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Conflicting Morphological, Molecular, Ecological, and Behavioral Evidence Requires Explicit Decision Rules in Integrative Insect Taxonomy

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ABSTRACT

Integrative insect taxonomy gains power from combining morphology, molecular data, ecology, behavior, and life-history information, yet disagreement among these domains creates an inferential problem that cannot be solved by simple evidence counting. This article develops a systematic framework for treating concordance and conflict as explicit taxonomic states. The framework separates what an evidence class measures from its reliability, independence, taxonomic relevance, and plausible causes of discordance. Published insect cases show that morphology and molecular evidence can strongly agree, but also that morphotypes, barcodes, phylogenomic relationships, coalescent partitions, ecological associations, and behavioral barriers may disagree at different biological and taxonomic scales. The proposed rules therefore reject a fixed hierarchy of evidence and instead require claim-level reconciliation. Ecology–genomics conflict is treated especially cautiously because host association, geography, environment, gene flow, and analytical design can produce overlapping signals. The framework is intended to structure transparent taxonomic reasoning, not to provide numerical weights, universal thresholds, or an empirically validated classifier. Its principal contribution is a reproducible vocabulary for deciding when concordance is informative, when discordance is explainable, and when uncertainty should remain unresolved pending stronger evidence.

Keywords: Integrative taxonomy, Species delimitation, Morphology–genomics discordance, Host-associated differentiation, Genomic structure, Evidence independence

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Introduction

Integrative taxonomy has become central to the practical problem of delimiting insect diversity when names, phenotypes, sequence clusters, distributions, and life histories do not map cleanly onto one another. Large-scale integrative taxonomy explicitly treats heterogeneous data as necessary for resolving difficult or poorly characterized taxa rather than assuming that a single data stream can carry every inferential task [1]. Tephritid species complexes illustrate the same point at an applied insect scale: morphology, molecular evidence, ecology, and behavior can contribute differently to resolution depending on the complex and its history [2]. The important unresolved issue is therefore not whether multiple evidence types are useful, but how disagreement among them should alter a taxonomic conclusion.

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Molecular partitions are particularly prone to being mistaken for decisions rather than evidence. DNA barcodes can be highly useful for identification, discovery, and association, but barcode evidence alone does not constitute a complete species description or automatically settle species limits [3]. Reanalysis of BIN-based taxonomic practice similarly shows that algorithmic barcode clusters should not be converted mechanically into species names without taxonomic interpretation and adequate access to the underlying evidence [4]. These cautions do not invalidate barcoding; they delimit what barcode partitions can legitimately establish.

This article addresses the narrower inferential problem created when morphology, molecular or genomic structure, ecology, and behavior point in different directions. The central contribution is a proposed conflict-adjudication framework rather than a new delimitation algorithm. It distinguishes evidence class from evidence reliability and independence, localizes disagreement to the biological or taxonomic level actually tested, and preserves an unresolved state when competing interpretations remain plausible. No evidence class is assigned a universal numerical weight, and no single form of concordance is treated as proof of species status.

Materials and Methods

This study used a non-empirical framework-construction approach. The source literature was examined at the level of the claim relevant to integrative insect taxonomy. For each study, the taxon, biological level, evidence class, life-stage or sex dependence where relevant, geographic setting, principal inference, conflicting or null result, methodological limitation, and transferability boundary were extracted. Evidence was then organized according to whether it addressed phenotype, molecular or genomic structure, ecological association, behavioral or reproductive differentiation, or a methodological property of delimitation. No new biological dataset, pooled effect estimate, species count, or accuracy statistic was generated.

Conflict was defined as disagreement between evidential propositions that bear on the same candidate taxonomic boundary but imply different interpretations after taxonomic level and measurement target are made explicit. This definition is process-aware: species-delimitation outputs depend on the biological process represented by the model, so algorithmic disagreement alone is not equivalent to biological conflict [5]. A second guardrail separates population structure from species inference because multispecies-coalescent methods can delimit structured populations under conditions where the inferred units should not automatically be interpreted as species [6].

Gene flow was not coded as a binary refutation of species boundaries. Delimitation under migration depends on the history and magnitude of gene flow and on the model used to represent it [7]. Accordingly, the proposed rules treat introgression or admixture as an interpretive condition that can weaken some inferences without forcing conspecificity. Likewise, method performance is conditional on the speciation and demographic scenario; comparative evaluations of molecular delimitation methods do not support a universally dominant algorithm [8]. Reliability was therefore treated qualitatively and contextually rather than converted into a score.

Four analytical questions were applied in sequence. First, what biological quantity or relationship was actually measured? Second, is that measurement and its inference reliable in the sampled taxon, stage, geography, marker set, and model? Third, does it contribute information that is genuinely distinct from other evidence already considered? Fourth, is the signal taxonomically relevant at the species-boundary level rather than at a neighboring level such as population structure or deeper phylogeny? Conflict explanations were retained as alternatives unless the underlying study directly discriminated among them. These operations constitute the article's proposed decision-rule construction and have not themselves been prospectively validated.

Results and Discussion

Concordance provides the necessary baseline for defining conflict. In the *Temnothorax salvini* ant group, phylogenomic and phenotypic evidence were integrated to formulate coherent species hypotheses, demonstrating that difficult boundaries can become more defensible when distinct data streams converge [9]. In Epyrinae wasps, combined morphological and molecular evidence helped resolve taxonomic and phylogenetic impasses that were not adequately represented by one partition alone [10]. These cases show the value of integration, but neither establishes a general evidential threshold for insects.

Concordance can also span biogeography and life-history information. Integrative work on *Agraulis* and *Dryas* butterflies used multiple domains to clarify species limits in groups previously treated as monotypic, while also showing that the informativeness of particular traits was uneven [11]. In overlapping *Psylliodes* flea beetles,

morphology, COI, and multilocus evidence jointly distinguished closely related entities, yet individual morphological characters differed in diagnostic reliability across populations and contexts [12]. Thus, "morphological support" is not a single homogeneous quantity: the relevant unit is the character system measured in the sampled taxon, sex, and geography.

Morphology can also provide independent corroboration without reproducing every molecular relationship. A character-based study of Euptychiina butterflies recovered substantial phylogenetic affinities compatible with molecular evidence while retaining localized discrepancies attributable to character coding, homoplasy, or taxon sampling [13]. Across ants, butterflies, and flea beetles, cross-domain concordance has therefore been demonstrated in taxonomically different insect systems [9, 11, 12]. In the proposed framework, this condition is termed bounded concordance: evidence classes agree on the focal inference, but confidence remains restricted to the sampling, characters, markers, models, and taxonomic level actually examined.

Morphology–molecule conflict

Morphology–molecule conflict becomes informative only after the unit of disagreement is specified. In the *Bactrocera frauenfeldi* complex, variable morphotypes and COI patterns did not map straightforwardly onto the broader nuclear phylogenomic evidence; nuclear loci and morphological reassessment supported synonymy where morphotype or barcode separation alone would have suggested a different reading [14]. This is not evidence that nuclear genomics is universally superior. It is evidence that, in that tephritid complex, morphotype identity and a single mitochondrial marker were insufficient proxies for the species-level history recovered from a broader evidential comparison.

Conflict can also occur at deeper taxonomic levels without directly settling species limits. Protein-encoding UCE phylogenomics in Oestroidea produced relationships that challenged parts of traditional morphology-based classification, while other established relationships were retained [15]. The proper inference is node- and level-specific: disagreement between a phylogenomic topology and a historical morphological grouping is not automatically a species-delimitation conflict. Conflating these scales would give molecular evidence apparent decisiveness over a question it did not directly test.

The Polleniidae provide an additional boundary condition. Mitogenomic analyses revised relationships that conflicted with earlier morphology-based groups, but adult morphology, terminalia, and COI could remain concordant for some species-level units [16]. The same study can therefore contain disagreement at one hierarchical level and agreement at another. The framework labels this hierarchical discordance, a proposed classification in which the first task is to localize the conflict to a claim—species diagnosis, species delimitation, genus-group relationship, or deeper topology—rather than label an entire evidence class "wrong."

Species-delimitation models create a related form of conflict. In Haeterini butterflies, classical taxonomy and multispecies-coalescent outputs required reconciliation rather than mechanical acceptance of either partition [17]. In *Phoebis*, several molecular approaches were evaluated together with morphology because alternative molecular partitions did not carry identical taxonomic implications [18]. These cases motivate a proposed model–diagnosis discordance state: when morphology or established diagnoses and model-based species partitions differ, adjudication should examine sampling, marker properties, prior assumptions, population structure, and alternative biological processes before assigning priority. The framework therefore treats conflict as a location for explanation, not as a vote in which one evidence class must win.

Because prose can obscure whether two studies conflict at the same inferential level, the reconciliation table below separates species-level phenotype–marker disagreement from deeper topological conflict, hierarchical discordance, and model-sensitive delimitation. Its purpose is to prevent visually similar "morphology versus molecules" cases from being treated as equivalent.

Table 1. Morphology–molecule conflict states differ by the inferential level at which phenotype, marker, and lineage evidence cease to agree

Conflict state or comparison		
Biological setting · Limits and uncertainty	**Evidence · Interpretation for taxonomic inference**	**Research or test**
Phenotype–single-marker discordance		
Variable morphotypes within a tephritid species complex	Adult morphotype and COI separation do not align cleanly with broader nuclear evidence	Expand independent nuclear sampling and reassess

Nuclear evidence remains sampling- and model-dependent	Morphotype or barcode partitions should not be treated as species-equivalent without reconciliation	phenotype stability across geography
Higher-level topological conflict		
Oestroidea phylogeny **Node support, locus choice, taxon sampling, and character homology remain relevant**	UCE relationships challenge selected morphology-based groupings Conflict revises a phylogenetic hypothesis, not automatically a species boundary	Test disputed nodes with alternative locus sets and explicitly homologized morphology
Proposed hierarchical discordance		
Polleniidae/Pollenia **Mitochondrial history is not equivalent to independent nuclear history**	Higher-group mitogenomic conflict coexists with species-level morphological or COI agreement Localize disagreement to the taxonomic level actually affected	Compare species-level and deeper-level evidence separately before revising names
Proposed model–diagnosis discordance		
Butterfly species-delimitation problems **Priors, structure, locus set, and demographic history can alter partitions**	Coalescent or multilocus partitions differ from classical diagnoses or from one another Model output is a species hypothesis requiring external taxonomic reconciliation	Re-estimate boundaries under alternative process assumptions and compare against independent traits
Character-level partial concordance		
Morphological systems with variable diagnostic characters **Character coding, sex, stage, and population coverage affect reliability**	Some traits support molecular groups while others are homoplastic or geographically variable "Morphology" should be decomposed into particular character systems	Identify which characters replicate across sex, stage, and range rather than weight morphology as one block
Concordant benchmark		
Integrative delimitation with phenotypic and molecular agreement **Shared sampling biases or hidden dependence can still inflate apparent corroboration**	Distinct data streams support the same focal boundary Concordance strengthens the species hypothesis but does not logically prove it	Test independence and coverage before treating agreement as cumulative support

Ecology–genomics conflict

Ecological differentiation is taxonomically informative only when the ecological axis and the genomic pattern are interpreted at the same spatial and biological scale. Comparative work on galling sawflies found contrasting degrees and patterns of host-associated genomic differentiation among closely related systems exposed to analogous host contrasts [19]. Host association therefore cannot be assigned a fixed taxonomic meaning: similar ecological differentiation may accompany strong genomic structure in one lineage and weaker or differently distributed structure in another.

Geography is a particularly important alternative explanation. In *Eumedonia eumedon*, larval host association was related to genomic differentiation after geographic comparisons, but isolation-by-distance relationships and inferred mechanisms changed with spatial scale [20]. This supports host association as a relevant explanatory axis while stopping short of demonstrating a universal causal route to speciation. A taxonomic rule that interprets host-associated clusters without explicit spatial comparison risks converting geographic covariance into ecological evidence.

Landscape-genomic studies reinforce this multicausal problem. In *Malacosoma disstria*, geography, climate, and host association jointly contributed to genomic differentiation rather than producing simple host-defined clusters [21]. In the specialist gall wasp *Belonocnema treatae*, host association and geography interacted in structuring genomic variation after spatial autocorrelation was considered [22]. These patterns are population-genomic evidence; by themselves they do not mandate recognition of species. In the proposed framework, ecology–genomics conflict therefore includes not only direct disagreement but also cases in which the same genomic pattern can be plausibly attributed to correlated ecological and geographic processes.

Host-linked divergence may nevertheless be consistent with a species-divergence scenario when genomic, ecological, and morphological information align. Phylogenomics of European *Ectoedemia* complexes clarified lineages that lower-resolution morphology or barcodes had not resolved and was consistent with host-linked divergence, but the historical mechanism remained inferential [23]. Conversely, work on admixing parapatric *Melitaea* butterflies showed that delimitation can remain continuous and method-sensitive even when genomic

datasets are rich; target-enrichment and ddRAD evidence on the same biological problem did not turn admixture into a naturally discrete boundary [24]. Across these insect systems, host-associated genomic differentiation is context-dependent and can covary with geography or other environmental structure [19-21].

The reconciliation logic is therefore asymmetric. Ecological association may explain why genomic differentiation is biologically plausible, but it does not automatically establish that observed genomic structure is species-level, caused by ecology, or sufficient for nomenclatural action. Conversely, weak genome-wide differentiation does not automatically erase ecological divergence when gene flow, recent divergence, or localized barriers remain plausible. The proposed decision rule is to separate three questions: ecological association, genomic differentiation, and taxonomic sufficiency. A claim may be well supported at the first two levels while remaining unresolved at the third.

This separation is difficult to retain in linear prose because host use, geography, genomic structure, and taxonomic interpretation cross-connect rather than form a single sequence. **Figure 1** therefore places these evidence layers in parallel, shows where covariance and method dependence enter, and marks the boundary at which empirical association ends and proposed taxonomic adjudication begins.

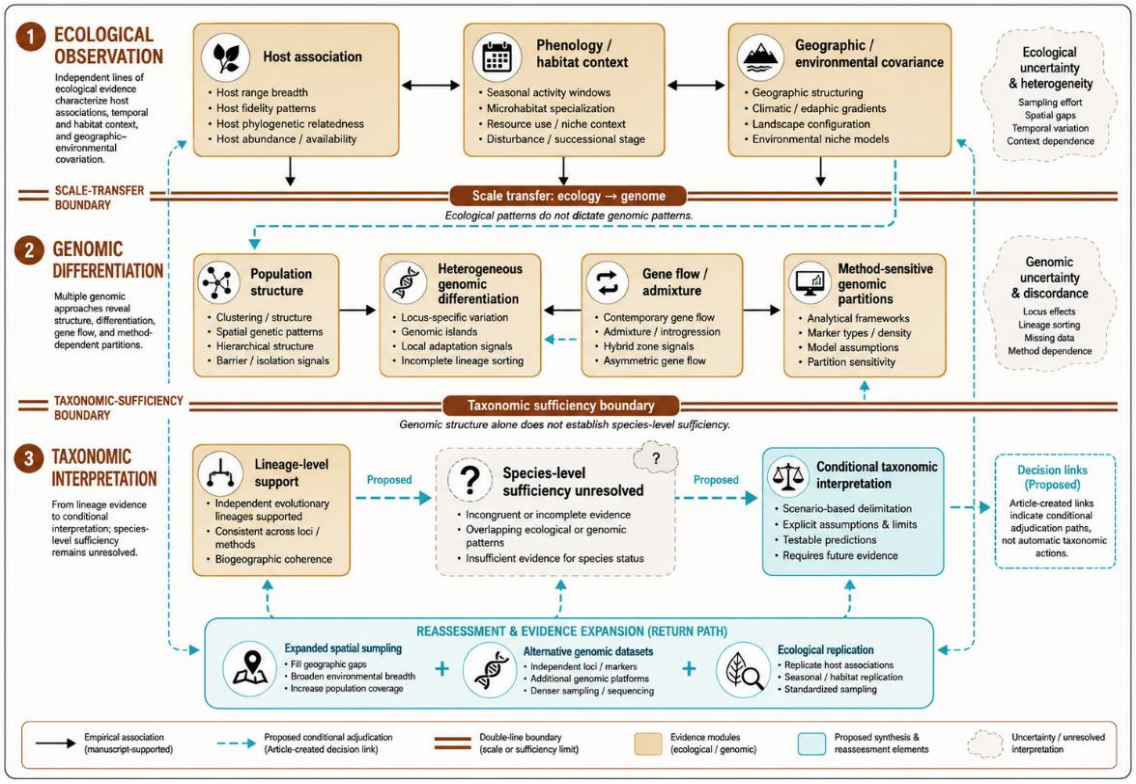


Figure 1. Ecological signals, genomic structure, and taxonomic sufficiency occupy different reconciliation layers under host-associated divergence

Behavioral isolation without genomic separation

Behavioral or reproductive differentiation need not coincide with complete genome-wide separation. In the *Andrena proxima* complex, genomic structure was evaluated alongside phenology and possible *Wolbachia*-associated incompatibility, with both mechanisms treated as plausible contributors to boundary maintenance rather than independently proven causes of speciation [25]. The taxonomic significance of phenological displacement therefore depends on whether it corresponds to reproducible reproductive separation rather than merely seasonal variation.

A contrasting configuration occurs when phenotype obscures rather than reveals lineage separation. Co-occurring *Morpho* butterflies combined convergent adult morphology with genetic isolation and divergent phenology, showing that similarity in visible phenotype can coexist with temporally segregated lineages [26]. Such cases weaken any rule that gives morphological similarity automatic precedence over independently measured behavioral, temporal, or genomic evidence.

Sexual traits can also diverge before uniform genomic isolation. In an incipient *Colias* species pair, a major male ultraviolet signal had a discrete genetic basis while substantial autosomal admixture persisted [27]. In *Ostrinia*, coincident temporal and behavioral barriers were associated with broader genomic differentiation than single barriers, indicating that barrier effects may depend on coupling rather than on the nominal number of isolating traits [28]. Consequently, "without genomic separation" is interpreted here as absence of complete, homogeneous genome-wide separation, not literal absence of genomic differentiation.

Behavioral evidence itself remains trait-specific. Comparative work across *Drosophila* documented extensive variation in sex-pheromone communication, but differences among chemical signals do not uniformly translate into equivalent reproductive barriers [29]. Direct comparison of coalescent delimitation and reproductive-isolation evidence likewise found substantial but incomplete correspondence, demonstrating that these evidential domains are not interchangeable [30]. Across the relevant bee and lepidopteran examples, isolating barriers may be partial, localized, heterogeneous, or coupled rather than uniformly expressed across the genome [25, 27, 28]. The proposed decision rule is therefore to treat behavioral isolation as an independent taxonomic contribution only when the behavior is functionally relevant, independently measured, and interpreted within its divergence stage and genomic context.

The following matrix separates forms of behavioral isolation that are easily collapsed into the same verbal category but have different taxonomic meanings.

Table 2. Behavioral isolation without complete genomic separation across divergence and evidence states

Behavioral-isolation state	Foundational dimensions	Interpretive and testing dimensions	
	Biological or divergence context · Evidence	**Taxonomic interpretation · Limits and uncertainty**	**Research or test**
Phenological boundary maintenance	Seasonally differentiated bee lineages Reproductive timing differs alongside genomic structure	Temporal segregation can support a boundary hypothesis Phenology alone does not establish causation	Measure realized mating overlap and replicate timing geographically
Convergent phenotype with temporal segregation	Co-occurring butterflies Similar adult appearance but lineage distinction and divergent phenology	Morphological similarity need not imply conspecificity System-specific coexistence mechanism	Test whether temporal separation persists across populations
Localized sexual-signal divergence	Incipient butterfly divergence Strong male signal difference with continuing admixture elsewhere	A reproductive signal may precede uniform genomic separation Trait difference alone is insufficient for full species status	Test mate discrimination and genomic distribution of differentiation
Coupled behavioral and temporal barriers	Contact-zone or divergence system Multiple barriers coincide with broader genomic differentiation	Corroboration increases only if barrier dependence is understood Coupled barriers are not independent votes	Compare single-barrier and coupled-barrier configurations
Chemical communication divergence	Sex-specific insect signaling systems Pheromone production, detection, and behavioral responses differ	Behavioral relevance must be established trait by trait Laboratory signal differences may not equal field isolation	Connect chemical divergence to realized assortative mating
Proposed unresolved behavioral–genomic state	Behavioral differentiation with incomplete genomic resolution Behavioral evidence is credible but genome-wide separation remains heterogeneous	Retain the boundary as plausible but not conclusively adjudicated Divergence stage, gene flow, sampling, and trait function remain uncertain	Expand genomic, behavioral, and geographic sampling before categorical action

Weighting independence and reliability

Evidence quantity is not equivalent to evidential strength. Mitochondrial loci illustrate the problem directly: genes within the mitochondrial genome share physical linkage and genealogical history, and mitochondrial multispecies-coalescent behavior can be sensitive to analytical configuration [31]. Agreement among several mitochondrial genes therefore cannot automatically be counted as several independent confirmations.

Morphological reliability is similarly conditional on what portion of the phenotype has actually been observed. Barcode-supported adult–larva matching in odonates expanded access to immature morphology that conventional adult-centered taxonomy could miss, while also illustrating dependence on reference-library quality [32]. Stage

and sex coverage therefore affect the completeness of morphological evidence even when the scored characters themselves are measured accurately.

The framework consequently separates reliability from independence. Reliability concerns whether a measurement and its inference are credible for the sampled taxon, marker, stage, geography, and analytical model. Independence concerns whether two apparently separate lines of support contain genuinely distinct information. A highly reliable datum may still be non-independent of another datum, while independent observations may individually be weak. Method sensitivity in molecular delimitation [8], character-specific variation in morphological diagnosis [12], genomic continuity under admixture [24], and geographic confounding of ecological differentiation [22] each show why these dimensions cannot be collapsed into a single hierarchy.

The proposed weighting rule is therefore qualitative rather than numerical: first appraise reliability, then appraise dependence, and only afterward ask how much corroborative value an additional stream contributes. Linked loci, correlated ecological variables, coupled behavioral barriers, and multiple algorithms using the same underlying dataset should not be treated as equivalent to genuinely independent replication. No universal coefficient follows from the current evidence.

The ledger below converts that principle into falsifiable expectations rather than unsupported scores.

Table 3. Predictions for testing whether additional evidence increases reliability or merely repeats dependent information

Proposed prediction or evidence	**Multiple linked mitochondrial signals will add less independent information than equivalent nuclear–phenotypic replication**	**Expanded stage or sex sampling can change apparent morphological reliability**	**Host-associated differentiation may weaken after spatial alternatives are controlled**	**Coupled isolating barriers should not be counted as separate independent confirmations**	**Delimitation instability across methods indicates conditional reliability**
Test that could challenge	Compare conclusions after adding independently inherited nuclear evidence	Repeat delimitation after holomorphological sampling	Replicate across spatially independent host contrasts	Compare populations where barriers occur separately	Reanalyse with process-explicit alternatives and independent evidence
Expected interpretation · Boundary condition	Agreement may increase internal consistency without proportionate independent corroboration Introgression and lineage sorting can alter mt history	Adult-only evidence may underrepresent the species phenotype Not every taxon has useful stage-specific characters	Apparent ecological corroboration may be partly dependent Host effects can remain after geographic control	Combined effect may be biologically important but evidentially dependent Degree of coupling is system-specific	Confidence should depend on process assumptions and data properties Method agreement can occur for the wrong biological reason
Taxonomic context · Evidence basis · Evidence	Molecular delimitation Concordant mt genes share one genomic history	Morphology-based diagnosis Diagnostic information differs among larvae, adults, males, or females	Ecological–genomic inference Host use covaries with geography or environment	Behavioral divergence Temporal and behavioral barriers covary	Genomic species inference Alternative methods partition the same specimens differently

Because reliability and independence operate through different mechanisms, a visual map is required to show where apparently increasing evidence fails to increase independent taxonomic information.

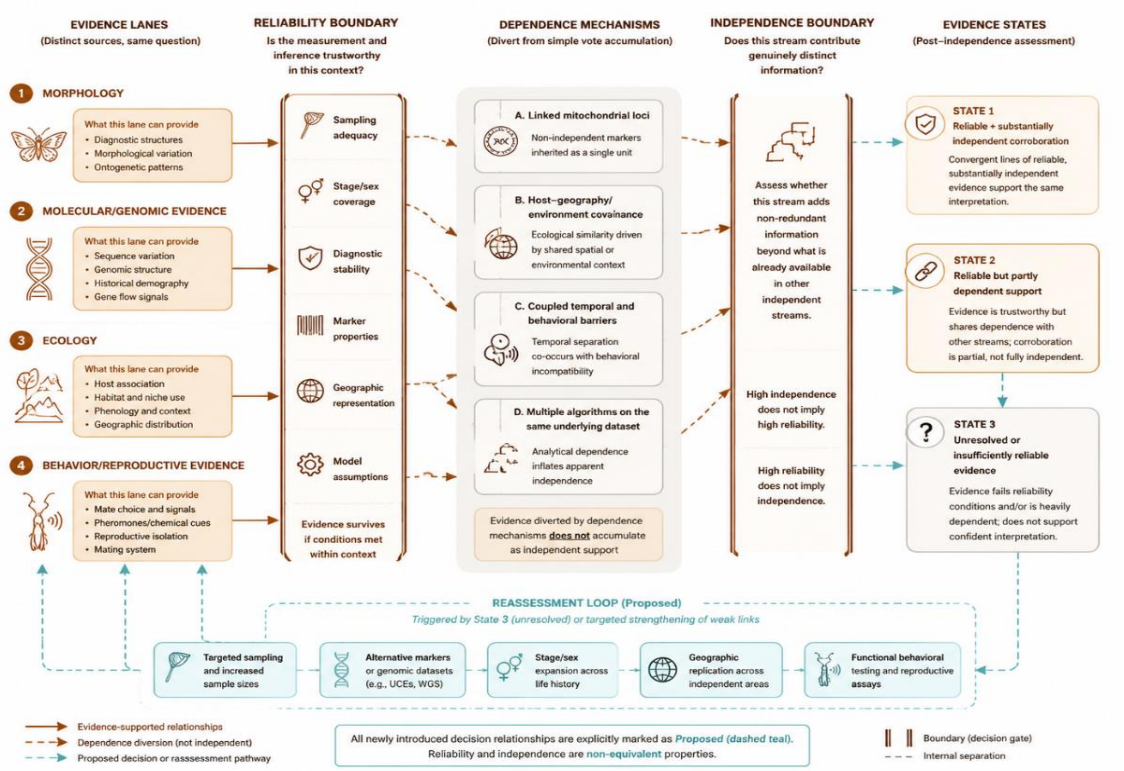


Figure 2. Reliability and independence create different boundaries on how much corroborative value an additional evidence stream can provide

Decision matrix for taxonomic outcomes

The proposed taxonomic decision architecture begins by asking what each evidence class actually measures rather than how many classes support a preferred conclusion. Integrative workflows require evidential provenance [1], while barcode partitions cannot be converted automatically into species decisions [3]. Process-aware delimitation further requires separating population or genomic structure from the biological interpretation assigned to that structure [5].

Three broad conflict states are proposed. Independent concordance occurs when sufficiently reliable and substantially independent evidence supports the same focal boundary. Explainable discordance occurs when conflict can plausibly be localized to marker history, taxonomic level, gene flow, geography, developmental stage, or another demonstrated boundary condition. Unresolved contradiction occurs when competing interpretations remain credible because reliability, independence, or biological mechanism cannot yet be discriminated. Population structure [6], gene flow [7], morphology–genomics disagreement [14], admixture [24], and barrier coupling [28] demonstrate why these states cannot be reduced to majority voting.

Taxonomic outcomes should consequently remain conditional. Strong bounded concordance may support recognition or retention of a species hypothesis. Concordance showing that historically separated morphotypes do not represent independent lineages may support synonymy when the evidential basis is sufficiently direct, as in the type of conflict exemplified by the *Bactrocera* case [14]. When methodological partitions remain unstable, however, forcing recognition or synonymy would exceed the evidence; method sensitivity itself argues for an unresolved state [8]. The proposed matrix therefore permits continued recognition, synonymy, retention of the existing treatment, targeted resampling, or provisional non-action without treating any outcome as automatically mandated.

Every decision should state its transferability boundary. Host-associated genomic structure can depend on lineage and geography [19]; spatial structure can interact with host association [22]; and stage representation changes what morphology is available [32]. The framework therefore does not attach universal confidence labels or numerical thresholds to its outcomes. Its intended function is to make the chain from evidence to taxonomic action explicit and contestable.

The central implication is that integrative taxonomy should adjudicate discordance rather than erase it. Difficult cases such as morphotype–phylogenomics conflict [14] and host-associated genomic heterogeneity [19] show

that disagreement may identify a biological or methodological boundary that would disappear if evidence streams were reduced to a consensus vote. At the same time, some disagreement will reflect sampling error, model misspecification, or weak characters; conflict is informative only after those possibilities are examined.

No fixed morphology-versus-molecules hierarchy follows from the selected insect literature. Character reliability varies within morphology [12], concordance can change with taxonomic level [16], and genomic partitions can remain method-sensitive under admixture [24]. Reproductive evidence also fails to map perfectly onto model-based species assignments [30]. The defensible conclusion is not that all data classes are equal, but that their reliability is conditional on the question and biological context.

Independence adds a separate constraint. Spatially correlated ecological variables [22], coupled isolating barriers [28], and physically linked mitochondrial loci [31] demonstrate distinct routes by which apparently multiple observations can carry overlapping information. A decision architecture that ignores these dependencies risks overstating corroboration even when every individual measurement is technically reliable.

The framework remains conceptual. Its conflict states and outcome rules require retrospective testing against well-resolved taxonomic revisions and prospective evaluation in cases where morphology, genomics, ecology, and behavior genuinely disagree. Such validation should assess whether different taxonomists applying the rules reach more transparent and reproducible interpretations, not assume that the framework itself supplies biological truth. Method sensitivity [8] and empirically difficult integrative cases [9] provide appropriate stress tests because they preserve uncertainty rather than eliminating it by design.

Conclusion

Conflicting evidence in insect taxonomy should not be resolved by assuming that morphology, barcodes, genomic clusters, ecology, or behavior has permanent priority. The proposed framework instead separates evidence class, reliability, independence, taxonomic relevance, and conflict explanation before a taxonomic outcome is considered. Concordance strengthens a species hypothesis only within its evidential boundaries; discordance may be biologically meaningful, method-generated, or genuinely unresolved. Explicitly preserving these alternatives makes taxonomic reasoning more transparent while avoiding unsupported numerical weighting or forced binary decisions. The framework is therefore a structured basis for future testing, not an empirically validated classifier of species boundaries.

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