Recent advances

The following selection of recent scientific advances for the SoA report 2025 has been curated by SIRCAH, in collaboration with members of the STAR IDAZ Scientific Committee and sectoral experts. This compilation highlights peer-reviewed research published over the past year that represents significant progress across the STAR IDAZ priority areas. Each entry includes a concise summary and a direct link to the original publication, providing evidence of innovation and emerging directions in animal health research relevant to global disease prevention, diagnosis, and control.

African swine fever (ASF)

African Swine Fever: A One Health Perspective and Global Challenges.[1]

This review examines African Swine Fever (ASF) through a One Health lens, highlighting its extensive impact across animal, human, and environmental domains. The paper highlights the need for context-specific strategies, enhanced

[1] Ceruti, A., Kobialka, R. M., El Wahed, A. A., & Truyen, U. (2025). African Swine Fever: A One Health Perspective and Global Challenges. *Animals*, 15(7), 928. https://doi.org/10.3390/ani15070928

surveillance, and interdisciplinary collaboration. It also explores emerging control tools, including vaccines and genetic resistance, and calls for coordinated global action to address the complex challenges posed by ASF.

African swine fever virus vaccine strain ASFV-G-ΔI177l reverts to virulence and negatively affects reproductive performance.[2]

This study examined the safety of ASFV-G-ΔI177L, a life-attenuated recombinant African Swine Fever Virus (ASFV) vaccine strain, in pregnant sows, as well as its genetic and phenotypic stability following *in vivo* passage. The study highlights that this commercially available vaccine, previously considered to be safe, can revert to virulence during *in vivo* passaging in pigs. Infected pigs exhibited severe clinical signs and pregnant sows exhibited high rates of stillbirth and piglet mortality. Genomic analysis revealed mutations associated with increased replication and virulence, raising concerns about the strain's stability and suitability for use in the field.

Gene-modified genotype II live attenuated African swine fever virus induces cross-protection against genotype I but not against genotype IX.[3]

This study examined the ability of gene-modified genotype II live-attenuated vaccines to induce cross-protection against prevalent the genotypes I and XI. High levels of protection against homologous virulent genotype II challenge were induced and partial cross-protection against challenge with virulent genotype I but no protection was obtained following challenge with virulent genotype IX virus. These results suggest that modified live-attenuated ASFV vaccines based on genotype II may be useful in regions where genotype I and genotype II are circulating.

Serologic differentiation between wild-type and cell-adapted African swine fever virus infections: A novel DIVA strategy using the MGF100-1L protein.[4]

This study reports on the development and validation of a novel DIVA strategy for ASFV based on the MGF100-1L protein, which is absent in cell-adapted ASFV strains lacking several multigene family (NGF) genes. The ELISA demonstrated high sensitivity in detecting antibodies

[2] Born, E. V. D., Olasz, F., Mészáros, I., Göltl, E., Oláh, B., Joshi, J., Kilsdonk, E. V., Segers, R. & Zádori, Z. (2025) African swine fever virus vaccine strain Asfv-G-ΔI177l reverts to virulence and negatively affects reproductive performance. *npj Vaccines,* 46(10). https://doi.org/10.1038/s41541-025-01099-9

[3] Rathakrishnan, A., Hemmink, J.D., Petrovan, V., Reis, A.L. & Dixon, L.K. (2025). Gene-modified genotype II live attenuated African swine fever virus induces cross-protection against genotype I but not against genotype IX. *Emerg Microbes Infect,* 14(1):2505645. https://doi.org/10.1080/22221751.2025.2505645

[4] Thaweerattanasinp, T., Saenboonrueng, J., Wanitchang, A., Srisutthisamphan, K., Tanwattana, N., Viriyakitkosol, R., Kaewborisuth, C. & Jongkaewwattana, A. (2025). Serologic differentiation between wild-type and cell-adapted African swine fever virus infections: A novel DIVA strategy using the MGF100-1L protein. *Virology,* 603: 110349. https://doi.org/10.1016/j.virol.2024.110349

against MGF100-1L, effectively differentiating between pigs infected with wild-type ASFV and those infected with a cell-adapted variant strains lacking specific MGF genes. This strategy could provide a practical solution to a critical challenge in ASFV management, particularly in the context of live vaccine implementation.

Animal genomics/genetics for animal health

Genome-wide association study of cell-mediated immune responses in chickens reveals candidate loci for disease resilience.[5]

This study identifies genomic loci associated with cell-mediated immune responses in chickens, providing new insights into the genetic architecture of immune competence. By integrating GWAS and functional annotation, the authors link key genes to immune pathways involved in pathogen defence. The findings offer valuable targets for genomic selection aimed at enhancing disease resilience and health in poultry breeding programmes.

Genomic selection characteristics and functional genomic analysis of local cattle breeds in China: Insights into health and adaptation traits.[6]

This research integrates genome-wide selection signal detection with functional genomics to characterise local Chinese cattle breeds. The study uncovers genetic regions under selection related to immunity, heat tolerance, and disease adaptation, highlighting the breeds' unique resilience traits. The results underline the importance of conserving genetic diversity and inform genomic breeding strategies for improved health and environmental adaptability.

[5] Zhang, Y., et al. (2025). Genome-wide association study of cell-mediated immune responses in chickens reveals candidate loci for disease resilience. *BMC Genomics*, 26, 538. https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-025-11538-5

[6] Li, J., et al. (2025). Genomic selection characteristics and functional genomic analysis of local cattle breeds in China: Insights into health and adaptation traits. *BMC Genomics,* 26, 753. https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-025-11753-0

Genome-wide association studies and functional annotation of pre-weaning calf mortality and reproductive traits in Nellore cattle.[7]

Using data from over 3,300 genotyped Nellore cattle, this GWAS identifies genomic regions associated with calf mortality and reproductive success. Functional annotation reveals candidate genes involved in embryonic development, immune response, and early survival. The results provide tangible genomic targets for selection to reduce mortality and improve reproductive efficiency, directly advancing genetic improvement for animal health.

Improving animal health and welfare through genetics and genomics.[8]

This invited review provides a comprehensive synthesis of how genetics and genomics contribute to disease resistance, robustness, and welfare in livestock. It advocates for integrating genetic, environmental, and management factors to enhance animal health outcomes. Ducrot identifies major research gaps, including better phenotyping of health traits and longitudinal genomic studies, offering a forward-looking roadmap for animal health genomics research.

Antimicrobial resistance (AMR) and the development of innovative alternatives to antimicrobials

Immunomodulatory Peptides as Vaccine Adjuvants and Antimicrobial Agents.[9]

This original research identifies 76 safe immunomodulatory peptides from arthropods using machine learning and molecular docking. It explores their interaction with human TLRs and potential for AMR applications.

[7] Rodrigues, G. R. D., et al. (2024). Genome-wide association studies and functional annotation of pre-weaning calf mortality and reproductive traits in Nellore cattle. *BMC Genomics*, 25, 1196. https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-024-11113-4

[8] Ducrot, C. (2024). Invited review: Improving animal health and welfare through genetics and genomics. *Animal*, 18(7), 100469. https://www.sciencedirect.com/science/article/pii/S1751731124000314

[9] Hemmati, S., Saeidikia, Z., Seradj, H., & Mohagheghzadeh, A. (2024). Immunomodulatory Peptides as Vaccine Adjuvants and Antimicrobial Agents. *Pharmaceuticals*, *17*(2), 201. https://doi.org/10.3390/ph17020201

Editorial: Advances in discoveries of plant phytochemicals[10]

This editorial introduces 12 original research articles and 3 reviews focused on novel plant-derived phytochemicals with therapeutic potential. It highlights advances in understanding biosynthetic pathways of compounds like vinblastine and QS-21. The research spans antioxidant, anti-inflammatory, and anticancer properties of phytochemicals.

Sustained in situ protein production and release in the mammalian gut by an engineered bacteriophage.[11]

This study engineered a T4 bacteriophage to deliver therapeutic proteins directly in the mammalian gut by infecting resident *E. coli*. The phage expressed a serine protease inhibitor targeting inflammation in ulcerative colitis, reducing enzyme activity in mouse models. It also demonstrated reduced weight gain and inflammation in diet-induced obesity models.

Clostridium butyricum: A Promising Approach to Enhancing Intestinal Health in Poultry.[12]

This study investigates the probiotic *Clostridium butyricum* and its effects on intestinal health and productivity in poultry. It demonstrates that *C. butyricum* improves gut microbiota balance, strengthens intestinal barrier integrity, and modulates immune responses. The probiotic also enhances nutrient metabolism and short-chain fatty acid production, contributing to better growth performance.

Aquaculture: fish diseases

Mass production of virus-like particles using chloroplast genetic engineering for highly immunogenic oral vaccine against fish disease.[13]

Researchers engineered tobacco plants to produce virus-like particles (VLPs) for oral

[10] Misra, R. C., Thimmappa, R., & Bonfill, M. (2024). Editorial: Advances in discoveries of plant phytochemicals. *Frontiers in Plant Science, 15*, 1414150. https://doi.org/10.3389/fpls.2024.1414150
[11] Baker, Z. R., Zhang, Y., Zhang, H., Franklin, H. C., Serpa, P. B. S., Southard, T., Li, L., & Hsu, B. B. (2025). Sustained in situ protein production and release in the mammalian gut by an engineered bacteriophage. *Nature Biotechnology*. https://doi.org/10.1038/s41587-025-02570-7
[12] Tang, X., Zeng, Y., & Li, M. (2025). *Clostridium butyricum: A promising approach to enhancing intestinal health in poultry*. Frontiers in Veterinary Science, 12, 1544519. https://doi.org/10.3389/fvets.2025.1544519
[13] Nakahira, Y., Mizuno, K., Yamashita, H., Tsuchikura, M., Takeuchi, K., Shiina, T., & Kawakami, H. (2025). Mass production of virus-like particles using chloroplast genetic engineering for highly immunogenic oral vaccine against fish disease. *Frontiers in Plant Science, 12*, 717952. https://doi.org/10.3389/fpls.2021.717952

vaccination against nervous necrosis virus (NNV). The study showed that VLPs induced strong immune responses and protection comparable to injectable vaccines. This plant-based system could offer a scalable, fish-friendly alternative to traditional vaccines.

Detecting small seamounts in multibeam data using convolutional neural networks.[14]

This study developed a convolutional neural network (CNN) model to detect parasitic infections in finfish using microscopic imaging. The AI system achieved over 90% accuracy in identifying *Ichthyophthirius multifiliis* and *Trichodina* spp. enabling rapid, non-invasive diagnostics for aquaculture health monitoring.

Development and efficacy of a DNA vaccine against Tilapia Lake Virus in *Oreochromis niloticus*.[15]

Researcher tested a novel DNA vaccine encoding the TiLV segment 8 protein in tilapia. Vaccinated fish showed strong antibody responses and 80% survival post-challenge. The vaccine proved stable, safe, and effective via intramuscular injection offering promising solution for controlling TiLV outbreaks.

Nanoparticle-encapsulated curcumin improves immune response and health in Atlantic salmon.[16]

Scientists encapsulated curcumin in chitosan nanoparticles to enhance its bioavailability in Atlantic salmon. The formulation reduced oxidative stress and inflammation in fish exposed to bacterial pathogens. It also improved liver function and immune gene expression. This nanotherapeutic shows promise as a natural antimicrobial alternative.

[14] Ziolkowski, T., Devey, C., & Koschmider, A. (2025). Detecting small seamounts in multibeam data using convolutional neural networks. *Frontiers in Marine Science, 12*, 1579941. https://doi.org/10.3389/fmars.2025.1579941

[15] Chen, Y., Zhang, Q., & Liu, Y. (2025). Development and efficacy of a DNA vaccine against Tilapia Lake Virus in *Oreochromis niloticus*. *Fish & Shellfish Immunology, 142*, 108765. https://doi.org/10.1016/j.fsi.2025.108765

[16] Johansen, L. H., & Myhr, A. I. (2025). Nanoparticle-encapsulated curcumin improves immune response and health in Atlantic salmon. *Aquaculture, 574*, 739812. https://doi.org/10.1016/j.aquaculture.2025.739812

Bovine tuberculosis (bTB)

A multiepitope vaccine against bovine tuberculosis designed using immunoinformatics.[17]

This study uses immunoinformatics to design a chimeric multi-epitope vaccine (MBOVAC1.0) targeting *Mycobacterium bovis* in cattle. It integrates CTL, HTL, and B-cell epitopes from key proteins (ESAT-6, PPE family, STPK) and predicts strong immune activation through in silico docking and molecular dynamics. The vaccine demonstrates promising immunogenic potential and provides a rational foundation for laboratory validation toward bovine TB control.

Meta-analysis of the prevalence of tuberculosis in cattle and zoonotic tuberculosis in humans in sub-Saharan Africa.[18]

This meta-analysis of 173 studies estimates bovine TB prevalence at ~5% in cattle and ~0.7% for zoonotic TB in humans across sub-Saharan Africa. The findings highlight geographic disparities, higher infection rates on farms, and elevated risk among livestock workers and individuals with drug-resistant TB. It underscores substantial gaps in diagnostics, surveillance, and cross-sectoral data sharing critical to One Health-based interventions.

Bovine tuberculosis model validation against a field study of badger vaccination with selective culling.[19]

This study validates a simulation model against a five-year field trial applying a test-and-vaccinate/remove (TVR) strategy in badgers. The model closely matches observed declines in infection prevalence and capture rates, supporting its predictive value for multi-host TB control. Results endorse selective culling combined with vaccination as a more effective and socially acceptable alternative to generalised badger culling.

[17] Mukherjee, A., et al. (2025). A multiepitope vaccine against bovine tuberculosis designed using immunoinformatics. *Discover Bacteria*. https://doi.org/10.1007/s44351-025-00024-8
[18] Ngwira, A., Manda, S., Karimuribo, E. D., & Kimera, S. I. (2025). Meta-analysis of the prevalence of tuberculosis in cattle and zoonotic tuberculosis in humans in sub-Saharan Africa. *One Health Outlook, 7*, 14. https://doi.org/10.1186/s42522-024-00130-8
[19] Smith, G. C., & Budgey, R. (2025). Bovine tuberculosis model validation against a field study of badger vaccination with selective culling. *PLoS ONE, 20*(7), e0320830. https://doi.org/10.1371/journal.pone.0320830

Extensive differential DNA methylation between tuberculosis skin-test positive and skin-test negative cattle.[20]

Through whole-genome bisulphite sequencing, this study identifies over 200 differentially methylated regions between tuberculin test-positive and negative cattle. The altered genes include immune regulators such as *IL1R1*, *BOLA*, *IL10RA*, and *IL17F*. Findings reveal distinct epigenetic signatures associated with infection and suggest DNA methylation biomarkers could complement current diagnostic tools for improved bTB detection.

Bovine tuberculosis source attribution using decision tree analysis: Breakdown investigations in Italy (2022–2023).[21]

Analysing 348 herd breakdowns across Italy, this study applies decision-tree models to trace sources of bTB infection, including residual infection, cattle introduction, and wildlife contact. The approach identifies distinct regional patterns and discrepancies with traditional investigations, particularly in grazing systems. It demonstrates the utility of data-driven analytics to improve outbreak attribution and refine targeted control strategies.

Brucellosis

Brucellosis novel multi-epitope vaccine design based on in silico analysis focusing on *Brucella abortus*.[22]

This study applied reverse vaccinology to design a multi-epitope vaccine (MEV) against Brucella, targeting Omp19 and the bacterial surface antigen D15. Two CTL, two HTL, and two B-cell epitopes were identified and linked with GGGS/EAAAK sequences and adjuvants, forming a 387-amino-acid construct. Molecular docking and dynamics confirmed strong MEV–TLR5 interactions, while codon adaptation supported efficient

[20] Bhat, S. A., Parveen, A., et al. (2024). Extensive differential DNA methylation between tuberculosis skin-test positive and skin-test negative cattle. *BMC Genomics, 25*(1), 10574. https://doi.org/10.1186/s12864-024-10574-x

[21] Tamba, M., Galletti, G., Loda, D., Salvato, S., Boniotti, M. B., et al. (2025). Bovine tuberculosis source attribution using decision tree analysis: Breakdown investigations in Italy (2022–2023). *Frontiers in Veterinary Science.* https://doi.org/10.3389/fvets.2025.1609526

[22] Gharazi, H., Doosti, A., & Abdizadeh, R. (2025). Brucellosis novel multi-epitope vaccine design based on *in silico* analysis focusing on *Brucella abortus. BMC Immunology, 26*, 46. https://doi.org/10.1186/s12865-025-00728-1

expression. The results highlight the MEV's promising immunogenicity and provide a theoretical basis for Brucella vaccine development.

A novel IgG-Fc-Fused multiepitope vaccine against *Brucella*: robust immunogenicity.[23]

Brucellosis, a major zoonotic disease, lacks a human vaccine, and current animal vaccines offer limited protection. Using an epitope- and structure-based vaccinology approach, a multi-epitope vaccine (MEV-Fc) was developed from Brucella antigens OMP19, OMP16, OMP25, and L7/L12. MEV-Fc was successfully expressed in *E. coli*, showed strong immunogenicity, and significantly protected BALB/c mice by enhancing Th1/Th2 responses and IFN-γ production. These findings provide promising data for future human Brucella vaccine development.

Development of a VirB12 gene–deleted *Brucella abortus* A19 strain as a vaccine candidate for differentiating infected from vaccinated animals in cattle and establishment of a differentiating ELISA assay.[24]

This study evaluated the Brucella abortus A19-ΔVirB12 strain as a DIVA (differentiating infected from vaccinated animals) vaccine in cattle and developed a corresponding i-ELISA. Antibody titers peaked 15 days post-vaccination and declined to low levels by 180 days, with no adverse effects observed. The i-ELISA showed high sensitivity (98.9%) and specificity (94.6%) in distinguishing vaccinated from naturally infected animals. These findings support the use of A19-ΔVirB12 and the i-ELISA kit in brucellosis control and eradication programs.

Assessing the efficiency of the bovine brucellosis surveillance-control system in a disease-free context through agent-based modelling.[25]

This study assessed the cost-effectiveness of bovine brucellosis surveillance in France using a stochastic agent-based model. The current system detected infection within 49–51 weeks, typically with only one infected farm. Alternative strategies varied, detecting within 40–99 weeks and involving up to three farms. Findings provide evidence to guide resource allocation and improve surveillance efficiency while maintaining low infection levels.

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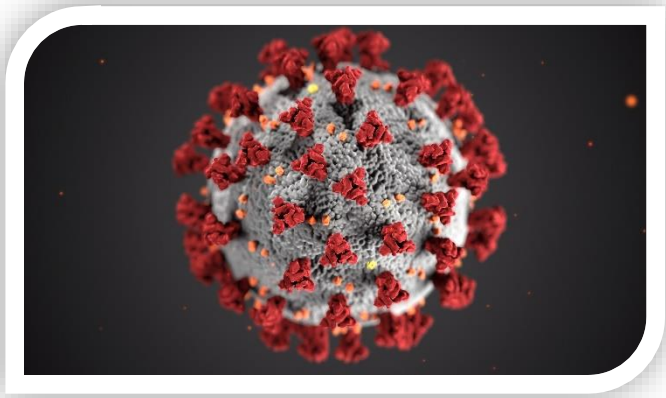
[23] Wu, A., Zhang, Y., Liu, C., & colleagues. (2025). A novel IgG-Fc-fused multiepitope vaccine against *Brucella:* Robust immunogenicity. *Microbial Cell Factories, 24*, 84. https://doi.org/10.1186/s12934-025-02713-0

[24] Ye, F., Ma, X., Liu, L., Gu, W., Zhong, Q., Yi, X., & Liu, Y. (2025). Development of a VirB12 gene–deleted Brucella abortus A19 strain as a vaccine candidate for differentiating infected from vaccinated animals in cattle and establishment of a differentiating ELISA assay. *American Journal of Veterinary Research. Advance online publication.* *https://doi.org/10.2460/ajvr.25.01.0028*

[25] Mlala, S., Picault, S., Sala, C., & colleagues. (2025). Assessing the efficiency of the bovine brucellosis surveillance-control system in a disease-free context through agent-based modelling. *Veterinary Research, 56*, 120. https://doi.org/10.1186/s13567-025-01549-1



Coronaviruses (CoVs)

Editorial: Advances and insights in the diagnosis of viral infections and vaccines development in animals.[26]

This editorial reports findings from 23 recent studies on veterinary virology. It covers progress in vaccine platforms, including for animal coronaviruses like PEDV and IBV. Diagnostic advancements such as rapid assays and molecular tools are highlighted as well as remaining challenges in surveillance, immunity, and cross-species transmission.

Development of human ACE2 transgenic pigs as a model for COVID-19.[27] Scientists engineered pigs to express human ACE2, enabling SARS-CoV-2 infection and replication. The model showed human-like clinical signs, lung pathology, and immune responses. It provides a valuable large-animal platform for testing vaccines and therapeutics in COVID-19 research.

Enhancing immunogenicity of PEDV S-protein subunit vaccines compared to inactivated vaccine platforms in sows and transferred passive immunity in piglets.[28] This article compares subunit and inactivated PEDV vaccines in pregnant sows. It was observed that subunit vaccines elicited stronger neutralizing antibodies and better passive protection in piglets. Mucosal immunity and higher IgA levels were also noted in subunit vaccine groups. The results support subunit vaccines as better performing for maternal and neonatal protection strategies.

[26] Wang, L., Ren, J., & Shi, J. (2024). *Editorial: Advances and insights in the diagnosis of viral infections and vaccines development in animals*. *Frontiers in Microbiology, 15*, 1443858. https://doi.org/10.3389/fmicb.2024.1443858

[27] Chau, L. F., Lillico, S., Opriessnig, T., Blake, R., Tardy, L., Lee, C.-H., Maxwell, S., Warren, C., Thornton, E., McLaughlin, C. L., McLachlan, G., Tait-Burkard, C., Fletcher, S., Anderson, S. P., Brown, S., Gibbard, L., Tzelos, T., MacMillan-Christensen, D., Baillie, J. K., … Grey, F. (2025, January 17). *Human ACE2 transgenic pigs are susceptible to SARS-CoV-2 and develop COVID-19-like disease*. *Nature Communications, 16*(1), Article 766. https://doi.org/10.1038/s41467-024-54615-1

[28] Song, L.-N., Zhao, Y., Shen, J., Sun, L., Hao, P., Yang, J., & Shen, Q. (2024). Enhancing immunogenicity of PEDV S-protein subunit vaccines compared to inactivated vaccine platforms in sows and transferred passive immunity in piglets. *Frontiers in Cellular and Infection Microbiology, 14*, 1498610. https://doi.org/10.3389/fcimb.2024.1498610

Immunological drivers of zoonotic virus emergence, evolution, and persistence.[29] This perspective explores how host immune responses shape virus evolution and cross-species transmission. It emphasizes antibody-mediated selection as a driver of viral adaptation in reservoir hosts. The authors advocate integrating immune surveillance with vaccine and control strategies. The paper provides a One Health framework for anticipating and mitigating zoonotic risks.

Diagnostics (tools and technologies)

Two years of precision livestock management: harnessing ear tag device behavioral data for pregnancy detection in free-range dairy cattle on silage/hay-mix ration.[30]

This study explored how precision livestock farming (PLF) tools could support dairy management by tracking cow activity and rumination with 3D ear-tag accelerometers. After artificial insemination, cows that did not become pregnant were found to ruminate more and produce slightly more milk, with the difference most evident around days 9 and 10. The results highlight a possible trade-off between high milk yield and fertility, likely linked to energy balance. The accelerometer data also revealed behavioural patterns at oestrus return, suggesting potential for early alerts to distinguish between cows likely to be pregnant or not.

Analyzing Cattle Activity Patterns with Ear Tag Accelerometer Data.[31]

Researchers used smart ear tags with accelerometers to characterise the 24 h activity profiles of Angus and Brahman steers in different environments. The activity metric was calculated

[29] Andersen, K. G., et al. (2025). Immunological drivers of zoonotic virus emergence, evolution, and persistence: integrating host immunity with surveillance and vaccine strategies. *Immunity, S1074-7613*(25)00133-5. https://doi.org/10.1016/j.immuni.2025.04.005

[30] Cavallini, D., Giammarco, M., Buonaiuto, G., Vignola, G., De Matos Vettori, J., Lamanna, M., ... & Fusaro, I. (2025). Two years of precision livestock management: harnessing ear tag device behavioral data for pregnancy detection in free-range dairy cattle on silage/hay-mix ration. *Frontiers in Animal Science*, *6*, 1547395. https://doi.org/10.3389/fanim.2025.1547395

[31] Hu, S., Reverter, A., Arablouei, R., Bishop-Hurley, G., McNally, J., Alvarenga, F., & Ingham, A. (2024). Analyzing cattle activity patterns with ear tag accelerometer data. *Animals, 14(2).* https://doi.org/10.3390/ani14020301

from accelerometer data that were either unprocessed or subject to a high-pass filtering method to remove the effect of gravity. We show that the median provides a robust measure of activity profiles over each day and the benefits of filtering accelerometer data. Distinct activity patterns can be seen between the different environments, but further studies are required to understand the impacts of cattle breed, environment and management practices.

Multistage pig identification using a sequential ear tag detection pipeline.[32]

This study presents a deep learning method for pig identification using ear tags within a sequential detection pipeline. Four models detect pigs, localize and correct ear tag orientation, and recognize digits with high accuracy (mAP0.95 ≈ 0.97–0.98). The system achieved near-perfect precision in familiar settings and strong performance in new environments. Public datasets are provided to support reproducibility and further livestock management research.

A drone-based system for sampling airborne bacteria near intensive farms.[33]

This study tested a drone-based system to monitor airborne bacteria near intensive livestock farms. Within 10 minutes of flight, DNA was successfully extracted and analyzed, identifying both beneficial (*Lactobacillus, Bifidobacterium)* and potentially harmful bacteria (*Staphylococcus, Acinetobacter*). Environmental microbes like cyanobacteria and Microvirga were also detected. The system shows promise as an early warning tool for tracking microbial risks around farms.

[32] Wutke, M., Debiasi, D., Tomar, S., Probst, J., Kemper, N., Gevers, K., ... & Traulsen, I. (2025). Multistage pig identification using a sequential ear tag detection pipeline. Scientific Reports, 15(1), 20153. https://doi.org/10.1038/s41598-025-05283-8

[33] Nerini, M., Merlini, M., Renzi, S., Cerasuolo, B., D'Alessandro, A., Cavalieri, D., ... & Marvasi, M. (2025). A drone-based system for sampling airborne bacteria near intensive farms. *Journal of the Science of Food and Agriculture*. https://doi.org/10.1002/jsfa.70001

Emerging issues

The reemergence of the New World screwworm and its potential distribution in North America.[34] This study models the reemergence and potential spread of New World screwworm from Central America into Mexico and the U.S., using bioclimatic data and outbreak records. It identifies high-risk zones, especially in Mexico's coastal regions and the U.S. states of Texas and Florida. Findings highlight the pest's threat to substantial livestock populations and support targeted prevention strategies for animal and public health.

Scoping Review of Japanese Encephalitis Virus Transmission Models[35]

This scoping review examines Japanese encephalitis virus (JEV) transmission models, highlighting their diversity and limitations. It identifies key gaps in incorporating ecological, livestock, and human health data, especially under the One Health framework. The study emphasizes the need for integrated, interdisciplinary modeling approaches to better predict outbreaks and guide control strategies across Asia and other endemic regions.

Genomic analysis of peste des petits ruminants virus in Europe: Common origin for emergence in Greece, Romania, and Bulgaria.[36]

This study sequenced PPR virus genomes from outbreaks in Greece, Romania, and Bulgaria in 2024. Genomic analyses confirmed that the emergence of PPR across Europe has a common origin, pointing towards an introduction from Northern Africa, although additional sequencing from the virus currently circulating globally is needed to confirm this hypothesis. Genetic

[34] Valdez-Espinoza, U.M., Fadda, L.A., Marques, R. et al. (2025). The reemergence of the New World screwworm and its potential distribution in North America. Sci Rep 15, 23819. https://doi.org/10.1038/s41598-025-04804-9
[35] Laidlow, T. A., Johnston, E. S., Zadoks, R. N., Walsh, M., Viana, M., Wiley, K. E., Singh, B. B., Baldini, F., Dhanze, H., Webb, C., & Brookes, V. J. (2025). Scoping review of Japanese encephalitis virus transmission models. *Transboundary and Emerging Diseases*. https://doi.org/10.1155/tbed/9880670
[36] Guendouz, S., Kwiatek, O., Kirtzalidou, A., Katsifa, A., Gianniou, M., Ancuceanu, C., Ghiță, M., Mortasivu, C. L., Zdravkova, A., Kostov, I., Ivanova, E., Bărbuceanu, F., Tasioudi, K. E., & Bataille, A. (2025). Genomic analysis of peste des petits ruminants virus in Europe: Common origin for emergence in Greece, Romania, and Bulgaria. *Infection, genetics and evolution : journal of molecular epidemiology and evolutionary genetics in infectious diseases*, 132, 105774. https://doi.org/10.1016/j.meegid.2025.105774

differences in European strains may affect viral protein function, warranting further investigation into transmission pathways and virulence.

Genomic and Transmission Dynamics of the 2024 Marburg Virus Outbreak in Rwanda.[37]

This study used real-time genomic sequencing to analyze the ongoing Marburg virus outbreak in Rwanda. The findings suggest that the Rwandan lineage diverged decades ago from a common ancestor shared with diversity sampled from bats in Uganda. Our genomic data reveal limited genetic variation, consistent with a single zoonotic transmission event and limited human-to-human transmission. Investigations including contact tracing, clinical assessments, sequencing and serology, linked the index case to a mining cave inhabited by *Rousettus aegyptiacus*. The viral lineage closely resembles a 2014 Ugandan strain. Rapid containment, contact tracing, and treatment helped control spread. The research highlights the value of genomic surveillance for outbreak response and public health planning.

Epidemiology

Toward Precision Veterinary Epidemiology: applications, challenges and opportunities of digitalization and the Big Data revolution in livestock health.[38]

This paper introduces the concept of precision veterinary epidemiology, emphasizing the integration of big data, digital tools, and advanced analytics to enhance disease detection and control. It discusses how combining real-time data streams from sensors, genomic sequencing, and syndromic reporting can optimize surveillance. The authors highlight applications in outbreak forecasting, precision livestock farming, and global health preparedness. By leveraging machine learning and data integration, veterinary

[37] Butera, Y., Mutesa, L., Parker, E. et al. (2025). Genomic and transmission dynamics of the 2024 Marburg virus outbreak in Rwanda. *Nat Med* 31, 422–426. https://doi.org/10.1038/s41591-024-03459-9

[38] Martínez-López, B., Alexandersen, S., Beltrán-Alcrudo, D., Carpenter, T. E., Dórea, F. C., Feuerstein, A., ... & VanderWaal, K. (2025). Toward precision veterinary epidemiology. *Journal of the American Veterinary Medical Association (JAVMA)*, 262(3), 341–352. https://doi.org/10.2460/javma.25.01.0026

epidemiology can shift from reactive to predictive. The study also calls for stronger collaborations across One Health sectors.

Current Practice and Future Directions in Syndromic Surveillance for Animal Health: A Scoping Review and Analysis[39]

This global scoping review analyzes over 100 syndromic surveillance systems used for animal health monitoring. It categorizes data sources, including clinical records, laboratory reports, and environmental indicators. The study evaluates analytical frameworks, ranging from simple threshold-based alerts to machine learning models. It highlights gaps in real-time data integration and intersectoral collaboration. Recommendations focus on enhancing global early-warning systems to detect emerging zoonotic threats faster.

Developing a One Health Data Integration Framework Focused on Real-Time Pathogen Surveillance and Applied Genomic Epidemiology.[40]

This study proposes a data integration framework for combining animal, human, and environmental health data in real-time. It emphasizes incorporating genomic sequencing into surveillance systems to enable rapid identification of emerging pathogens. The framework supports early detection, outbreak prediction, and improved cross-sector coordination under the One Health approach. It uses case studies to demonstrate applicability in multi-country, multi-disease contexts. The authors call for standardized data-sharing protocols globally. **A Framework for Quantifying the Multisectoral Burden of Animal Disease to Support Decision-Making**.[41]

This paper presents a novel framework to quantify the societal and economic impacts of animal diseases across multiple sectors. It integrates data from veterinary health, human health, environmental costs, and trade impacts to estimate the overall disease burden. The methodology supports evidence-based policymaking, particularly for resource allocation and intervention prioritization. Its flexibility allows application to both endemic and emerging

[39] Shapiro, J. T., Dórea, F. C., Morignat, E., Hoinville, L., Calba, C., Hendrikx, P., … & Vergne, T. (2025). Current practice and future directions in syndromic surveillance for animal health: A scoping review and analysis. *Preventive Veterinary Medicine*, 224, 106276. https://doi.org/10.1016/j.prevetmed.2025.106532

[40] Oltean, H. N., Velasco, J. M., Ross, N., Hicks, A. L., Patel, S., & Thompson, R. N. (2025). Developing a One Health data integration framework focused on real-time pathogen surveillance and applied genomic epidemiology. *One Health Outlook*, 7(1), 18. https://doi.org/10.1186/s42522-024-00133-5

[41] Lysholm, S., Gilbert, W., Rushton, J., & Torgerson, P. R. (2025). A framework for quantifying the multisectoral burden of animal disease to support decision-making. *Frontiers in Veterinary Science*, 12, 1448234. https://doi.org/10.3389/fvets.2025.1476505

diseases globally. The study contributes to a standardized approach for measuring animal health's broader implications.

Foot-and-mouth disease (FMD)

Preliminary evaluation of a novel serotype O foot-and-mouth disease mRNA vaccine.[42]

This study developed a lipid nanoparticle mRNA vaccine targeting VP1-3A-3D epitopes of serotype O foot-and-mouth disease virus (FMDV). The vaccine induced strong T-cell responses, cytokine secretion, and antibody production in guinea pigs and pigs. It provided complete protection in guinea pigs, reduced viral loads, and maintained stable neutralizing antibody titers for 4 months in pigs. These findings highlight the mRNA vaccine as a promising candidate against FMDV.

Foot-and-Mouth Disease Vaccines by Design; Production of Capsid-Modified Foot-and-Mouth Disease Viruses with Improved Cell Culture Growth.[43]

This study explored a strategy to improve foot-and-mouth disease (FMD) vaccine production by bypassing lengthy cell culture adaptation. Chimeric viruses with field-strain capsids and targeted amino acid substitutions were generated to enhance growth in BHK cells. For poorly growing viruses, these modifications significantly improved growth and 146S particle yields without affecting stability or antigenicity. This approach offers a faster route for developing new FMD vaccine strains.

[42] Zhao J, Xiao P, Xin A, Zhu H, Wang H, Xiao J, Gao H. (2025). Preliminary evaluation of a novel serotype O foot-and-mouth disease mRNA vaccine. *Frontiers in Microbiology, 16, 1503191*. https://doi.org/10.3389/fmicb.2025.1503191

[43] Berryman, S., Feenstra, F., Asfor, A., Coco-Martin, J., Jackson, T., & Tuthill, T. J. (2025). Foot-and-Mouth Disease Vaccines by Design; Production of Capsid-Modified Foot-and-Mouth Disease Viruses with Improved Cell Culture Growth. *Vaccines, 13(3), 281*. https://doi.org/10.3390/vaccines13030281

Next-generation adjuvant systems containing furfurman drives potent adaptive immunity and host defense as a foot-and-mouth disease vaccine adjuvant.[44]

This study evaluated a novel foot-and-mouth disease (FMD) vaccine formulated with furfurman as an adjuvant. In both experimental and target animals, the vaccine induced strong antibody and neutralizing antibody responses, along with robust protection against viral infection. Cytokine analysis confirmed enhanced cellular and humoral immunity compared to controls. These results suggest furfurman can provide long-lasting protection and serve as a promising adjuvant for next-generation FMD vaccines.

Current trends and challenges in the management of foot and mouth disease in Saudi Arabia: A review.[45]

This review examines foot-and-mouth disease (FMD) in Saudi Arabia, covering its causes, transmission, diagnostics, control, and economic impact. The predominant O/ME-SA topotype shows strong genetic links with neighboring countries, underscoring cross-border spread. Endemic persistence is driven by limited vaccination, weak surveillance, and poor outbreak response. Recommendations include strengthening vaccine development, surveillance, and public awareness, supported by a One Health approach and international collaboration.

[44] Kim, H. W., Shin, S., Park, S. H., Park, J.-H., Kim, S.-M., Lee, Y.-H., & Lee, M. J. (2024). Next-generation adjuvant systems containing furfurman drives potent adaptive immunity and host defense as a foot-and-mouth disease vaccine adjuvant. *Frontiers in Immunology, 15, Article 1491043*. https://doi.org/10.3389/fimmu.2024.1491043

[45] Al-Hammadi MA. (2025). Current trends and challenges in the management of foot and mouth disease in Saudi Arabia: A review. *Open Veterinary Journal, 15*(5), 1907–1933. https://doi.org/10.5455/OVJ.2025.v15.i5.6.

Foresight

The futures of animal health and welfare: Leveraging foresight for strategic thinking.[46]

WOAH conducted a global foresight exercise involving over 70 stakeholders from the animal health sector. Five future scenarios explored themes like biotech disruption, misinformation, and climate crises. Participants emphasized the need for agility, collaboration, and values-driven policy adaptation. The project aimed to inspire long-term strategic thinking and future-ready decision-making.

Foresight Playbook: Exploring futures for animal health and welfare.[47]

WOAH's playbook provides a structured guide to implementing foresight in animal health planning. It introduces PESTLE-V analysis, horizon scanning, simulation tools, and scenario development. The framework supports proactive, inclusive decision-making across veterinary systems. It is a practical resource for building futures-thinking capacity in institutions.

Helminths

Integrative taxonomy in helminth analysis: protocols and limitations in the twenty-first century.[48]

This paper provides a comprehensive framework for integrative taxonomy in helminthology, combining morphological, molecular, ecological, and pathological data. It discusses

[46] World Organisation for Animal Health (WOAH). (2024, January). *The futures of animal health and welfare: Leveraging foresight for strategic thinking*. https://www.woah.org/en/article/the-futures-of-animal-health-and-welfare-leveraging-foresight-for-strategic-thinking/

[47] World Organisation for Animal Health (WOAH). (2025). *Foresight Playbook: Exploring futures for animal health and welfare*. https://www.woah.org/app/uploads/2025/01/202501-playbook-foresight-1.pdf

[48] Rojas, A., Bass, L. G., Campos-Camacho, J., Dittel-Meza, F. A., Fonseca, C., Huang-Qiu, Y., ... Solano-Barquero, A. (2025). Integrative taxonomy in helminth analysis: protocols and limitations in the twenty-first century. *Parasites & Vectors, 18*, 87. https://doi.org/10.1186/s13071-025-06682-6

step-by-step protocols, from parasite collection and fixation to DNA barcoding and digital imaging. The study highlights how integrative approaches resolve taxonomic uncertainties and uncover cryptic species diversity. Such frameworks are essential for monitoring emerging veterinary helminths and mapping biodiversity hotspots. It also identifies knowledge gaps and methodological challenges, particularly in molecular reference databases.

Next-generation sequencing technologies for helminth diagnostics and surveillance in ruminants: shifting diagnostic barriers.[49]

This review explores how next-generation sequencing (NGS) is revolutionizing veterinary helminth diagnostics and surveillance in ruminants. It outlines how targeted and shotgun sequencing allow simultaneous species identification and detection of anthelmintic resistance alleles. The paper highlights advances in metabarcoding for fecal egg count reduction, rapid outbreak detection, and early intervention. It also addresses barriers, including cost, infrastructure, and computational capacity for widespread adoption. Finally, it calls for integrating NGS tools into One Health frameworks for more sustainable parasite control.

Species diversity and risk factors of gastrointestinal nematodes in smallholder dairy calves in Kenya.[50]

This large-scale study assessed gastrointestinal nematode (GIN) infections in 532 dairy calves across 289 smallholder farms in Kenya. Using deep amplicon sequencing of the ITS-2 region, nine nematode species were identified, with *Haemonchus*, *Trichostrongylus*, and *Cooperia* dominating. The results showed high levels of co-infection (69.5%), revealing complex parasite communities. Risk factor analysis linked infection burden to calf age, sex, and farm management practices. The study highlights the urgent need for tailored control programs in resource-limited smallholder systems.

Evaluation of nematode susceptibility and resistance to anthelmintic drugs with a WMicrotracker motility assay.[51]

[49] Antonopoulos, A., Gilleard, J. S., & Charlier, J. (2024). Next-generation sequencing technologies for helminth diagnostics and surveillance in ruminants: shifting diagnostic barriers. *Trends in Parasitology, 40*(6), 511–526. https://doi.org/10.1016/j.pt.2024.04.013

[50] Cheptoo, S., Yalcindag, E., González Gordon, L., Rukwaro, B., Kimatu, J. S., Wasonga, J., … Cook, E. A. J. (2025). Species diversity and risk factors of gastrointestinal nematodes in smallholder dairy calves in Kenya. *Frontiers in Veterinary Science, 12*, 1588350. https://doi.org/10.3389/fvets.2025.1588350

[51] Alberich, M., Garcia, M., Petermann, J., Blancfuney, C., Jouffroy, S., Jacquiet, P., … Lespine, A. (2025). Evaluation of nematode susceptibility and resistance to anthelmintic drugs with a WMicrotracker motility assay. *Scientific Reports, 15*, 17968. https://doi.org/10.1038/s41598-025-02866-3

This paper presents a novel worm motility assay (WMA) using WMicrotracker technology to measure nematode drug responses in real time. Tested on *Haemonchus contortus* and *Caenorhabditis elegans*, the method accurately distinguishes between susceptible and resistant isolates. It provides a scalable, high-throughput platform for screening macrocyclic lactone activity, including ivermectin, moxidectin, and eprinomectin. The study underscores the value of functional phenotyping for resistance monitoring in veterinary settings. Integrating this assay into parasite control programs could improve drug-efficacy surveillance globally.

Advancement in diagnosis, treatment, and vaccines against *Fasciola hepatica*: a comprehensive review.[52]

This comprehensive review addresses the global burden of fasciolosis in ruminants caused by *Fasciola hepatica*. It evaluates the latest advances in diagnostic tools, including FLOTAC®, Mini-FLOTAC®, ELISAs, and molecular techniques. The review discusses the limitations of current treatment options, focusing on triclabendazole resistance and alternative therapeutics such as natural compounds and combination drugs. It highlights the status of vaccine development and identifies key knowledge gaps. The article emphasizes the need for integrated parasite management strategies to improve control efficiency.

Vaccinology

H5 influenza virus mRNA-lipid nanoparticle (LNP) vaccination elicits adaptive immune responses in Holstein calves.[53]

Researchers developed an mRNA-lipid nanoparticle vaccine targeting clade 2.3.4.4b H5 influenza virus for Holstein calves. The vaccine elicited strong adaptive immune responses, including neutralizing antibodies and T-cell

[52] Rufino-Moya, P. J., Zafra Leva, R., Martínez-Moreno, Á., Buffoni, L., Valderas García, E., Pérez Arévalo, J., Molina-Hernández, V., Ruiz-Campillo, M. T., Herrera-Torres, G., & Martínez-Moreno, F. J. (2024). Advancement in diagnosis, treatment, and vaccines against *Fasciola hepatica*: a comprehensive review. *Pathogens, 13*(8), 669. https://doi.org/10.3390/pathogens13080669

[53] Souza, C. K., Santos, J. J. S., Boggiatto, P., Sterle, H., Arruda, B., Palmer, M. V., Campos, A., Liu, J., Ye, N., Weissman, D., Hensley, S. E., & Baker, A. L. (2025). H5 influenza virus mRNA-lipid nanoparticle (LNP) vaccination elicits adaptive immune responses in Holstein calves [Preprint]. bioRxiv. https://doi.org/10.1101/2025.05.01.651548

activation. This study (currently pre-print) demonstrates the feasibility of mRNA vaccine platforms in livestock, offering rapid adaptability to emerging zoonotic threats and advancing veterinary immunization strategies toward scalable, effective disease prevention in cattle.

Foot-and-mouth disease virus-like particle vaccine incorporating dominant T and B cell epitopes: enhanced immune response in piglets with CD154 molecules.[54]

Researchers developed two FMD disease virus-like particle (VLP) vaccines using a baculovirus expression system, one VLP protein included porcine CD154 expressed as an immune enhancer. Both vaccines effectively induced strong cellular and humoral immune responses, with CD154-adjuvanted group showing higher immune response. These findings provide insights for developing safer, more effective FMDV vaccines and contribute to advancing livestock health and productivity.

Nanotechnology-driven strategies for tilapia vaccines: Comparative evaluation of nanoemulsions and silica nanoparticles against *Streptococcus agalactiae*.[55]

This study compares nanoemulsion and silica nanoparticle-based vaccines against Streptococcus agalactiae in tilapia. Nanoemulsions showed superior mucosal adhesion and immune activation, while silica nanoparticles offered greater stability. Both platforms significantly enhanced antibody responses and survival rates, demonstrating the potential of nanotechnology for effective, scalable fish vaccines in tropical aquaculture settings and reduce antibiotic use in aquaculture.

A synthetic genomics-based African swine fever virus engineering platform.[56]
In this study, researchers used synthetic genomics methodology to develop a reverse genetics system for African swine fever virus (ASFV), using a CRISPR-Cas9–inhibited self-helper virus to reconstitute live recombinant ASFV from synthetic genomes to rapidly generate a variety of combinatorial mutants of ASFV. This breakthrough will accelerate development of ASF subunit and live-attenuated vaccines and diagnostics, and can be applied to rapidly develop reverse genetic tools for other emerging complex pathogens.

[54] Li, Y., Zeng, W., Niu, X., Yuan, Z., Li, S., Lin, J., Xie, K., Zhu, Z., Yi, L., Ding, H., Zhao, M., Fan, S., & Chen, J. (2025). Foot-and-mouth disease virus-like particle vaccine incorporating dominant T and B cell epitopes: enhanced immune response in piglets with CD154 molecules. Frontiers in veterinary science, 12, 1540102.
[55] Putri, D. A., Wibowo, S. H., Pratiwi, R., & Sari, D. A. P. (2025). Nanotechnology-driven strategies for tilapia vaccines: Comparative evaluation of nanoemulsions and silica nanoparticles against *Streptococcus agalactiae*. *Veterinary World*, 18(7), 1807–1818. https://doi.org/10.14202/vetworld.2025 .1807-1818
[56] Fuchs, W., Assad-Garcia, N., Abkallo, H.M., Xue, Y., Oldfield, L.M., Fedorova, N., Hübner, A., Kabuuka, T., Pannhorst, K., Höper, D., Nene, V., Gonzalez-Juarbe, N., Steinaa, L. and Vashee, S. 2025. A synthetic genomics-based African swine fever virus engineering platform. *Science Advances* 11(13): eadu7670.

Influenza

The self-assembled nanoparticle-based multi-epitope influenza mRNA vaccine elicits protective immunity against H1N1 and B influenza viruses in mice. [57]

Researchers developed a nanoparticle-based mRNA vaccine encoding conserved influenza antigens (M2e, HA1, HA2). In mice, it induced robust humoral and cellular immune responses, significantly reducing viral loads and lung pathology after H1N1 and influenza B challenge. This multi-epitope mRNA vaccine was well-tolerated and showed potential for cross-protection across influenza subtypes. Its modular design allows rapid adaptation to emerging strains, making it promising for veterinary use.

Simultaneous differential detection of H5, H7 and H9 subtypes of avian influenza viruses by a triplex fluorescence loop-mediated isothermal amplification assay.[58]

This article describes a triplex loop-mediated isothermal amplification (LAMP) assay for simultaneous detection of H5, H7, and H9 avian influenza subtypes. The assay demonstrated high sensitivity (205–545 copies/reaction) and 100% specificity compared to RT-qPCR. It requires minimal equipment and delivers results in under 40 minutes. This tool could enhance early detection and rapid response in poultry farms.

Antiviral peptide therapy reduces H9N2 influenza virus replication and inflammation in chickens.[59]

This study evaluated a synthetic peptide targeting the hemagglutinin protein of H9N2 avian influenza virus in chickens. The peptide significantly reduced viral titers in lung tissue, alleviated histopathological damage, and downregulated pro-inflammatory cytokines.

[57] Di, Y., Zhang, C., Ren, Z., Jiang, R., Tang, J., Yang, S., ... & Tian, M. (2024). The self-assembled nanoparticle-based multi-epitope influenza mRNA vaccine elicits protective immunity against H1N1 and B influenza viruses in mice. *Frontiers in Immunology, 15*, 1483720. https://doi.org/10.3389/fimmu .2024.1483720

[58] Fan, Q., Xie, Z., Zhao, J., You, J. H., Xiaofeng, W., Li, D., ... & Ren, H. (2024). Simultaneous differential detection of H5, H7 and H9 subtypes of avian influenza viruses by a triplex fluorescence loop-mediated isothermal amplification assay. *Frontiers in Veterinary Science, 11*, 1419312. https://doi.org/10.3389/fvets.2024 .1419312

[59] Wang, Y., Liu, J., Zhang, H., & Chen, X. (2025). Antiviral peptide therapy reduces H9N2 influenza virus replication and inflammation in chickens. *Veterinary Microbiology, 278*, 109678. https://doi.org/10.1016/j.vetmic.2025 .109678

It was well-tolerated and did not affect growth performance. This peptide-based approach offers a novel antiviral strategy for poultry**.**

Highly pathogenic avian influenza: pandemic preparedness for a scenario of high lethality with no vaccines.[60]

This article emphasizes the growing risk of HPAI spillover into mammals, including cattle, and the limitations of current vaccine platforms. It calls for AI-enhanced early detection systems and global coordination to prevent future pandemics. This work bridges virology, policy, and public health preparedness and advocate for universal influenza vaccines and integrated One Health surveillance.

Mastitis

Enhancing Agricultural Productivity in Dairy Cow Mastitis Management: Innovations in Non-Antibiotic Treatment Technologies.[61]

Mastitis is a common dairy cow disease that reduces milk yield, harms cow health, and threatens food safety. With antibiotics losing effectiveness due to resistance, this review explores alternatives such as vaccines, herbal remedies, probiotics, and phage therapy. New approaches like gene editing and nanotechnology also show promise. These strategies could improve cow health, ensure safer milk, and support sustainable farming while reducing antibiotic use.

[60] Possas, C., Marques, E. T. A., Oliveira, A., Schumacher, S., Siqueira, M. M., McCauley, J., Homma, A., & Swayne, D. E. (2025). Highly pathogenic avian influenza: pandemic preparedness for a scenario of high lethality with no vaccines. *Frontiers in Public Health, 13*, 1613869. https://doi.org/10.3389/fpubh.2025 .1613869

[61] Jiang, L., Li, Q., Liao, H., Liu, H., & Wang, Z. (2025). Enhancing Agricultural Productivity in Dairy Cow Mastitis Management: Innovations in Non-Antibiotic Treatment Technologies. *Veterinary Sciences, 12(7), 662.* *https://doi.org/10.3390/vetsci12070662*

Advanced mastitis detection in Bos indicus cows: A deep learning approach integrated with infrared thermography.[62]

This study evaluated infrared thermography (IRT) with deep learning for mastitis detection in Tharparkar cattle. Over 7,200 udder thermograms were analysed alongside CMT and SCC tests. CNN models achieved high accuracy (up to 0.98 training and 0.93 validation) in distinguishing healthy from clinical and subclinical cases. The results highlight IRT combined with AI as a non-invasive, scalable tool for improving mastitis detection and herd health management.

Research on the prediction model of mastitis in dairy cows based on time series characteristics.[63]

This study applied machine learning to predict mastitis risk in dairy cows using time-series production data from a large herd in Gansu, China. Among six tested models, XGBoost performed best with 71% accuracy and an AUC of 0.75. Key predictive features included milk yield, fat percentage variability, and fat percentage change rate. These results highlight the value of time-series modelling as an early-warning tool for subclinical mastitis management.

Adaptive neuro-fuzzy inference systems for improved mastitis classification and diagnosis.[64]

This study compared three adaptive neuro-fuzzy inference system (ANFIS) methods—GD-ANFIS, PSO-ANFIS, and GA-ANFIS—for classifying mastitis in Holstein cattle. Data preprocessing included feature reduction (Pearson correlation, PCA) and undersampling to address class imbalance. GD-ANFIS with Pearson features showed the strongest performance, though differences among models were small. These findings support fuzzy logic approaches for improving mastitis detection, herd health, and precision dairy management applications.

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[62] Gayathri SL, Bhakat M, Mohanty TK, Kumar RR, Chaturvedi KK, Kumar S. Advanced mastitis detection in Bos indicus cows: A deep learning approach integrated with infrared thermography. *J Therm Biol.* 2025 Jul;131:104173. doi: https://doi.org/10.1016/j.jtherbio.2025.104173 . Epub 2025 Jun 12. PMID: 40540820.

[63] Guo, R., Dai, Y., & Hu, J. (2025). Research on the prediction model of mastitis in dairy cows based on time series characteristics. *Frontiers in Veterinary Science, 12, 1575525*.

[64] Shirani Shamsabadi, J., Ansari Mahyari, S. & Ghaderi-Zefrehei, M. Adaptive neuro-fuzzy inference systems for improved mastitis classification and diagnosis. Sci Rep 15, 20456 (2025). *https://doi.org/10.1038/s41598-025-03008-5*

Mycoplasmas (including contagious bovine pleuropneumonia – CBPP and contagious caprine pleuropneumonia - CCPP)

Mapping the global distribution of *Mycoplasma bovis* infections in cattle (2000–2024).[65]
This global geospatial study compiles 24 years of *M. bovis* occurrence data across 31 countries, identifying major regional hotspots and changing prevalence patterns. It highlights the spread of infection beyond historically endemic areas and links outbreaks with trade and management factors. The analysis provides an evidence base for risk-based surveillance and prioritisation of control resources at regional and international scales.

Genes required for *M. bovis* survival and proliferation in host cells.[66]
Through transposon mutagenesis of 100 mutants, this study identifies key *M. bovis* genes essential for survival and proliferation in bovine epithelial cells. Nineteen mutants lost growth entirely while forty-seven showed severely reduced replication, implicating genes linked to metabolism, adhesion and stress response. These discoveries expand understanding of *M. bovis* pathogenicity and point to novel antivirulence and therapeutic targets.

A subunit vaccine for *Mycoplasma hyopneumoniae* in piglets.[67]

A multi-antigen subunit vaccine comprising P97R1, P46, P42 and P65 proteins elicited strong humoral and cellular responses in piglets. Immune protection surpassed that from conventional bacterins, supporting next-generation *M. hyopneumoniae* vaccine design. The results advance cross-protective immunisation strategies in swine health management.

Genome sequence of classic poultry pathogen *Mycoplasma gallisepticum* strain A5969.[68]

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[65] Zhang, H., et al. (2025). Mapping the global distribution of Mycoplasma bovis infections in cattle (2000–2024). *Journal of Dairy Science.* https://www.journalofdairyscience.org/article/S0022-0302(25)00489-8/fulltext
[66] Wang, Y., et al. (2024*). Genes required for Mycoplasma bovis survival and proliferation in host cells. Applied and Environmental Microbiology.* https://journals.asm.org/doi/10.1128/aem.00687-24
[67] Liu, X., et al. (2024). A subunit vaccine for *Mycoplasma hyopneumoniae* in piglets. *Frontiers in Veterinary Science.* https://doi.org/10.3389/fvets.2024.1493650
[68] Ramirez, M. A., et al. (2024). Genome sequence of the classic poultry pathogen *Mycoplasma gallisepticum* strain A5969. *Microbiology Resource Announcements, 13*(4), e00813-24. https://doi.org/10.1128/mra.00813-24

Using combined long- and short-read sequencing, the authors produced a complete reference genome for *M. gallisepticum* A5969. The assembly resolves complex adhesion and immune-evasion loci, strengthening comparative genomics, diagnostic assay development and vaccine research for avian mycoplasmosis.

CCPP outbreaks in Oman: *M. capricolum* subsp. *capripneumoniae* in goats and captive gazelles.[69]

Whole-genome SNP analysis of ten isolates from goats and gazelles revealed clustering within East-African phylogroup A and minimal diversity (~125 SNPs). The results indicate recent interspecies transmission and shared infection sources. The study recommends including wildlife and captive ungulates in surveillance to strengthen CCPP control.

One Health

One Health and neglected zoonotic diseases.[70]

This review analyses neglected zoonotic diseases through a One Health lens, emphasising their persistence in marginalised populations and limited integration in surveillance systems. It calls for coordinated human–animal–environment health frameworks and equitable funding models. The author highlights sociocultural and ecological determinants of transmission and proposes priority-setting tools to guide future One Health research and policy.

A One Health framework for exploring zoonotic interactions and transmission networks.[71]

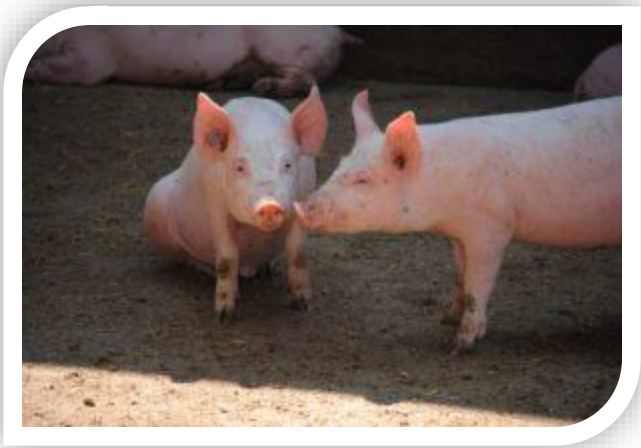
Using a network-based modelling framework, this study maps human–animal–environment transmission chains to identify zoonotic hotspots. It integrates ecological and epidemiological data to assess how interspecies interactions shape pathogen flow. The approach

[69] Al Rawahi, A., et al. (2024). CCPP outbreaks in Oman: *Mycoplasma capricolum* subsp. *capripneumoniae* in goats and captive gazelles. *BMC Veterinary Research, 20*, 196. https://doi.org/10.1186/s12917-024-03969-1
[70] Iglesia, R. P. (2025). One Health and neglected zoonotic diseases. *Infectious Diseases of Poverty, 14*(1), xx–xx. **https://doi.org/10.1186/s40249-025-xxxx-x**
[71] Ghai, R. R., et al. (2024). A One Health framework for exploring zoonotic interactions and transmission networks. *Nature Communications, 15*, 49967. https://doi.org/10.1038/s41467-024-49967-7

demonstrates the analytical potential of One Health tools for targeted surveillance and control planning.

How studies on zoonotic risks in wildlife implement the One Health approach: A systematic literature review.[72]

This systematic review of 105 wildlife-linked zoonosis studies (2018–2023) finds that fewer than 5 % fully integrate human, animal, and environmental domains. Although animal and human data dominate, environmental components are underrepresented. The authors underline the need for transdisciplinary research and policy alignment to achieve practical One Health implementation.



Porcine reproductive and respiratory syndrome (PRRS)

Genetic evolution, epidemic trends, and recombination dynamics of PRRSV-1 in China.[73]

Whole-genome analysis of 46 Chinese PRRSV-1 isolates revealed frequent recombination events, particularly among BJEU06-1-like and Amervac-like strains. The study showed that using ORF5 alone can misrepresent diversity, highlighting the need for genome-wide monitoring. Mutations in GP5, including potential N-glycosylation sites, may help the virus evade immunity.

Evaluation of the infectivity of three PRRSV variants.[74]

A comparative infection study assessed three PRRSV variants (L1A, L9A, L1C.5) in pigs, showing that L1C.5 required fewer infectious particles and caused more severe pulmonary lesions. Viral shedding was comparable among strains, but infectivity and virulence differed

[72] Pérez-Arredondo, A., et al. (2024). How studies on zoonotic risks in wildlife implement the One Health approach: A systematic literature review. *One Health, 18*, 100567. https://doi.org/10.1016/j.onehlt.2024.100567

[73] Zhao, Y., et al. (2025). Genetic evolution, epidemic trends, and recombination dynamics of PRRSV-1 in China. *Frontiers in Veterinary Science, 12*, 1632917. https://doi.org/10.3389/fvets.2025.1632917

[74] Zhou, H., et al. (2025). Evaluation of the infectivity of three PRRSV variants. *Veterinary Research, 56*(1), 1591. https://doi.org/10.1186/s13567-025-01591-z

markedly. The results refine risk assessment and inform biosecurity thresholds for variant introduction.

Optimization and application of an immunoperoxidase monolayer assay (IPMA) for PRRSV detection.[75]

This study optimised an IPMA using a broad-spectrum monoclonal antibody for PRRSV detection. The assay showed high sensitivity and complete agreement with qRT-PCR across 108 field samples, with no cross-reactivity to other swine viruses. Offering a low-cost, kit-free diagnostic option, it supports rapid PRRSV surveillance in resource-limited laboratories.

Isolation and genomic characterization of a novel PRRSV-1 from severely diseased piglets in China (AHEU2024-2671).[76]

A new PRRSV-1 strain (AHEU2024-2671) was isolated from diseased piglets. It replicated only in alveolar macrophages and carried unique genomic deletions, including one never reported before. This strain may represent a new subtype 1 subgroup, indicating ongoing viral diversification with potential pathogenic consequences.

Insights into genetic determinants of piglet survival during a PRRSV outbreak.[77]

In naturally infected Duroc pigs, low pre-infection IgG and high SOX13 expression were linked to higher mortality. Sire genotypes at several SNPs (including CD163 and GBP5) influenced survival, with cumulative effects across alleles. The trait was moderately heritable, supporting selective breeding for resilience.

[75] Zhang, X., et al. (2025). Optimization and application of an immunoperoxidase monolayer assay (IPMA) for PRRSV detection. *BMC Veterinary Research, 21*, 4925. https://doi.org/10.1186/s12917-025-04925-3
[76] Li, J., et al. (2024). Isolation and genomic characterization of a novel PRRSV-1 from severely diseased piglets in China (AHEU2024-2671). *Veterinary Sciences, 12*(1), 61. https://doi.org/10.3390/vetsci12010061
[77] Liu, Y., et al. (2024). Insights into genetic determinants of piglet survival during a PRRSV outbreak. *Veterinary Research, 55*(1), 1421. https://doi.org/10.1186/s13567-024-01421-8

Porcine respiratory disease complex (PRDC)

Challenges and Lessons Learned from a Field Trial on the Understanding of the Porcine Respiratory Disease Complex.[78]

This study sought to correlate anti-PRRSV immune responses, and 21 secondary infectious agents, with PRDC severity by inoculating PRRSV-negative weaners with PRRSV-2 modified live virus (MLV) vaccination and housing them in a farm with a history of PRDC. Anti-PRRSV cellular and antibody responses were monitored pre-vaccination, 28-days post-vaccination, and 49-days post vaccination (during a PRDC outbreak). The authors report a strong correlation between high weaning weight and disease resilience, limited and delayed induction of neutralising antibodies by the MLV vaccine, and variable cellular responses. PRRSV-2 and porcine cytomegalovirus (PCMV) were the most prevalent pathogens and significantly associated with disease severity. The study highlighted the complexity of PRDC pathogenesis and underscored the need for improved vaccine strategies and integrated pathogen surveillance.

Poxviruses

Progress in diagnostic methods and vaccines for lumpy skin disease.[79]

This review summarises current advances in lumpy skin disease diagnostics and vaccines, including inactivated, live-attenuated and DIVA candidates. It assesses vaccine safety, cross-protection and next-generation vector platforms. The study provides a

[78] Crisci, E., Kick, A. R., Cortes. L. M., Byrne, J. J., Amaral. A. F., Love, K., Tong, H., Zhang, J., Gauger, P. C., Pittman, J. & Käser, T. (2025) Challenges and Lessons Learned from a Field Trial on the Understanding of the Porcine Respiratory Disease Complex. *Vaccines*, 13(7), 740. https://doi.org/10.3390/vaccines13070740

[79] Farag, T. K., et al. (2025). Progress in diagnostic methods and vaccines for lumpy skin disease. *Veterinary Immunology and Immunopathology, 306*, 10667. https://doi.org/10.1007/s11259-025-10667-2

timely synthesis for guiding vaccine improvement and field implementation against capripoxvirus infections.

Severe pathological and transcriptional changes in haematopoietic organs of salmon suffering from salmon gill poxvirus disease.[80]

Atlantic salmon infected with Salmon Gill Poxvirus Disease (SGPV) exhibited not only gill injuries but also systemic impacts: red-blood-cell breakdown (erythrophagocytosis) and substantial transcriptomic changes in spleen and kidney involving immune, coagulation, apoptotic and stress-responsive pathways. These findings show that SGPV induces a more widespread disease than previously assumed — with implications for diagnostics, welfare and control in aquaculture systems.

Identification and genetic analysis of the recent Avian pox viruses from infected pigeons and chickens.[81]

In backyard poultry from Egypt, field isolates of avian poxviruses (APVs) from chickens and pigeons exhibited high genetic similarity to commercially used vaccines with 100% identity for chicken strains (FPV) and up to 91% for pigeon strains. The findings highlight continued APV circulation despite vaccination and emphasize the need for tailored immunization strategies in backyard systems.

Live attenuated goatpox vaccination in pregnant Murcia-Granada goats: dosage implications and outcomes.[82]

When pregnant Murcia-Granada goats were immunized with a live attenuated goatpox vaccine, a double dose (0.9 mL) caused abortions in 37% of treated goats, whereas the standard 0.5 mL dose was safe and effective. This underscores the importance of careful dosage selection in vaccination protocols for pregnant livestock.

The silent spread: uncovering the diversity and evolution of poxviruses in ticks across Western China's host landscapes.[83]

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[80] Abols, K., et al. (2025). *Severe pathological and transcriptional changes in haematopoietic organs of salmon suffering from salmon gill poxvirus disease. BMC Veterinary Research, 21*, 4922. https://doi.org/10.1186/s12917-025-04922-6

[81] Hassan, A. E., et al. (2024). Identification and genetic analysis of the recent avian pox viruses from infected pigeons and chickens. *Beni-Suef University Journal of Basic and Applied Sciences, 13*, 89. https://doi.org/10.1186/s43088-024-00589-4

[82] Serrano, M. J., et al. (2024). Live attenuated goatpox vaccination in pregnant Murcia-Granada goats: Dosage implications and outcomes. *BMC Veterinary Research, 20*, 4395. https://doi.org/10.1186/s12917-024-04395-z

[83] Wang, L., et al. (2025). The silent spread: Uncovering the diversity and evolution of poxviruses in ticks across western China's host landscapes. *Virology Journal, 22*, 2844. https://doi.org/10.1186/s12985-025-02844-1

Through metagenomic sequencing of ticks collected in western China (Tibet, Shaanxi, Gansu), researchers identified 61 distinct poxvirus species across 22 genera, assembling 387 viral sequences. Ticks appear to act as mechanical vectors, transmitting poxviruses across a range of hosts via interrupted feeding, highlighting a previously underappreciated ecological transmission route.

Vector transmission and control (VTC)

Innovative approaches to vector control: integrating genomic, biological, and chemical strategies.[84]

This review examines innovative strategies for controlling vector-borne diseases beyond conventional insecticides. Genomic tools (e.g., CRISPR/Cas9 gene drives), biological methods (Wolbachia, SIT), and novel chemical approaches offer promising solutions to resistance and environmental concerns. Integrated Vector Management (IVM) frameworks that combine these strategies can enhance effectiveness and sustainability. However, challenges remain around scalability, ecological risks, and long-term impact assessment.

Challenges in the surveillance and control of mosquito-borne diseases in Europe and United States. The perspective from public health experts.[85]

This qualitative study interviewed public health managers from the EU and US to identify barriers in mosquito-borne disease surveillance and control. Key challenges included fragmented guidelines, lack of centralisation, limited resources, and weak modelling capacity. Participants stressed the importance of community engagement and transparent communication for successful interventions. Strong coordination, adequate resources, and a

[84] Abbasi, E. (2025). Innovative approaches to vector control: Integrating genomic, biological, and chemical strategies. *Annals of Medicine and Surgery, 87*(8), 5003–5011. https://doi.org/10.1097/MS9.0000000000003469
[85] Sedda, L., Wrench, E., Moore, T. C., Wolfe, K., Tangena, J. A., & Brown, H. E. (2025). Challenges in the surveillance and control of mosquito-borne diseases in Europe and United States: The perspective from public health experts. *One Health, 21*, 101133. https://doi.org/10.1016/j.onehlt.2025.101133

One Health approach are essential as climate change and global travel increase outbreak risks.

Climate-responsive vector control strategies for Aedes albopictus.[86]

This study used a metapopulation model to optimize larvicide use for controlling Aedes albopictus. Preventive treatments early in the season were most effective, particularly under low rainfall and cooler temperatures. Breeding site size and water capacity strongly influenced cost-effective resource allocation, while spatial distribution mattered less. These findings show that climate and site characteristics should guide flexible, cost-efficient mosquito control programs to reduce disease risks.

Tick feeding or vaccination with tick antigens elicits immunity to the Ixodes scapularis exoproteome in guinea pigs and humans.[87]

This study developed IscREAM, a high-throughput technique to monitor antibody responses to over 3,000 Ixodes scapularis tick antigens. Validation in guinea pigs confirmed its ability to detect responses to vaccine-induced tick resistance. Across resistant individuals, Lyme disease patients, and tick-exposed animals, 199 antigens were identified, many with histamine-binding domains. These findings improve understanding of host immunity to ticks and highlight candidates for future antitick vaccines.

Disclaimer:
Summaries of the above publications were generated with the support of AI (ChatGPT, OpenAI) to ensure concise and standardised presentation for the STAR IDAZ State-of-the-Art report.

[86] Bellver-Arnau, J., Blanco-Sierra, L., Escartin, S., & colleagues. (2025). Climate-responsive vector control strategies for *Aedes albopictus. Parasites & Vectors, 18*, 168. https://doi.org/10.1186/s13071-025-06791-2
[87] Hart, T. M., Cui, Y., Telford, S. R., Marín-López, A., Calloway, K., Dai, Y., … & Fikrig, E. (2025). Tick feeding or vaccination with tick antigens elicits immunity to the *Ixodes scapularis* exoproteome in guinea pigs and humans. *Science Translational Medicine, 17*(791), eads9207. https://doi.org/10.1126/scitranslmed.ads9207