



Epidemiological investigation and management of a case of VHS detected in Atlantic salmon in a French fish farming in 2015

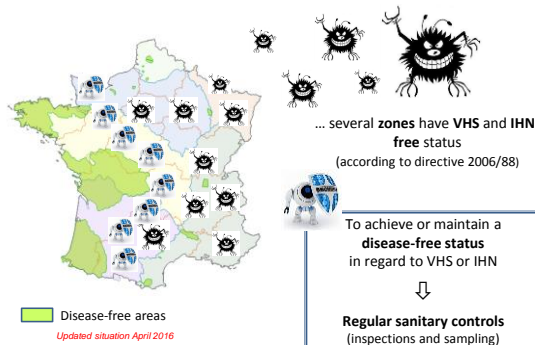
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CONTEXT

France is not declared free from non exotic listed diseases VHS and IHN but...

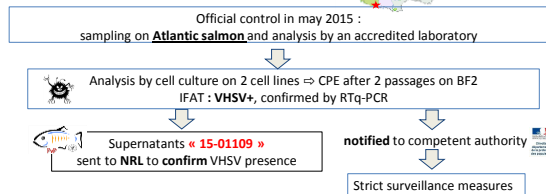


CONTEXT

Fish farm X: the only fish farm in a free-disease compartment, located upstream a large disease-free zone where a lot of free-disease status establishments are in activity (mainly producing rainbow trout)



Purpose: restocking (atlantic salmon, lake trout, brown trout and arctic char)

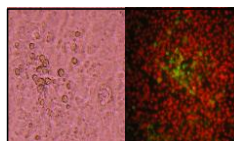


LABORATORY ANALYSIS

① Cell culture :

- ⇒ CPE on BF2 and EPC cells
- ⇒ IFAT **positive for VHSV**

Notification to competent authority

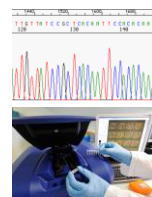


Declaration of infection for the farm X
 Surveillance for the downstream zone

② Characterization of the isolate by sequencing :

- ⇒ G gene (Einer-Jensen)
- ⇒ Full length / Next Generation Sequencing

anses
 Sequencing Platform
 (Dr Y. Blanchard et al.)



LABORATORY ANALYSIS

⇒ Sequence analysis (G gene) on 1524 nt
 Comparison with other French isolates (from rainbow trouts and other host species)



Sequences	Identity (%)	Number of differences
AY546616(07/71)Fr\1971\TAC	99.9	1
AY546617(Fr_23_75\1975)Fr_27\ario	98.1	28
EU708786(Dsa6915_02\2002)Germany\TAC	97.9	31
Isolat_L59x\1987)Fr_44\Civelles	90.5	144
Isolat_4164_91\1991)Fr_65\salar	99.9	1
Isolat_N14165_1\2004)Fr_63)Brochet	97.7	34
Isolat_KX35\2012)Fr_21\TAC	97.1	43
Isolat\002921\2014)Fr_55)TAC	97.0	45
Isolat_001534-1\2015)Fr_57)TAC	97.3	41

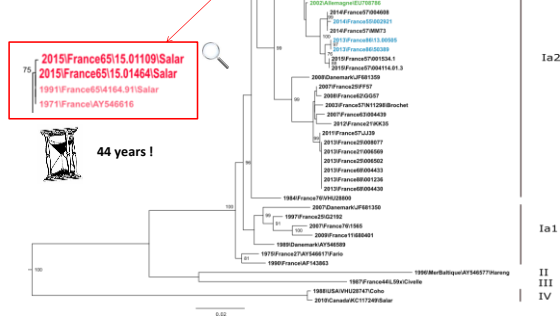
Last French identified isolates

Isolate described in 1971 - used as positive control in the French accredited labs

French isolate identified in the same area in 1991 in Atlantic salmon

LABORATORY ANALYSIS

G GENE ANALYSIS: PhyML tree (with genotype IV as outgroup)

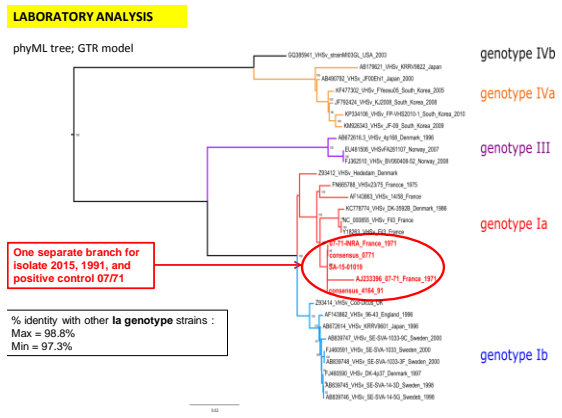


LABORATORY ANALYSIS

FULL LENGTH ANALYSIS:

10852 nt	Identity			Number of snp		
	0.999	0.998		5	14	17
consensus_0771	4164_91	15-01109	consensus_0771	4164_91	15-01109	
EJ481506_VHSV strain FA281107	0.917	0.917	0.916	900	897	909
GG385941_VHSV_strainMI03GL	0.869	0.869	0.868	1423	1422	1435
KF477302_VHSV isolate PRees05	0.86	0.86	0.859	1521	1520	1533
KF524306_VHSV strain FRVHSV2010-1	0.861	0.861	0.859	1509	1508	1521
JF792424_VHSV strain KJ2008	0.861	0.861	0.86	1499	1498	1511
KM926343_VHSV isolate JF-09	0.86	0.86	0.859	1512	1511	1524
NC_008855_VHSV F12	0.988	0.988	0.987	229	226	236
FJ460590_VHSV isolate DK-4p37	0.979	0.98	0.978	219	215	228
FJ460591_VHSV isolate SE-5VA-1033	0.979	0.979	0.978	222	218	231
AB179621_VHSV_KORV0822	0.855	0.855	0.854	1570	1569	1582
AB672616_3_VHSV_4p168	0.918	0.918	0.917	884	881	893
AB839745_VHSV_SE-5VA-14-3D	0.979	0.98	0.979	218	214	227
AB839746_VHSV_SE-5VA-14-5G	0.979	0.979	0.978	222	218	231
AB839747_VHSV_SE-5VA-1033-9C	0.978	0.978	0.977	232	228	241
AB839748_VHSV_SE-5VA-1033-3F	0.979	0.979	0.978	222	218	231
KC778774_VHSV strain DK-35928	0.987	0.987	0.986	139	136	148
Y12623_VHSV F13	0.988	0.988	0.987	129	126	138
FJ362510_VHSV isolate BV060408-52	0.917	0.917	0.916	900	897	909
AB490792_VHSV_H00LH1	0.862	0.862	0.861	1495	1494	1507
AB672614_VHSV_KORV0601	0.98	0.981	0.979	210	206	219
FN65788_VHSV strain 23-75	0.989	0.989	0.988	112	109	121
AF143863_VHSV 14-58	0.983	0.983	0.982	176	175	187
AF143862_VHSV 96-43	0.98	0.98	0.979	216	212	225
Z93414_VHSV strain Cod Ulfus	0.982	0.983	0.981	188	184	197
Z93412_VHSV Hededeam	0.982	0.983	0.982	186	182	195
AJ233596_0771	0.974	0.974	0.973	282	280	292
0771_inhA	0.999	0.999	0.998	3	3	3

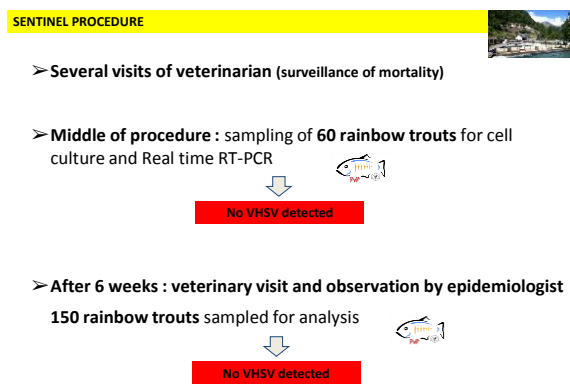
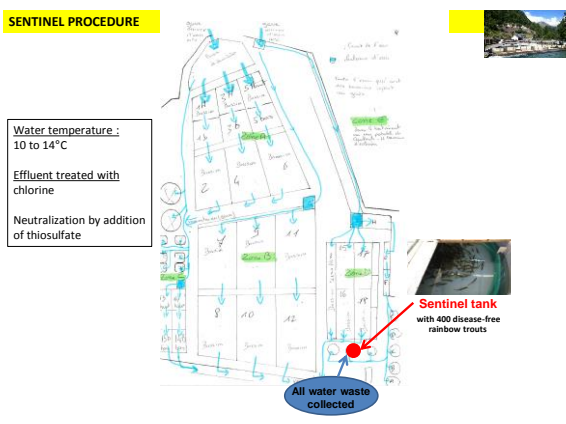
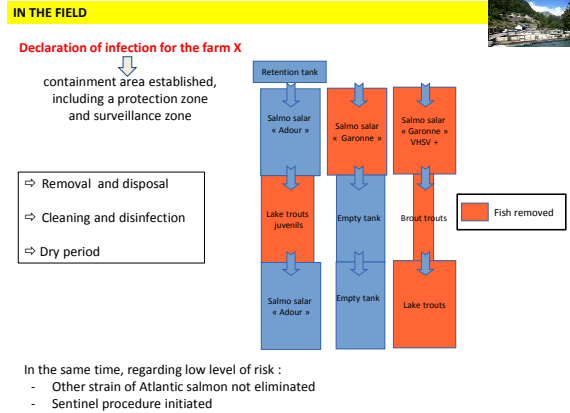
- Similarity at ~99% with the French isolate 0771 (INRA)
- Several mistakes on Genbank sequence AJ233396 (strain 0771)



BIBLIOGRAPHIC INVESTIGATIONS

Salmo salar & VHSV

- ◉ Susceptible species (OIE 2015)
- ◉ Regarding natural infections and experimental contaminations :
 - infectable in the wild by genotype IV but low mortality (Garver et al, 2013)
 - isolation **only in few cases** in Europe
 - **very low prevalence** in France (study carried on at the end of 1990s)
 - **moderate pathogenicity** of European strains
 - no mortality after infection by bath with **genotype Ia** and **III** strains (De kinkelin and castic, 1982 ; Dale et al, 2009)
 - significant mortality after infection by bath with **IVa** genotype isolate ⇒ **potential vector?** (Loy et al, 2013)
- ◉ **VHSV evolution rate**
 - ◉ Between **1.74x10⁻³** and **6.01x10⁻⁴** substitution / site / year (-0.91 to 2.65 nucleotides/year for G gene) (Einer-Jensen, 2004)
 - ◉ Evolution rate potentially **lower in less susceptible species...**
but ... such a long time in host without mutations??
 - ◉ EURL knowledge : similar cases = cross contamination



CONCLUSION

Surveillance of the investigated zone and **restriction lift** the week following negative result obtained by cell culture analysis.

No more case of VHSV detected in the farms located downstream

Estimated cost of 160 000€ for removal and disposal



October 2015 :
The X farm was eventually qualified again with disease-free status

ANSES report : https://www.anses.fr/fr/system/files/L_ABO2015sa0161.pdf