CHAPTER 2.2.3.

INFECTION WITH DECAPOD IRIDESCENT VIRUS 1

1. Scope

Infection with decapod iridescent virus 1 means infection with the pathogenic agent decapod iridescent virus 1 (DIV1), Genus *Decapodiridovirus*, Subfamily *Betairidovirinae*, Family *Iridoviridae*.

2. Disease information

2.1. Agent factors

2.1.1. Aetiological agent

DIV1 is the only species of the genus *Decapodiridovirus* assigned to the subfamily *Betairidovirinae*, family *Iridovirus* (ICTV, 2023). DIV1 is a 150–158 nm, enveloped icosahedral double-stranded DNA virus, with a linear genome of 165 kb composed of 34.6% G + C content and 170–178 putative open reading frames (ORFs) (Li *et al.*, 2017; Qiu *et al.*, 2017; 2018a; Xu *et al.*, 2016). Although *Cherax quadricarinatus* iridovirus (CQIV) (Xu *et al.*, 2016) and shrimp haemocyte iridescent virus (SHIV) (Qiu *et al.*, 2017) have been reported from the redclaw crayfish (*C. quadricarinatus*), and the whiteleg shrimp (*L. vannamei*), respectively, they are classified as different isolates (strains) within the DIV1 species.

2.1.2. Survival and stability in processed or stored samples

DIV1-infected cephalothoraxes are infectious after homogenisation, centrifugation, filtration and storage at –80°C (Qiu *et al.*, 2022a; Xu *et al.,* 2016).

2.1.3. Survival and stability outside the host

Not available.

For inactivation methods, see Section 2.4.5.

2.2. Host factors

2.2.1. Susceptible host species

Species that fulfil the criteria for listing as susceptible to infection with DIV1 according to chapter 1.5. *Aquatic Animal Health Code* (*Aquatic Code*) are:

Family	Scientific name	Common name
Cambaridae	*Procambarus clarkii*	red swamp crawfish
Palaemonidae	*Macrobrachium nipponense*	Oriental river prawn
	Macrobrachium rosenbergii	giant river prawn
	Palaemon carinicauda	ridgetail prawn
Parastacidae	*Cherax quadricarinatus*	red claw crayfish
Penaeidae	*Penaeus japonicus*	kuruma prawn
	Penaeus vannamei	whiteleg shrimp
Portunidae	*Portunus trituberculatus*	swimming crab

2.2.2. Species with incomplete evidence for susceptibility

Species for which there is incomplete evidence to fulfil the criteria for listing as susceptible to infection with DIV1 according to Chapter 1.5 of the *Aquatic Code* are:

Family	Scientific name	Common name
Penaeidae	*Penaeus chinensis*	fleshy prawn
	Penaeus monodon	giant tiger prawn

In addition, pathogen-specific positive polymerase chain reaction (PCR) results have been reported in the following species, but an active infection has not been demonstrated:

Family	Scientific name	Common name
Ampullariidae	*Pomacea canaliculata*	channeled applesnail
Palaemonidae	*Macrobrachium superbum*	no common name
Salticidae	*Plexippus paykulli*	no common name
Varunidae	*Helice tientsinensis*	no common name
	Hemigrapsus penicillatus	Japanese shore crab

2.2.3. Likelihood of infection by species, host life stage, population or sub-populations

All live stages are potentially susceptible to infection; DIV1 has been detected in post-larvae (PL), juvenile and sub-adult stages of shrimp (*Penaeus vannamei*, *P. chinensis*, *Exopalaemon carinicauda*, *Macrobrachium nipponense, M. rosenbergii*, crayfish [*Cherax quadricarinatus, Procambarus clarkia*] and crab [*Portunus trituberculatus*]) as natural infection or by experimental (*per os*) exposure (Chen *et al.*, 2019; Qiu *et al.*, 2018; 2019b; 2020b; 2021b; 2022b). Species with a positive DIV1 polymerase chain reaction (PCR) result, without an active infection include: *Penaeus monodon, Pomacea canaliculata, Macrobrachium superbum, Plexippus paykulli and Hemigrapsus penicillatus* (Qiu *et al.,* 2021; 2019a; 2022b; Srisala *et al.,* 2021).

2.2.4. Distribution of the pathogen in the host

The principal target tissues for DIV1 include lymphoid organ, haematopoietic tissues, as well as epithelia and haemocytes in gills, muscle, hepatopancreas, pereiopods, pleopods, uropods, and antenna (Qiu *et al.*, 2017; 2019a; 2021a; Sanguanrut *et al.*, 2021).

2.2.5. Aquatic animal reservoirs of infection

There is evidence that crustacean species may become reservoirs of DIV1 infection. DIV1 was detected in non-clinical adult wild giant tiger prawn (*P. monodon*) (Srisala *et al.*, 2021), wild crabs (*Helis tientsinensis, Hemigrapsus penicillatus*) in drainage ditches (Qiu *et al.*, 2022a), and *Macrobrachium superbum* in affected shrimp ponds (Qiu *et al.*, 2019a).

Subclinical infection has been reported in gazami crab, *Portunus trituberculatus*, which is widely distributed in environmental waters in Asia and could be a potential source of DIV1 infection on shrimp farms (Qiu *et al.,* 2022a).

2.2.6. Vectors

There are no confirmed vectors of DIV1.

2.3. Disease pattern

2.3.1. Mortality, morbidity and prevalence

Mortality can be high (80–100%) after a natural infection with DIV1 and mostly reported in the adult stage of shrimp (Liao *et al.,* 2022) and crayfish species, which has been confirmed by experimental infection through intramuscular injection or oral administration in *P. vannamei*, *Cherax quadricarinatus*, *Procambarus clarkii* and *Macrobrachium rosenbergii* (Qiu *et al.*, 2017; 2019a; Xu *et al.*, 2016). Experimental infection with DIV1 administered orally or by intramuscular injection resulted in 50% and 100% mortality, respectively, in the gazami crab (*Portunus trituberculatus*) (Qiu *et al.*, 2022a).

In pathogenicity studies of crustacean species, mortalities rose more rapidly in *Litopenaeus vannamei* compared with *Cherax quadricarinatus* or *Procambarus clarkii* in experimental infections (Xu *et al*., 2016).

The prevalence of DIV1 infection was 15.5, 15.2, and 50% in *P. vannamei, P. chinensis*, and *M. rosenbergii,* respectively, in a survey of shrimp farms tested in the period 2014 to 2016 (Qiu *et al*., 2017).

2.3.2. Clinical signs, including behavioural changes

Clinical signs in affected whiteleg shrimp (*P. vannamei*) are reddish bodies, white atrophied hepatopancreas, soft shells and empty stomachs and intestines, while giant freshwater shrimp (*M. rosenbergii*) showed a white discoloration at the base of the rostrum (white head) and hepatopancreatic atrophy (Qiu *et al.,* 2017; 2019a). However, these disease signs are not always distinctive because the course of the disease varies in affected animals.

2.3.3 Gross pathology

See Section 2.3.2.

2.3.4. Modes of transmission and life cycle

Based on experimental and natural infections, DIV1 is thought to be transmitted horizontally by oral routes and contaminated water (Qiu *et al*., 2017; 2019a; 2022a; Xu *et al*., 2016).

2.3.5. Environmental factors

Temperature and co-culture play an important role in DIV1 infection. DIV1 has been detected in shrimp and crayfish reared at 16–32°C, but not at temperatures above 32°C in a 2017–2018 survey (Qiu *et al.,* 2018b; 2019b; 2020b; 2021b 2022b). In shrimp farm management, polyculture with different species of crustaceans increases the risk of DIV1 infection in farmed shrimp due to cross-species transmission (Qiu *et al.,* 2019a; 2022a).

2.3.6. Geographical distribution

DIV1 has been reported in farmed shrimp and crayfish in the Asia-Pacific region (Qiu *et al*., 2017; Xu *et al*., 2016).

See WAHIS (https://wahis.woah.org/#/home) for recent information on distribution at the country level.

2.4. Biosecurity and disease control strategies

2.4.1. Vaccination

Not available.

2.4.2. Chemotherapy including blocking agents

Not available.

2.4.3. Immunostimulation

Not available.

2.4.4. Breeding resistant strains

Not available.

2.4.5. Inactivation methods

Not known.

2.4.6. Disinfection of eggs and larvae

Not available

2.4.7. General husbandry

Biosecurity practices can be used to reduce the risk of DIV1 infection. These includes PCR pre-screening of broodstock and larvae, PCR pre-screening of polychaetes and food organisms for broodstock and larvae, disinfection of rearing water and farming equipment, controlled stocking density, and avoidance of polyculture with different crustacean species.

Using an experimental protocol of 15-day thermal treatment at 36°C combined with 15-day restoration treatment at 28°C, *P. vannamei* infected by intramuscular injection of DIV1 showed no clinical signs, no DNA replication, no histopathology and *in-situ* DIG-labelling, loop-mediated DNA amplification (ISDL) results, indicating DIV1 could be eliminated from challenged shrimp after 36°C treatment (Guo *et al.*, 2022).

3. Specimen selection, sample collection, transportation and handling

This section draws on information in Sections 2.2, 2.3 and 2.4 to identify populations, individuals and samples that are most likely to be infected.

3.1. Selection of populations and individual specimens

For diagnosis during a disease outbreak, moribund and apparently healthy crustacean specimens of susceptible species (see Section 2.2.3) from the same ponds, especially in polyculture mode, are selected as samples for identification testing. Apparently healthy or even dead and dried samples from crustacean farms next to the affected farms can be used as sources of materials for examination (Qiu *et al.*, 2019a). For surveillance in apparently healthy populations, all life stages of samples reared at 16–32°C should be suitable for testing (see Section 2.3.5)

Shrimp and crayfish that are 4–7 cm in body length provide the highest detection rate of DIV1 when used for examination (Qiu *et al.*, 2018b ;2019b ;2020b; 2021b ;2022b).

3.2. Selection of organs or tissues

Suitable tissues for testing are lymphoid organ, haematopoietic tissues, muscle, gills, hepatopancreas, pereiopods, pleopods, uropods, and antennae (Qiu *et al.*, 2017; 2019a; 2021a; Srisala *et al.*, 2021). Quantitative virus analysis from different tissues of naturally infected *Macrobrachium rosenbergii* showed that muscle and hepatopancreas had lower virus load compared with that of the lymphoid organ, haematopoietic tissues, gills, pereiopods, pleopods, uropods and antennae (Qiu *et al.*, 2019a).

3.3. Samples or tissues not suitable for pathogen detection

Autolytic and compound eyes samples are not suitable for PCR-based pathogen detection.

3.4. Non-lethal sampling

If non-lethal tissue sample types differ from recommended tissues (see Section 3.2.), or from the tissue samples used in validation studies, the effect on diagnostic performance should be considered.

3.5. Preservation of samples for submission

For guidance on sample preservation methods for the intended test methods, see Chapter 2.2.0 *General information* (diseases of crustaceans).

3.5.1. Samples for pathogen isolation

The success of pathogen isolation and results of bioassay depend strongly on the quality of samples (time since collection and time in storage). Fresh specimens should be kept on ice and preferably sent to the laboratory within 24 hours of collection. To avoid degradation of samples, use alternative storage methods only after consultation with the receiving laboratory.

3.5.2. Preservation of samples for molecular detection

Tissue samples for PCR testing should be preserved in 70–90% (v/v) analytical/reagent-grade (undenatured) ethanol. The recommended ratio of ethanol to tissue is 10:1 based on studies in terrestrial animal and human health. The use of lower grade (laboratory or industrial grade) ethanol is not recommended. If material cannot be fixed, it may be frozen.

Standard sample collection, preservation and processing methods for molecular techniques can be found in Section B.5.5 of Chapter 2.2.0 *General information* (diseases of crustaceans).

3.5.3. Samples for histopathology, immunohistochemistry or *in-situ* hybridisation

Standard sample collection, preservation and processing methods for histological techniques can be found in Section B.5.3 of Chapter 2.2.0 *General information* (diseases of crustaceans).

3.5.4. Samples for other tests

Not available

3.6. Pooling of samples

Pooling of samples from more than one individual animal for a given purpose is only recommended where robust supporting data on diagnostic sensitivity and diagnostic specificity have been evaluated and found to be suitable. If the effect of pooling on diagnostic sensitivity has not been thoroughly evaluated, larger shrimp (or other decapod crustaceans) should be processed and tested individually. Small life stages such as larvae or PLs can be pooled to obtain the minimum amount of material for virus isolation or molecular detection.

4. Diagnostic methods

The methods currently available for pathogen detection that can be used in i) surveillance of apparently healthy animals, ii) presumptive diagnosis in clinically affected animals and iii) confirmatory diagnostic purposes are listed in Table 4.1. by animal life stage.

Ratings for purposes of use. For each recommended assay a qualitative rating for the purpose of use is provided. The ratings are determined based on multiple performance and operational factors relevant to application of an assay for a defined purpose. These factors include appropriate diagnostic performance characteristics, level of assay validation, availability cost, timeliness, and sample throughput and operability. For a specific purpose of use, assays are rated as:

+++ =   Methods are most suitable with desirable performance and operational characteristics.

++ =   Methods are suitable with acceptable performance and operational characteristics under most circumstances.

+ =   Methods are suitable, but performance or operational characteristics may limit application under some circumstances.

Shaded boxes = Not appropriate for this purpose.

Validation stage. The validation stage corresponds to the assay development and validation pathway in chapter 1.1.2. The validation stage is specific to each purpose of use. Where available, information on the diagnostic performance of recommended assays is provided in Section 6.3.

WOAH Reference Laboratories welcome feedback on diagnostic performance of recommended assays, in particular PCR methods. Of particular interest are any factors affecting expected assay sensitivity (e.g. tissue components inhibiting amplification) or expected specificity (e.g. failure to detect particular genotypes, detection of homologous sequences within the host genome). These issues should be communicated to the WOAH Reference Laboratories so that advice can be provided to diagnostic laboratories and the standards amended if necessary.

Table 4.1. WOAH recommended diagnostic methods and their level of validation for surveillance of apparently healthy animals and investigation of clinically affected animals

Method [amend or shade in as relevant]	Surveillance of apparently healthy animals				Presumptive diagnosis of clinically affected animals				Confirmatory diagnosis1 of a suspect result from surveillance or presumptive diagnosis			
	Early life stages[2]	Juveniles[2]	Adults	LV	Early life stages[2]	Juveniles[2]	Adults	LV	Early life stages[2]	Juveniles[2]	Adults	LV
Wet mounts												
Histopathology						++	++	1				
Cell culture												
Real-time PCR	++	+++	+++	NA	+++	+++	+++	1	+++	+++	+++	1
Conventional PCR	++	++	++	NA	++	++	++	NA				
Conventional nested PCR followed by amplicon sequencing									+	+	+	1
Conventional PCR followed by amplicon sequencing									+++	+++	+++	1
In-situ hybridisation						++	++	1		+++	+++	1
Bioassay					+	+	+	NA				
LAMP	+	+	+	NA	+	+	+	NA				
Quantitative LAMP	++	++	++	NA	++	++	++	1				
Ag-ELISA												
RPA	++	++	++	NA	++	++	++	1				
Other methods[3]												

LV = level of validation, refers to the stage of validation in the WOAH Pathway (chapter 1.1.2); NA = not available;

PCR = polymerase chain reaction; LAMP = loop-mediated isothermal amplification

Ag-ELISA = antigen enzyme-linked immunosorbent assay; RPA = recombinase polymerase amplification

[1]For confirmatory diagnoses, methods need to be carried out in combination (see Section 6). [2]Susceptibility of early and juvenile life stages is described in Section 2.2.3.

[3]Specify the test used. Shading indicates the test is inappropriate or should not be used for this purpose.

4.1. Wet mounts

Not relevant

4.2. Histopathology and cytopathology

Histopathological examination revealed pathognomonic dark eosinophilic cytoplasmic inclusion bodies in the karyopyknotic cells of haemopoietic tissues and lymphoid organs, and in the haemocytes of gills, pereopods and sinus of the hepatopancreas (Qiu *et al.,* 2017; 2019a), as well as cuticular epithelium under the cuticles (Chen *et al.,* 2019).

4.3. Cell culture for isolation

Not available.

4.4. Nucleic acid amplification

PCR assays should always be run with the controls specified in Section 5.5 '*Use of molecular and antibody-based techniques for confirmatory testing and diagnosis*' of Chapter 2.2.0 *General information* (diseases of crustaceans). Each sample should be tested in duplicate.

Extraction of nucleic acids

Different kits and procedures can be used for nucleic acid extraction. The quality and concentration of the extracted nucleic acid is important and can be checked using a suitable method as appropriate to the circumstances.

4.4.1. Real-time PCR

Table 4.4.1.1. Primers and probes (sequences) and cycling conditions for DIV1 real-time PCR

Target gene	Primer/probe (5'–3')	Concentration	Cycling parameters[a]
Method 1: Qiu *et al.,* 2018a; GenBank Accession No.: MF599468.1			
ATPase	SHIV-F: AGG-AGA-GGG-AAA-TAA-CGG-GAA-AAC SHIV-R: CGT-CAG-CAT-TTG-GTT-CAT-CCA-TG Probe: FAM-CTG-CCC-ATC-TAA-CAC-CAT-CTC-CCG-CCC-TAMRA	500 nM 200 nM	40 cycles of 95°C/100 sec and 60°C/30 sec
Method 2: Qiu *et al.,* 2020a; GenBank Accession No.: MF599468.1			
MCP	142F: AAT-CCA-TGC-AAG-GTT-CCT-CAG-G 142R: CAA-TCA-ACA-TGT-CGC-GGT-GAA-C Probe: FAM- CCA-TAC-GTG-CTC-GCT-CGG-CTT-CGG-TAMRA	500 nM 200 nM	40 cycles of 95°C/10 sec and 60°C/30 sec
Method 3: Gong *et al.,* 2021; GenBank Accession No.: MF599468.1			
ATPase	DIV1-F: AGG-AAA-GGA-AAC-GAA-AGA-AAT-TAT-ACC DIV1-R: GCT-TGA-TCG-GCA-TCC-TTG-A Probe: FAM-CAC-ATG-ATT-TGC-AAC-AAG-CTT-CCA-GCA-TAMRA	400 nM 200 nM	40 cycles of: 95°C/10 sec and 60°C/30 sec

[a]A denaturation step prior to cycling has not been included.

4.4.2. Conventional PCR/nested PCR

Table 4.4.2.1. Primer sequences and cycling conditions for DIV1 PCR and nested PCR

Target gene	Primer (5'–3')	Concentration	Cycling parameters[a]
Method 1: Xu *et al.,* 2016; GenBank Accession No.; amplicon size: 103 bp			
MCP	CQIV-MCP-F: GAA-ACT-TTA-TGC-ACA-ATC-TTA-T CQIV-MCP-R: CCA-ATC-ATG-TTG-TCG-TAT-CC	NA	25 cycles of: 94°C/30 sec, 55°C/30 sec and 72°C/30 sec
Method 2: Qiu *et al.,* 2017; GenBank Accession No.: KY618040; amplicon size: 457 and 129 bp			
ATPase	Primary step: SHIV-F1: GGG-CGG-GAG-ATG-GTG-TTA-GAT SHIV-R1: TCG-TTT-CGG-TAC-GAA-GAT-GTA Nested PCR: SHIV-F2: CGG-GAA-ACG-ATT-CGT-ATT-GGG SHIV-R2: TTG-CTT-GAT-CGG-CAT-CCT-TGA	400 nM 400 nM	Primary and nested steps: 95°C/3 min; 35 cycles of 95°C/30 sec, 59°C/30 sec and 72°C/30 sec

[a]A denaturation step prior to cycling has not been included.

4.4.3. Other nucleic acid amplification methods

Table 4.4.3 Primers and probes (sequences) for DIV1 LAMP, RPA and qLAMP

Method/target gene	Primer (5'–3')	Concentration	Cycling parameters[a]/ method
Method 1: Chen *et al.,* 2019; GenBank Accession No.: xxx			
LAMP/DNA-directed RNA polymerase II	SHIV-FIP (F1C + F2): TGG-GGT-TTC-ATA-TGG-GCA-AA T-GAT-TTT-AAG-AAT-GGA-AAG-ATC-CTA-TCA-GC SHIV-BIP (B1C + B2): AGG-AGA-AAA-GGT-TGG-ATT-GGT-TAC-TTT-TAC-TTC-TGT-TAC-TGC-GAT-GG SHIV-LF: GAG-AGG-CGT-GCA-ACT-TTC-TG SHIV-LB: TTT-GGC-ATT-GTC-TGC-TAC-AAT-TTC-C SHIV-F3: GAT-GGC-CAT-TCC-TTC-AAA-C SHIV-B3: AAA-ATA-GTC-ATC-CTG-AAA-TCC-T	1600 nM 1600 nM 800 nM 800 nM 200 nM 200 nM	60 cycles of: 60°C 85°C/5 min:
Method 2: Chen *et al.,* 2020; GenBank Accession No.:xxx			
RPA/ MCP	RPA-F : CAG-ATC-AGA-GCG-CAT-TCG-ATC-CCA-TAG-GCA-CCG-C RPA-R: CGT-AAG-AGA-ACA-TGT-GGT-ATC-CGG-TGA-GTT-CGG-G RPA- Probe: ATA-CGA-ATC-TTC-AGA-TCG-TAT-TCC-CGT-GA(FAM-dT)G(THF)C(BHQ1-dT)GCC-GAT-TAC-TTC-TC (phosphorylation)	400 nM 400 nM 120 nM	40 cycles of: 39°C/45 sec, and 39°C/15 sec
Method 3: Gong *et al.,* 2021; GenBank Accession No.: xxx			
qLAMP/ ATPase	F3: GGC-TTG-GTA-TCT-TAT-TCA-GAG-AT B3: ATT-CAC-AAC-ATC-GTC-ACC-AT FIP: CTC-TTG-ATG-GAT-ACA-CTG-ATC-TTC-GGA-GCC-AGA-GAT-TGT-AAC-GG BIP: ATT-CAG-TAT-TCA-AGG-ATT-GGT-TCA-AAA-GTT-CTT-CCA-TCT-ACC-TCT-C LF: TTC-GGT-ACG-AAG-ATG-TAG-C LB: GAA-GAG-TAT-CCT-AAT-ATG-ACC-ATC-C	200 nM 200 nM 1600 nM 1600 nM 800 nM 800 nM	63°C/30 sec 40 cycles of: 63°C/60 sec

[a]A denaturation step prior to cycling has not been included.

4.5. Amplicon sequencing

The size of the PCR amplicon should be verified, for example, by agarose gel electrophoresis. Both DNA strands of the PCR product must be sequenced and analysed in comparison with reference sequences.

4.6. *In-situ* hybridisation

In-situ hybridisation has been applied to paraffin sections to determine the specific location of DIV1 in target tissues by either DIG-labelled oligonucleotide probe or DIG-labelling-loop-mediated DNA amplification (ISDL) (Chen *et al.*, 2019; Sanguanrut *et al.,* 2021). ISDL is the preferred method to use because it is highly sensitive through simultaneous pathogen DNA amplification and labelling techniques, compared with routine probe-based *in-situ* hybridisation.

4.7. Immunohistochemistry

Not available.

4.8. Bioassay

Bioassay has application in presumptive diagnosis, but cost, accuracy, labour, timing, or other factors limit its application (Qiu *et al.*, 2017; Xu *et al.*, 2016).

4.9. Antibody- or antigen-based detection methods

Not available.

4.10. Other methods

Not available.

5. Test(s) recommended for surveillance to demonstrate freedom in apparently healthy populations

Any of the real-time PCR assays is recommended for surveillance to demonstrate freedom in apparently health populations.

6. Corroborative diagnostic criteria

This section only addresses the diagnostic test results for detection of infection in the absence (Section 6.1.) or in the presence of clinical signs (Section 6.2.) but does not evaluate whether the infectious agent is the cause of the clinical event.

The case definitions for a suspect and confirmed case have been developed to support decision making related to trade and confirmation of disease status at the country, zone or compartment level. Case definitions for disease confirmation in endemically affected areas may be less stringent. If a Competent Authority does not have the capability to undertake the necessary diagnostic tests it should seek advice from the appropriate WOAH Reference Laboratory, and if necessary, refer samples to that laboratory for confirmatory testing of samples from the index case in a country, zone or compartment considered free.

6.1. Apparently healthy animals or animals of unknown health status[1]

Apparently healthy populations may fall under suspicion, and therefore be sampled, if there is an epidemiological link(s) to an infected population. Hydrographical proximity to, or movement of animals or animal products or equipment, etc., from a known infected population equate to an epidemiological link. Alternatively, healthy populations are sampled in surveys to demonstrate disease freedom.

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1   For example transboundary commodities.

6.1.1. Definition of suspect case in apparently healthy animals

The presence of infection with DIV1 shall be suspected if at least one of the following criteria is met:

    i)   Positive result by real-time PCR

    ii)   Positive result by conventional PCR,

    iii)   Positive result by LAMP

    iv)   Positive result by RPA

6.1.2. Definition of confirmed case in apparently healthy animals

The presence of infection with DIV1 is considered to be confirmed if at least one of the following criteria is met:

    i)   Positive result by real-time PCR followed by conventional PCR and amplicon sequencing.

    ii)   Positive result by real-time PCR followed by conventional nested PCR and amplicon sequencing.

6.2 Clinically affected animals

Clinical signs are not pathognomonic for a single disease; however, they may narrow the range of possible diagnoses.

6.2.1. Definition of suspect case in clinically affected animals

The presence of infection with DIV1 shall be suspected if at least one of the following criteria is met:

    i)   Gross pathology or clinical signs associated with the disease as described in this chapter, with or without elevated mortality

    ii)   Positive result by real-time PCR

    iii)   Positive result by conventional PCR

    iv)   Positive result by LAMP

    v)   Positive result by RPA

    vi)   Histopathological changes consistent with the presence of the pathogen or the disease

    vii)   Positive result by *in-situ* hybridisation

6.2.2. Definition of confirmed case in clinically affected animals

The presence of infection with DIV1 is considered to be confirmed if at least at least one of the following criteria is met:

    i)   Positive result by real-time PCR and positive result by conventional PCR followed by amplicon sequencing

    ii)   Positive result by real-time PCR and positive result by conventional nested PCR and amplicon sequencing

    iii)   Positive result by real-time PCR and positive result by *in-situ* hybridisation

6.3. Diagnostic sensitivity and specificity for diagnostic tests

The diagnostic performance of tests recommended for surveillance or diagnosis of infection with DIV1 are provided in Tables 6.3.1. and 6.3.2 (no data are currently available for either). Data are only presented where tests are validated to at least level 2 of the validation pathway described in Chapter 1.1.2. and the information is available within published diagnostic accuracy studies.

6.3.1. For presumptive diagnosis of clinically affected animals

Test type	Test purpose	Source populations	Tissue or sample types	Species	DSe (*n*)	DSp (*n*)	Reference test	Citation

DSe = diagnostic sensitivity, DSp = diagnostic specificity, *n* = number of animals used in the validation study,
PCR: = polymerase chain reaction.

6.3.2. For surveillance of apparently healthy animals

Test type	Test purpose	Source populations	Tissue or sample types	Species	DSe (*n*)	DSp (*n*)	Reference test	Citation

DSe = diagnostic sensitivity, DSp = diagnostic specificity, *n* = number of animals used in the validation study
PCR: = polymerase chain reaction.

7. References

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NB: There is a WOAH Reference Laboratory for infection with decapod iridescent virus 1
(please consult the WOAH web site:
https://www.woah.org/en/what-we-offer/expertise-network/reference-laboratories/#ui-id-3).
Please contact the WOAH Reference Laboratories for any further information on
infection with decapod iridescent virus 1

NB: FIRST ADOPTED IN 2024.