Veterinærinstituttet
Norwegian Veterinary Institute

Water currents may explain the transmission of the new subtype of Pancreas Disease virus in Norway.

Britt Bang Jensen[1*], Hildegunn Viljugren[1] & Anne Stene[2]

1. Norwegian Veterinary Institute, Oslo. 2. Ålesund University college, Ålesund. *Corresponding author: Britt-bang.jensen@vetinst.no

INTRODUCTION

Pankreas Disease (PD) is an infectious disease causing major losses in Norwegian salmonid farming. PD is caused by a virus, *Salmonid alphavirus* (SAV), of which there are several different subtypes (see factbox 1).

Until recently, only SAV3 had been identified in Norway In 2011, a new subtype was identified. Genetic characterisation places this subtype together with SAV2, but with some discrepancies. The subtype have therefore been referred to as 'SAV2-like'.

It is not known how the new subtype was introduced to the Norwegian salmonid population, or how it is transmitted. Here we propose a possible route of transmission by use of integrated hydrodynamic models and epidemiological data on disease outbreaks

SAV2-LIKE EPIDEMIOLOGY

The first isolation of 'SAV2-like' was from fish slaughtered due to an outbreak of Cardiac Myopathy Syndrome outside the endemic zone in mid-Norway in April 2011. This was an isolated finding, and in spite of vigorous surveillance and screening in the area, no more virus was found. Then, in October 2011, the subtype was found again, now in a sea site within the endemic zone on the west coast of Norway. Since then, 'SAV2-like' has been found on several sites in this area, both within and outside of the endemic zone. To date, 'SAV2-like' have been isolated from 14 PD-cases (figure 1).

METHODOLOGY

Of the 14 cases, 9 were on sites in the same water current network. For this network, a hydrodynamic model has previously been developed (see factbox 2). The model was used to analyse whether it was possible for transmission to have occurred between locations by water contact. From monthly reporting of production data from the locations, it was possible to identify the period where there were fish at each location. Date of diagnosis was obtained from the journal system of the Veterinary Insitute.

RESULTS

Results from the network model is presented in table 1. From the table, it is evident that transmission between sites can have occurred via water currents. The locations A, B, C and D were all diagnosed within the same quarter, and it is not possible to tell which was infected first. But the tables shows, that infection could have spread from A to D, from C to A and/or D, and from D to either of A, B and C. It is likely that F was infected via water currents from B, and that the infection was then spread to G and H, either directly from F, or via one or the other. E and I did not receive water from any other locations, thus the spread to these locations cannot be explained by this model.

All locations and possible routes of transmission is also illustrated on the map in figure 2.

Table 1. Water current network. Letters denotes individual locations, corresponding to figure 2. Distributing locations are at the top, and receiving locations within the matrix. Green shading denotes when there were fish at the distributing location. Receiving locations are in the matrix at the time (quarter and year) when it is in water current network with the distributing location. Red color denotes when PD-outbreak was diagnosed at the location in the network.

Quarter and year	Distributing location															
	A	B	C		D			E	F			G			H	
4 2009			A		A	B	C									
1 2010	D															
2 2010	D		A	D	A				B	H	G	B	F	H	F	G
3 2010	D	F	A	D	A	B	C*	H	B*	H		B	F	H		
4 2010			A		A	B	C	H		H		B	F	H	F	G
1 2011		F						H	B	H	G	B	F	H	F	G
2 2011		F						H		H	G	B	F	H	F	G
3 2011		F						H		H		B	F	H		
4 2011								H		H					F	G

*** The location was not in water current network at the time of diagnosis.**

FACTBOX 1: PD-subtypes

There are 6 known subtypes of SAV:

- SAV1 is the cause of PD in Scotland and Ireland
- SAV2 is known to cause Sleeping Disease in Rainbow trout in freshwater aquaculture in France and Scotland. A variant of SAV2 have been associated with PD in Atlantic salmon in Scotland
- SAV3 is endemic in Norway where it causes PD in Atlantic salmon and rainbow trout
- SAV4 has been found in Scotland and Ireland
- SAV5 has only been found in Ireland
- SAV6 has only been found in Scotland

(McLoughlin &Graham)

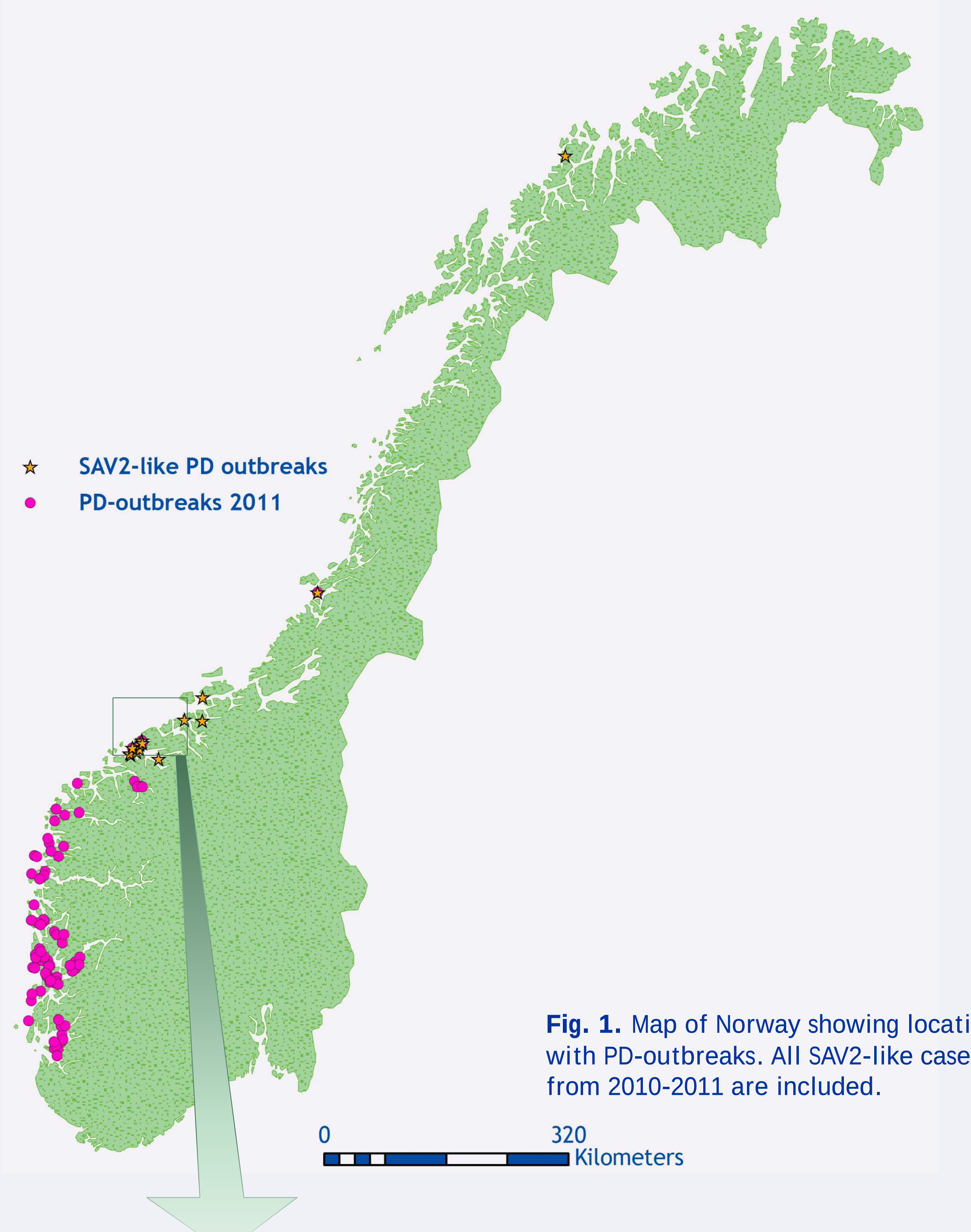

Fig. 1. Map of Norway showing locations with PD-outbreaks. All SAV2-like cases from 2010-2011 are included.

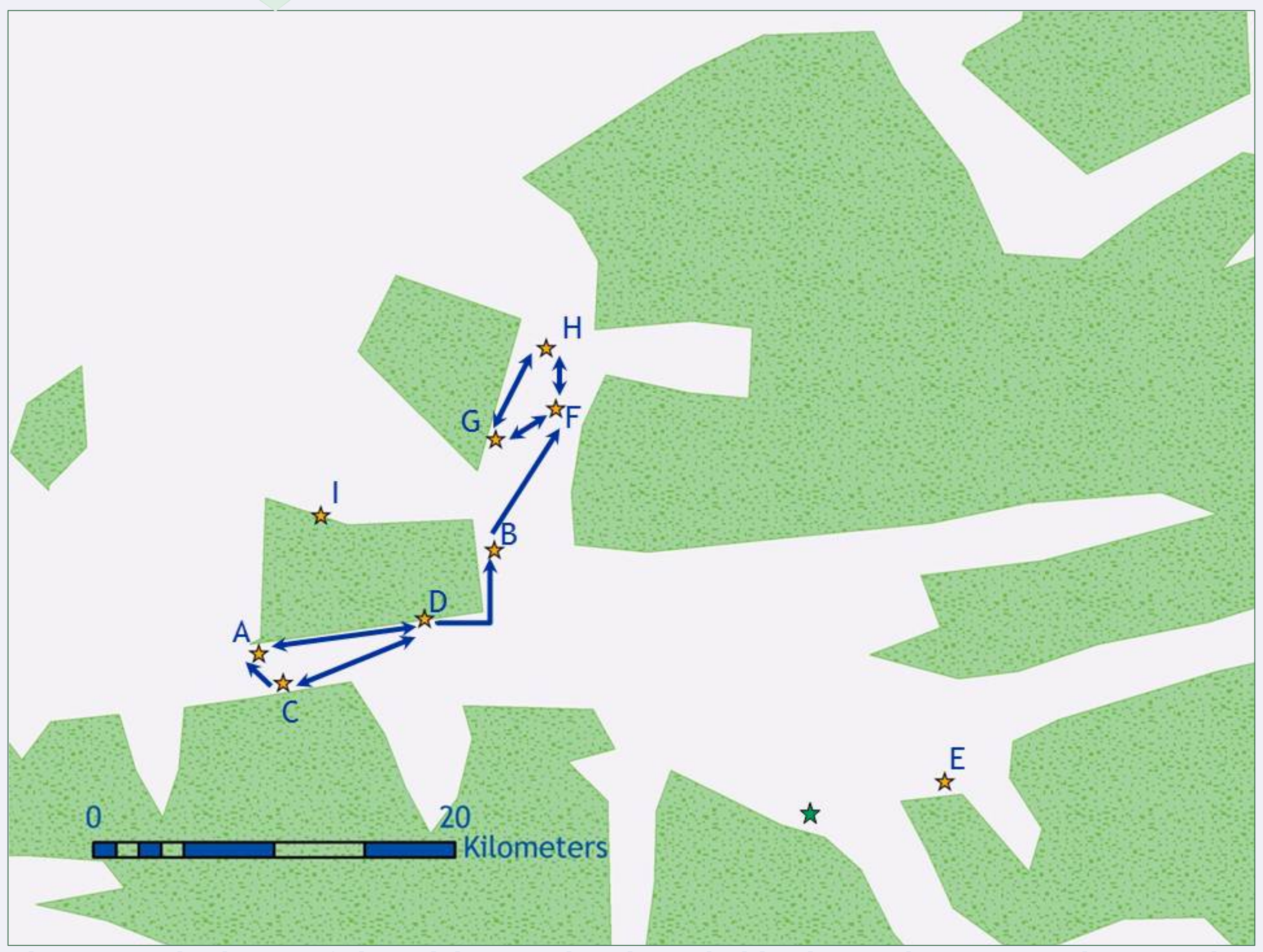

Fig. 2. Detailed map of the eight sea-sites included in the model. Arrows simulate the most likely spread of SAV2-like via water currents.

DISCUSSION

The results indicate that it is likely that the new 'SAV2-like' virus has been spread by water currents between infected sites. The model does not explain transmission to site E and I. However, only the parameter settings explained in factbox 2 have been used, and thus it is not unlikely that the transmission could be explained if for example a longer half-life is assumed. Further, the parameter settings are based on knowledge of the physical properties of SAV3, as little is known about 'SAV2-like'.

The model can not give the time of infection of a location, as only time of diagnosis is available. Infection can easily have occurred long before diagnosis, especially in the cold winter months when virus can be dormant in the fish population. It is therefore important to include time intervals before diagnosis on the distributing location in the matrix.

The work presented here are preliminary results of a test-modelling, meant to generate a hypothesis of spread of 'SAV2-like' via water current networks. The authors plan to include this hypothesis in a future study, including several other hypothesis for spread.

CONCLUSION

Transmission via water current networks is a likely route for 'SAV2-like' virus, and this should be taken into account both in future modelling of SAV-transmission, and when considering strategies for control of PD.

FACTBOX 2:

The Ocean Modeling System: "SINMOD" was used to identify farms being hydrographically linked by sea currents (Slagstad & McClimans). SINMOD is a 3D coupled hydro-dynamic, chemical and biological model system. It has a horizontal resolution of 160 m up to 33 different depth layers. A particle-tracking module uses currents, tides, wind, runoff, temperature, and salinity fields as input. A new positions of virus are calculated at 2 meters depth every hour. The mean annual share of particles moving between the sites in question is identified. The concentration of virus particles is 100% at release, regardless of biomass on site. It is assumed that the concentration is decreasing exponentially with a half life of 4.3 days in the winter and 1 day in the summer.

References

Mcloughlin & Graham (2007) Alphavirus infections in salmonids –a review. Journal of Fish Diseases 30, 511-531
Slagstad & McClimans (2005) Modelling the ecosystem dynamics of the Barents Sea including the marginal ice zone: I. Physical and chemical oceanography. Journal of Marine Systems, 58, 1-18

www.vetinst.no