Metaheuristic Optimization Review
◆ ISSN: 3066-280X Vol: 07, No. 01, 2026 ◆ PP. 29–40
Article DOI: https://doi.org/10.54216/MOR.070104

REVIEW ARTICLE

Artificial Intelligence and Deep Learning in Hantavirus Research: A Comprehensive Review

Elham Edkndarnia[1,*]
[1] Arab open university-Bahrain
Email: Elham.mohamed@aou.org.bh

Received: February 10, 2026 Revised: April 11, 2026 Accepted: June 10, 2026 ⋆ Corresponding author

ABSTRACT

Hantavirus remains an important zoonotic threat because of its association with severe human diseases, including hemorrhagic fever with renal syndrome and hantavirus pulmonary syndrome. Its transmission is strongly influenced by rodent reservoirs, environmental conditions, human exposure patterns, and regional ecological variability. Recent advances in artificial intelligence (AI) and deep learning have created new opportunities for improving Hantavirus detection, outbreak prediction, ecological risk mapping, diagnostic support, and public health surveillance. This review examines the role of AI-driven methods in Hantavirus research, with emphasis on how machine learning, deep learning, image-based analysis, epidemiological modeling, and data-driven surveillance can support earlier detection and more informed decision-making. The review also discusses the potential of AI to integrate heterogeneous data sources, including clinical records, environmental variables, remote sensing indicators, genomic information, and epidemiological reports. Despite these advances, several challenges remain, including limited datasets, geographic bias, model generalization, lack of clinical validation, data imbalance, interpretability concerns, and the need for real-time deployment. Overall, AI and deep learning offer promising tools for strengthening Hantavirus surveillance and response, but their practical value depends on transparent models, high-quality data, interdisciplinary validation, and integration into public health systems.

Keywords: Hantavirus; Artificial intelligence; Deep learning; Disease surveillance; Outbreak prediction

1. INTRODUCTION

Hantavirus represents an important zoonotic viral threat because of its capacity to cause severe human disease, its dependence on wildlife reservoirs, and its close relationship with ecological, environmental, and human behavioral factors. Unlike many directly transmitted viral infections, Hantavirus transmission is strongly associated with rodent reservoirs and human exposure to contaminated excreta, aerosols, or infected environments. This makes Hantavirus not only a biomedical concern, but also an ecological and public health challenge that requires integration between virology, epidemiology, environmental monitoring, clinical diagnosis, and surveillance science. The continuing concern surrounding Hantavirus is reinforced by its pandemic potential, severe clinical outcomes, and capacity to emerge or re-emerge when environmental and human conditions favor spillover events [1].

The clinical importance of Hantavirus is mainly linked to two major disease patterns: hemorrhagic fever with renal syndrome and Hantavirus pulmonary syndrome. These syndromes differ in their geographical distribution, dominant viral lineages, clinical presentation, and disease severity, but both reflect the broader ability of Hantaviruses to produce serious systemic illness. The public health burden of these infections is intensified by diagnostic difficulty, symptom overlap with other febrile or respiratory diseases, and the need for early recognition before progression to severe manifestations. Because Hantavirus infection can involve complex host-pathogen interactions and region-specific epidemiological profiles, surveillance systems must be able to capture both clinical and ecological signals rather than relying on isolated case reporting [2]. A central challenge in Hantavirus control is that viral circulation is deeply connected to rodent ecology. Reservoir abundance, host distribution, biodiversity, land-use transformation, climate variability, and human intrusion into natural habitats can influence the probability of viral maintenance and spillover. Modern research increasingly recognizes that Hantavirus risk cannot be understood only through confirmed human cases, because human infection often represents the final stage of a longer ecological chain involving reservoir dynamics, environmental exposure, and behavioral risk. Machine learning-based ecological analysis has shown particular value in examining how land-use conditions affect the presence of rodent hosts associated with New World Hantaviruses, thereby supporting broader risk mapping and surveillance strategies [3]. The need for advanced data-driven approaches is further strengthened by spatial and temporal variability in Hantavirus reservoirs. Rodent hosts do not remain constant across regions or seasons, and their infection patterns may shift according to habitat structure, food availability, climate conditions, and anthropogenic disturbance. Recent surveillance-oriented studies have emphasized that rodent-associated Hantavirus patterns can vary over time and across geographic locations, making static monitoring insufficient for long-term risk assessment [4]. Therefore, predictive tools that can learn from ecological, epidemiological, genomic, and environmental data may provide stronger support for identifying risk zones before human outbreaks occur. Artificial intelligence has become increasingly relevant in infectious disease research because it can identify complex nonlinear relationships within heterogeneous datasets. In the context of Hantavirus, AI may support multiple tasks, including early warning, ecological risk prediction, clinical decision support, molecular screening, viral classification, and public health surveillance. Unlike traditional statistical methods that may require strong assumptions about variable relationships, AI models can learn hidden patterns from high-dimensional data and adapt to different data types. This capability is especially useful for zoonotic diseases, where risk may depend on interactions among host ecology, pathogen genetics, climate, land use, human behavior, and health-system detection capacity [5]. Deep learning is particularly important because it can process complex data structures such as genomic sequences, medical images, environmental signals, and large-scale temporal data. For Hantavirus research, deep learning may contribute to viral sequence interpretation, host-pathogen interaction analysis, molecular inhibitor screening, and disease prediction. Some recent studies have already explored deep learning frameworks for identifying molecular inhibitors and understanding Hantavirus-related pathogenic mechanisms, showing that computational approaches can extend beyond surveillance into therapeutic discovery and molecular-level investigation [6]. This reflects a broader shift from purely descriptive virology toward computationally assisted biological interpretation. AI also has potential value in diagnostic and therapeutic development. Emerging research on antiviral peptide prediction, epitope identification, vaccine design, and computer-aided drug discovery shows that computational models can reduce the time required to screen candidate molecules or predict biologically meaningful targets. Although such methods do not replace laboratory validation, they can prioritize candidates, reduce experimental burden, and support faster response to emerging viral threats. In this context, machine learning and deep learning tools used for antiviral peptide prediction provide a relevant foundation for future Hantavirus-focused therapeutic research [7]. Despite these opportunities, the application of AI and deep learning to Hantavirus remains limited compared with more widely studied infectious diseases. Much of the available AI literature focuses on pandemic-scale pathogens, respiratory infections, general infectious disease prediction, or broad zoonotic surveillance rather than Hantavirus-specific modeling. Systematic reviews of machine learning and deep learning for infectious disease preparedness indicate that AI can improve forecasting, detection, and response planning, but they also highlight recurring limitations such as inconsistent datasets, lack of external validation, limited interpretability, and weak integration into real public health workflows [8]. These limitations are highly relevant to Hantavirus because available data are often fragmented across ecological, clinical, and laboratory domains. Another important issue is that Hantavirus surveillance requires integration across multiple scales. At the molecular scale, AI can support sequence classification, epitope prediction, molecular docking prioritization, and host adaptation analysis. At the clinical scale, AI can assist in distinguishing Hantavirus infection from other febrile, renal, or respiratory conditions when sufficient validated data are available. At the ecological scale, AI can model reservoir distribution, environmental suitability, and spillover risk. At the public health scale, AI can support early warning systems, outbreak preparedness, and decision-making. The growing use of AI for early detection of infectious diseases demonstrates that data-driven systems can strengthen public health response when they are transparent, validated, and connected to surveillance infrastructure [9]. However, the practical use of AI in Hantavirus research faces several barriers. First, Hantavirus datasets are often small, geographically uneven, and inconsistent in quality. Second, ecological and clinical datasets may not be easily integrated because they differ in spatial scale, temporal resolution, and data standards. Third, deep learning models may require large labeled datasets that are difficult to obtain for rare or regionally concentrated diseases. Fourth, AI outputs may lack interpretability, which limits clinical and public health trust. Fifth, models trained in one region may fail to generalize to another because reservoir species, viral genotypes, land-use patterns, healthcare access, and reporting practices differ. These concerns are consistent with broader discussions on AI and machine learning for emerging and re-emerging viral diseases, where methodological promise is often balanced by concerns regarding validation, deployment, and ethical use [10]. Accordingly, this review aims to examine the intersection between Hantavirus research, artificial intelligence, and deep learning. It focuses on how AI-driven methods can contribute to Hantavirus detection, prediction, ecological surveillance, molecular analysis, diagnostic support, and public health preparedness. Rather than treating AI as a single solution, this review considers it as a set of computational approaches that must be evaluated according to data type, application context, model transparency, validation strategy, and practical deployment potential. The review also discusses current gaps in the literature, including limited Hantavirus-specific datasets, weak model generalization, lack of real-world validation, and insufficient integration between ecological intelligence and clinical surveillance. By synthesizing existing research, this paper highlights both the promise and limitations of AI and deep learning in advancing Hantavirus monitoring, understanding, and response.

2. LITERATURE REVIEW

The literature on Hantavirus research has gradually expanded from classical epidemiological and clinical descriptions toward a broader multidisciplinary field that includes ecology, molecular biology, public health surveillance, computational modeling, artificial intelligence, and deep learning. This transition is important because Hantavirus does not represent a single-dimensional infectious disease problem. Instead, it exists at the intersection of reservoir-host ecology, environmental exposure, viral evolution, human behavior, diagnostic uncertainty, and healthcare preparedness. Earlier research was largely concerned with identifying disease patterns, describing clinical syndromes, and documenting reservoir-host relationships. More recent work has increasingly emphasized predictive modeling, sequence-based interpretation, risk mapping, automated diagnosis, and data-driven public health decision support. This shift reflects the growing recognition that Hantavirus prevention and response require more than retrospective case reporting; they require tools capable of detecting hidden patterns across complex biological, ecological, and epidemiological data.

Figure 1 presents Hantavirus research as a data-to-impact process. The figure emphasizes that Hantavirus risk arises from the interaction between reservoir ecology, environmental drivers, viral persistence, and human exposure. This is directly relevant to artificial intelligence-based modeling because predictive systems must integrate diverse forms of evidence rather than focusing on one isolated data source. The figure identifies several AI and deep learning methods that may be applied in Hantavirus research, including machine learning, deep learning, spatiotemporal modeling, natural language processing, and generative AI. It also summarizes the major data categories that can support these methods, including ecological, environmental, epidemiological, clinical, genomic, and socio-behavioral data. By linking data sources, AI workflow stages, benefits, challenges, future directions, and public health response, Figure 1 provides a comprehensive visual summary of the review's analytical framework.

A major body of Hantavirus literature focuses on human disease prevalence, genotype distribution, and epidemiological characterization. These studies are important because they provide the foundation for understanding how Hantavirus infections appear in human populations, how disease patterns differ across regions, and which viral genotypes are associated with specific clinical outcomes. Retrospective observational analyses have shown that human Orthohantavirus disease is not uniformly distributed, but rather shaped by regional genotype circulation, exposure pathways, and surveillance capacity [11]. This is particularly relevant for artificial intelligence-based review work because machine learning and deep learning models require high-quality epidemiological data to detect temporal trends, classify risk profiles, and support early warning. However, the uneven distribution of reported cases also creates methodological difficulties. If data are concentrated in specific regions or diagnostic centers, AI models may learn geographically biased patterns rather than generalizable disease signals. Therefore, epidemiological datasets must be interpreted not only as evidence of disease occurrence, but also as products of surveillance intensity, healthcare access, diagnostic availability, and reporting infrastructure. Mathematical modeling has also contributed significantly to Hantavirus research by formalizing the relationship between infected rodents, susceptible hosts, environmental conditions, and human infection risk. Such models are valuable because they translate ecological and epidemiological assumptions into structured systems that can be analyzed, simulated, and compared under different transmission scenarios. Transmission models among rodents and humans demonstrate that human infection is not independent of reservoir dynamics, and that changes within rodent populations can influence downstream human risk [12]. Although traditional mathematical models are different from deep learning systems, they provide an important conceptual foundation for AI-based approaches. Mathematical models often rely on explicitly defined equations and assumptions, while AI models learn relationships from data. Combining both directions may be useful in future Hantavirus studies, where mechanistic models can provide biological interpretability and AI models can improve predictive flexibility. This hybrid direction is especially promising for diseases where ecological processes are known but difficult to measure continuously. Another important research direction concerns the molecular and bioinformatics characterization of Hantavirus proteins. Molecular studies help explain how viral components contribute to infection, immune recognition, host interaction, and disease pathogenesis. Bioinformatics analysis of envelope glycoproteins associated with Hantavirus cardiopulmonary syndrome and hemorrhagic fever with renal syndrome has provided insight into structural and functional features that may influence viral behavior and immune response [13]. This type of work is highly relevant to deep learning because modern neural models can process protein sequences, structural representations, and molecular features at scales that are difficult to analyze manually. In future Hantavirus research, deep learning may be used to identify conserved antigenic regions, predict host-interaction patterns, support vaccine target discovery, and classify viral variants according to biologically meaningful sequence features. However, such applications require careful validation because computational predictions in molecular virology cannot be treated as equivalent to laboratory-confirmed biological function. Reservoir-host research remains one of the strongest foundations of Hantavirus science. Since Hantaviruses are maintained mainly in rodent reservoirs, understanding reservoir ecology is essential for predicting human risk. Broader work on bat and rodent reservoirs of zoonotic viruses has emphasized that reservoir species often maintain viruses through complex immune, ecological, and behavioral mechanisms that differ from those observed in humans [14]. For Hantavirus, this means that disease prevention cannot be limited to clinical surveillance alone. Rodent abundance,

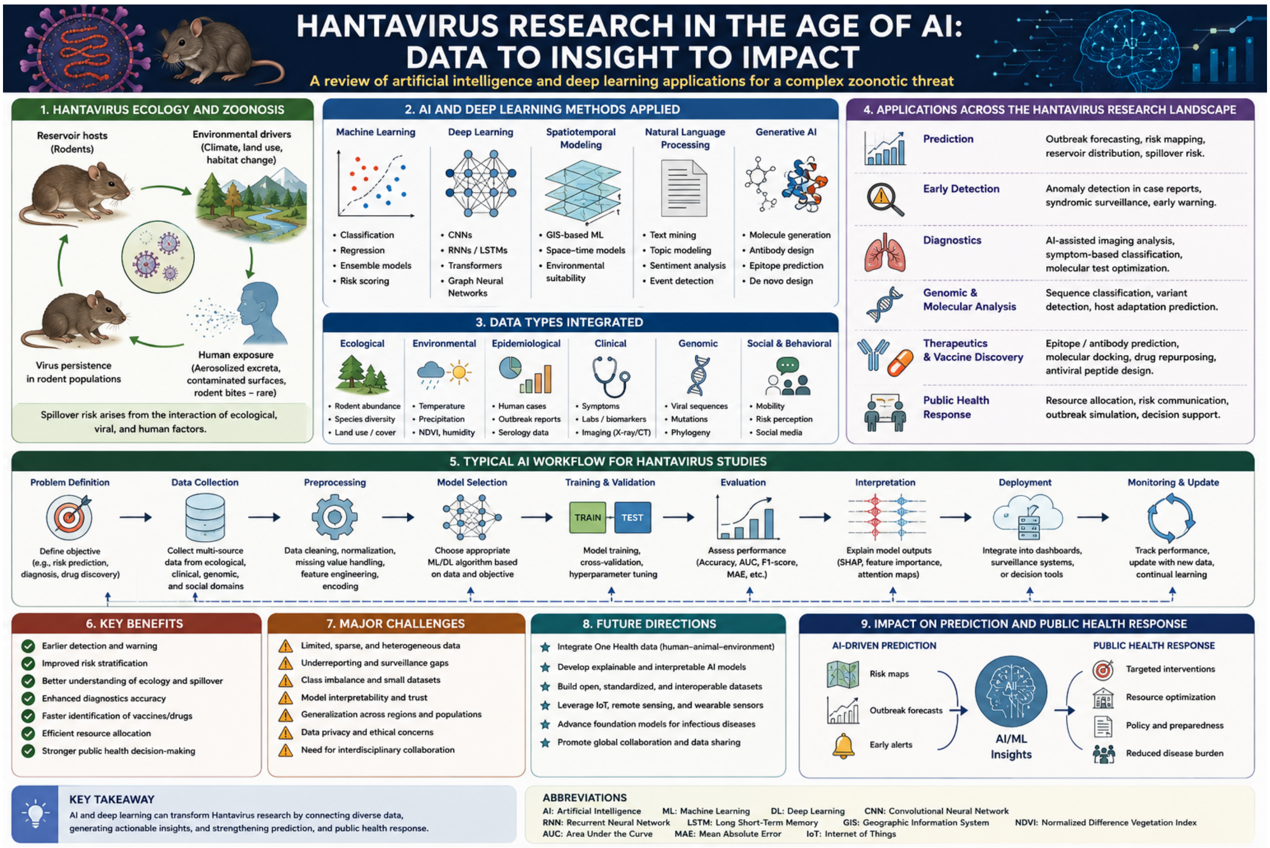

Figure 1. Data-to-impact framework for Hantavirus research in the age of artificial intelligence, showing ecological drivers, AI methods, data types, research applications, workflow stages, benefits, challenges, future directions, and public health response.

habitat suitability, seasonal movement, interspecies contact, and environmental disturbance must also be monitored. Artificial intelligence can contribute to this area by integrating reservoir occurrence records, environmental variables, land-use data, climate indicators, and viral sequence information. Nevertheless, reservoir-based AI models face several difficulties, including incomplete wildlife sampling, inconsistent geographic coverage, uncertain host-virus associations, and temporal gaps in ecological data. These limitations make interpretability and uncertainty estimation essential when AI models are used for zoonotic risk mapping. Recent work has also started to connect generative artificial intelligence with Hantavirus-related biological discovery. Experiment-aware generative pipelines designed for pan-Hantavirus antibody development indicate that computational systems may help reduce the gap between simulation and laboratory applicability [15]. This direction is important because antibody discovery, vaccine development, and therapeutic screening often require substantial experimental resources. Generative AI can support candidate design by proposing molecular structures, optimizing antibody features, or prioritizing candidates before experimental testing. However, such models must be approached carefully. A generative model may produce biologically plausible candidates, but plausibility is not the same as efficacy, safety, or manufacturability. Therefore, the role of generative AI in Hantavirus research should be understood as an acceleration tool rather than a replacement for laboratory validation. In a review context, this point is essential because it separates computational promise from biomedical proof. The diagnostic literature has also begun to incorporate machine learning and nanotechnology as complementary tools for zoonotic disease control. Advances in microbial diagnostics show that machine learning can support pattern recognition, biosignal interpretation, molecular detection, and diagnostic decision-making when integrated with emerging laboratory technologies [16]. This has clear implications for Hantavirus, where early diagnosis may be difficult because symptoms can resemble other febrile, renal, or respiratory diseases. AI-supported diagnostics could help classify patients based on clinical variables, laboratory values, exposure history, and regional epidemiological risk. Deep learning may also support molecular diagnostics by improving sequence classification or assay design. Yet, diagnostic AI models require high-quality labeled clinical data, external validation, and clear clinical pathways. Without these conditions, a model may perform well in development datasets but fail when applied to real patient populations. Clinical decision support is another emerging theme within Hantavirus-related literature. A simple clinical score for reducing unnecessary Puumala Hantavirus testing shows that structured decision rules can improve diagnostic efficiency and reduce avoidable testing when applied to appropriate clinical contexts [17]. Although this type of scoring system is not necessarily a deep learning model, it is highly relevant to AI-based research because it demonstrates the practical value of decision support in Hantavirus diagnosis. In many clinical settings, the goal is not only to maximize sensitivity or specificity, but also to use limited diagnostic resources effectively. Future AI models may build on such clinical scoring principles by incorporating broader variables and learning more complex relationships. However, the interpretability of clinical decision support remains critical. Physicians and public health practitioners are more likely to trust models that provide understandable reasoning, particularly when the disease is rare, severe, or diagnostically ambiguous. Deep learning for disease prediction has expanded across infectious disease research, especially where climatic, environmental, and linguistic or contextual variables are combined to infer outbreak risk or disease patterns. Deep learning-driven disease prediction models that integrate climatic and linguistic attributes illustrate how heterogeneous data sources can be fused for predictive health applications [18]. This direction is particularly relevant for Hantavirus because environmental and climatic factors influence rodent population dynamics, vegetation patterns, food availability, and human exposure. Social, behavioral, and textual data may also provide indirect signals of outbreak concern, public awareness, or reporting changes. Nevertheless, the integration of heterogeneous data introduces methodological challenges. Different data sources vary in reliability, temporal resolution, geographic coverage, and noise level. A model that combines climate data, epidemiological reports, and textual information must therefore be carefully designed to avoid learning spurious correlations. For Hantavirus, this is especially important because outbreaks may be rare and regionally specific.

Viral classification has become another important area where deep learning may support infectious disease research. Hierarchical deep learning models for interpretable viral classification show that neural networks can be designed not only to classify viruses, but also to preserve meaningful relationships across viral taxonomic or biological levels [19]. This is relevant to Hantavirus because viral diversity, host association, and genotype distribution are central to understanding disease emergence and clinical risk. An interpretable hierarchical classifier could potentially support Hantavirus sequence classification, reservoir association analysis, or detection of unusual viral patterns. However, viral classification models must address the problem of dataset imbalance, since some viruses and genotypes are much better represented in sequence databases than others. If deep learning models are trained on imbalanced viral datasets, they may perform well on common lineages while failing to recognize rare or emerging variants.

Figure 2 presents the future-oriented direction of AI-enabled Hantavirus research. The figure emphasizes that the next stage of development should move beyond isolated computational models and toward integrated surveillance and decision-support systems. Such systems should combine reservoir monitoring, environmental sensing, clinical information, genomic sequencing, laboratory diagnostics, social and behavioral data, and public health reporting. This integrated structure is important because Hantavirus risk is shaped by interactions among animal reservoirs, environmental conditions, viral biology, human exposure, clinical progression, and surveillance capacity. By connecting these domains, AI and deep learning can support earlier warning, stronger risk stratification, more accurate diagnostic prioritization, and better coordination between researchers, clinicians, epidemiologists, and public health authorities. Therefore, Figure 2 supports the main conclusion of this review: artificial intelligence is most useful when it is transparent, validated, interpretable, and connected to practical public health action.

Vaccine and epitope prediction literature further demonstrates how artificial intelligence can support infectious disease preparedness. AI-driven epitope prediction has been reviewed as a growing field that can assist vaccine development by identifying candidate immune targets and comparing computational strategies [20]. In the Hantavirus context, epitope prediction may contribute to vaccine design by identifying conserved regions that could generate protective immune responses across relevant viral strains. Such approaches could be especially useful when experimental screening is costly or when rapid prioritization is needed. However, epitope prediction remains a probabilistic computational task, and predicted epitopes require immunological validation. A major challenge for Hantavirus vaccine-related AI is the genetic and antigenic diversity of viral strains, which may complicate the design of broadly protective candidates. Therefore, AI can support vaccine research most effectively when combined with immunology, structural biology, and experimental validation. Across the reviewed literature, a clear pattern emerges: Hantavirus research is moving toward more integrated computational frameworks, but the field remains fragmented. Epidemiological studies provide essential human disease data, ecological studies explain reservoir and environmental risk, molecular studies clarify viral structure and function, diagnostic studies improve detection pathways, and AI-oriented studies introduce new computational possibilities. However, these streams are not yet fully unified. Many AI models in infectious disease research are developed on general viral datasets or non-Hantavirus case studies, while Hantavirus-specific AI applications remain comparatively limited. This creates both a gap and an opportunity. The gap is that Hantavirus has not yet benefited from the same volume of AI research seen in diseases such as COVID-19, influenza, or dengue. The opportunity is that existing AI methods from viral classification, disease prediction, molecular screening, epitope prediction, and diagnostic support can be adapted carefully to Hantavirus-specific problems. The literature also shows that AI and deep learning should not be treated as universal solutions. Their value depends on data availability, model design, validation quality, interpretability, and practical integration into surveillance or clinical workflows. For Hantavirus, the most useful future systems may be multimodal rather than single-purpose. A strong surveillance platform could combine rodent reservoir data, land-use variables, climate indicators, viral sequences, human case reports, clinical symptoms, and diagnostic results. Deep learning could analyze high-dimensional sequence or image data, while traditional machine learning could model structured ecological and clinical variables. Mechanistic models could add biological interpretability, and public health dashboards could translate model outputs into actionable decisions. Such integration would move Hantavirus research from isolated prediction tasks toward intelligent decision-support systems. In summary, the existing literature provides a strong foundation for reviewing artificial intelligence and deep learning in Hantavirus research, even though direct Hantavirus-specific AI studies remain relatively limited. Epidemiological and clinical studies define the disease burden and surveillance needs. Ecological and reservoir studies explain why environmental and host-related data are essential for prediction. Molecular and bioinformatics studies cre-

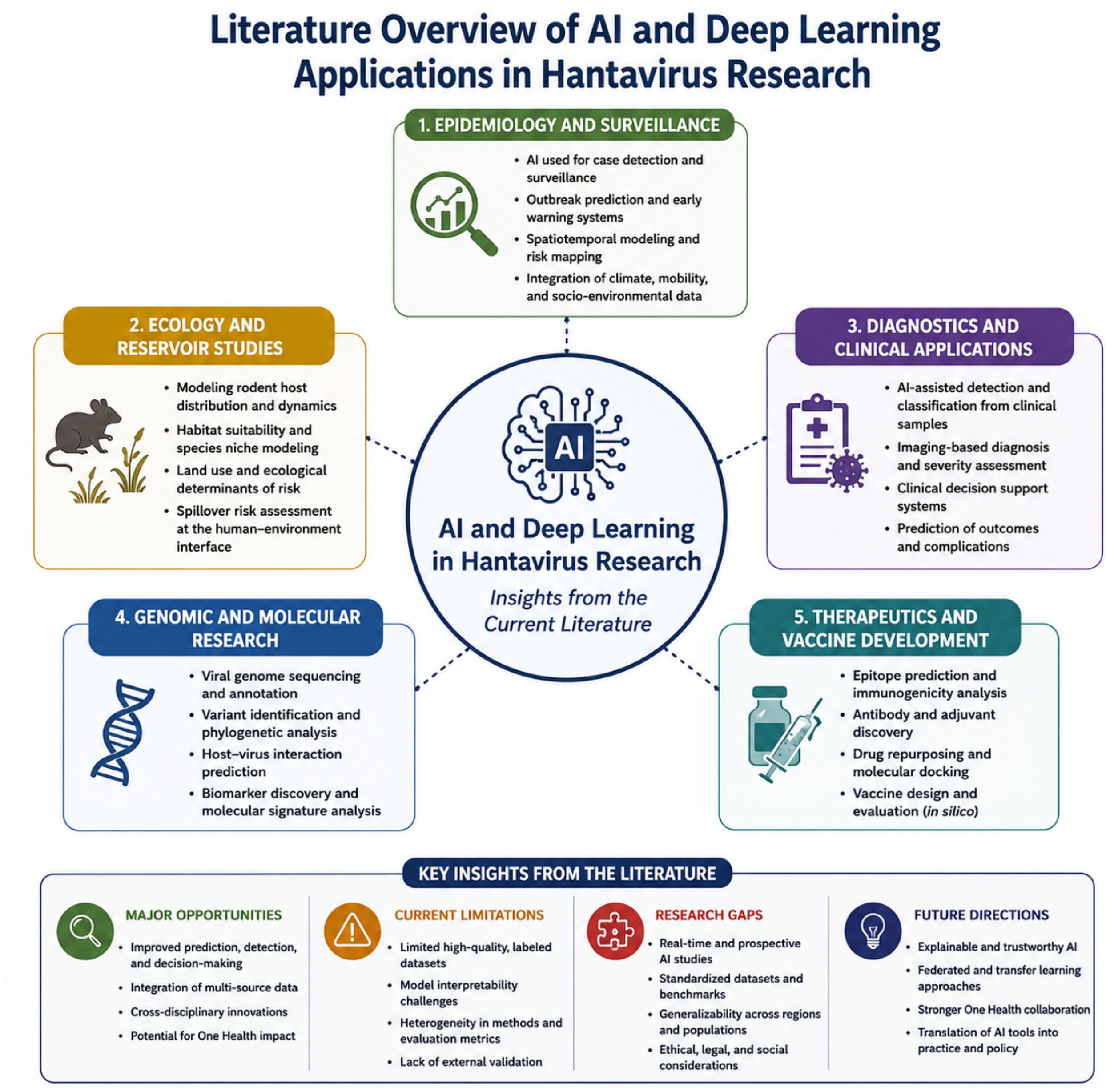

Figure 2. Integrated future framework for AI-enabled Hantavirus surveillance, prediction, clinical support, therapeutic discovery, and public health decision-making.

ate opportunities for sequence-based modeling, therapeutic screening, and vaccine target discovery. Broader AI studies in infectious disease prediction, diagnostics, viral classification, and epitope prediction provide transferable methods that can be adapted to Hantavirus. The main challenge is to transform these separate research directions into validated, interpretable, and deployable AI systems that can support real-world Hantavirus detection, prediction, and public health response. The first reference in Table 1 focuses on Hantavirus vaccine design through a computational immunoinformatics framework. Its methodological value lies in showing how candidate vaccine components can be identified, assembled, and evaluated before experimental validation. This is important for the present review because it demonstrates that computational approaches can contribute to Hantavirus prevention, not only to diagnosis or surveillance. By supporting antigen identification and vaccine-candidate prioritization, this reference represents the preventive biomedical side of artificial intelligence-supported Hantavirus research.

The second reference frames Hantavirus within the broader context of pandemic potential and emerging infectious disease preparedness. Its value is not primarily methodological in the technical sense, but rather contextual. It helps justify why Hantavirus deserves attention from public health researchers, surveillance specialists, and computational scientists. Since Hantavirus can cause severe disease and is influenced by ecological exposure, it requires preparedness frameworks that can detect risk early and guide coordinated response. This reference therefore supports the public health motivation for applying artificial intelligence and deep learning to Hantavirus monitoring.

The third reference examines self-attention-based deep learning for regional influenza forecasting. Although it is not Hantavirus-specific, it is highly relevant methodologically because it demonstrates how attention mechanisms can im-

Table 1. Methodological comparison of studies related to Hantavirus, artificial intelligence, deep learning, diagnostics, therapeutic discovery, and infectious disease surveillance.

Ref.	Research focus	Methodological approach	Relevance
[21]	Hantavirus vaccine design	Multi-epitope vaccine construction with immunoinformatics validation	Supports computational vaccine design and antigen identification.
[22]	Pandemic potential	Public health comparison between Hantavirus and COVID-19	Frames Hantavirus as a potential emerging infectious disease threat.
[23]	Hantavirus pathogenesis	Experimental comparison of endothelial responses	Explains disease severity and host-cell mechanisms.
[24]	Land-use and infection	Ecological analysis of infection in small mammals	Supports reservoir monitoring and ecological-risk prediction.
[25]	Antibody characterization	Antigenic mapping of neutralizing antibodies	Relevant to antibody discovery and vaccine research.
[26]	Community perceptions	Ethnonursing and socio-cultural investigation	Highlights behavioral and local prevention factors.
[27]	Case reporting	Public health report of a detected Hantavirus case	Supports surveillance and outbreak investigation.
[28]	Antiviral activity	In vitro testing of carrageenans and fucoidans	Provides background for antiviral candidate screening.
[29]	Severe treatment	Clinical discussion of high-volume hemofiltration	Supports clinical management and intervention planning.
[30]	Serological evidence	Detection of Hantavirus antibodies in a regional population	Provides historical exposure and epidemiological context.
[31]	Pulmonary syndrome	Analysis of VEGF in edema fluid and PBMCs	Explains severe pulmonary manifestations.
[32]	Outbreak preparedness	Case-based preparedness and response discussion	Supports emergency planning and outbreak response.
[33]	Host–parasite prediction	Machine learning using ecological and evolutionary traits	Supports reservoir–pathogen and spillover-risk prediction.

prove infectious disease forecasting. Attention-based models are useful because they can identify which temporal patterns or input features contribute most strongly to prediction. For Hantavirus, this idea is important because ecological and environmental drivers may influence disease risk with time delays. A model that can learn delayed relationships between environmental change, reservoir activity, and human infection risk may be valuable for future surveillance systems.

The fourth reference investigates Hantavirus pathogenesis by experimentally comparing endothelial responses to pathogenic and nonpathogenic Hantaviruses. This study contributes biological depth to the review because it helps explain how severe disease develops at the host-cell level. Since Hantavirus disease severity is strongly associated with vascular dysfunction and endothelial involvement, this type of biological evidence is essential for interpreting clinical risk. It also provides a foundation for future artificial intelligence models that may aim to predict severity, identify therapeutic targets, or connect molecular mechanisms with patient outcomes.

The fifth reference focuses on the relationship between land use and Hantavirus infection in small mammals. This is directly relevant to ecological-risk prediction because Hantavirus circulation depends strongly on reservoir hosts and their environments. Land-use change can alter rodent abundance, species composition, habitat suitability, and contact between humans and infected reservoirs. For artificial intelligence applications, this reference supports the inclusion of ecological and environmental variables in predictive models. It also shows that Hantavirus surveillance should not rely only on human case data, because reservoir and habitat information may provide earlier warning signals.

The sixth reference discusses antibody characterization through antigenic mapping of neutralizing antibodies. Its relevance lies in connecting Hantavirus research with immune protection, antibody discovery, and vaccine development. This type of work is important because artificial intelligence and deep learning can support future antibody modeling, epitope prediction, and vaccine-candidate prioritization when high-quality immunological data are available. In the context of the review, the reference strengthens the biomedical and therapeutic side of Hantavirus AI research by showing that immune-response data can inform computational discovery.

The seventh reference explores community perceptions of Hantavirus using a socio-cultural and ethnonursing perspective. This reference is important because Hantavirus prevention depends not only on scientific monitoring, but also on how communities understand risk, rodents, exposure, disease symptoms, and prevention practices. Public health interventions may fail if they ignore local beliefs and behavioral realities. For artificial intelligence-supported public health systems, this means that social and behavioral data should be considered alongside clinical and environmental variables. The reference therefore highlights the human-centered side of Hantavirus prevention.

The eighth reference presents a public health report of a detected Hantavirus case. Its importance lies in showing how Hantavirus appears within real surveillance and reporting systems. Individual case reports may seem limited, but they often trigger outbreak investigation, public communication, environmental assessment, and preventive action. In future artificial intelligence systems, such reports could serve as surveillance signals when combined with regional exposure information, ecological data, and clinical indicators. This reference therefore supports the practical surveillance dimension of Hantavirus monitoring.

The ninth reference examines antiviral activity through in vitro testing of carrageenans and fucoidans against Hantavirus. This reference is valuable because it provides experimental therapeutic background. Artificial intelligence can support antiviral discovery by screening candidate molecules, predicting interactions, and prioritizing compounds, but experimental studies remain necessary to confirm biological activity. Therefore, this reference helps connect computational therapeutic discovery with laboratory validation. It shows that antiviral development for Hantavirus must remain grounded in experimental evidence.

The tenth reference discusses targeted high-volume hemofiltration for severe Hantavirus disease. Its relevance is clinical because it focuses on intervention planning and management of severe cases. Hantavirus can progress to life-threatening disease, so treatment-related evidence is important for understanding the clinical burden. In the future, artificial intelligence may help identify patients at higher risk of deterioration and support earlier treatment decisions. However, such predictive systems must be built on clinically meaningful outcomes and validated patient data. This reference therefore supports the clinical-management dimension of the review.

The eleventh reference provides serological evidence of Hantavirus exposure in a regional population. Serological evidence is important because it can reveal previous exposure that may not be captured by confirmed clinical case records. This helps improve understanding of hidden disease burden, population-level exposure, and regional epidemiology. For artificial intelligence-based surveillance, serological data could support more accurate estimation of risk and exposure patterns. The reference therefore contributes historical and epidemiological context to the review.

The twelfth reference investigates vascular endothelial growth factor in Hantavirus pulmonary syndrome. Its significance is biological and clinical because it helps explain severe pulmonary manifestations, including vascular leakage and edema. This is important for artificial intelligence research because biomarkers and pathophysiological indicators may eventually be used in severity-prediction models. Rather than relying only on symptoms or demographic data, future models could integrate biological markers that reflect disease mechanisms. This reference therefore supports the connection between clinical biology and predictive modeling.

The thirteenth reference addresses outbreak preparedness and response. Its relevance lies in emphasizing that surveillance is meaningful only when it leads to action. Artificial intelligence can generate predictions, but those predictions must be connected to emergency planning, public health communication, risk assessment, and intervention strategies. For Hantavirus, this is especially important because outbreaks may be geographically localized and influenced by environmental or reservoir conditions. This reference supports the need to integrate AI-based prediction into operational public health response systems.

The fourteenth reference presents a machine learning framework for predicting host–parasite interactions using ecological and evolutionary traits. Its relevance to Hantavirus is strong because spillover risk depends on reservoir–pathogen relationships and ecological compatibility. Although the study is not limited to Hantavirus, its methodological logic can be adapted to reservoir-virus prediction. Machine learning can help identify ecological and evolutionary patterns that influence host association, transmission potential, and spillover risk. This reference therefore supports one of the central arguments of the review: artificial intelligence can help connect ecological complexity with Hantavirus prediction and public health response.

Figure 3 provides a general biological overview of Hantavirus and establishes the virological and public health foundation of this review. The figure summarizes the essential structural properties of Hantavirus, including its enveloped structure, negative-sense RNA genome, glycoproteins, nucleocapsid protein, and segmented genome organization. This visual representation is important because it connects the molecular identity of the virus with its epidemiological behavior and clinical consequences. It also highlights the natural transmission cycle, where rodents act as reservoir hosts and shed the virus through saliva, urine, and feces. Human infection mainly occurs through inhalation of aerosolized contaminated particles, making environmental contamination and rodent exposure central elements in disease prevention. In addition, the figure distinguishes the two major clinical syndromes associated with Hantavirus infection, namely Hantavirus pulmonary syndrome and hemorrhagic fever with renal syndrome. By presenting viral structure, reservoir transmission, clinical disease, genome organization, important species, and prevention measures in one framework, Figure 3 supports the introductory argument that Hantavirus is a complex zoonotic disease requiring biological, ecological, clinical, and public health understanding.

3. DISCUSSION

The reviewed literature shows that the integration of artificial intelligence and deep learning into Hantavirus research remains an emerging but highly promising direction. Hantavirus is not only a clinical infection; it is also an ecological, environmental, molecular, and public health problem. This makes it suitable for data-driven investigation because multiple interacting factors shape disease emergence and transmission risk. Rodent reservoir distribution, land-use change, climate variability, viral genetics, human exposure behavior, diagnostic capacity, and public health preparedness all influence the probability of infection. Traditional epidemiological methods remain essential, but they may be limited when the relationships between these factors are nonlinear, spatially heterogeneous, or temporally delayed. AI-based methods can help address these challenges by identifying hidden patterns across complex datasets and supporting earlier detection, risk estimation, and decision-making. One of the strongest themes emerging from the reviewed studies is the importance of ecological intelligence in Hantavirus prediction. Since Hantavirus transmission depends heavily on reservoir hosts, surveillance systems that focus only on confirmed human cases may detect risk too late. Rodent population changes, habitat disturbance, land-use patterns, environmental variation, and seasonal dynamics may provide earlier indicators of possible spillover. Machine learning models are especially suitable for this task because they can integrate spatial, ecological, and environmental predictors into risk maps or forecasting systems. However, the success of such models depends on the availability of reliable reservoir data, consistent geographic sampling, and accurate environmental records. Without these inputs, AI models may produce predictions that appear statistically strong but lack ecological reliability. Another important finding is that deep learning can contribute to Hantavirus research at the molecular and biomedical levels. Sequence-based models, antibody-design pipelines, epitope prediction frameworks, and computer-aided drug-discovery systems suggest that AI may accelerate the identification of vaccine targets, antiviral candidates, and biologically meaningful viral features. These

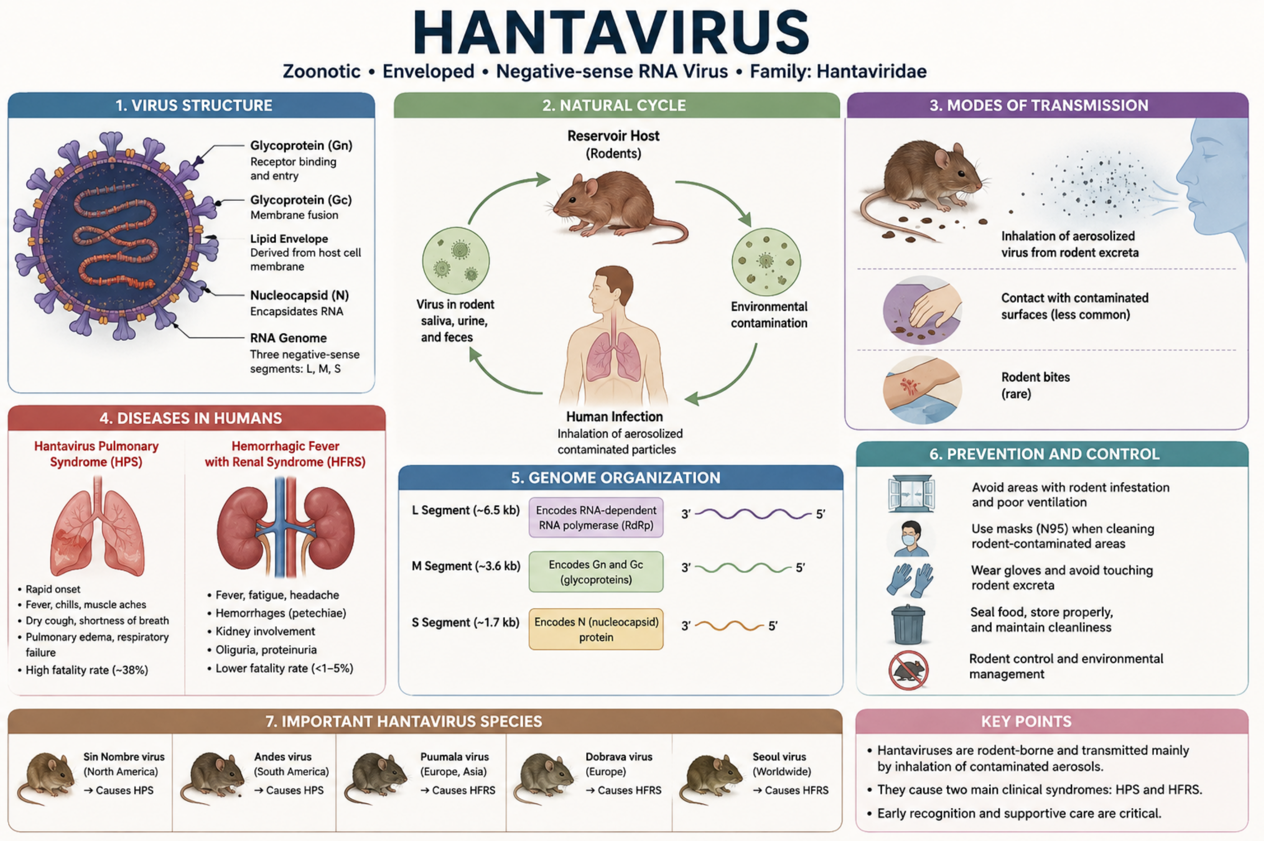

Figure 3. General biological overview of Hantavirus structure, transmission, clinical syndromes, genome organization, major species, and prevention strategies.

approaches are particularly valuable because experimental screening can be costly and time-consuming. Nevertheless, computational prediction must not be treated as biological confirmation. Any AI-generated vaccine candidate, antibody design, antiviral peptide, or molecular interaction requires laboratory validation before it can be considered clinically meaningful. Therefore, AI should be viewed as a prioritization and discovery-support tool rather than a replacement for experimental virology. The diagnostic potential of AI is also significant. Hantavirus infection may be difficult to recognize early because its symptoms can overlap with other febrile, renal, or respiratory diseases. AI-based diagnostic tools could support clinicians by integrating symptoms, laboratory markers, exposure history, geographic risk, and imaging or molecular data. Such tools may help reduce diagnostic delay, improve triage, and support testing decisions. However, clinical AI systems require carefully labeled datasets, external validation, interpretability, and integration into healthcare workflows. For rare or regionally concentrated diseases such as Hantavirus, dataset scarcity remains a major barrier. Models trained on small or geographically narrow datasets may fail when applied to different populations or viral lineages. The reviewed literature also highlights the importance of interpretability. In public health and clinical settings, model accuracy alone is insufficient. Clinicians, epidemiologists, and decision-makers must understand why a model produces a certain prediction, especially when the output may influence diagnosis, treatment, surveillance priorities, or resource allocation. Interpretable models are particularly important for Hantavirus because risk is shaped by biological, ecological, and social factors. A black-box model that predicts high risk without explaining whether the signal comes from reservoir density, climate conditions, land-use change, case history, or clinical biomarkers may be difficult to trust or act upon. Therefore, future Hantavirus AI systems should prioritize explainable artificial intelligence, transparent feature importance, uncertainty estimation, and domain-informed validation. A further issue is the need for multimodal data integration. Hantavirus research cannot rely on one data type alone. Human case data provide clinical relevance but often arrive late. Rodent surveillance data provide ecological insight but may be difficult to collect continuously. Environmental data provide broad spatial coverage but may not directly indicate infection. Genomic data provide molecular detail but may be unevenly available. Social and behavioral data provide exposure context but may be difficult to quantify. The most effective AI systems will likely combine several of these sources into unified surveillance frameworks. Such multimodal integration could improve early warning by connecting environmental suitability, reservoir infection, viral evolution, human exposure, and clinical detection.

Figure 4 illustrates the central theme of this review by showing how artificial intelligence and deep learning can be integrated into different stages of Hantavirus research and public health response. The figure begins with the natural history of Hantavirus, moving from reservoir hosts and virus shedding to environmental contamination, human exposure, and clinical disease. This sequence is important because AI-based Hantavirus research cannot depend on clinical data alone. Instead, effective prediction requires information from ecological, environmental, epidemiological, molecular, and social sources. The figure also presents the major application do-

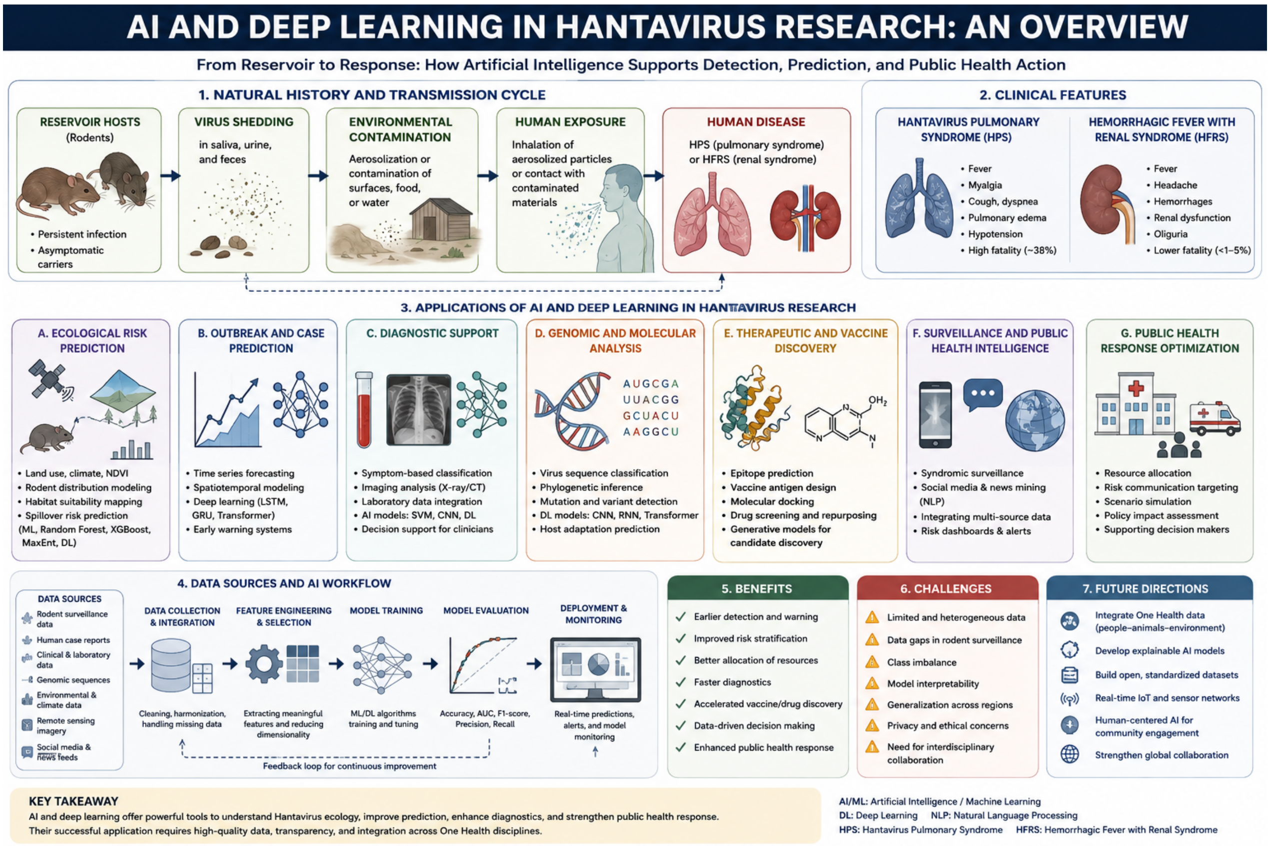

Figure 4. Overview of artificial intelligence and deep learning applications in Hantavirus research, from ecological exposure to prediction, diagnostics, molecular analysis, therapeutic discovery, surveillance, and public health response.

mains of AI in Hantavirus research, including ecological risk prediction, outbreak forecasting, diagnostic support, genomic and molecular analysis, therapeutic and vaccine discovery, surveillance intelligence, and public health response optimization. Therefore, Figure 4 supports the review's argument that AI and deep learning can strengthen Hantavirus detection, prediction, and public health response when connected to high-quality data and validated surveillance infrastructure. Despite these opportunities, several limitations must be acknowledged. First, Hantavirus-specific AI literature remains limited compared with AI research on more widely studied infectious diseases. Many methods discussed in this review are transferable from broader viral, zoonotic, diagnostic, or deep learning studies rather than fully developed for Hantavirus. Second, data quality remains a major constraint. Inconsistent surveillance, underreporting, missing ecological records, and limited sequence availability can reduce model reliability. Third, geographic bias may affect model generalization, since Hantavirus species, reservoir hosts, and clinical syndromes differ across regions. Fourth, many AI models are developed in experimental or retrospective settings without real-world deployment. Fifth, ethical and practical concerns must be considered, especially when AI predictions influence public health interventions, community risk communication, or clinical decision-making. Overall, the discussion shows that AI and deep learning can strengthen Hantavirus research when used carefully and contextually. Their strongest contributions are likely to emerge in ecological risk prediction, molecular analysis, diagnostic decision support, therapeutic discovery, and integrated surveillance. However, their practical impact will depend on interdisciplinary collaboration among virologists, epidemiologists, ecologists, clinicians, public health authorities, data scientists, and local communities. Future work should move beyond isolated models and toward validated, interpretable, field-ready systems that support real decisions in Hantavirus monitoring and response.

4. CONCLUSION

This review examined the role of artificial intelligence and deep learning in advancing Hantavirus research, with attention to detection, prediction, surveillance, diagnostics, molecular analysis, therapeutic discovery, and public health preparedness. The reviewed literature indicates that Hantavirus is a complex zoonotic disease whose risk is shaped by interactions among viral biology, reservoir-host ecology, environmental change, human exposure, and healthcare detection capacity. Because of this complexity, AI-based approaches offer meaningful opportunities to improve how Hantavirus risk is understood, modeled, and managed. The main conclusion is that artificial intelligence can support Hantavirus research across several interconnected levels. At the ecological level, machine learning can help identify environmental and reservoir-related predictors of spillover risk. At the molecular level, deep learning and computational biology can support sequence interpretation, epitope prediction, antibody design, and antiviral candidate prioritization. At the clinical level, AI may contribute to diagnostic support, severity prediction, and treatment decision-making. At the public health level, intelligent surveillance systems can help integrate heterogeneous data sources and improve early warning. These contributions show that AI should not be viewed as a single method, but as a broad computational framework that can support different stages of Hantavirus monitoring and response. However, the field remains at an early stage. Hantavirus-specific AI applications are still relatively limited, and many available methods are adapted from broader infectious disease research. Major challenges include limited datasets, geographic bias, lack of external validation, weak interpretability, fragmented data systems, and insufficient integration with real-world surveillance infrastructure. These limitations must be addressed before AI and deep learning can be reliably deployed in Hantavirus decision-making. Future research should prioritize the development of high-quality Hantavirus datasets that combine clinical, ecological, genomic, environmental, and socio-behavioral information. Greater attention should also be given to explainable AI, model validation across different geographic regions, low-resource deployment, and integration with public health workflows. In addition, computational predictions in vaccine design, therapeutic discovery, and molecular diagnostics must be supported by experimental validation. By combining robust data, transparent models, and interdisciplinary collaboration, artificial intelligence and deep learning can become valuable tools for strengthening Hantavirus surveillance, preparedness, and disease control.

REFERENCES

[1] Abbas Khan, Mazhar Khan, Saeed Ullah, and Dong-Qing Wei. Hantavirus: The Next Pandemic We Are Waiting For? *Interdiscip Sci Comput Life Sci*, 13(1):147–152, March 2021.

[2] Jan Clement, Piet Maes, and Marc Van Ranst. Hemorrhagic fever with renal syndrome in the new, and hantavirus pulmonary syndrome in the old world: paradi (se) gm lost or regained? *Virus Research*, 187:55–58, 2014.

[3] Gabriel E. García-Peña and André V. Rubio. Unveiling the impacts of land use on the phylogeography of zoonotic New World Hantaviruses. *Ecography*, 2024(10):e06996, October 2024.

[4] Francisca Astorga, Abdelghafar Alkishe, Paanwaris Paansri, Gabriel Mantilla, and Luis E. Escobar. Hantavirus in rodents in the United States: Temporal and spatial trends and report of new hosts. *Ecosphere*, 16(3):e70209, March 2025.

[5] Daniel Zeng, Zhidong Cao, and Daniel B. Neill. Artificial intelligence–enabled public health surveillance—from local detection to global epidemic monitoring and control. In *Artificial intelligence in medicine*, pages 437–453. Elsevier, 2021.

[6] Yash Srivastav Srivastav, Stuti Verma Verma, Vaishali Bhagwani Bhagwani, Ankuj Pandey Pandey, Vasu Tiwari Tiwari, Neha Rawat Rawat, and Anup Kumar Sirbaiya Sirbaiya. Hantavirus Reservoirs in Human-to-Human Transmission: Deep Learning Frameworks for the Identification of Molecular Inhibitors Targeting and Virus Interhuman Pathogenesis. *Journal of Pharmacology, Genetics and Molecular Biology*, pages 44–56, 2026.

[7] Nicolás Lefin, Lisandra Herrera-Belén, Jorge G. Farias, and Jorge F. Beltrán. Review and perspective on bioinformatics tools using machine learning and deep learning for predicting antiviral peptides. *Mol Divers*, 28(4):2365–2374, August 2024.

[8] Ravikiran Keshavamurthy, Samuel Dixon, Karl T. Pazdernik, and Lauren E. Charles. Predicting infectious disease for biopreparedness and response: A systematic review of machine learning and deep learning approaches. *One Health*, 15:100439, 2022.

[9] Adekunle Adeoye, Chibuzo Okechukwu Onah, Enibokun Theresa Orobator, Elizabeth Anuoluwa Akintayo, Jacob Ukpabio Inuaeyen, Daniel Ojonugwa Umoru, Isaiah Olumeko, Gladys Jacob Dick, Kelechi Wisdom Elechi, and Ubalaeze Solomon Elechi. AI and machine learning for early detection of infectious diseases in the US: Opportunities and challenges. *Journal of Medical Science, Biology, and Chemistry*, 2(1):54–63, 2025.

[10] Rc Theijeswini, Soumya Basu, Rayapadi G. Swetha, Jayaraman Tharmalingam, Sudha Ramaiah, R Calaivanane, V. Raja Sreedharan, Paul Livingstone, and Anand Anbarasu. Prophylactic and therapeutic measures for emerging and re-emerging viruses: artificial intelligence and machine learning - the key to a promising future. *Health Technol.*, 14(2):251–261, March 2024.

[11] Shannon LM Whitmer, Amy Whitesell, Melissa Mobley, Emir Talundzic, Elizabeth Shedroff, Caitlin M. Cossaboom, Sharon Messenger, Mojgan Deldari, Julu Bhatnagar, and Lindsey Estetter. Human Orthohantavirus disease prevalence and genotype distribution in the US, 2008–2020: a retrospective observational study. *The Lancet Regional Health–Americas*, 37, 2024.

[12] Asep K. Supriatna, Herlina Napitupulu, Meksianis Z. Ndii, Bapan Ghosh, and Ryusuke Kon. A Mathematical Model for Transmission of Hantavirus among Rodents and Its Effect on the Number of Infected Humans. *Computational and Mathematical Methods in Medicine*, 2023(1):9578283, January 2023.

[13] Carlos Polanco, Alberto Huberman, Vladimir N. Uversky, Martha Rios Castro, Enrique Hernandez-Lemus, Thomas Buhse, Gilberto Vargas Alarcon, Gabriela Calvo-Leroux Corona, Erika Jeannette Lopez Oliva, Claudia Pimentel-Hernandez, Mireya Martinez-Garcia, Brayans Becerra-Luna, Juan Luciano Diaz Gonzalez, Raul Martinez-Memije, Francisco J. Roldan Gomez, Pedro L Flores Ch, and Carlos Rafael Sierra Fernandez. A Bioinformatics Analysis of the Envelope Glycoproteins Expressing the Hantavirus Cardiopulmonary Syndrome and Hemorrhagic Fever with Renal Syndrome. *CAC*, 21(8):936–959, October 2025.

[14] Aaron T. Irving, Tony Schountz, Nolwenn Jouvenet, Ansalna Ansari, Michelle Baker, and Arinjay Banerjee. Lessons learned from bat and rodent reservoir hosts of zoonotic viruses. *Trends in Microbiology*, 2026.

[15] Bala Bhaskar Kumbhagiri. Gen-YSD: An Experiment-Aware Generative AI Pipeline for Closing the Sim-to-Real Gap in Pan-Hantavirus Antibody Design. *Available at SSRN 6752081*, 2026.

[16] Narges Lotfalizadeh, Cinzia Santucciu, Valentina Chisu, Helia Sepahvand, Abbas Rahdar, Razieh Behzadmehr, Octavio Luiz Franco, Guettari Moez, and Luiz Fernando Romanholo Ferreira. Advances in Microbial Diagnostics: Machine Learning and Nanotechnology for Zoonotic Disease Control. *WIREs Nanomed Nanobiotechnol*, 18(1):e70050, January 2026.

[17] Justus Brockmann, Michael Kleines, Narmin Ghaffari Laleh, Jakob Nikolas Kather, Stephanie Wied, Jürgen Floege, and Gerald S. Braun. A simple clinical score to reduce unnecessary testing for Puumala hantavirus. *Plos one*, 19(5):e0304500, 2024.

[18] Kommalapati Prasanthi and J. Rakesh Babu. Deep Learning-Driven Disease Prediction Combining Linguistic with Climatic Attributes. In *2026 Second International Conference on Multi-Agent Systems for Collaborative Intelligence (ICMSCI)*, pages 780–785. IEEE, 2026.

[19] M. Saqib Nawaz, Philippe Fournier-Viger, Shoaib Nawaz, Youxi Wu, and Wei Song. HieRMVir: Interpretable Viral Classification via Hierarchical Deep Learning. *IEEE Journal of Biomedical and Health Informatics*, 2025.

[20] Francisca Villanueva-Flores, Javier I. Sanchez-Villamil, and Igor Garcia-Atutxa. AI-driven epitope prediction: a systematic review, comparative analysis, and practical guide for vaccine development. *npj Vaccines*, 10(1):207, 2025.

[21] Taghreed N. Almanaa, Ayman Mubarak, Muhammad Sajjad, Asad Ullah, Muhammad Hassan, Yasir Waheed, Muhammad Irfan, Saifullah Khan, and Sajjad Ahmad. Design and validation of a novel multi-epitopes vaccine against hantavirus. *Journal of Biomolecular Structure and Dynamics*, 42(8):4185–4195, May 2024.

[22] AI Contact Center. Hantavirus: Ein Vergleich mit COVID-19 und das Pandemiepotenzial.

[23] Erika Geimonen, Sherry Neff, Tracy Raymond, Salih S. Kocer, Irina N. Gavrilovskaya, and Erich R. Mackow. Pathogenic and nonpathogenic hantaviruses differentially regulate endothelial cell responses. *Proc. Natl. Acad. Sci. U.S.A.*, 99(21):13837–13842, October 2002.

[24] Jérémy Dubrulle, Kayla Kauffman, Voahangy Soarimalala, Toky Randriamoria, Steven M. Goodman, James Herrera, Charles Nunn, and Pablo Tortosa. Effect of Land-Use on Hantavirus Infection Among Introduced and Endemic Small Mammals of Madagascar. *Ecology and Evolution*, 15(4):e70914, April 2025.

[25] Taylor B. Engdahl, Elad Binshtein, Rebecca L. Brocato, Natalia A. Kuzmina, Lucia M. Principe, Steven A. Kwilas, Robert K. Kim, Nathaniel S. Chapman, Monique S. Porter, and Pablo Guardado-Calvo. Antigenic mapping and functional characterization of human New World hantavirus neutralizing antibodies. *Elife*, 12:e81743, 2023.

[26] Janeth Agrazal Garcia, Lydia Gordón de Isaacs, Elsa Lucia Escalante-Barrios, and Sergi Fàbregues. Beliefs and socio-cultural perspectives on hantavirus in a rural community in Panama: An ethnonursing study. *PLOS Global Public Health*, 5(10):e0005320, 2025.

[27] B. T. P. Principal. Erster Hantavirus-Fall in Illinois: Gesundheitsbehörden untersuchen.

[28] Stanislav N. Pavliga, Galina G. Kompanets, and Vasiliy Yu. Tsygankov. The Experimental Research (In Vitro) of Carrageenans and Fucoidans to Decrease Activity of Hantavirus. *Food Environ Virol*, 8(2):120–124, June 2016.

[29] René López, Rodrigo Pérez-Araos, Álvaro Salazar, Mauricio Espinoza, Cecilia Vial, Analia Cuiza, Pablo A. Vial, and Jerónimo Graf. Targeted high volume hemofiltration could avoid extracorporeal membrane oxygenation in some patients with severe Hantavirus cardiopulmonary syndrome. *Journal of Medical Virology*, 93(8):4738–4747, August 2021.

[30] Walter G. Wasser, Cindy A. Rossi, and Gregory E. Glass. Hantavirus Antibodies in New York. *Ann Intern Med*, 127(2):166–167, July 1997.

[31] Irina Gavrilovskaya, Elena Gorbunova, Frederick Koster, and Erich Mackow. Elevated VEGF Levels in Pulmonary Edema Fluid and PBMCs from Patients with Acute Hantavirus Pulmonary Syndrome. *Advances in Virology*, 2012:1–8, 2012.

[32] Attila J. Hertelendy, Lawrence O. Gostin, and Gregory R. Ciottone. The MV Hondius Hantavirus Outbreak—Lessons for Pandemic Preparedness. *JAMA*.

[33] Angel Luis Robles Fernandez. *Ecointeraction: A Machine Learning Framework to Predict Host-Parasite Interactions Through Ecological and Evolutionary Covariates*. PhD Thesis, Arizona State University, 2025.