

Fish Databases and Evolution of Fomed for Disease Transmission Prevention and Management Modeling

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Abstract

The emergence of fish diseases poses a significant threat to aquaculture sustainability and public health. Fish diseases, transmissible between animals and humans, pose major public health and economic challenges worldwide. Efficient surveillance, timely detection, and rapid response are critical to preventing outbreaks. Databases play a pivotal role by storing, integrating, and analyzing diverse biological, epidemiological, and environmental data. This review examines the utility of genomic repositories, pathogen surveillance databases, ecological and vector data platforms, and integrative One Health systems. In recent years, fish-specific molecular and epidemiological databases have become vital tools in understanding disease mechanisms, transmission pathways, and prevention strategies. These databases integrate genomic, transcriptomic, proteomic, and ecological data to facilitate early detection, molecular epidemiology, and predictive modeling.

This paper reviews the development, structure, and applications of fish databases, emphasizing their role in disease surveillance, host–pathogen interaction analysis, and policy development within the One Health framework. Newly designed Fish Organ-Specific Molecular Electronic Database (FOMED) by the author, exemplifies this evolution, integrating organ-specific molecular, physiological, and pathological data.

We discuss how these databases support risk assessment, outbreak modeling, molecular epidemiology, and preventive strategies, while highlighting challenges such as data fragmentation and lack of interoperability.

Future directions include development of intelligent, interoperable databases, machine learning integration, and enhanced global collaboration to improve disease management.

Keywords: Databases; Surveillance; Genomics; Disease Prevention; Modeling; Data Integration

Introduction

Fish diseases contribute to significant global economic losses in aquaculture and can also have zoonotic implications (FAO, 2024). With the intensification of aquaculture and the growing human–fish interface, early disease surveillance and control have become critical. The advent of bioinformatics and high-throughput sequencing technologies has led to the creation of specialized fish databases containing genetic, taxonomic, and environmental information (Becker, et al., 2021). These resources support both molecular-level investigations and macro-ecological disease assessments.

Fish databases function as knowledge repositories that facilitate the integration of host, pathogen, and environmental data. They play a pivotal role in correlating molecular signatures with disease phenotypes, thereby strengthening the ability to forecast outbreaks and inform management strategies (Singh, et al., 2023).

Fish databases have evolved as indispensable digital infrastructures for managing, integrating, and analyzing aquatic biological, environmental, and epidemiological data. These databases support sustainable fisheries, aquaculture health, and facilitate genomic, ecological, and disease surveillance information.

Zoonotic diseases account for more than 60% of all human infectious diseases and around 75% of emerging pathogens (Jones et al., 2008; WHO, 2020). Their emergence is often influenced by ecological disruption, agricultural intensification, wildlife trade, and climate change (Allen et al., 2017). Early detection, accurate tracking, and rapid response are crucial for preventing large-scale outbreaks.

The growth of genomic sequencing, molecular surveillance, and environmental monitoring has generated vast quantities of data relevant to zoonotic diseases. These include pathogen genomes, host and vector distributions, environmental variables, clinical case reports, and experimental data. Databases provide structured platforms for storing, curating, and analyzing these diverse data streams. Properly designed, they support transmission modeling, risk mapping, and targeted interventions (Gardy & Loman, 2018; Grubaugh et al., 2019).

Conventional databases such as Fish Base (Froese & Pauly, 2019), ZFIN (Howe et al., 2013), and Ensembl Fish have been extensively used for cataloging taxonomic and genomic information. However, they lack organ-specific molecular and Genomic applications which limits their application in understanding disease mechanisms at the tissue level.

To address this gap, the Fish Organ-Specific Molecular Electronic Database (FOMED) was developed to integrate organ-level gene expression, disease phenotypes, and environmental metadata within a single framework. FOMED provides a model for how fish health databases can evolve toward precision aquaculture and integrative fish disease analytics.

This review synthesizes current knowledge on the utility of databases in disease transmission and prevention, focusing on surveillance, molecular epidemiology, and predictive modeling. The Fish Organ-specific Molecular Electronic Database (FOMED) extends this paradigm by offering a dedicated platform that links organ-level molecular signatures with disease-associated genes and environmental factors. This multidimensional approach enables targeted disease modeling and surveillance for both aquatic and zoonotic pathogens.

Categories of Fish Databases

The emergence of digital data systems has revolutionized aquatic health research, enabling large-scale integration of genetic, environmental, and epidemiological information. Fish databases now play a crucial role in understanding disease dynamics, biodiversity conservation, and aquaculture management. Databases play an essential role in disease prediction, vaccine development, epidemiological modeling, **and** environmental risk assessment To facilitate multidisciplinary research, fish databases can be broadly classified into four categories (Fig.1): Genomic and Molecular Databases, Epidemiological Surveillance Databases, Ecological and Vector Databases, and Integrative One Health Databases and Platforms. Each category contributes uniquely to the understanding of aquatic health and disease dynamics. The figure provides the visual overview of how different types of fish databases interconnect within the aquatic health research ecosystem.

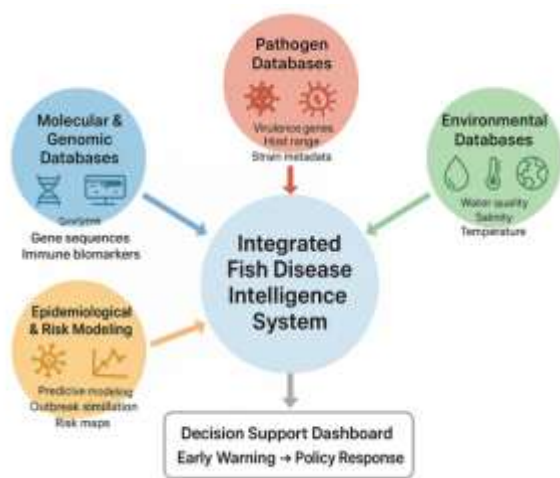


Figure 1. Conceptual Framework of Fish Database Categories

Each category serves a distinct purpose within the framework of aquatic disease monitoring, molecular epidemiology, and sustainable aquaculture practices. Fish constitute a vital component of global food security, biodiversity, and livelihoods. However, increasing disease outbreaks, environmental changes, and anthropogenic stressors have

amplified the need for systematic data-driven approaches to manage aquatic health (FAO, 2023). The rapid advancement in bioinformatics and molecular biology has led to the development of diverse databases dedicated to fish genomics, pathogen surveillance, and ecological monitoring.

Fish databases represent the cornerstone of modern aquatic research, enabling multi-disciplinary integration of molecular, epidemiological, and environmental data (Prasad et al., 2021; Luo et al., 2020). The growing challenges in fish disease surveillance, zoonotic transmission, and aquaculture sustainability have necessitated database systems capable of linking genomic information with real-world aquatic health outcomes. Various specialized databases, such as FishBase, AquaFish, and ZFIN, have emerged to catalog taxonomic, physiological, and genomic data, while integrative platforms now link molecular and ecological datasets for disease forecasting (Froese & Pauly, 2019; Howe et al., 2013).

Genomic and Molecular Databases

Genomic and molecular databases provide fundamental resources for understanding the genetic architecture and molecular mechanisms underlying fish biology and disease resistance. These repositories store nucleotide sequences, annotated genomes, proteomes, and transcriptomic datasets. They serve as essential tools for comparative genomics, functional annotation, and pathogen-host interaction studies (Yuan et al., 2022).

Platforms such as NCBI FishBase Genomes and Ensembl Fish Genomes provide comprehensive assemblies and annotations for numerous fish species. Specialized databases like FishTEDB (Fish Transposable Elements Database) catalog repetitive genetic elements across over 500 fish genomes (Chalopin et al., 2015). Similarly, AquaPathogen DB and FISH-DiseaseBase integrate molecular and pathogen-specific data for aquaculture health research.

These databases are crucial for identifying genes associated with immunity, stress tolerance, and disease resistance. They underpin the development of molecular diagnostics, marker-assisted breeding, and genomic selection, advancing precision aquaculture and aquatic molecular epidemiology. iFish, includes genetic variants along with detailed annotations such as genomic coordinates, minor allele frequencies, and functional consequences, at the genomic level, which will accelerate both genetic and evolutionary investigations (Ruoyan et al., 2025)

Genomic databases are repositories of DNA, RNA, and protein sequences, often linked with gene annotations, transcriptome data, and proteomic information. Examples include FishBase, NCBI GenBank, Ensembl Fish, and ZFIN (Zebrafish Model Organism Database), which provide access to genome assemblies and molecular markers for model and non-model fish species (Howe et al., 2013). Fig. 2. Illustrates how molecular data (e.g., gene sequences, proteomic profiles) are collected, annotated, and used for downstream applications like disease gene discovery, vaccine design, and phylogenetic analysis in molecular epidemiology and aquaculture genetics.

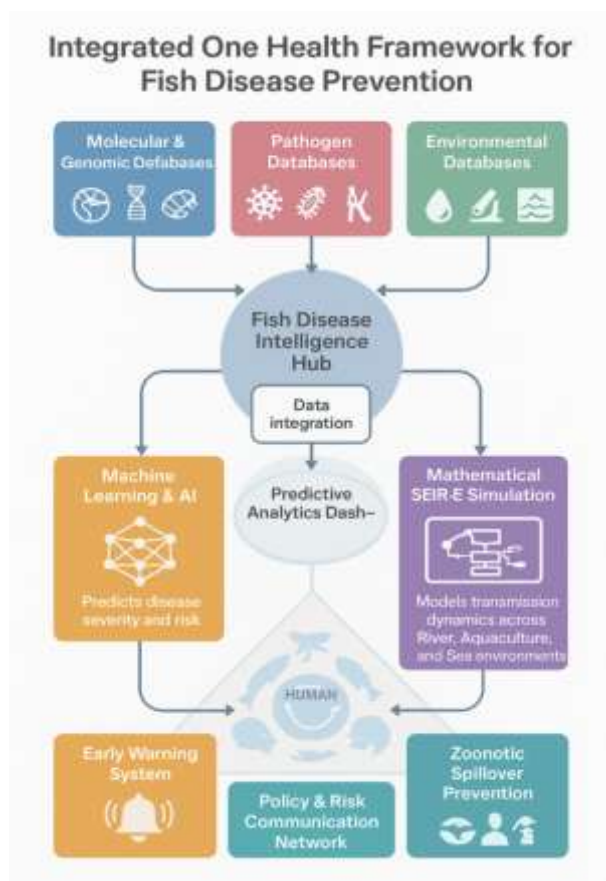


Figure 2. Workflow of Genomic and Molecular Fish Databases

Core Components:

- Sequence Repositories: Genomic, transcriptomic, and proteomic datasets.
- Annotation Layers: Functional gene information, orthologs, and variant data.
- Bioinformatics Tools: BLAST search engines, pathway mapping, and gene ontology visualization.

These molecular resources are vital for identifying disease-associated genes, studying host-pathogen interactions, and supporting selective breeding for disease resistance (Chen et al., 2022).

Epidemiological Surveillance Databases

Epidemiological surveillance databases are instrumental in tracking and analyzing fish disease outbreaks. They support the collection of real-time data on disease prevalence, spatial distribution, and transmission dynamics, thereby facilitating biosecurity planning and early warning systems (OIE, 2023).

The World Animal Health Information System (WAHIS), managed by the World Organization for Animal Health (WOAH/OIE), compiles global reports of noticeable aquatic diseases. Similarly, the Asia Regional Aquatic Animal Health Information System (NACA-AIS) functions as a regional hub for disease surveillance and capacity building (Bondad-Reantaso et al., 2019). The EU Fish Pathogens Database also provides data on regulated fish pathogens across European aquaculture systems.

By enabling risk analysis and outbreak mapping, epidemiological databases strengthen international cooperation in disease surveillance, trade regulation, and pathogen containment, aligning with global aquatic health policies and the Sustainable Development Goals (SDG 3 and SDG 14). Fig.3. Illustrates the structure of aquatic disease monitoring and early warning systems. The diagram shows how disease outbreak data move from field sampling and laboratory testing to national and global reporting systems.

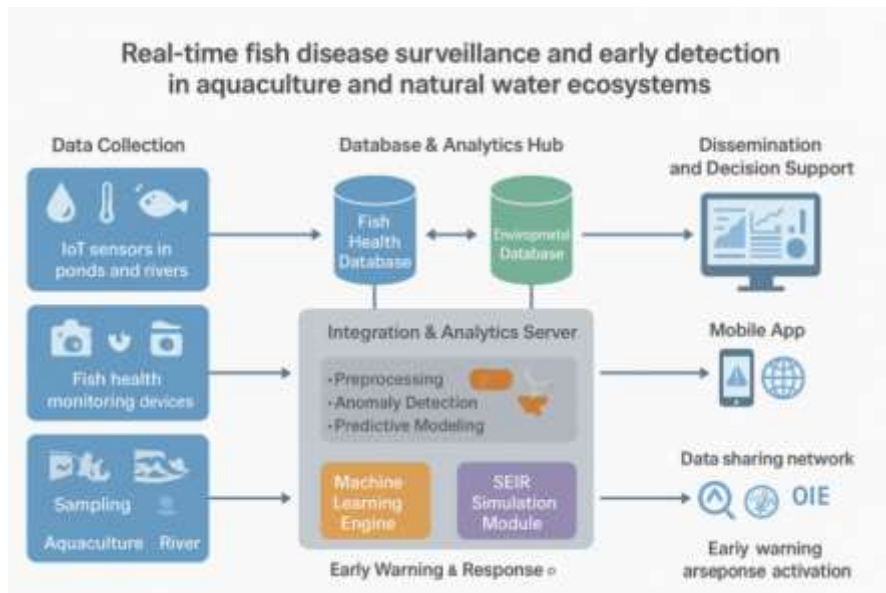


Figure 3. Data Flow in Fish Disease Epidemiological Surveillance Systems

Epidemiological databases track disease incidence, prevalence, and outbreak data across aquaculture and wild fish populations. Systems such as FAO's Global Aquaculture Production Database and World Organisation for Animal Health (WOAH) Aquatic Animal Health Database collect standardized reports on noticeable aquatic diseases (WOAH, 2023).

Core Components:

- Pathogen Metadata: Information on bacterial, viral, fungal, and parasitic agents.
 - Spatio-Temporal Surveillance Layers: Geographical mapping of outbreaks and disease vectors.
 - Host and Population Data: Details of species affected, environmental factors, and case outcomes.
- These systems enable early-warning surveillance, supporting policies on transboundary aquatic diseases and biosecurity (Subasinghe et al., 2021).

Ecological and Vector Databases

Fish health is deeply influenced by environmental conditions and vector-borne disease transmission. Ecological and vector databases provide integrated datasets on habitat parameters, vector species, and climatic factors affecting aquatic ecosystems. These repositories link ecological data with pathogen prevalence, supporting the study of disease-environment interactions (Rogers et al., 2020).

Databases such as AquaMaps predict species distribution under varying environmental scenarios, while the Global Biodiversity Information Facility (GBIF) provides geospatial data on fish and associated vectors. Organizations like NOAA and FAO Fisheries maintain repositories of oceanographic and limnological data relevant to aquaculture sustainability.

These systems help detect environmental triggers of disease emergence, such as changes in temperature, salinity, or pollution levels. By correlating disease outbreaks with ecological changes, these databases contribute to ecosystem-based disease management and climate-resilient aquaculture strategies. Figure 4. Conceptual ecological model illustrating how environmental stressors (temperature, pH, salinity, dissolved oxygen) and biological vectors (copepods, snails) interact to influence pathogen transmission and disease susceptibility in fish within an aquatic ecosystem.

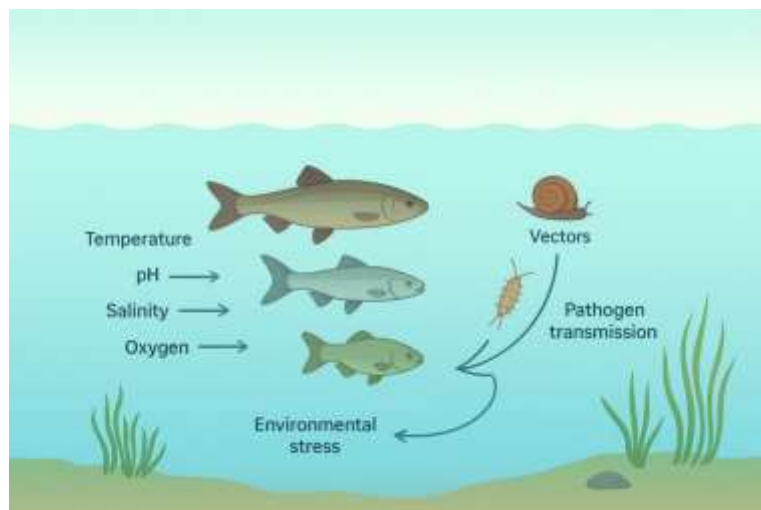


Figure 4. Environmental and Vector Interaction Model in Fish Disease Ecology

Ecological databases integrate environmental parameters—such as water temperature, salinity, and dissolved oxygen—with habitat and population data. Vector databases, in turn, focus on species that transmit pathogens between aquatic hosts (Soto et al., 2020). Examples include AquaMaps, OBIS (Ocean Biodiversity Information System), and FishTraits databases.

Core Components:

- Environmental Layers: Oceanographic and limnological datasets from in-situ or satellite monitoring.
- Species Distribution Models: Predictive habitat models for understanding species ecology.
- Vector-Pathogen Interfaces: Metadata linking vector species to pathogen transmission routes. Such data are integral to ecological risk assessments and to understanding the environmental determinants of fish diseases (Kebede et al., 2022).

Integrative One Health Databases and Platforms

Integrative One Health databases represent the most advanced form of aquatic health data systems. They combine molecular, epidemiological, and environmental data to address zoonotic and ecosystem health challenges through a unified framework (Destoumieux-Garzón et al., 2018).

The FAO-OIE-WHO Tripartite Zoonotic Guide Platform coordinates data exchange across animal, human, and environmental sectors. Similarly, initiatives like the AquaOneHealth Network and EcoHealth Alliance Datasets integrate cross-sectoral data for zoonotic pathogen tracking and risk modeling.

These integrative systems support the prediction and control of zoonotic infections such as *Mycobacterium marinum* and *Streptococcus iniae*, which pose risks to both fish and humans. By merging multi-source datasets, One Health databases promote holistic disease surveillance, policy integration, and sustainable aquatic ecosystem management in accordance with SDGs 2, 3, 6, 14, and 15.

Integrative platforms merge molecular, ecological, and epidemiological data under integrated paradigm, recognizing the interconnection among fish, human, and environmental health. Examples include the Aquatic Pathogen Information System (APIS) and FishPathogenDB, which aggregate host-pathogen-environment data for predictive modeling and policy development (Shen et al., 2023). Table 1. Categorizes primary uses, Key data types and focus of the major fish databases.

Core Components:

- Data Integration Modules: Link genomic, environmental, and epidemiological inputs.
 - Predictive Modeling Engines: Machine learning and AI-based modules for disease forecasting.
 - Visualization Dashboards: Interactive geospatial and network analytics for decision support.
- Such integrative frameworks enable real-time monitoring and improve preparedness for zoonotic spillovers and aquaculture disease management (Buller et al., 2021).

Table 1. Category and primary uses of databases

Category	Focus	Key Data Types	Primary Use	Examples
Genomic Molecular	& DNA, RNA, proteins	Gene sequences, markers	Molecular diagnostics, genomics	NCBI, Ensembl, FishTEDB
Epidemiological	Disease monitoring	Outbreak reports, host-pathogen records	Surveillance, biosecurity	OIE-WAHIS, NACA-AIS
Ecological Vector	& Environmental data	Habitat, water quality, vector species	Ecosystem management	AquaMaps, GBIF
Integrative Health	One Multi-sectorial	Genomic + Epidemiological + Environmental	Zoonotic risk modeling	FAO-OIE-WHO Platform, Aqua One Health

The growing complexity of aquatic ecosystems and disease transmission pathways necessitates comprehensive and interoperable data platforms. Fish databases—ranging from molecular-level genomic repositories to ecosystem-wide One Health networks—form the backbone of modern aquaculture research and management.

Future advancements should focus on interoperability, AI-driven analytics, and cloud-based data integration to enhance predictive modeling and cross-disciplinary collaboration. Strengthening these databases will be vital for achieving sustainable aquaculture, biodiversity conservation, and global health security.

Fish databases are evolving from single-domain molecular repositories to integrated, cross-disciplinary platforms that support predictive aquatic health intelligence. Their modular components—ranging from genomic annotations to environmental surveillance—facilitate comprehensive risk assessment and management within the One Health context. Continued global collaboration and data standardization will enhance the utility of these systems in mitigating aquatic disease threats and sustaining biodiversity.

Utility of Fish Databases in Disease Transmission Studies

Fish databases have become indispensable tools in understanding the transmission dynamics of aquatic and zoonotic pathogens. The integration of molecular, ecological, and epidemiological data within such databases enables scientists to explore host–pathogen relationships, track emerging infections, and assess their potential risks to human and environmental health. These databases function as data integration platforms, combining gene expression, microbial, and environmental parameters for enhanced surveillance and modeling of disease transmission routes.

Molecular and Genomic Databases

Molecular-level databases such as NCBI GenBank, Ensembl Fish, and FishBase play a central role in linking genomic variability to disease susceptibility in fish populations. These resources allow researchers to retrieve annotated sequences of immune-related genes (e.g., *MHC*, *TLR*, *IL*, *IFN*) to study host–pathogen co-evolution and adaptive immune responses under pathogen pressure (Becker, 2021; Froese and Pauly, 2024). For instance, comparative genomic analyses of *Cyprinus carpio* (Common Carp) and *Danio rerio* (Zebrafish) have revealed genetic markers associated with viral hemorrhagic septicemia and Koi herpesvirus (KHV), providing key insights into molecular mechanisms underlying disease transmission (Yates et al., 2023; O’Leary et al., 2016).

These databases enable phylogenetic analyses, detection of mutation patterns, and tracing of transmission chains (Gardy and Loman, 2018).

Pathogen and Epidemiological Databases

Pathogen-specific repositories like FishPathogens.eu, ViPR (Virus Pathogen Resource), and AquaPathogen Database (APD) serve as centralized hubs for storing pathogen genomes, virulence factors, and strain-specific metadata. Such data support phylogenetic tracking of aquatic pathogens, allowing for the identification of potential zoonotic spillovers through shared reservoirs or genetic similarities (Kasprzyk, 2020; Peeler and Thrush, 2019). Epidemiological databases

further integrate spatial and temporal patterns of disease occurrence, offering evidence-based decision support for containment and surveillance strategies [Chen et al., 2022].

Environmental and Ecological Databases

Environmental drivers—such as temperature, salinity, dissolved oxygen, and nutrient availability—strongly influence the prevalence and virulence of aquatic pathogens (Pickett et al. 2012). Databases like AquaMaps, OBIS (Ocean Biodiversity Information System), and FAO Fish Disease Database provide critical environmental layers that can be integrated with host and pathogen information to model outbreak probabilities across regions (Leung and Bates, 2013; Ready et al., 2010). By linking these datasets, researchers can identify climatic thresholds and ecological “hotspots” where zoonotic transmission risks may increase due to environmental stress or anthropogenic influence.

Integrated Databases and Predictive Modeling

The Integrated approach emphasizes interconnectedness among human, animal, and environmental health. Integrated data platforms such as GBADs (Global Burden of Animal Diseases), EcoHealthNet, and AquaONE embody this principle by linking multi-omics fish data with epidemiological and socio-economic variables (OBIS, 2023; FAO, 2024). Such integration facilitates the use of predictive modeling frameworks, including machine learning (Random Forest, ANN) and mathematical SEIR models, to forecast disease dynamics under varying environmental and biological conditions (Grace et al., 2021). These models, powered by well-curated fish databases, aid in designing early-warning systems for zoonotic and aquaculture-associated outbreaks.

Implications for Zoonotic Transmission and Global Surveillance

Given that fish serve as intermediate or reservoir hosts for several zoonotic pathogens (e.g., *Mycobacterium marinum*, *Streptococcus iniae*, *Vibrio vulnificus*), data-driven approaches using fish databases are vital in cross-species transmission studies (Rushton et al., 2021). Integrative database analytics enable real-time linkage between genetic diversity, environmental perturbations, and epidemiological outcomes, forming the backbone of digital disease surveillance systems [17]. In doing so, fish databases not only strengthen aquatic health monitoring but also serve as strategic instruments in global zoonotic disease prevention.

Role of Fish Databases in Molecular Epidemiology and Predictive Modeling

In contrast to descriptive epidemiology, which uses molecular biology to describe the distribution of disease in a population, molecular epidemiology still mainly depends on the integration of standard (or analytical) epidemiological techniques to determine the etiological factors influencing these relationships (Michael Snow, 2011). Fish databases have emerged as essential tools in molecular epidemiology since they enable researchers to examine the genetic basis of disease susceptibility, pathogen evolution, and transmission dynamics in aquatic species. These platforms make it easier to identify important molecular determinants of infection and analyse outbreak patterns by combining environmental, pathogen, and host genomics datasets. (Becker, L. et al., 2021; Austin and Austin, 2016). We thoroughly obtained genome assembly datasets from the National Centre for Biotechnology Information (NCBI) (Sayers et al., 2025) and Ensembl (Dyer et al., 2025) to cover an extensive range of fish species.

Molecular Epidemiology Applications

Molecular epidemiology relies on genomic and transcriptomic information to track the spread of infectious agents within and between fish populations. Databases such as NCBI GenBank, Ensembl Fish, and pathogen-specific repositories like ViPR or FishPathogens.eu provide annotated sequences of both hosts and pathogens, enabling comparative analyses of virulence genes, immune response markers, and zoonotic determinants (Benson, 2018; Yates, 2023).

For instance, studies on Koi herpesvirus (KHV) and *Streptococcus iniae* utilize fish genome and pathogen sequence databases to trace infection routes, identify high-risk strains, and determine host susceptibility markers (Raida and Buchmann, 2008; Palaioikostas and Houston, 2017). The ability to correlate genomic variation with disease incidence enhances the understanding of transmission networks, facilitating targeted surveillance and risk-based management strategies in aquaculture and natural water bodies (Peeler and Thrush, 2019).

Predictive Modeling Applications

In addition to descriptive epidemiology, predictive modelling frameworks that assess the likelihood of outbreaks, the severity of diseases, and possible zoonotic spillover are supported by fish databases. Databases support mathematical simulation models (e.g., SEIR-E models; Peterson et al., 2015) and machine learning models (e.g., Random Forest, Artificial Neural Networks) by combining multi-dimensional datasets, such as genomic, pathogen, environmental, and ecological information. For instance, predictive models can replicate the dynamics of disease transmission across rivers, aquaculture farms, and marine ecosystems by fusing host immune gene expression data with environmental factors like water temperature, salinity, and dissolved oxygen. These models guide preventive interventions, inform policy decisions, and produce early warning signals for emerging diseases (Harvell et al., 2002; Kaschner et al., 2019).

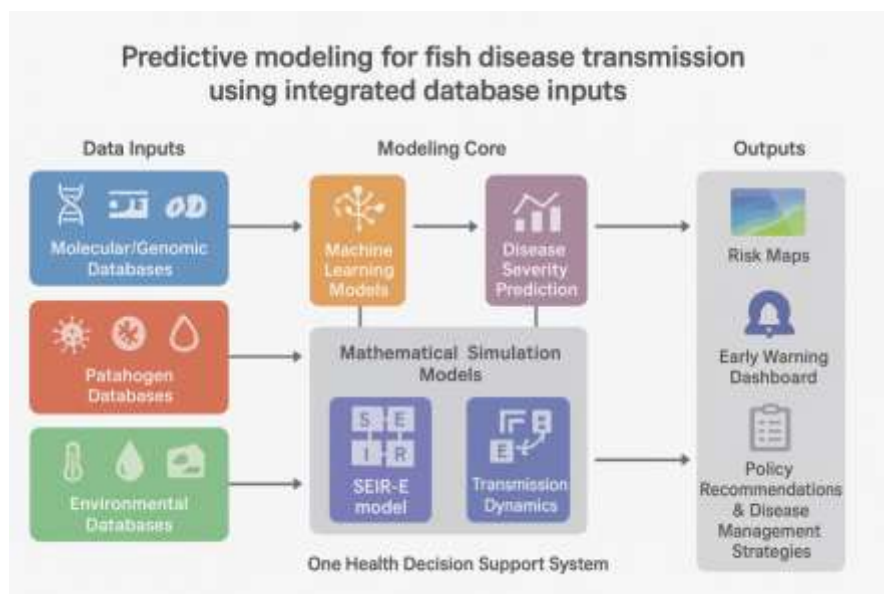


Figure 5. Integrative Database Architecture for Aquatic Systems

Fig.5.represents the multidisciplinary approach linking aquatic animal health, human health, and environmental sustainability.The layered architecture diagram shows data integration across molecular, epidemiological, ecological, and human health domains shows data exchange among FAO, OIE, WHO, Aqua One Health, and Eco Health Alliance systems, with a central “One Health Data Hub.”

Integrative Role in One Health Surveillance

By linking aquatic health data to indicators of human and environmental health, fish databases also make it easier to integrate molecular epidemiology and predictive modelling within a One Health framework. This integration facilitates data-driven policymaking, allows for thorough risk assessment for zoonotic pathogens, and supports early detection and real-time surveillance systems for newly emerging aquatic diseases (Grace et al., 2021; Morse et al., 2012).

Fish databases are essential tools in contemporary aquatic health management because they enable researchers and public health authorities to predict outbreaks, create focused interventions, and lower the risks of zoonotic transmission by fusing molecular insights, ecological factors, and predictive analytics.

Utility of Databases in Disease Transmission, Policy Making, and Management Strategies

Aquaculture is a vital component of global food security, but it faces significant challenges from infectious diseases. These diseases have the potential to disrupt food supply chains, endanger biodiversity, and result in significant financial losses. Strong surveillance systems, well-informed policymaking, and strategic management techniques are necessary for the effective management of these diseases. Because they offer centralised platforms for data collection, analysis, and decision-making support, databases are essential in these domains. Databases are used aqua resource management and real-time monitoring applications for stakeholders (Kimothi et al.,2023)

Role of Databases in Disease Transmission

Databases make it easier to research and comprehend how diseases spread in aquaculture by:

- **Centralizing Data:** Combining information from multiple sources, such as fish farms, labs, and environmental sensors, into a single platform.
 - **Tracking Disease Spread:** Tracking the spread of pathogens over time and space, looking for trends and possible hotspots.
 - **Finding Transmission Routes:** figuring out how diseases move from farm to farm via personnel, equipment, or water.
- To help track and study disease transmission pathways, the Fishpathogens.eu database, for example, offers comprehensive information on a variety of fish pathogens, their sequences, and related metadata.

Informing Policy Making

Databases help with aquaculture policymaking by:

- **Providing Evidence-Based Data:** Giving access to thorough information on disease prevalence, impacts, and patterns of spread helps guide policy decisions.

- **Supporting in Risk Assessment:** promoting the identification of high-risk practices and areas, directing the creation of specific policies.
- **Promoting International Collaboration:** This improves international disease control initiatives by enabling data exchange and coordination between nations.

Enhancing Management Strategies

By offering resources for real-time monitoring and quick identification of disease outbreaks, databases improve disease management strategies.

- **Directing Biosecurity Measures:** Providing guidance for the creation of biosecurity procedures to stop the introduction and spread of disease.
- **Assessing Intervention Effectiveness:** Enabling the evaluation of management initiatives and their results, thereby promoting ongoing enhancement.

The AquaNet-Mod framework (James et al., 2023) is a data-driven, stochastic, state-transition model that helps assess management approaches by applying to the spread and control of aquatic diseases. FOMED facilitates molecular-to-environmental correlation, which supports One Health applications. Its organ-specific datasets can identify tissue-level biomarkers of exposure to environmental pollutants or pathogens with zoonotic potential. As a link between molecular biology and ecosystem health, FOMED integrates with ecological and surveillance data to form a comprehensive aquatic information infrastructure.

FOMED Database: Design and Utility

The Fish Organ-Specific Molecular Electronic Database (FOMED), which integrates genomics, transcriptomics, and bioinformatics components, was created as a centralized web-based repository for research on diseases specific to fish organs (Isaac, 2025).

FOMED, which was created for species like *Cyprinus carpio*, allows for the following:

- **Data Retrieval:** Gene information specific to an organ with chromosomal mapping and annotation.
 - **Analysis Modules:** Visualisation of differential expression, RNA coding potential, and ORF detection.
 - **Interactivity:** dynamic genome exploration through web-based querying integrated with GFF3.
 - **Visualisation:** Diagrams showing the relationships between organs and genes and chromosome mapping.
 - **Export options** include the creation of CSV and PDF reports for outputs that are ready for publication.
- FOMED is a cutting-edge bioinformatics model for aquatic disease diagnostics because of its distinct emphasis on organ-level molecular integration. It may eventually expand to machine learning-based biomarker discovery and One Health data harmonization.

Challenges and Limitations

Despite their advantages, there are a number of difficulties:

- Analyses can become challenging due to differences in data quality and a lack of standardization.

- Data Security and Privacy: Collaboration and data sharing may be hampered by issues about disclosing private information.
 - Resource Limitations: It takes a lot of resources to create and maintain extensive databases.
- For databases to be as useful as possible in disease transmission research and policymaking, these issues must be resolved.

Future Directions

Technological and methodological developments are expected to increase databases' usefulness:

- Artificial Intelligence Integration: Applying AI to the analysis and pattern recognition of massive datasets.
- Global database expansion: incorporating information from various geographical areas to offer a more thorough understanding.
- Real-time surveillance system development: putting in place mechanisms that enable prompt analysis and reaction in the event of an outbreak.

The ongoing creation and use of databases to facilitate research and guide public health decisions is essential to the future of disease transmission studies and aquaculture policymaking.

Conclusion

There are significant advancement in fish databases. Fish disease informatics has advanced significantly with the creation and use new databases. It closes the gap between genomics research and practical disease management by combining environmental and pathogen data with organ-specific molecular data. Fish databases support global efforts in aquatic biosecurity, predictive modelling, and zoonotic disease prevention when linked together within frameworks such as FOMED.

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