

WOAH Reference Laboratory for EHNV, YHV1 and AbHV

Regional Workshop for WOAH Focal Points for Aquatic Animals

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WOAH Reference Laboratory for
Epizootic Haematopoietic Necrosis Virus,
Yellow Head Virus genotype 1 and Abalone
Herpesvirus

Reference Centre



World Organisation
for Animal Health



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for Animal Health



Australian Government
Department of Agriculture,
Fisheries and Forestry

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Tokyo University of Marine Science and Technology



WOAH ad hoc Group for *Megalocytivirus pagrus 1*

Mission:

Review peer-reviewed literature for validated methods and develop a shortlist ✓

1. Koda real-time PCR (Koda et al., 2023)
2. Cummins real-time PCR (Kawato et al., 2021)
3. Rimmer real-time PCR (Rimmer et al., 2012)
4. Rimmer conventional nested PCR (Rimmer et al., 2012)

Develop WOAHA technical disease card ✓

(<https://www.woah.org/en/document/technical-disease-card-megalocytivirus-pagrus1/>)

Plan and undertake interlaboratory comparability (ILC) for the shortlisted assays

- 40 sample panel, 10 labs internationally (+ AFDL) containing RSIV, ISKNV and TRBIV

Author the WOAHA *Aquatic Manual* Chapter for infection with *M. pagrus1*

Report to the Aquatic Animal Health Standards Commission, July 2026



Infection with *Megalocytivirus pagrus1*

Pathogen Information

1. CAUSATIVE AGENT

1.1. Pathogen type

Virus.

1.2. Disease name and synonyms

Infection with *Megalocytivirus pagrus1*.

Red sea bream individual disease has been used to describe an infection with the *M. pagrus1* genogroup red sea bream iridovirus (RSIV). Reddish body syndrome has been used to describe infection with the *M. pagrus1* genogroup turbot reddish body iridovirus (TRBIV).

1.3. Pathogen common names and synonyms

There is no common name or synonyms for *M. pagrus1*.

1.4. Taxonomic affiliation

M. pagrus1 is a species within the genus *Megalocytivirus*, which is within the family Iridoviridae. There are three genogroups of *M. pagrus1* currently recognised. The genogroups are RSIV, infectious spleen and kidney necrosis virus (ISKNV), and TRBIV (ICTV, 2024). The International Committee for the Taxonomy of Viruses recognises *Megalocytivirus pagrus1*, with RSIV, ISKNV and TRBIV genogroups within this species (ICTV, 2024).

1.5. Authority (first scientific description, reference)

White disease caused by TRBIV has been reported since the 1980s in ornamental fish (Go et al., 2016), the first outbreak of disease associated with RSIV was recorded in Japan in 1990 (Inoue et al., 1992). Infectious spleen and kidney necrosis virus was the first genogroup of *M. pagrus1* identified, and Chinese perch (*Siniperca chuatsi*) was the first reported host of ISKNV (Ito et al., 2001; Kurita & Nakajima, 2012). In 2004, TRBIV was first reported (Siti et al., 2004).

1.6. Pathogen environment (fresh, brackish, marine waters)

Infection with *M. pagrus1* can occur in freshwater, brackish, and marine environments (Johan et al., 2020).

2. MODES OF TRANSMISSION

2.1. Routes of transmission (horizontal, vertical, indirect)

Horizontal transmission of *M. pagrus1* can occur through water, cohabitation, ingestion of infected waste, and cannibalism (Go et al., 2016; Johan et al., 2020). More recently, Kawato et al. (2023) demonstrated that the risk of horizontal transmission through infected seawater increases with increasing viral load in the water. Further, RSIV was shown to be more likely to spread between open-system fish farms through fomites rather than seawater (Kawato et al., 2023).

There is no evidence of vertical transmission of *M. pagrus1*.

2.2. Reservoir

Populations of farmed fish (Kawato et al., 2023) and ornamental fish in the retail trade (Mohr et al., 2015) are known reservoirs of *M. pagrus1*.

2.3. Risk factors (temperature, salinity, etc.)

Outbreaks of disease caused by RSIV have mostly been seen in the summer months at water temperatures of 20°C and above (Kurita et al., 2012). He et al. (2003) showed that ISKNV caused disease in Chinese perch (*Siniperca chuatsi*) at temperatures above 20°C only.

The ISKNV genogroup has been shown to transmit between freshwater and marine environments, demonstrating a potential pathway for pathogen spread between marine and freshwater populations through euryhaline species (Go et al., 2016).

Less is known about the epidemiology (including risk factors) of TRBIV. This is likely due to fewer records of disease outbreaks caused by TRBIV (as opposed to RSIV and ISKNV), and difficulty in obtaining TRBIV-positive material for experimental research (Mohr et al., 2015).

3. HOST RANGE

3.1. Susceptible species

The host range of *M. pagrus1* includes over 50 species of marine and freshwater fish from 30 families (WOAH, 2025).

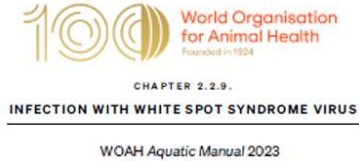


Effect of pooling on DSe and DSp

From the WOAHA Aquatic Manual for WSSV...

3.6. Pooling of samples

Pooling of samples from more than one individual animal for a given purpose should only be recommended where robust supporting data on diagnostic sensitivity and diagnostic specificity have been evaluated and found to be suitable. The effect of pooling on diagnostic sensitivity has not been thoroughly evaluated, therefore larger specimens should be processed and tested individually. Small life stages can be pooled to obtain the minimum amount of material for virus isolation or molecular detection.



We need estimates of DSe for testing individuals. Using apparently healthy, experimentally exposed animals, of known C_T value we determined DSe for individual animals for *Megalocytivirus pagrus1* and WSSV. Will also be calculated for YHV1.

Using apparently healthy, experimentally exposed animals, of known C_T value, we generated pools and applied the proportion testing positive to individual animal DSe using $DSe_{POOL} = DSe_{IND} \times (ObsPOS/ExpPOS)$

Recalculating using Bayesian Latent Class Models (BLCM)



Effect of pooling on DSe and DSp

How it all works

$WSSV_{IND}$ DSe is 83% and $WSSV_{POOL}$ DSe (preliminary) is 61%.

Using 95% confidence of 2% prevalence:

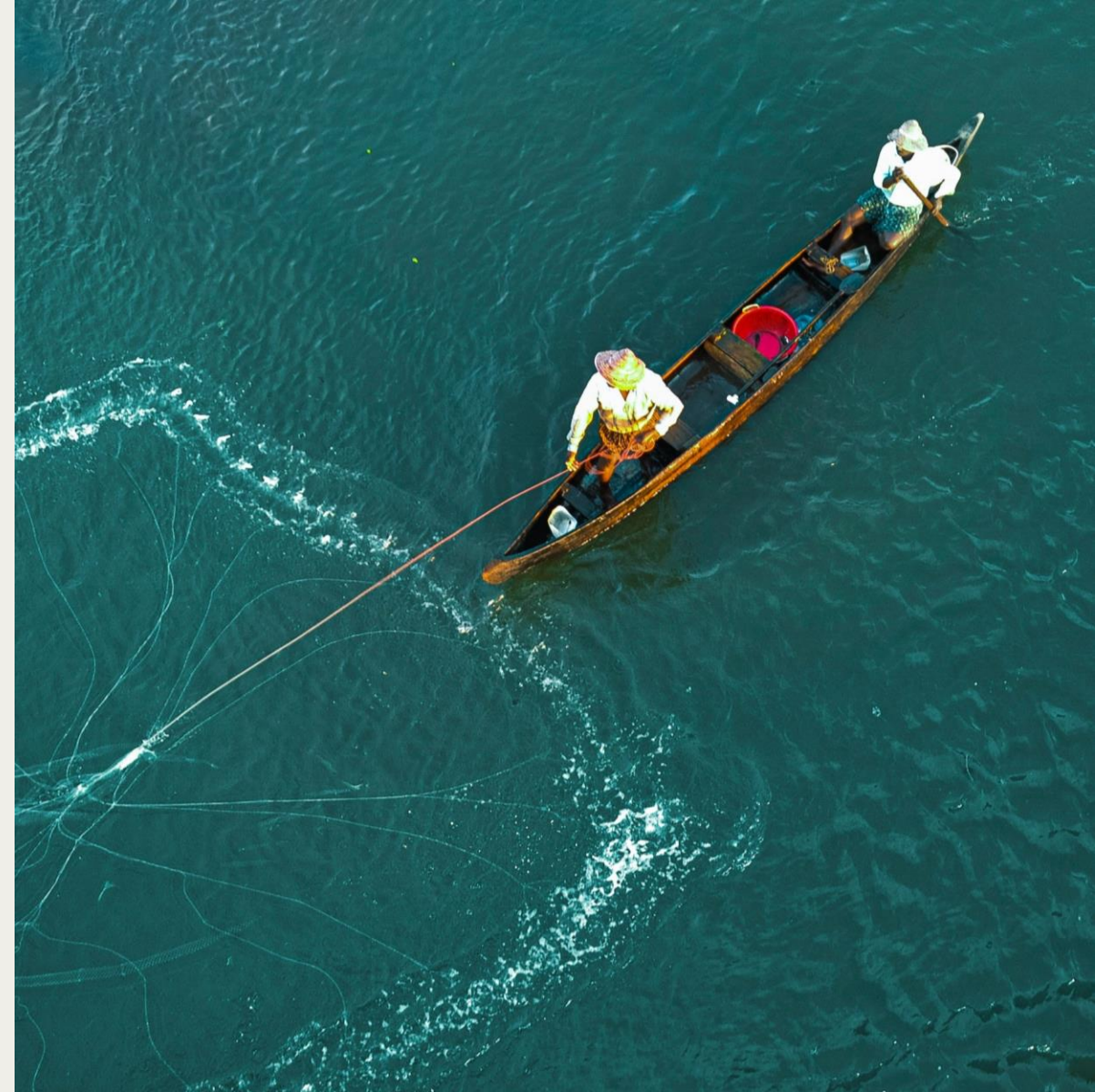
- Individuals: require 178 samples = 178 tests
- Pools: require 243 samples (tested as pools of 5) = 49 tests

Using AFDL's charges (\$600 for the first sample and \$100 for the rest)

- Individuals: 178 tests = \$18,000
- Pools: 49 tests = \$5,400

Pooling requires more samples ($\uparrow$ 65) but test costs are cheaper ($\downarrow$ \$12,600)

Thank you



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