

Critical Review of Epsilonretrovirus : Taxonomy, Distribution and Evolution

Athirah Shaharum^a, Roziyah Kambol^{a*}

Structured Abstract

Background: Due to their distinct evolutionary and ecological effects, epsilonretroviruses members of the *Retroviridae* family are essential to comprehending piscine retroviruses. Although they are found in many fish species around the world, little is known about their distribution and evolutionary history, especially in Malaysia and other Southeast Asian countries. In order to clarify their classification, evolutionary patterns, and geographic distribution, this review attempts to collect information from a compilation of existing literature.

Literature Review: Epsilonretroviruses, which belong to the Orthoretrovirinae subfamily, are highly host-specific and genetically diverse. These retroviruses have conserved long terminal repeats (LTRs) and structural genes (*gag*, *pol*, and *env*) that are necessary for replication and host genome integration. Research shows that they can become endogenous retroviruses (ERVs) and integrate into host genomes, impacting evolution and genetic diversity. The evolutionary adaptation and host-virus coevolution of endogenous epsilonretroviruses are highlighted by their phylogenetic resemblance to their exogenous counterparts.

Epsilonretroviruses have an extensive evolutionary history, with Southeast Asia showing the greatest phylogenetic diversity. Novel strains in native fish species, including gigantic gourami (*Osphronemus goramy*) and striped snakehead (*Channa striata*), have been identified by high-throughput genomic analysis, indicating dynamic host-virus interactions. These results highlight how aquaculture methods and environmental conditions influence the evolution and dynamics of retroviral transmission.

Geographically, freshwater and marine fish species have been shown to harbor epsilonretroviruses. The varied ecosystems found in Malaysian waters make them the perfect place for viral evolution. The identification of *Salmon Swimbladder Sarcoma Virus* (SSSV) and *Snakehead Retrovirus* (SnRV) in aquaculture settings are noteworthy instances that highlight the necessity of focused study on disease management and conservation tactics.

Conclusion: As models for exploring host-virus coevolution and genetic innovation, epsilonretroviruses exhibit significant ecological and evolutionary value. Fish populations in Southeast Asia offer valuable insights into the possibility of finding new retroviral taxa and comprehending their effects on fish health and aquaculture viability. In order to identify the molecular mechanisms underlying retroviral variety and adaptation, future research should concentrate on utilizing cutting-edge genomic technologies.

Keywords: Epsilonretrovirus, Endogenous Retroviruses, Piscine Hosts, Evolution, Southeast Asia

*Correspondence: roziyah1259@uitm.edu.my

^aSchool of Biology, Faculty of Applied Sciences, Universiti Teknologi MARA, Shah Alam, Malaysia