

Appendix C: Evidence for changes to the risk species lists that were not included in the draft update

Host species	Pathogen	Reference	Pathway of infection	Identification	Replication and growth	Viable pathogen	Pathology	Location	Outcome of procedure
<i>Acanthopagrus schlegelii</i> and <i>A. latus</i>	Causative agent of RSIVD	OIE (2019)	n/a	n/a	n/a	n/a	n/a	n/a	1
<i>Leiognathus equulus</i>	Causative agent of RSIVD	Wang et al. (2009)	Natural	Yes – PCR followed by sequencing	nd	nd	Yes – Affected fish showed abnormal swimming behaviour and lethargy and cumulative mortality of 30-50% within one month	Yes – positive PCR from spleen tissue	2a
<i>Mugil cephalus</i>	Causative agent of RSIVD	OIE (2019)	n/a	n/a	n/a	n/a	n/a	n/a	1
<i>Rhabdosargus sarba</i>	Causative agent of RSIVD	Wang et al. (2009)	Natural	Yes – PCR followed by sequencing	nd	nd	Yes – Affected fish showed abnormal swimming behaviour and lethargy and cumulative mortality of 30-50% within one month	Yes – positive PCR from spleen tissue	2a
<i>Sciaenops ocellatus</i>	Causative agent of RSIVD	OIE (2019)	n/a	n/a	n/a	n/a	n/a	n/a	1

RSIVD Red sea bream iridoviral disease. **n/a** Not applicable as recognised as susceptible by the World Organisation for Animal Health (OIE). **nd** Not done in the scientific paper. **PCR** Polymerase Chain Reaction. **TEM** Transmission electron microscopy. **Outcome of procedure** The combination of evidence of susceptibility (1, 2a or 2b) that the evidence fulfills as outlined in the 'Procedure to determine finfish susceptibility to infection with a specific pathogenic agent' (Appendix A).

Note: A causative agent of RSIVD is defined here as either red sea bream iridovirus (RSIV) or infectious spleen and kidney necrosis virus (ISKNV) (OIE 2019).

References

OIE 2019, *Manual of diagnostic tests for aquatic animals* 2019, World Organisation for Animal Health (OIE), Paris, available at <http://www.oie.int/en/standard-setting/aquatic-manual/access-online/> accessed 25 June 2021.

Wang CS, Chao SY, Ku CC, Wen CM, Shih HH (2009) PCR amplification and sequence analysis of the major capsid protein gene of megalocytiviruses isolated in Taiwan. *Journal of Fish Diseases* 32 pp.543-550.