

REPORTING FORMAT FOR FISH DISEASE DATA

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REPORTING FORMAT FOR FISH DISEASE DATA

1 OVERVIEW OF THE FISH DISEASE SYSTEM

The fish disease reporting format – data type ‘DF’ – is used for reporting data from fish disease surveys conducted according to the standard methodology described in ‘Methodology of Fish Disease Surveys’ (ICES, 1989, ICES Coop. Res. Rep. No. 166) and for reporting new disease outbreaks.

Version 2.2 is a total revision of the fish disease reporting formats, and earlier versions may not be used.

The types of disease which can be reported at present are listed in the Environmental reference codes found on the web at www.ices.dk/env/ (choose Codes). When new disease codes are necessary, the ICES Environment Department should be contacted so that the data formats can be expanded.

Each data type has a number of record types associated with it. The record types available for fish disease data are: the *Sample Master Record* (RECID: 01), the *Haul Information Record* (RECID: 02), the *Fish Disease Specimen/Sub-sample Record* (RECID: 06), the *Fish Disease Data Record* (RECID: 08), and the *Plain Language Comment Record* (RECID: 13).

2 FISH DISEASE DATA FILE

2.1 Data file structure

The data file comprises a series of (one or more) *Sample Master Records*, each followed by (one or more) *Haul Information Records*, (one or more) *Fish Disease Specimen/Sub-sample Records* and (one or more) *Fish Disease Data Records*.

Figure A is a schematic representation of the data file structure, illustrating the hierarchy of the file.

Figure A – Fish disease data file structure

```

01 – Sample master record
    02 – Haul Information record
        06 – Fish Disease Specimen/Sub-sample Record
            08 – Fish disease data record
            08 – Fish disease data record
            08 – Fish disease data record
            :
        06 – Fish Disease Specimen/Sub-sample Record
            08 – Fish disease data record
            08 – Fish disease data record
            08 – Fish disease data record
            :
    02 – Haul Information record
        06 – Fish Disease Specimen/Sub-sample Record
            08 – Fish disease data record
            08 – Fish disease data record
            08 – Fish disease data record
            :
        06 – Fish Disease Specimen/Sub-sample Record
            08 – Fish disease data record
            08 – Fish disease data record
            08 – Fish disease data record
            :
End of file

```

2.2 Data records included in the fish disease format

The guidelines for conducting fish disease surveys detail the species to be sampled, the number of specimens to be collected, length ranges to be sampled, etc. The format for reporting fish disease data utilizes the following types of data records:

- *The Sample Master Record (RECID: 01)*
The *Sample Master Record* includes general information such as when and where the sample was obtained, together with administrative information in relation to the intended use of the data for specimens collected as part of a single sample of fish.
- *The Haul Information Record (RECID: 02)*
The sample can be reported as one or more hauls, utilizing the *Haul Information Record*. This record gives more detailed information concerning the gear, the total number and sex of individuals in the haul, and the scientists involved in examining the specimens.
- *The Fish Disease Specimen/Sub-sample Record (RECID: 06)*
A given haul of fish is sub-divided via *Fish Disease Specimen/Sub-sample Records* into different length class/sex categories for individuals or bulks which represent a sub-sample. The total number of diseases looked for, the number of specimens examined in the specified category and general information concerning length and age of the specimens are given in this record type.

- *The Fish Disease Data Record (RECID: 08)*

Each *Fish Disease Data Record* records the number of individuals affected by a particular disease in a given sub-sample.

- *The Plain Language Comment Record (RECID: 13)*

Plain Language Comment Records can be inserted at any point in the data file to supply additional information to aid the interpretation of the data reported on the preceding data record. If the explanatory text does not fit on a single *Plain Language Comment Record*, several of these records can be included in a block. It should be noted that, whilst information reported as plain language text will be stored at the data centre, and, where possible, retrieved and presented together with the data, data handling systems do not generally take account of plain language text. The comments are likely to become dissociated from the coded data, for example during exchange of data in non-ICES format for import into software packages used for data evaluation purposes. Thus, *Plain Language Comment Records* should be avoided unless they are specifically required by the reporting format.

2.3 Fish Disease Link-keys

The fish disease data reporting format does not involve any link-keys; the only items of method-related information are included on the *Haul Information Records*.

3 FISH DISEASE SAMPLE AND SUB-SAMPLE DEFINITIONS

A fish disease sample comprises specimens of a single species, collected in a given area within a limited time period, and is designated by the *Sample Master Record*. A sample can consist of specimens obtained using one or more hauls.

A given haul of fish is sub-divided via *Fish Disease Specimen/Sub-sample Records* into different length class/sex categories for individuals or bulks. Each of the individuals/bulks reported there are considered to be a sub-sample. The sub-sample is referred to by stating both the haul number and the sub-sample number.

4 RECORD LAYOUT DESCRIPTIONS FOR FISH DISEASE DATA

4.1 File headers

The first record of every file must be a file header, i.e., a 00-record, specifying the version numbers of the reporting format, the screening program, and the valid code list file (for example: **00 RF2.2 SV1.34 LR1**). The header numbers should coincide with the latest updates

4.2 General field specifications

The following sections describe the layout of each record type found in the fish disease data reporting format. Each record is presented in the form of a table where the following are described for each data field of the record: the data field code, the data field name, the field column numbers, the valid values for the field, the format for the field, and whether the field is mandatory.

The data **field codes** and the data **field names** are described in detail in the section on Data Field Descriptions of this manual.

The **column** numbers refer to the column placement of the field in a given record.

The **valid values** for the field describe predefined values and ranges, and refer to Environmental reference codes found on the web at www.ices.dk/env/ (choose Codes).

The **format** column for the field indicates the type of variable included in the indicated data field according to one of the following:

SPC n a 'space filled' character field, consisting of n spaces

CHAR n a character field of n characters. Character fields are formatted as left-justified, space filled.

NUM n a numeric (integer) field of width n . Integer fields are formatted as right justified, zero filled – e.g., the number 43 in a field NUM4:

0	0	4	3
---	---	---	---

NUM n m a numeric field of width n , including an **implied** decimal point; the rightmost m positions in the field are decimal positions. Values are formatted as decimal justified, zero filled – e.g., the number 3.7 in a field NUM4i2:

0	3.	7	0
---	----	---	---

The **mandatory**, or ‘M’, column indicates those data fields which are mandatory in the context of the reporting formats, i.e., data which **must be reported**; the following codes apply:

- m mandatory;
- m? mandatory in some cases, e.g., when reporting data for a specific programme;
- mH mandatory when reporting data to HELCOM (BMP/COMBINE);
- mO mandatory when reporting data to OSPARCOM (JMP/JAMP);
- x mandatory and predefined (i.e., insert the characters specified in the valid values column).

4.3 Sample Master Record (01)

RECORD: Sample Master Record					
Code	Field name	Columns	Valid values	Format	M
RECID	Record identifier	1–2	'01'	NUM2	x
DTYPE	Data type	3–4	'DF'	CHAR2	x
RLABO	Reporting institute code	5–8	cf. RLABO	CHAR4	m
MYEAR	Monitoring year	9–10	'74' to present year	NUM2	m
SEQNO	Sample sequence number	11–14	0001–9999	NUM4	m
CNTRY	Country code	15–16	cf. CNTRY	CHAR2	m
SHIPC	Ship code	17–18	cf. SHIPC	CHAR2	m
CRUIS	Cruise identifier	19–22	A–z, 0–9	CHAR4	m
SDATE	Sampling date	23–28	000000–999999	CHAR6	m
STIME	Sampling time	29–32	0000–2359 or spaces	CHAR4	
	Sampling area coordinates				
LATDG	Latitude degrees	33–34	00–90 (north)	NUM2	m
LATMI	Latitude minutes	35–36	00–59	NUM2	m
LATMF	Latitude decimal minutes	37–38	00–99	NUM2	m
LONDG	Longitude degrees	39–40	00–99	NUM2	m
LONMI	Longitude minutes	41–42	00–59	NUM2	m
LONMF	Longitude decimal minutes	43–44	00–99	NUM2	m
QEORW	Quadrant	45–45	'E', 'e', 'W' or 'w' (cf. Data Field Descriptions)	CHAR1	m
JMPAR	JMP area code	46–54	cf. JMPAR and Data Field Descriptions, or spaces	CHAR9	mO
ICEAR	ICES statistical rectangle	55–59	cf. ICEAR	CHAR5	m
OTHAR	Other area or station code	60–64	A–z, 0–9 or spaces	CHAR5	mH
SPECI	Species (RUBIN) code	65–72	cf. SPECI	CHAR8	m
NOINS	<i>Field not used in disease data</i>	73–75	spaces	SPC3	x
WADEP	Water depth	76–79	0000–9999 or spaces	NUM4	m?
COREL	<i>Field not used in disease data</i>	80–82	spaces	SPC2	x
ESTSR	<i>Field not used in disease data</i>	83–85	spaces	SPC3	x
SMLNK	<i>Field not used in disease data</i>	86–87	spaces	SPC2	x
ORGNZ	Organization codes	88–92	cf. ORGNZ	CHAR5	m
PURPM	Purpose of monitoring codes	93–97	cf. PURPM	CHAR5	m
RLIST	RUBIN code list	98–99	cf. RLIST	CHAR2	m
VESSL	Vessel type	100–100	cf. VESSL	CHAR1	m
GEART	Gear type used	101–103	cf. GEART	CHAR3	m
NOHAU	Number of hauls reported	104–105	01–99	NUM2	m
SPSEA	Spawning season code	106–106	'Y' or 'N'	CHAR1	m
TOTIN	Total number of individuals	107–110	0001–9999	NUM4	m
ASTSA	<i>Field not used in disease data</i>	111–111	spaces	SPC1	x
STTYP	Station type	112–112	cf. STTYP	CHAR1	m
PTSRC	Point source of contamination	113–113	cf. PTSRC	CHAR1	
		114–120	spaces	SPC	x

4.4 Haul Information Record (02)

RECORD: Haul Information record					
Code	Field name	Columns	Valid values	Format	M
RECID	Record identifier	1–2	'02'	NUM2	x
DTYPE	Data type	3–4	'DF'	CHAR2	x
RLABO	Reporting institute code	5–8	cf. RLABO	CHAR4	m
MYEAR	Monitoring year	9–10	'74' to present year	NUM2	m
SEQNO	Sample sequence number	11–14	0001–9999	NUM4	m
	<i>Field reserved</i>	15–15	space	SPC1	x
HAULN	Haul sequence number	16–17	01–99	NUM2	m
	<i>Field reserved</i>	18–18	space	SPC1	x
DAMAG	Gear damage	19–19	'Y', 'N' or space	CHAR1	
CEMSH	Cod end mesh size (mm)	20–22	000–999	NUM3	m
NETOP	Net opening (m)	23–25	000–999 or spaces	NUM3i1	
SPEED	Trawl speed (knots)	26–27	00–99	NUM2i1	m
DURAT	Duration of haul (min)	28–29	00–99 or spaces	NUM2	
STRAT	Stratified sampling	30–30	cf. STRAT	CHAR1	m
	<i>Field reserved</i>	31–33	spaces	SPC3	x
NOMAL	Number of males in haul	34–37	0000–9999	NUM4	m
NOFEM	Number of females in haul	38–41	0000–9999	NUM4	m
NOUNK	Number of individuals – unknown sex	42–45	0000–9999	NUM4	m
	<i>Field reserved</i>	46–46	space	SPC1	x
SCIEN	Scientist in charge	47–56	A–z	CHAR10	m
OBSER	Observer	57–66	A–z	CHAR10	m
INSPT	Inspection time per fish (min)	67–69	000–999	NUM3i1	m
OTHHA	Other haul code	70–72	A–z, 0–9 or spaces	CHAR3	
		73–120	spaces	SPC	x

4.5 Fish Disease Specimen/Sub-sample Record (06)

RECORD: Fish Disease Specimen/Sub-sample Record					
Code	Field name	Columns	Valid values	Format	M
RECID	Record identifier	1–2	'06'	NUM2	x
DTYPE	Data type	3–4	'DF'	CHAR2	x
RLABO	Reporting institute code	5–8	cf. RLABO	CHAR4	m
MYEAR	Monitoring year	9–10	'74' to present year	NUM2	m
SEQNO	Sample sequence number	11–14	0001–9999	NUM4	m
	<i>Field reserved</i>	15–15	space	SPC1	x
HAULN	Haul sequence number	16–17	01–99	NUM2	m
	<i>Field reserved</i>	18–18	space	SPC1	x
INORB	Individual or bulk code	19–19	cf. INORB	CHAR1	m
SUBNO	Sub-sample number	20–23	0001–9999	NUM4	m
	<i>Field reserved</i>	24–24	space	SPC1	x
NODIS	Number of diseases examined for	25–26	01–99	NUM2	m
	<i>Field reserved</i>	27–27	space	SPC1	x
SIZEC	Size class	28–32	'<<-', '00-99', '->>' or spaces (cf. Data Field Descriptions)	CHAR5	m?
	<i>Field reserved</i>	33–33	space	SPC1	x
SEXCO	Sex code	34–34	cf. SEXCO	CHAR1	m?
	<i>Field reserved</i>	35–35	space	SPC1	x
NOEXA	Number of specimens examined	36–39	0001–9999	NUM4	m
	<i>Field reserved</i>	40–40	space	SPC1	x
LNMIN	Length – minimum (mm)	41–45	00001–99999 or spaces	NUM5	
LNMAX	Length – maximum (mm)	46–50	00001–99999 or spaces	NUM5	
LNMEA	Length – mean (mm)	51–55	00001–99999 or spaces	NUM5	m?
LNSTD	Length – standard deviation (mm)	56–60	00000–99999 or spaces	NUM5	
AGMIN	Age – minimum	61–62	00–99 or spaces	NUM2	
AGMAX	Age – maximum	63–64	00–99 or spaces	NUM2	
AGMEA	Age – mean	65–66	00–99 or spaces	NUM2	
AGDET	Age determination	67–67	cf. AGDET	CHAR1	m?
SPAWN	Spawning code	68–68	'S', 'N' or space (cf. Data Field Descriptions)	CHAR1	
		69–120	spaces	SPC	x

4.6 Fish Disease Data Record (08)

RECORD: Fish Disease Data Record					
Code	Field name	Columns	Valid values	Format	M
RECID	Record identifier	1–2	'08'	NUM2	x
DTYPE	Data type	3–4	'DF'	CHAR2	x
RLABO	Reporting institute code	5–8	cf. RLABO	CHAR4	m
MYEAR	Monitoring year	9–10	'74' to present year	NUM2	m
SEQNO	Sample sequence number	11–14	0001–9999	NUM4	m
	<i>Field not used in disease data</i>	15–15	space	SPC1	x
HAULN	Haul sequence number	16–17	01–99	NUM2	m
	<i>Field not used in disease data</i>	18–18	space	SPC1	x
INORB	Individual or bulk code	19–19	cf. INORB	CHAR1	m
SUBNO	Sub-sample number	20–23	0001–9999	NUM4	m
	<i>Field not used in disease data</i>	24–34	spaces	SPC11	x
DISEA	Disease	35–42	cf. DISEA	CHAR8	m
	<i>Field not used in disease data</i>	43–43	space	SPC1	x
NOAFF	Total number affected	44–47	0000–9999	NUM4	m
		48–120	spaces	SPC	x

4.7 Plain Language Comment Record (13)

RECORD: Plain Language Comment Record					
Code	Field name	Columns	Valid values	Format	M
RECID	Record identifier	1-2	'13'	NUM2	x
PTEXT	Plain text	3-87		CHAR85	
		88-120	spaces	SPC	x

5 FISH DISEASE EXAMPLES

5.1 Example 1

Two hauls were taken at the same station. From each haul a sample of 3 dabs was taken and examined for *skin ulcers* and *lymphocystis*. The results were:

Haul #1, specimen #1: *skin ulcer, lymphocystis*

Haul #1, specimen #2: *skin ulcer, lymphocystis*

Haul #1, specimen #3: *lymphocystis*

Haul #2, specimen #1: (neither disease)

Haul #2, specimen #2: (neither disease)

Haul #2, specimen #3: *skin ulcer*

This information should be reported as

01 – Sample Master Record	(SPECI = LIMA LIM; NOHAU = 2 TOTIN = 6)
02 – Haul information Record	(HAULN = 01)
06 – Sub-sample Record	(SUBNO = 01 ; NODIS = 2; NOEXA = 1)
08 – Fish Disease Record	(DISEA = ‘SKIN ULC’; NOAFF = 1)
08 – Fish Disease Record	(DISEA = ‘LYMP CYS’; NOAFF = 1)
06 – Sub-sample Record	(SUBNO = 02 ; NODIS = 2; NOEXA = 1)
08 – Fish Disease Record	(DISEA = ‘SKIN ULC’; NOAFF = 1)
08 – Fish Disease Record	(DISEA = ‘LYMP CYS’; NOAFF = 1)
06 – Sub-sample Record	(SUBNO = 03 ; NODIS = 2; NOEXA = 1)
08 – Fish Disease Record	(DISEA = ‘SKIN ULC’; NOAFF = 0)
08 – Fish Disease Record	(DISEA = ‘LYMP CYS’; NOAFF = 1)
02 – Haul information Record	(HAULN = 02)
06 – Sub-sample Record	(SUBNO = 01 ; NODIS = 2; NOEXA = 1)
08 – Fish Disease Record	(DISEA = ‘SKIN ULC’; NOAFF = 0)
08 – Fish Disease Record	(DISEA = ‘LYMP CYS’; NOAFF = 0)
06 – Sub-sample Record	(SUBNO = 02 ; NODIS = 2; NOEXA = 1)
08 – Fish Disease Record	(DISEA = ‘SKIN ULC’; NOAFF = 0)
08 – Fish Disease Record	(DISEA = ‘LYMP CYS’; NOAFF = 0)
06 – Sub-sample Record	(SUBNO = 03 ; NODIS = 2; NOEXA = 1)
08 – Fish Disease Record	(DISEA = ‘SKIN ULC’; NOAFF = 1)
08 – Fish Disease Record	(DISEA = ‘LYMP CYS’; NOAFF = 0)

A single *Sample Master Record* heads two *Haul Information Records*, one for each haul. Since each specimen in the hauls is reported as a sub-sample, there are three *Fish Disease Specimen/Sub-sample Records* reported under each *Haul Information Record*. Each specimen is examined for two diseases, thus two *Fish Disease Records* follows each *Fish Disease Specimen/Sub-sample Record*. It should be noted that when a specimen is analysed individually, NOAFF = 1 means that the specimen was infected by the disease it was examined for, while NOAFF = 0 means that the specimen showed no sign of the disease.