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Emerging Zoonotic and Transboundary Infectious Threats at Wildlife–Livestock–Human Interfaces: A Living Systematic Review of Surveillance Signals, Reservoir Dynamics, Transmission Pathways, Exposure Networks, Intervention Evidence, and Preparedness, 2017–2026

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ABSTRACT

Zoonotic and transboundary infectious threats increasingly emerge through dynamic wildlife–livestock–human interfaces in which reservoir circulation, livestock amplification, exposure networks, and surveillance intensity can change faster than conventional periodic reviews. This living systematic review examines how heterogeneous signals should be interpreted without conflating pathogen detection with validated transmission, reservoir attribution, outbreak magnitude, or intervention effectiveness. Peer-reviewed evidence published from 2017–2026 was organized using a prespecified living-review framework covering surveillance signals, reservoir dynamics, transmission pathways, exposure networks, intervention evidence, preparedness, and methodological uncertainty. Search, selection, extraction, appraisal, and synthesis procedures were designed for reproducibility and version control. Heterogeneous evidence was synthesized without forced quantitative pooling. No search-derived count is reported where a reconciled value was unavailable in the review-selection record. The evidence indicates that actionable warning can arise from genomic surveillance, serology, aggregated livestock sampling, slaughterhouse sentinels, wildlife sampling, and integrated human–animal–vector systems, but these signals differ fundamentally in what they establish. Reservoir inference is sensitive to species, specimen, timing, and assay choice; transmission evidence ranges from field association to controlled experimentation and model-based inference; and much preparedness evidence remains observational or operational rather than causal. A proposed evidence-state architecture therefore separates detection, interpretation, cross-interface attribution, and response consequence. One Health preparedness benefits from linking heterogeneous surveillance streams while retaining explicit boundaries between signal and event, association and pathway, reservoir evidence and reservoir proof, and implementation activity and demonstrated effectiveness. Living updating is most defensible when changes are versioned, uncertainty is retained, and new evidence can revise rather than merely accumulate prior interpretations.

Keywords: Emerging infections, Living systematic review, One health, Reservoir surveillance, Transboundary animal disease, Zoonoses

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Introduction

Recent H5N1 emergence in United States dairy cattle demonstrated that a pathogen historically framed around avian reservoirs can acquire a consequential livestock interface, with surveillance and genomic evidence

documenting interstate spread [1]. Independent outbreak investigations confirmed spillover into dairy cattle and established a new mammalian production context without, by themselves, defining population prevalence or human risk [2]. Mpox genomics likewise shows that zoonotic introductions and sustained human transmission can coexist, making source events analytically distinct from onward propagation [3]. Rift Valley fever investigations further illustrate how livestock surveillance can initiate One Health response while leaving the causal contribution of particular control measures unresolved [4].

The problem is therefore not simply whether a pathogen is detected. It is whether a signal identifies reservoir circulation, cross-species transmission, networked exposure, or an event requiring coordinated action. This review addresses those distinctions through an explicitly living synthesis that preserves uncertainty and separates observed evidence from proposed integration.

Review objective and living-review scope

The objective is to synthesize evidence from 2017–2026 on emerging zoonotic and transboundary infectious threats where wildlife, livestock, people, vectors, production systems, or surveillance infrastructures interact. The scope is organized around six linked but non-equivalent domains: surveillance signals, reservoir dynamics, transmission pathways, exposure networks, intervention evidence, and preparedness.

The review treats detection as an evidential state rather than a diagnosis of transmission mechanism. Serologic, molecular, genomic, clinical, ecological, and operational observations are interpreted according to what each design can establish. Evidence about a wildlife or livestock host is not automatically treated as proof of reservoir competence, and evidence of response implementation is not treated as proof of effectiveness. The proposed integrative contribution is a boundary-conscious interface architecture that can be revised as new evidence changes host attribution, pathway confidence, or response relevance.

Materials and Methods

A living systematic-review design was used to accommodate an evidence base expected to change with new outbreaks, host detections, genomic analyses, and surveillance technologies. Review procedures were prespecified around reproducible searching, explicit eligibility decisions, structured extraction, design-sensitive appraisal, non-pooled synthesis, and version control. The analytical unit was the evidence contribution relevant to one or more locked domains rather than a generic pathogen mention.

Methods were constructed to keep three layers separate: what a study directly measured, what its design reasonably permits investigators to infer, and what this review newly proposes when integrating evidence across host and system levels. Search-derived quantities were to be reported only when traceable to the reconciled review-selection record. Because that record does not contain reconciled retrieval, deduplication, screening, exclusion, or inclusion values, no such numbers are introduced in this manuscript version.

Protocol and reporting framework

Reporting was structured around PRISMA 2020 principles for transparent systematic-review methods and selection accounting [5]. The explanation-and-elaboration guidance informed the operational interpretation of reporting items, particularly eligibility decisions, information-source documentation, selection flow, and distinctions between methods performed and results obtained [6]. Protocolization was treated as a transparency mechanism rather than evidence that a review is automatically current or unbiased; comparative methodological work shows that published protocols can coexist with older searches and greater review effort [7].

For the living component, each review version is conceptually separated into an initial evidence state and subsequent dated updates. Changes in eligibility interpretation, evidence classification, or synthesis are intended to be logged rather than silently overwritten. This framework permits correction and reclassification when emerging data challenge earlier assumptions while preserving a readable account of why interpretation changed.

Eligibility criteria

Eligible evidence comprised peer-reviewed journal articles published from 2017 through 2026 with a verifiable DOI and direct relevance to the wildlife–livestock–human interface, transboundary animal-disease surveillance, zoonotic transmission, reservoir dynamics, exposure, intervention, preparedness, or necessary review methodology. Sources had to provide sufficient information on species or population, setting, design,

measurement, exposure or intervention where applicable, and outcome or inferential target to bound the claim supported.

Topic-adjacent papers were excluded when they could not support a specific review domain or when their species, exposure, outcome, setting, or decision context was materially incompatible with the intended inference. Duplicate article versions were not eligible as independent evidence units. Non-peer-reviewed material, preprints, conference abstracts, dissertations, and sources without verifiable DOI information were outside scope. Transboundary diseases without zoonotic potential were admissible only when explicitly used as bounded surveillance comparators, not as evidence of human risk.

Information sources

Information-source planning was designed to span veterinary, biomedical, infectious-disease, public-health, and multidisciplinary literature because relevant evidence is distributed across host, pathogen, clinical, ecological, and surveillance traditions. Database searching was therefore conceived as complementary rather than interchangeable: broad biomedical coverage can recover human and laboratory evidence, whereas veterinary and multidisciplinary indexing is needed for livestock, wildlife, farm-system, and transboundary-threat studies.

Source documentation was specified at the platform and search-date level so that later updates could distinguish genuinely new records from changes in indexing or database coverage. Citation chasing and publisher verification were treated as supplementary verification procedures rather than substitutes for reproducible database searches. Information-source completeness was not assumed from the presence of highly relevant records; coverage remains a methodological boundary requiring reassessment when terminology, hosts, pathogens, or indexing practices change.

Search strategy and update schedule

Search reporting followed PRISMA-S principles, requiring exact information sources, platforms, dates, and reproducible strategies for each search or update [8]. Update searches were not assumed to be safely compressible: simplified strategies may improve efficiency in some settings, but their performance must be tested against the topic and database being updated [9]. Search effectiveness was interpreted multidimensionally because recall, precision, yield, and workload can produce different judgments about the same strategy [10]. Filters were considered only when their performance was appropriate to the database, design, and topic rather than presumed transferable [11].

For a living review, the proposed operational rule is to intensify reassessment when terminology, host range, outbreak geography, or surveillance technology changes. This creates distinct search states rather than a fixed calendar-only routine. Because search design and update timing jointly alter evidential confidence, their adjudication is more efficiently distinguished in a comparative matrix than by treating search updates as interchangeable repetitions. **Table 1** presents event-triggered search adaptations for a living review of changing zoonotic interfaces.

Table 1. Event-triggered search adaptations for a living review of changing zoonotic interfaces

Evidence-change trigger	Search-vocabulary change	Update timing	Retrieval signal monitored	Methodological safeguard	Next trigger and basis
Stable terminology	Retain validated core concepts	Routine interval	**Context:** Stable host and pathogen vocabulary **Observed:** Similar retrieval profile	**Action:** Maintain strategy **Risk:** Indexing drift remains possible	**Recheck:** Check yield against known records **Basis:** Proposed synthesis
New host/interface	Add host, setting, and pathway terms	Immediate targeted update	**Context:** Novel livestock or wildlife interface **Observed:** New host detection or exposure context	**Action:** Broaden retrieval **Risk:** Initial reports may be unstable	**Recheck:** Search complementary sources **Basis:** Proposed synthesis
Outbreak escalation	Expand geography and surveillance terminology	Shortened interval	**Context:** Rapidly changing outbreak context **Observed:** Accelerating publication volume	**Action:** Increase update intensity **Risk:** Duplicate or preliminary reporting	**Recheck:** Reconcile versions before screening **Basis:** Proposed synthesis

Sparse or discordant signal	Preserve sensitive reservoir terminology	Event-triggered reassessment	**Context:** Intermittent shedding or heterogeneous sampling **Observed:** Negative or discordant detection	**Action:** Avoid premature narrowing **Risk:** Specimen and timing dependence	**Recheck:** Reassess ecological and assay coverage **Basis:** Proposed synthesis
Search-method change	Benchmark revised syntax or filter	Before replacement	**Context:** Platform or indexing change **Observed:** Shift in recall, precision, or workload	**Action:** Adopt only after comparison **Risk:** Performance may be platform-specific	**Recheck:** Retain prior strategy for validation **Basis:** Evidence-informed rule

Study selection

Study selection was designed as a staged, auditable process in which records progress from identification and deduplication to title/abstract assessment and full-text eligibility review. PRISMA reporting principles require those transitions to be transparent rather than reconstructed retrospectively [5]. Where eligibility depends on host role, transmission interpretation, or surveillance context, decisions must retain the reason for exclusion instead of reducing complex judgments to a generic "not relevant" label [6].

For living updates, a previously screened record may require re-evaluation if new evidence changes its relevance—for example, when a host initially treated as incidental becomes epidemiologically important. Such reclassification should be versioned rather than treated as an unrecorded correction. Numerical flow reporting is withheld because the available review-selection record does not contain a reconciled identification-to-inclusion count chain; those values are therefore not estimated or derived from the reference list.

Data extraction

Extraction fields were structured to preserve species or population, setting, sample size when reported, design, exposure or intervention, comparator, measurement source, analytical method, main finding, uncertainty, and transferability. Comparative evidence on review conduct remains limited for several selection, abstraction, and appraisal procedures, supporting explicit rather than implicit extraction rules [12]. Qualitative or implementation evidence was retained with its context and methodological limitations rather than converted into effect claims [13].

Missing outcomes or incompletely reported variables were recorded as unavailable rather than inferred, because methodological surveys show that missing-data handling is often inadequately reported in systematic reviews [14]. Where statistical pooling was not defensible, extraction retained the information needed for transparent synthesis without meta-analysis, consistent with SWiM guidance [15]. The resulting evidence structure distinguishes direct observation, study-level inference, and review-level synthesis so that subsequent analytical claims cannot silently exceed the underlying design.

Risk-of-bias assessment

Risk-of-bias assessment was specified as design-sensitive because the evidence base spans outbreak investigations, surveillance studies, seroepidemiology, genomic analyses, experimental models, modeling, and reviews. A single undifferentiated instrument would falsely imply that identical bias domains and inferential vulnerabilities apply across these designs. Methodological evidence also indicates that comparative support for many appraisal procedures is limited, reinforcing the need to make assessment rules explicit [12].

For qualitative or implementation-oriented evidence, methodological limitations and contextual coherence were retained as part of confidence interpretation rather than collapsed into a numerical score [13]. Missingness and incomplete reporting were treated as distinct sources of uncertainty because absence of reported information cannot be assumed to mean absence of bias or absence of an outcome [14]. No distribution of risk-of-bias judgments is reported because such findings require a finalized screened evidence set and completed design-specific appraisal.

Evidence synthesis

Synthesis was organized by the article's interface domains rather than by pathogen alone. This permits evidence from different threats to inform common interpretive problems—such as non-detection, reservoir attribution, pathway inference, exposure aggregation, or response escalation—without implying biological interchangeability.

When designs, outcomes, and measurements were too heterogeneous for defensible pooling, synthesis remained structured and non-quantitative in accordance with SWiM principles [15].

The review therefore uses a proposed evidence-state logic: signals are first classified by what was observed, then by the level of inference the design permits, and finally by their possible decision consequence. This last layer is proposed synthesis, not a validated prediction rule. Contradictory findings, negative surveillance, model dependence, and setting-specific constraints are retained as evidence boundaries rather than averaged away, preserving the distinction between uncertainty that should prompt further observation and uncertainty that limits transferability.

Living-review updating and version control

A living review requires continuing evidence surveillance and an explicit updating process rather than a simple intention to revisit the topic [16]. Human oversight remains necessary even where machine-assisted screening or prioritization is used, because automation can reduce workload without eliminating classification error or the need for validation [17]. Repeated quantitative updating introduces statistical concerns when meta-analysis is appropriate, but living status does not justify pooling heterogeneous evidence that should remain separate [18]. Evidence updating is also distinct from updating recommendations: a new signal can change evidential confidence without automatically changing policy [19].

Accordingly, each update is treated as a versioned state transition. New evidence may add support, create contradiction, alter host or pathway attribution, or force reclassification of earlier interpretations. The different consequences of those transitions are separated below so that evidence change is not mistaken for recommendation change. **Table 2** presents version-control operations for additions, contradictions, reclassifications, and method changes.

Table 2. Version-control operations for additions, contradictions, reclassifications, and method changes

Evidence change	Version operation	Claim affected	Historical safeguard	Validation before release
No material change	Preserve prior synthesis	**Observed:** No eligible evidence altering interpretation **Synthesis consequence:** Maintain current version	Search sensitivity remains finite	**Context:** Stable evidence environment **Check:** Continue scheduled surveillance **Basis:** Established method
New surveillance signal	Add dated evidence entry	**Observed:** Signal changes evidence landscape **Synthesis consequence:** Reopen affected domain	Signal may not establish pathway	**Context:** New host, geography, assay, or outbreak **Check:** Seek confirmatory evidence **Basis:** Proposed synthesis
Evidence contradiction	Record competing interpretation	**Observed:** New result conflicts with prior pattern **Synthesis consequence:** Lower or split confidence	Discordance may be methodological	**Context:** Design or setting divergence **Check:** Re-extract comparable conditions **Basis:** Proposed synthesis
Reclassification	Amend interpretation while retaining history	**Observed:** Earlier evidence acquires new meaning **Synthesis consequence:** Update affected synthesis	Retrospective interpretation risk	**Context:** Changed host or pathway understanding **Check:** Document rationale and affected claims **Basis:** Proposed synthesis
Method change	Fork and benchmark revised procedure	**Observed:** Retrieval or appraisal behavior shifts **Synthesis consequence:** Protect cross-version comparability	Tool performance can drift	**Context:** Platform, filter, or tool change **Check:** Validate before full adoption **Basis:** Evidence-informed rule

Results and Discussion

The evidence framework prepared for synthesis spans multiple observational and analytical scales, including wildlife and livestock surveillance, human–animal exposure assessment, outbreak investigation, genomics, experimental transmission research, modeling, and preparedness operations. These designs cannot be interpreted through one common evidential hierarchy because they answer different questions: whether a pathogen is

detectable, whether hosts show prior exposure, whether a route is experimentally plausible, whether transmission is inferred from sequence data, or whether a response was implemented.

Accordingly, the results are organized in the subsequent sections around study-selection flow, evidence characteristics, surveillance signals, reservoir dynamics, transmission pathways, exposure networks, intervention evidence, preparedness, and design-specific bias. No numerical search, screening, exclusion, inclusion, subgroup, or evidence-category result is stated because the available selection record does not contain a reconciled count chain. Substantive synthesis therefore proceeds only with claim-level evidence traceable to the approved reference set, while numerical review-flow reporting remains withheld rather than estimated.

Study-selection flow

The selection process was defined as identification, deduplication, title/abstract screening, full-text eligibility assessment, exclusion with reason, and inclusion, repeated for later living-review updates. These transitions follow systematic-review reporting requirements [5] and should remain traceable across versions [6]. The available review record, however, does not contain a reconciled numerical chain for retrieval, duplicate removal, screening, full-text exclusion, or inclusion. Such values are therefore not estimated. **Figure 1** retains the verified procedural topology but marks numerical accounting as unavailable, preventing the bibliography size from being misrepresented as an included-study count.

Because transparent incompleteness is preferable to reconstructed selection statistics, the review-selection architecture is shown with its accounting boundary visible.

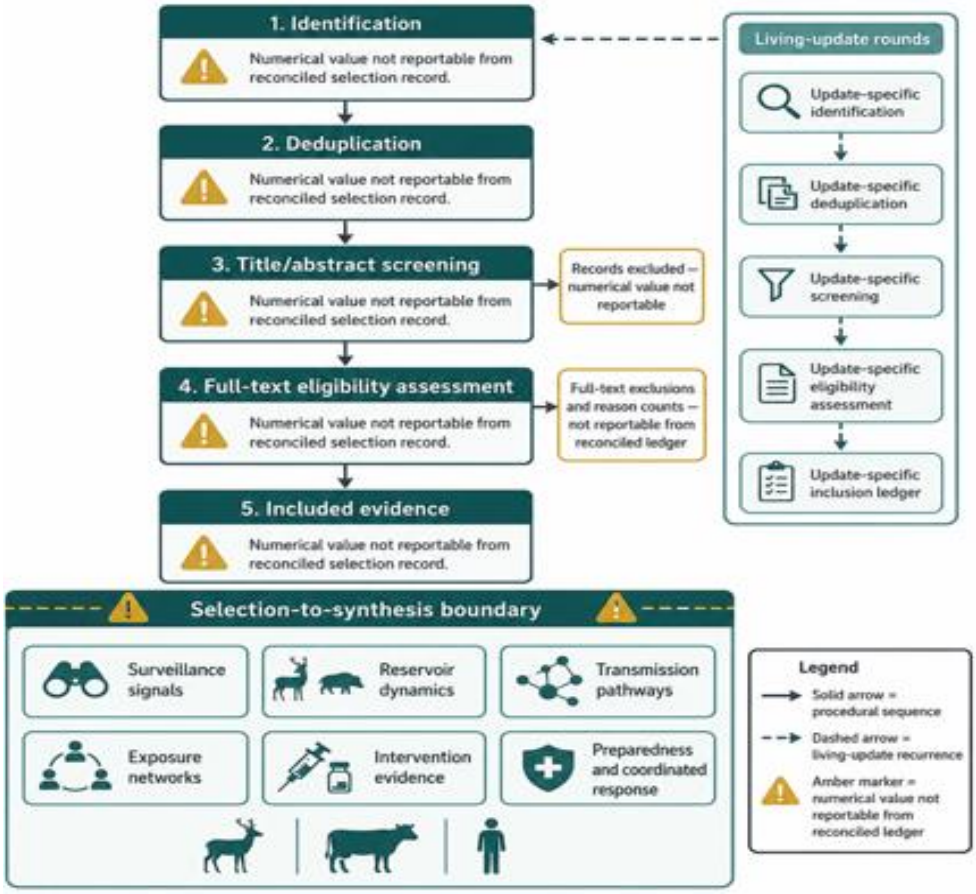

Figure 1. Versioned selection-accounting boundary for wildlife–livestock–human interface evidence

Included-evidence characteristics

The evidence framework spans several surveillance designs. Targeted Nipah investigation in *Pteropus medius* represents wildlife reservoir-oriented sampling [20]. Parallel human–livestock RVF serosurveillance demonstrates cross-interface exposure detection where routine outbreak recognition may be limited [21]. Aggregated livestock sampling provides population-level viral surveillance without individual-animal attribution [22]. CCHFV livestock serosurveillance adds a sentinel model in which animal exposure informs geographic

human-risk context without directly measuring human infection [23]. These designs differ in host, specimen, timing, and inferential target; consequently, evidence is characterized by what was sampled, measured, and attributable rather than by treating all positive observations as equivalent proof of reservoirs or transmission.

Surveillance signals

Surveillance signals differ in what they establish. Human–livestock RVF serology can reveal prior exposure, but antibodies do not establish active infection or transmission direction [21]. Aggregated livestock samples improve population-level observability while sacrificing individual attribution [22]. Wildlife surveillance is sensitive to shedding, timing, specimen choice, and assay performance [20], whereas livestock seropositivity can indicate CCHFV circulation without estimating human incidence [23]. The proposed distinction is between detection, interpreted circulation, and action-triggering signals. Escalation should depend on sampling adequacy, host relevance, temporal consistency, corroboration, and consequence if the signal is genuine.

Table 3 presents biological time windows and attribution limits of molecular, serologic, pooled, and discordant surveillance signals.

Table 3. Biological time windows and attribution limits of molecular, serologic, pooled, and discordant surveillance signals

Surveillance modality	Biological time window	Unit of attribution	Signal gained	Pathway claim unavailable	Confirmatory pairing
Molecular detection	Current/recent infection signal	Specimen and timing	Positive nucleic acid	**Limit:** Detection ≠ pathway **Basis:** Evidence-informed	**Use:** Confirm context **Pairing:** Repeat or triangulate
Serologic exposure	Prior exposure	Assay specificity	Antibody signal	**Limit:** Exposure ≠ active infection **Basis:** Evidence-informed	**Use:** Map exposure pressure **Pairing:** Compare molecular evidence
Aggregated livestock signal	Population warning	Pooling and prevalence	Positive pooled sample	**Limit:** No individual attribution **Basis:** Evidence-informed	**Use:** Target source investigation **Pairing:** Follow-up sampling
Discordant signal	Uncertain circulation	Sampling adequacy	Mixed results	**Limit:** Measurement may explain discordance **Basis:** Proposed synthesis	**Use:** Intensify verification **Pairing:** Reassess specimen/timing

Reservoir dynamics

Reservoir attribution requires more than demonstrating exposure or pathogen carriage. Nipah surveillance in *Pteropus medius* supports a bat reservoir context, yet detectability varies with sampling window and specimen type [20]. CCHFV antibodies in livestock identify enzootic exposure pressure but not infectiousness at sampling or direct transmission to people [23]. Molecular assays preferentially capture current or recent infection, whereas antibodies may represent historical exposure. Reservoir confidence should therefore rise only when repeated detection, host ecology, temporal persistence, pathogen characterization, and epidemiological linkage converge. Isolated positivity or non-detection remains bounded evidence rather than definitive confirmation or exclusion of reservoir status.

Transmission pathways

Transmission-pathway evidence occupies different inferential levels. A bovine-outbreak-associated human H5N1 isolate was transmissible and pathogenic in animal models, supporting mammalian concern without proving sustained human transmission [24]. A contemporary H5N1 cattle synthesis integrates origin, evolution, and cross-species evidence but depends on rapidly changing primary studies [25]. Controlled cattle experiments support mouth-to-teat transmission under studied conditions without establishing farm-level dominance [26]. MERS-CoV genomic modeling further shows that inferred zoonotic transition counts depend on analytical assumptions and sampling [27]. The review therefore separates field linkage, experimental route demonstration, mechanistic plausibility, and model-inferred transition rather than treating them as interchangeable.

Exposure networks

Exposure is often networked rather than reducible to one infected animal contacting one person. Parallel RVF seropositivity in people and livestock can reflect shared ecological or vector exposure rather than direct animal-

to-human transmission [21]. Aggregated livestock samples represent group and production-environment signals [22], while CCHFV livestock serology identifies settings where animals, ticks, workers, and movement may intersect [23]. The proposed exposure-network interpretation distinguishes source, amplifier, connector, and sentinel roles. A livestock population may therefore be epidemiologically useful as a sentinel without being the immediate source of every human infection; directional claims require evidence that actually measures those links.

Intervention evidence

Intervention evidence was graded by design. Kerala Nipah outbreak reports document rapid case identification, contact surveillance, and containment activity but cannot isolate the effect of individual measures [28]. H5N1 cattle containment analysis emphasizes surveillance and implementation constraints without constituting a controlled efficacy trial [29]. Integrated RVF surveillance in Tanzania detected otherwise unreported human–livestock–vector transmission [30], while slaughterhouse surveillance in Kenya revealed unreported livestock circulation [31]. These findings support an intervention ladder separating detection infrastructure, response implementation, mechanistic plausibility, and demonstrated effectiveness. Only the last category would justify a causal effectiveness claim.

Preparedness and coordinated response

Preparedness depends on moving credible information across animal-health, public-health, laboratory, and operational boundaries. Kerala Nipah experience supports rapid detection and contact-focused coordination while remaining observational [28]. H5N1 analysis shows how incomplete surveillance and production-system connectivity can constrain containment [29]. Integrated RVF surveillance demonstrates the value of observing humans, livestock, and vectors together [30], and slaughterhouse sampling shows how production-chain nodes can act as sentinels [31]. The proposed response architecture conditions escalation on signal credibility, host or network relevance, confirmation, exposure opportunity, and feasibility rather than on positivity alone.

Table 4 presents preparedness configurations for early signals, contact-linked outbreaks, silent multi-host circulation, and persistent uncertainty.

Table 4. Preparedness configurations for early signals, contact-linked outbreaks, silent multi-host circulation, and persistent uncertainty

Preparedness question	Credible early signal	Outbreak with contact risk	Silent multi-host circulation	Persistent uncertainty
Coordination focus	Cross-sector verification	Case/contact coordination	Integrated surveillance	Proportionate precaution
Resource or ecological constraint	Consequence severity	Response capacity	Vector/production ecology	Resource limits
Evidence that opens action	Repeated/confirmed signal	Cases plus exposure links	Cross-compartment signals	Sparse/discordant evidence
Preparedness move	Intensify investigation	Target controls	Broaden surveillance	Avoid premature closure
Claim still bounded	Pathway may remain unknown	Effectiveness uncertain	Attribution incomplete	Escalation not automatic
Review trigger	Seek convergence	Monitor transmission	Repeat sampling	Reassess trigger
Basis	Proposed synthesis	Evidence-informed	Evidence-informed	Proposed synthesis

Risk-of-bias findings

A numerical distribution of risk-of-bias judgments cannot be reported because the available record lacks a completed design-specific appraisal ledger for a finalized included set. The principal interpretive vulnerabilities are nevertheless clear. Surveillance studies can be distorted by site, host, specimen, and timing selection; seroepidemiology adds assay specificity and temporal ambiguity; outbreak investigations often lack complete ascertainment and counterfactuals; genomic models depend on sequencing coverage and assumptions; experimental transmission may have limited field transferability; and reviews inherit weaknesses of their underlying evidence. These domains are consistent with the design-sensitive appraisal approach specified in the Methods [12].

The same biological event can appear differently depending on where surveillance is positioned. Persistent MERS-CoV circulation and evolution in Saudi Arabian camels shows why reservoir surveillance can remain important despite fluctuating human disease [32]. African mpox data demonstrate that observed epidemiology is shaped by heterogeneous confirmation and surveillance capacity [33]. Emerging clade Ib evidence further shows how rapidly changing data can destabilize early assumptions [34]. Concurrent CCHFV serology among livestock and farmers in the Democratic Republic of the Congo supports shared occupational exposure while leaving individual transmission direction unresolved [35]. The proposed synthesis therefore separates detection, attribution, pathway confidence, network relevance, and response consequence; it is organizational rather than prospectively validated.

Implications for One Health preparedness

One Health preparedness should connect surveillance streams rather than simply increase isolated testing. Integrated RVF surveillance illustrates the gain from observing people, livestock, and vectors together [30], while slaughterhouse surveillance shows how production-chain nodes can reveal silent circulation [31]. Persistent camel MERS-CoV evolution supports reservoir surveillance even during quieter human periods [32], and linked livestock–farmer CCHFV exposure highlights occupational interfaces [35]. The proposed operational rule is conditional escalation: weak or discordant signals prompt verification; convergent host, laboratory, temporal, or network evidence justifies broader investigation; intervention decisions remain distinct from claims of demonstrated effectiveness.

Evidence gaps

Important gaps remain. Genomic estimates of zoonotic transitions require sensitivity analysis and external validation because model assumptions can change inferred events [27]. H5N1 containment remains limited by uncertainty about surveillance completeness, transmission structure, and measure-specific effects [29]. Rapidly changing mpox evidence likewise requires reassessment as lineage epidemiology and confirmation coverage evolve [34]. Prospective comparative studies should determine when wildlife, farm, market, slaughterhouse, vector, environmental, and human surveillance are complementary. Transmission studies should connect controlled biological plausibility with field frequency, while intervention studies should separate process completion from causal reduction in infection. These studies would test rather than presume the validity of the proposed synthesis.

Limitations

The underlying evidence has important boundaries. A large Gabon wildlife survey found no MPXV detection in sampled putative reservoirs, but non-detection cannot exclude unsampled species, tissues, places, or infection windows [36]. Age-stratified H5N1 serosurveillance shows how cross-reactive immunity can complicate susceptibility inference and cannot be equated with cattle-virus infection [37]. African swine fever risk mapping offers wildlife–livestock surveillance lessons, but ASF is non-zoonotic and cannot support human-risk claims [38]. Nipah surveillance in Indian *Pteropus* populations further shows that molecular non-detection can coexist with serologic evidence because the assays capture different temporal states [39]. Review-flow and appraisal summaries also remain unavailable because reconciled ledgers were absent.

Conclusion

This living systematic review organizes emerging interface threats around what surveillance can legitimately establish: detection, reservoir evidence, pathway confidence, exposure-network relevance, intervention evidence, and preparedness consequence. The proposed evidence-state architecture is intended to prevent positive signals from being mistaken for proof of transmission or effectiveness and to make uncertainty explicit. Its usefulness depends on reproducible updating, design-sensitive interpretation, and version control. It should be revised as stronger prospective surveillance, field transmission, and intervention evidence accumulates across wildlife, livestock, human, vector, and production-system interfaces.

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