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Continuous Genomic Variation Challenges Insect Species Boundaries When Taxonomic Decisions Depend on Artificial Thresholds

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ABSTRACT

Genome-scale data have expanded the resolution of insect systematics, yet greater resolution does not guarantee that categorical species boundaries become biologically clearer. Population structure, introgression, geographic clines, recombination landscapes and marker-specific histories can generate discontinuities that are real in the data while remaining ambiguous in taxonomic meaning. This article develops a proposed threshold-sensitivity framework for deciding when genomic partitions are sufficiently stable and biologically corroborated to inform species hypotheses without treating analytical cut-offs as species criteria. The framework separates continuous population structure from biological discontinuity, represents gene flow as graded and potentially asymmetric, interprets geographic clines as spatial evidence rather than categorical boundaries, and distinguishes barrier-consistent genomic islands from differentiation amplified by genomic architecture. Taxonomic conclusions are then evaluated across a reasonable analytical neighborhood comprising defensible changes in marker set, data quantity, method, parameterization and reference geography. Stability across that neighborhood increases confidence only when supported by evidence with partly independent error processes; instability instead identifies where taxonomic rank remains contingent on analytical choice. The framework is qualitative and requires prospective evaluation across insect radiations, hybrid zones and cryptic species complexes. Its purpose is not to eliminate thresholds from analysis, but to prevent operational thresholds from being mistaken for biological discontinuities.

Keywords: Species delimitation, Population genomics, Gene flow, Geographic clines, Genomic islands, Integrative taxonomy

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Introduction

Genomic species delimitation in insects increasingly operates at a resolution where biological continua can be partitioned into apparently discrete entities. The analytical problem is not simply whether a method detects structure, but whether the taxonomic conclusion survives plausible changes in sampling, model assumptions, population structure and geography. Genomic delimitation can over- or under-partition diversity under different demographic and analytical conditions, making robustness of the inferred partition a separate question from the magnitude of genomic differentiation itself [1]. DNA barcodes illustrate the same inferential distinction at a simpler marker scale: a barcode cluster or gap can be operationally useful while still requiring biological and geographic interpretation before it is treated as a species boundary [2].

This distinction matters especially in insect complexes in which molecular, genomic, ecological and reproductive data operate with different failure modes. Work on the *Bemisia tabaci* complex shows that these evidence classes are not interchangeable and that robust delimitation depends on their joint interpretation rather than on a single marker or threshold [3]. Whole-genome analyses of the *Papilio machaon* complex further show that genomic differentiation can be hierarchical across population, subspecific and species scales while historical gene flow remains detectable [4]. Conversely, integrative phylogenomics in the *Acromyrmex octospinosus* complex has supported revision in both directions, retaining some lineages while synonymizing historical names that were not independently supported [5]. Genomic resolution therefore does not imply a one-way tendency towards taxonomic splitting.

The central problem addressed here is consequently one of inferential dependence. When a categorical taxonomic outcome exists only because an analyst chose one distance threshold, clustering level, marker subset or model configuration, the discontinuity is partly analytical even if the underlying genomic variation is genuine. This article proposes a threshold-sensitivity framework that asks whether a species hypothesis remains stable across a reasonable analytical neighbourhood and whether the stable portion of that hypothesis is supported by evidence that approaches the biological boundary independently. The framework does not define a universal threshold-free species concept. Instead, it separates observed genomic pattern, biological process and taxonomic inference so that uncertainty remains visible when continuous variation is forced into categorical nomenclature.

Materials and Methods

The framework was constructed as a qualitative comparative architecture rather than as a new empirical delimitation analysis. Evidence was organized around five sources of taxonomic sensitivity: data quantity, marker composition, delimitation method or model, geographic reference scope and independence of corroborating evidence. These dimensions were selected because the literature contains direct examples in which changing one of them changes the inferred partition or its interpretation. No numerical sensitivity score, optimal parameter range or universal pass threshold is proposed.

Data-volume sensitivity is included because phylogenomic delimitation of *Stylops* demonstrated that inferred species number can change with the number of loci analysed under a specific delimitation workflow [6]. The inference permitted by that result is limited: locus number can affect the partition, not that adding loci generally causes oversplitting. Reference-neighbourhood sensitivity is included because insect identification outcomes can vary with similarity threshold, taxon and geographic distance to reference material [7]. Although identification and species delimitation are not equivalent, this result establishes that an apparently discrete molecular assignment can depend on the composition and spatial scope of the comparison set.

A second component separates analytical entities from species hypotheses. The multispecies coalescent can delimit population structure that should not automatically be interpreted as species [8]. Single-locus delimiters likewise differ in assumptions and can generate non-equivalent partitions from the same general class of sequence evidence [9]. Accordingly, the proposed framework treats algorithmic entities as intermediate analytical objects: they may support a species hypothesis, but they do not contain the taxonomic conclusion within the model output. The final component is integrative adjudication. In the *Bactrocera frauenfeldi* complex, strong island-associated genomic structure did not justify all historical species partitions; phylogenomics combined with morphology and biogeography instead supported synonymy and exposed limitations of COI-based diagnosis [10]. This case motivates a framework rule that analytical stability must be evaluated alongside evidence independence. Stability across correlated algorithms is weaker evidence than stability accompanied by morphology, ecology, reproductive information or genomic histories that fail for different biological reasons. The proposed framework therefore asks two sequential questions: how sensitive is the partition to defensible analytical change, and what independent evidence supports interpreting its stable component as a biological discontinuity?

Results and Discussion

The evidence resolves several states between panmixia and strongly corroborated species separation. Range-wide population genomics of *Lymantria dispar* reveals nested geographic structure useful for phylogeographic and subspecific interpretation, but such operational population assignment is not itself a species test [11]. At the other end of the interpretive spectrum, *Plagiolepis pyrenaica* was supported as a cryptic species by concordant

phylogenomic, morphometric and demographic evidence [12]. These contrasting cases demonstrate why the magnitude of structure cannot be mapped directly onto taxonomic rank without considering what other evidence converges on the same partition.

Intermediate cases are particularly informative. In an alpine diving beetle, genomic, morphological and physiological differentiation coexists with introgression, supporting interpretation as rapid ecotypic differentiation and incipient speciation rather than requiring an already completed species boundary [13]. A genomically distinctive form within the *Anopheles gambiae* complex similarly warranted provisional recognition while limited regional sampling and incomplete validation constrained stronger taxonomic claims [14]. Candidate or incipient status is therefore not an evidential failure; it is a legitimate representation of uncertainty when the genomic pattern is stronger than the available evidence for a discrete biological boundary.

The strongest warning against what is here proposed as structure-to-boundary slippage comes from a grasshopper species complex in which deep genomic structure was strongly associated with geography and connectivity yet did not support the current taxonomic designations [15]. This does not imply that geographic structure is never taxonomic. It establishes that structure and species rank are different inference targets. Within the proposed framework, continuous population structure is therefore represented not as a single gradient of weak to strong divergence but as potentially nested partitions whose taxonomic relevance depends on analytical stability, geography, historical process and independent corroboration.

Gene flow gradients

Gene flow provides another domain in which binary criteria are poorly matched to observed insect genomic patterns. In *Formica* wood ants, extensive hybridization occurs among several species while multiple parental species remain genomically distinguishable, producing semipermeable rather than simply open or closed boundaries [16]. *Melitaea* butterflies provide an even stronger challenge to a simple cut-off: substantial introgression can be highly asymmetric while differentiated species remain recognizable [17]. These findings do not establish a general amount of gene flow compatible with species status; they show that gene flow must be characterized by magnitude, direction and genomic distribution.

The opposite end of the spectrum is equally important. Replicated Alpine contact zones between *Erebia* sibling species show rare hybridization and little or no detectable introgression, illustrating a low-permeability boundary without providing a universal criterion for species status [18]. Other systems demonstrate why the mechanism behind restricted gene flow also requires caution. In the *Andrena proxima* complex, low gene flow and phenological differences accompany species differentiation, whereas a possible contribution of *Wolbachia* remains mechanistically plausible rather than proven [19]. Correlation between a putative isolating factor and a genomic discontinuity should therefore not be promoted to a causal species mechanism without targeted evidence. Gene flow can also be marker-specific. In a large tephritid pest complex, mitochondrial introgression reduced COI diagnosticity while nuclear genomic data retained differentiation among taxa [20]. A threshold applied to one genome can consequently describe the permeability of that marker history rather than the permeability of the lineage as a whole. The proposed gene-flow gradient therefore has four non-equivalent dimensions: overall extent, directionality, genomic localization and geographic context. Temporal scale is a fifth qualifier because present-day hybridization and historical introgression need not indicate the same boundary state.

Because these dimensions cannot be recovered efficiently from a single “gene flow present/absent” statement, the cross-scale grid below separates permeability states from the additional tests required before they are translated into taxonomic conclusions.

Table 1. Gene-flow gradients as cross-scale boundary states rather than a binary species criterion

Boundary state	Taxonomic context	Genomic signal	Boundary interpretation and condition	Validation and status
Semipermeable, asymmetric, and low-permeability states				
Semipermeable boundary	Differentiated species with recurrent hybridization	Genome-wide ancestry remains structured while admixture occurs	Gene flow does not by itself collapse the species hypothesis Permeability may differ among species pairs, loci and localities	Test ancestry and barrier strength across multiple populations Evidence-derived

Asymmetric introgression	Directionally unequal exchange between differentiated lineages	Introgressed ancestry is stronger in one direction or lineage	One amount of gene flow cannot represent the boundary Historical demography and genomic region may alter inferred direction	Estimate direction and genomic localization separately Evidence-derived
Low-permeability contact	Closely related taxa in geographic contact	Hybrids are rare and introgression is minimal across replicate contacts	Stronger support for discontinuity, but not a universal cutoff Contact history and opportunity for hybridization remain relevant	Replicate the boundary across contact zones Evidence-derived
Multifactor and marker-specific permeability				
Multi-factor restricted flow	Differentiation coincides with phenology or another candidate isolating factor	Genetic and ecological separation covary	Candidate mechanisms strengthen interpretation without proving causation Association is insufficient for mechanistic attribution	Test candidate isolating processes directly Evidence-derived
Marker-specific permeability	Mitochondrial and nuclear histories disagree	One genomic compartment crosses the boundary more readily	Marker failure need not indicate lineage collapse Introgression and incomplete lineage sorting affect markers differently	Compare independently inherited genomic compartments Evidence-derived
Integrated graded boundary				
Graded boundary state	Synthesis spanning the states above	Joint pattern across extent, direction, loci, geography and time	Use multidimensional permeability rather than zero/nonzero gene flow No validated numerical boundary is assumed	Prospectively test the proposed representation Proposed

Geographic clines

Geographic clines turn genomic continuity into an explicitly spatial problem. Cline location, width and shape encode different information, and their interpretation depends on model specification rather than on visual sharpness alone [21]. A steep ancestry transition may be consistent with a barrier, but neither slope nor width constitutes a universal taxonomic threshold. Spatial sampling therefore determines not only the precision of a cline estimate but also which portion of the genomic continuum becomes visible to the analyst.

Historical processes further complicate interpretation. Genomic structure in *Aglaia urticae* reflects repeated differentiation and admixture through glacial cycles, showing that present-day geographic transitions can integrate earlier isolation and secondary contact rather than represent a single contemporary barrier process [22]. In *Anopheles messeae* and *Anopheles daciae*, differentiation, inversion frequencies and hybridization vary across Eurasia, demonstrating that a boundary characterized at one locality may not retain the same genomic form elsewhere [23]. Species-level inference must therefore record where a discontinuity occurs and how consistently it is expressed across the range.

Hybrid-zone genomics can add biological depth without removing this spatial conditionality. In scarce swallowtail butterflies, genomic regions showing reduced current hybridization also carry evidence of longer-term resistance to gene flow [24]. This strengthens a barrier interpretation for those regions, yet the result remains heterogeneous across the genome. The proposed framework consequently treats geographic clines as spatial evidence that can support, weaken or localize a species hypothesis, not as a geometric substitute for that hypothesis. A robust boundary should remain interpretable when sampling is extended across adjacent geography and when historical and current processes are distinguished.

Genomic islands

Genomic islands are especially vulnerable to being converted from descriptive patterns into categorical taxonomic evidence. Their interpretation becomes stronger when differentiated regions are tied to independently characterized traits or barriers. In *Heliconius*, a small set of genomic regions carrying ecological and reproductive

differences remained differentiated amid extensive genomic homogenization in a documented hybrid-speciation system [25]. This provides a strong positive case in which localized genomic differentiation has biological content beyond an arbitrary outlier threshold.

The converse failure mode is equally well supported. Between *Drosophila yakuba* subspecies, many divergence islands are associated predominantly with chromosomal inversions and low-recombination regions [26]. In a seaweed fly, large inversions structure pronounced genomic variation across multiple geographic scales within a species [27]. High differentiation can therefore be generated or amplified by genomic architecture without mapping directly onto a species boundary. Recombination rate, structural variation and linked genomic effects must be considered before an island is interpreted as evidence of a barrier locus.

Replication offers one route to stronger inference. Comparative use of replicate hybrid zones can test whether the same genomic regions repeatedly resist gene flow rather than appearing as local or stochastic outliers [28]. Repetition is not equivalent to causality, but it increases the ability to distinguish a persistent barrier-consistent pattern from one produced by local genomic context.

The interpretive problem is therefore better represented as conditional states than as a ranking of island “strength.” The matrix below separates cases in which biological interpretation is independently supported from those in which genome architecture or incomplete validation can generate the same visual signature of localized differentiation.

Table 2. Conditional interpretation of genomic islands when localized differentiation has multiple biological and analytical causes

Island state	Genomic pattern	Biological setting needed for interpretation	Failure mode	Taxonomic consequence with validation state
Barrier-consistent versus architecture-amplified				
Trait-linked barrier-consistent island	Localized differentiation persists despite extensive background introgression	Independent ecological or reproductive traits are linked to the region	Treating an exceptional system as a universal rule	Can strengthen a boundary hypothesis when other evidence converges Link genotype, trait and restricted gene flow independently Evidence-derived
Architecture-amplified island	High differentiation coincides with inversions or low recombination	Structural and recombination landscapes are characterized	Mistaking suppressed recombination for a barrier locus	Weak species evidence if architecture explains the peak Reanalyse after controlling for inversions and recombination Evidence-derived
Intraspecific versus replicated candidates				
Intraspecific inversion island	Strong regional differentiation occurs within a recognized species	Structural variants segregate across populations or environments	Inferring species rank from differentiation magnitude	Demonstrates that large peaks can remain population-level Test interpretation across geographic scales Evidence-derived
Replicated barrier candidate	Similar differentiated regions recur across independent contact zones	Comparable hybrid-zone histories and sampling are available	Assuming repeatability proves mechanism	Stronger barrier-consistent evidence, but not a species criterion Replicate clines and introgression patterns independently Evidence-derived
Unresolved and context-qualified states				
Unresolved island	Localized differentiation lacks independent biological or architectural explanation	Functional, structural or recombination evidence is incomplete	Converting an outlier statistic directly into a taxonomic character	Retain uncertainty rather than force a split Target structural, functional and gene-flow validation Proposed
Context-qualified island class	Synthesis integrating the states above	Recombination, trait, replication and boundary	Creating a hidden numerical	Supports qualitative evidence weighting, not a cutoff

evidence are considered together	hierarchy of island importance	Test stability across defensible analytical choices
		Proposed

Arbitrary delimitation thresholds

A threshold becomes taxonomically problematic when changing it within a defensible analytical range changes the categorical conclusion while the underlying biological observations remain essentially unchanged. Marker selection is one source of such contingency. Universal single-copy orthologs improve genomic coverage and marker independence, but their performance still depends on completeness, taxon representation and analytical implementation; they do not generate a universal number of loci sufficient for delimitation [29]. Cross-method agreement can nevertheless be informative. In *Chanohirata*, several molecular delimitation approaches broadly converged with morphology, strengthening the species hypotheses in that particular leafhopper system [30]. Agreement is therefore useful when it reflects genuinely complementary information rather than repeated analysis of the same signal under closely related assumptions.

Geographic reference scope creates a second form of threshold sensitivity. An Italian odonate barcode inventory revealed apparent splits and taxonomic warnings whose interpretation changed when Holarctic variation was considered [31]. A locally conspicuous barcode gap can therefore become part of a wider geographic continuum. Conversely, a threshold-originated hypothesis need not remain weak indefinitely: cryptic skipper species initially suggested by barcode and ecological differences received independent support from nuclear genomic evidence [32]. The relevant distinction is not threshold versus no threshold, but threshold dependence versus evidence convergence.

The framework therefore proposes a reasonable analytical neighbourhood: the set of scientifically defensible marker subsets, sampling scopes, model choices and parameterizations over which the same taxonomic proposition is stress-tested. No numerical width is assigned to this neighbourhood. A partition that disappears after minor defensible analytical changes should remain taxonomically provisional. A partition that remains stable gains analytical credibility, but species-level interpretation still requires evidence approaching biological discontinuity independently.

This relationship between analytical stability and biological corroboration is difficult to express as a linear decision sequence. **Figure 1** therefore places genomic partitions in a qualitative state space in which the same apparent discontinuity can carry different taxonomic meaning depending on sensitivity to analytical choice and the strength of independent biological evidence.

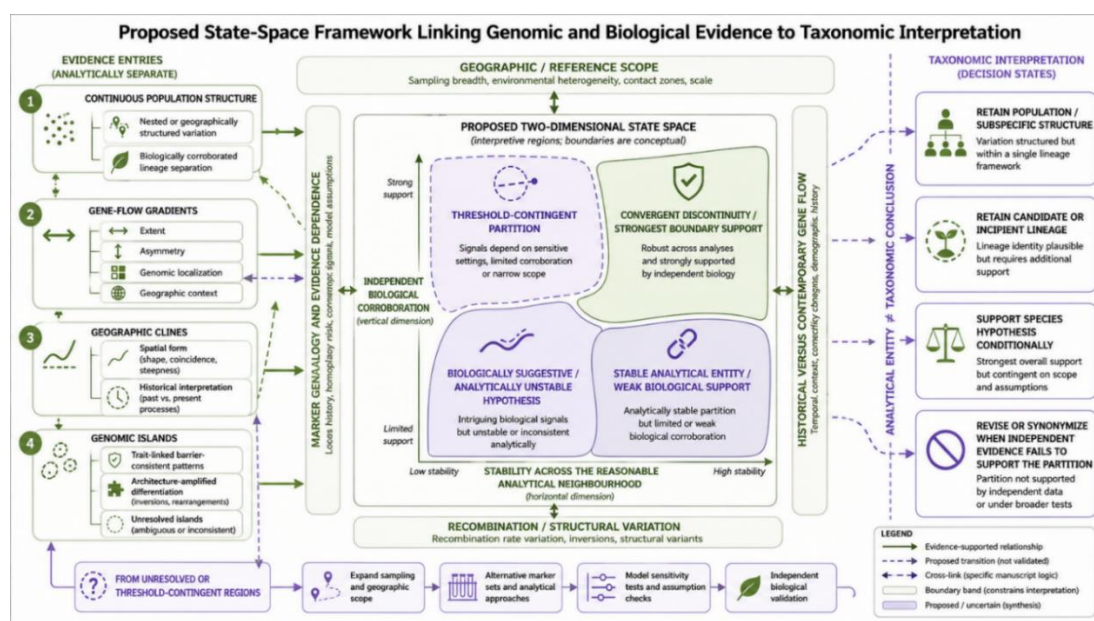


Figure 1. When the same genomic discontinuity changes meaning: analytical stability versus biological corroboration in insect species delimitation

Biological versus analytical discontinuities

The preceding evidence supports a distinction between a discontinuity that exists in measured data and one that justifies a biological species hypothesis. Multispecies-coalescent analyses illustrate why these cannot be collapsed: in butterflies, classical taxonomy and coalescent delimitation recovered partly different entities, and their reconciliation allowed cryptic diversity to be recognized without elevating every structured population to species rank [33]. The analytical boundary therefore lies between the entity constructed by a method and the biological proposition that the entity represents an independently evolving species-level lineage.

Analytical error can operate in the opposite direction as well. In the *Melanoplus scudderi* complex, species that appeared paraphyletic with limited molecular information became supported by larger phylogenomic datasets, demonstrating that apparent conflict may result from insufficient phylogenetic signal rather than genuine biological continuity [34]. Thus, neither splitting nor lumping is intrinsically the conservative outcome. The critical question is whether an apparent discontinuity persists after the major known analytical alternatives have been examined.

The article therefore proposes three distinct inference objects: observed or evidential discontinuity, describing a detectable break or concentration in measured data; biological discontinuity, describing independently supported restriction, differentiation or lineage processes relevant to species separation; and analytical discontinuity, describing a categorical partition produced or materially sharpened by data processing, model choice, marker properties or sampling. These categories can overlap. Their value is to prevent the taxonomic conclusion from being silently embedded inside the analytical procedure.

Because the consequences of confusing these states are easier to compare by inference pathway than by narrative description, **Table 3** maps characteristic signals to their biological alternatives and taxonomic consequences.

Table 3. Separating observed genomic breaks, biological processes and analytical partitions before assigning insect species rank

Focal discontinuity	Observed signal	Candidate biological process	Analytical mimic	Taxonomic consequence	Discriminator	Decision state
Geographic and coalescent partitions						
Geography-aligned deep structure	Strong genomic clustering	Restricted dispersal, historical separation or lineage divergence	Isolation by distance, uneven sampling or landscape connectivity	Species rank remains unresolved from structure alone	Broaden geographic sampling and test independent biological evidence	Evidence-derived
Coalescent-delimited entity	Genealogical population partition	Independent lineage history	Population structure captured by the species model	Analytical entity must not be equated directly with species	Compare morphology, ecology, reproductive evidence and geography	Evidence-derived
Introgression and localized islands						
Introgressed but differentiated lineage	Distinct ancestry with gene exchange	Semipermeable reproductive boundary	Marker-specific history or asymmetric sampling	Gene flow does not automatically negate species status	Resolve direction, locus distribution and spatial consistency of introgression	Evidence-derived
Localized differentiation island	Strong regional genomic divergence	Barrier-linked ecological or reproductive differences	Inversion, low recombination or linked selection	Island strengthens species inference only when mechanism is independently supported	Characterize recombination, structural variation and associated traits	Evidence-derived

Cross-evidence conflict and final separation						
Apparent molecular–morphological conflict	Gene tree conflicts with morphological species	Rapid radiation or complex lineage history	Insufficient genomic signal or model sensitivity	Conflict is not automatically biological discordance	Increase independent information and retest phylogenetic stability	Evidence-derived
Observed–biological–analytical separation	Any discontinuity requiring interpretation	Process compatible with lineage separation	Partition contingent on method, threshold or sampling	Keep taxonomic conclusion outside the measurement procedure	Stress-test the partition and seek independently generated support	Proposed

Threshold-free decision logic

A threshold-free decision rule does not require analyses without thresholds. Most clustering, alignment, filtering and model-selection procedures contain operational choices. The proposed logic instead prevents a particular operational cut-off from becoming the biological definition of a species.

First, the observed variation is characterized without immediately assigning species rank. Second, any candidate partition is stress-tested across defensible changes in markers, data quantity, parameterization, sampling scope and delimitation method. Third, the analysis asks whether the stable partition corresponds to evidence approaching a biological boundary. Mitonuclear discordance in Central European bees demonstrates the value of this separation: independent nuclear phylogenomics can clarify species limits when mitochondrial history is discordant, but this does not justify assigning universal supremacy to nuclear data [35]. Evidence is weighted by the failure mode relevant to the proposition, not by a fixed hierarchy of molecular technologies.

Fourth, evidence with partly independent error processes is compared. Genome-scale UCE data in *Sericomyrmex* resolved a recent ant radiation and revised historical species hypotheses without relying on a universal genetic-distance threshold [36]. The relevant outcome was not “more loci therefore more species,” but a revised taxonomic interpretation conditioned by phylogenomic structure and systematic context.

The resulting proposed threshold-free decision logic has four legitimate outcomes: retain population or subspecific structure; retain a candidate, ecotypic or incipient lineage; support a species hypothesis conditionally when analytical stability and independent biological evidence converge; or revise/synonymize a named taxon when the genomic partition lacks independent support. These are not certainty grades and are not ordered numerically. They are inference states designed to preserve uncertainty instead of converting a continuous genomic landscape into a categorical result prematurely.

The principal implication is that the reliability of an insect species boundary depends less on crossing one analytical threshold than on whether the conclusion survives the alternatives that could plausibly have generated it. Contemporary genomic delimitation already recognizes substantial model, sampling and geographic sensitivity [1]. The proposed framework reorganizes these known limitations around the stability of the taxonomic conclusion, rather than around performance of any particular algorithm.

Several evidence patterns make this distinction necessary. The *Stylops* result demonstrates that altering genomic data volume can change the number of inferred entities [6]. The grasshopper counterexample shows that deep genomic structure can be strongly geographic without supporting existing species designations [15]. Conversely, extensive asymmetric introgression can coexist with differentiated *Melitaea* species [17]. Together these cases make a universal genomic-distance or gene-flow boundary scientifically difficult to justify.

Spatial and genomic heterogeneity add further complications. Cline geometry is informative only within an explicit spatial model [21], while hybrid-zone evidence can identify regions with persistent resistance to introgression without making the remainder of the genome uniformly impermeable [24]. Likewise, genomic islands may be magnified by inversions or suppressed recombination rather than uniquely marking reproductive barriers [26]. The same observed peak of differentiation can therefore support different biological interpretations after genomic architecture and spatial history are considered.

The framework also avoids an opposite error: treating uncertainty as evidence that species cannot be delimited. Integrative reconciliation can distinguish structured populations from supported species hypotheses [33], and independent nuclear phylogenomics can clarify boundaries when mitochondrial histories conflict [35]. Threshold

sensitivity should therefore operate as a diagnostic test of inference, not as an argument for systematic agnosticism.

Three validation priorities follow. First, future delimitation studies should report whether principal taxonomic conclusions are stable across defensible analytical alternatives rather than only reporting the selected analysis. Second, stability should be evaluated against evidence independence: agreement among several procedures operating on the same marker history should not be treated as equivalent to concordance among genomic, spatial, morphological, ecological or reproductive evidence. Third, difficult cases should be deliberately retained as candidate, incipient or population-level entities where evidence remains threshold-dependent. Such terminology better represents the current inferential state than a forced binary classification.

The framework remains conceptual. Its proposed analytical neighbourhood has no empirically validated width, and its decision states have not been prospectively benchmarked across insect orders. Taxa with unusual reproductive systems, extensive asexuality, hybrid origin, endosymbiont-associated incompatibilities or extreme geographic fragmentation may require additional criteria. Validation should therefore compare how often taxonomic conclusions remain stable when the framework is applied independently to well-characterized species complexes, recent radiations and broad geographic continua.

Conclusion

Continuous genomic variation does not eliminate species boundaries, but it makes the route from genomic pattern to taxonomic decision more explicit. Population structure, introgression, clines and genomic islands can each be biologically meaningful without carrying a fixed species-level interpretation. The proposed threshold-sensitivity framework therefore separates analytical partitions from biological discontinuities and asks whether taxonomic conclusions persist across defensible analytical choices and independent evidence. Where they do, species hypotheses become stronger; where they do not, uncertainty should remain visible. Taxonomy is thereby treated as evidence-bounded inference rather than the automatic consequence of crossing an analytical threshold.

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