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Congruence, Conflict, and Evidential Weight Across Morphological, Molecular, Ecological, and Behavioral Data in Integrative Insect Taxonomy

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ABSTRACT

Integrative insect taxonomy increasingly combines morphology, DNA barcodes, multilocus and genome-scale data, ecology, geography, and reproductive evidence, yet agreement among these sources is often treated more simply than the underlying inference permits. This critical review examines how evidential classes contribute to species delimitation and higher-level taxonomic interpretation when they converge, conflict, or share non-independent sources of error. The central problem is not whether molecular evidence should replace morphology, or whether several agreeing datasets automatically justify a taxonomic decision, but how observations generated at different biological and analytical levels are translated into species-level inference. Morphological characters may be diagnostic, convergent, life-stage restricted, or difficult to quantify; molecular signals may reflect population structure, introgression, incomplete lineage sorting, marker-specific histories, or model misspecification; ecological differences may provide independent context without proving reproductive separation; and reproductive evidence may directly test biological isolation but is unevenly available across insect systems. The review therefore distinguishes evidence acquisition from taxonomic interpretation and argues that evidential weight should depend on relevance, independence, error structure, inferential distance, and explicit consideration of competing explanations rather than on a fixed ranking of data classes. This dependence-aware view provides a basis for interpreting both concordance and conflict while preserving uncertainty, taxonomic scope, and the distinction between lineage detection and species recognition.

Keywords: Integrative taxonomy, Species delimitation, Phylogenomics, Morphological evidence, Ecological divergence, Reproductive isolation

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Introduction

Integrative taxonomy has become central to the resolution of insect species complexes because no single evidence class consistently captures every dimension of lineage differentiation. Work on tephritid fruit flies illustrates why difficult complexes require coordinated interpretation of morphological, molecular, ecological, and other evidence rather than reliance on a single diagnostic channel [1]. The difficulty is not merely technical. Different datasets can describe different biological levels, and the taxonomic conclusion is an inference made from those observations rather than another observation of the same kind.

This distinction is especially important for genetic evidence. Multispecies-coalescent methods can delimit population structure even when the inferred entities should not automatically be interpreted as species, showing that statistically discrete genetic clusters and taxonomically defensible species hypotheses are not equivalent [2].

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The evidence available for testing those hypotheses is also shaped by collections, digitization, specimen quality, and the expanding connection of museum material to molecular and informatic resources [3]. Taxonomic disagreement can therefore arise because organisms have complex histories, because different characters evolve at different rates, or because the evidence itself is unevenly sampled and preserved.

The problem addressed here is consequently narrower than a catalogue of techniques. The review asks how evidential weight should change when morphology, molecular or genomic data, ecology, and behavior or reproduction converge, partially overlap, or conflict. It also asks when apparent agreement is genuinely corroborative rather than a consequence of shared specimens, shared genealogy, correlated characters, or common analytical assumptions. The article develops a proposed dependence-aware interpretation in which data classes are not given permanent ranks. Instead, their contribution is judged by what they measure, how directly they bear on the taxonomic question, what errors they may share, and which alternative explanations remain plausible.

Review scope and evidential framework

The review treats species delimitation as a staged inference. First, investigators observe variation in characters, sequences, genomes, ecological associations, distributions, or reproductive interactions. Second, analytical methods convert those observations into clusters, trees, distances, assignments, or tests of differentiation. Third, those results are interpreted in relation to a species hypothesis. The boundaries between these stages matter because biological processes can violate the assumptions that connect them. Models that explicitly accommodate gene flow demonstrate that lineage divergence need not occur under complete isolation, while migration can complicate the interpretation of genetic distinctness [4].

Model fit is therefore part of evidential quality rather than a technical afterthought. Simulations of multispecies-coalescent inference show that violations of model assumptions can alter inferred species boundaries, so high statistical support cannot by itself establish that the biological model is appropriate [5]. Comparative evaluations of molecular delimitation methods likewise show that performance varies across divergence histories and demographic scenarios; no method can be assigned universal priority independently of the conditions under which it is applied [6].

This review accordingly separates five properties that are often conflated: detectability, diagnosticity, independence, biological relevance, and inferential reliability. Detectability concerns whether a difference can be measured. Diagnosticity concerns whether it distinguishes candidate taxa in the sampled material. Independence concerns whether the signal is generated by a genuinely distinct evidence process rather than by the same genealogy or correlated character system. Biological relevance concerns how directly the observation bears on lineage separation. Inferential reliability concerns whether sampling, model assumptions, and analytical choices support the conclusion being drawn. These properties are used qualitatively, not as a numerical scoring system, and their combination is proposed here as an interpretive framework, rather than as an empirically validated weighting algorithm.

Morphological evidence

Morphology remains indispensable because formal taxonomy is anchored to organisms and specimens, but "morphological evidence" is not a single uniform class. Its availability changes across life stages, preservation states, sexes, and character systems. Next-generation barcode matching of immature and adult insects can link life stages that cannot readily be associated by morphology alone, illustrating that a morphological diagnosis may be limited by ontogeny even when the species hypothesis itself is not [7]. In the long-horn moth *Nemophora degeerella* complex, morphology, DNA barcodes, and genome-wide ddRAD data jointly revealed cryptic diversity, yet not every nuclear or morphological character discriminated the same entities [8]. Integrative revision of *Sea* and *Cybdelis* butterflies likewise showed how morphological and molecular evidence can converge in a revised systematic interpretation without requiring that every character partition carry identical weight [9].

Conflict can also reveal the evolutionary limitations of morphology. Phylogenomics of net-winged beetles identified parallel evolution of morphological traits, demonstrating that similarity in phenotype may reflect convergence rather than close common ancestry [10]. Conversely, quantitative morphology can recover information that categorical inspection misses. Wing geometric morphometrics has been used to assign type material within cryptic bumblebee complexes, although its diagnostic performance remains contingent on the focal taxa and reference material [11].

Digital image analysis further changes how morphological evidence is acquired without eliminating the distinction between identification and taxonomic inference. Convolutional-network transfer learning has achieved expert-level performance in defined insect identification tasks [12]. Computer-vision approaches may therefore scale the extraction of morphological information, but their performance depends on training data, image conditions, and transfer to new taxa or settings [13]. A classifier that accurately labels images is not, by that fact alone, evidence that the named categories represent independently evolving species.

Morphological evidence should therefore be evaluated at the level of the actual character system. A genital trait, wing-shape configuration, larval character, color pattern, or automated image feature may differ in developmental stability, environmental sensitivity, evolutionary convergence, and dependence on other traits. The relevant question is not whether morphology as a whole agrees with DNA, but which morphological observations are diagnostic, how they were measured, and whether the processes generating them are sufficiently independent to add information to the species hypothesis.

Molecular and genomic evidence

Molecular evidence has transformed insect systematics, but it also comprises non-equivalent signals. Mitochondrial loci, nuclear markers, reduced-representation genomic data, ultraconserved elements, and multilocus coalescent models differ in inheritance, effective population history, genomic representation, and analytical assumptions. Multilocus delimitation of Mesoamerican *Scaptotrigona* stingless bees supported cryptic diversity while also illustrating that marker choice and delimitation procedure can influence the resulting species hypotheses [14]. Molecular delimitation of Afrotropical *Culicoides* similarly demonstrated the value of multigene evidence for resolving species relationships within difficult complexes while remaining dependent on regional sampling and marker performance [15].

At broader phylogenetic scales, molecular evidence can revise long-standing taxonomic boundaries. Analysis of *Choristoneura* supported changes to generic delimitation and reconstructed biogeographic history from sampled molecular loci [16]. Yet greater genomic breadth does not make all molecular partitions interchangeable. In *Stenocorse* parasitoid wasps, nuclear 3RAD and mitochondrial data were both informative, but mitochondrial evidence generated additional lineage structure that did not map identically onto the nuclear genomic signal [17]. Such discrepancies should not be reduced to a contest in which one marker is declared correct without evaluating introgression, lineage sorting, sampling, or the scale of the question.

The *Phoebis* butterfly study provides a complementary case: barcode, morphology, and model-based species delimitation yielded different raw partitions that could be reconciled into a more defensible species hypothesis [18]. This illustrates why algorithmic agreement is not a substitute for interpretation. Delimitation procedures may identify operational clusters, whereas the taxonomic decision must account for what each cluster represents biologically.

Genome-scale methods expand resolution but also magnify the consequences of analytical design. Data-driven reconstruction of insect phylogeny has benefited from rapidly growing sequence resources, yet coverage and support remain uneven across the insect tree [19]. Nested anchored hybrid enrichment has provided substantial resolution in tiger moth phylogeny, showing the power of dense, targeted genomic sampling at shallow evolutionary levels [20]. However, large comparative analyses of molecular species delimitation demonstrate that dataset properties affect method efficiency and agreement [21]. In Adephaga, phylogenomic inference was shown to be sensitive to model misspecification and excessive data trimming, with analytical choices capable of generating strongly supported artefacts [22]. Protein-encoding ultraconserved elements have likewise revised relationships among oestroid flies, emphasizing that genomic evidence can overturn previous classifications while remaining conditional on locus choice, taxon sampling, and model specification [23].

The implication is not that genomic evidence is weaker than morphology. Rather, genomic evidence is strongest when its scale, marker properties, sampling design, and model assumptions match the taxonomic question. More loci generally reduce stochastic sampling error, but they do not eliminate systematic error, nor do they convert a gene-tree pattern automatically into a species-level conclusion.

Ecological evidence

Ecological evidence becomes taxonomically informative when candidate lineages differ in environmental association, host use, geography, or other dimensions that are measured independently of the characters used to delimit them. Its evidential role is nevertheless contextual. Integrative work on the endangered weevil

Pachyrhynchus sonani combined genetic, morphological, and geographic information to evaluate island lineages, showing how spatial context can strengthen interpretation without making geographic separation itself sufficient for species recognition [24]. In the *Bombus monticola* complex, geographic differentiation across refugial regions was associated with genetic and eco-chemical structure, but such differentiation should not be equated automatically with completed speciation [25].

Host use can provide a more direct ecological contrast. Cryptic species within the fungivorous beetle *Octotemnus laminifrons* differed in host association alongside genetic and morphological evidence, making host use an informative component of the delimitation problem [26]. Nearctic ambush bugs provide a more complicated example: molecular data, geometric morphometrics, and ecological associations were integrated, yet mitochondrial and nuclear patterns were not uniformly concordant and alternative historical explanations remained relevant [27]. Ecological evidence therefore gains weight when it contributes a distinct observation about lineage ecology, but it should lose weight when it is merely a correlate of geography, sampling design, or the same population structure already captured genetically.

The practical interpretive problem is to determine when ecology contributes independent discrimination and when it merely redescribes structure already visible in another data class. The mechanism–boundary matrix below is needed because those conditions are more readily compared across inference states than narrated serially, while ecological association must remain separate from claims about reproductive isolation or adaptive divergence.

Table 1. Ecological evidence states that strengthen, qualify, or fail to resolve insect species-boundary inference

Ecology observed			Species-boundary use
Ecological signal	**Taxon and ecological setting**	**Ecological basis**	**Taxonomic contribution and adjudication**
Spatially structured concordance	Island, refugial, or geographically partitioned lineages	Distributional separation accompanies morphological or genetic differentiation	Geography can increase plausibility of persistent lineage separation. Geographic structure may reflect isolation by distance or historical fragmentation rather than species boundaries. Test whether differentiation persists across contact zones and independent character systems. Evidence-derived synthesis.
Eco-chemical differentiation	Lineages occupying historically distinct environmental regions	Chemical or ecological phenotype covaries with geographic-genetic structure	Adds organismal context beyond sequence divergence. Environmental plasticity and shared geography can generate correlated differences. Separate environmentally induced variation from stable lineage-associated differences. Evidence-derived synthesis.
Host-associated divergence	Phytophagous or fungivorous insects using distinct resources	Candidate lineages show repeatable host-use differences	Host association may provide an independent ecological discriminator. Host availability, geographic segregation, or learned use may mimic lineage specificity. Sample sympatric populations and test host association independently of genetic assignment. Evidence-derived synthesis.
Multiclass ecological concordance	Candidate taxa assessed with morphology, molecules, and ecological associations	Ecological differences align with more than one non-ecological evidence class	Concordance is stronger when ecological information is measured independently. Shared sampling structure can create pseudo-independence among evidence classes. Evaluate covariance among evidence streams before treating agreement as replication. Proposed dependence-aware interpretation.
Ecological–molecular discordance	Candidate lineages with conflicting mitochondrial, nuclear, or ecological patterns	Host or habitat association does not map cleanly onto all molecular partitions	Discordance should trigger alternative-history testing rather than forced consensus. Introgression, incomplete lineage sorting, recent divergence, or sampling may remain unresolved. Retain competing explanations and avoid taxonomic action based on ecological association alone. Proposed dependence-aware interpretation.

Behavioral and reproductive evidence

Behavioral and reproductive data occupy a distinctive position because they can test interactions among candidate lineages rather than merely characterize differences between them. Their value, however, depends on what is measured. Courtship behavior, mate recognition, pheromonal divergence, mating frequency, hybrid viability, and fertility address different stages of reproductive isolation and should not be collapsed into a single binary variable.

Comparative analysis of model-based species delimitation against reproductive isolation in *Drosophila* showed substantial, but incomplete, correspondence between coalescent-delimited entities and biologically measured reproductive separation [28]. The importance of this result lies in the mismatch as much as the agreement: genomic or coalescent structure may anticipate, lag behind, or diverge from reproductive boundaries, and reproductive isolation itself can be partial. Consequently, reproductive evidence can provide an unusually direct test of biological separation without functioning as a universal criterion that every insect taxon must satisfy.

Behavioral evidence is also especially vulnerable to extrapolation. Differences observed under laboratory choice tests may not transfer to field encounter rates, while absence of observed mating can reflect geography, seasonality, sex ratio, or experimental design rather than intrinsic isolation. Conversely, shared host use or geographic overlap cannot be treated as evidence of free interbreeding unless mating or gene-exchange processes are actually assessed. In this review, behavioral and reproductive observations therefore receive high interpretive relevance when they directly address lineage interaction, but their evidential weight remains conditional on ecological realism, life stage, sex, opportunity for encounter, and the specific component of reproductive isolation measured.

Patterns of congruence

Congruence is most informative when evidence classes interrogate different properties of the same candidate boundary and nevertheless support compatible interpretations. Genome-wide data in the *Melanoplus scudderi* complex resolved relationships that had appeared paraphyletic with earlier markers and supported morphologically recognized species, showing that genomic evidence can corroborate rather than displace organismal diagnosis [29]. In nymphalid butterflies, reconciliation of classical taxonomy with multispecies-coalescent inference similarly demonstrated that genetic structure can be interpreted alongside existing species hypotheses rather than converted automatically into additional species [30].

The strongest integrative cases also expose why independence matters. Phylogenomic delimitation of the *Temnothorax salvini* group combined genomic, morphological, and geographic information to support additional diagnosable species [31]. Molecular delimitation of *Gnaptorina* likewise produced broad correspondence between molecular hypotheses and morphospecies while retaining method-dependent uncertainty [32]. Agreement therefore becomes more persuasive when independently acquired observations converge at the same boundary, not simply when several analyses reuse the same sequences or specimens.

Scale also changes the meaning of concordance. Agreement between morphology and genome-wide structure across a regional species complex is not equivalent to agreement among a few populations sampled from one locality. The *Melanoplus* example shows that genome-scale data may clarify relationships while retaining correspondence with established morphology [29]. The *Temnothorax* analysis similarly illustrates that concordance becomes more interpretable when geography and morphology are evaluated beside phylogenomics rather than treated as consequences of the same clustering result [31]. Thus, congruence is strongest when it survives changes in analytical scale and when the evidence classes were not defined using one another.

For this review, congruence is consequently divided into independent concordance, conditional concordance, and pseudo-concordance. Independent concordance occurs when distinct evidence-generating processes support a compatible boundary. Conditional concordance occurs when agreement is meaningful but limited by geography, sampling, life stage, or analytical assumptions. Pseudo-concordance is proposed for apparent replication that derives substantially from shared genealogy, shared sampling, correlated characters, or repeated analysis of the same underlying data. This distinction does not assign numerical weights; it identifies when agreement can and cannot reasonably be treated as corroboration.

Because these forms of agreement differ in biological scale and inferential independence, their taxonomic meaning is more clearly contrasted in a cross-scale grid than through simple vote counting.

Table 2. When concordant insect evidence constitutes corroboration rather than repeated measurement

Congruence mode	Evidence classes compared	Agreement pattern	Independence-adjusted meaning	Dependence audit
Independent concordance	Candidate lineages measured through genuinely different evidence processes	Compatible morphological, genomic, ecological,	Stronger corroboration because major error sources are less likely to	Independence is rarely absolute. Verify that sampling and classification were not conditioned on the same prior grouping

		or reproductive boundaries	be shared. Proposed interpretation.	
Conditional concordance	Geographic, life-stage, or taxon-restricted comparisons	Multiple classes agree within the sampled context	Supports a bounded species hypothesis. Proposed interpretation.	Agreement may disappear with broader sampling. Extend sampling across contact zones, sexes, stages, and populations
Within-class replication	Multiple loci, algorithms, or morphological characters	Similar partitions recur within one evidence family	Increases confidence in that measurement domain. Proposed interpretation.	Shared genealogy or character development limits independence. Test an evidence class generated by a different biological process
Cross-scale concordance	Organismal diagnosis and population/genomic structure coincide	Phenotypic and genomic boundaries align	Links diagnosability with lineage structure. Evidence-derived synthesis.	Neither class alone establishes every species property. Examine ecological or reproductive consequences where feasible
Algorithmic concordance	Several delimiters recover similar clusters	Analytical outputs agree	Supports robustness to some method choices. Evidence-derived synthesis.	Same input data can make outputs statistically dependent. Change data type or biological test, not only algorithm

The figure below compresses this reasoning by retaining evidence classes as parallel analytical lanes, then separating genuine corroboration from dependence and unresolved conflict before taxonomic interpretation.

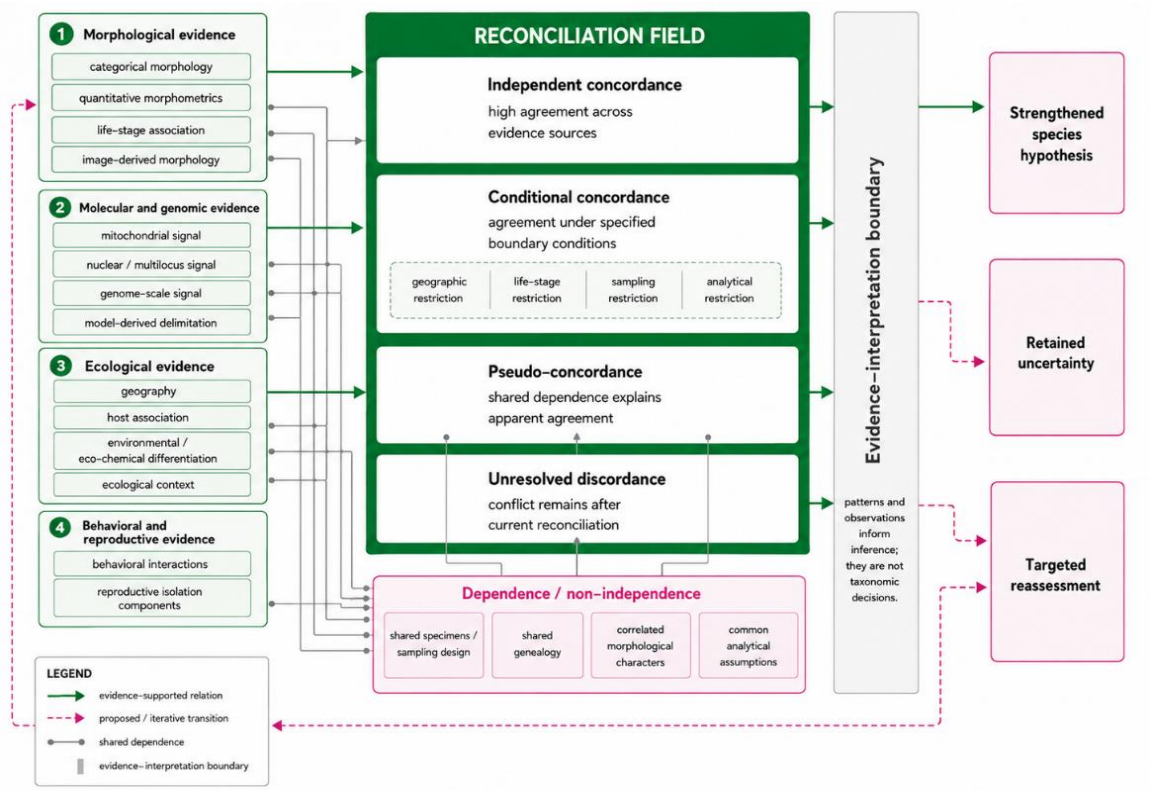


Figure 1. Congruence gains taxonomic force only after dependence and inference boundaries are exposed

why data classes conflict

Conflict is not a single biological signal. In Megasternini water scavenger beetles, molecular phylogeny aligned more closely with geography than with some traditional morphological groupings, consistent with repeated parallel evolution of morphological traits [33]. In *Gymnosoma* parasitoid flies, extensive genome-wide data did not cleanly differentiate all named morphospecies, showing that morphological diagnosis and genomic differentiation can remain incongruent even with thousands of loci [34]. Anchored-hybrid-enrichment analysis of

flesh flies likewise challenged traditional classification and implicated convergence in characters previously treated as phylogenetically informative [35].

These cases illustrate three non-equivalent sources of discordance: biological history, measurement limitation, and inferential failure. Introgression or incomplete lineage sorting can cause loci to record histories different from a species history; convergent morphology can make unrelated lineages appear similar; limited sampling can miss geographic or life-stage variation; and model misspecification can generate confident but misleading genomic relationships. The reviewed evidence does not justify diagnosing any one process from discordance alone. Conflict should instead be treated as a request for competing explanations, with targeted data capable of discriminating among them.

Marker disagreement deserves the same restraint. Mitochondrial and nuclear 3RAD evidence in *Stenocorse* did not delimit lineage structure identically [17]. Ambush-bug analyses likewise retained mitochondrial–nuclear discordance despite the addition of morphometric and ecological information [27]. These examples make introgression, incomplete lineage sorting, or population history legitimate alternatives, but they do not allow any one process to be inferred merely from the existence of discordance. Analytical conflict can also imitate biological conflict: the Adephaga study showed that model choice and excessive trimming could alter apparently well-supported phylogenomic relationships [22]. Before taxonomic revision, conflict should therefore be localized to the evidence-generating stage at which it first appears.

evidential weighting and dependence

Evidential weight should therefore be conditional rather than assigned by data class. Phylogenomic scholarship emphasizes that large datasets reduce some forms of sampling error while leaving orthology problems, taxon sampling, model choice, and systematic error capable of influencing inference [36]. The same logic applies across evidence classes: a highly diagnostic trait can be weak evidence for history if convergence is plausible, while a genomic split can be weak evidence for species status if it primarily reflects population structure.

The dependence-aware scheme proposed here evaluates five questions: what is directly observed; how close that observation is to the taxonomic proposition; whether another evidence stream is genuinely independent; which error processes could generate the same pattern; and what competing explanation remains viable. Weight rises when evidence is relevant, independently generated, robust to plausible analytical alternatives, and informative against competing hypotheses. Weight falls when agreement is produced by reused data, correlated characters, restricted sampling, or an untested model assumption. These are qualitative conditions, not scores.

Relevance also depends on the proposition being tested. Reproductive isolation addresses lineage interaction more directly than a sequence cluster, but its absence from a study does not negate a species hypothesis; comparative *Drosophila* evidence shows that coalescent boundaries and measured isolation correspond incompletely [28]. Conversely, the demonstrated tendency of multispecies-coalescent methods to delimit population structure means that strong genetic partitioning requires interpretation beyond model support [2]. Evidential weight is therefore proposition-specific: evidence useful for identification, historical relationship, reproductive separation, or geographic structure should not automatically be transferred to another inferential task.

The principal failure modes and corrective tests are summarized below because their interaction is easier to compare as conditional states than as a ranked evidence hierarchy.

Table 3. Dependence conditions that change the meaning of evidential weight in integrative insect taxonomy

	Relevance × independence		**Dependence control**
Evidential-weight condition	**Observed configuration**	**How weight should change**	**Failure and corrective independence test**
High relevance, low independence	Several analyses support one boundary from the same loci or specimens	Confidence within the dataset increases more than cross-class corroboration. Proposed.	Pseudo-replication of evidence. Add independently generated organismal, ecological, or reproductive observations
High independence, limited relevance	Distinct ecological or phenotypic differences occur without direct evidence of lineage separation	Adds context but cannot alone settle species status. Proposed.	Inferential overreach. Test whether the difference persists independently of geography or environment
High dimensionality, uncertain model fit	Genome-scale results have strong internal support	Data volume does not neutralize systematic error. Evidence-derived synthesis.	Model-driven false confidence. Conduct sensitivity analyses and alternative model checks

Diagnostic morphology, convergence plausible	Candidate taxa are readily distinguished phenotypically	Diagnosis remains useful but historical interpretation is uncertain. Evidence-derived synthesis.	Homoplasy. Compare independent genomic history and character evolution
Multiple independent classes, bounded sampling	Distinct evidence processes converge in sampled populations	Species hypothesis is strengthened within sampled scope. Proposed.	Geographic or life-stage overgeneralization. Expand taxonomic, geographic, sex, and stage coverage

Critical synthesis

The review supports neither molecular supremacy nor equal weighting of all observations. The more defensible unit of appraisal is the evidence-generating relationship between a measurement and the taxonomic proposition. Morphology may provide direct diagnosability yet share developmental correlations among characters. Mitochondrial and nuclear signals may appear to offer independent replication while recording partially different genealogical histories. Ecology may contribute an external axis of differentiation but remain confounded with geography. Reproductive evidence may directly address lineage interaction but be unavailable or experimentally unrealistic for many insects.

The central proposal is therefore a dependence-aware reconciliation architecture: preserve evidence classes separately through measurement, expose dependencies before interpreting concordance, represent conflict as competing explanations rather than a failed vote, and cross an explicit interpretation boundary before taxonomic action. This architecture organizes existing evidence; it is not itself validated as a predictive or quantitative decision rule.

Future standards

Future integrative taxonomy should report not only which datasets agree but why they can reasonably be regarded as independent. Specimen vouchers, linked life stages, accessible image and sequence data, transparent analytical code, and explicit sensitivity analyses would make disagreements more diagnosable. Genome-scale studies should demonstrate robustness to plausible model and filtering choices rather than treating locus number as sufficient assurance, while morphological and ecological studies should document sampling across sex, stage, geography, and environmental conditions relevant to the claimed boundary.

Taxonomic conclusions should also retain unresolved alternatives when available evidence cannot distinguish convergence, introgression, lineage sorting, plasticity, or population structure.

Digitized collections can connect historical specimens with molecular and occurrence data, but uneven preservation and representation must remain explicit [3]. Computer-vision tools can increase morphological throughput, yet taxonomic use requires validation beyond the training domain [13]. Future datasets should preserve provenance linking specimen, image, life stage, sequence, locality, ecological observation, and analytical decision. Such linkage would make concordance and conflict auditable rather than merely reported.

Progress depends less on accumulating nominal “lines of evidence” than on designing observations that discriminate among those explanations.

Conclusion

Integrative insect taxonomy is strongest when congruence is interpreted rather than counted. Morphological, molecular, ecological, and behavioral evidence differ in what they measure, how errors arise, and how directly they bear on species boundaries. A dependence-aware approach preserves those differences, treats conflict as scientifically informative, and separates detection from interpretation. Its value is therefore not a universal weighting formula, but a disciplined way to decide when agreement corroborates a taxonomic hypothesis and when uncertainty should remain visible.

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