



Wildlife health, disease surveillance, emerging infectious diseases and zoonotic disease risks in wild animal populations

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Abstract

Background: Wild animal populations serve as reservoirs for a substantial share of pathogens capable of infecting humans and domestic animals, and intensifying anthropogenic pressure is bringing wildlife, livestock, and human communities into closer and more frequent contact.

Objective: This narrative review synthesises the scientific literature on wildlife health monitoring, disease surveillance systems, the ecological drivers of emerging infectious disease (EID) in wild animal populations, and the zoonotic risks these diseases pose to public health.

Methods: Peer-reviewed articles, systematic reviews, and institutional and governmental reports, largely published between 2012 and 2026, were identified through structured searches of biomedical, veterinary, and ecological literature and synthesised thematically; no primary data were collected. Results: Land-use change, climate-driven range redistribution, wildlife trade, and urbanisation emerge as principal drivers that reshape host communities and expand the human-wildlife-livestock interface at which spillover occurs. Case evidence drawn from bat-associated coronaviruses, the 2020-2024 clade 2.3.4.4b highly pathogenic avian influenza panzootic, and fungal wildlife diseases such as white-nose syndrome and chytridiomycosis illustrates both the zoonotic and the conservation dimensions of disease emergence in wildlife. Surveillance capacity remains geographically and technically uneven: passive carcass-based reporting, targeted sentinel-species sampling, genomic sequencing, and emerging environmental DNA (eDNA) tools offer complementary but unevenly resourced detection pathways.

Conclusion: Strengthening integrated, One Health-aligned wildlife disease surveillance, particularly in under-resourced high-risk regions, is essential to narrow the interval between pathogen emergence in wildlife and detection of spillover risk to humans and domestic animals.

Keywords: Wildlife health, disease surveillance, emerging infectious diseases, zoonotic spillover, One Health, pathogen ecology

Introduction

Infectious disease emergence has, over the past three decades, become inseparable from the health of wild animal populations. A widely cited analysis of emerging infectious disease events found that roughly sixty per cent of such events are zoonotic in origin, and that more than seventy per cent of zoonotic pathogens originate in wildlife rather than domestic animals, underscoring wild fauna as the principal upstream source of novel human pathogens. The COVID-19 pandemic, whatever its precise origin, sharpened global attention on this relationship and exposed how thinly resourced wildlife health surveillance remains relative to its consequence for human and animal health security.

Wildlife health surveillance is the systematic collection, analysis, and interpretation of data on disease, mortality, and pathogen circulation in free-ranging animal populations, undertaken to detect emerging threats before they cross into humans or domestic animals, and to protect biodiversity from novel pathogens in their own right. Unlike human or livestock disease surveillance, which benefit from established clinical reporting infrastructure, wildlife disease surveillance depends on opportunistic carcass discovery, targeted field sampling, and diagnostic capacity that is unevenly distributed across regions and taxa. This asymmetry matters because the ecological conditions that generate spillover risk, tropical forest margins, wildlife trade networks, and climate-altered habitats, are frequently located precisely where surveillance infrastructure is weakest.

This review synthesises current literature across three interlinked themes: the ecological and anthropogenic drivers that increase the frequency and risk of pathogen emergence in wild animal populations; illustrative disease systems, spanning bat-associated coronaviruses, the ongoing avian influenza panzootic, and non-zoonotic but ecologically catastrophic fungal wildlife diseases, that demonstrate these dynamics in practice; and the surveillance approaches, technologies, and persistent gaps that shape how quickly emerging threats are detected. The review closes by considering governance implications for One Health-aligned surveillance and prevention.

Conceptual Framework: Wildlife Health within One Health

The One Health concept holds that human, animal, and environmental health are interdependent and best safeguarded through coordinated, cross-sectoral action rather than siloed disease-specific responses. Within this framework, wildlife health occupies a pivotal but historically under-resourced position: wild animals are simultaneously reservoirs of pathogens with zoonotic potential, sentinels whose morbidity and mortality can provide early warning of environmental or infectious hazards, and a conservation concern in their own right when disease itself threatens population persistence.

It is useful to distinguish between a zoonotic disease case, an instance in which a specific individual or group has been diagnosed with a defined illness, and a zoonotic disease event, the broader constellation of ecological, environmental, and epidemiological conditions surrounding transmission, including situations that elevate future outbreak probability without yet producing a diagnosed case. Reactive surveillance, built around confirmed human cases, systematically lags behind the ecological processes that create risk. Figure 1 summarises the conceptual pathway from upstream anthropogenic drivers, through wildlife reservoir disruption and the human-wildlife-livestock interface, to downstream health outcomes and the feedback role of One Health surveillance in shortening detection-to-response timelines.

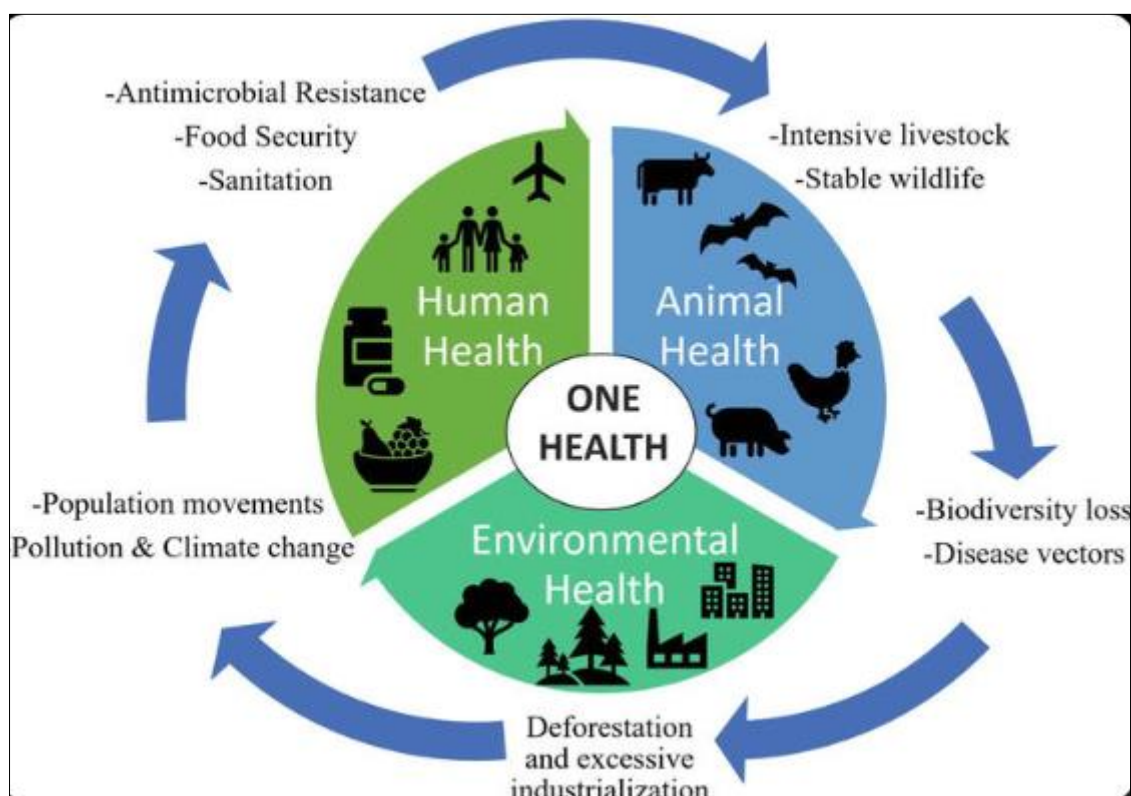


Fig 1: Conceptual framework linking anthropogenic drivers, wildlife reservoirs, the spillover interface, and One Health surveillance feedback in the emergence of zoonotic and wildlife-associated infectious disease.

Review Methodology

This review adopts a narrative, thematic synthesis approach rather than a formal systematic review or meta-analysis; it was not registered on a systematic-review platform, and no protocol-driven risk-of-bias scoring was applied, a methodological choice appropriate to the breadth of the topic but noted here as a transparent limitation. Literature was identified through structured searches of biomedical and life-science databases and search engines, including PubMed/MEDLINE, Web of Science, Scopus, and Google Scholar, together with institutional sources such as the World Organisation for Animal Health (WOAH), the U.S. Geological Survey National Wildlife Health Center, and peer-reviewed preprint servers, using combinations of terms including "wildlife disease surveillance", "zoonotic spillover", "emerging infectious disease", "One Health", "bat coronavirus", "avian influenza wild birds", and "environmental DNA pathogen detection".

Sources were prioritised for inclusion where they represented primary empirical research, systematic reviews or meta-analyses, or authoritative institutional guidance published predominantly between 2012 and 2026, with older landmark studies retained where they remain foundational to the field. Because this is a synthesis of previously published, publicly available literature and involves no new data collection, animal handling, or human participants, no ethics approval or informed consent was required.

No original experimental, epidemiological, or laboratory data are reported; all quantitative figures and case findings cited below are attributed to their original published sources and should not be interpreted as new findings generated by this review.

Drivers of Emerging Infectious Disease in Wild Animal Populations

1. Land-Use Change and Habitat Fragmentation

Deforestation and other forms of land-use change are among the most consistently implicated drivers of zoonotic disease emergence in the literature. Clearing intact forest for agriculture, logging, or settlement increases the length of ecological edges, or ecotones, between human-modified and natural habitat, bringing humans, livestock, and wildlife into more frequent and closer contact. Emerging infectious disease hotspots, though comprising a small fraction of global land area, disproportionately account for global spillover risk, because dense human and domestic animal populations there live in close proximity to remaining wildlife habitat and to wildlife trade activity. Notably, spillover risk does not disappear once cleared land begins to regenerate: modelling work indicates that regenerating secondary forest can retain elevated spillover risk relative to mature forest for an extended period, depending on how quickly it regains the species composition and structural complexity of primary habitat, meaning that reforestation efforts require accompanying wildlife-management and human-exposure awareness to avoid inadvertently prolonging risk.

Large-scale land transactions and agricultural conversion further concentrate this risk geographically: global analyses of large-scale land acquisitions show that Southeast Asia and Latin America host both extensive land-use transformation and elevated overlap with zoonotic reservoir species distributions, positioning these regions as priorities for both deforestation prevention and ecological restoration.

Across the land-use literature, several recurring ecological mechanisms link habitat change to spillover risk:

- Expansion of ecotones and habitat edges, increasing the frequency of human, livestock, and wildlife contact.
- Community disassembly favouring generalist, disturbance-tolerant reservoir species (for example, certain rodents and bats) over specialist species less able to persist in degraded habitat.
- Loss of roosting, denning, or feeding habitat, which can concentrate wildlife populations and increase intraspecific contact and pathogen transmission.
- Erosion of any protective "dilution effect" that diverse host communities may otherwise provide, a hypothesis that remains actively debated in the disease-ecology literature.
- Increased human presence and mobility into newly accessible or regenerating landscapes.

2. Climate Change and Host Range Redistribution

Climate change is increasingly recognised as a driver of disease emergence that operates largely through its effects on host and vector geography rather than through direct pathogen effects alone. As temperature and precipitation patterns shift, the ecological niches of many wildlife species are projected to move poleward or to higher elevations, bringing previously isolated host species, and the pathogens they carry, into contact for the first time. Phylogeographic modelling of mammalian host-virus networks projects that a very large number of first-time viral sharing events between mammal species could occur by 2070 under combined climate and land-use change scenarios, with the geographic areas of greatest projected range overlap concentrated in tropical and subtropical regions that are also human population centres.

Regional case evidence supports this pattern. In Australia, climate-driven southward range expansion of flying-fox populations has been associated with a substantial increase in the estimated number of horses geographically exposed to Hendra virus spillover risk, illustrating how climate-mediated reservoir movement can materially expand the human and animal population at risk without any change in the pathogen itself. Similarly, ecological niche modelling of monkeypox virus reservoir species in the Congo Basin indicates that forest clearing and climate variables jointly shape current and projected transmission risk to humans. Beyond individual case studies, trait-based vulnerability assessments of mammal species show that many species most vulnerable to climate-driven range and population change are not consistently prioritised within existing national wildlife disease surveillance programmes, indicating a structural mismatch between where disease-emergence risk is rising and where surveillance effort is concentrated.

3. Wildlife Trade, Markets, and Direct Human-Wildlife Contact

Legal and illegal wildlife trade and live-animal markets create some of the most direct and highest-risk opportunities for pathogen spillover, because they physically co-locate multiple wild and domestic species, along with humans, under conditions of stress, close confinement, and limited biosecurity. Historical precedent is well established: viral surveillance following the 2002-2004 severe acute respiratory syndrome (SARS) outbreak identified SARS-related coronaviruses in civets and other wildlife sold in live-animal markets, and a substantial reservoir of related bat coronaviruses was subsequently documented in the region. The COVID-19 pandemic renewed this concern, with early epidemiological and environmental evidence linking the outbreak's origins to a live-animal market in Wuhan, prompting calls to restrict the sale of wild-caught and exotic animals in such settings and to integrate wildlife-trade monitoring more closely with zoonotic disease surveillance.

4. Urbanisation and Agricultural Intensification

Urban expansion and the intensification of livestock production compound the drivers described above by increasing the density and proximity of human, domestic animal, and synanthropic wildlife populations. Species that adapt well to human-modified environments, including many bats, rodents, and wild bird species, often persist or even thrive at the urban-wild interface, sustaining pathogen circulation in close proximity to dense human populations and creating durable, long-term spillover opportunities rather than isolated events tied to a single land-clearing episode.

Illustrative Wildlife Disease Systems

1. Bat-Associated Coronaviruses and Pandemic Preparedness

Bats host a notably diverse assemblage of coronaviruses, and interest in systematic bat coronavirus surveillance increased sharply following the emergence of SARS-CoV-2. A systematic review and meta-analysis of bat coronavirus sampling conducted between 1996 and 2019 compiled data from well over one hundred studies and nearly ninety thousand bat samples, and found that viral detection was maximised through repeated sampling of the same site and through analysis of rectal or faecal rather than blood samples. Importantly, the same analysis found that pre-pandemic sampling effort was heavily concentrated in China, leaving substantial surveillance gaps across South Asia, the Americas, and sub-Saharan Africa, regions that host considerable undersampled bat diversity and correspondingly uncertain zoonotic risk.

Since the COVID-19 pandemic, several national and regional programmes have sought to close these gaps, including harmonised passive wildlife coronavirus surveillance in Italy, dedicated bat and coronavirus tracking by the United States Geological Survey's National Wildlife Health Center, coordinated frameworks for coronavirus surveillance across African bat and wildlife populations, and targeted SARS-CoV-2 reverse-spillover surveillance in North American urban wildlife populations, reflecting concern that an established wildlife reservoir could complicate long-term pandemic control. Collectively, this body of work illustrates both the value and the current unevenness of bat-focused surveillance as a pandemic-preparedness tool.

2. The 2020-2024 Highly Pathogenic Avian Influenza Panzootic in Wild Birds

The clade 2.3.4.4b lineage of highly pathogenic avian influenza (HPAI) H5N1, first detected causing unusual wild bird mortality in Europe in 2021, has since produced what has been described as the largest avian panzootic on record, marking a notable departure from earlier HPAI outbreaks in which wild birds served mainly as an asymptomatic reservoir rather than as victims of severe disease themselves. Surveillance reports and field investigations have documented mass mortality events across multiple continents, illustrating both the scale of the outbreak and the diversity of surveillance approaches used to track it:

1. A large die-off of migratory waterbirds on Maliy Zhemchuzhniy Island in the Caspian Sea, Russia, in May 2022, confirmed as clade 2.3.4.4b H5N1 through post-mortem virological investigation.
2. Mass mortality among wild birds across eastern Canada from 2021 onward, following the first detection of the clade in North America in a gull at a wildlife rehabilitation facility in Newfoundland.
3. Severe mortality in black-legged kittiwake breeding colonies in northern Norway in 2023, with tens of thousands of carcasses recorded in a single region over one month.
4. Spillover from wild birds into farmed fur-bearing mammals (foxes, minks, and raccoon dogs) in Finland in 2023, a development of particular concern because mammalian infection increases opportunity for viral adaptation toward mammalian, and potentially human, transmissibility.
5. Community-based surveillance of found-dead birds in Galveston County, Texas, in 2025-2026, combining citizen reporting with molecular diagnostics and genomic sequencing to characterise circulating genotypes and offer antiviral prophylaxis to exposed residents, without documented human infection.

Taken together, these events demonstrate how wild bird mortality surveillance functions simultaneously as a wildlife health concern, an agricultural biosecurity early-warning system for poultry, and a sentinel for pathogen evolution with pandemic potential, while also revealing how unevenly resourced and coordinated such surveillance remains across different countries and regions.

3. Fungal Wildlife Diseases: White-Nose Syndrome and Chytridiomycosis

Not all consequential wildlife diseases are zoonotic, and two fungal diseases illustrate why wildlife health surveillance retains intrinsic conservation value independent of direct human health risk. White-nose syndrome, caused by the cold-adapted fungal pathogen now classified as *Pseudogymnoascus destructans*, was first documented in hibernating bats in New York State in 2006 and has since spread across much of North America, disrupting hibernation physiology and causing premature arousal, exhaustion, and death; estimates place cumulative bat mortality in the millions, with some analyses projecting that roughly a third of North American bat species face conservation-status deterioration as a result. Chytridiomycosis, caused by the fungal pathogen *Batrachochytrium dendrobatidis*, has independently driven catastrophic amphibian population declines and extinctions worldwide, with several hundred amphibian species affected. Comparative analysis of the two diseases has identified striking parallels in their emergence dynamics, environmental persistence, and host-pathogen interactions, suggesting that lessons from managing one may usefully inform management of the other and of future emerging fungal pathogens more broadly.

These fungal disease systems reinforce a broader point relevant to surveillance design: an exclusively zoonosis-focused surveillance architecture risks overlooking wildlife pathogens with severe ecological and biodiversity consequences that do not directly threaten human health but that can destabilise ecosystems, insect population regulation, and, indirectly, agricultural and public health outcomes that depend on ecosystem services.

Wildlife Disease Surveillance: Approaches, Technologies, and Gaps

Wildlife disease surveillance systems are commonly organised along a spectrum from passive to active monitoring. Passive surveillance relies on opportunistic reporting of found-dead or visibly diseased animals, often by members of the public, wildlife rehabilitators, or hunters, and is comparatively low-cost but subject to substantial detection bias toward conspicuous, large-bodied, or urban-adjacent species. Active or targeted surveillance instead involves systematic field sampling of specific sentinel species, chosen for their susceptibility to infection, ecological exposure, or likelihood of encountering a pathogen of concern, as in the routine sampling of wild bird populations for avian influenza or of bat populations for coronaviruses.

Molecular and genomic technologies have substantially expanded what surveillance programmes can detect and how quickly. Real-time polymerase chain reaction (PCR), multiplex qPCR panels, and next-generation sequencing now allow simultaneous screening for multiple pathogens and rapid genomic characterisation of detected strains, as demonstrated in the genomic reassortment analysis performed during recent community-based avian influenza surveillance. Emerging CRISPR-based diagnostic methods offer further potential for rapid, field-deployable pathogen detection, although high costs, complex data-analysis requirements, and incomplete reference genome databases currently constrain their large-scale deployment, particularly in resource-limited, high-risk regions.

Environmental DNA (eDNA) and environmental RNA approaches represent a further advance, enabling pathogen and host detection from water, soil, or air samples without requiring direct animal capture or handling. In aquatic systems, eDNA-based detection of the crayfish plague pathogen *Aphanomyces astaci* has been shown to precede visible mortality events by roughly three weeks compared with conventional detection methods, illustrating the genuine early-warning potential of environmental sampling. Complementary advances in wildlife biologging and tracking, when integrated with disease surveillance data, have been proposed as a means of achieving near-real-time, spatially explicit assessment of outbreak dynamics in tracked animal populations, supporting both disease management and conservation decision-making simultaneously.

Despite these technological advances, several structural gaps persist across the wildlife disease surveillance literature:

1. Geographic concentration of historical surveillance effort in a small number of well-resourced countries, leaving substantial gaps in tropical and subtropical regions that combine high biodiversity with elevated spillover risk.
2. Under-reporting of negative or baseline surveillance results, which limits the ability to distinguish genuine pathogen emergence from simple detection-effort bias.
3. Limited longitudinal, repeat sampling at the same sites, despite evidence that repeated sampling substantially improves pathogen detection sensitivity.
4. A mismatch between species identified as most vulnerable to climate-driven disease emergence and the species actually prioritised within existing national surveillance programmes.
5. Fragmented data-sharing arrangements across wildlife, agricultural, and public health agencies, slowing the translation of wildlife surveillance findings into public health or biosecurity action.

One Health Governance, Policy, and Zoonotic Risk Mitigation

Post-pandemic assessments of global health security frameworks have consistently identified wildlife and environmental health as the most neglected pillar relative to its contribution to pandemic risk. Reviews of national and multisectoral health-security evaluations conducted between 2007 and 2020 found persistent, unaddressed gaps specifically related to wildlife and environmental drivers of spillover, despite these same evaluations existing well before the COVID-19 pandemic exposed the practical consequences of that neglect. International initiatives such as the United States Agency for International Development's PREDICT programme, and the World Organisation for Animal Health's dedicated Working Group on Wildlife, represent attempts to institutionalise wildlife health surveillance within broader pandemic-preparedness architecture, though sustained funding and coordination across such initiatives remain ongoing challenges.

Economic analyses reinforce the case for shifting investment upstream, toward prevention at the source, rather than concentrating resources on outbreak response after spillover has already occurred. Spatial prioritisation modelling of deforestation-prevention and ecological-restoration interventions across fifty countries estimates that hundreds of thousands of square kilometres of land could meaningfully reduce zoonotic spillover risk if protected or restored, most of it currently outside existing protected-area networks; the same analyses note that prevention-oriented investment costs only a fraction of reactive outbreak mitigation, yet funding remains disproportionately weighted toward the latter. Complementary measures, including stronger regulation of wildlife trade, expanded genomic surveillance in under-resourced hotspots, and formal integration of wildlife health data into pandemic early-warning systems, are widely recommended across the literature, though implementation remains uneven.

Synthesis and Discussion

The literature reviewed here converges on a consistent narrative: wildlife disease emergence is not a series of isolated, unpredictable events but a reasonably well-characterised outcome of anthropogenic pressure on natural systems, operating through identifiable ecological mechanisms that increase the frequency and intimacy of contact at the human-wildlife-livestock interface. The case evidence examined, spanning bat coronavirus ecology, the ongoing avian influenza panzootic, and fungal wildlife diseases, shows that these mechanisms operate across diverse pathogen types and taxa, reinforcing the case for broad, taxonomically inclusive surveillance rather than pathogen-specific vigilance alone. Yet detection capacity has not kept pace with this understanding of risk: the same tropical forest-margin regions repeatedly identified as ecological spillover hotspots also recur as areas of comparatively sparse surveillance effort, a spatial mismatch that stands out as the single most actionable structural gap in current wildlife health and zoonotic risk governance.

Limitations of This Review

Several limitations should be acknowledged. This is a narrative rather than a formally registered systematic review: search terms and inclusion criteria were structured and transparent, but the process does not follow a PRISMA-type protocol, was not independently duplicated by a second reviewer, and does not apply a formal risk-of-bias or evidence-quality scoring system. The reference list was deliberately limited to preserve readability, so some relevant regional or species-specific literature could not be incorporated, and the review draws mainly on English-language, openly indexed sources, which may under-represent regional grey literature. This field is also evolving rapidly, particularly regarding the ongoing avian influenza panzootic and post-pandemic surveillance policy reform, so the synthesis presented here reflects the literature current to the time of writing rather than a static account. Finally, because this is a synthesis of secondary literature rather than an analysis of primary data, no

new statistical findings or original results are reported; all quantitative claims are attributed to, and should be verified against, their original cited sources.

Conclusion

Wild animal populations sit at the ecological origin of most emerging infectious diseases affecting humans, yet wildlife health surveillance remains structurally under-resourced relative to this role, particularly in the tropical and subtropical regions where anthropogenic pressure on wildlife habitat is most intense. This review has synthesised evidence on the drivers of wildlife disease emergence, land-use change, climate-driven host redistribution, wildlife trade, and urbanisation, alongside illustrative disease systems and the surveillance technologies, from passive carcass reporting to genomic sequencing and environmental DNA, that are used to detect them. The consistent conclusion across this literature is that proactive, upstream investment in wildlife health surveillance and habitat-based spillover prevention offers a more cost-effective and timely path to reducing zoonotic and wildlife disease risk than reactive outbreak response alone. Realising this potential will require sustained cross-sectoral funding, closer integration of wildlife, agricultural, and public health data systems, and deliberate prioritisation of surveillance capacity in the geographic and taxonomic gaps identified throughout this review.

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