satisfies a stated criterion for recognizing more than one lineage.

Historical name usage

Genomic delimitation identifies biological patterns; nomenclature determines how historically established names apply to those patterns. These tasks interact but cannot be collapsed. An inferred genomic lineage has no automatically determined scientific name, because name application depends on type specimens, original descriptions, subsequent usage, specimen identity and the rules governing nomenclatural priority.

The revision of *Cerurina* and *Afrocerura* demonstrates why this distinction is operationally important. Examination of type-associated and historical material was integrated with morphology, COI and anchored-hybrid-enrichment genomic evidence to resolve confused species identities and prior misidentifications [26]. The decisive provenance chain therefore connected contemporary lineage evidence to historical specimens and names. Without that link, even a strongly supported genomic unit could remain nomenclaturally ambiguous.

Dense phylogenomic sampling can magnify this issue by altering classification across many lineages simultaneously. A large reconstruction of Euptychiina combined target-enrichment and Sanger data across extensive taxon sampling and resulted in numerous changes to generic placement and synonymic treatment [27]. Such revisions require more than a final list of accepted combinations. To remain reproducible, they should preserve how prior names map onto newly delimited or reclassified entities and which evidence supported each transition.

Digital taxonomic infrastructure adds another layer of temporal uncertainty. Name harmonization can depend on the database, software, authority file and version selected, and comparative evaluation of available resources shows that different workflows have distinct strengths and failure modes [28]. An "accepted name" retrieved from a database is therefore not a timeless observation. It is a database-mediated statement at a particular version or date.

The proposed framework treats historical name usage as its own provenance domain. For each taxonomic entity undergoing revision, the record should distinguish the biological evidence supporting the entity from the evidence supporting application of a particular name. Type linkage, historical combinations, synonymic history, database source and unresolved identification problems are retained as traceable components rather than compressed into the final accepted name. This separation becomes especially important when genomic evidence changes, because the biological entity may be reassessed without necessarily changing its name, while a nomenclatural correction may occur without altering the underlying species hypothesis.

Genomic evidence updates

A genomic update should be treated as a change in the evidential state of a revision, not automatically as correction of an earlier taxonomy. Aphid phylogenomics illustrates why: thousands of genes produced substantial gene-tree discordance attributable to competing processes including incomplete lineage sorting, introgression and an anomaly-zone history, so individual gene histories could not simply be equated with the inferred species history [29]. The provenance problem is therefore temporal as well as analytical. A later dataset may alter support for relationships without making every earlier observation erroneous.

Marker-specific diagnostic performance creates a different update. In Dacini fruit flies, large-scale evaluation of COI showed that identification success depended on the lineage and on whether monophyly- or distance-based criteria were used [30]. A genomic revision should consequently record whether a previous marker remains diagnostic, becomes ambiguous, or is contradicted by nuclear evidence rather than replacing the older result without explanation.

Increasing genomic scale can improve resolution while preserving conflict. HiMAP demonstrated efficient recovery of hundreds of phylogenetically informative amplicons across many tephritid specimens, yet multilocus expansion does not logically guarantee concordance among histories [31]. A revision should therefore distinguish evidence supplementation from evidence supersession. New nuclear loci may add resolution while leaving older morphological or mitochondrial observations valid within their original diagnostic scope; alternatively, they may reveal that an earlier marker tracked geography, introgression or another history poorly aligned with the lineage question. The update record should state which interpretation changed and which observations remain usable, rather than presenting the newest dataset as if it erased prior evidence.

We therefore propose three separable update questions: what new evidence has become observable; which analytical inference changes; and whether that change is sufficient, under the declared species criterion, to alter the taxonomic treatment. These questions prevent "more genomic data" from becoming an implicit species criterion and make disagreement over changed evidence distinguishable from disagreement over its taxonomic meaning.

Because these update scenarios differ in what they permit a taxonomist to infer, a reconciliation table is more informative than treating every genomic discrepancy as stronger or weaker support.

Table 1. Reconciliation of genomic evidence updates that can alter taxonomic interpretation without constituting species decisions by themselves

Discordance, diagnosis, and scale updates			
Genomic update comparison dimension	**Gene-tree/species-history discordance**	**Marker-diagnostic conflict**	**Increased genomic scale**
Taxonomic setting and evidence	Deep or recent lineage relationships Conflicting locus histories, alternative species-tree signal	Identification or preliminary delimitation COI monophyly or distance signal compared with broader evidence	Phylogenomic or delimitation update Larger multilocus datasets and expanded locus recovery
Interpretive change	Support for relationships and inferred lineage history	Confidence that a marker diagnoses an already hypothesized entity	Resolution, support and visibility of discordance
Decision boundary	Incomplete lineage sorting, introgression and model-related discordance may be difficult to separate	Diagnostic failure is lineage- and criterion-dependent	Additional loci do not guarantee a unique species history
Revision handling and state	Retain competing histories and reassess the inference connecting loci to the taxonomic hypothesis Evidence-supported distinction	Preserve marker performance as evidence; do not convert a failed threshold directly into lumping or splitting Evidence-supported distinction	Reanalyse the hypothesis while retaining dataset, locus and model provenance Evidence-supported distinction
Evidence-to-decision reassessment			
Genomic update comparison dimension	**Evidence-to-decision reassessment**		
Taxonomic setting and evidence	Any revision receiving materially new evidence Combined updated evidence interpreted under an explicit species criterion		
Interpretive change	Whether a prior treatment remains adequate		
Decision boundary	Evidence change and taxonomic change are not equivalent		
Revision handling and state	Reaffirm, revise, split or synonymize only after the inferential transition is documented Proposed synthesis		

The principal argument is therefore best represented as a validation architecture in which genomic observations cannot bypass analytical and nomenclatural boundaries.

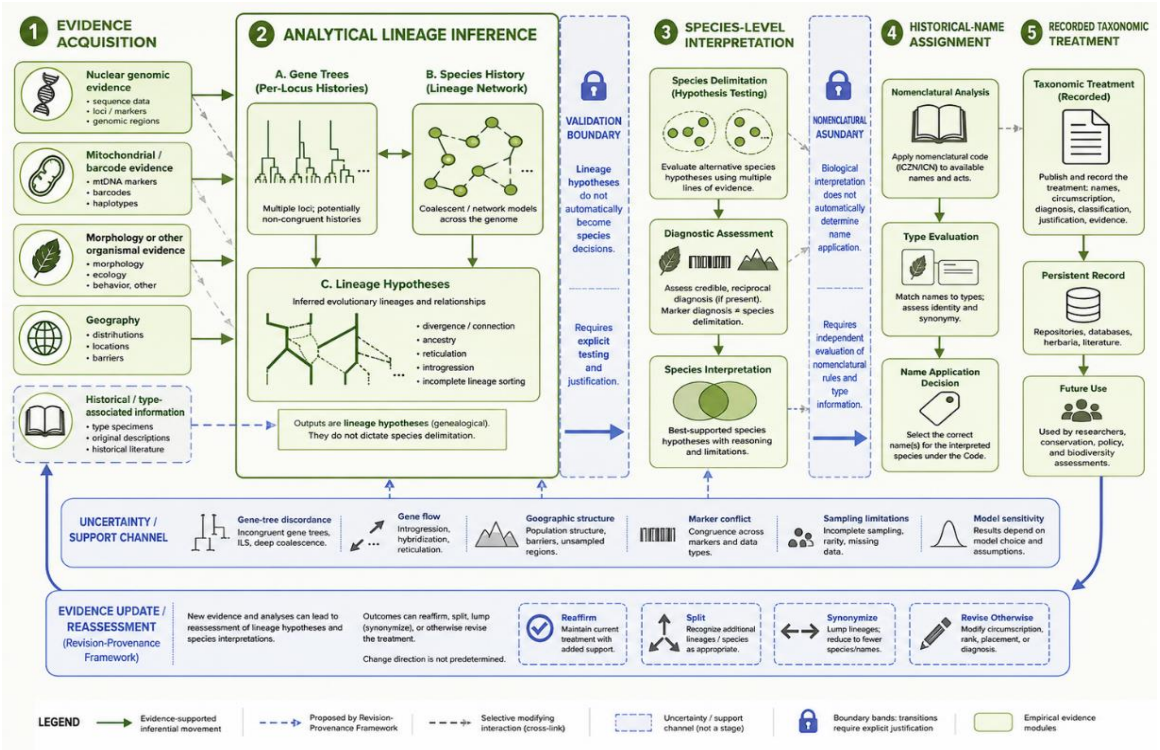


Figure 1. Validation boundaries that prevent genomic updates from becoming automatic taxonomic actions

Read left to right, the figure separates genomic and complementary observations from analytical lineage inference, species-level interpretation, historical name application and the resulting taxonomic treatment. Parallel evidence lanes remain distinct until an explicit interpretation step. Solid arrows indicate relationships established as legitimate inferential steps by the cited literature; dashed arrows identify transitions organized by the proposed Revision-Provenance Framework. An uncertainty channel carries gene-tree discordance, migration, geographic structure, marker conflict and model sensitivity alongside—not downstream of—the main inference. A return path from later evidence to the recorded decision represents reassessment rather than presumed.

Traceable decision records

A reproducible revision must preserve enough information for a later investigator to identify where disagreement enters the inference. Reference databases are part of that chain because mislabeled sequences, taxonomic conflict, inadequate resolution and incomplete coverage can affect downstream assignments [32]. Recording a database name without its relevant version, taxonomic scope or unresolved conflicts may therefore be inadequate.

Specimen representation is equally important. Arthropod taxonomy often privileges particular semaphoronts, especially adults or one sex, even though DNA-assisted association can expose systematic information from females and immature stages that conventional sampling leaves underused [33]. This does not mean every revision must sample every life stage. It means the decision record should state which stages, sexes and specimen classes actually support the diagnosis.

The proposed decision record therefore links specimen and name provenance, evidence classes, sampling geography, analytical assumptions, alternative outputs, declared species criterion, taxonomic interpretation and the versioned nomenclatural action. It should also distinguish information that was unavailable from evidence that was examined but discordant. That distinction matters when a later revision asks whether a conclusion changed because genuinely new evidence became available or because the same evidence was reinterpreted under another criterion. Where specimen vouchers, sequence accessions or type-associated material are available, the record should connect them to the relevant inferential step without treating repository identifiers as evidence of taxonomic correctness. These are audit fields, not a numerical confidence score.

Reproducible revision workflow

Reproducibility also requires preserving methodological alternatives. SPdel illustrates how outputs from multiple single-locus delimitation procedures can be generated and compared within a common workflow [34]. Agreement

among methods can reveal robustness to algorithm choice, while disagreement identifies method sensitivity; neither outcome independently validates species status.

We propose that revision proceed through separable checkpoints: establish candidate entities and associated specimens; declare the species concept and operational criterion; document evidence classes and geographic sampling; record model assumptions and competing analytical outputs; evaluate concordance and discordance; connect biological entities to historical names; state the taxonomic action and its justification; and archive the decision in a form that can be updated. Not every taxon requires every evidence class, and straightforward revisions need not become administratively burdensome. The minimum standard is that omitted evidence or inapplicable checkpoints remain distinguishable from evidence that was examined and found contradictory.

When later genomic, morphological, geographic or nomenclatural information becomes available, reassessment returns to the affected checkpoint. A new dataset may strengthen the existing treatment, expose an analytical failure, change the inferred species hypothesis, or alter only name application. The workflow therefore separates an update trigger from an update outcome. A trigger may be a newly sampled population, a different life stage, improved type association, genomic data, an alternative model or correction of a reference-database conflict. None specifies in advance whether the accepted treatment should change. Versioning preserves that distinction and prevents revision history from being overwritten by the newest conclusion. It also allows a later author to state precisely which part of a previous decision is being challenged while leaving unaffected evidence intact.

The central implication is that inferential reproducibility in taxonomy is broader than computational reproducibility. Species are defensible scientific hypotheses when their evidential basis and criteria can be reconstructed [3], while transparent versioning allows later changes to be understood rather than merely observed [13]. Database harmonization adds the same requirement at the name-data interface [28]. The proposed framework integrates these principles at revision scale without claiming that they eliminate legitimate disagreement.

A particularly important safeguard concerns genomic structure. Multispecies-coalescent structure, gene flow and model misspecification can each alter delimitation inference [5, 9, 10]. Consequently, a strongly supported genomic partition is evidence requiring biological interpretation, not a nomenclatural command. The framework is deliberately neutral about whether reassessment should increase or decrease recognized diversity.

That neutrality is empirically necessary. Recent insect revisions show that genomic evidence can support synonymy, simultaneously expose synonymy and previously unrecognized diversity, or reveal species obscured by mitochondrial diagnostics [18, 19, 23]. These examples demonstrate possible directions of revision rather than their frequencies across insects. Taxon history, geographic sampling, reproductive biology, marker behavior, model assumptions and the available phenotypic evidence all limit transfer from one revision to another.

The framework also has practical limits. Historical types may be unsuitable for genomic sampling; geographically important populations may be inaccessible; life stages may remain unassociated; reference databases can propagate uncertain names; and alternative models may remain difficult to discriminate. Some insect groups will also have evidence architectures dominated by morphology, host association, reproductive traits or geography rather than genome-scale data, so a provenance framework should not privilege genomics merely because it is available. Reproducible documentation cannot manufacture missing evidence, overcome sparse sampling or adjudicate among equally defensible species concepts. Its benefit is narrower but important: uncertainty can be located rather than concealed inside a final taxonomic statement, and subsequent authors can determine whether disagreement concerns observations, analysis, interpretation or nomenclature.

Prospective evaluation is therefore required before claiming that this architecture improves accuracy, stability or efficiency. Useful tests would compare whether independent taxonomists can reconstruct the same evidence-to-decision path, identify the same points of disagreement, and update a treatment without losing the rationale for earlier versions. Evaluation should also examine whether provenance remains usable across legacy museum material, recently sampled populations, contrasting insect orders and revisions with strongly discordant evidence. Such tests would reveal where the proposed fields are excessive, insufficient or taxon-specific. Evaluation should focus on auditability and interpretive transparency rather than assume that agreement itself is evidence of biological

Conclusion

Genomic evidence has made insect taxonomic revision more informative without making species concepts, nomenclature or interpretation automatic. Reproducibility requires preserving the path from observations through analytical assumptions and species criteria to historical name application and taxonomic action. The proposed Revision-Provenance Framework separates these stages while retaining discordance, geographic limits and subsequent evidence updates. Its purpose is not to standardize every species decision, but to make the reasoning behind synonymy, splitting, retention and later reassessment recoverable. In genomic-era systematics, a revision should remain scientifically inspectable even when its conclusion eventually changes.

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