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Poultry and Livestock Disease Surveillance, Diagnosis, and Control

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Systematic Review

Keywords: Poultry, ruminants, transboundary animal diseases, zoonoses, diagnostics, surveillance, One Health

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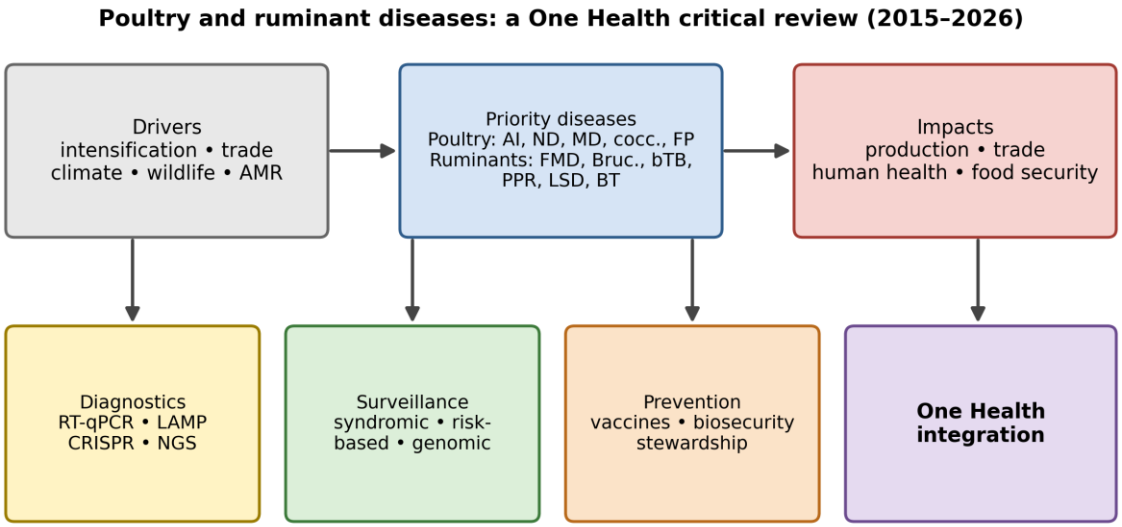
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Poultry and Livestock Disease Surveillance, Diagnosis, and Control

Highlights

- Priority poultry and ruminant diseases are chosen using explicit criteria
- Diagnostic tools are compared by purpose, specimen, speed and field suitability
- Leaky Marek's vaccines and FMD carriers show vaccines can reshape pathogens
- H5N1 in dairy cattle shows why surveillance must cross species boundaries
- A tiered One Health workflow is proposed for resource-limited settings

Graphical abstract



Graphical abstract. Drivers, priority diseases and impacts addressed in this review, and the four intervention domains (diagnostics, surveillance, prevention and One Health integration).

Abstract

Infectious diseases of poultry and ruminants limit production, disrupt trade and threaten human health. The last decade brought panzootic H5N1 avian influenza, its spillover into dairy cattle, and incursions of foot-and-mouth disease (FMD), peste des petits ruminants (PPR) and lumpy skin disease into Europe. This critical review compares diagnostic, surveillance and prevention approaches for priority diseases of poultry (avian influenza, Newcastle disease, Marek's disease, coccidiosis, fowlpox) and ruminants (FMD, brucellosis, bovine tuberculosis, PPR, lumpy skin disease, bluetongue) in literature published between 2015 and 2026, with global coverage and attention to low- and middle-income countries. Diseases were prioritised using five explicit criteria. The synthesis shows that test performance depends on purpose, specimen and prevalence, and that access and logistics limit diagnosis more often than assay chemistry. Vaccines can reshape pathogen populations, as leaky Marek's disease vaccines and FMD carrier animals illustrate, so vaccination needs matched monitoring. Economic estimates rest on incompatible methods, cross-species surveillance is needed after H5N1 emerged in cattle, and antimicrobial stewardship is essential in poultry. We propose a tiered surveillance–diagnostic–intervention workflow for resource-limited settings and list research priorities, including field validation of rapid and genomic tools and harmonised economic frameworks.

Keywords: Poultry; ruminants; transboundary animal diseases; zoonoses; diagnostics; surveillance; One Health

1. Introduction

Poultry and ruminant production underpins the diets and incomes of billions of people, and the sector keeps growing as populations urbanise and demand for animal protein rises. Chickens are the most numerous farmed animals on the planet, and cattle, buffalo, sheep and goats are spread across nearly every agricultural region (Gilbert et al., 2018; Robinson et al., 2014). Infectious disease is one of the main brakes on this system. It lowers growth, fertility and yield, closes export markets, and, for a sizeable group of pathogens, moves into people. Roughly six in ten human pathogens are zoonotic, and about three-quarters of those that have newly emerged have an animal origin (Taylor et al., 2001; Jones et al., 2008). Agricultural intensification and land-use change are among the strongest drivers of that flow (Jones et al., 2013; Rohr et al., 2019).

The last decade has made this concern concrete. Clade 2.3.4.4b H5N1 avian influenza has become a panzootic that has reached most continents, including Antarctica, infected a wide range of wild and domestic mammals, and in 2024 was found in dairy cattle in the United States (Peacock et al., 2025; Caserta et al., 2024). Foot-and-mouth disease (FMD) returned to Germany, Hungary and Slovakia in 2025, peste des petits ruminants (PPR) and lumpy skin disease (LSD) entered southern and south-

eastern Europe in 2024–2025, and antimicrobial resistance (AMR) continues to erode treatment options (Murray et al., 2022; Department of Agriculture, Environment and Rural Affairs [DAERA], 2026). These events share a feature that single-disease reviews rarely stress: they cross species, sectors and borders faster than the surveillance and diagnostic systems built to catch them.

Many narrative reviews describe individual diseases, and a smaller number address a single sector. What is harder to find is a comparison of how the two largest animal-source food systems, intensive poultry and mostly extensive ruminant production, differ in the way diagnosis, surveillance and control work in practice, and what that implies for low- and middle-income countries (LMICs). This review aims to fill that gap. Its objective is to critically compare diagnostic, surveillance and prevention approaches for priority transboundary and zoonotic diseases of poultry and ruminants published between 2015 and 2026, and to derive a practical, tiered framework for applying them within a One Health perspective. Three questions guide the analysis. (1) Which diseases deserve priority, and by what criteria? (2) How do test performance, access and purpose shape diagnostic and surveillance choices in the two systems? (3) Which control measures have the strongest evidence, and where do vaccines, antimicrobials or biosecurity create unintended consequences?

2. Scope, Selection Criteria and Review Approach

2.1 Boundaries of the review

The review covers chickens and other domestic poultry, and cattle, buffalo, sheep and goats, at global scale with particular attention to LMICs and South Asia, where disease burden and diagnostic constraints are greatest. The literature window is January 2015 to October 2026. Earlier papers were retained only where they report primary mechanistic findings or assay development that later work still relies on (for example, the original description of PB2 adaptive mutations or of loop-mediated isothermal amplification). Pigs, equids and companion animals fall outside the species scope. African swine fever (ASF) is mentioned once, as a comparator, because it illustrates what happens when no effective vaccine exists.

2.2 Literature search

Searches were designed for Scopus, Web of Science and PubMed using combinations of disease names, "diagnosis", "surveillance", "vaccin*", "biosecurity", "antimicrobial resistance", "One Health", "poultry" and "ruminant*". Peer-reviewed articles in English were eligible. Outbreak status for 2024–2026 changes quickly and is not yet fully captured in journals, so official sources (WOAH, ECDC, national veterinary authorities) were used for event dates only and are labelled as such. No formal risk-of-bias scoring was applied. Field-validated findings were given more weight than in vitro or modelling results, and conflicting evidence is reported rather than averaged. Because designs and outcomes vary widely, no meta-analysis was attempted.

2.3 Disease selection

A starting pool of about twenty WOAH-listed or production-limiting diseases was screened against five criteria: zoonotic potential (C1), transboundary spread (C2), economic burden (C3), outbreak frequency in 2015–2026 (C4) and the size of the diagnostic or control gap in LMICs (C5). Each criterion was rated high, moderate or low from the sources cited in this paper. A disease was prioritised if it was rated high on at least two criteria. Fowlpox and babesiosis did not meet that rule but were kept as mechanistic exemplars of mechanical and tick-borne transmission, respectively. Table 1 shows the outcome and Figure 1 the workflow. The ratings are the author's qualitative appraisal, not a computed score, and should be read as a transparent starting point for debate.

Infectious bronchitis virus (IBV) and infectious bursal disease virus (IBDV) also meet the rule. They are not reviewed in depth because the paper already spans two production systems, and this is acknowledged as a limitation. IBV is included in the differential-diagnosis matrix (Table 3) because it is routinely confused with the respiratory diseases discussed here.

Table 1. Disease prioritisation matrix. H = high, M = moderate, L = low. Ratings are the author's qualitative appraisal from the sources cited in this review. C1 zoonotic potential; C2 transboundary spread; C3 economic burden; C4 outbreak frequency 2015–2026; C5 diagnostic or control gap in LMICs.

Disease	Main hosts	C1	C2	C3	C4	C5	Decision
HPAI	Poultry, wild birds, mammals	H	H	H	H	M	Included
Newcastle disease	Poultry	L	H	H	H	H	Included
Marek's disease	Chickens	L	M	H	M	H	Included
Coccidiosis	Poultry	L	L	H	M	H	Included
Fowlpox	Poultry	L	L	M	M	M	Exemplar
Infectious bronchitis	Chickens	L	H	H	H	M	Qualifies; not in depth
Infectious bursal disease	Chickens	L	H	H	M	M	Qualifies; not in depth
Foot-and-mouth disease	Cattle, buffalo, sheep, goats	L	H	H	H	M	Included
Brucellosis	Cattle, sheep, goats	H	M	H	M	H	Included
Bovine tuberculosis	Cattle	H	M	H	M	H	Included
PPR	Sheep, goats	L	H	H	H	H	Included
Lumpy skin disease	Cattle, buffalo	L	H	M	H	M	Included
Bluetongue	Ruminants	L	H	M	H	M	Included
Babesiosis	Cattle	L	L	M	M	M	Exemplar

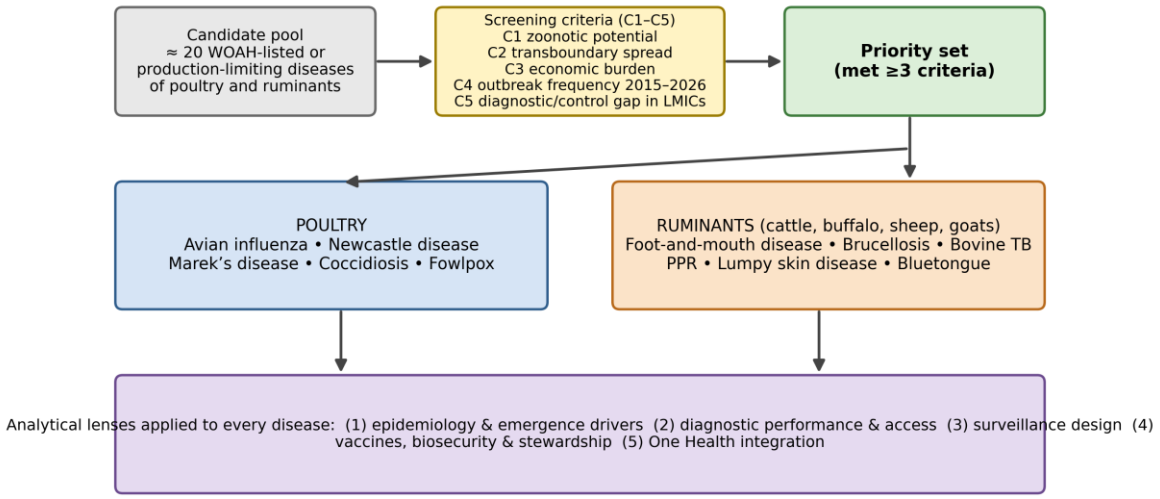


Figure 1. Workflow used to define the review scope and select priority diseases. Candidate diseases were screened against five criteria (C1–C5), and those rated high on at least two criteria were prioritised.

3. Epidemiological Context and Drivers

3.1 How diseases move

Pathogens reach and spread within farms by a limited set of routes, but the weight of each route differs by disease (Figure 2). Avian influenza virus (AIV) and Newcastle disease virus (NDV) spread through direct contact, respiratory droplets over short distances, faecal contamination of water and feed, and fomites such as crates, vehicles and boots. Live-bird markets and shared transport create dense contact networks that move virus between farms that never meet. In ruminants, FMD virus is shed in breath, milk, semen and lesion material, and spreads through animal movement, contaminated vehicles and, over short distances, aerosols. Brucellosis passes mainly through aborted fetuses, placental membranes and milk. Bluetongue, LSD and babesiosis depend on arthropods, though in different ways: *Culicoides* midges biologically transmit bluetongue virus, biting flies and mosquitoes carry LSD virus mechanically, and *Rhipicephalus* ticks transmit *Babesia* (Bock et al., 2004; Maclachlan et al., 2019; Sprygin et al., 2019).

Two points of earlier confusion are worth fixing. First, coccidiosis is not vector-borne. Chickens ingest sporulated *Eimeria* oocysts from contaminated litter, feed or water. Oocysts leave the bird unsporulated and become infective after one to two days in warm, moist, oxygenated litter, which is why litter moisture is the most practical lever on the farm (Chapman, 2014; Blake & Tomley, 2014). Insects, rodents, workers and equipment can carry oocysts mechanically, but they are not required for the life cycle. Second, fowlpox virus is spread mechanically by mosquitoes (including *Culex* and *Aedes* species) and other biting insects, and by contact with scabs and abrasions, whereas the wet form follows inhalation or ingestion of virus-laden material (Giotis & Skinner, 2019; Bolte et al., 1999). Red mites have been proposed as additional mechanical carriers, but the evidence is thin.

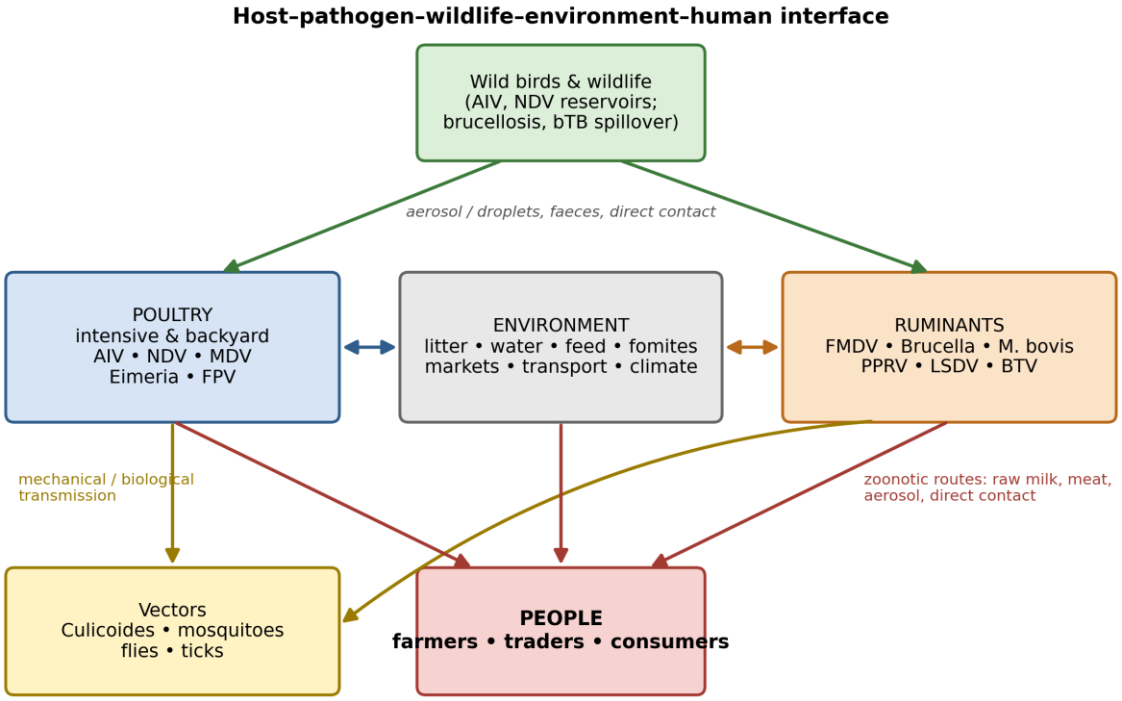


Figure 2. Conceptual schematic of the host–pathogen–wildlife–environment–human interface for poultry and ruminant diseases, showing the principal transmission routes discussed in Section 3 (author's schematic).

3.2 Risk factors with evidence behind them

Stocking density, poor ventilation, high litter moisture, mixed-age and mixed-species premises, frequent off-farm movement of animals, lapses in cleaning and disinfection, and shared equipment recur across the farm-level studies reviewed (Wu et al., 2023; Gelaude et al., 2014; Van Limbergen et al., 2018). In backyard systems the relevant risks are different: scavenging, contact with wild birds and the absence of any all-in/all-out routine (Conan et al., 2012). Seasonal demand matters too. In Vietnam, festival-driven demand for poultry meat shaped the timing of avian influenza transmission, which suggests that surveillance can be intensified before predictable peaks (Delabouglise et al., 2017).

Poor air quality deserves a mechanistic explanation because it quietly underlies many respiratory outbreaks (Figure 3). Ammonia from wet litter, together with respirable dust, impairs mucociliary clearance, damages the tracheal epithelium and promotes inflammation. Even moderate ammonia exposure has been linked to poorer broiler performance (Miles et al., 2004), and a systematic review linked particulate matter in poultry houses to respiratory disease (Wang et al., 2023). Damaged mucosa is then colonised by avian pathogenic *Escherichia coli* (APEC), usually after a viral or *Mycoplasma* primary insult, producing airsacculitis, septicaemia and carcass condemnation (Guabiraba & Schouler, 2015; Kathayat et al., 2021). Heat and other stressors add to this by impairing intestinal integrity and macrophage function (Quinteiro-Filho et al., 2010).

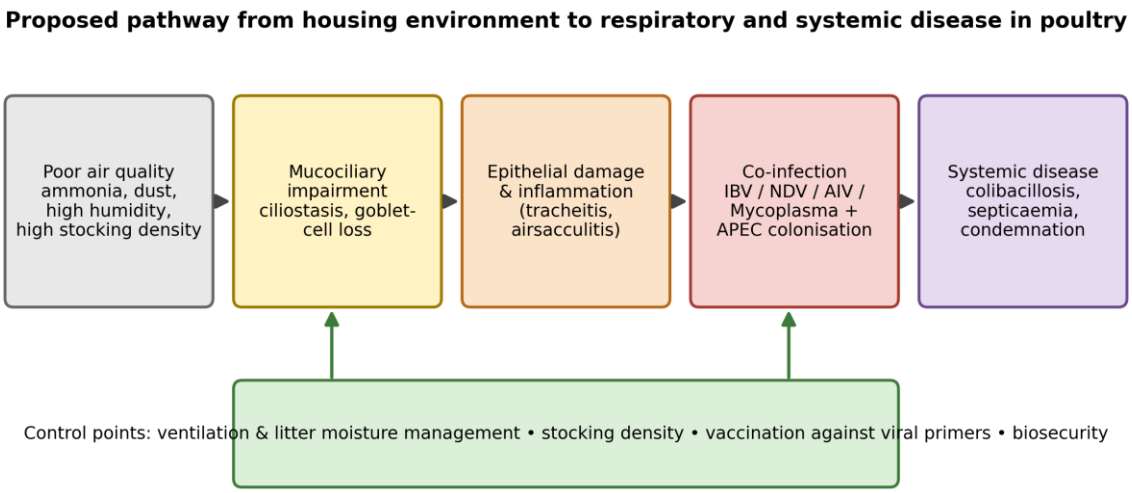


Figure 3. Proposed pathway from poor housing air quality to respiratory and systemic disease in poultry, with control points

3.3 Wildlife, climate and trade

Wild waterbirds are the natural reservoir of AIV, and the wild–domestic interface is a recurring entry route into poultry. Dabbling ducks, geese and swans are the classic reservoir hosts, and gulls, terns and other seabirds have featured prominently in the clade 2.3.4.4b panzootic (Verhagen et al., 2021; Elmberg et al., 2017). The risk is not uniform. It depends on the virus subtype, the species involved, and on contact conditions such as shared wetlands, open water sources and feed storage. Wildlife also acts as a maintenance host for brucellosis and bovine tuberculosis (bTB) in some regions (Miller et al., 2013a).

Climate change widens the range of vectors and lengthens their active season, which is the main way it alters host–pathogen contact; the north-ward spread of bluetongue in Europe is the standard example (Purse et al., 2005; Baylis, 2017; Rupasinghe et al., 2022). Legal and illegal trade in live animals, products and fomites moves viruses across continents, and the 2025 European FMD and LSD incursions are recent reminders (DAERA, 2026; Department for Environment, Food and Rural Affairs [Defra], 2026a). Figure 4 summarises the main emergence and re-emergence events since 2016. In this review "emerging" means a disease that has newly appeared in a host population or region, or whose incidence or range has recently increased, and "re-emerging" means one that returns after a period of control or absence (Taylor et al., 2001).

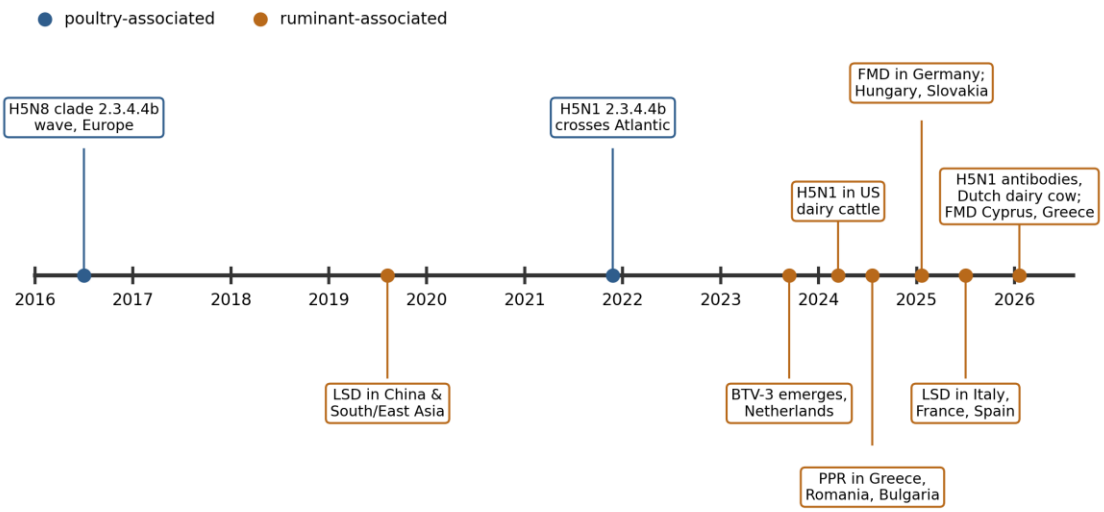


Figure 4. Selected emergence and re-emergence events in poultry- and ruminant-associated diseases, 2016–2026. "Emergence" means newly appeared in a host population or region, or reappeared after absence. Dates for 2024–2026 events come from official sources cited in Sections 4 and 5.

4. Priority Diseases of Poultry

4.1 Avian influenza

High pathogenicity avian influenza (HPAI) of the A/goose/Guangdong lineage first appeared in 1996, and its descendants have since diversified into many clades (Lycett et al., 2019). Clade 2.3.4.4b was responsible for the large European epizootics from 2016 and, from 2020, a panzootic that crossed the Atlantic in 2021 and reached the Americas (Verhagen et al., 2021; Caliendo et al., 2022; Wille & Barr, 2022). It has caused large losses in poultry, mass mortality in wild birds and repeated infections in mammals (Peacock et al., 2025).

Two features make the current situation different from earlier waves. The first is spillover into livestock. In March 2024 H5N1 was identified in US dairy cattle, where transmission appears to involve milk and milking equipment and where infected herds have been reported in more than a dozen states (Caserta et al., 2024; Nguyen et al., 2025). In January 2026 antibodies against H5N1 were found in one dairy cow in the Netherlands, the first such finding in European cattle. No virus was detected and no wider circulation was found (Defra, 2026b). The second is human exposure. Since April 2024 more than 70 human cases have been reported in the United States, most of them mild and many linked to dairy or poultry work (European Centre for Disease Prevention and Control [ECDC], 2026; Garg et al., 2025).

Surveillance targets should therefore include molecular markers of mammalian adaptation (Figure 5). Substitutions such as PB2 E627K and D701N raise polymerase activity at the lower temperature of the mammalian upper airway (Hatta et al., 2001; Steel et al., 2009), and PB2 E627K was found in the first dairy-farm worker infected in 2024 (Uyeki et al., 2024). Changes in haemagglutinin that shift

preference from avian-type (α2,3) towards human-type (α2,6) receptors are a second watch-list item, and sequencing every H5-positive sample is the only way to track both (Mostafa et al., 2018; Kandeil et al., 2023). A marker panel is a risk indicator, not a prediction. Several mutations act in combination, and their effects depend on the genetic background of the virus (Abdelwhab & Mettenleiter, 2023).

Other subtypes also deserve a place on the watch-list. H7N9 caused repeated human infections in China between 2013 and 2019, most of them linked to live-poultry markets, and illustrates how a virus of low pathogenicity in birds can still be a serious zoonotic threat (Mostafa et al., 2018).

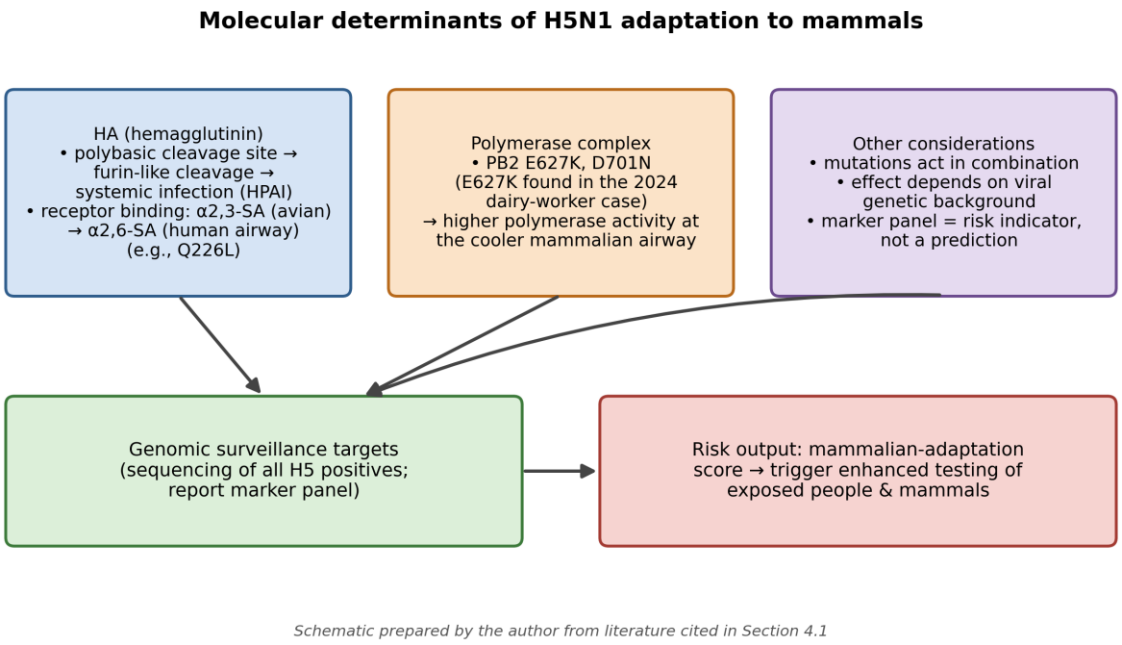


Figure 5. Molecular determinants relevant to mammalian adaptation of H5N1 viruses, and their use as genomic surveillance targets. Prepared from Hatta et al. (2001), Steel et al. (2009), Mostafa et al. (2018), Kandeil et al. (2023) and Uyeki et al. (2024).

For poultry, stamping-out and zoning remain the foundation of control in most countries. Vaccination is used in several others, but it creates trade and surveillance trade-offs because vaccinated flocks must be monitored using strategies that can tell vaccine response from infection.

4.2 Newcastle disease

Newcastle disease (ND) is caused by avian orthoavulavirus 1, and virulence is governed mainly by the amino acid motif at the fusion-protein cleavage site. Virulent strains carry multiple basic residues that allow cleavage by ubiquitous host proteases, giving systemic and neurotropic disease (Cattoli et al., 2011). The virus is classified into genotypes under a unified system, and genotype VII viruses have driven panzootic spread since the late 1990s (Dimitrov et al., 2019). ND is endemic across much of Asia, Africa and parts of Latin America, where village flocks suffer heavy and under-reported losses, and wild birds contribute to persistence in some regions (Brown & Bevins, 2017; Dimitrov et al., 2017).

Vaccination is the central tool, but it is not a complete solution. Vaccines prevent clinical disease well, yet they differ in how far they reduce shedding. Genotype-matched vaccines reduced shedding in challenge experiments, which supports updating vaccine strains in endemic regions, although the practical benefit under field conditions is debated (Miller et al., 2013b; Dimitrov et al., 2017). Experimental and field outcomes diverge because vaccine take depends on cold-chain integrity, application method and maternal antibody, which are often poorly controlled in smallholder settings (Mayers et al., 2017).

4.3 Marek's disease

Marek's disease (MD) is a lymphoproliferative disease caused by Gallid alphaherpesvirus 2. Vaccines based on herpesvirus of turkeys, SB-1 and the Rispens CVI988 strain, often given in ovo, protect against tumours and clinical disease but do not block infection or shedding of virulent virus (Gimeno, 2008; Bertzbach et al., 2020). This is the textbook case of a "leaky" vaccine. In experiments with chickens, imperfect vaccination allowed more virulent strains to be transmitted and enhanced their spread, which supports the hypothesis that vaccine use has selected for increasingly virulent field strains over decades (Read et al., 2015). The consequence is practical. Producers rely on vaccine protection that must keep being upgraded, and MD becomes a monitoring problem that depends on pathotyping and routine sequencing, not just a vaccination decision.

4.4 Coccidiosis

Coccidiosis in chickens is caused by seven *Eimeria* species that differ in site of infection and pathogenicity. A re-estimation that combined production losses, prevention and treatment put the global cost at about US$14.5 billion (2016 prices), far above the figure of roughly US$3 billion that is still often quoted (Blake et al., 2020). Control has historically depended on in-feed anticoccidials, and resistance is common (Chapman & Jeffers, 2014; Noack et al., 2019). Live vaccines, shuttle and rotation programmes, and management of litter moisture all form part of the response (Dalloul & Lillehoj, 2006; Peek & Landman, 2011). Section 8.4 returns to the pharmacology.

4.5 Fowlpox

Fowlpox, caused by an avipoxvirus, is the poultry exemplar of mechanical vector transmission. It produces cutaneous nodules on unfeathered skin (dry form) or lesions of the upper digestive and respiratory tract (wet form), and the second is more lethal. Control combines mosquito management and wing-web vaccination with live virus, and fowlpox is also the backbone of several vectored vaccines (Giotis & Skinner, 2019). Its importance is greatest in backyard and layer systems with limited vector control.

5. Priority Diseases of Ruminants

5.1 Foot-and-mouth disease

FMD virus occurs in seven serotypes, and cross-protection between them is poor, which makes vaccine matching essential (Paton et al., 2009; Jamal & Belsham, 2013). Endemic virus pools in Africa, the Middle East and Asia supply periodic incursions elsewhere (Brito et al., 2017). Persistently infected carriers complicate eradication and trade. The costs are large: estimates put annual direct losses in endemic regions between US$6.5 and 21 billion and a further US$1.5 billion or more each year from outbreaks in FMD-free countries (Knight-Jones & Rushton, 2013). Those figures are direct production and vaccination costs, not "trade losses" as sometimes cited. In January 2025 Germany reported FMD in water buffalo, its first outbreak since 1988, and in March 2025 serotype O was confirmed in Hungary and Slovakia, with outbreaks also reported in Cyprus and Greece in late 2025 and early 2026 (DAERA, 2026). Germany, Hungary and Slovakia all later regained FMD-free status without vaccination. Inactivated vaccines need boosters, a reliable cold chain and strain matching, and they perform best when combined with movement control (Diaz-San Segundo et al., 2017). Proactive vaccination strategies appear feasible where outbreaks occur in recurring waves (Casey-Bryars et al., 2018).

5.2 Brucellosis

Brucella abortus mainly affects cattle, *B. melitensis* sheep and goats, and *B. suis* pigs, but host ranges overlap, and camelids and wildlife are also involved. Brucellosis causes abortion, retained placenta and infertility, and humans acquire infection from raw milk, dairy products and contact with birth material (Godfroid et al., 2011; Dadar et al., 2019). The burden on people is substantial and often under-recognised. Pappas et al. (2006) estimated over half a million new human cases a year. In sub-Saharan Africa and other LMICs, diagnostic access, poor reporting and low farmer awareness stand in the way of control (Ducrotoy et al., 2017; Godfroid et al., 2013). Control depends on surveillance, movement control, removal of infected animals and vaccination (for example, strain RB51 or S19 in cattle and Rev-1 in small ruminants). Antibiotic treatment of infected livestock is not a control strategy, because intracellular persistence and relapse limit cure (Blasco & Molina-Flores, 2011; Khurana et al., 2021).

5.3 Bovine tuberculosis

Bovine tuberculosis (bTB) is caused by *Mycobacterium bovis*, which infects a wide range of hosts, including wildlife reservoirs in some regions. Zoonotic transmission occurs through unpasteurised milk and, more rarely, aerosols, and the human burden is thought to be underestimated (Müller et al., 2013; Olea-Popelka et al., 2017). Control rests on test-and-cull programmes that depend on the quality of the test. Vaccination with BCG is not routine in cattle, partly because it interferes with skin-test

interpretation. Evidence from India and other LMICs suggests a high but poorly characterised prevalence, and diagnostic capacity and compensation schemes are the main obstacles (Srinivasan et al., 2018). *M. bovis* is also intrinsically resistant to pyrazinamide, and drug-resistant strains have been described (Borham et al., 2022).

5.4 Peste des petits ruminants

PPR virus causes a severe morbillivirus disease of sheep and goats with high morbidity and mortality. It is endemic across Africa, the Middle East and much of Asia (Parida et al., 2015; Banyard et al., 2010). A highly effective live attenuated vaccine providing long immunity is the basis of the Global Strategy for PPR eradication, which aims for eradication by 2030 (Baron et al., 2016; Food and Agriculture Organization of the United Nations [FAO] & World Organisation for Animal Health [WOAH], 2015). The successful eradication of rinderpest demonstrated that a morbillivirus disease can be eliminated (Mariner et al., 2012). An economic analysis found eradication to be favourable in benefit-cost terms (Jones et al., 2016). In 2024–2025 PPR was reported in Greece, Romania, Bulgaria and Hungary, and in Albania (WOAH Regional Representation for Europe, 2025), so the threat is no longer confined to LMICs.

5.5 Lumpy skin disease and bluetongue

LSD virus is a capripoxvirus transmitted mechanically by biting flies, mosquitoes and ticks (Sprygin et al., 2019; Tuppurainen et al., 2017). From the Middle East it spread into the Balkans and later across Asia, including China in 2019 (Lu et al., 2021). In 2025 it appeared in Sardinia and northern Italy and in Savoie, France, and later in Catalonia, Spain (Defra, 2026a). Vector-borne spread explains why movement bans alone may be insufficient and why vaccination features strongly in control. Bluetongue is a vector-borne orbiviral disease of ruminants, and its re-emergence in northern Europe illustrates the link between climate and vector competence (Maclachlan et al., 2019; Purse et al., 2005). Babesiosis, caused by *Babesia bovis* and *B. bigemina*, is included as a tick-borne exemplar. Control relies on tick management and live attenuated vaccines, both of which face resistance and cold-chain constraints (Bock et al., 2004; Florin-Christensen et al., 2014).

5.6 Economic evidence

The economic evidence behind the headlines varies sharply in method. Table 2 sets out what each figure includes and where it comes from. Disease costs are rarely estimated on a common basis, which makes cross-disease comparison unreliable and helps explain why different reports give very different numbers for the same disease (Kappes et al., 2023; Jones et al., 2018).

Table 2. Reported economic impact of priority diseases: what each estimate includes. No pooled global figure exists for several diseases.

Disease	Reported estimate	What it includes	Source
HPAI	No pooled global estimate	Outbreak- and country-specific; depopulation, indemnity, control and trade restrictions dominate	Kappes et al. (2023)
Newcastle disease	No standardised global estimate	Mainly mortality and lost output in village flocks; under-reported	Dimitrov et al. (2017)
Marek's disease	Not comparable across studies	Mortality, condemnation and vaccination costs within production-disease reviews	Jones et al. (2018)
Coccidiosis	≈ US$14.5 billion (2016 prices), global	Production losses plus prevention and treatment; replaces the older ≈ US$3 billion figure	Blake et al. (2020)
FMD	US$6.5–21 billion per year (endemic regions); > US$1.5 billion per year (FMD-free countries)	Direct production losses and vaccination in endemic regions; outbreak costs in free countries	Knight-Jones & Rushton (2013)
Brucellosis	> 500,000 new human cases per year	Human burden; animal losses (abortion, milk) not pooled	Pappas et al. (2006)
Bovine tuberculosis	Zoonotic burden poorly measured	Human cases likely underestimated; animal losses vary by programme	Olea-Popelka et al. (2017)
PPR	Eradication favourable in benefit–cost terms	Programme cost versus avoided losses	Jones et al. (2016)

6. Diagnosis

6.1 Choosing a test by purpose

A diagnostic test has no fixed quality. Its usefulness depends on purpose, target, specimen, timing and the prevalence of infection in the tested population. A test that is excellent for confirming disease in a sick flock can give many false positives when used to certify freedom in a low-prevalence population, because positive predictive value falls with prevalence. The questions to ask are the following. Is the aim screening, confirmation, surveillance or certification for trade? Does the assay detect the pathogen, its antigen, its nucleic acid or the host antibody response? What are the specimen type and optimal time of sampling? How do vaccination and previous exposure alter interpretation? These considerations are used to structure the sections below.

6.2 Clinical and pathological diagnosis

Clinical signs rarely identify a disease on their own, but they decide when to sample and which differentials to rule out. In poultry the key problem is the overlap among respiratory and nervous syndromes (Table 3). HPAI typically causes sudden high mortality with oedema of the head and haemorrhage of the shanks in chickens, whereas ducks may be infected without obvious signs. Virulent ND often features greenish diarrhoea and nervous signs such as torticollis. Infectious laryngotracheitis (ILT) is marked by gasping and expectoration of blood-stained mucus, and IBV usually causes milder respiratory signs with egg-quality changes (Cattoli et al., 2011; World Organisation for Animal Health [WOAH], 2024). In ruminants, vesicular lesions of the mouth and feet suggest FMD but must be separated from other vesicular diseases, abortion storms point to

brucellosis among other causes, and skin nodules suggest LSD. Necropsy and histopathology (including immunohistochemistry where available) extend the clinical picture, and radiography has a limited role in field practice.

Table 3. Differential diagnosis of clinically similar respiratory diseases in chickens. Sources: WOAH (2024); Cattoli et al. (2011).

Feature	HPAI	Virulent Newcastle disease	Infectious laryngotracheitis	Infectious bronchitis
Typical signs	Sudden death, depression, facial oedema, cyanotic combs; ducks may be subclinical	Depression, greenish diarrhoea, respiratory distress, torticollis, paralysis	Gasping, head extension, blood-stained mucus, conjunctivitis	Sneezing, tracheal rales, watery eyes; fall in egg quality
Mortality	Up to about 100% in chickens	Variable; very high in naïve flocks	Low to moderate in severe form	Usually low; higher with APEC or nephropathogenic strains
Characteristic lesions	Haemorrhage on shanks; visceral necrosis	Haemorrhagic lesions of proventriculus and intestinal lymphoid tissue	Haemorrhagic or diphtheritic tracheitis; intranuclear inclusions	Mucoid tracheitis, airsacculitis; nephritis in some strains
Confirmatory test	RT-qPCR (M gene, H5/H7); cleavage-site sequencing	RT-qPCR; virus isolation; F-cleavage-site sequencing	PCR; histopathology	RT-PCR; S1 sequencing

6.3 Laboratory methods

Table 4 compares the main laboratory approaches. Real-time reverse-transcription PCR (RT-qPCR) is the workhorse for AIV and NDV, with validated assays for the influenza matrix gene, H5 and H7 subtypes and for NDV (Spackman et al., 2002; Wise et al., 2004). PCR is not restricted to viruses. Species-level assays for *Eimeria*, *Brucella* and *M. bovis* exist as well, and they are most informative when matched to the right specimen: oropharyngeal and cloacal swabs for AIV and NDV, tissue and aborted material for *Brucella*, and faeces or intestinal scrapings for *Eimeria* (WOAH, 2024). Virus isolation remains important for characterisation but requires appropriate biocontainment for HPAI. Serology (haemagglutination inhibition, ELISA) is useful for flock-level screening and monitoring, but its interpretation depends on vaccination history, which is one of the reasons that vaccination needs a DIVA strategy.

Beyond the assay itself, five practical issues determine whether a result can be trusted. The first is validation. A test needs to be validated for the species, specimen and purpose for which it is used, and kit performance claims from the manufacturer do not replace local verification. The second is false results. False negatives arise from poor sampling, degraded RNA or sampling too late in infection, while false positives arise from cross-reactivity, carry-over contamination or testing at low prevalence. The third is the distinction between screening and confirmatory tests. A rapid test may justify immediate movement restrictions, but notification and culling decisions normally rest on a confirmatory laboratory result. The fourth is biosafety and transport. HPAI, FMD and *Brucella* samples need appropriate containment and a reliable cold chain, and in practice poor sample transport

causes more failed confirmations than poor assays. The fifth is interpretation in vaccinated populations. Vaccination masks serology for AIV and NDV, and a positive RT-qPCR in a vaccinated flock may reflect vaccine virus, so sequencing is used to separate vaccine strains from field strains (Cattoli et al., 2011; WOAH, 2024).

Table 4. Comparison of laboratory approaches for priority diseases. Sources as cited in the table and WOAH (2024).

Method	Detects	Typical specimen	Strengths	Limitations and setting
RT-qPCR	Nucleic acid	Oropharyngeal and cloacal swabs; tissues	High sensitivity and specificity; results in hours; subtype and pathotype assays (Spackman et al., 2002; Wise et al., 2004)	Needs equipped laboratory and cold chain; detects non-viable RNA
Virus isolation	Live virus	Swabs and tissues in SPF eggs or cells	Provides an isolate for characterisation	Days to result; biocontainment for HPAI; low throughput
Serology (HI, ELISA)	Antibody	Serum, egg yolk, milk	Flock-level screening; low cost	Retrospective; vaccination confounds; needs DIVA strategy
Lateral-flow antigen test	Antigen	Swabs; epithelium	Minutes; pen-side	Lower sensitivity than RT-qPCR; positives need confirmation
LAMP	Nucleic acid	Swabs; tissues	Under one hour; visual readout; suits district laboratories (Notomi et al., 2000)	Primer design; amplicon contamination; local validation needed
CRISPR-Cas lateral flow	Nucleic acid	Extracted RNA or DNA	Sensitive; potentially instrument-free (Chen et al., 2018; Gootenberg et al., 2017)	Few veterinary validations; reagent access
Nanopore or NGS	Genome	Positive samples	Pathotype, lineage and adaptation markers; portable (Quick et al., 2016)	Cost, power supply, bioinformatics, data-sharing rules
Culture with susceptibility testing	Live bacteria	Tissue, faeces, milk	Isolates for AMR testing	Slow; biosafety (e.g., *Brucella*)

For ruminants, WOAH-recommended approaches are summarised in Table 5. Brucellosis serology is widely used (Rose Bengal test as a screen, ELISA or fluorescence polarisation assay for confirmation), but cross-reactivity of smooth lipopolysaccharide with other Gram-negative bacteria such as *Yersinia enterocolitica* O:9 can produce false positives, and vaccination with S19 complicates interpretation (Nielsen, 2002; Godfroid et al., 2011). For bTB, the single intradermal comparative cervical test and the interferon-gamma release assay are the main tools. Skin-test sensitivity is imperfect and specificity can be reduced by exposure to environmental mycobacteria or *M. avium* complex (de la Rua-Domenech et al., 2006). For FMD, RT-qPCR and antigen detection confirm acute cases, and antibodies against non-structural proteins help to distinguish infected from vaccinated animals, with the caveat that repeated vaccination with insufficiently purified products can produce non-specific reactions.

Table 5. Diagnostic approaches and known pitfalls for priority ruminant diseases. Sources: WOAH (2024) and the references cited in the table.

Disease	Screening	Confirmation	Known limitations
Brucellosis	Rose Bengal test; milk ring test	ELISA (indirect or competitive), fluorescence polarisation; culture; PCR	Cross-reaction with *Yersinia enterocolitica* O:9 and other smooth-LPS bacteria; S19 vaccine antibodies (Nielsen, 2002)

Disease	Screening	Confirmation	Known limitations
Bovine tuberculosis	Comparative intradermal test; interferon-gamma assay	Culture; PCR; histopathology	Imperfect skin-test sensitivity; environmental mycobacteria reduce specificity (de la Rua-Domenech et al., 2006)
FMD	Antigen lateral-flow test; NSP ELISA	RT-qPCR; virus isolation; serotyping	NSP-based DIVA affected by repeated vaccination with impure products; carriers need probang sampling (WOAH, 2024)
PPR	Competitive ELISA	RT-qPCR; sequencing	Serology reflects past exposure or vaccination (Parida et al., 2015)
Lumpy skin disease	Clinical signs	PCR; virus isolation	Subclinical infection; relatedness of capripoxviruses (Tuppurainen et al., 2017)
Bluetongue	Competitive ELISA	RT-qPCR; serotyping	Serotype-specific vaccines and assays; vector surveillance needed (Maclachlan et al., 2019)

6.4 Rapid and advanced platforms

Conventional PCR is no longer the only option. Isothermal methods such as loop-mediated isothermal amplification (LAMP) amplify target nucleic acid at a constant temperature in under an hour and can be read by eye, which suits district laboratories and some field use (Notomi et al., 2000). Their weak points are primer design complexity, amplicon contamination and variable performance across lineages, so they are best validated against RT-qPCR locally. CRISPR-Cas-based assays use collateral nuclease activity for sensitive nucleic acid detection and can be combined with lateral flow readouts (Chen et al., 2018; Gootenberg et al., 2017). These systems have mostly been developed and validated for human pathogens, and veterinary validation, including for AIV and NDV, is at an early stage. Portable nanopore sequencing has proved field-deployable for outbreak genomics (Quick et al., 2016). It has an obvious role in pathotyping, in tracking spread and in screening for adaptation markers, but cost, power supply, bioinformatic capacity and data-sharing rules limit uptake in LMICs. Biosensors are another active area (Vidic et al., 2017). A realistic expectation is that these tools complement, and do not replace, laboratory confirmation.

7. Surveillance

Surveillance converts diagnostic results into decisions. Following the standard terminology, passive surveillance relies on reports from farmers and veterinarians, active surveillance involves planned sampling, syndromic surveillance uses non-specific indicators such as mortality, milk drop or abortion, and risk-based surveillance directs effort to higher-risk animals, places or times (Hoinville et al., 2013; Stärk et al., 2006; Dórea et al., 2011). Genomic surveillance adds sequence data to any of these. Each design has costs. Passive systems are cheap but suffer from underreporting, and active sampling gives more precise estimates at a higher price.

The two production systems favour different mixes. In intensive poultry, high flock mortality and frequent veterinary contact make syndromic triggers and routine submission of dead birds effective for detecting HPAI and ND, and the extreme number of birds makes batch testing and risk-based

sampling around wild-bird activity economical. In ruminant systems, animals are often dispersed, mobile and owned by smallholders or pastoralists, so detection depends on village reporting, abattoir inspection, milk or herd-level testing, and cross-border coordination. Studies from LMICs explored whether syndromic information from rural poultry farmers could supplement formal reporting, and the findings stress the importance of farmer engagement and feedback (Mubamba et al., 2018).

Wildlife and genomic components need separate mention. Passive surveillance of dead wild birds is the usual early-warning tool for HPAI, and it works best when it is linked to poultry-farm reporting so that detections in wild birds trigger enhanced checks on nearby farms (Verhagen et al., 2021). Sequence data add the ability to distinguish new introductions from local spread and to read adaptation markers, but they are only useful if sequences are shared quickly and metadata (host, date, location) are complete (Quick et al., 2016). For LMICs, a pragmatic approach is to sequence a defined subset of positives, for example all first detections in a region and all cases in unusual hosts, at a regional laboratory, instead of aiming for complete coverage.

Integrated systems link human, animal and environmental data. Experience from East Africa shows that joint surveys of people and livestock can reveal health and economic links that sector-specific surveys miss (Thumbi et al., 2015), and that endemic and emerging zoonoses share surveillance bottlenecks that can be addressed together (Halliday et al., 2012). Proposals for brucellosis control in LMICs make a similar point: move away from improvisation and towards shared planning (Godfroid et al., 2013). Figure 6 shows a tiered workflow that follows these lessons. Syndromic reporting is the base, district laboratories use rapid screening, national laboratories confirm and sequence, and reference laboratories provide characterisation and notification. The workflow is a proposal derived from the evidence reviewed. It has not been tested as a whole, and its components would need local adaptation.

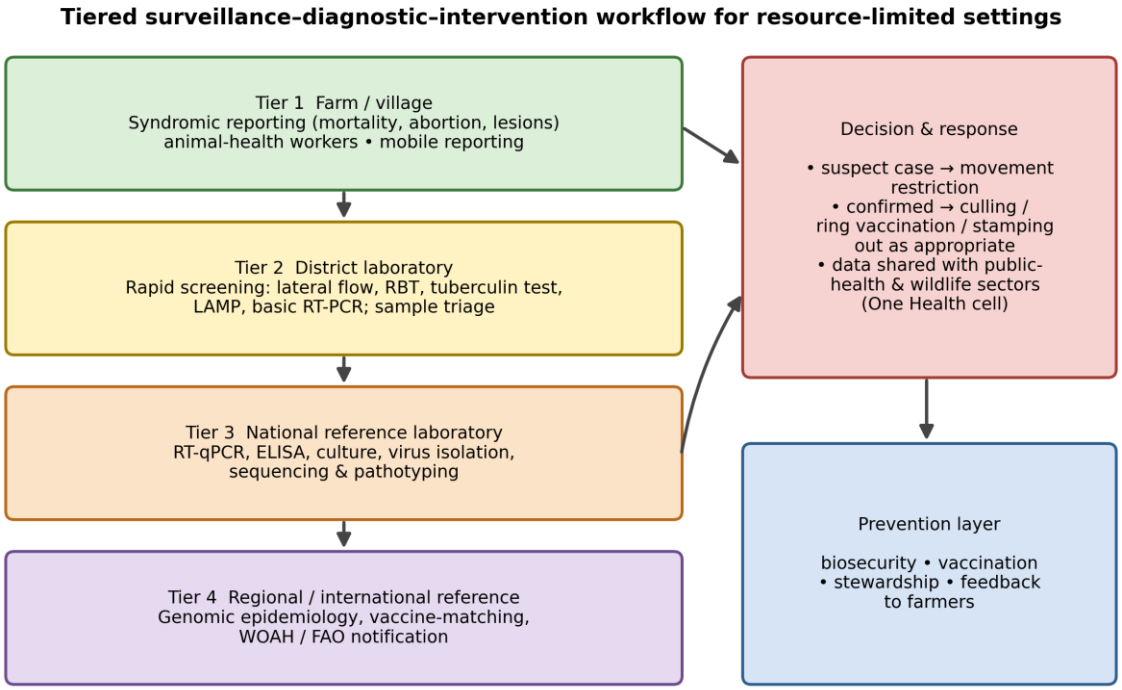


Figure 6. Tiered surveillance–diagnostic–intervention workflow proposed for resource-limited settings (author's synthesis of the evidence reviewed; not field-tested).

8. Prevention and Control

8.1 Terminology

The terms prevention, control, containment, elimination and eradication are used in this paper as follows. Prevention means stopping introduction of a pathogen. Control means reducing incidence or prevalence to an acceptable level. Containment means restricting spread within a defined zone or population. Elimination means zero cases in a defined region with continued intervention, and eradication means permanent worldwide zero incidence.

8.2 Vaccines

Vaccination remains the foundation for many diseases, yet "vaccination" is not a single approach. Table 6 compares the main platforms. Live attenuated vaccines (ND, PPR, fowlpox, Rev-1) are cheap and induce strong immunity but need cold chains and carry reversion or recombination risks. Inactivated adjuvanted vaccines (AI, FMD, some ND) are safe but require injection and boosters, and may not stop shedding. Viral-vectored vaccines such as HVT-vectored products allow DIVA strategies and in ovo delivery. DNA and mRNA platforms are attractive for rapid strain updating but remain largely experimental or conditionally licensed for animals and are expensive for commercial poultry.

Table 6. Vaccine platforms used or under development for poultry and ruminant diseases.

Platform	Examples	Strengths	Limitations
Live attenuated	ND, PPR, fowlpox, Rev-1, S19	Low cost; strong, long immunity (PPR) (Baron et al., 2016)	Cold chain; reversion or recombination risk; S19 interferes with serology (Blasco & Molina-Flores, 2011)
Inactivated, adjuvanted	AI, FMD, some ND	Safe; strains can be updated	Injection and boosters; may not stop shedding (Diaz-San Segundo et al., 2017)
Cell-associated herpesvirus	HVT, SB-1, CVI988 (Marek's disease)	Tumour protection; in ovo use	Leaky; do not block shedding (Gimeno, 2008; Read et al., 2015)
Viral-vectored	HVT-ND, HVT-AI, fowlpox-vectored	DIVA potential; in ovo delivery; long immunity	Cost; pre-existing immunity to the vector (Dimitrov et al., 2017)
Subunit, DNA, mRNA	Largely experimental or conditionally licensed	Rapid strain updating	Cost; limited field evidence; cold chain

Claims that vaccine success depends "exclusively" on timing and administration are too narrow. Performance also depends on antigenic match, cold-chain integrity, maternal antibody, host immune status, coverage and concurrent immunosuppressive infections. FMD and ND show the problem of antigenic match. MD shows the problem of vaccines that protect the host but not the population (Read et al., 2015). A quantitative comparison of ND, MD and AI vaccination programmes is not possible, because the available studies use different challenge models and outcomes, and this is itself a gap.

8.3 Biosecurity

Biosecurity is the set of measures that keep pathogens out of a farm and limit their spread within it. Quantitative tools such as Biocheck.UGent link biosecurity scores with performance and antimicrobial use on broiler farms (Gelaude et al., 2014; Van Limbergen et al., 2018). Core measures are controlled access, cleaning and disinfection of vehicles and equipment, all-in/all-out management, wild-bird and rodent exclusion, safe water and carcass disposal, and quarantine for new stock. In backyard systems, simplified, culturally acceptable measures have a better chance of being adopted than complex protocols, though evidence of effectiveness is weak (Conan et al., 2012). Table 7 collates control measures for each priority disease.

Table 7. Prevention and control measures for priority diseases (biosecurity, immunisation, therapeutic limits, and statutory reporting). Practices vary by country; consult national regulations.

Disease	Biosecurity	Immunisation	Therapeutic limits	Reporting and quarantine	Key sources
HPAI	Controlled access; vehicle disinfection; wild-bird exclusion; all-in/all-out	Selective use of inactivated or vectored vaccines with DIVA monitoring	No treatment of infected commercial flocks	Notifiable to WOAH; zoning, movement control, stamping-out	WOAH (2024); Verhagen et al. (2021)
Newcastle disease	As above, plus strict visitor control	Live and inactivated, genotype-matched where possible	Supportive; antimicrobials only for secondary bacterial infection	Notifiable; quarantine in outbreaks	Dimitrov et al. (2017)
Marek's disease	Hatchery hygiene; age segregation; cleaning	In ovo or day-old HVT with CVI988	No treatment	Generally not notifiable; pathotype monitoring	Gimeno (2008); Read et al. (2015)

Disease	Biosecurity	Immunisation	Therapeutic limits	Reporting and quarantine	Key sources
Coccidiosis	Dry litter; moisture control; clean bedding	Live vaccines; anticoccidial programmes with rotation	Anticoccidials or sulfonamides in outbreaks; observe withdrawal periods	Not notifiable; farm-level monitoring	Chapman (2014); Noack et al. (2019)
Fowlpox	Mosquito control; insect screening	Wing-web vaccination	Supportive; antimicrobials for secondary infection	Generally not notifiable	Giotis & Skinner (2019)
FMD	Gate disinfection; restricted introductions; vehicle sanitation	Inactivated vaccine in endemic or high-risk zones; ring vaccination	No antiviral therapy; supportive care	Immediate notification to WOAH; movement bans; stamping-out or ring vaccination	Diaz-San Segundo et al. (2017); DAERA (2026)
Brucellosis	Separate calving areas; disposal of aborted material; pasteurisation	S19 or RB51 (cattle); Rev-1 (small ruminants)	Antibiotics not recommended for herd control	Test-and-slaughter; herd accreditation; movement control	Godfroid et al. (2011); Blasco & Molina-Flores (2011)
Bovine tuberculosis	Pre-movement testing; reducing wildlife contact	BCG not routine in cattle	Treatment not used	Test-and-cull; herd restrictions	de la Rua-Domenech et al. (2006); Olea-Popelka et al. (2017)
PPR	Quarantine of new stock; market hygiene	Live attenuated vaccine	Supportive	Notifiable; zoning, stamping-out	Baron et al. (2016); FAO & WOAH (2015)
Lumpy skin disease	Insecticides and repellents; movement control	Live attenuated vaccines	Supportive	Notifiable; zoning and vaccination	Tuppurainen et al. (2017); Defra (2026a)
Bluetongue	Vector control; housing at peak midge activity	Serotype-specific vaccines	Supportive	Notifiable in many regions	Maclachlan et al. (2019)

8.4 Antimicrobial use, resistance and stewardship

Antibiotics treat bacterial infections, whereas coccidiostats and anticoccidials act on protozoa, and the two should not be conflated. Ionophores such as monensin and salinomycin act by disrupting ion gradients across parasite membranes, and synthetic chemicals such as diclazuril and nicarbazin target other parasite-specific processes. The two classes differ in resistance patterns, regulation and the way they are used in rotation programmes (Noack et al., 2019; Peek & Landman, 2011). Withdrawal periods and maximum residue limits are label-specific and set by national regulators, and compliance is what protects the food chain. The use of antibiotics as growth promoters has been banned in the European Union since 2006 and restricted in a growing number of other countries (Castanon, 2007).

Global antimicrobial use in food animals is high and is projected to remain so (Van Boeckel et al., 2015; Mulchandani et al., 2023; Tiseo et al., 2020). Resistance in animals is concentrated in hotspots in several LMICs (Van Boeckel et al., 2019), poultry is a major reservoir of resistant *E. coli* (Roth et al., 2019; Hedman et al., 2020; Nhung et al., 2017), and plasmid-mediated colistin resistance (*mcr-1*)

emerged from animal production in China (Liu et al., 2016). The human consequences are large. Bacterial AMR was associated with almost five million deaths in 2019 (Murray et al., 2022). Transmission from animals to people occurs through food, direct contact and the environment, though attribution is difficult (Ma et al., 2021). Stewardship measures include limiting preventive use, treating under veterinary prescription, replacing antibiotics with vaccination and better husbandry, and monitoring use and resistance. Probiotics, phytogenics and other alternatives are promising, but the evidence for field-scale benefits is mixed (Mehdi et al., 2018; Hosain et al., 2021).

8.5 Husbandry, nutrition and welfare

Stressors such as heat, crowding and abrupt feed changes impair immunity and raise susceptibility, so management is a legitimate disease-control tool, not merely a production matter (Quinteiro-Filho et al., 2010; Bessei, 2018). Nutrient deficiency and gut health also modulate disease outcomes, particularly for enteric infections (Wickramasuriya et al., 2022). The evidence linking particular nutritional interventions to reduced outbreak risk at farm scale is still modest.

9. Emerging Diseases and the One Health Approach

Emergence and re-emergence in animals are best explained by identifiable drivers, not by pathogens "adapting to how people live". The drivers include farm intensification and land-use change, expanding trade and market chains, climate-related shifts in vector ranges, changes in wildlife–livestock contact and antimicrobial use (Jones et al., 2013; Rohr et al., 2019; Karesh et al., 2012). Perry et al. (2013) discuss how such systemic changes in production and trade are likely to shape livestock disease dynamics. High-consequence transboundary threats in ruminants, namely PPR and LSD, deserve to be assessed alongside avian threats, which is why they are included in this review. ASF is not addressed in detail because it affects pigs, and its main lesson is that, without an effective vaccine, control depends on biosecurity and movement restrictions. It should be noted that vaccines are used to prevent disease, not to treat established infection.

One Health is defined by the One Health High-Level Expert Panel as an integrated approach that balances and optimises the health of people, animals and ecosystems (One Health High-Level Expert Panel [OHHLEP], 2022). The idea is not new (Zinsstag et al., 2011; Destoumieux-Garzón et al., 2018), and its value lies in operational detail (Mackenzie & Jeggo, 2019). In practice, integration means shared case definitions, joint outbreak investigations, coordinated sampling, interoperable data systems, and written agreements on who notifies whom within which timeframe.

Several steps seem realistic for LMICs where resources are constrained. First, build on existing animal-health workers and district laboratories, and keep tiers few and well linked (Figure 6). Second, use multi-pathogen panels and shared specimen transport to reduce unit cost. Third, put data-sharing

and sample-sharing agreements in place before outbreaks, so wildlife, veterinary and public-health authorities can exchange results quickly. Fourth, include farmer feedback and compensation schemes, because these affect reporting behaviour (Mubamba et al., 2018). Multi-agency coordination works best when roles are written down before an event. A standing national One Health committee with veterinary, public-health and wildlife representation can agree case definitions, set who tests which specimens, and define triggers for joint investigation, such as human cases of avian influenza in people with poultry contact or clusters of abortions with human fever in livestock-keeping households. Joint risk assessments and simulation exercises help to test these arrangements (Halliday et al., 2012; Cleaveland et al., 2017).

Evidence that integrated systems improve outcomes is still mainly descriptive and based on case studies, and rigorous comparative evaluations remain scarce (Cleaveland et al., 2017; Thumbi et al., 2015).

10. Critical Synthesis, Knowledge Gaps and Research Priorities

Comparing the two sectors yields four lessons. First, the same intervention behaves differently in different systems. Stamping out suits short-cycle, high-value poultry, where the economic and welfare calculus is favourable, but is harder to justify and enforce in extensive ruminant systems and informal trade, where ring vaccination, movement control and compensation matter more. Second, vaccines can reshape pathogen populations as well as protect hosts. Leaky MD vaccines, carriers after FMD vaccination and incomplete shedding control for ND all show that vaccination programmes need matched monitoring. Third, diagnostic accuracy is not a fixed property but depends on purpose and prevalence, and many LMIC testing failures are failures of access, logistics and interpretation more than of assay chemistry. Fourth, H5N1 in dairy cattle shows that species-based surveillance silos can leave gaps. A virus that circulated in birds was detected in cattle only after clinical signs were linked to it, and the human health consequences followed (Caserta et al., 2024).

Important gaps remain. There are few head-to-head field evaluations of rapid tests against reference methods in LMIC conditions. Economic estimates use incompatible methods. Evidence for the effectiveness of backyard biosecurity is thin. Comparative data on the performance of integrated One Health surveillance are limited, and long-term data on vaccine-driven evolution outside MD are scarce. Priorities for the next decade should include prospective validation of LAMP, lateral flow and portable sequencing for HPAI, ND, PPR and FMD, harmonised cost frameworks, and trials of stewardship interventions in smallholder poultry.

11. Limitations

This is a narrative review and not a systematic review, so selection bias is possible even though the criteria are explicit. Only English-language publications were considered. Several relevant diseases, including IBV, IBDV, ASF, anthrax and mastitis, are not covered in depth. Outbreak information for 2024–2026 comes partly from official sources that are updated frequently, and the situation will have moved by the time of reading. The criteria ratings are qualitative and reflect the author's judgement.

12. Conclusions

Priority diseases of poultry and ruminants threaten food security, trade and human health. Their control rests on tools that are individually well known but are applied under very different conditions in intensive poultry and extensive ruminant systems. The main conclusions are these. Diseases should be prioritised using explicit criteria. Diagnostic tools should be selected by purpose and by their fit with local resources. Surveillance should be risk-based, tiered and cross-species. Vaccination should be accompanied by monitoring that detects pathogen evolution. Antimicrobial use should be governed by stewardship. The recent events in cattle, in European ruminants and in wild and domestic birds show that waiting for a pathogen to appear in the sector where it is expected is no longer enough. Future work should test the proposed tiered framework in the field and standardise economic and diagnostic evidence.

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