IMNV surveillance plan

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FAO Expert on Aquatic Disease Epidemiology
Qingdao, 2-5 November 2017
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Learned behaviors of the emergence of infectious diseases in aquaculture

Table I. Emerging viral pathogens of finfish.

Virus	Abbreviation	Genome	Taxonomic classification[1]	Known geographic distribution	OIE listed[2]
DNA viruses					
Epizootic haematopoietic necrosis virus and other ranaviruses	EHNV	dsDNA	*Iridoviridae, Ranavirus*	Australia, Europe, Asia, North America, Africa	Yes
Red sea bream iridovirus	RSIV	dsDNA	*Iridoviridae, Megalocytivirus*	Asia	Yes
Koi herpesvirus	KHV	dsDNA	*Alloherpesviridae, Cyprinivirus*	Asia, Europe, North America, Israel, Africa	Yes
RNA Viruses					
Infectious haematopoietic necrosis virus	IHNV	(−) ssRNA	*Mononegavirales, Rhabdoviridae, Novirhabdovirus*	Europe, North America, Asia	Yes
Viral haemorrhagic septicaemia virus	VHSV	(−) ssRNA	*Mononegavirales, Rhabdoviridae, Novirhabdovirus*	Europe, North America, Asia	Yes
Spring viraemia of carp virus	SVCV	(−) ssRNA	*Mononegavirales, Rhabdoviridae, Vesiculovirus*	Europe, Asia, North and South America	Yes
Infectious salmon anaemia virus	ISAV	(−) ssRNA	*Orthomyxoviridae, Isavirus*	Europe, North and South America	Yes
Viral nervous necrosis virus	VNNV	(+) ssRNA	*Nodaviridae, Betanodavirus*	Australia, Asia, Europe, North America, Africa, South Pacific	No

[1] ICVT, 2009.
[2] OIE, 2009.

Walker and Winton, 2010

Learned behaviors of the emergence of infectious diseases in aquaculture

Table II. Emerging viral pathogens of marine and freshwater shrimp.

Virus	Abbreviation	Genome	Taxonomic classification[1]	Year emerged	Known geographic distribution	OIE listed disease[2]
DNA viruses						
Monodon baculovirus	MBV	dsDNA	*Baculoviridae*	1977	Asia-Pacific, Americas, Africa	No
Baculoviral midgut gland necrosis virus	BMNV	dsDNA	*Baculoviridae*	1971	Asia, Australia	No
White spot syndrome virus	WSSV	dsDNA	*Nimaviridae, Whispovirus*	1992	Asia, Middle-East, Mediterranean, Americas	Yes
Infectious hypodermal and haematopoietic necrosis virus	IHHNV	ssDNA	*Parvoviridae, Densovirus*	1981	Asia-Pacific, Africa, Madagascar, Middle-East, Americas	Yes
Hepatopancreatic parvovirus	HPV	ssDNA	*Parvoviridae, Densovirus*	1983	Asia-Pacific, Africa, Madagascar, Middle-East, Americas	No
RNA viruses						
Yellow head virus	YHV	(+) ssRNA	*Nidovirales, Roniviridae, Okavirus*	1990	East and Southeast Asia, Mexico	Yes
Taura syndrome virus	TSV	(+) ssRNA	*Picornavirales, Dicistroviridae*	1992	Americas, East and Southeast Asia	Yes
Infectious myonecrosis virus	IMNV	(+) ssRNA	Totivirus (unclassified)	2002	Brazil, Indonesia, Thailand, China	Yes
Macrobrachium rosenbergii nodavirus	MrNV	(+) ssRNA	Nodavirus (unclassified)	1995	India, China, Taiwan, Thailand, Australia, Caribbean	Yes
Laem-Singh virus	LSNV	(+) dsRNA	Luteovirus-like (unclassified)	2003	South and Southeast Asia	No
Mourilyan virus	MoV	(−) ssRNA	Bunyavirus-like (unclassified)	1996	Australia, Asia	No

[1] ICTV, 2009.
[2] OIE, 2009.

Walker and Winton, 2010

FAO's Global Biosecurity Framework

From largest aquaculture-related disease epidemics

- White spot syndrome virus (WSSV)
- Epizootic ulcerative syndrome (EUS)
- Infectious salmon anemia virus (ISAV) in Chile, 2007.
- AHPNV
- Tilapia-Lake Virus
- Infectious myonecrosis virus, etc.

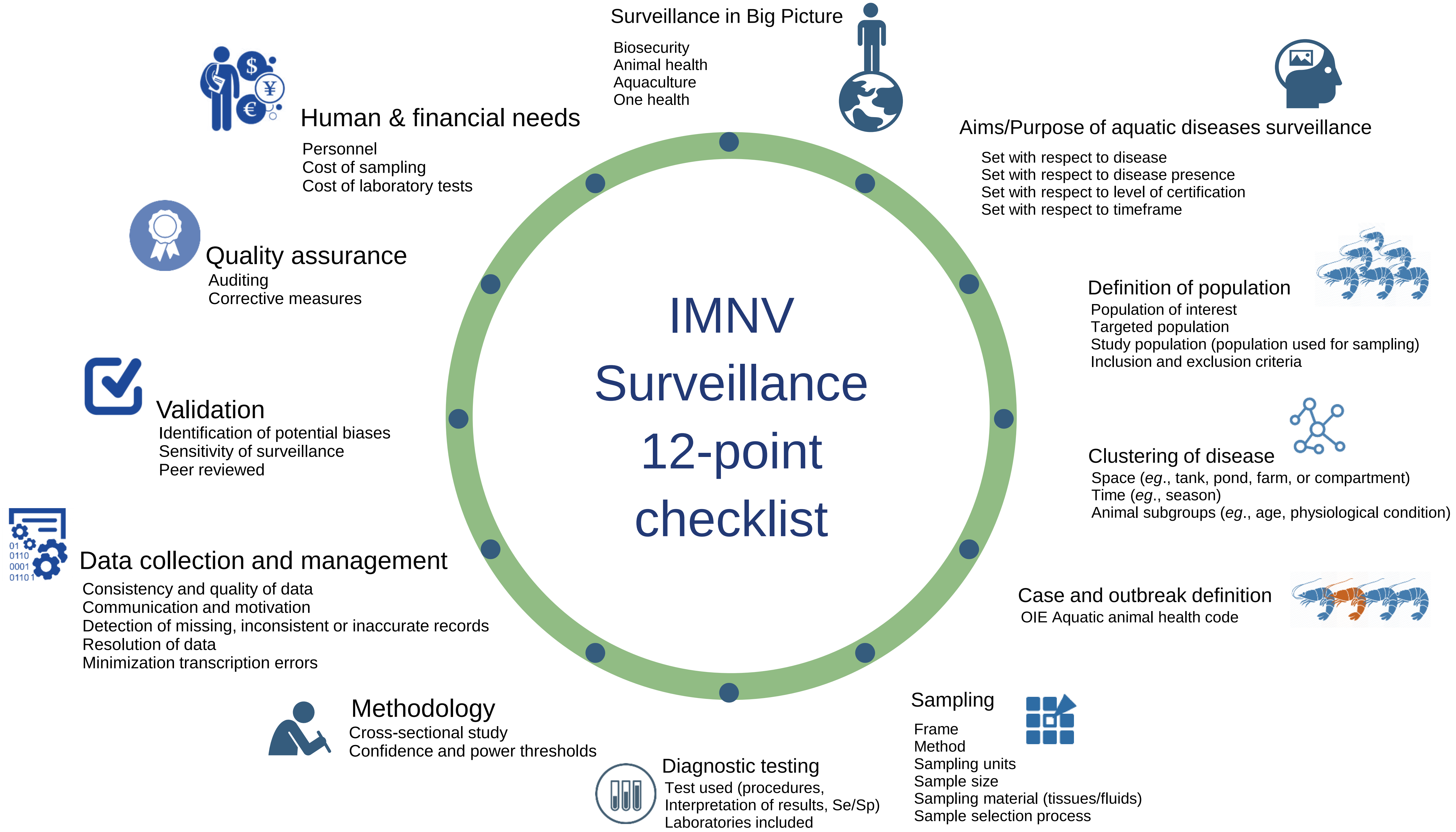
Disease
The development of an unknown disease in a farm

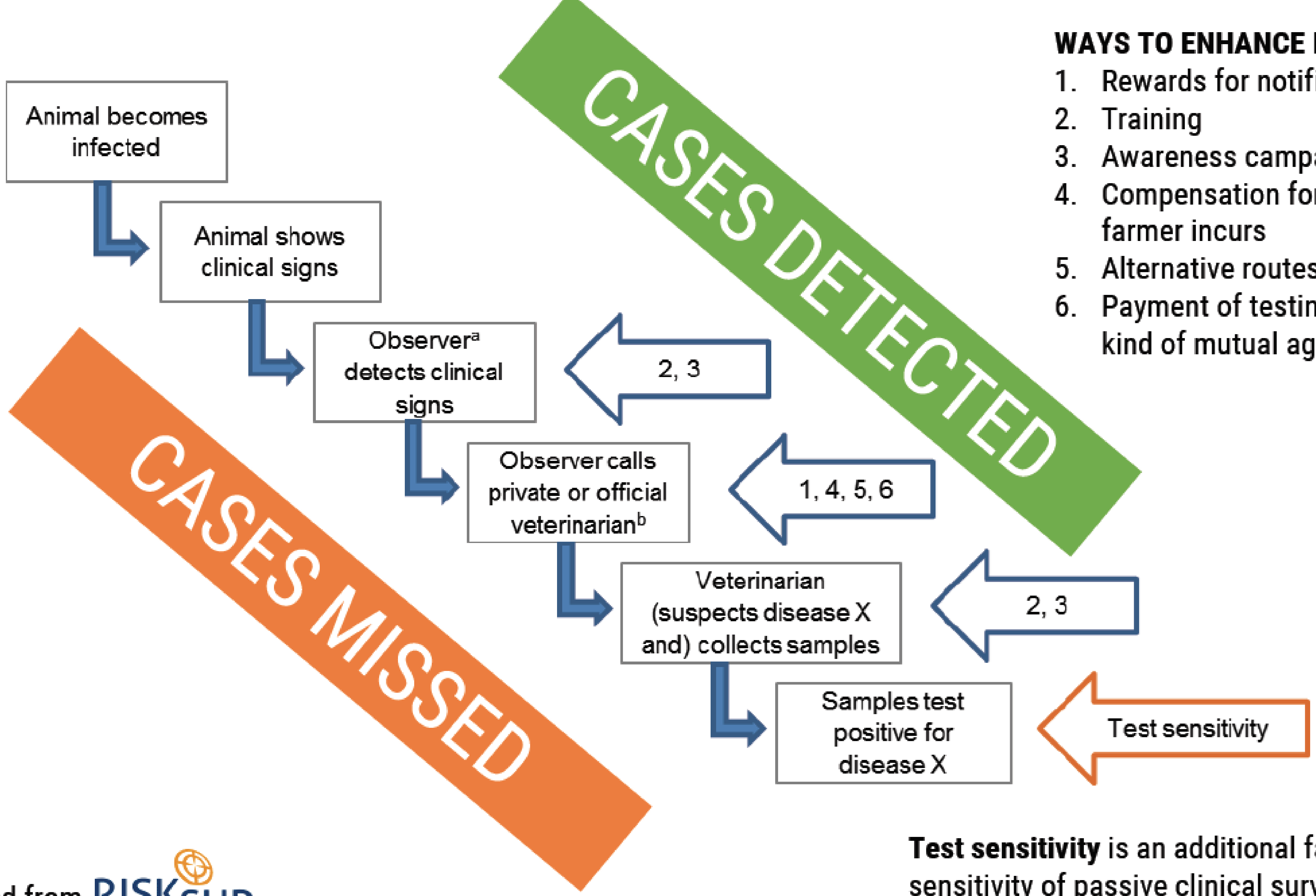
Diagnostic
The development of a diagnostic test

Reporting
The reporting and communication (national and OIE)

Vaccination
Development of an effective vaccine

Control
Effective diseases control implementations (cost-benefit)


IMNV Surveillance 12-point checklist
Surveillance in Big Picture
Biosecurity
Animal health
Aquaculture
One health
Aims/Purpose of aquatic diseases surveillance
Set with respect to disease
Set with respect to disease presence
Set with respect to level of certification
Set with respect to timeframe
Definition of population
Population of interest
Targeted population
Study population (population used for sampling)
Inclusion and exclusion criteria
Clustering of disease
Space (eg., tank, pond, farm, or compartment)
Time (eg., season)
Animal subgroups (eg., age, physiological condition)
Case and outbreak definition
OIE Aquatic animal health code
Sampling
Frame
Method
Sampling units
Sample size
Sampling material (tissues/fluids)
Sample selection process
Diagnostic testing
Test used (procedures,
Interpretation of results, Se/Sp)
Laboratories included
Methodology
Cross-sectional study
Confidence and power thresholds
Data collection and management
Consistency and quality of data
Communication and motivation
Detection of missing, inconsistent or inaccurate records
Resolution of data
Minimization transcription errors
Validation
Identification of potential biases
Sensitivity of surveillance
Peer reviewed
Quality assurance
Auditing
Corrective measures
Human & financial needs
Personnel
Cost of sampling
Cost of laboratory tests



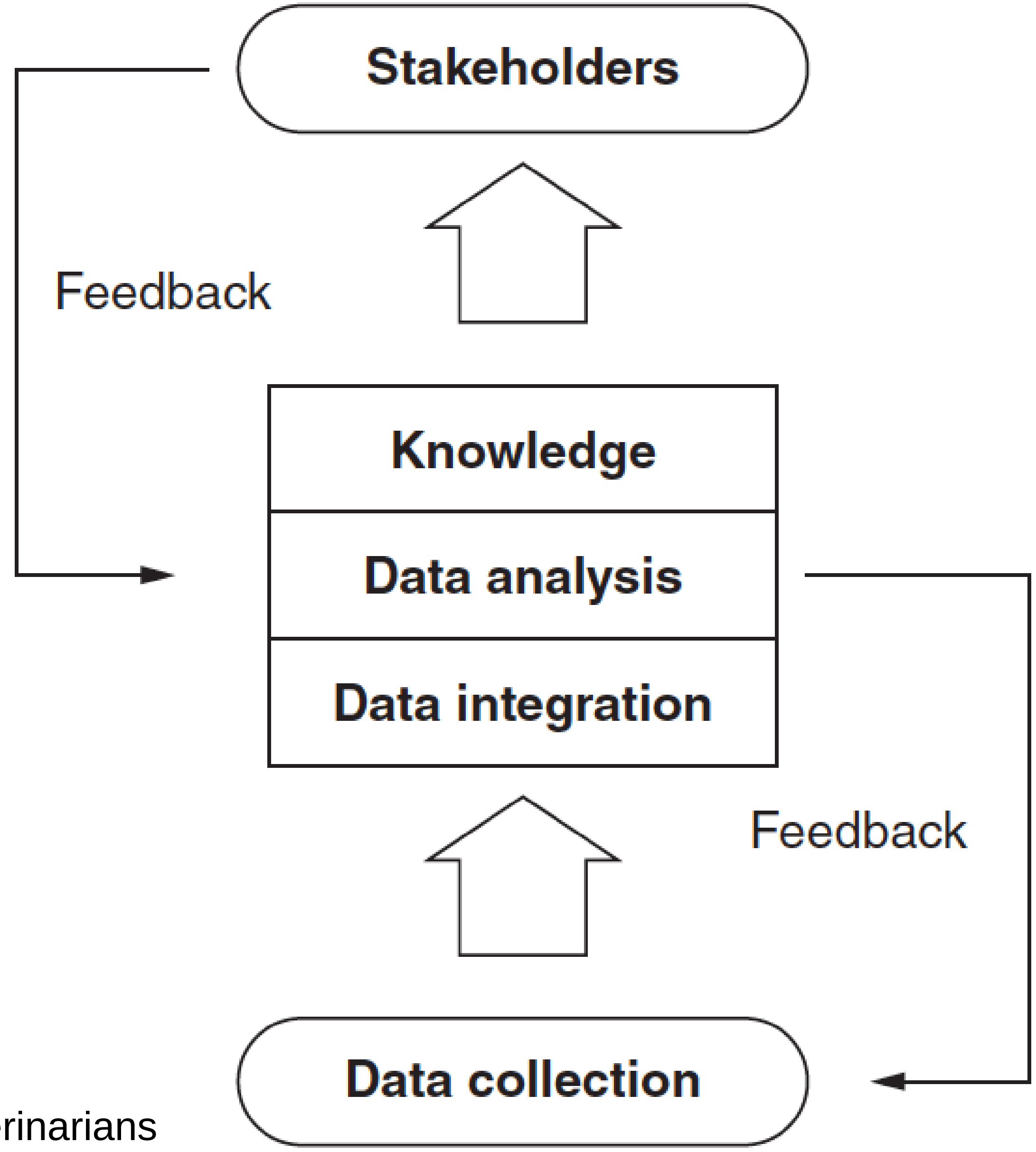
WAYS TO ENHANCE PASSIVE SURV.

1. Rewards for notifications
2. Training
3. Awareness campaigns
4. Compensation for losses the farmer incurs
5. Alternative routes of reporting
6. Payment of testing cost or other kind of mutual agreement.

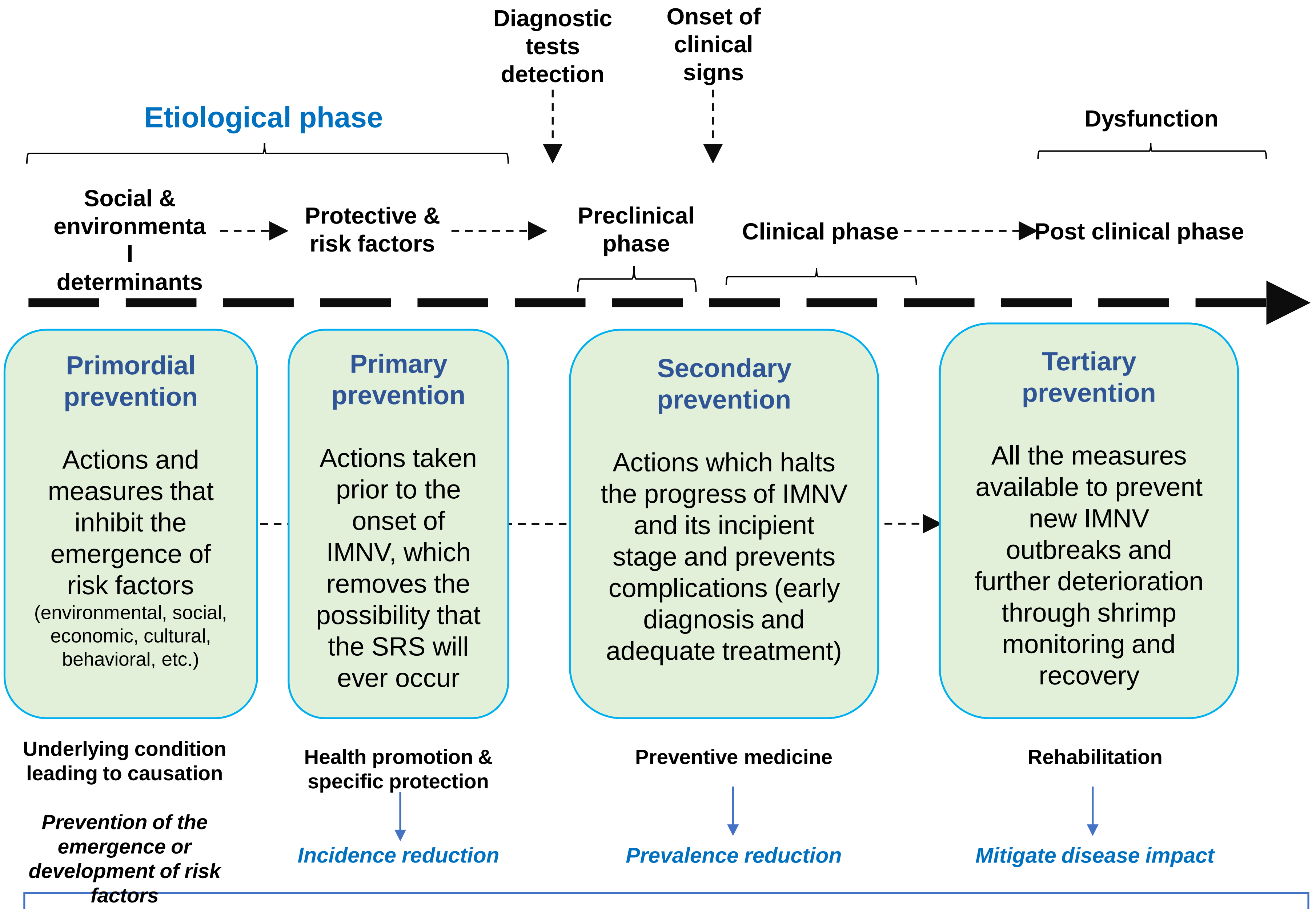
Test sensitivity is an additional factor influencing sensitivity of passive clinical surveillance.

Adapted from RISKSUR

The broad concept of disease surveillance

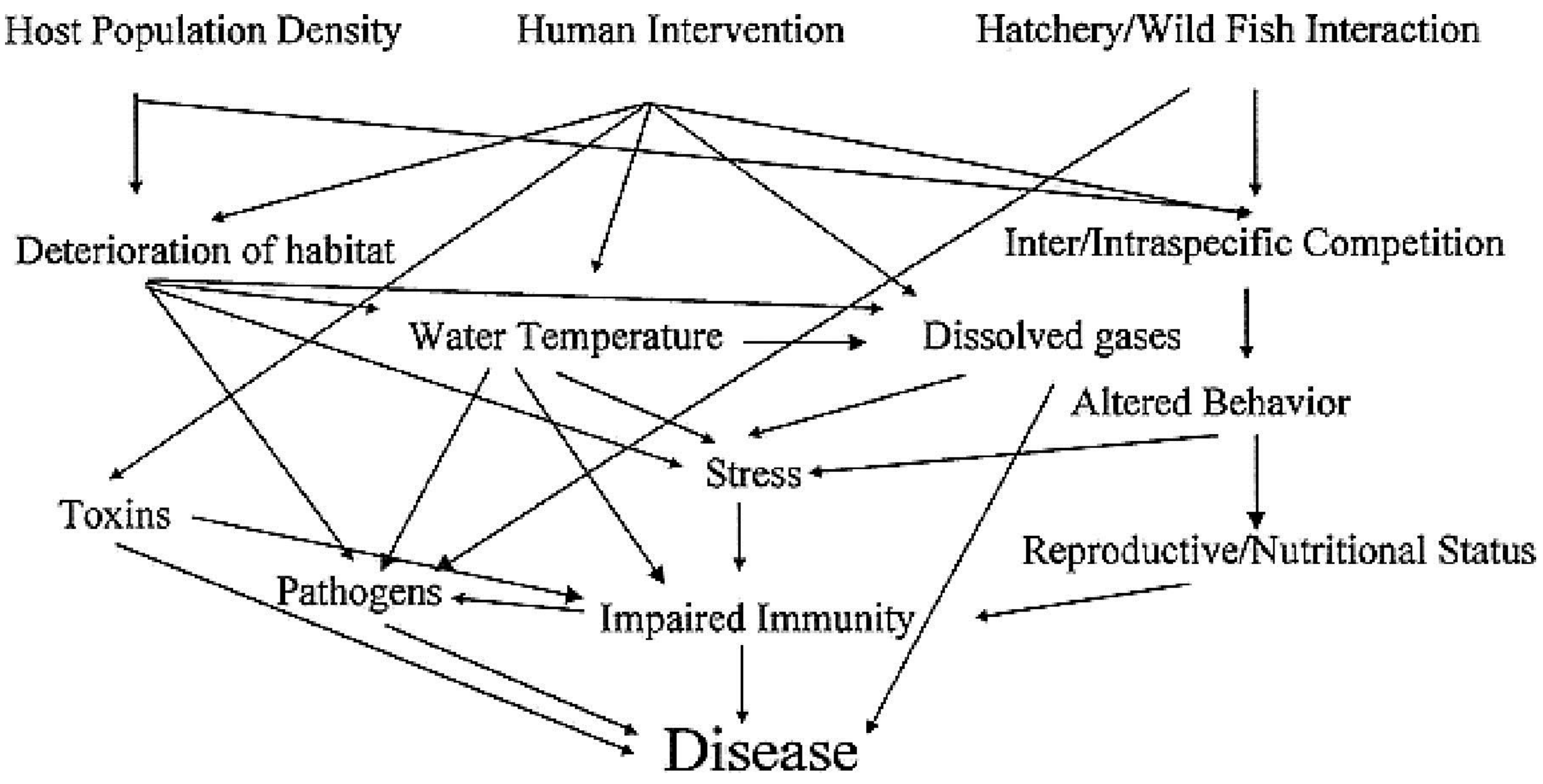


From book: Epidemiology for field veterinarians



Best management practices for shrimp health

Disease dynamics



Ronald P Hedrick 1998

Modern concepts of disease

Bradford–Hill criteria

Criteria	Description
Strength of association	Strong associations with higher risk ratios are more likely to be causal than a weak association
Consistency	Consistently finding an association between a putative cause and a disease outcome in multiple studies by different investigators
Specificity	If a factor is only associated with a specific disease it was said to be specific and considered more likely to be causal
Temporality	The causal factor should precede the outcome it is proposed to be causing
Biological gradient	A dose-response association is supportive of a causal relationship
Plausibility	Is the association biologically plausible?
Coherence	The proposed causal association should not contradict current scientific knowledge
Experiment	A causal association is more likely if it is supported by results from controlled, randomized trials
Analogy	A causal association may be more likely if there are other examples of causal associations for analogous exposures and outcomes

AMERICAN
Journal of Epidemiology
Formerly AMERICAN JOURNAL OF HYGIENE

VOL. 104 DECEMBER, 1976 NO. 6

Reviews and Commentary

CAUSES

KENNETH J. ROTHMAN

PUBLIC HEALTH MATTERS

Causation and Causal Inference in Epidemiology

Kenneth J. Rothman, DrPH, Sander Greenland, MA, MS, DrPH, C Stat

Total factors = 10
5 sufficient causes to disease
One necessary factor

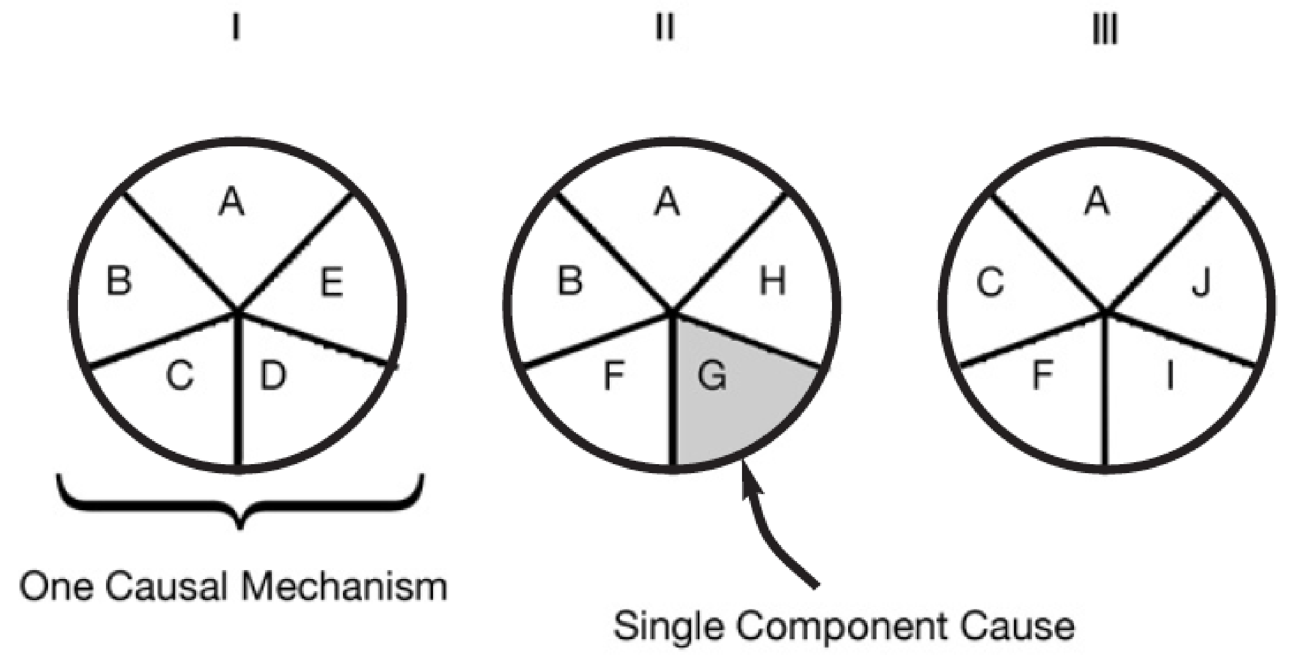


FIGURE 1—Three sufficient causes of disease.

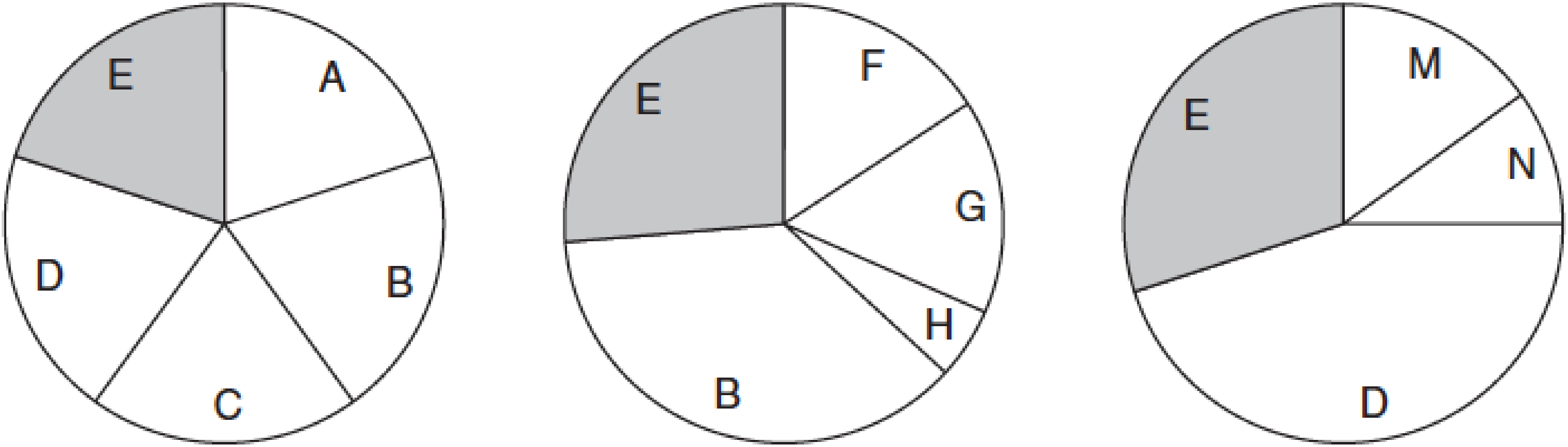
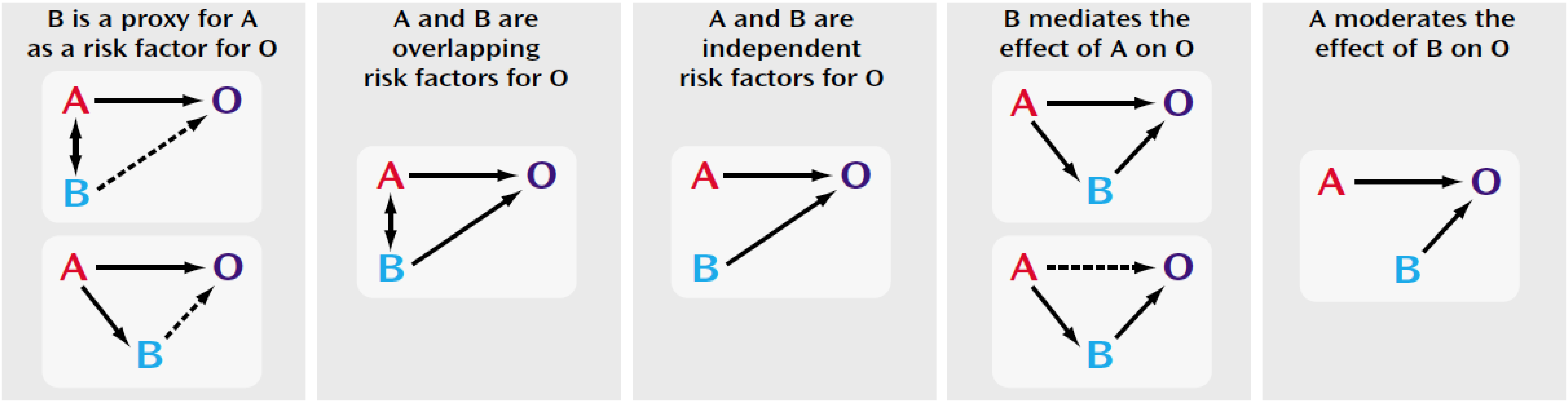


Fig. 4.1. Use of pie charts to demonstrate three separate sufficient causal mechanisms, each made up of multiple component causes identified by letters. There is one candidate necessary cause (E) that is the only component cause found in every sufficient causal mechanism (adapted from Rothman and Greenland, 2005).

How Do Risk Factors Work Together? Mediators, Moderators, and Independent, Overlapping, and Proxy Risk Factors

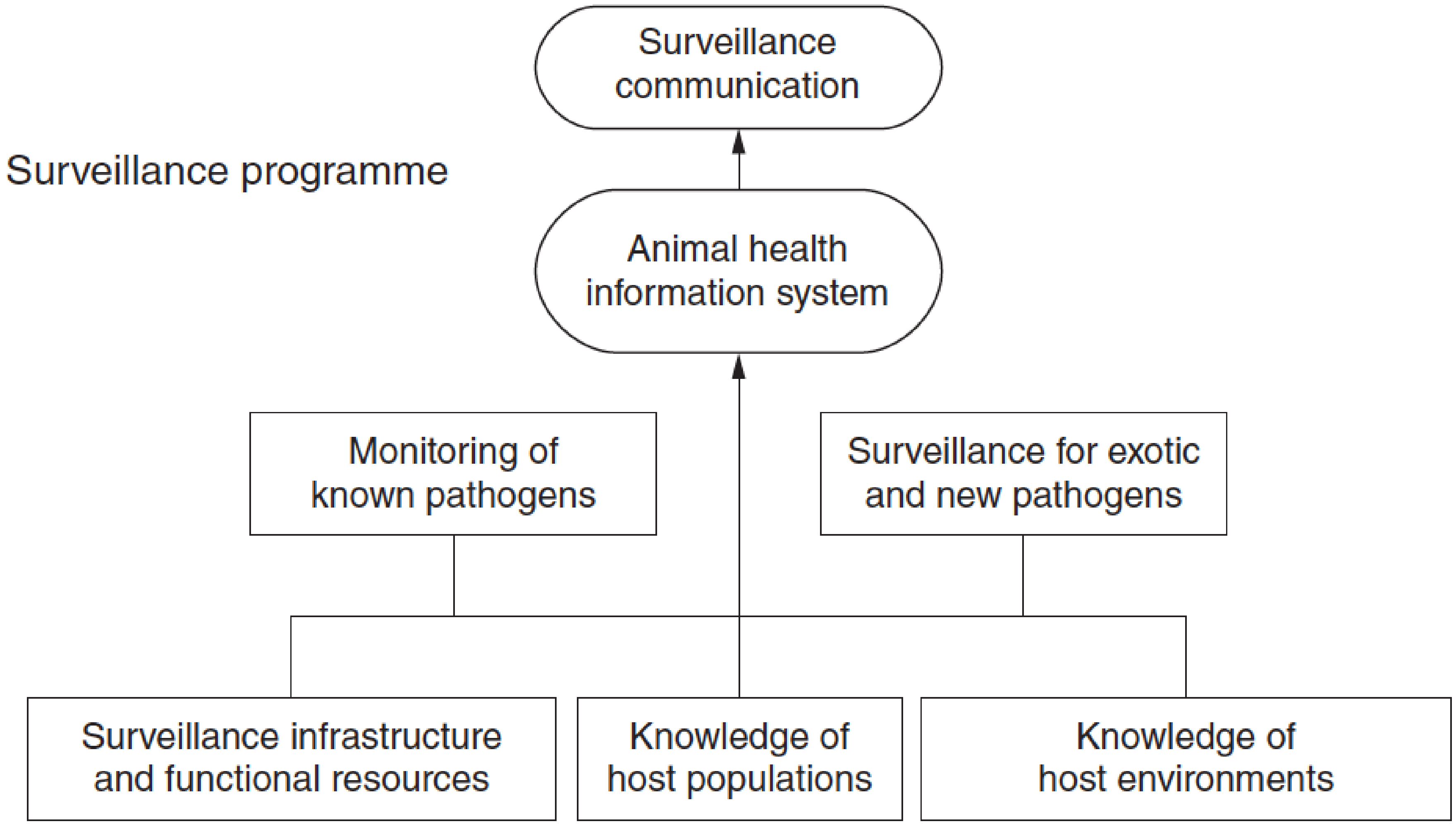
Kraemer, Stice, Kazdin et al. Am J Psychiatry 2001; 158:848–856

FIGURE 1. Five Ways Risk Factors A and B Can Work Together to Affect Outcome O[a]



[a] Left to right positioning indicates temporal order. A solid arrow indicates a correlation. A dotted arrow indicates a correlation that weakens or disappears when the other risk factor is considered.

Relationships among different components of a population health surveillance program incorporating OIE Code concepts



From book: Epidemiology for field veterinarians

Agreed on previous Natal workshop

- **Thailand, Ecuador, Mexico and China** – recall historical surveillance info to demonstrate freedom from IMNV or surveillance sensitivity.
- **Indonesia** – surveillance data to gain insight into the spatial epidemiology (definition of risk zones or zones of influence)
- **Brazil** – surveys to farmers to gain best management practices knowledge and biosecurity measures

Agreed on previous Natal workshop

- ~~**Thailand, Ecuador, Mexico and China** – recall historical surveillance info to demonstrate freedom from IMNV or surveillance sensitivity.~~
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- **Brazil** – surveys to farmers to gain best management practices knowledge and biosecurity measures

India (June and July, 2016)

- Adult *L. vannamei* with body weight ranging from 7.2 to 15.3 g were collected from grow-out ponds located at different localities in Purba Medinipur and North 24 Parganas districts, West Bengal, India.
- The mortality of shrimp in all disease outbreak ponds ranged from 20% to 50% and increased gradually.
- The possibility is that it could have entered either from Indonesia or Brazil through smuggled broodstock or post-larvae for use in a commercial hatchery.
- Very likely Ganges Delta will spread as in the NE Brazil


INDEX
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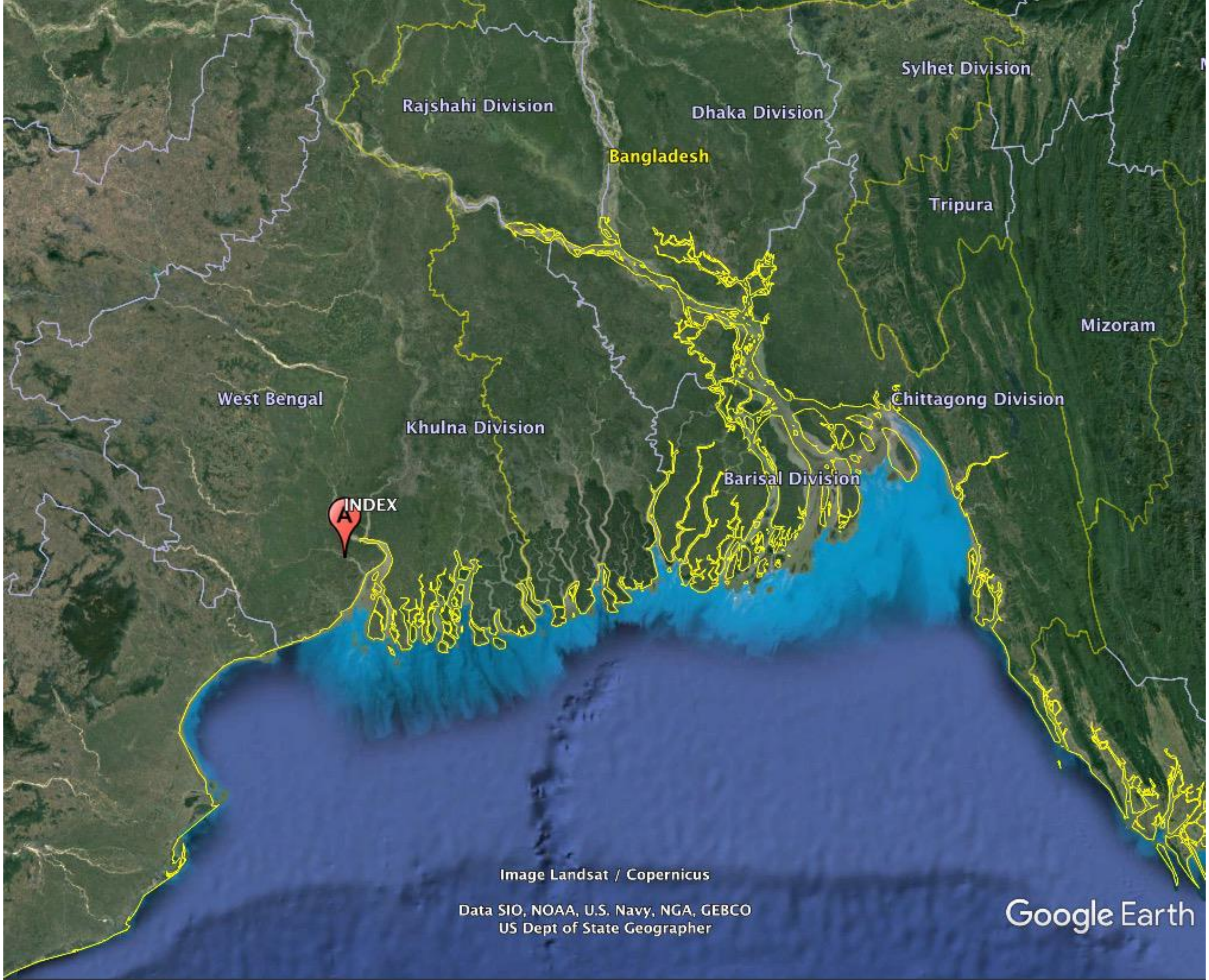
Sylhet Division
Rajshahi Division
Dhaka Division
Bangladesh
Tripura
Mizoram
West Bengal
Chittagong Division
Khulna Division
Barisal Division
A
INDEX
Image Landsat / Copernicus
Data SIO, NOAA, U.S. Navy, NGA, GEBCO
US Dept of State Geographer
Google Earth

Estimation of the probability of freedom from ISAV in farmed Coho salmon in Chile using scenario tree modeling

Alba A, Monti G, Ibarra R, Tello A, Lara M, Montecinos K, Gallardo A, Sergeant E, Perez AM, **Mardones FO***.

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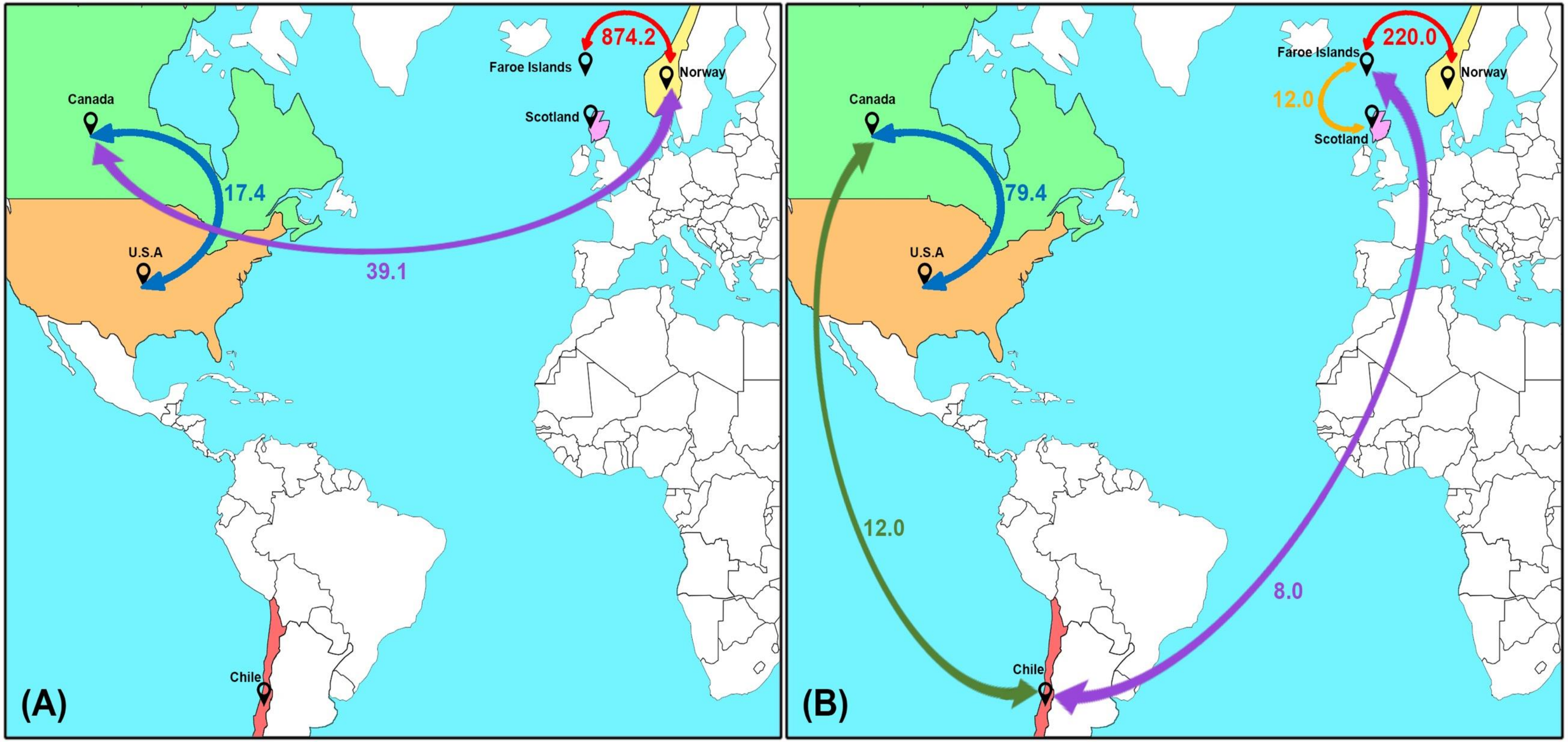
INFECTIOUS SALMON ANEMIA

- Affects Atlantic salmon (*Salmo salar*), rainbow trout (*O. mykiss*) are considered as carriers.

- World Animal Health Organization (OIE) notifiable disease

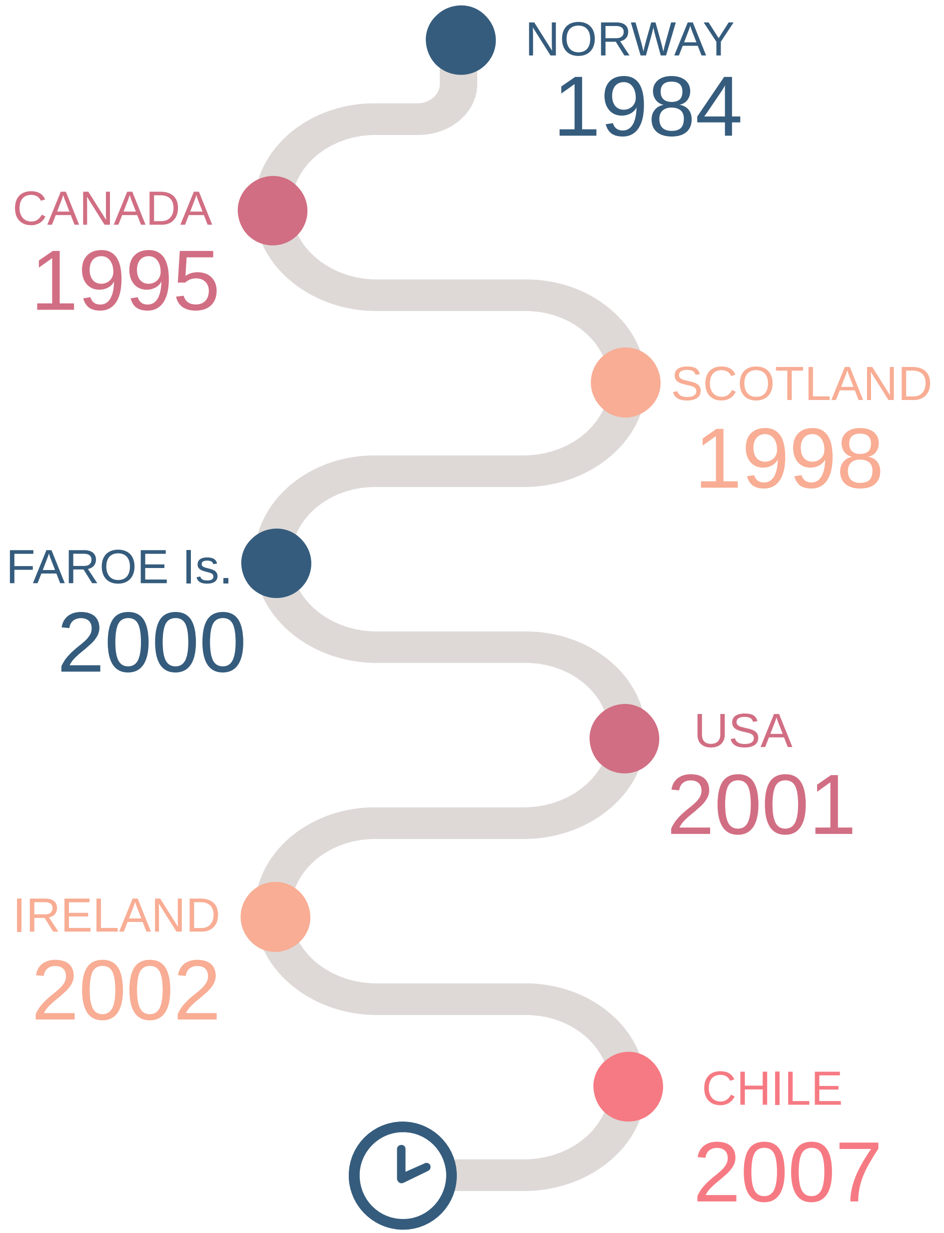
- Norway 1984, Canada 1995, Scotland 1998, Faroe Is. 2000, USA 2001, Ireland 2002, **Chile 2001 y 2007**.

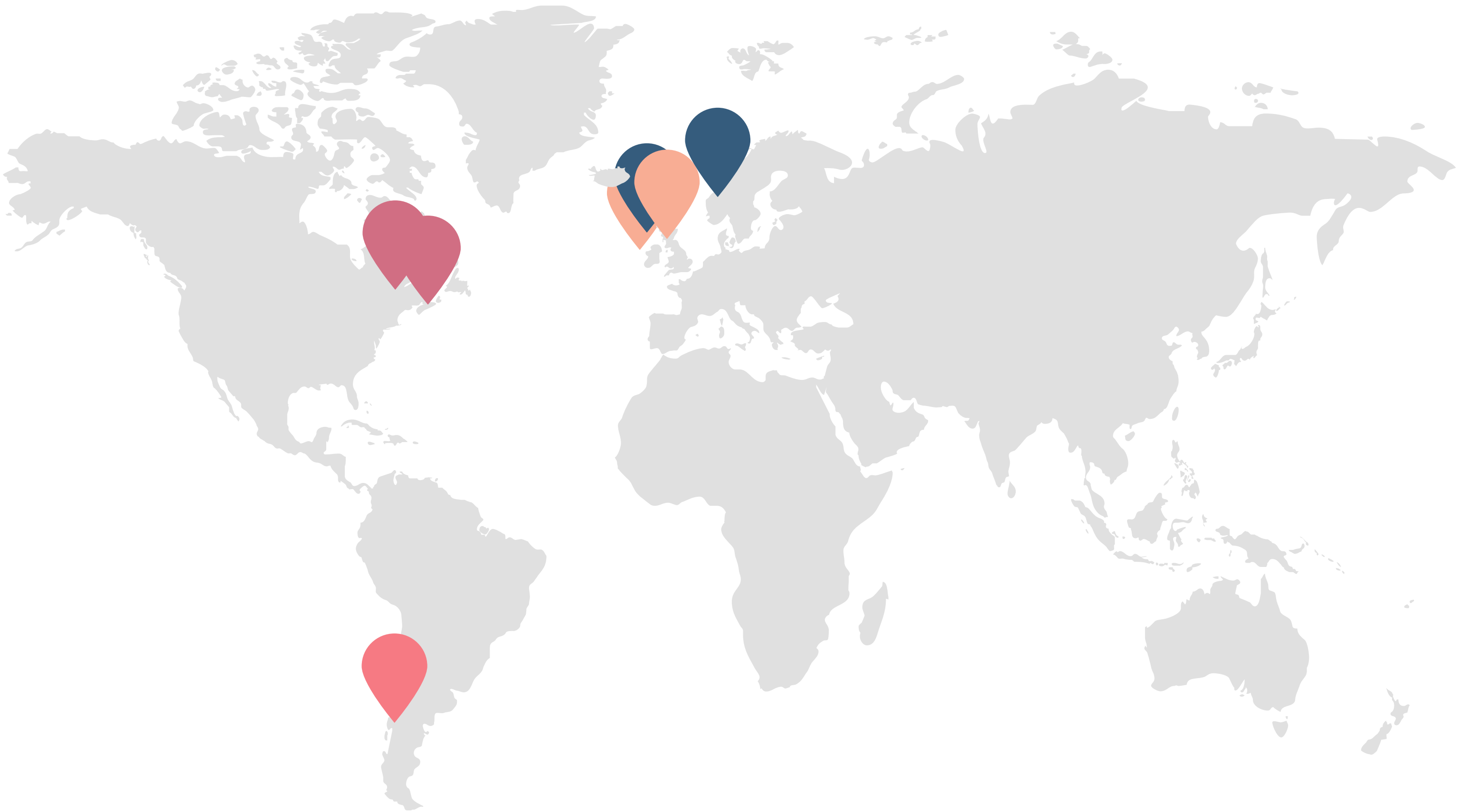
ISAV likely dispersal routes



Our team used BSSVS to fit phylogeographic models to the FP gene (A) and HE gene (B) sequence dataset, and inferred geographic connections (transmission routes) using Bayes factors (BF).

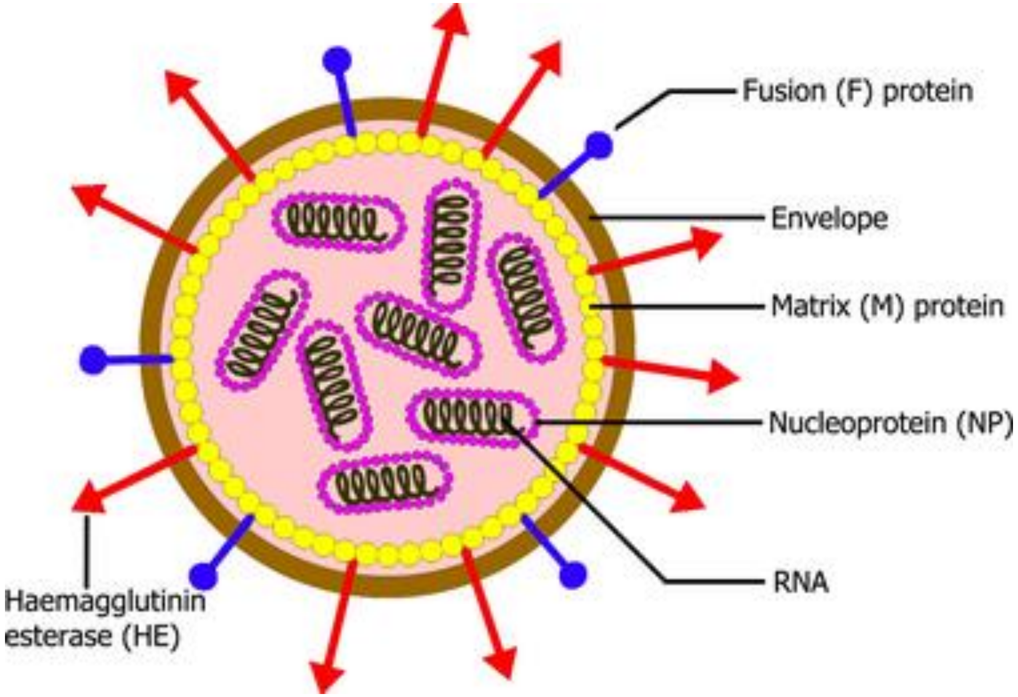
ISAV in a global context

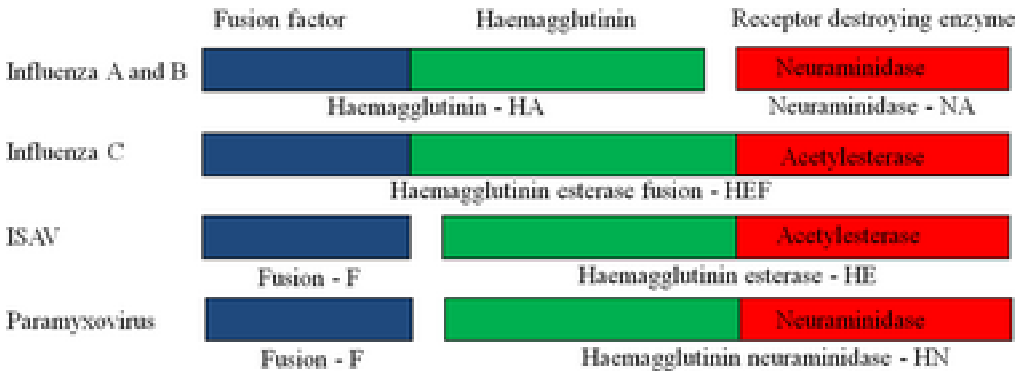




INFECTIOUS SALMON ANEMIA virus (ISAV)

RNA virus;
family *Orthomyxoviridae*
("fish flu")





Localization of the functional activities of the surface proteins of ortho- and paramyxovirus.

Model of infectious salmon anaemia virus (ISAV) genome segment 6 encoding the HE surface glycoprotein.

Aamelfot et al. 2014. Infectious salmon anaemia – pathogenesis and tropism. J Fish Dis 37(4).

CHAPTER 2.3.5.

INFECTION WITH INFECTIOUS SALMON ANAEMIA VIRUS

Natural outbreaks of ISA have only been recorded in farmed Atlantic salmon, and in Coho salmo
(*Oncorhynchus kisutch*) in Chile (Kibenge et al., 2001). Subclinically infected feral Atlantic salmon, brow

Natural outbreaks of ISA have only been recorded in farmed Atlantic salmon, and in Coho salmon (*Oncorhynchus kisutch*) in Chile (Kibenge et al., 2001). Subclinically infected feral Atlantic salmon, brown trout and sea trout (*S. trutta*) have been identified by RT-PCR (Kibenge et al., 2004; Plarre et al., 2005). In marine fish, detection of ISAV by RT-PCR has been reported in tissues of pollock (*Pollachius virens*) and cod (*Gadus morhua*), but only in fish collected from cages with Atlantic salmon exhibiting ISA (MacLean et al., 2003). Following experimental infection by bath immersion, ISAV has been detected by RT-PCR in rainbow trout (*Oncorhynchus mykiss*) (Biacchesi et al., 2007) and herring (*Clupea harengus*), the latter in a subsequent transmission to Atlantic salmon. Attempts have been made to induce infection or disease in pollock, *Pollachius virens*, but with negative results.

2.2.2. Susceptible stages of the host

In Atlantic salmon, disease outbreaks are mainly reported in seawater cages, and only a few cases have been reported in the freshwater stage, including one case in yolk sac fry (Rimstad et al., 2011). ISA has been experimentally induced in both Atlantic salmon fry and parr kept in freshwater. Genetics may also play an

2.2.3. Species or subpopulation predilection (probability of detection)

ISA is primarily a disease of Atlantic salmon.

CHILEAN SALMON INDUSTRY

Started mid-80s

Exotic species

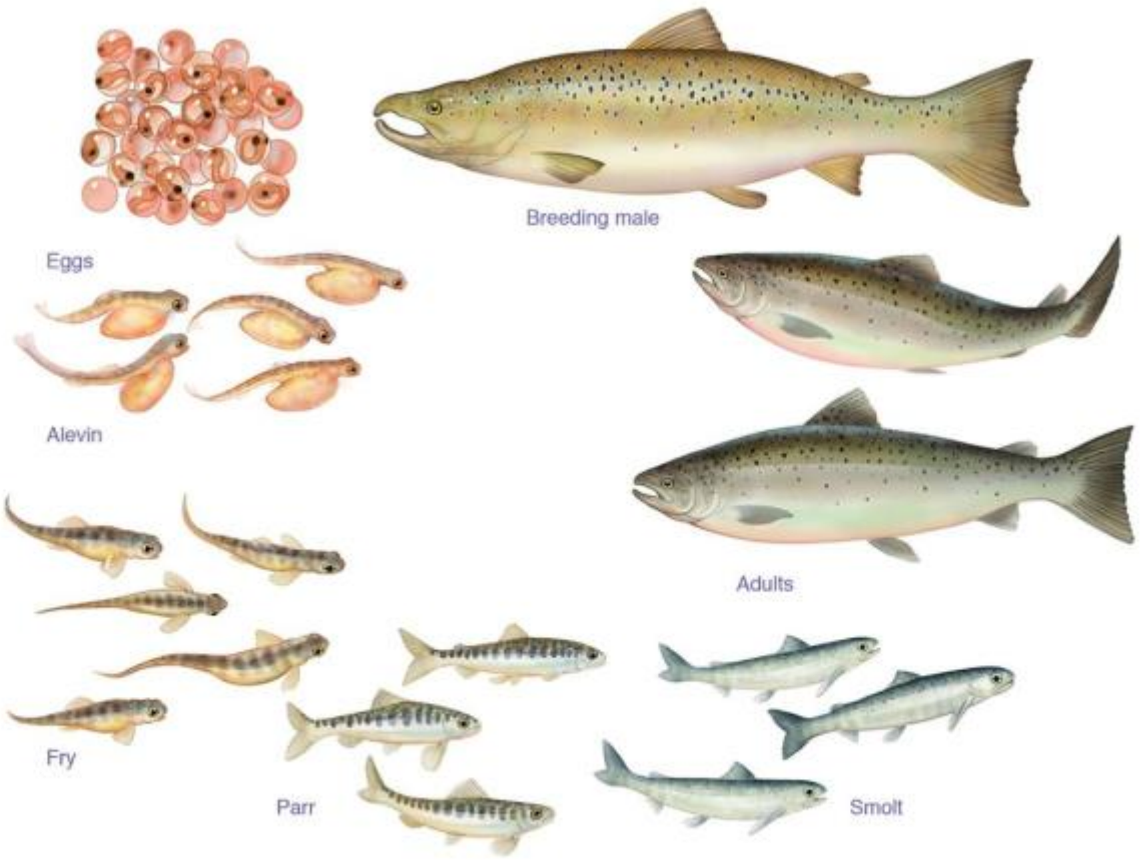
2nd largest producer

USD 4 bill. yearly

Half of the country

SALMON FARMING INDUSTRY

Natural life cycle



Artificial salmon farming

Photos: M. Godoy

CONTROVERSIES between STUDIES related to the ISAV infection in Coho salmon in Chile

EVIDENCES of ISAV infection in farmed Coho salmon in Chile

Vol. 45: 9–18, 2001	DISEASES OF AQUATIC ORGANISMS Dis Aquat Org	Published May 4

Isolation and identification of infectious salmon anaemia virus (ISAV) from Coho salmon in Chile

Frederick S. B. Kibenge[1,*], Oscar N. Gárate[2], Gerald Johnson[1], Roxana Arriagada[4], Molly J. T. Kibenge[2], Dorota Wadowska[3]

[1]Department of Pathology and Microbiology, [2]AVC Inc., and [3]EM Laboratory, Atlantic Veterinary College, University of Prince Edward Island, 550 University Ave., Charlottetown, Prince Edward Island C1A 4P3, Canada
[4]Aquatic Health Chile Ltda, Benavente 952, Puerto Montt, Chile

EVIDENCES of resistence to ISAV infection in Pacific salmon in Chile

Journal of Fish Diseases 2003, 26, 511–520

Relative resistance of Pacific salmon to infectious salmon anaemia virus

J B Rolland and J R Winton

Western Fisheries Research Center, Seattle, WA, USA

Other diseases similar to ISAV infection in Coho salmon in Chile

Journal of Fish Diseases 2006, 29, 709–715

Infectious haemolytic anaemia causes jaundice outbreaks in seawater-cultured coho salmon, *Oncorhynchus kisutch* (Walbaum), in Chile

P A Smith[1], J Larenas[1], J Contreras[1], J Cassigoli[2], C Venegas[1], M E Rojas[1], A Guajardo[1], S Pérez[1] and S Díaz[1]

1 Unit of Pathology of Aquatic Animals, Department of Animal Pathology, Faculty of Veterinary Sciences, University of Chile, Santiago de Chile, Chile
2 Instituto Tecnológico del Salmón (INTESAL), Asociación de la Industria del Salmón (Salmón Chile), Puerto Montt, Chile

Characterization of ISAV associated with clinical disease uniquely in farmed Atlantic salmon in Chile

BMC Veterinary Research

BioMed Central

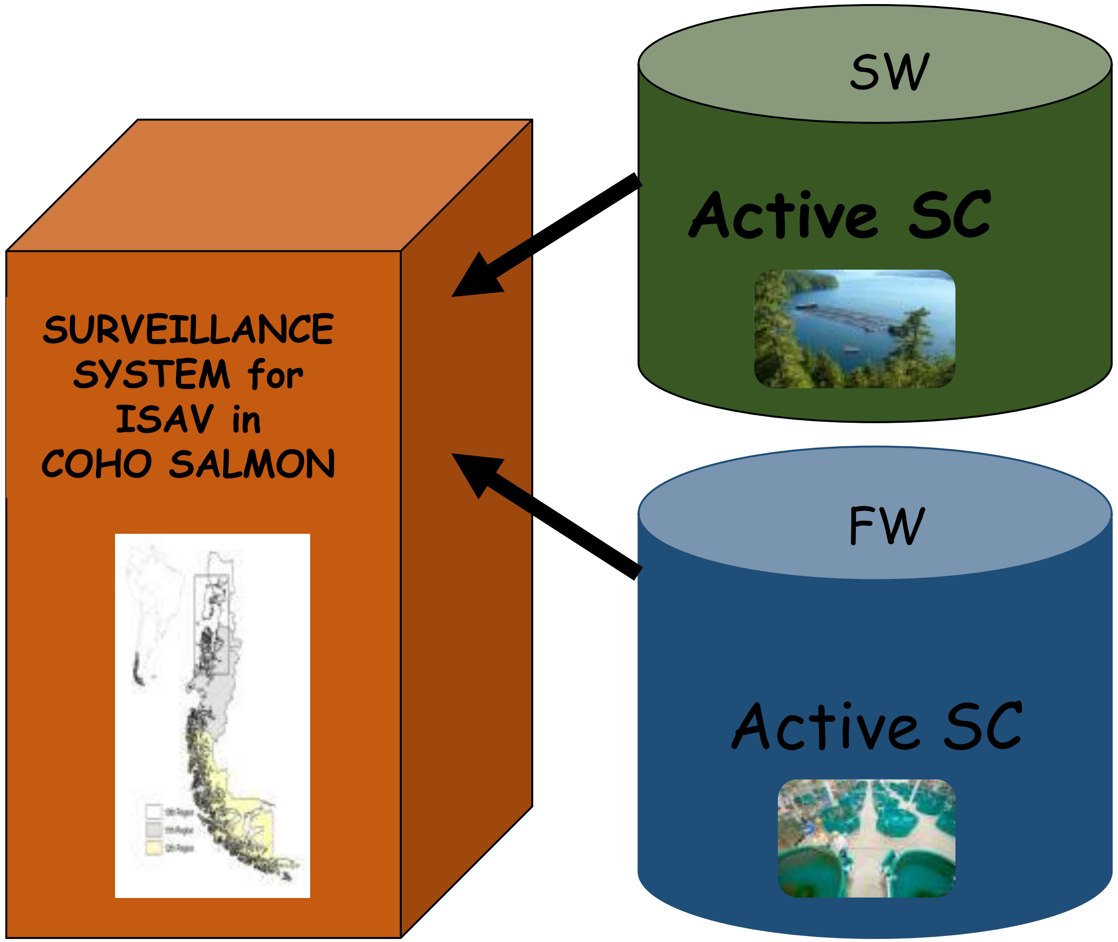
Research article

Open Access

First detection, isolation and molecular characterization of infectious salmon anaemia virus associated with clinical disease in farmed Atlantic salmon (*Salmo salar*) in Chile

Marcos G Godoy[1], Alejandra Aedo[1], Molly JT Kibenge[2], David B Groman[3], Carmencita V Yason[4], Horts Grothusen[1], Angelica Lisperguer[4], Marlene Calbucura[1], Fernando Avendaño[5], Marcelo Imilán[5], Miguel Jarpa[5] and Frederick SB Kibenge*[2]

Since 2001 SURVEILLANCE SYSTEM for ISAV in COHO SALMON in CHILE



A **two-stage systematic random sampling** of all farmed salmon at both fresh and marine sites

At least **two visits per year with a minimum interval of 4 months.**

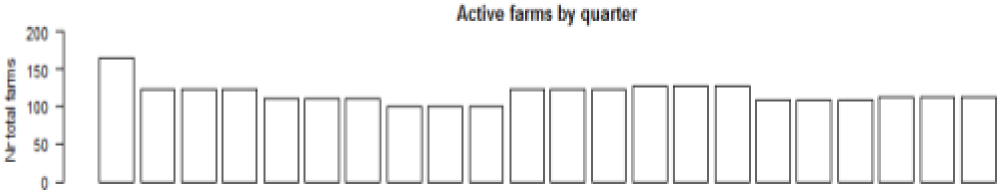
Mandatory

Coordinated by Sernapesca and **co-paid by both farmers and Sernapesca.**

TARGETED POPULATION
Coho salmon farms in Chile (Sep 2007-Dec 2014)

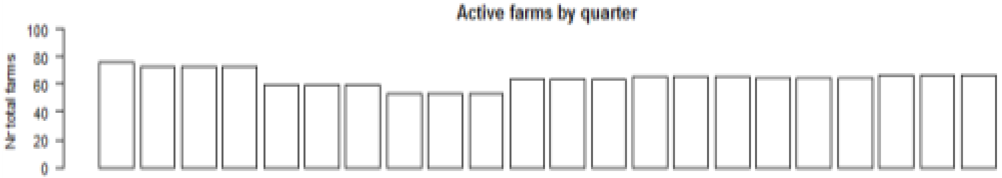
~363 sites in salt-water

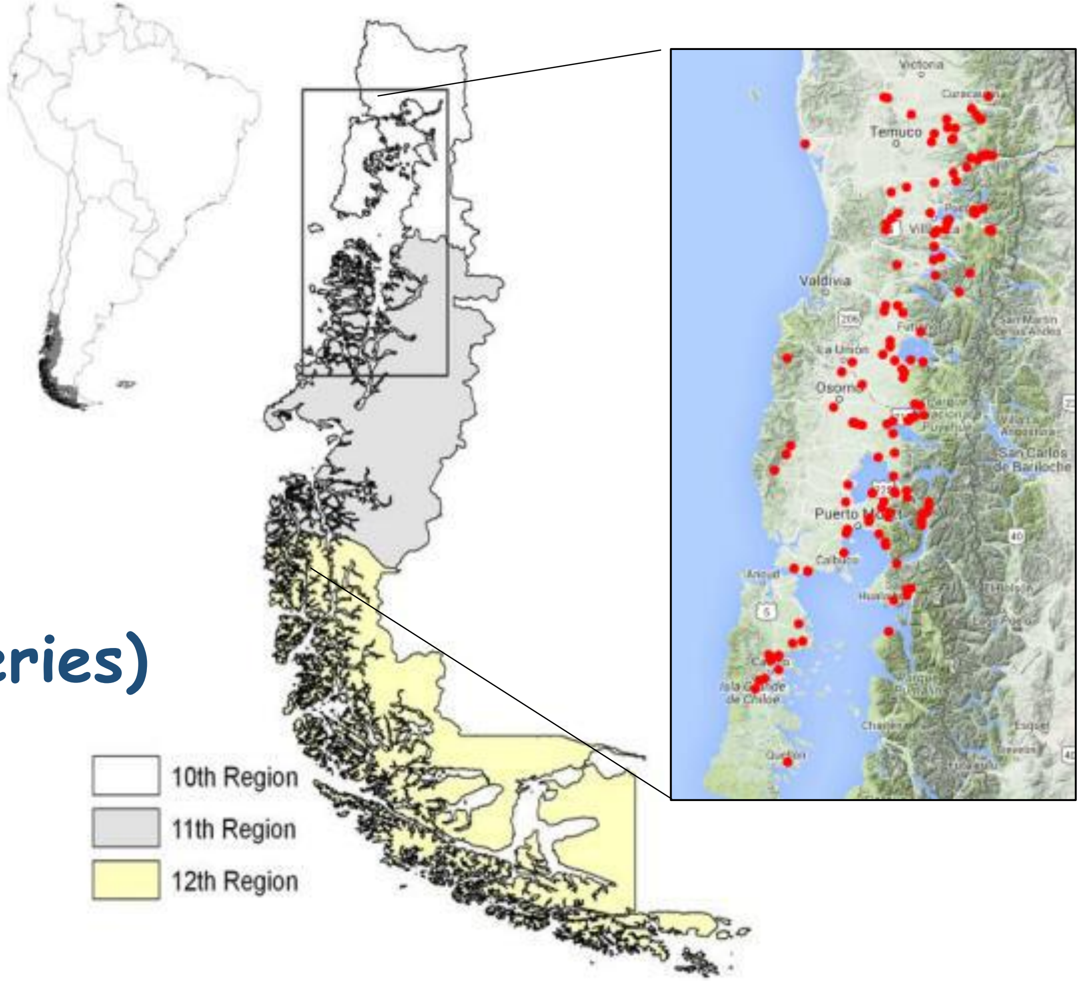
(a median = 109 per year, range: 86-167)



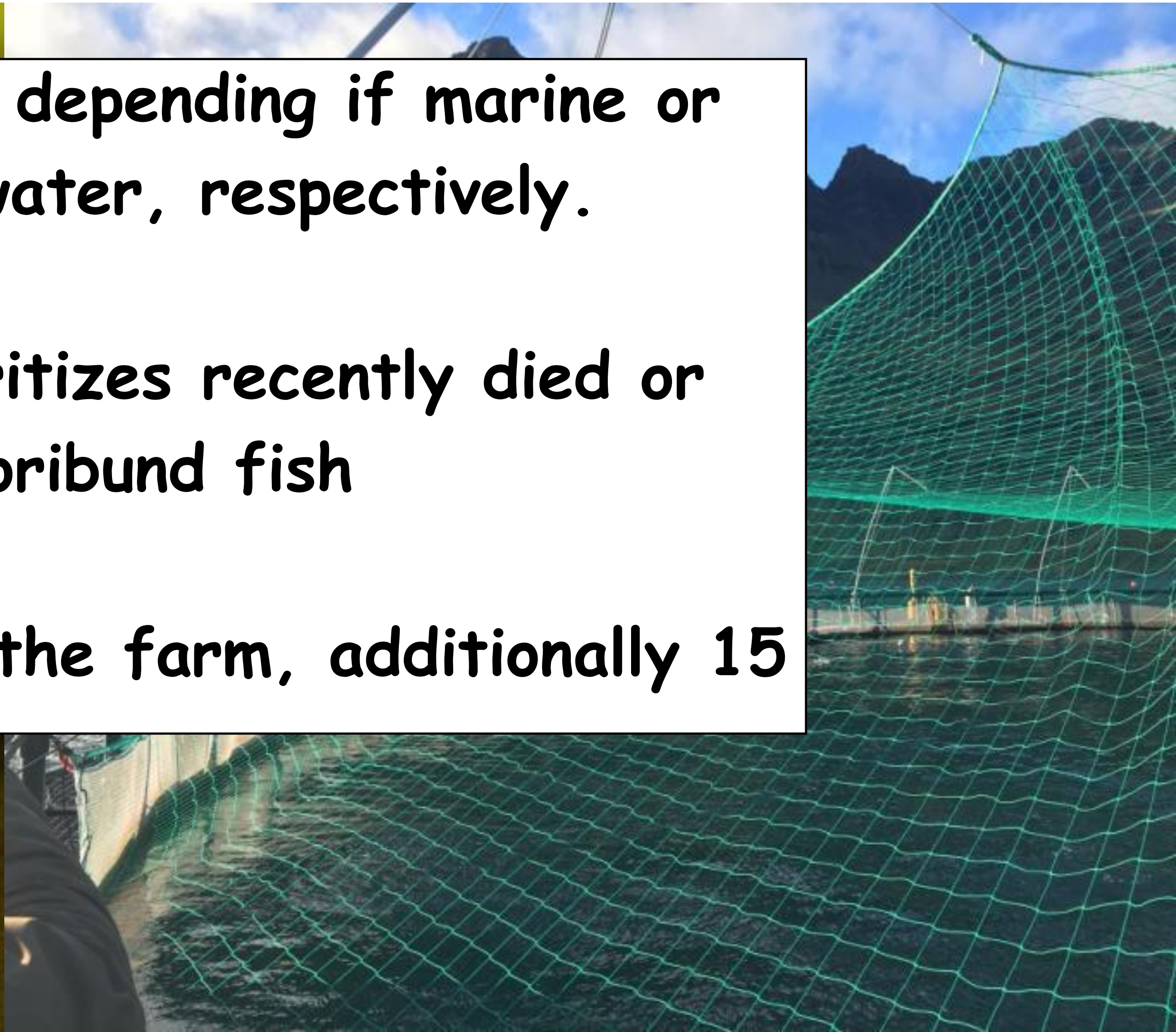
~187 sites in fresh-water (hatcheries)

(a median = 87 per year, range: 74-102)





Samplings



30 to 60 fish depending if marine or freshwater, respectively.

Samples prioritizes recently died or moribund fish

If breeders at the farm, additionally 15

AIMS of the STUDY

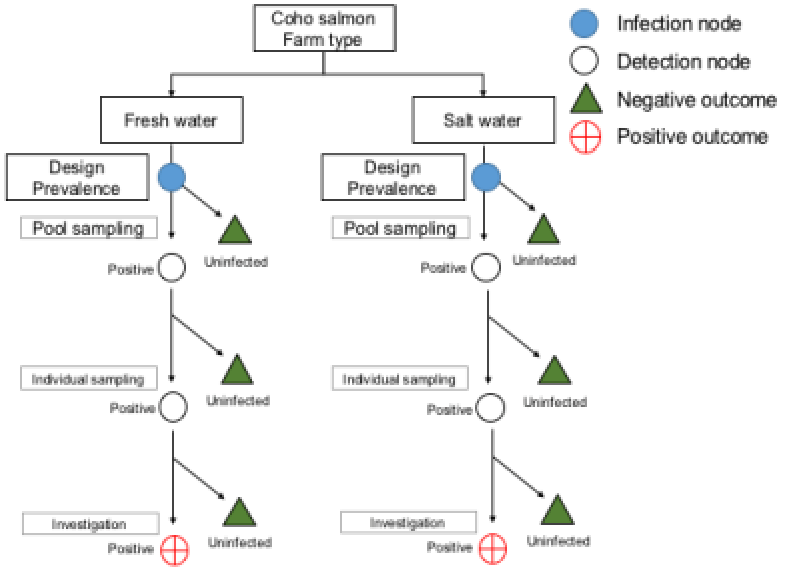
To assess the **sensitivity of the surveillance program** and the **probability of freedom from ISAV** in the **Chilean population of farmed coho salmon**

Period : Sep 2007 and Dec 2014

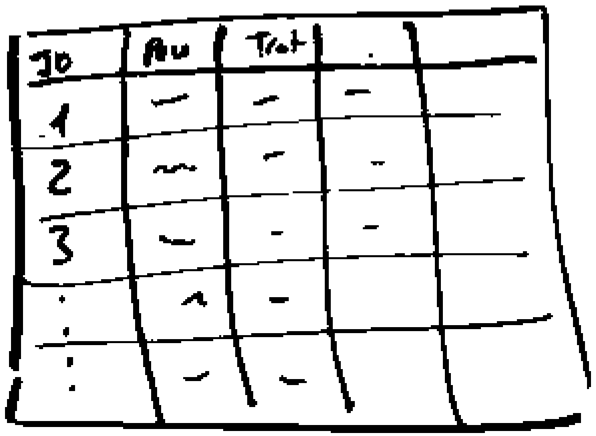
Why? To evaluate the need for sustaining surveillance activities for the disease in this species and contribute to increase the efficiency in the use of resources for disease surveillance in farmed salmon in Chile and other regions.

Stochastic scenario tree model (Martin et al, 2007)

- To estimate:
  - sensitivity of the surveillance system
  - probability of freedom from ISAV in the coho sub-population
- Assessed every 4 months
- The model builds up information from quarter to quarter, taking the confidence gained from consecutive testing and the probability of introduction of the disease into the coho subpopulation over time.



SURVEILLACE and POPULATION DATA of the ANALYSIS



SOURCE:

SERNAPESCA
Ministerio de Economía, Fomento y Turismo
Gobierno de Chile

- Identification - farm code
- Location of the farm - region
- Type of site: fresh water (FW) or salt water (SW)
- Number of farmed coho salmon in each site
- Sampling date
- Number of pools
- Pool size
- Testing results to rtRTPCR

PERIOD: Sep 2007 –Dec 2014

ASSESSMENT OF THE SENSITIVITY SYSTEM BY QUARTER

Probability of detecting the ISAV infection by quarter if the coho salmon population is infected in farmed farms of fresh or salt water in Chile

PERIOD Sep 2007 - Dec 2014

Estimation of the sensitivity by quarter for the ISAV surveillance activities carried out

Sensitivity **at pool level** → Se_{pool}

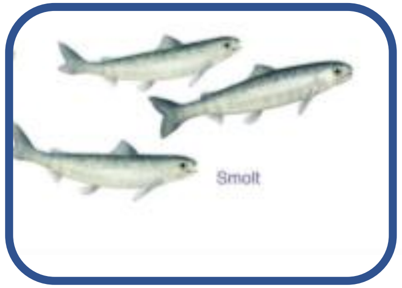
Sensitivity **at farm level** → Se_F

Sensitivity **at component level** → Se_C
being C=SW or FW

System sensitivity **at population level** combining both components → **SeP**

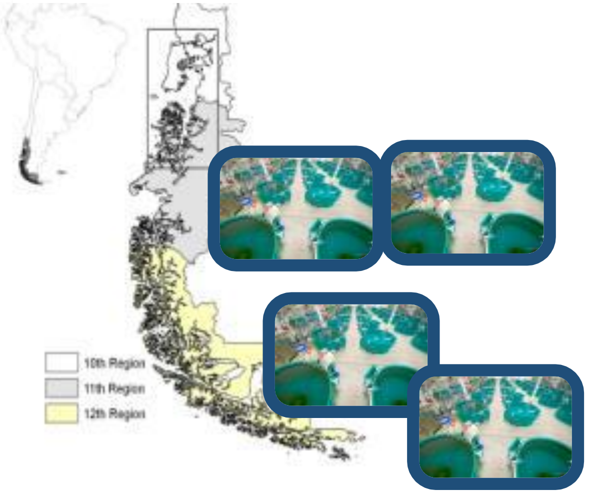
DIFFERENT UNITS OF STUDY TO ASSESS THE SENSITIVITY OF THE SYSTEM

Pool
Se_{Pool}

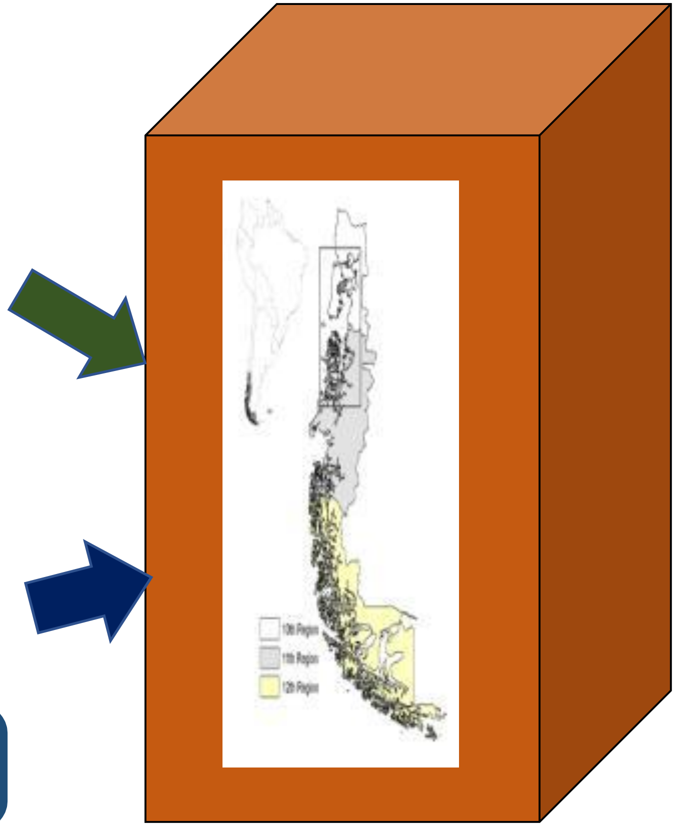


FARM
Se_F

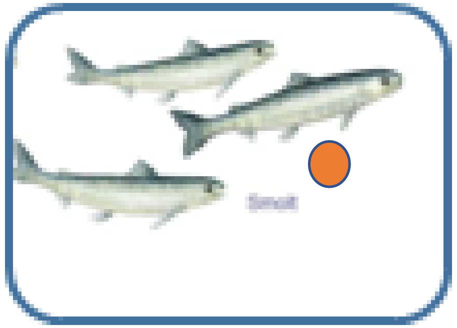
COMPONENT
Se_C



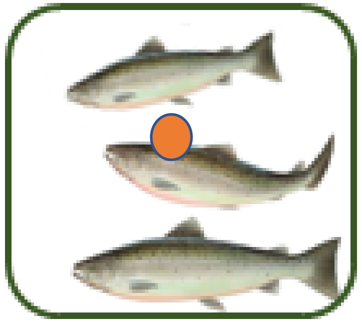
POPULATION
Se_P



SENSITIVITY AT POOL LEVEL → Se_{pool}



P(detecting an infected pool with rtRT-PCR)



Depending on:

- **Pool size**: 3 (1-8)
- **Tissues collected:** Tissues including kidney, heart and gills.
- **Se of diagnostic test**: RT-qPCR and confirmatory sequencing

Pert (min: 90%, mode: 95%, max: 99 %) (*Ring test Sernapesca*)

SENSITIVITY AT FARM LEVEL → Se_F

or

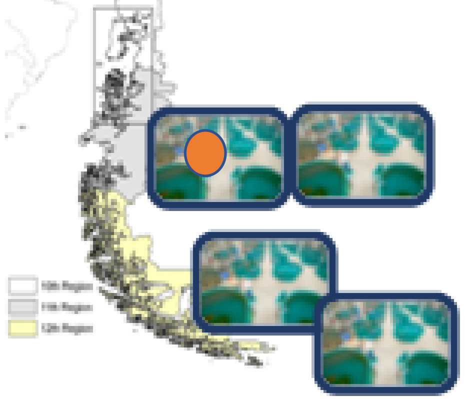
P(detecting at least a positive pool in an infected farm)

Depending on:

Se_{Pool}
Design Prev within farm P^*_U 5%.
Number of pools tested in each farm **n**

SENSITIVITY AT EACH COMPONENT LEVEL: Se_C

or



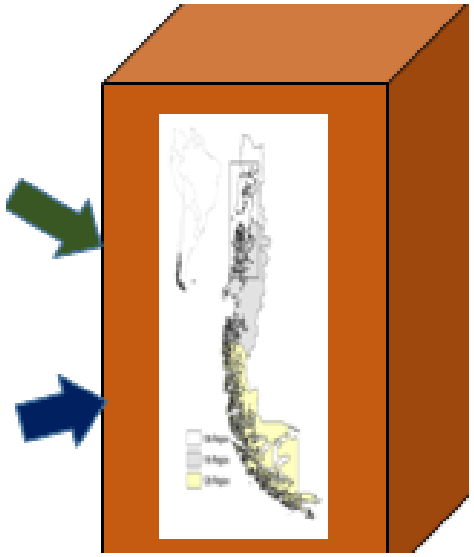
P(detecting at least a positive farm in an infected component)

Depending on:

$$Se_C = 1-(1-Se_F \times n/N)^{PH \times N}$$

- **Se_F**
- Design Prev among farms **P^*_H 5%.**
- No. farms tested **n**
- No. farms in each component **N**

SENSITIVITY AT POPULATION LEVEL → Se_P



P(detecting at least a positive component)

Assuming that both components (SW and FW) are indepent

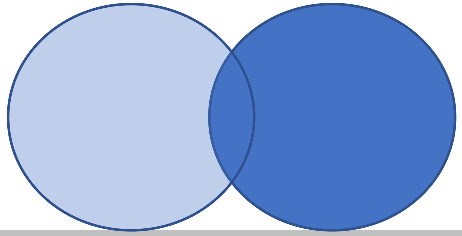
$$Se_P = 1-[(1-Se_{SW}) \times [(1-Se_{FW})]$$

PROBABILITY OF FREEDOM FROM ISAV OVER TIME IF ALL TESTS RESULT NEGATIVE

$$PFree_Q = \frac{1 - PIntro_Q}{1 - Se_{P_Q} X PIntro_Q}$$

Using a Bayesian approach

$$PInfec_Q = 1 - PFree_Q$$



Combining PInfec + PIntro

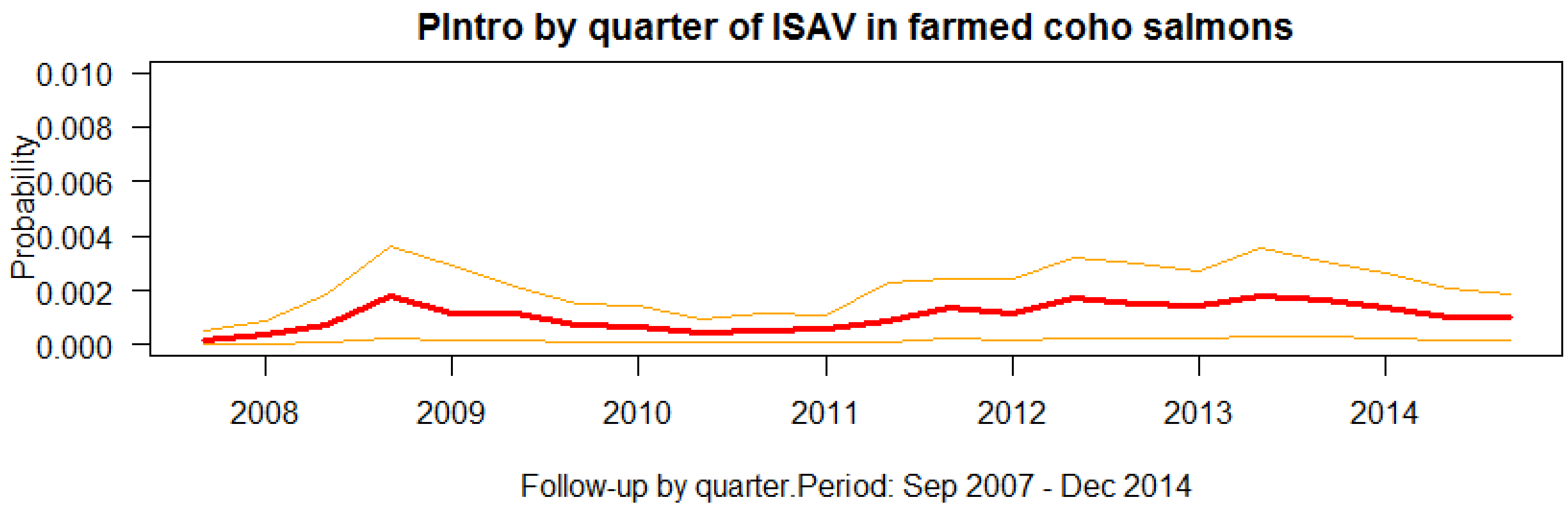
$$PInfecTot_Q = PInfec_Q + PIntro_Q - PInfec_Q X PIntro_Q$$

Proxi measure→ $PIntro_Q$

$Pintro_{t=0}$ → 0.5

Incidence detected in Atlantic salmon over this period

Experimental studies about susceptibility of Atlantic salmon and Coho salmon



PFree over all period → Area under the curve

PFree over the entire period expressed as AUC

$$AUC = \Delta t\left(\frac{PFree_{t=1}}{2} + PFree_{t=2} + PFree_{t=3} + \cdots + \frac{PFree_{t=12}}{2}\right)$$

Statistical Software

Associated packages

"RSurveillance"
"learnBayes"
"reshape"
"zoo"

RESULTS

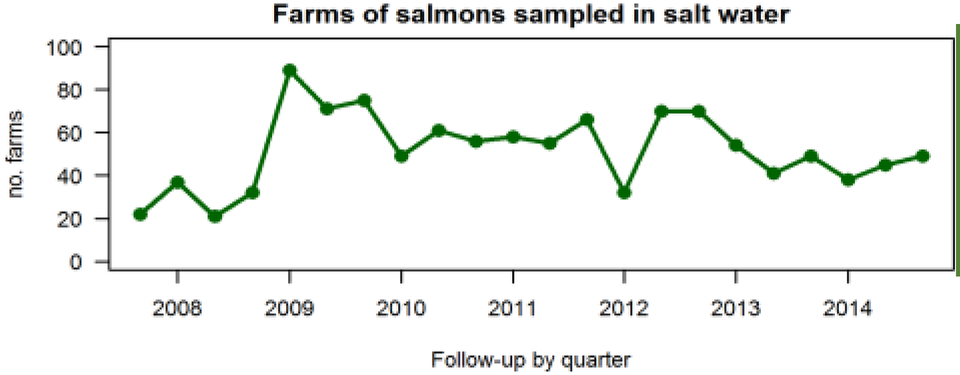
Follow up of the surverveillance for ISAV in Coho salmon (Sep 2007-Dec 2014)

- Sampled a total of 164 FW and 299 SW farms
- 86,382 tested pools
- All NEGATIVE results RT-qPCR

Component	Saltwater (SW)	Freshwater (FW)
Population range under surveillance (median)	86 – 167 (109)	74-102 (87)
Surveyed range farms	43 – 82 (55)	18-58 (32)
Average coho population per farm	0.73 mill (95% CI = 0.4, 1.04)	3.8 mill (95% CI = 1.8, 5.8)

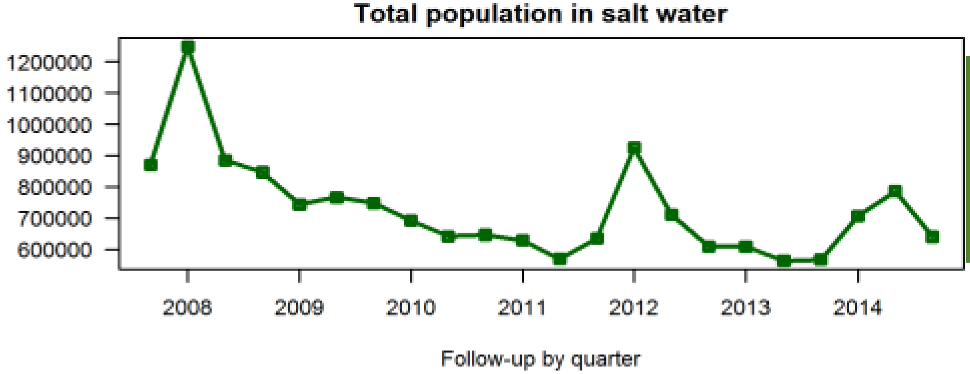
FOLLOW UP of SURVEILLANCE

SALT WATER
50% sites sampled



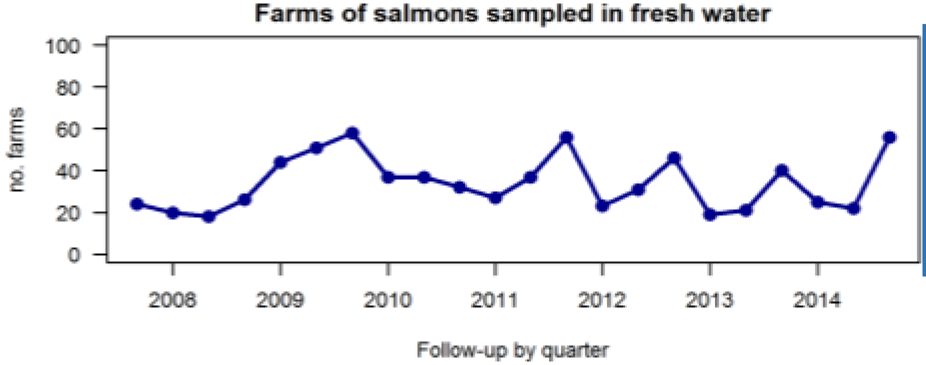
No. farms
Min: 21
Med: 52
Max: 89

No. pools
Min: 209
Med: 1058
Max: 3427

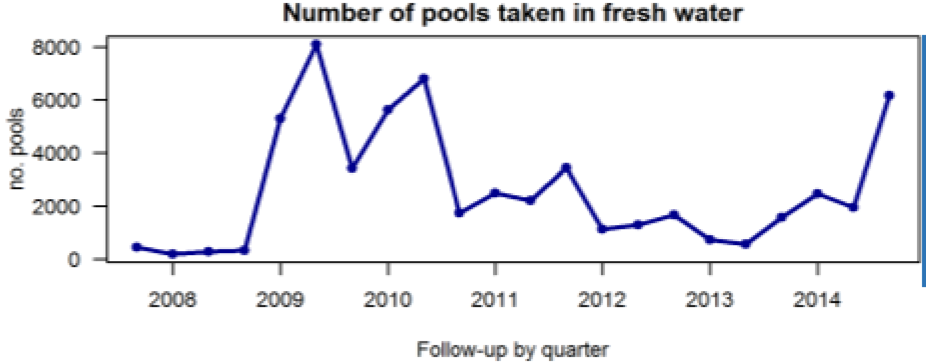


Population
Min: $5.6X10^5$
Med: $6.9X10^5$
Max: $1.2X10^6$

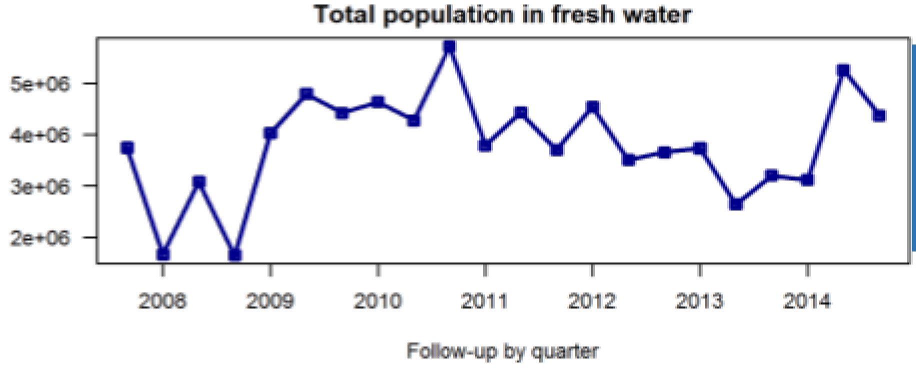
FRESH WATER
38% sites sampled



No. farms
Min: 18
Med: 34
Max: 58

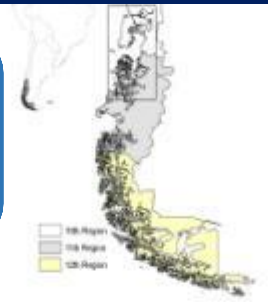


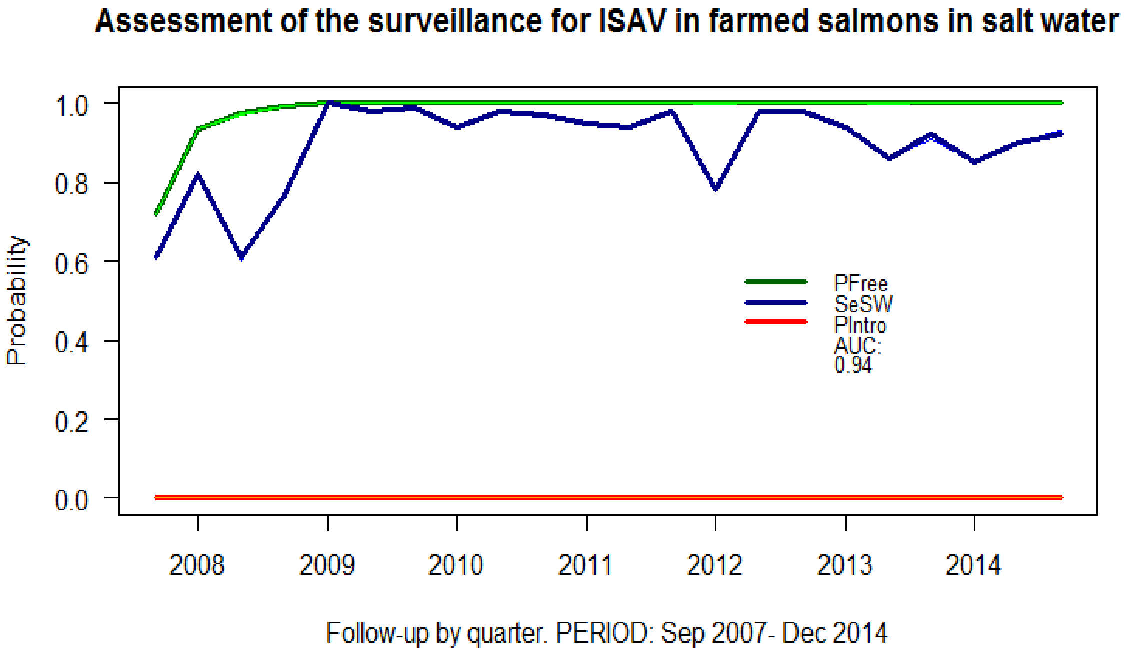
No. pools
Min: 190
Med: 1834
Max: 8088

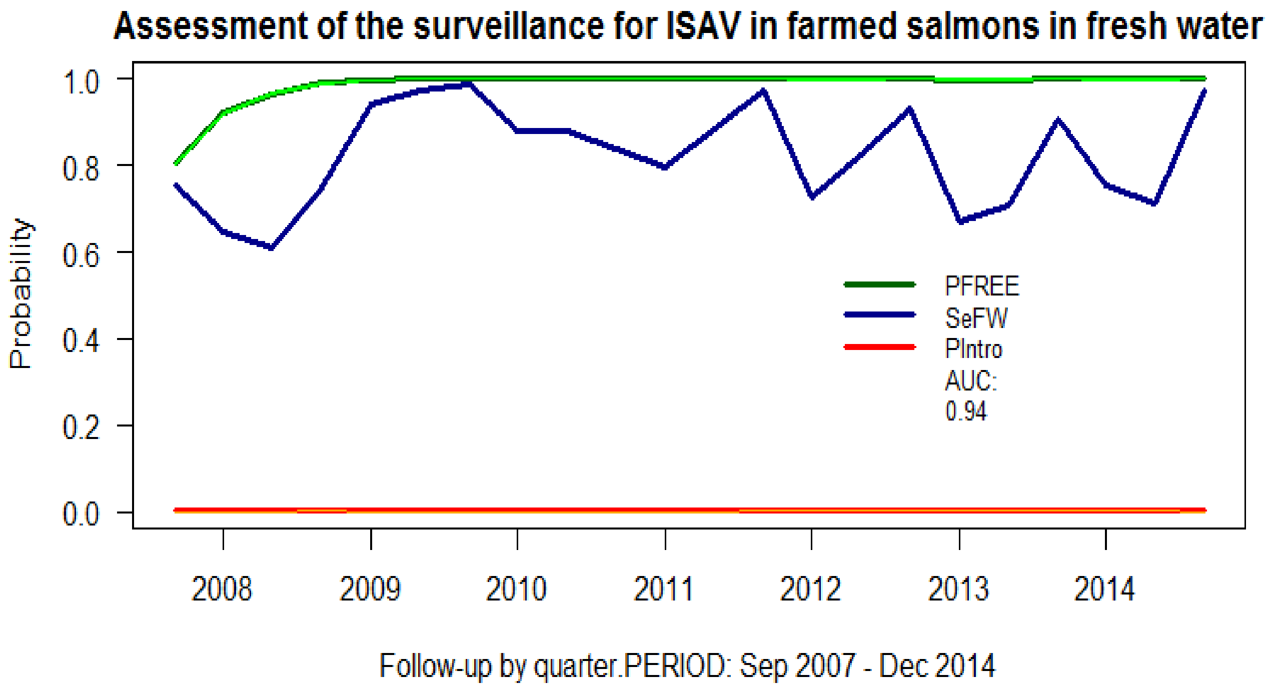


Population
Min: $1.6X10^6$
Med: $3.8X10^6$
Max: $5.7X10^6$

Estimation of PFree and Se for each SSC



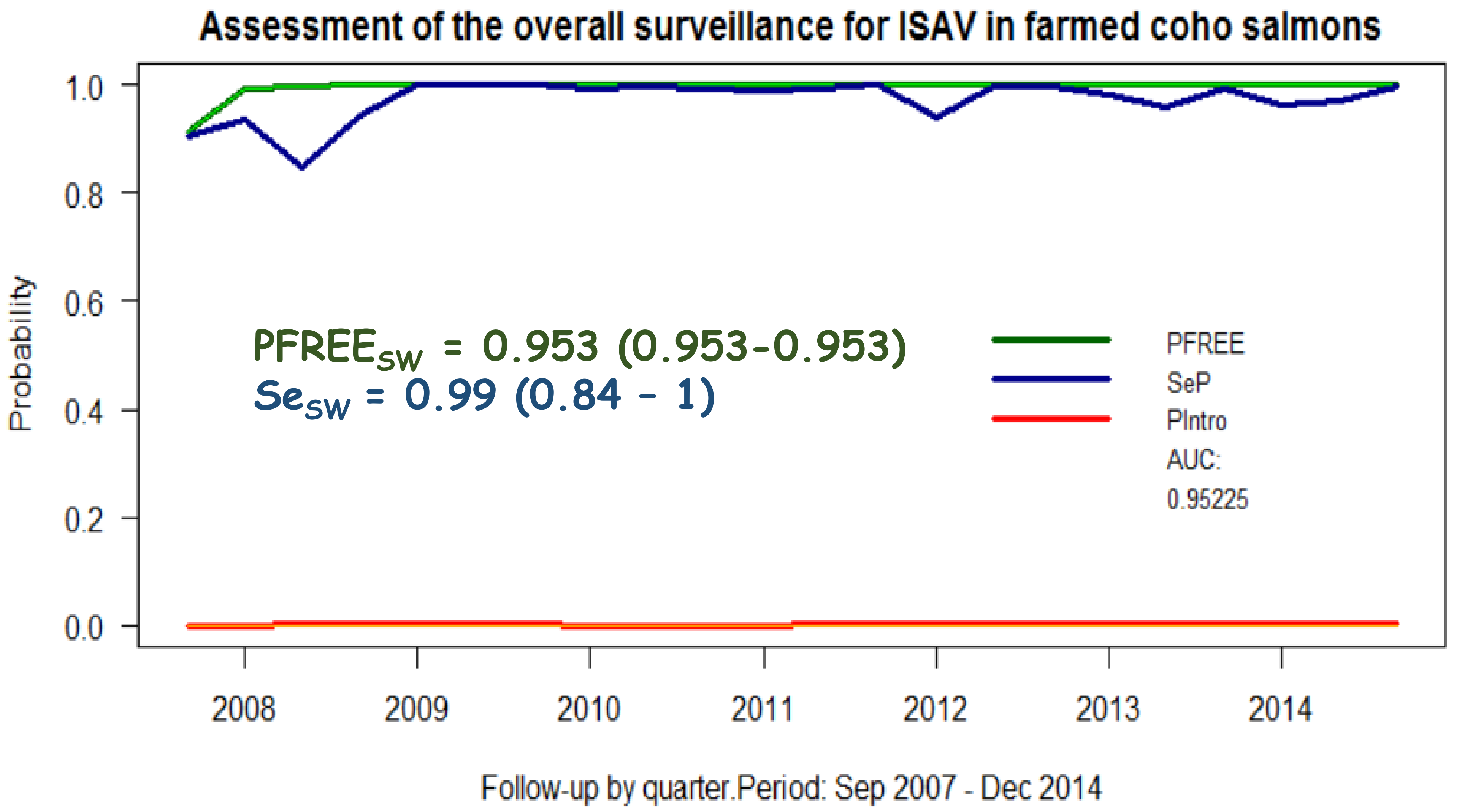




$PFREE_{SW}$ = 0.943 (0.943-0.944)
Se_{SW} = 0.94 (0.61 – 1)

$PFREE_{FW}$ = 0.94 (0.94-0.94)
Se_{FW} = 0.83 (0.61 – 0.99)

Overall PFree and Se for the System of Surveillance for ISAV in farmed Coho salmon



Discussion

- High probability (>0.95) of being free of ISAV
- Kibenge et al 2001 confirmed ISAV from diseased coho salmon farmed with Atlantic salmon, however **Atlantic salmon** did not developed any clinical signs.
- Similar in British Columbia

Journal of Fish Diseases 2016, 39, 117–128 doi:10.1111/jfd.12329

Piscine reovirus, but not Jaundice Syndrome, was transmissible to Chinook Salmon, *Oncorhynchus tshawytscha* (Walbaum), Sockeye Salmon, *Oncorhynchus nerka* (Walbaum), and Atlantic Salmon, *Salmo salar* L.

K A Garver[1], G D Marty[2], S N Cockburn[1], J Richard[1], L M Hawley[1], A Müller[1], R L Thompson[3], M K Purcell[3] and S Saksida[4]

1 Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo, BC, Canada
2 Animal Health Centre, Ministry of Agriculture, Abbotsford, BC, Canada
3 Western Fisheries Research Center, U.S. Geological Survey, Seattle, WA, USA
4 British Columbia Centre for Aquatic Health Sciences, Campbell River, BC, Canada

Relevance in Disease Management

- **Coho salmon has shown a lower susceptibility to most diseases** that currently affect farmed salmonids

  Eg: *sea lice,*

  Piscirickettsia salmonis,

  infectious pancreatic necrotic virus

  ISAV

- Epidemiological 'firebreak' between more susceptible species, e.g. Atlantic salmon.

Associated costs to survey for nothing?

- Individual pool sample 22 USD
- Overall study period 86,382 samples tested
- Equivalent to US 1,8 million or roughly 260,000 USD per year
- Resources that can be allocated to other diseases, e.g., *Piscirickettsia salmonis*

This study

...may benefit other areas where Coho salmon is produced and routinely sampled.

...hihglights that it is relevant to evaluate the need for sustaining surveillance activities for the disease in this species,

increase the efficiency in the use of resources for disease surveillance in farmed salmon in Chile and other regions.

Agreed on previous Natal workshop

- ~~**Thailand, Ecuador, Mexico and China** – recall historical surveillance info to demonstrate freedom from IMNV or surveillance sensitivity.~~
- ~~**Indonesia** – surveillance data to gain insight into the spatial epidemiology (definition of risk zones or zones of influence)~~
- **Brazil** – surveys to farmers to gain best management practices knowledge and biosecurity measures

A survey to farmers in Northern Brazil

- Short survey with ~70 questions
- IMNV epidemiological features
- Capturing also Best Management Practices, biosecurity, water and environmental monitoring, and shrimp movements control.
- Used previously for WSS in Sinaloa, Mexico.

Highlights IMNV

- Total of 21 respondents (targeted >30)

- All believe that the index case at the farm is random (no clustering at this level)
- 8/21 (40%) believe that rainy season is a risk factor, however, still 3/21 believe all year.
- 9/21 (43%) considers IMN as a low incidence disease.
- Expected mortality in an infected unit ~ 10-20%

IMNV surveillance plan

Fernando O Mardones
Assistant Professor UNAB
FAO Expert on Aquatic Disease Epidemiology
Qingdao, 2-5 November 2017
fomardones@gmail.com

Disease outbreak

- A disease outbreak is a short-term epidemic or a series of disease events that are clustered in time and space.
- In many cases, the cause of the outbreak is unknown, at least initially.
- The disease events are usually new cases of a known disease occurring at a higher frequency than that normally expected, or cases of a previously unrecognized disease.

Disease outbreak

- An outbreak, by its nature, requires a **rapid investigation** and **implementation of control measures**, often before a final etiological diagnosis can be confirmed.
- An outbreak investigation is therefore a systematic process to identify risk factors for the disease that can be manipulated to prevent the further transmission of the disease-causing agent, control or stop the outbreak, and prevent future outbreaks.

Disease outbreak

- Prompt and effective investigation of outbreaks is also an essential component of disease surveillance, particularly for new and emerging diseases.
- Active investigation of disease incidents provides ongoing surveillance for the detection and characterization of new and emerging diseases.

Disease outbreak

- The epidemiological approach is based on the premise that cases of a disease are not distributed randomly, but occur in patterns within the population at risk.

- The occurrence of most diseases depends on a whole range of factors relating to
  - the host (e.g. breed, species, age)
  - the agent (e.g. strain virulence, methods of transmission, etc.) and,
  - the environment (e.g. housing, nutrition, management)

It is not only the presence of the age

Basic steps for an outbreak investigation

From book: Epidemiology for field veterinari

1. Establish or confirm a provisional diagnosis.
2. Define a case.
3. Confirm that an outbreak is actually occurring.
4. Collect data on cases and non-cases.
5. Analyze the data:
    a) Exploratory analysis to verify and check the data.
    b) Identify potential patterns of disease in time, space and by animal characteristics.
    c) Descriptive and statistical analysis of any potential risk factors.
6. Formulate working hypotheses in an attempt to identify the type of epidemic, the possible source and mode of spread.
7. Implement control and preventive measures.
8. Undertake intensive follow-up investigations to identify high-risk groups and possible further outbreaks.
9. Report the findings of the investigation with recommendations for dealing with future possible outbreaks of the same disease.

Table 3.4. Examples of case definitions for epizootic ulcerative syndrome (EUS) in fish.

Study unit	Case definition
Animal	A fish with necrotizing, granulomatous dermatitis and/or myositis and/or granulomas in internal organs with *Aphanomyces piscicida/invadans* found within the lesion
	A fish with one or more granulomas with *Aphanomyces piscicida/invadans* found within the lesion
	A fish with lesions in which *Aphanomyces piscicida/invadans* can be found
	A fish with one or more surface lesions, each of which could be described as a red spot
Pond	A pond with one or more fish meeting the selected case definition for an individual animal
River	A river with one or more fish meeting the selected case definition for an individual animal

From book: Epidemiology for field veterinarians

Exploratory Data Analysis

1. What is the exact time period of the outbreak?
2. Given the diagnosis, what is the probable period of exposure?
3. Is the outbreak most likely from a common source, propagated or both?
4. Is the outbreak still spreading or has it peaked and started to decline?
5. What are the significant features of the geographical distribution of cases?
6. Are there any particular groups of animals that appear to be at greater risk than others?
7. Which animals have the highest and which have the lowest risk of disease?
8. What are the relevant attack rates in different groups of animals?
9. Are there clusters of disease in time and/or space that might help explain why the disease has occurred?

From book: Epidemiology for field veterinarians

Table 6.2. Comparison of measures of disease frequency.

	Incidence rate	Cumulative incidence	Prevalence
Numerator	New cases occurring during a period of time among a group initially free of the disease in question	New cases occurring during a period of time among a group initially free of the disease in question	Existing cases at a point in time
Denominator	Sum of time periods during which individuals could have developed disease	All at-risk individuals present at the beginning of the period	All at-risk individuals examined, including cases and non-cases
Time	From beginning of follow-up until disease occurs for each individual	Duration of period of observation	Single point in time
How measured	Prospective cohort study	Prospective cohort study	Cross-sectional study
Interpretation	Rapidity with which new cases develop over a defined time period	Risk of developing disease in defined time period	Risk of having disease at a particular point in time

From book: Epidemiology for field veterinarians

Prevalence

- The prevalence of a condition is the proportion of existing cases of disease present in a population at a given point in time.
- Prevalence = number of cases/Population at risk

Incidence

- The incidence is the number of new cases that arise in a population over a specified period of time.
- Incidence = number of new cases in a given time period/total PAR

- Unlike prevalence, incidence reflects risk, or the likelihood of an individual animal contracting the disease in a given period of time. Incidence can be calculated as a risk rate (or cumulative incidence) or a true rate (incidence density).

Calculation of the Odds Ratio (OR)

	Disease status	
Presence of the hypothesized Risk factor	**Diseased**	**Non-Diseased**
Yes	a	b
No	c	d

Odds Ratio (OR) = (ad)/(bc)

***<u>INTERPRETATION</u>**: "The risk to develop IMNV in shrimp farms with presence of the hypothesized risk factor would be x times (the OR estimation) to develop IMNV in shrimp farms with the absence of the hypothesized risk factor"*