# The phylogenetics and pathogen population dynamics of Infectious Hypodermal and Hematopoietic Necrosis Virus (IHHNV) in global shrimp populations

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## Abstract

Infectious Hypodermal and Hematopoietic Necrosis Virus (IHHNV) has posed a persistent threat to global shrimp aquaculture since its emergence in the 1980s, with transmission exacerbated by intensified farming and international trade. While previous studies have focused on regional outbreaks, the global evolutionary dynamics of IHHNV remain poorly understood. Here, we analyse 126 IHHNV capsid protein sequences (107 sequences extracted from GenBank and 19 newly collected sequences from northern Queensland, Australia) and 63 NS1 gene sequences (44 from GenBank and 19 from northern Queensland, Australia) collected from 12 countries between 1986 and 2022. Bayesian coalescent analyses estimate a mean nucleotide substitution rate of $4.5 \times 10^{-4}$ (95% HPD $2.8 \times 10^{-4}$, $6.4 \times 10^{-4}$) substitutions/site/year for the capsid region and $1.9 \times 10^{-4}$ (95% HPD $1.1 \times 10^{-4}$, $2.8 \times 10^{-4}$) for NS1, consistent with earlier region-specific results. The time to the most recent common ancestor was dated to the early 1980s (95% HPD: 1976–1986). Demographic reconstruction revealed periods of exponential growth in the 1990s and early 2000s, followed by a decline in the mid-2010s. Phylogenetic analysis revealed marked genetic diversity and strong geographic structuring, with some evidence of international viral exchange. Distinct regional SNP patterns mirrored the phylogenetic structure, supporting geographically constrained viral evolution and diversification. The high evolutionary rates and structured global distribution of IHHNV underscore the need for continued molecular surveillance and enhanced biosecurity to mitigate the risk of future outbreaks.

## Introduction

- IHHNV is a single-stranded DNA virus causing mortality and growth deformities in farmed shrimp.
- The ~4 kb genome contains NS1, NS2, and capsid genes, with infectious and endogenous genotypes.
- Global spread followed shrimp trade and farming intensification, shaping species replacement in aquaculture.
- Global evolutionary structure remains poorly resolved due to limited sampling and inclusion of endogenous sequences.
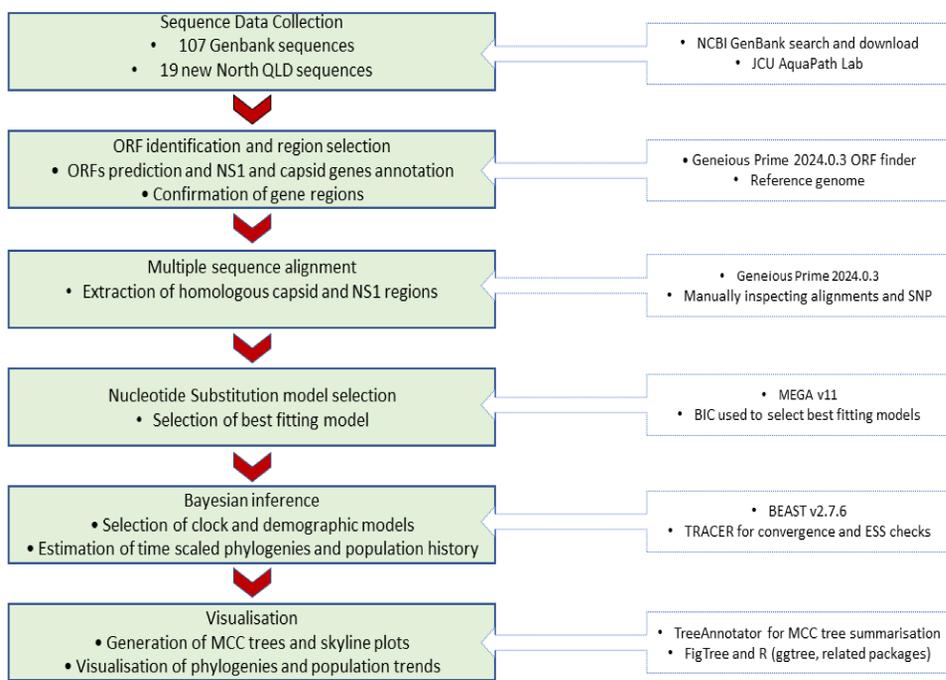
## Methodology



Fig. 1 Overview of the analytical workflow for phylogenetic and phylodynamic analysis of IHHNV sequences in this study. Summary of the processing pipeline, showing major steps and associated software used for ORF extraction, alignment, model selection, BEAST analysis, tree summarisation and visualisation.

## Results



**Countries:** Mexico, USA, Brazil, Ecuador, Peru, Venezuela, China, Philippines, South Korea, Taiwan, Vietnam, Australia
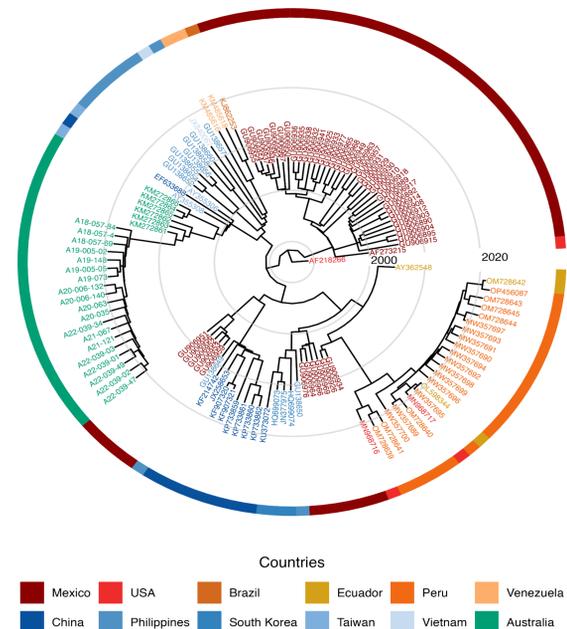
Fig. 2 Maximum Clade Credibility (MCC) time-scaled tree of 126 Global IHHNV Capsid Sequences. Branch lengths are proportional to calendar time. Nodes with low posterior support (<0.80) were collapsed..
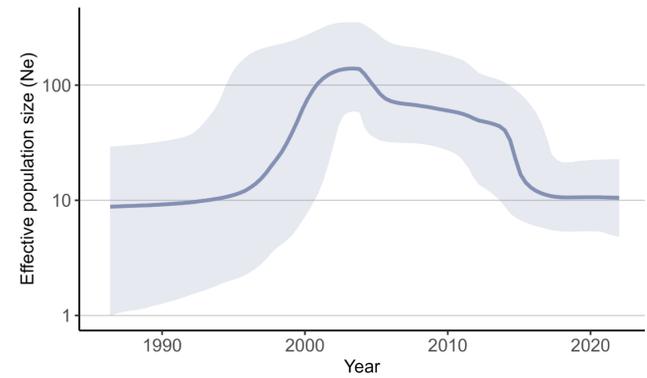


Fig. 3 Bayesian Skyline Plot of IHHNV (Capsid Region) Population dynamics of IHHNV over time, inferred from Bayesian Skyline analysis of the capsid region of 126 sequences, highlighting fluctuations in effective viral population size. The central blue line is the mean effective population size through time, and the shaded region is the 95% highest posterior density interval.
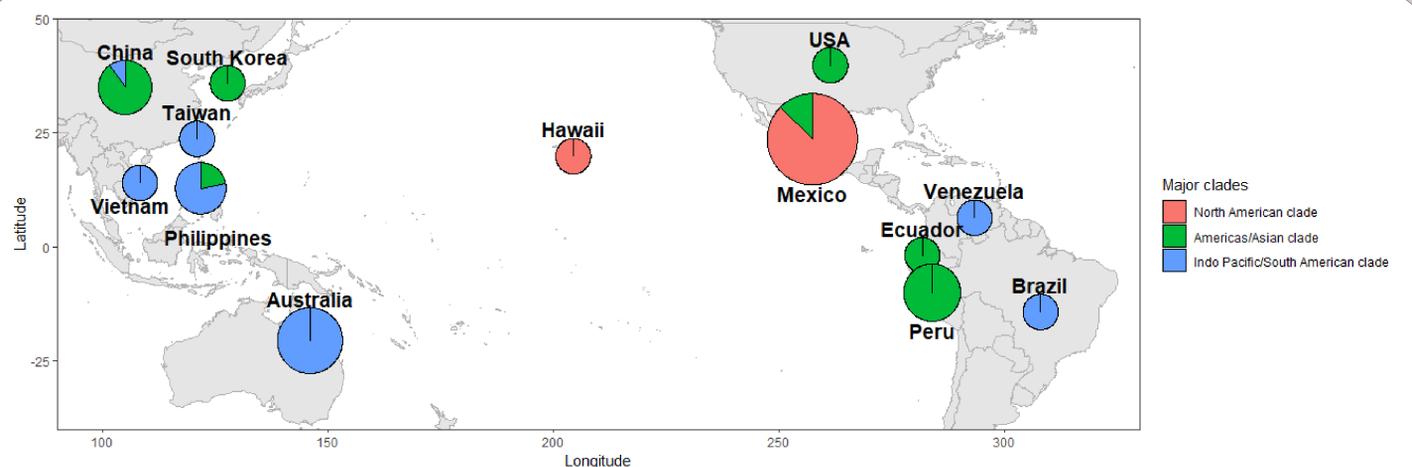
## Conclusion

- NS1 and capsid genomes show consistent phylogenetic topologies and recent shared ancestry.
- IHHNV shows rapid evolution with clear regional genetic structure.
- Regional SNPs enable lineage tracking and strengthen biosecurity response.
- Field-deployable diagnostics and global surveillance remain essential.

**Study link** ➡



**Major clades:** North American clade, Americas/Asian clade, Indo Pacific/South American clade

Fig. 4 Global Spatial Distribution of Major IHHNV Clades Represented in this Study. Spatial phylogeography map showing the relative proportion of sequences belonging to each of the three major phylogenetic clades at each sampling location. Pie-chart size is proportional to the total number of sequences obtained from that region. Clade colours correspond to major clades as described in the legend.