Report of the WOAH *ad hoc* Group on susceptibility of fish species to infection with WOAH listed diseases

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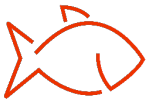

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1. Introduction

This report covers the work of the WOAH *ad hoc* Group on Susceptibility of fish species to infection with WOAH listed diseases (the *ad hoc* Group). This group met electronically in April and November/December 2022.

The list of participants and the Terms of Reference are presented in Annex I and Annex II, respectively.

***Ad hoc* Group's recommendation, rationale and decision-making to the Aquatic Animals Commission:**

After reviewing the references it became clear to the *ad hoc* Group that it was not possible to identify the viruses to the level of genogroup (i.e. red seabream iridovirus (RSIV), infectious spleen and kidney necrosis virus (ISKNV) and turbot reddish body iridovirus (TRBIV) genogroups) for many of the susceptible host species. The distinction to genogroup requires nucleic acid sequence and/or phylogenetic tree analyses; and methodologies for this level of taxonomic differentiation are varied (not yet standardized) and only available for recent publications. Members of the *ad hoc* Group were confident in their ability to identify host species that are susceptible to ISKNV at the viral species level (which includes RSIV, ISKNV, TRBIV genogroups) but without additional sequencing evidence could not provide a comprehensive list of susceptible host species to the individual virus genogroups.

The *ad hoc* Group noted that infection with the three genogroups (RSIV, ISKNV and TRBIV) of the ISKNV species presents with the same clinical signs, histopathology and epidemiological information and the only difference between the genogroups is the sequencing information.

The *ad hoc* Group is recommending the title of the proposed chapter be listed as Infection with *Megalocytivirus* instead of Infection with infectious spleen and kidney necrosis virus as there could be confusion between ISKNV species and ISKNV genogroup. The *ad hoc* Group recommends that both Article 10.8.1. of Chapter 10.8. of the WOAH *Aquatic Animal Health Code* (the *Aquatic Code*) and Section 1. of Chapter 2.3.7. of the WOAH *Manual of Diagnostic Tests for Aquatic Animals* (the *Aquatic Manual*) be updated to reflect the three specific genogroups (RSIV, ISKNV and TRBIV) that would be included within an infection with *Megalocytivirus* chapter.

Assessing fish species susceptible to infection with *Megalocytivirus* at the viral species level allows the inclusion of the early studies using the monoclonal antibody M10 to identify the fish species with RSIV/ISKNV genogroup infections. Many of these fish species are important aquaculture (traded) species. Consequently, failing to recognize them as susceptible to *Megalocytivirus* could have significant disease transmission implications. Furthermore, it is likely that the monoclonal antibody M10 would cross-react with TRBIV but not Scale drop disease virus (SDDV). If this was confirmed (Takano *et al*., 2020) then M10 could become a key diagnostic tool.

The *ad hoc* Group considered when making this recommendation to the Aquatic Animals Commission that the specific PCR (Kawato *et al*., 2021a) could be a recommended test in an infection with *Megalocytivirus* chapter of the *Aquatic Manual* since it detects the three genogroups of concern (RSIV, ISKNV and TRBIV). This test would not detect SDDV and would not cross-react with ranaviruses. The *ad hoc* Group noted that while this PCR is validated for both RSIV and ISKNV, it is not validated for TRBIV. This validation would need to be completed if the Aquatic Animals Commission elected to include all three genotypes under a listing of infection with *Megalocytivirus*.

2. Methodology

The *ad hoc* Group applied the *Aquatic Code* criteria, as outlined in Chapter 1.5. Criteria for listing species as susceptible to infection with a specific pathogen, to potential host species in order to determine susceptibility to one or more of the following: infection with RSIV (genogroup), infection with ISKNV (genogroup), infection with TRBIV (genogroup) or infection with *Megalocytivirus* (infectious spleen and kidney necrosis virus species). RSIV, ISKNV and TRBIV are all distinct genogroups of *Megalocytivirus* (excluding SDDV) (https://talk.ictvonline.org/ictv-reports/ictv_online_report/dsdna-viruses/w/iridoviridae/615/genus-megalocytivirus).

The assessments were done using a three-stage approach, as outlined in Article 1.5.3. of Chapter 1.5., and further considerations are described below:

2.1. Stage 1: Criteria to determine whether the route of transmission is consistent with natural pathways for the infection (as described in Article 1.5.4.):

Table 1 describes the routes of infection accepted by the *ad hoc* Group for the assessments, as well as some considerations when applying Stage 1 criteria to support susceptibility to one of the following: infection with RSIV (genogroup), infection with ISKNV (genogroup), infection with TRBIV (genogroup) or infection with *Megalocytivirus* (excluding SDDV). Consideration was given to whether, if experimental, the procedures mimic natural pathways for disease transmission. Consideration was also given to host stressors, e.g. environmental factors, or co-infections, that may affect host response, virulence and transmission.

Table 1: Route of transmission

Route of transmission	Considerations
1. Natural exposure including situations where infection has occurred without experimental intervention (e.g. infection in wild or farmed populations). **OR** 2. Non-invasive experimental procedures: e.g. cohabitation with infected hosts, infection by immersion, or by ingestion.	References that reported invasive experimental procedures as the route of transmission were not used as evidence for infection (i.e. Article 1.5.4.). References that reported co-infections were noted as such and were interpreted with caution.

2.2. Stage 2: Criteria to determine whether the pathogenic agent has been adequately identified (as described in Article 1.5.5.):

Table 2 describes the pathogen identification methods accepted by the *ad hoc* Group for the assessments, as well as some considerations when applying Stage 2 to support susceptibility to one of the following: infection with RSIV (genogroup), infection with ISKNV (genogroup), infection with TRBIV (genogroup) or infection with *Megalocytivirus* (excluding SDDV).

Table 2: Pathogen identification

Pathogen Identification to the level of *Megalocytivirus* genus excluding SDDV (i.e. RSIV, ISKNV and TRBIV genogroups only)	Pathogen Identification to the level of genogroup (RSIV, ISKNV, TRBIV)	Considerations
Immunological methods (e.g. IFAT or IHC) (e.g. Kurita & Nakajima, 2012) **OR** PCR (e.g. Mohr *et al.*, 2015)	PCR **AND** Sequence analysis (e.g. Kurita & Nakajima, 2012)	Antibodies for RSIV cross react with, and cannot be used to differentiate between, the genogroups, RSIV, ISKNV and TRBIV (IFAT alone is not sufficient to differentiate the three viruses). Consequently, they were adequate for identifying ISKNV at the species (but not genogroup) level. Monoclonal antibody (M10) provided by the WOAH reference lab can be used to indicate infection with the three genogroups of *Megalocytivirus* (RSIV, ISKNV and TRBIV). Further, it does not react with SDDV. PCR and sequence analysis can target various (and single or multiple) regions of the genome (e.g. MCP, ATPase, myristylated membrane protein gene, K2, laminin-like protein, and phosphatase, genes). MCP or ATPase loci or multi-loci analyses were primarily used but other regions were not excluded when phylogenetic analysis demonstrated strong homology with reference strains. Lack of standardized or validated measures of discrimination lend uncertainty to genogroup differentiation.

2.3. Stage 3: Criteria to determine whether the evidence indicates that presence of the pathogenic agent constitutes an infection (as described in Article 1.5.6.):

Criteria A to D, as described in Article 1.5.6. and presented below, were used to determine if there was sufficient evidence for one of the following: infection with RSIV (genogroup), infection with ISKNV (genogroup), infection with TRBIV (genogroup) or infection with *Megalocytivirus* (excluding SDDV) in the suspected host species:

A. The pathogenic agent is multiplying in the host, or developing stages of the pathogenic agent are present in or on the host[1];

B. Viable pathogenic agent is isolated from the proposed susceptible species, or infectivity is demonstrated by way of transmission to naïve individuals;

C. Clinical or pathological changes are associated with the infection;

D. The specific location of the pathogen corresponds with the expected target tissues.

Evidence to support criterion A alone was sufficient to determine infection. In the absence of evidence to meet criterion A, satisfying at least two of criteria B, C or D were required to determine infection.

Table 3 describes the criteria for assessment of Stage 3 to support susceptibility to infection with RSIV (genogroup), infection with ISKNV (genogroup), infection with TRBIV (genogroup) and infection with *Megalocytivirus* (excluding SDDV).

Table 3: Evidence of infection (note this criterion is the same for all assessments)

Evidence of infection			
A: Replication	**B: Viability / Infectivity**	**C: Pathology / Clinical signs***	**D: Location**
1. Sequential virus titration over time **OR** 2. Demonstration of increasing copy number over time by qPCR with confirmatory PCR/sequencing **OR** 3. TEM showing virions in host cells **OR** 4. Products (e.g. antigens) of virus replication detected	1. Isolation by cell culture **OR** 2. Cohabitation with passage to a susceptible host **OR** 3. Isolation of virus from a host and IP injection into a susceptible host	1. Pale gills, erratic swimming, lethargy, enlarged spleen **OR** 2. Presence of abnormally enlarged cells in tissue imprint or histological sections of the spleen, heart, kidney, liver, intestine or gill **OR** 3. Mortality in experimental virus-exposed group but not in control group	1. Infection found in gill lamellae or intestine** **OR** 2. Identification in visceral organs such as spleen, heart, kidney or liver

* Pathology/Clinical signs may be non-specific, variable and include some or all of the characteristics listed.

** As demonstrated by histology, immunohistochemistry (IHC) or in-situ hybridisation (ISH).

3. Results

If Chapter 10.8. of the *Aquatic Code* and Chapter 2.3.7. of the *Aquatic Manual* are maintained as Infection with RSIV, the species proposed to be listed in the respective articles are included below. However, the *ad hoc* Group report also shows the impact to the list of susceptible species in the *Aquatic Code* and list of susceptible species and species with incomplete evidence in the *Aquatic Manual* if the chapter was amended to Infection with *Megalocytivirus*. For species assessed for infection with *Megalocytivirus* (excluding SDDV), the *ad hoc*

[1] For the purposes of the assessments for susceptibility to infection with red sea bream iridovirus and infection with infectious spleen and kidney necrosis virus, replication 'on the host' was not considered to apply.

Group report also includes the specific genogroup (if possible) assessed, which aligns with the approach taken for infection with viral haemorrhagic septicaemia.

Infection with red seabream iridovirus

The *ad hoc* Group agreed that five of the species currently included in Article 10.8.2 as susceptible to infection with red seabream iridovirus (genogroup), and nine additional species, not previously listed, meet the criteria for listing as susceptible to infection with red seabream iridovirus in accordance with Chapter 1.5. of the *Aquatic Code*. These are proposed to be listed in Article 10.8.2. of Chapter 10.8. Infection with red seabream iridovirus.

Family	Scientific name	Common name
Butidae	*Oxyeleotris marmorata*	marble goby
Carangidae	*Seriola quinqueradiata*	Japanese amberjack[2]
	Trachinotus carolinus	Florida pompano
Centrarchidae	*Lepomis macrochirus*	bluegill
Latidae	*Lates calcarifer*	barramundi
Oplegnathidae	*Oplegnathus fasciatus*	barred knifejaw[3]
	Oplegnathus punctatus	spotted knifejaw
Osphronemidae	*Macropodus opercularis*	paradise fish
Paralichthyidae	*Paralichthys olivaceus*	bastard halibut
Sciaenidae	*Larimichthys crocea*	large yellow croaker
Sinipercidae	*Siniperca chuatsi*	Mandarin fish
Sparidae	*Acanthopagrus schlegelii*	blackhead seabream
	Pagrus major	red sea bream
Synanceiidae	*Inimicus japonicus*	no common name

[2] Based on FAOTERM and www.fishbase.se the common name for *Seriola quinqueradiata* is Japanese amberjack.

[3] Based on FAOTERM and www.fishbase.se the common name for *Oplegnathus fasciatus* is barred knifejaw.

Seven species, bluefin tuna (*Thunnus thynnus*), flathead grey mullet (*Mugil cephalus*), greater amberjack (*Seriola dumerili*), groupers (*Epinephelus spp.*), red drum (*Sciaenops ocellatus*), sea bass (*Lateolabrax sp.*) and striped jack (*Pseudocaranx dentex*) were assessed as not meeting the criteria and were proposed to be removed from Article 10.8.2. of Chapter 10.8. of the *Aquatic Code.*

Five species, goldlined seabream (*Rhabdosargus sarba*), Japanese seabass (*Lateolabrax japonicus*), pearl gourami (*Trichopodus leerii*), rockfish (*Sebastes schlegeli*) and silver pomfret (*Pampus argenteus*) were assessed as having incomplete evidence of susceptibility and were proposed to be included in Section 2.2.2., of Chapter 2.3.7. of the *Aquatic Manual*.

Pathogen-specific positive PCR results were reported in the following two species, common ponyfish (*Leiognathus equulus*) and giant grouper (*Epinephelus lanceolatus*), but an active infection had not been demonstrated. These species were proposed to be included in the second paragraph of Section 2.2.2. of Chapter 2.3.7. of the *Aquatic Manual*.

Infection with *Megalocytivirus* (excluding SDDV)

The following species were assessed to meet the criteria for listing as susceptible to infection with *Megalocytivirus*, in accordance with Chapter 1.5., and the *ad hoc* Group has proposed these species to be included in Article 10.8.2. of a revised Chapter 10.8. Infection with *Megalocytivirus*. These species are shown in the table below:

Family	Scientific name	Common name	Assessed for:
Apogonidae	*Pterapogon kauderni*	Banggai cardinalfish	ISKNV (genogroup)
Butidae	*Oxyeleotris marmorata*	marble goby	RSIV (genogroup)
			ISKNV (genogroup)

Family	Scientific name	Common name	Assessed for:
Carangidae	*Pseudocaranx dentex*	white trevally	*Megalocytivirus* (excluding SDDV)
	Seriola dumerili	greater amberjack	*Megalocytivirus* (excluding SDDV)
	Seriola lalandi	goldstripe amberjack	*Megalocytivirus* (excluding SDDV)
	Seriola quinqueradiata	Japanese amberjack	RSIV (genogroup)
	Seriola quinqueradiata x Seriola lalandi	Buri-hira hybrid	*Megalocytivirus* (excluding SDDV)
	Trachinotus blochii	snubnose pompano	*Megalocytivirus* (excluding SDDV)
	Trachinotus carolinus	Florida pompano	RSIV (genogroup)
	Trachurus japonicus	Japanese jack mackerel	*Megalocytivirus* (excluding SDDV)
Centrarchidae	*Lepomis macrochirus*	bluegill	RSIV (genogroup)
Cichlidae	*Astronotus ocellatus*	Oscar	ISKNV (genogroup)
			TRBIV (genogroup)
	Etroplus suratensis	pearlspot	ISKNV (genogroup)
	Oreochromis niloticus	Nile tilapia	ISKNV (genogroup)
	Pterophyllum altum	deep angelfish	ISKNV (genogroup)
	Pterophyllum scalare	freshwater angelfish	ISKNV (genogroup)
Cyprinidae	*Epalzeorhynchos frenatum*	rainbow sharkminnow	ISKNV (genogroup)
Danionidae	*Danio rerio*	zebrafish	ISKNV (genogroup)
Ephippidae	*Platax orbicularis*	orbiculate batfish	ISKNV (genogroup)
Girellidae	*Girella punctata*	largescale blackfish	*Megalocytivirus* (excluding SDDV)
Haemulidae	*Parapristipoma trilineatum*	chicken grunt	*Megalocytivirus* (excluding SDDV)
	Plectorhinchus cinctus	crescent sweetlips	*Megalocytivirus* (excluding SDDV)
Latidae	*Lates calcarifer*	barramundi	RSIV (genogroup)
			ISKNV (genogroup)
			TRBIV (genogroup)
Lethrinidae	*Lethrinus haematopterus*	Chinese emperor	*Megalocytivirus* (excluding SDDV)
	Lethrinus nebulosus	spangled emperor	*Megalocytivirus* (excluding SDDV)
Mugilidae	*Mugil cephalus*	flathead grey mullet	*Megalocytivirus* (excluding SDDV)
Nothobranchiidae	*Aphyosemion gardneri*	steel blue killifish	ISKNV (genogroup)
Oplegnathidae	*Oplegnathus fasciatus*	barred knifejaw	RSIV (genogroup)
			ISKNV (genogroup)
	Oplegnathus punctatus	spotted knifejaw	RSIV (genogroup)
			ISKNV (genogroup)
Osphronemidae	*Macropodus opercularis*	paradise fish	RSIV (genogroup)
	Osphronemus goramy	giant gourami	ISKNV (genogroup)
	Trichogaster lalius	dwarf gourami	ISKNV (genogroup)
			TRBIV (genogroup)
	Trichopodus leerii	pearl gourami	ISKNV (genogroup)
	Trichopodus microlepis	moonlight gourami	ISKNV (genogroup)
Paralichthyidae	*Paralichthys olivaceus*	bastard halibut	RSIV (genogroup)

Family	Scientific name	Common name	Assessed for:
			TRBIV (genogroup)
			Megalocytivirus (excluding SDDV)
Percichthyidae	*Maccullochella peelii*	Murray cod	ISKNV (genogroup)
Pleuronectidae	*Verasper variegatus*	spotted halibut	*Megalocytivirus* (excluding SDDV)
Poeciliidae	*Poecilia latipinna*	sailfin molly	ISKNV (genogroup)
	Poecilia reticulata	guppy	*Megalocytivirus* (excluding SDDV)
	Xiphophorus hellerii	green swordtail	ISKNV (genogroup)
	Xiphophorus maculatus	southern platyfish	ISKNV (genogroup)
Procatopodidae	*Poropanchax normani*	Norman's lampeye	*Megalocytivirus* (excluding SDDV)
Rachycentridae	*Rachycentron canadum*	Cobia	*Megalocytivirus* (excluding SDDV)
Sciaenidae	*Larimichthys crocea*	large yellow croaker	RSIV (genogroup)
	Sciaenops ocellatus	red drum	ISKNV (genogroup)
Scombridae	*Scomber japonicus*	chub mackerel	*Megalocytivirus* (excluding SDDV)
	Scomberomorus niphonius	Japanese Spanish mackerel	*Megalocytivirus* (excluding SDDV)
	Thunnus orientalis	Pacific bluefin tuna	*Megalocytivirus* (excluding SDDV)
Scophthalmidae	*Scophthalmus maximus*	turbot	TRBIV (genogroup)
Serranidae	*Epinephelus akaara*	Hong Kong grouper	*Megalocytivirus* (excluding SDDV)
	Epinephelus awoara	yellow grouper	*Megalocytivirus* (excluding SDDV)
	Epinephelus bruneus	longtooth grouper	*Megalocytivirus* (excluding SDDV)
	Epinephelus coioides	orange-spotted grouper	*Megalocytivirus* (excluding SDDV)
	Epinephelus fuscoguttatus	brown-marbled grouper	*Megalocytivirus* (excluding SDDV)
	Epinephelus fuscoguttatus ♀ × ♂*E. lanceolatus*	pearl gentian grouper (hybrids)	ISKNV (genogroup)
	Epinephelus malabaricus	Malabar grouper	*Megalocytivirus* (excluding SDDV)
	Epinephelus septemfasciatus	convict grouper	*Megalocytivirus* (excluding SDDV)
Sinipercidae	*Siniperca chuatsi*	Mandarin fish	RSIV (genogroup)
			ISKNV (genogroup)
Sparidae	*Acanthopagrus schlegelii*	blackhead seabream	RSIV (genogroup)
	Dentex tumifrons	yellowback seabream	*Megalocytivirus* (excluding SDDV)
	Pagrus major	red sea bream	RSIV (genogroup)
Stromateidae	*Pampus argenteus*	silver pomfret	RSIV (genogroup)
Synanceiidae	*Inimicus japonicus*	no common name	RSIV (genogroup)
Tetraodontidae	*Takifugu rubripes*	tiger pufferfish	*Megalocytivirus* (excluding SDDV)

The following species were assessed as having incomplete evidence of susceptibility to infection with *Megalocytivirus*, in accordance with Chapter 1.5., and the *ad hoc* Group has proposed these species to be included in Section 2.2.2. of a revised Chapter 2.3.7. Infection with *Megalocytivirus* of the *Aquatic Manual*.

Family	Scientific name	Common name	Assessed for:
Cichlidae	*Cleithracara maronii*	keyhold cichlid	TRBIV (genogroup)
	Mikrogeophagus ramirezi	ram cichlid	ISKNV (genogroup)
	Pterophyllum scalare	freshwater angelfish	TRBIV (genogroup)
Helostomatidae	*Helostoma temminckii*	kissing gourami	ISKNV (genogroup)
Lateolabracidae	*Lateolabrax japonicus*	Japanese seabass	RSIV (genogroup)
Oplegnathidae	*Oplegnathus fasciatus*	barred knifejaw	TRBIV (genogroup)
Osphronemidae	*Betta splendens*	siamese fighting fish	*Megalocytivirus* (excluding SDDV)
	Trichopodus leerii	pearl gourami	RSIV (genogroup)
	Trichopodus trichopterus	three spot gourami	ISKNV (genogroup)
			TRBIV (genogroup)
Poeciliidae	*Poecilia sphenops*	molly	ISKNV (genogroup)
	Poecilia velifera	sail-fin molly	*Megalocytivirus* (excluding SDDV)
	Xiphophorus variatus	variable platyfish	ISKNV (genogroup)
Sebastidae	*Sebastes schlegeli*	rockfish	RSIV (genogroup)
Sparidae	*Rhabdosargus sarba*	goldlined seabream	RSIV (genogroup)
			ISKNV (genogroup)

Pathogen-specific PCR results for infection with *Megalocytivirus* had been reported in the following species but an active infection had not been demonstrated. These species were proposed to be included in the second paragraph of Section 2.2.2. of a revised Chapter 2.3.7. Infection with *Megalocytivirus* in the *Aquatic Manual*. These species are shown in the table below:

Family	Scientific name	Common name	Assessed for:
Carangidae	*Alepes djedaba*	shrimp scad	ISKNV (genogroup)
	Caranx sexfasciatus	bigeye trevally	ISKNV (genogroup)
	Decapterus maruadsi	Japanese scad	ISKNV (genogroup)
	Scomberoides lysan	doublespotted queenfish	ISKNV (genogroup)
	Scomberoides tala	barred queenfish	ISKNV (genogroup)
	Selaroides leptolepis	yellowstripe scad	ISKNV (genogroup)
Characidae	*Moenkhausia costae*	tetra fortune	*Megalocytivirus* (excluding SDDV)
Clupeidae	*Konosirus punctatus*	dotted gizzard shad	ISKNV (genogroup)
Cobitidae	*Misgurnus anguillicaudatus*	pond loach	*Megalocytivirus* (excluding SDDV)
Cynoglossidae	*Cynoglossus sinicus*	no common name	ISKNV (genogroup)
Cyprinidae	*Carassius auratus*	goldfish	ISKNV (genogroup)
	Cyprinus carpio	common carp	ISKNV (genogroup)
Danionidae	*Danio albolineatus*	pearl danio	ISKNV (genogroup)
Engraulidae	*Thryssa mystax*	moustached thryssa	ISKNV (genogroup)
Haemuliae	*Plectorhinchus pictus*	trout sweetlips	ISKNV (genogroup)
Hemiodontidae	*Hemiodus gracilis*	no common name	*Megalocytivirus* (excluding SDDV)
Leiognathidae	*Deveximentum insidiator*	pugnose ponyfish	ISKNV (genogroup)

Family	Scientific name	Common name	Assessed for:
	Leiognathus brevirostris	shortnose ponyfish	ISKNV (genogroup)
	Leiognathus equulus	common ponyfish	RSIV (genogroup)
	Photopectoralis bindus	orangefin ponyfish	ISKNV (genogroup)
Loricariidae	*Hypostomus plecostomus*	suckermouth catfish	*Megalocytivirus* (excluding SDDV)
Lutjanidae	*Lutjanus argentimaculatus*	mangrove red snapper	ISKNV (genogroup)
	Lutjanus johnii	John's snapper	ISKNV (genogroup)
	Lutjanus russelli	Russell's snapper	ISKNV (genogroup)
	Lutjanus sanguineus	humphead snapper	ISKNV (genogroup)
Monacanthidae	*Paramonacanthus japonicus*	hair-finned leatherjacket	ISKNV (genogroup)
Osphronemidae	*Macropodus opercularis*	paradise fish	ISKNV (genogroup)
	Trichogaster labiosa	thick lipped gourami	*Megalocytivirus* (excluding SDDV)
Osteoglossidae	*Arapaima gigas*	araipama	*Megalocytivirus* (excluding SDDV)
Pangasiidae	*Pangasianodon hypothalymus*	striped catfish	*Megalocytivirus* (excluding SDDV)
Polynemidae	*Eleutheronema tetradactylum*	fourfinger threadfin	ISKNV (genogroup)
Pomacanthidae	*Pomacanthus navarchus*	bluegirdled anglefish	*Megalocytivirus* (excluding SDDV)
Sciaenidae	*Dendrophysa russelii*	goatee croaker	ISKNV (genogroup)
	Otolithes ruber	tigertooth croaker	ISKNV (genogroup)
	Pennahia argentata	silver croaker	ISKNV (genogroup)
	Pennahia macrocephalus	big-head pennah croaker	ISKNV (genogroup)
Scombridae	*Scomberomorus commerson*	narrow-barred Spanish mackerel	ISKNV (genogroup)
Serranidae	*Cephalopholis boenak*	chocolate hind	ISKNV (genogroup)
	Epinephelus bleekeri	duskytail grouper	ISKNV (genogroup)
	Epinephelus chlorostigma	brownspotted grouper	ISKNV (genogroup)
	Epinephelus fasciatomaculosus	rock grouper	ISKNV (genogroup)
	Epinephelus lanceolatus	giant grouper	RSIV (genogroup)
	Epinephelus merra	honeycomb grouper	ISKNV (genogroup)
Serrasalmidae	*Pygocentrus nattereri*	red piranha	ISKNV (genogroup)
	Serrasalmus gibbus	no common name	*Megalocytivirus* (excluding SDDV)
Siganidae	*Siganus canaliculatus*	rabbitfish	ISKNV (genogroup)
Stromateidae	*Pampus argenteus*	silver pomfret	ISKNV (genogroup)
Synodontidae	*Saurida elongata*	slender lizardfish	ISKNV (genogroup)
Syphyraenidae	*Sphyraena forsteri*	bigeye barracuda	ISKNV (genogroup)
Terapontidae	*Pelates quadrilineatus*	fourline grunter	ISKNV (genogroup)
	Terapon jarbua	Jarbua terapon	ISKNV (genogroup)
Tetraodontidae	*Lagocephalus spadiceus*	half-smooth golden pufferfish	ISKNV (genogroup)

Family	Scientific name	Common name	Assessed for:
	Takifugu alboplumbeus	no common name	ISKNV (genogroup)
	Takifugu xanthopterus	yellowfin pufferfish	ISKNV (genogroup)

4. Assessments

Host species were determined to be susceptible based on the combination of assessment outcomes as outlined in Article 1.5.7.

Table 4 below describes the different scores and outcomes of the assessments undertaken by the *ad hoc* Group.

Table 4: Scores and Outcome of assessments

Score	Outcome
1	Species assessed as susceptible (as described in Article 1.5.7.). Infection with red seabream iridovirus (genogroup): These species were proposed for inclusion in Article 10.8.2. of Chapter 10.8., Infection with red seabream iridovirus, of the *Aquatic Code* and Section 2.2.1. of Chapter 2.3.7., Infection with red seabream iridovirus, of the *Aquatic Manual*. Infection with infectious spleen and kidney necrosis virus (genogroup): These species were proposed to the Commission for decision. Infection with turbot reddish body iridovirus (genogroup): These species were proposed to the Commission for decision. Infection with *Megalocytivirus* (excluding SDDV): These species were proposed to the Commission for decision.
2	Species assessed as having incomplete evidence for susceptibility (as described in Article 1.5.8.). Infection with red seabream iridovirus (genogroup): These species for infection with red seabream iridovirus were proposed for inclusion in Section 2.2.2., Species with incomplete evidence for susceptibility of Chapter 2.3.7., Infection with red seabream iridovirus, of the *Aquatic Manual*. Infection with infectious spleen and kidney necrosis virus (genogroup): These species were proposed to the Commission for decision. Infection with turbot reddish body iridovirus (genogroup): These species were proposed to the Commission for decision. Infection with *Megalocytivirus* (excluding SDDV): These species were proposed to the Commission for decision.
3	Species assessed as not meeting the criteria or for which there was unresolved or conflicting information. However, this category also included species where pathogen-specific positive PCR results had been reported, but an active infection had not been demonstrated. These species were proposed as follows. Infection with red seabream iridovirus (genogroup): These species were proposed for inclusion in a separate paragraph in Section 2.2.2, Species with incomplete evidence for susceptibility, of Chapter 2.3.7. of the *Aquatic Manual*. Infection with infectious spleen and kidney necrosis virus (genogroup): These species were proposed to the Commission for decision. Infection with turbot reddish body iridovirus (genogroup): These species were proposed to the Commission for decision. Infection with *Megalocytivirus* (excluding SDDV): These species were proposed to the Commission for decision.
4	Species assessed as non-susceptible.

Score	Outcome
NS	Species not scored due to insufficient or irrelevant information.

Assessments for host susceptibility to infection with red seabream iridovirus (genogroup), infectious spleen and kidney necrosis virus (genogroup), turbot reddish body iridovirus (genogroup) and *Megalocytivirus* (excluding SDDV) together with the outcomes and relevant references are shown in the tables below.

Table 5: Assessments for RSIV genogroup

Family	Scientific name	Common name	Stage 1: Route of transmission	Stage 2: Pathogen identification	Stage 3: Evidence of infection				Outcome	References
					A	B	C	D		
Score 1										
Butidae	*Oxyeleotris marmorata*	marble goby	N	PCR and sequence analysis	ND	ND	Y	Y	1	Chen *et al.*, 2013
			N	PCR and sequence analysis	ND	ND	ND	Y	2	Huang *et al.*, 2011
Carangidae	*Seriola quinqueradiata*	Japanese amberjack	N	qPCR, PCR and sequence analysis	Y	ND	ND	Y	1	Kawato *et al.*, 2021a
			E	PCR and sequence analysis[4]	ND	Y	Y	Y	1	Ito *et al.*, 2014
			N and E	PCR and sequence analysis[4]	Y	Y	Y	Y	1	Ito *et al.*, 2013
	Trachinotus carolinus	Florida pompano	N	PCR, sequence and phylogenetic analyses	ND	ND	Y	Y	1	Koda *et al.*, 2019
			N	PCR and sequence analysis	ND	ND	Y	Y	1	Koda *et al.*, 2018
			N	PCR and sequence analysis	Y	ND	Y	Y	1	Lopez-Porras *et al.*, 2018
Centrarchidae	*Lepomis macrochirus*	bluegill	N	PCR and sequence analysis	Y	Y	Y	Y	1	Liu *et al.*, 2019
Latidae	*Lates calcarifer*	barramundi	N	PCR and sequence analysis	Y	ND	Y	Y	1	Sumithra *et al.*, 2022
			N	PCR and sequence analysis	ND	ND	Y	Y	2	Wang *et al.*, 2009
Oplegnathidae	*Oplegnathus fasciatus*	barred knifejaw	N	PCR and sequence analysis[5]	ND	ND	Y	Y	1	Jeong *et al.*, 2008b
			N	PCR and sequence analysis	ND	Y	Y	ND	1	Do *et al.*, 2004
			N	PCR and sequence analysis	ND	ND	Y	Y	1	Jeong *et al.*, 2003

Family	Scientific name	Common name	Stage 1: Route of transmission	Stage 2: Pathogen identification	Stage 3: Evidence of infection				Outcome	References
					A	B	C	D		
	Oplegnathus punctatus	spotted knifejaw	N	PCR and sequence analysis	Y	Y	ND	Y	1[6]	Dong *et al.*, 2010
Osphronemidae	*Macropodus opercularis*	paradise fish	N	PCR and sequence analysis	Y	Y	Y	Y	1	Liu *et al.*, 2019
Paralichthyidae	*Paralichthys olivaceus*	bastard halibut	N	PCR and sequence analysis	Y	Y	Y	Y	1	Jung *et al.*, 2016
Sciaenidae	*Larimichthys crocea*	large yellow croaker	N	PCR and sequence analysis	Y	Y	Y	Y	1	Chen *et al.*, 2003
Sinipercidae	*Siniperca chuatsi*	Mandarin fish	N	PCR and sequence analysis	ND	Y	Y	Y	1	Dong *et al.*, 2013
Sparidae	*Acanthopagrus schlegelii*	blackhead seabream	N	PCR and sequence analysis	ND	ND	Y	Y	1	Jeong *et al.,* 2003
	Pagrus major	red sea bream	N	PCR and sequence analysis	ND	ND	ND	ND	1	Kurita *et al.*, 2002
			N	PCR, sequence analysis and qPCR	Y	Y	ND	Y	1	Kawato *et al.*, 2021b
			N	VI[7]	Y	Y	Y	Y	1	Inouye *et al.*, 1992
Synanceiidae	*Inimicus japonicus*[8]		N	qPCR, PCR and sequence analysis	Y	Y	Y	Y	1	Kawato *et al.* 2017c
Score 2										
Lateolabracidae	*Lateolabrax japonicus*	Japanese seabass	N	PCR and sequence analysis	ND	ND	ND	Y	2	Do *et al.*, 2005
			N	IFAT	Y	ND	Y	Y	NS	Matsuoka *et al.*, 1996
Osphronemidae	*Trichopodus leerii*	pearl gourami	N and E	PCR and sequence analysis[5]	ND	ND	Y	Y	2[9]	Jeong *et al.*, 2008b
Sebastidae	*Sebastes schlegeli*	rockfish	N	PCR and sequence analysis	ND	ND	Y	Y	2	Do *et al.*, 2005
			N	PCR and sequence analysis	ND	ND	ND	Y	3	Kim *et al.*, 2002
Sparidae	*Rhabdosargus sarba*	goldlined seabream	N	PCR and sequence analysis	ND	ND	Y	Y	2[9]	Wang *et al.,* 2009
Stromateidae	*Pampus argenteus*	silver pomfret	N	PCR and sequence analysis	Y	ND	Y	Y	2	Ni *et al.*, 2021

Family	Scientific name	Common name	Stage 1: Route of transmission	Stage 2: Pathogen identification	Stage 3: Evidence of infection				Outcome	References
					A	B	C	D		
Score 3										
Leiognathidae	*Leiognathus equulus*	common ponyfish	N	PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2009
Serranidae	*Epinephelus lanceolatus*	giant grouper	N	PCR and sequence analysis	ND	ND	ND	Y	3	Huang *et al.*, 2011
			N	PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2009
Not scored (NS)										
Moronidae	*Morone saxatilis x Morone chrysops*	striped sea bass x white bass hybrid	N	PCR and sequence analysis	ND	ND	ND	ND	NS	Kurita & Nakajima, 2012
Serranidae	*Cromileptes altivel*	humpback grouper	EI	PCR	Y	Y	Y	Y	NS	Mahardika *et al.*, 2004
	Epinephelus tauvina	greasy grouper	N	PCR and sequence analysis	ND	Y	Y	Y	NS	Sudthongkong *et al.,* 2002a
Sparidae	*Acanthopagrus latus*	yellowfin sea bream	N	PCR and sequence analysis	ND	ND	ND	ND	NS	Kurita & Nakajima, 2012

[4] Stock isolate (RSIV KagYT-96) has been sequenced and identified as RSIV in Kawato *et al.*, 2020.

[5] The sequence analysis is by extension as it relies on previous sequence analysis (Jeong *et al.*, 2003) of the isolate used in the challenge study.

[6] The WOAH Reference Laboratory for RSIV has isolated RSIV genogroup from spotted knifejaw giving this unique paper a second line of evidence.

[7] The full genome of the virus isolate (Ehime-1) from Inouye *et al.*, 1992 was sequenced in Kurita *et al.*, 2002.

[8] No common name was available on FAOTerm or www.fishbase.se.

[9] Only one study was available for assessment. The evidence provided was assessed by the *ad hoc* Group as having met the criteria for susceptibility and was scored as a '1'. However, the *ad hoc* Group was unable to find any additional studies or corroborative evidence within the study, and determined that this study alone was not sufficient for a final assessment of a '1'. As a result the *ad hoc* Group assessed this species as an overall score of a '2'.

Table 6: Assessments for ISKNV genogroup

Family	Scientific name	Common name	Stage 1: Route of transmission	Stage 2: Pathogen identification	Stage 3: Evidence of infection				Outcome	References
					A	B	C	D		
Score 1										
Apogonidae	*Pterapogon kauderni*	Banggai cardinalfish	N	PCR and sequence analysis	Y	ND	Y	Y	1	Weber *et al.*, 2009
Butidae	*Oxyeleotris marmorata*	marble goby	N	PCR and sequence analysis	Y	Y	Y	Y	1	Wang *et al.*, 2011
Cichlidae	*Astronotus ocellatus*	Oscar	N	PCR and sequence analysis	ND	ND	Y	Y	1	Baoprasertkul & Kaenchan, 2019
			N	PCR and sequence analysis	Y	ND	ND	Y	1	Go *et al.*, 2016
	Etroplus suratensis	pearlspot	N	PCR and sequence analysis	Y	Y	Y	Y	1	Swaminathan *et al.*, 2022
	Oreochromis niloticus	Nile tilapia	N	PCR, sequence and phylogenetic analyses	Y	ND	Y	Y	1	Figueiredo *et al.*, 2021
			N	PCR and sequence analysis	Y	Y	Y	Y	1	Ramírez-Paredes *et al.*, 2020
			N	PCR and sequence analysis	Y	ND	Y	Y	1	Subramaniam *et al.*, 2016
	Pterophyllum scalare	freshwater angelfish	N	PCR and sequence analysis	ND	Y	ND	Y	1	Kawato *et al.*, 2020
			N	PCR and sequence analysis	ND	ND	ND	Y	2	Go *et al.*, 2016
Cyprinidae	*Epalzeorhynchos frenatum*	rainbow sharkminnow	N	PCR, sequence and phylogenetic analyses	ND	Y	Y	Y	1	Koda *et al.*, 2021
Danionidae	*Danio rerio*	zebrafish	N	PCR, sequence and phylogenetic analyses	Y	ND	Y	Y	1	Bermudez *et al.*, 2018
			N	PCR and sequence analysis	ND	ND	ND	Y	2	Subramaniam *et al.*, 2014

Family	Scientific name	Common name	Stage 1: Route of transmission	Stage 2: Pathogen identification	Stage 3: Evidence of infection				Outcome	References
					A	B	C	D		
Ephippidae	*Platax orbicularis*	orbiculate batfish	N	PCR and sequence analysis	Y	ND	Y	Y	1	Sriwanayos *et al*., 2013
Latidae	*Lates calcarifer*	barramundi	N	PCR and sequence analysis	ND	Y	Y	Y	1	Kerddee *et al*., 2021
			N	PCR, sequence and phylogenetic analyses	Y	Y	Y	Y	1	Zhu *et al*., 2021
Nothobranchiidae	*Aphyosemion gardneri*	steel blue killifish	N	PCR and sequence analysis	ND	ND	Y	Y	1	Nolan *et al*., 2015
Oplegnathidae	*Oplegnathus fasciatus*	barred knifejaw	N	PCR and sequence analysis	ND	ND	Y	Y	1	Jeong *et al*., 2008b
			N	PCR and sequence analysis	ND	ND	ND	Y	2	Song *et al*., 2008
	Oplegnathus punctatus	spotted knifejaw	N	PCR and sequence analysis	ND	Y	Y	Y	1	Huang *et al*., 2021
Osphronemidae	*Osphronemus goramy*	giant gourami	N	PCR and sequence analysis	Y	Y	Y	Y	1	Swaminathan *et al*., 2021
	Trichogaster lalius	dwarf gourami	N	PCR and sequence analysis	Y	Y	ND	ND	1	Rimmer *et al.,* 2017
			N	PCR and sequence analysis	ND	Y	Y	Y	1	Go & Whittington, 2006
			N	PCR and sequence analysis	ND	Y	Y	Y	1	Sudthongkong *et al*., 2002b
	Trichopodus leerii	pearl gourami	N	PCR and sequence analysis	ND	ND	Y	Y	1	Jeong *et al*., 2008a
			N	PCR and sequence analysis	ND	ND	Y	Y	1	Jeong *et al*., 2008b
	Trichopodus microlepis	moonlight gourami	N	PCR and sequence analysis	ND	ND	Y	Y	1	Jeong *et al*., 2008a
Percichthyidae	*Maccullochella peelii*	Murray cod	E	PCR and sequence analysis	Y	ND	Y	Y	1	Go & Whittington, 2006
			N	PCR and sequence analysis	Y	ND	Y	Y	1	Go *et al*., 2006

Family	Scientific name	Common name	Stage 1: Route of transmission	Stage 2: Pathogen identification	Stage 3: Evidence of infection				Outcome	References
					A	B	C	D		
Poeciliidae	*Poecilia latipinna*	sailfin molly	N	Nested PCR and sequence analysis	ND	ND	Y	Y	1	Nolan *et al.,* 2015
			N	Nested PCR, qPCR and sequence analysis	ND	ND	Y	Y	1[10]	Baoprasertkul & Kaenchan, 2019
	Xiphophorus hellerii	green swordtail	N	PCR and sequence analysis	ND	ND	ND	Y	2	Zainathan *et al*., 2017
			N	Nested PCR and sequence analysis	ND	ND	Y	Y	1	Nolan *et al.,* 2015
			N	PCR and sequence analysis	ND	ND	ND	Y	2	Subramaniam *et al*., 2014
	Xiphophorus maculatus	southern platyfish	N	Nested PCR, qPCR and sequence analysis	ND	ND	Y	Y	1	Baoprasertkul & Kaenchan, 2019
			N	PCR and sequence analysis	Y	ND	Y	Y	1	Jung-Schroers *et al*., 2016
			N	Nested PCR and sequence analysis	ND	ND	Y	Y	1	Nolan *et al.,* 2015
Sciaenidae	*Sciaenops ocellatus*	red drum	N	PCR and sequence analysis	Y	ND	Y	Y	1	Oseko *et al*., 2004
			N	PCR and sequence analysis	Y	ND	Y	Y	1	Weng *et al*., 2002
Serranidae	*Epinephelus fuscoguttatus*♀ ×♂*E. lanceolatus*	pearl gentian grouper (hybrids)	N	PCR and sequence analysis	Y	Y	Y	Y	1	Huang *et al*., 2020
Sinipercidae	*Siniperca chuatsi*	Mandarin fish	N	PCR and sequence analysis	Y	ND	Y	Y	1	Tanaka *et al*., 2014
			N	sequence analysis[11]	Y	Y	Y	Y	1	He *et al*., 2001
Score 2										
Cichlidae	*Mikrogeophagus ramirezi*	ram cichlid	N	PCR and sequence analysis	ND	ND	ND	Y	2	Subramaniam *et al.,* 2014
			N	PCR and sequence analysis	ND	ND	ND	Y	2	Zainathan *et al*., 2019

Family	Scientific name	Common name	Stage 1: Route of transmission	Stage 2: Pathogen identification	Stage 3: Evidence of infection				Outcome	References
					A	B	C	D		
	Pterophyllum altum	deep angelfish	N	PCR and sequence analysis	Y	Y	Y	Y	2[12]	Jung-Schroers *et al.*, 2016
Helostomatidae	*Helostoma temminckii*	kissing gourami	N	PCR and sequence analysis	ND	ND	ND	Y	2	Rimmer *et al.*, 2015
Osphronemidae	*Trichopodus trichopterus*	three spot gourami	N	PCR and sequence analysis	ND	ND	ND	Y	2	Zainathan *et al.*, 2017
			N	PCR and sequence analysis	ND	ND	ND	Y	3	Rimmer *et al.*, 2015
Poeciliidae	*Poecilia sphenops*	molly	N	PCR and sequence analysis	ND	ND	ND	Y	2	Zainathan *et al.*, 2017
			N	PCR	ND	ND	ND	Y	3	Rimmer *et al.*, 2015
	Xiphophorus variatus	variable platyfish	N	Nested PCR, qPCR and sequence analysis	ND	ND	Y	Y	2[13]	Baoprasertkul & Kaenchan, 2019
Sparidae	*Rhabdosargus sarba*	goldlined seabream	N	PCR and sequence analysis	ND	ND	ND	Y	2	Huang *et al.,* 2011
Score 3										
Carangidae	*Alepes djedaba*	shrimp scad	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Caranx sexfasciatus	bigeye trevally	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Decapterus maruadsi	Japanese scad	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Scomberoides lysan	doublespotted queenfish	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Scomberoides tala	barred queenfish	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Selaroides leptolepis	yellowstripe scad	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
Clupeidae	*Konosirus punctatus*	dotted gizzard shad	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
Cynoglossidae	*Cynoglossus sinicus*[14]		N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007

Family	Scientific name	Common name	Stage 1: Route of transmission	Stage 2: Pathogen identification	Stage 3: Evidence of infection				Outcome	References
					A	B	C	D		
Cyprinidae	*Carassius auratus*	goldfish	N	PCR and sequence analysis	ND	ND	ND	Y	3[15]	de Lucca Maganha *et al.*, 2018
	Cyprinus carpio	common carp	N	PCR and sequence analysis	ND	ND	ND	Y	3[15]	de Lucca Maganha *et al.*, 2018
Danionidae	*Danio albolineatus*	pearl danio	N	PCR and sequence analysis	ND	ND	ND	Y	3[15]	de Lucca Maganha *et al.*, 2018
Engraulidae	*Thryssa mystax*	moustached thryssa	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
Haemulidae	*Plectorhinchus pictus*	trout sweetlips	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
Leiognathidae	*Deveximentum insidiator*	pugnose ponyfish	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Leiognathus brevirostris	shortnose ponyfish	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Photopectoralis bindus	orangefin ponyfish	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
Lutjanidae	*Lutjanus argentimaculatus*	mangrove red snapper	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Lutjanus johnii	John's snapper	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Lutjanus russelli	Russell's snapper	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Lutjanus sanguineus	humphead snapper	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
Monacanthidae	*Paramonacanthus japonicus*	hair-finned leatherjacket	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
Osphronemidae	*Macropodus opercularis*	paradise fish	N	PCR and sequence analysis	ND	ND	ND	Y	3[15]	de Lucca Maganha *et al.*, 2018
			N	PCR and sequence analysis	ND	ND	ND	Y	3	Kim *et al.*, 2010
Polynemidae	*Eleutheronema tetradactylum*	fourfinger threadfin	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
Sciaenidae	*Dendrophysa russelii*	goatee croaker	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007

Family	Scientific name	Common name	Stage 1: Route of transmission	Stage 2: Pathogen identification	Stage 3: Evidence of infection				Outcome	References
					A	B	C	D		
	Otolithes ruber	tigertooth croaker	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Pennahia argentata	silver croaker	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Pennahia macrocephalus	big-head pennah croaker	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
Scombridae	*Scomberomorus commerson*	narrow-barred Spanish mackerel	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
Serranidae	*Cephalopholis boenak*	chocolate hind	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Epinephelus bleekeri	duskytail grouper	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Epinephelus chlorostigma	brownspotted grouper	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Epinephelus fasciatomaculosus	rock grouper	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Epinephelus merra	honeycomb grouper	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
Serrasalmidae	*Pygocentrus nattereri*	red piranha	N	PCR and sequence analysis	ND	ND	ND	Y	3[15]	de Lucca Maganha *et al.*, 2018
Siganidae	*Siganus canaliculatus*	rabbitfish	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
Stromateidae	*Pampus argenteus*	silver pomfret	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
Synodontidae	*Saurida elongata*	slender lizardfish	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
Syphyraenidae	*Sphyraena forsteri*	bigeye barracuda	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
Terapontidae	*Pelates quadrilineatus*	fourline grunter	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Terapon jarbua	Jarbua terapon	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
Tetraodontidae	*Lagocephalus spadiceus*	Half-smooth golden pufferfish	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007

Family	Scientific name	Common name	Stage 1: Route of transmission	Stage 2: Pathogen identification	Stage 3: Evidence of infection				Outcome	References
					A	B	C	D		
	Takifugu alboplumbeus[14]		N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
	Takifugu xanthopterus	yellowfin pufferfish	N	Nested PCR and sequence analysis	ND	ND	ND	Y	3	Wang *et al.*, 2007
Not scored (NS)										
Centrarchidae	*Micropterus salmoides*	largemouth bass	EI	N	ND	Y	Y	ND	NS	He *et al*., 2002
Xencyprididae	*Ctenopharyngodon idella*	grass carp	EI	N	ND	ND	ND	ND	NS	He *et al.*, 2002

[10] Pathogen identification was not completed to the level of genogroup for this species. The *ad hoc* Group included this study as supporting evidence.

[11] PCR was not performed in this study. The authors cloned DNA fragments for sequencing.

[12] The assessed study included two different species of angelfish and the molecular analysis was performed on pool tissues that included gill tissue. As a result the *ad hoc* Group determined the evidence was not sufficient for a final assessment of '1' and assessed this species as an overall score of '2'.

[13] Only one study was available for assessment and only one fish within that study showed clinical signs. The *ad hoc* Group determined that the evidence from the single fish was not sufficient for a final assessment of a '1'. As a result the *ad hoc* Group assessed this species as an overall score of a '2'.

[14] No common name was available on FAOTerm or www.fishbase.se.

[15] The findings from this study were obtained from wild surveys of multiple fish species. The *ad hoc* Group had concerns about possible cross contamination resulting from this sampling methodology. As a result the *ad hoc* Group assessed the evidence provided from this study as a score of '3'.

Table 7: Assessments for TRBIV genogroup

Family	Scientific name	Common name	Stage 1: Route of transmission	Stage 2: Pathogen identification	Stage 3: Evidence of infection				Outcome	References
					A	B	C	D		
Score 1										
Cichlidae	*Astronotus ocellatus*	Oscar	N	PCR and sequence analysis	ND	Y	Y	Y	1	Koda *et al*., 2018
Latidae	*Lates calcarifer*	barramundi	N	PCR and sequence analysis	Y	ND	Y	Y	1	Tsai *et al*., 2020
Osphronemidae	*Trichogaster lalius*	dwarf gourami	N	PCR and sequence analysis	Y	ND	Y	Y	1	Go *et al*., 2016

Family	Scientific name	Common name	Stage 1: Route of transmission	Stage 2: Pathogen identification	Stage 3: Evidence of infection				Outcome	References
					A	B	C	D		
			N	PCR and sequence analysis	Y	Y	ND	ND	1	Rimmer *et al.,* 2015
Paralichthyidae	*Paralichthys olivaceus*	bastard halibut	N	PCR and sequence analysis	Y	Y	Y	Y	1	Jung *et al*., 2016
Scophthalmidae	*Scophthalmus maximus*	Turbot	N	PCR and sequence analysis[16]	ND	ND	Y	Y	1	Shi *et al*., 2010
			N	N[17]	Y	ND	Y	Y	NS	Shi *et al*., 2004
Score 2										
Cichlidae	*Cleithracara maronii*	keyhold cichlid	N	PCR and sequence analysis	ND	Y	ND	ND	2	Koda *et al*., 2018
	Pterophyllum scalare	freshwater angelfish	N	PCR, sequence and phylogenetic analyses	ND	ND	Y	Y	1[18]	Go *et al*., 2016
Olegnathidae	*Oplegnathus fasciatus*	barred knifejaw	N	PCR and sequence analysis	ND	ND	ND	Y	2	Song *et al*., 2008
Osphronemidae	*Trichopodus trichopterus*	three spot gourami	N	PCR and sequence analysis	ND	Y	ND	ND	2	Koda *et al.,* 2018

[16] Virus isolated later sequenced in Shi et *al.*, 2010.

[17] Complete genome virus isolated by Shi *et al.*, 2004.

[18] Only one study was available for assessment and only one fish within that study showed clinical signs. The *ad hoc* Group determined that the evidence from the single fish was not sufficient for a final assessment of a '1'. As a result, the *ad hoc* Group assessed this species as an overall score of a '2'.

Table 8: Assessments for *Megalocytivirus* (excluding SDDV)

Family	Scientific name	Common name	Stage 1: Route of transmission	Stage 2: Pathogen identification	Stage 3: Evidence of infection				Outcome	References
					A	B	C	D		
Score 1										
Carangidae	*Pseudocaranx dentex*	white trevally	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
			N	IFAT	Y	ND	Y	Y	1	Matsuoka *et al*., 1996
			N	IFAT	Y	ND	Y	Y	1	Nakajima *et al*., 1995b
	Seriola dumerili	greater amberjack	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002

Family	Scientific name	Common name	Stage 1: Route of transmission	Stage 2: Pathogen identification	Stage 3: Evidence of infection				Outcome	References
					A	B	C	D		
			N	IFAT	Y	ND	Y	Y	1	Matsuoka *et al.*, 1996
			N	IFAT	Y	ND	Y	Y	1	Nakajima *et al.*, 1995b
	Seriola lalandi	goldstripe amberjack	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
			N	IFAT	Y	ND	Y	Y	1	Matsuoka *et al.*, 1996
			N	IFAT	Y	ND	Y	Y	1	Nakajima *et al.*, 1995b
	Seriola quinqueradiata x Seriola lalandi	Buri-hira hybrid	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
	Trachinotus blochii	snubnose pompano	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
			N	IFAT	Y	ND	Y	Y	1	Matsuoka *et al.*, 1996
	Trachurus japonicus	Japanese jack mackerel	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
			N	IFAT	Y	ND	Y	Y	1	Matsuoka *et al.*, 1996
Girellidae	*Girella punctata*	largescale blackfish	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
			N	IFAT	Y	ND	Y	Y	1	Matsuoka *et al.*, 1996
Haemulidae	*Parapristipoma trilineatum*	chicken grunt	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
			N	IFAT	Y	ND	Y	Y	1	Matsuoka *et al.*, 1996
	Plectorhinchus cinctus	crescent sweetlips	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
Lethrinidae	*Lethrinus haematopterus*	Chinese emperor	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
	Lethrinus nebulosus	spangled emperor	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
Mugilidae	*Mugil cephalus*	Flathead grey mullet	N	PCR, TEM and IFAT	Y	Y	Y	Y	1	Gibson-Kueh *et al.*, 2004
Paralichthyidae	*Paralichthys olivaceus*	bastard halibut	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
			N	IFAT	Y	ND	Y	Y	1	Matsuoka *et al.*, 1996
Pleuronectidae	*Verasper variegatus*	spotted halibut	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
Poeciliidae	*Poecilia reticulata*	guppy	N	Nested PCR, qPCR	ND	ND	Y	Y	1[19]	Baoprasertkul & Kaenchan, 2019
			N	PCR and sequence analysis	ND	ND	ND	Y	2[20]	Zainathan *et al.*, 2019
			N	PCR and sequence analysis	ND	ND	ND	Y	3[20]	de Lucca Maganha *et al.*, 2018

Family	Scientific name	Common name	Stage 1: Route of transmission	Stage 2: Pathogen identification	Stage 3: Evidence of infection				Outcome	References
					A	B	C	D		
Procatopodidae	*Poropanchax normani*	Norman's lampeye	N	PCR and sequence analysis	Y	Y	Y	Y	1	Sudthongkong *et al.,* 2002b
Rachycentridae	*Rachycentron canadum*	cobia	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
Scombridae	*Scomber japonicus*	chub mackerel	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
	Scomberomorus niphonius	Japanese Spanish mackerel	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
	Thunnus orientalis[21]	Pacific bluefin tuna	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
			N	IFAT	Y	Y	ND	ND	1	Nakajima *et al*., 1998c
			N	IFAT	Y	ND	Y	Y	1	Matsuoka *et al*., 1996
Serranidae	*Epinephelus akaara*	Hong Kong grouper	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
			N	IFAT	Y	ND	Y	Y	1	Matsuoka *et al*., 1996
	Epinephelus awoara	yellow grouper	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
			N	IFAT	Y	ND	Y	Y	1	Matsuoka *et al*., 1996
	Epinephelus bruneus	longtooth grouper	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
	Epinephelus coioides	orange-spotted grouper	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
			N	PCR and sequence analysis	ND	Y	Y	ND	2^{22}	Ma *et al*., 2012
			N	PCR and sequence analysis	ND	ND	ND	Y	2^{20}	Huang *et al.,* 2011
			N and E	PCR and sequence analysis	ND	ND	ND	Y	2^{22}	Lu *et al.,* 2005
	Epinephelus fuscoguttatus	brown-marbled grouper	N	PCR and IFAT	Y	Y	Y	Y	1	Gibson-Kueh *et al*., 2004
	Epinephelus malabaricus	Malabar grouper	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
			N	PCR	Y	Y	Y	Y	1	Danayadol *et al*., 1997
	Epinephelus septemfasciatus	convict grouper	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
			N	IFAT	Y	ND	Y	Y	1	Matsuoka *et al*., 1996
Sparidae	*Dentex tumifrons*[23]	yellowback seabream	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002
			N	IFAT	Y	ND	Y	Y	1	Matsuoka *et al.,* 1996
			N	IFAT	Y	ND	Y	Y	1	Nakajima *et al*., 1995b
Tetraodontidae	*Takifugu rubripes*	tiger pufferfish	N	IFAT	Y	ND	Y	Y	1	Kawakami & Nakajima, 2002

Family	Scientific name	Common name	Stage 1: Route of transmission	Stage 2: Pathogen identification	Stage 3: Evidence of infection				Outcome	References
					A	B	C	D		
			N	IFAT	Y	ND	Y	Y	1	Matsuoka *et al.*, 1996
			N	IFAT	Y	ND	Y	Y	1	Nakajima *et al.*, 1995b
Score 2										
Osphronemidae	*Betta splendens*	siamese fighting fish	N	PCR and sequence analysis	ND	ND	Y	Y	2[24]	Baoprasertkul & Kaenchan, 2019
Poeciliidae	*Poecilia velifera*	sail-fin molly	N	PCR and sequence analysis	ND	ND	Y	Y	2[24]	Baoprasertkul & Kaenchan, 2019
Score 3										
Characidae	*Moenkhausia costae*	tetra fortune	N	PCR	ND	ND	ND	Y	3	de Lucca Maganha *et al.*, 2018
Cobitidae	*Misgurnus anguillicaudatus*	pond loach	N	PCR	ND	ND	ND	Y	3	de Lucca Maganha *et al.*, 2018
Hemiodontidae	*Hemiodus gracilis*[25]		N	PCR	ND	ND	ND	Y	3	de Lucca Maganha *et al.*, 2018
Loricariidae	*Hypostomus plecostomus*	suckermouth catfish	N	PCR	ND	ND	ND	Y	3	de Lucca Maganha *et al.*, 2018
Osphronemidae	*Trichogaster labiosa*	thick lipped gourami	N	PCR	ND	ND	ND	Y	3	Rimmer *et al.*, 2015
Osteoglossidae	*Arapaima gigas*	araipama	N	PCR	ND	ND	ND	Y	3	de Lucca Maganha *et al.*, 2018
Pangasiidae	*Pangasianodon hypothalymus*	striped catfish	N	PCR	ND	ND	ND	Y	3	de Lucca Maganha *et al.*, 2018
Pomacanthidae	*Pomacanthus navarchus*	bluegirdled anglefish	N	PCR	ND	ND	ND	Y	3	de Lucca Maganha *et al.*, 2018
Serrasalmidae	*Serrasalmus gibbus*[25]		N	PCR	ND	ND	ND	Y	3	de Lucca Maganha *et al.*, 2018
Not scored (NS)										
Cichlidae	*Apistogramma cacatuoides*	cockatoo cichlid	N	N[26]	ND	ND	Y	ND	NS	Nolan *et al.*, 2015
Serranidae	*Cromileptes altivelis*	humpback grouper	EI	N[27]	Y	Y	Y	Y	NS	Mahardika *et al.*, 2004

[19] Pathogen identification was not completed to the level of genogroup for this species.

[20] This study was assessed at the level of the ISKNV genogroup but the *ad hoc* Group determined the evidence supported susceptibility at the level of infection with *Megalocytivirus*. As a result, the genogroup level assessments are included within the infection with *Megalocytivirus* assessment table.

[21] Prior to 1999 bluefin tuna (*Thunnus thynnus*) and Pacific bluefin tuna (*Thunnus orientalis*) were considered to be one species, collectively called bluefin tuna (*Thunnus thynnus*). Collette *et al*., 1999 suggested separation of the species and it is recognised as such in www.fishbase.se. Nakajima *et al*., 1998c and Matsuoka et al., 1996 were published prior to 1999, and Kawakami & Nakajima, 2002 was published when the species had just been proposed. Based on the sampling locations in these three studies, and the geographic distribution of Pacific bluefin tuna (*Thunnus orientalis*), the *ad hoc* Group determined the species included in these studies to be Pacific bluefin tuna (*Thunnus orientalis*).

[22] This study was assessed at the level of the RSIV genogroup but the *ad hoc* Group determined the evidence supported susceptibility at the level of infection with *Megalocytivirus*. As a result, the genogroup level assessments are included within the infection with *Megalocytivirus* assessment table.

[23] On www.fishbase.se, *Dentex tumifrons* (yellowback seabream) is the accepted taxonomy. *Evynnis japonica* (crimson seabream) is considered an invalid synonym.

[24] Only one study was available for assessment and only one fish within that study showed clinical signs. The *ad hoc* Group determined that the evidence from the single fish was not sufficient for a final assessment of a '1'. As a result, the *ad hoc* Group assessed this species as an overall score of a '2'.

[25] No common name was available on FAOTerm or www.fishbase.se.

[26] Histology alone was used for identification of the pathogen.

[27] Infected fish were PCR positive but sequence analysis was not undertaken to confirm virus identification.

Assessment Table Key

N: Natural infection

E: Experimental (non-invasive)

EI: Experimental invasive

Y: Demonstrates criterion is met

N: Criterion is not met

ND: Not determined

NS: Not scored

5. Naming convention for susceptible species

The scientific names of the species are in accordance with www.fishbase.se.

The common names of fish species are in accordance with FAOTERM (http://www.fao.org/faoterm/collection/faoterm/en/). Where the common fish name was not found in FAOTERM, the naming was done in accordance with https://www.fishbase.se.

6. General Comments

The *ad hoc* Group agreed to focus initially on studies published from 2000 onwards, when molecular testing was available. Papers published in earlier years were referred to when necessary to increase confidence of an assessment, when no recent paper was available for the assessment of a specific host species, or to assess susceptibility to infection with ISKNV species viruses (RSIV, ISKNV and TRBIV genogroups). When necessary to corroborate pathogen identification, the *ad hoc* Group:

a) contacted authors of the studies or Reference Laboratory experts to further describe pathogen identification methods, or

b) utilized molecular information from parallel or subsequent studies on the same source population.

The *ad hoc* Group agreed that while the ideal situation to categorize a fish species as susceptible was the presence of two papers with a score of '1', a single strong study scoring '1' was also sufficient to conclude susceptibility of a species in the absence of conflicting evidence. A study was considered strong if there were multiple fish examined and multiple lines of evidence (e.g. temporal or geographic separation, or different challenge experiments) within the study as well as no inconsistencies. Consequently, additional studies were still reviewed to check for any supporting or conflicting evidence. When additional papers were identified but the *ad hoc* Group did not feel that they were necessary to assess as the species had already been determined as susceptible by other studies, these studies were included in the list of references.

7. Listing of Susceptible species at a taxonomic ranking of Genus or Higher

The *ad hoc* Group completed the assessments of susceptible species but did not have sufficient time to determine if Article 1.5.9. was applicable for infection with *Megalocytivirus*. The *ad hoc* Group noted that no species were assessed as a '4' with evidence of non-susceptibility.

The *ad hoc* Group agreed to request guidance from the Aquatic Animals Commission for the review of listing of susceptible species at the taxonomic ranking of Genus or higher.

The *ad hoc* Group identified several studies where the species was only identified to the level of genus. In these cases, the *ad hoc* Group assessed the species to the level of genus in case this information was of assistance in the application of Article 1.5.9. This information is provided in Table 9 below.

Table 9: Infection with *Megalocytivirus* assessed for hosts that were identified only to the genus level

Family	Scientific name	Stage 1: Route of transmission	Stage 2: Pathogen identification	Stage 3: Evidence of infection				Outcome	Assessed for	References
				A	B	C	D			
Score 1										
Cichlidae	*Pterophyllum sp.*	N	Nested PCR, qPCR and sequence analysis	ND	ND	Y	Y	1	*Megalocytivirus* (excluding SDDV)	Baoprasertkul & Kaenchan, 2019
Lateolabracidae	*Lateolabrax sp.*	N	IFAT	Y	ND	Y	Y	1	*Megalocytivirus* (excluding SDDV)	Nakajima *et al.*, 1995b
		N	IFAT	Y	ND	Y	Y	1	*Megalocytivirus* (excluding SDDV)	Matsuoka *et al.*, 1996
		N	IFAT	Y	ND	Y	Y	1	*Megalocytivirus* (excluding SDDV)	Kawakami & Nakajima, 2002
		N	PCR and sequence analysis	Y	ND	Y	Y	1	RSIV (genogroup)	Jeong *et al.*, 2003
Serranidae	*Epinephelus sp.*	N	PCR and sequence analysis	ND	ND	Y	Y	1	*Megalocytivirus* (excluding SDDV)	Fusianto *et al.*, 2021
		N	PCR and sequence analysis	Y	Y	Y	Y	1	ISKNV (genogroup)	Chao *et al.*, 2004
Score 2										
Cichlidae	*Cichlasoma sp.*	N	Nested PCR, qPCR and sequence analysis	ND	ND	Y	Y	2[26]	*Megalocytivirus* (excluding SDDV)	Baoprasertkul & Kaenchan, 2019
	Symphysodon sp.	N	PCR	ND	ND	ND	Y	2[26]	*Megalocytivirus* (excluding SDDV)	Baoprasertkul & Kaenchan, 2019
Osphronemidae	*Trichogaster sp.*	N	PCR and sequence analysis	ND	ND	Y	Y	2[26]	*Megalocytivirus* (excluding SDDV)	Baoprasertkul & Kaenchan, 2019

[28] Only one study was available for assessment. The evidence provided was assessed by the *ad hoc* Group as having met the criteria for susceptibility and was scored as a '1'. However, the *ad hoc* Group was unable to find any additional studies or corroborative evidence within the study, and determined that this study alone was not sufficient for a final assessment of a '1'. As a result, the *ad hoc* Group assessed this species as an overall score of a '2'.

Assessment Table Key

N: Natural infection

E: Experimental (non-invasive)
EI: Experimental invasive
Y: Demonstrates criterion is met
N: Criterion is not met
ND: Not determined
NS: Not scored

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…/Annexes

Annex I. List of Participants

AD HOC GROUP ON SUSCEPTIBILITY OF FISH SPECIES TO INFECTION WITH WOAH LISTED DISEASES

April & November/December 2022

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WOAH *AD HOC* GROUP ON SUSCEPTIBILITY OF FISH SPECIES TO INFECTION WITH WOAH LISTED DISEASES

Paris, April & November/December 2022

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Background

Chapter 1.5. Criteria for listing species as susceptible to infection with a specific pathogenic agent, of the *Aquatic Code*, adopted in 2014, provides criteria for determining which host species are listed as susceptible in Article X.X.2. of each disease-specific chapter in the *Aquatic Code.* The list of susceptible species included in Article X.X.2. of all disease-specific chapters are being progressively reviewed against the criteria in Chapter 1.5.

The *ad hoc* Group on Susceptibility of fish species to infection with WOAH listed diseases has undertaken assessments for all of the WOAH listed diseases of fish, except for infection with red sea bream iridovirus, tilapia lake virus and infection with *Aphanomyces invadans* (epizootic ulcerative syndrome).

Purpose

The *ad hoc* Group on Susceptibility of fish species to infection with WOAH listed diseases will undertake assessments in accordance with criteria described in Chapter 1.5. for infection with red sea bream iridovirus.

Given that infectious spleen and kidney necrosis virus (ISKNV) is a closely related virus in the Genus *Megalocytivirus*, and that there is likely to be an overlap with RSIV in its epidemiology, pathology and diagnostic test methods, the *ad hoc* Group should also undertake assessments of susceptible species to ISKNV in its work.

Terms of Reference

1) Consider evidence required to satisfy the criteria in Chapter 1.5.

2) Review relevant literature documenting susceptibility of species for infection with red sea bream iridovirus and infection with infectious spleen and kidney necrosis virus.

3) Undertake assessments in accordance with Article 1.5.3. for potential host species in order to determine susceptibility to infection with red sea bream iridovirus and infection with infectious spleen and kidney necrosis virus.

4) Based on the assessments, propose a list of susceptible species for infection with red sea bream iridovirus and infection with infectious spleen and kidney necrosis virus in accordance with Article 1.5.7.

5) Based on the assessments, propose a list of species with incomplete evidence for susceptibility for infection with red sea bream iridovirus and infection with infectious spleen and kidney necrosis virus in accordance with Article 1.5.8.

Expected outputs of the *ad hoc* Group

1) Propose a list of susceptible species for inclusion in Article 10.8.2. in the *Aquatic Code.*

2) Propose a list of species with incomplete evidence for susceptibility for inclusion in Section 2.2.2. of the *Aquatic Manual.*

3) Propose a list of susceptible species and species with incomplete evidence for susceptibility for infection with ISKNV.

4) Draft a report for consideration by the Aquatic Animal Health Standards Commission at its September 2022 meeting.

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