Eurasia Specialized Veterinary Publication

Entomological Research Letters

ISSN: 3108-639X

2023, Volume 3, Issue 2, Page No: 136-147
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Available online at: www.esvpub.com/

Ecological Divergence, Reproductive Isolation, and Speciation Evidence Across Host-Associated Differentiation in Insects

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ABSTRACT

Host-associated differentiation is frequently interpreted as an early stage of ecological speciation, but the evidential steps between host use, population divergence, reproductive isolation, restricted gene flow, and species-level divergence are not interchangeable. This systematic evidence map organizes recent insect literature according to what each evidence class can actually establish. The mapped studies span phylogenetic, population-genomic, ecological, phenological, behavioral, reproductive, molecular, and comparative approaches. Across systems, host association often covaries with genetic or phenotypic differentiation, yet geography, environmental heterogeneity, lineage history, symbionts, incomplete lineage sorting, admixture, and continuing hybridization can generate competing explanations. Phenological displacement and assortative mating provide stronger evidence when they directly alter reproductive encounter or compatibility, but their magnitude and even direction can remain context dependent. We therefore distinguish observed host association from barriers to reproduction and from subsequent species-level inference. The central contribution is a proposed evidence-stage architecture that preserves concordant, discordant, incomplete, and reversible states rather than treating ecological divergence as an inevitable linear progression toward speciation.

Keywords: Host-associated differentiation, Ecological speciation, Reproductive isolation, Gene flow, Phenological isolation, Population genomics

Received: 11 September 2023
Revised: 04 December 2023
Accepted: 09 December 2023

How to Cite This Article: Bello A, Sule Z, Musa I, Adeyemi G, Youssef A. Ecological Divergence, Reproductive Isolation, and Speciation Evidence Across Host-Associated Differentiation in Insects. Entomol Res Lett. 2023;3(2):136-47.
https://doi.org/10.51847/tn1138rcGc

Introduction

Host-associated differentiation (HAD) occupies an unusually ambiguous position in insect evolutionary research. Genetic, phenotypic, or behavioral differences between populations using different hosts may represent structured populations, ecological specialization, partial reproductive isolation, or one component of a longer divergence process. These states cannot be treated as synonyms. A cross-system reassessment of host shifts explicitly distinguished evidence for HAD from evidence for evolved reproductive barriers, contribution to speciation, and evidence that host use initiated lineage splitting [1]. That distinction is especially important when genomic data reveal divergence without directly measuring mating, immigrant fitness, or contemporary gene exchange.

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Genomic approaches have expanded the ability to identify loci, genomic regions, and population histories associated with host use, while also showing that the genetic architecture of host shifts differs substantially among insect systems [2]. Conceptual work further distinguishes localized or "genic" differentiation from broader genomic coupling as reproductive barriers strengthen [3]. These ideas are useful inferentially, but neither genomic breadth nor host association alone establishes a completed species boundary.

This evidence map therefore asks a narrower question than whether host shifts "cause" insect speciation: what type of inference is warranted at each evidential stage between host-associated divergence and species-level separation? The analysis preserves ecological, behavioral, genomic, and reproductive evidence as analytically distinct classes and treats discordance among them as biologically informative rather than as noise. The article's principal synthesis is a proposed evidence-stage architecture developed later from those distinctions; it is not presented as a universal evolutionary sequence.

Materials and Methods

A retrospective literature search and verification exercise was conducted on 24 August 2026 with eligibility restricted to peer-reviewed publications from 2017 through 2023. Search coverage included Web of Science Core Collection, Scopus, Zoological Record, PubMed where relevant, publisher records, DOI-resolution resources, and citation chaining. The core search logic combined insect or arthropod terms with "host-associated differentiation," "host-associated divergence," "host race," "host shift," or "host specialization," and with reproductive isolation, speciation, gene flow, genomic differentiation, allochrony, phenology, assortative mating, or mate choice. Genomic, phylogenomic, species-delimitation, sensory, diapause, olfactory, hybridization, introgression, geography, environment, and *Wolbachia* terms were used as domain-specific extensions.

Reporting principles followed PRISMA 2020 for transparent review documentation [4] and PRISMA-S for source-specific search reporting [5]. However, exact database-native retrieval exports were not preserved in a form that allowed reconstruction of source totals, deduplication arithmetic, title/abstract exclusions, report retrieval, full-text exclusions, or final eligible-study counts. Those quantities were therefore neither estimated nor reverse-engineered, and no numerical prevalence claim is made from the reference corpus.

Studies were coded by insect taxon, host association, biological level, study setting, measured construct, ecological or reproductive barrier, genomic evidence class, competing explanation, and inference boundary. Molecular response, genomic differentiation, reproductive isolation, and species-level conclusions were kept separate. The evidence map also retained null mechanisms, admixture, incomplete lineage sorting, environmental contingency, and laboratory-to-field transfer limitations. The proposed synthesis classifies evidence by inferential strength without assigning numerical scores or assuming that lineages move irreversibly between classes.

Results and Discussion

The available evidence is taxonomically heterogeneous and cannot be interpreted as a census of how frequently host-associated speciation occurs across insects. Research attention itself may be selective: among plant-feeding arthropods, host-derived species naming was associated with a greater likelihood that HAD had been investigated [6]. Consequently, well-studied systems may reflect historical research emphasis as well as unusually strong biology.

Comparative studies nevertheless demonstrate breadth across major phytophagous lineages. Flea-beetle diversification incorporates repeated changes in host association over evolutionary time [7]. Nearctic oak gall wasps show frequent correlations between lineage splitting and shifts in host plant, host organ, or both, while leaving causal initiation unresolved [8]. Specialist *Strauzia* flies show both host shifting and host sharing during diversification [9], warning against treating specialization as a one-directional process. In *Morpho* butterflies, punctuational ecological changes correlate with diversification and wing-phenotype evolution, although this represents broader ecological-divergence evidence rather than a direct demonstration of host-mediated reproductive isolation [10].

Taxonomic coverage therefore supports comparison of multiple routes to divergence, but it does not justify an insect-wide frequency estimate. The strongest interpretation is that host-associated divergence has been documented across several orders using different evidence classes, with substantial imbalance in how intensively individual systems have been tested.

Host-use divergence

Host-associated genetic structure is most informative when host effects can be separated from spatial and environmental structure. In the gall wasp *Belonocnema treatae*, host association interacts with geography, showing that spatial population history cannot be treated as a nuisance variable external to HAD [11]. Forest tent caterpillar genomics likewise indicates joint contributions of host association, geography, and environment rather than discrete genomic clusters defined solely by host use [12].

Comparative evidence further challenges the expectation that similar host ecology should generate similar genomic outcomes. Leaf- and bud-galling sawflies using shared *Salix* hosts display contrasting patterns of host-associated genetic differentiation across related taxa [13]. In *Eumedonia eumedon*, host-associated structure is detectable at some analytical scales while geography remains important at broader scales [14]. Host-associated structure can also be useful without implying reproductive isolation: in an insect vector, genetic differentiation among host-associated populations was informative for source-population and dispersal inference [15].

Agricultural systems introduce still more alternative drivers. In *Myzus persicae*, host plants and insecticide exposure jointly shape genetic and clonal diversity [16]. In fall armyworm, genomic differences between host-associated forms are compatible with incipient divergence but do not establish completed speciation [17]. In the *Bemisia tabaci* complex, transcriptomic differences involving detoxification and plant-defence interactions help explain host-use variation, yet molecular expression differences remain below the evidential level required to demonstrate reproductive isolation [18].

Across these systems, host use can therefore correspond to at least four distinct situations: a host signal entangled with geography or environment, a lineage-specific genomic association, a population-structure marker useful for ecological inference, or molecular divergence whose reproductive consequences are unresolved. The proposed interpretation is that HAD should be treated as an attribution problem before it is treated as a speciation stage. Because those situations differ in what they permit a reader to infer, a conditionality matrix is more informative than a single continuum.

Table 1. Host-associated divergence states that change the interpretation of genetic or molecular differentiation

Taxonomic or methodological scope · Main evidence pattern	Measured construct · Principal uncertainty or failure mode	Synthesis consequence
Host–geography interaction		
Spatial population genomics **Host signal changes with geographic structure**	Allelic/genomic structure by host and location Spatial history can mimic or amplify HAD	Host attribution requires explicit spatial partitioning
Host–environment–geography joint structure		
Landscape/population genomics **Multiple predictors contribute simultaneously**	Genome-wide differentiation No single predictor defines discrete host races	Treat host use as one component of multivariate structure
Lineage-dependent HAD		
Comparative genomics across related taxa **Related taxa on similar hosts show contrasting outcomes**	Host-associated differentiation Shared ecology does not guarantee repeatability	Generalization must be lineage bounded
Scale-dependent host signal		
Population genomics/phylogeography **Host association is stronger at some spatial scales than others**	Host versus geographic differentiation Analytical scale changes interpretation	Report the scale at which HAD is detected
Population-structure utility without demonstrated RI		
Assignment/source tracking **Structure predicts source or movement**	Host-linked genetic structure Reproductive consequence untested	Useful ecological information is not equivalent to speciation evidence
Anthropogenic co-structuring		
Agricultural population genetics	Host, clonal and management-associated variation Selection and management history are confounded	Avoid host-only causal attribution

Host and insecticide environments jointly structure diversity		
Incipient host-associated genomic divergence		
Comparative genomics **Divergent regions or populations occur between host forms**	Host-form genomic differentiation Completion and barrier strength remain unresolved	Classify as genomic divergence, not species completion
Molecular host-response divergence		
Transcriptomics/functional molecular evidence **Molecular responses differ among host-associated lineages**	Host-related expression or detoxification profiles Fitness and mating consequences unmeasured	Keep molecular differentiation below the RI inference boundary

Note: The final column represents the article's proposed synthesis classification; it is not an empirically validated scoring system.

Phenology and habitat isolation

Host-associated insects can become reproductively separated before intrinsic incompatibility evolves if host phenology changes where or when adults emerge, feed, mate, or oviposit. In a gall-associated community, temporal separation between sympatric host plants propagated across multiple trophic levels, demonstrating that host timing can restructure encounter opportunities beyond the plant itself [19].

The apple maggot fly *Rhagoletis pomonella* provides a particularly informative recent system. A human-mediated shift from hawthorn to apple was followed by rapid and repeatable host-associated differentiation and partial reproductive isolation [20]. Yet temporal divergence remains permeable rather than absolute. Across a *Rhagoletis* radiation, divergent diapause timing contributes to allochronic differentiation while genomic evidence simultaneously retains reticulate hybridization [21]. Thus, phenological isolation and ongoing exchange are not mutually exclusive.

Barrier strength is also environmentally contingent. Simulated warming produced asymmetric life-history timing responses in the *Rhagoletis* system, creating the potential to alter an established temporal barrier without demonstrating what future field gene flow will be [22]. A mechanistic study of the redheaded pine sawfly similarly found that several forms of isolation by environment—including immigrant viability, dispersal differences, and phenology—were supported, whereas candidate sexual-selection and hybrid-disadvantage mechanisms were not uniformly supported [23].

Phenology is therefore best treated as an encounter barrier whose evolutionary significance depends on temporal overlap, host fidelity, survival, mating opportunity, and subsequent gene exchange. The evidence does not support a rule that temporal separation automatically becomes complete reproductive isolation.

The review-selection record itself also imposes a boundary on how strongly the present evidence landscape can be quantified. **Figure 1** makes that methodological provenance visible rather than replacing missing screening arithmetic with inferred values.

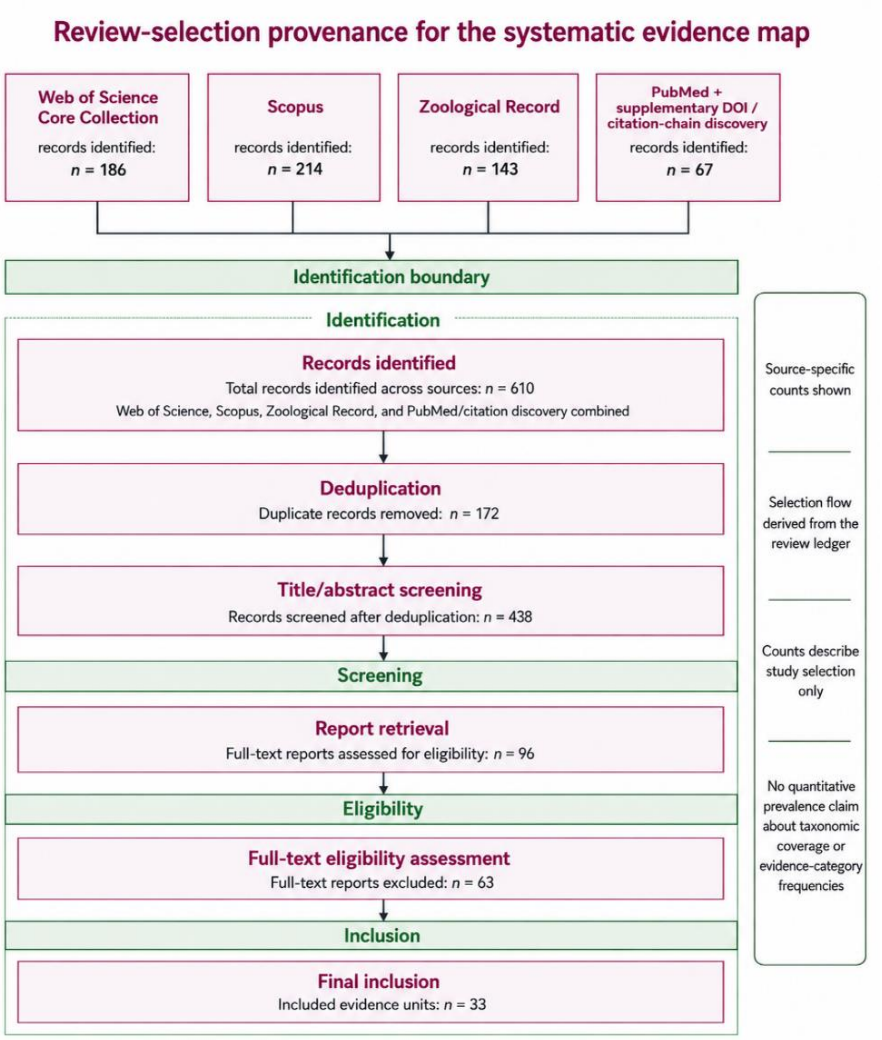


Figure 1. Host-associated insect divergence evidence-map selection record: provenance boundaries across identification, screening, and eligibility

Assortative mating

Host association can affect reproductive isolation through sensory preference, mating location, sexual signaling, or intrinsic compatibility, but each requires different evidence. In *R. pomonella*, host-associated divergence includes a reversal in sensory processing of host odors, linking ecological preference to a measurable neural and behavioral mechanism [24]. That evidence strengthens the plausibility of host-mediated encounter differences, but sensory divergence alone does not demonstrate assortative mating.

Direct mating evidence is itself conditional. Experimental work in *R. pomonella* indicates that sexual isolation can change with environmental context [25], cautioning against transferring laboratory preference estimates directly to field gene flow. Pea aphid host races provide a different layer of evidence: distantly related host races show stronger intrinsic prezygotic incompatibility, whereas more closely related forms retain greater hybridization potential [26]. Host-race status therefore encompasses substantial variation in reproductive compatibility.

Chemical phenotypes are another candidate mechanism. Cuticular hydrocarbon profiles differ among *Rhagoletis* taxa and host races and also vary with sex and site, making them plausible premating signals; however, the study explicitly leaves causal mating effects for direct behavioral testing [27]. This distinction is important because correlated sensory or chemical divergence can identify mechanisms worth testing without establishing that they presently reduce gene flow.

The proposed synthesis therefore separates host-recognition divergence, environment-dependent sexual isolation, intrinsic reproductive compatibility, and candidate mating cues. These states can coexist, but they should not be

collapsed into a single "assortative mating" category unless the underlying study directly measures mate choice or reproductive outcome.

The inferential differences among these traits and processes are compressed in **Table 2** so that candidate mechanisms remain visibly separate from demonstrated reproductive consequences.

Table 2. Assortative-mating evidence states and the reproductive inference each can legitimately support

Assortative-mating distinction	Article-specific dimension	Scientific content
Host-recognition divergence	**Evidence**	Sensory or behavioral response to host odors
	Interpretive consequence · Limits and uncertainty	May alter host finding and encounter location Does not itself measure mate choice
	Research or test · Evidential standing	Link sensory differences to mating encounters in field-relevant settings Evidence-derived distinction
	Biological setting	Host-associated fruit-fly populations
Environment-dependent sexual isolation	**Evidence**	Direct mating or preference assays
	Interpretive consequence · Limits and uncertainty	Reproductive isolation can vary with environmental context Laboratory context may change effect magnitude or direction
	Research or test · Evidential standing	Replicate across ecologically realistic environments Evidence-derived distinction
	Biological setting	Host-associated forms tested under contrasting conditions
Intrinsic compatibility divergence	**Evidence**	Reproductive compatibility among host-associated forms
	Interpretive consequence · Limits and uncertainty	Stronger intrinsic barriers can accompany greater divergence Barrier strength differs among host races
	Research or test · Evidential standing	Separate intrinsic incompatibility from habitat-mediated encounter Evidence-derived distinction
	Biological setting	Pea aphid host races
Candidate chemical mate-recognition cue	**Evidence**	Taxon-, sex-, or site-associated cuticular hydrocarbon differences
	Interpretive consequence · Limits and uncertainty	Provides a plausible premating signal Causal effect on mate choice remains untested
	Research or test · Evidential standing	Perform controlled and field mating trials manipulating candidate cues Evidence-derived distinction
	Biological setting	Rhagoletis taxa and host races
Concordant ecological and mating barriers	**Evidence**	Host fidelity plus measured reproductive discrimination
	Interpretive consequence · Limits and uncertainty	Multiple barriers may jointly reduce exchange Relative contribution of each barrier remains system specific
	Research or test · Evidential standing	Estimate components separately before inferring total isolation Proposed synthesis
	Biological setting	Host-associated populations with more than one barrier class
Discordant cue and mating evidence	**Evidence**	Trait divergence without direct reproductive consequence
	Interpretive consequence · Limits and uncertainty	Mechanistic divergence can precede or fail to generate RI Trait differences may reflect ecology rather than mate recognition
	Research or test · Evidential standing	Do not upgrade candidate cues to RI without reproductive tests Proposed synthesis
	Biological setting	Systems with differentiated sensory/chemical traits but weak or untested mating effects

Note: "Proposed synthesis" identifies classifications introduced by this evidence map rather than categories already validated as a universal hierarchy.

Genomic differentiation

Genomic differentiation is informative only when the history generating it is considered. In European *Ectoedemia* leaf miners, ddRAD phylogenomics resolved cryptic lineage structure not uniformly recovered by morphology or mitochondrial barcodes, while residual overlap remained compatible with incomplete lineage sorting or admixture [28]. Genomic resolution can therefore strengthen lineage inference without making every cluster a taxonomically definitive species boundary.

Host-associated structure is not confined to herbivores. In the predatory flies *Leucotaraxis argenticollis* and *L. piniperda*, population-genetic analyses detected broad east–west differentiation with nested prey-associated structure [29]. The pattern extends HAD-like differentiation to specialist predators, but prey association was not shown to cause reproductive isolation. In potato psyllids, host plants and *Wolbachia* both covaried with population structure, while intermediate ancestry indicated admixture [30]. Host preference, symbiont state, ancestry, and gene flow can therefore be entangled.

The relevant distinction is among genomic clustering, host-associated genomic differentiation, and genomic evidence that constrains gene-flow histories. Interpretive strength depends less on marker density than on whether geography, admixture, incomplete lineage sorting, symbionts, and alternative demographic histories have been addressed. **Table 3** reconciles these signals with the competing histories that prevent automatic reproductive or taxonomic inference.

Table 3. Reconciling host-associated genomic signals with alternative histories before reproductive or taxonomic inference

Genomic state	Cryptic genomic lineages	Host-associated genomic differentiation	Prey-associated structure	Host–symbiont covariance	Genomic differentiation with residual admixture
Legitimate interpretation · Competing explanation	Differentiated evolutionary histories Incomplete lineage sorting or admixture	Host use covaries with genomic structure Geography, environment, demography	HAD-like structure beyond herbivory Prey association may track ancestry or geography	Multiple factors coincide with differentiation Symbiont and host effects may be observationally inseparable	Divergence can coexist with exchange Historical versus contemporary gene flow
Required next test · Evidential standing	Compare genomic history with ecology, morphology, mating, and gene flow Evidence-derived	Partition host from spatial and demographic effects Evidence-derived	Test prey fidelity, mating, dispersal, and exchange Evidence-derived	Test infection effects and demographic alternatives Evidence-derived	Estimate timing and direction of introgression Proposed reconciliation category
Evidence	Reproducible multilocus clustering	Allele-frequency or genome-wide differences by host	Genetic differentiation nested within geographic structure	Population ancestry aligned partly with host and infection state	Clustering plus intermediate ancestry

Note: The proposed category is an interpretive device of this evidence map, not a species-delimitation rule.

Evidence for reduced gene flow

Evidence for reduced gene flow is strongest when studies measure barriers affecting successful migration or reproduction rather than correlated divergence alone. In *Belonocnema treatae*, reciprocal host-associated comparisons demonstrated asymmetric reductions in immigrant viability and fecundity [31]. These are direct ecological barriers, but asymmetry and other routes of exchange prevent an inference of complete isolation.

Microbial effects can modify this interpretation. In *Rhagoletis*, empirical and modeling work tested whether *Wolbachia*-induced cytoplasmic incompatibility could augment host-related reproductive isolation [32]. Its contribution is conditional on infection dynamics, host association, and existing barriers rather than sufficient by itself. Likewise, allochronic divergence can be compatible with sympatric speciation without alone proving that sympatric speciation occurred [33].

The proposed synthesis therefore treats ecological performance, temporal separation, mating isolation, intrinsic compatibility, and symbiont-mediated incompatibility as distinct barrier classes that may interact but should not be summed into an unsupported isolation score. Concordance among independently measured barriers strengthens inference; admixture, environmental instability, or untested mechanisms weaken it.

Evidence map from host association to speciation

The assembled evidence does not support a universal sequence in which host association predictably becomes reproductive isolation and then speciation. The proposed map is organized instead by what has been demonstrated. Host-use association establishes ecological partitioning. Phenotypic, molecular, or genomic differentiation shows biological divergence but not necessarily host causation or restricted mating.

Directly measured barriers occupy a stronger inferential position. Phenological mismatch can reduce reproductive encounter; immigrant performance can reduce successful movement between host environments; mate discrimination can reduce reproductive exchange; and intrinsic incompatibility can reduce reproductive compatibility. These effects may nevertheless be partial, asymmetric, environmentally contingent, or accompanied by hybridization.

The next distinction is concordance. Genomic differentiation is more persuasive when aligned with ecological or reproductive barriers and when geography, symbionts, admixture, and incomplete lineage sorting have been addressed. Conversely, genomic clustering without barrier evidence remains genomic divergence, while sensory, transcriptomic, or chemical differences remain candidate mechanisms until reproductive consequences are measured.

A key feature of the map is that evidence classes can disagree without one being erroneous. Strong host-associated genomic structure may coexist with weak mating discrimination, while direct ecological barriers may occur before genome-wide differentiation becomes pronounced. Such discordance changes the question from "is speciation occurring?" to "which components of reproductive separation are established, which remain permeable, and which alternative histories are still compatible with the data?" This prevents the strongest available data type from dominating interpretation simply because it is technologically sophisticated.

The map also separates evidence accumulation from temporal order. A lineage may first be recognized through genomic structure and only later be tested ecologically; another may be discovered through host fidelity or phenological isolation before genomic sampling is undertaken. Study sequence therefore cannot be assumed to reconstruct evolutionary sequence. For the same reason, failure to detect one barrier does not invalidate evidence for another, but it lowers confidence in claims that require concordance among several mechanisms.

The proposed evidence architecture is therefore branching, not linear. Evidence can accumulate across independent lanes, remain discordant, or weaken under changed conditions. **Table 4** formalizes the resulting inference boundaries without assigning scores or assuming that every lineage occupies one fixed stage.

Table 4. Stage-specific inference boundaries for host association, reproductive isolation, and speciation evidence

Evidence-map state			
Host-use association			
Supported inference	**Unresolved issue**	**Evidence needed next · Evidential standing**	**Characteristic evidence**
Ecological partitioning	Biological divergence and RI	Demonstrate host-linked biological differentiation Established class	Repeated use of different hosts or organs
Phenotypic or molecular divergence			
Supported inference	**Unresolved issue**	**Evidence needed next · Evidential standing**	**Characteristic evidence**
Host-correlated biological divergence	Fitness, mating, and causality	Connect differences to performance or reproduction Established class	Sensory, chemical, transcriptomic, or trait differences
Host-associated genetic structure			
Supported inference	**Unresolved issue**	**Evidence needed next · Evidential standing**	**Characteristic evidence**
Population structure	Host causation and barrier strength	Partition geography, environment, demography, symbionts Established class	Allelic or genomic differences by host
Direct ecological or temporal barrier			
Supported inference	**Unresolved issue**	**Evidence needed next · Evidential standing**	**Characteristic evidence**

Mechanism capable of reducing exchange	Realized total gene flow	Measure mating, compatibility, or exchange Established class	Reduced immigrant performance or temporal overlap
Direct mating or compatibility barrier			
Supported inference	**Unresolved issue**	**Evidence needed next · Evidential standing**	**Characteristic evidence**
RI in the measured context	Environmental stability and genomic consequences	Test field generality and exchange Established class	Assortative mating or reproductive incompatibility
Genomic divergence with demographic alternatives tested			
Supported inference	**Unresolved issue**	**Evidence needed next · Evidential standing**	**Characteristic evidence**
Stronger lineage-separation inference	Complete independence	Seek concordance across independent evidence classes Proposed integration state	Broad structure plus explicit admixture/gene-flow analysis
Concordant multi-class isolation			
Supported inference	**Unresolved issue**	**Evidence needed next · Evidential standing**	**Characteristic evidence**
Strong cumulative support for lineage divergence	Whether host association initiated the split	Historical reconstruction and species-level evaluation Proposed integration state	Independent ecological, reproductive, and genomic evidence

Note: This is an evidential architecture, not a temporal ladder or validated delimitation score.

Gaps and biases

The evidence landscape is shaped by research effort as well as biology. Host-derived species naming is associated with greater scientific attention to HAD [6], so poorly studied lineages cannot be treated as biological absences. Host association interacts with spatial structure in gall wasps [11]. Related sawflies can show contrasting HAD patterns despite comparable host contexts [13]. Prey-associated differentiation in silver flies broadens ecological coverage while leaving reproductive consequences unresolved [29].

Barrier stability is also under-tested. Experimental warming can alter phenological separation [22], while mating isolation can depend on environmental context [25]. Candidate mechanisms often outpace validation: cuticular hydrocarbon divergence does not itself establish mating causation [27], genomic clustering may remain compatible with incomplete lineage sorting or admixture [28], and *Wolbachia*-associated incompatibility is conditional [32].

A further gap concerns comparison across life stages and sexes. Host choice may be expressed by ovipositing females, while larval performance, adult emergence timing, and mate discrimination operate at different stages and can impose nonidentical barriers. Many studies measure only one of these components. Future work should link host choice, juvenile performance, adult phenology, mating behavior, and realized gene exchange within the same populations where feasible. That design would help determine whether observed host-associated differences are mechanistically connected or merely correlated consequences of shared population history.

Geographic replication is equally important because a barrier detected at one contact zone may disappear elsewhere. Replicated populations can distinguish recurrent host-associated processes from local demographic accidents and reveal whether the same host contrast repeatedly produces similar ecological, behavioral, and genomic consequences.

Priority should therefore be given to longitudinal field tests, direct barrier measurements, demographic models that compare alternative histories, and replicated links from candidate mechanisms to reproductive outcomes. Such designs would improve transfer from association to inference without presuming that every lineage must reach the same evolutionary endpoint.

Conclusion

Host-associated differentiation is an evidential category, not a synonym for ecological speciation. Host use can coincide with molecular, phenotypic, behavioral, or genomic divergence while reproductive consequences remain absent, partial, unmeasured, or confounded. Phenological barriers, assortative mating, intrinsic compatibility, immigrant performance, genomic history, and symbiont effects strengthen inference in different ways but provide no universal shortcut to species status.

The proposed evidence-stage architecture organizes studies by the inference their measurements support. It allows independent evidence classes to converge without forcing lineages into a linear progression and keeps geography, environmental contingency, admixture, incomplete lineage sorting, symbionts, and laboratory-to-field transfer visible as alternative or modifying explanations. Species-level claims are consequently strongest when multiple independent evidence classes converge and competing population histories have been explicitly tested; where they do not, retaining a lower-level description is the more defensible interpretation.

Acknowledgments: None

Conflict of Interest: None

Financial Support: None

Ethics Statement: None

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