

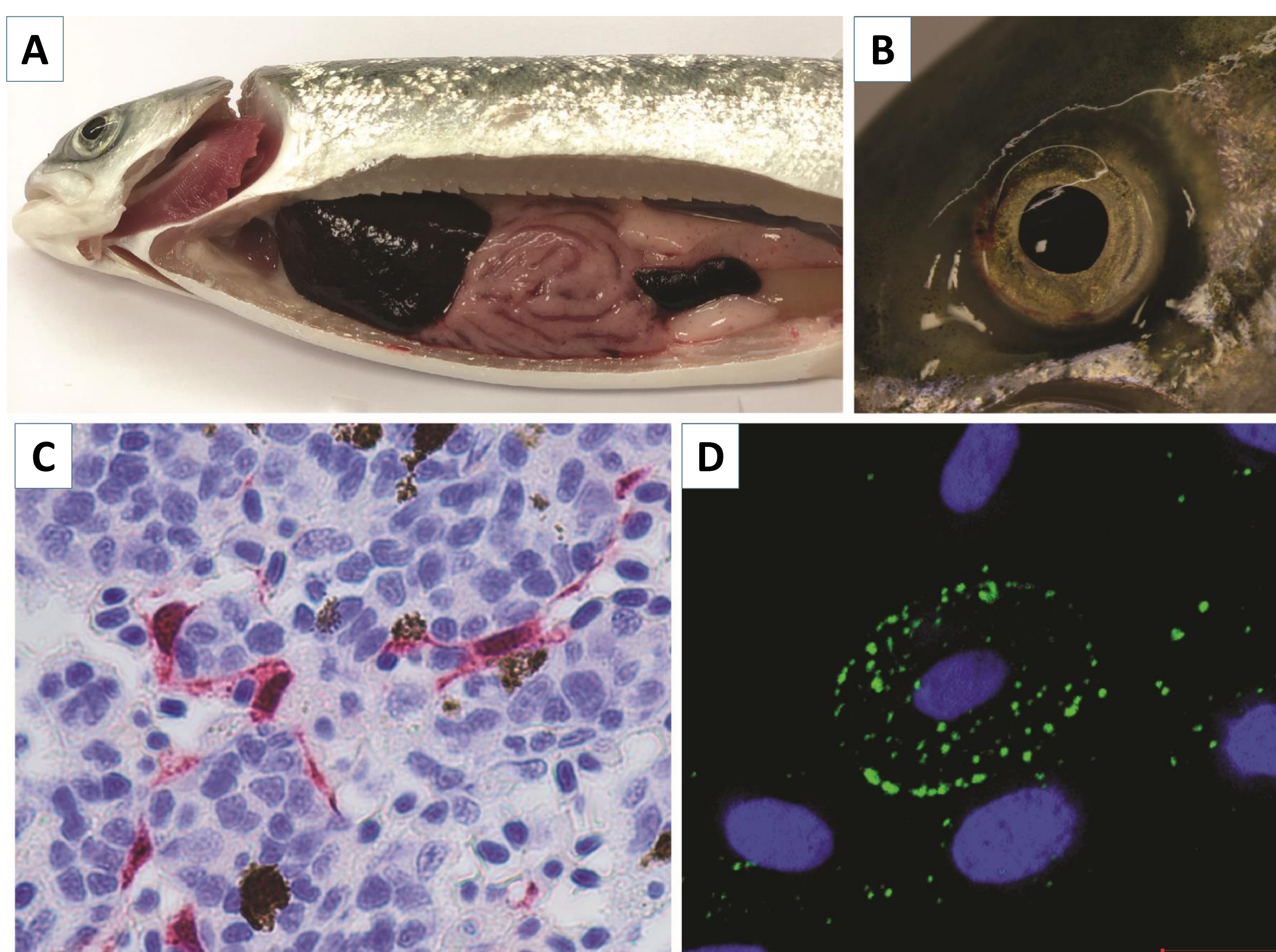
# INSIDE THE ZONE:

## a historical assessment of infectious salmon anemia (ISA) control regulations in Norway

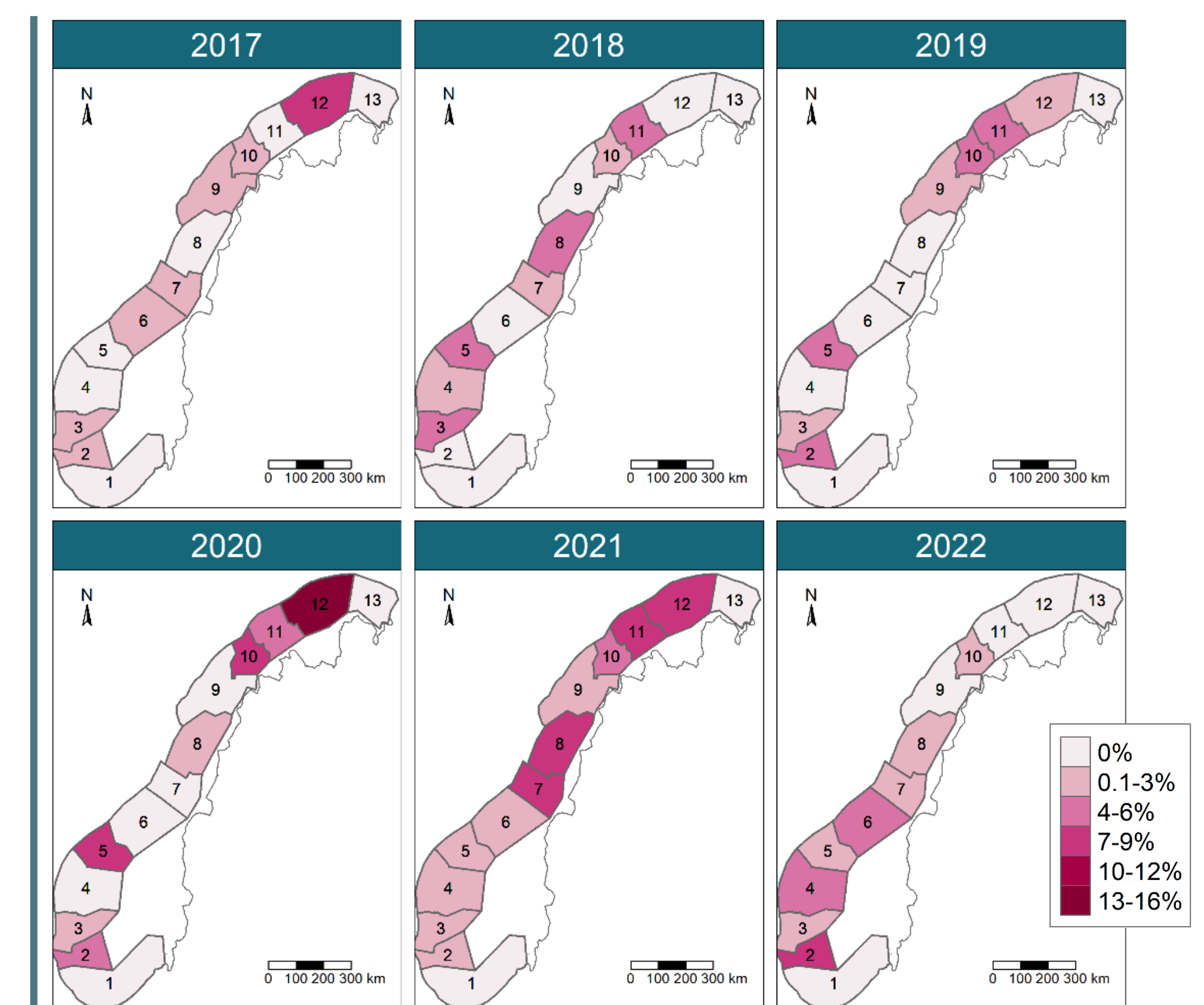
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### About ISA

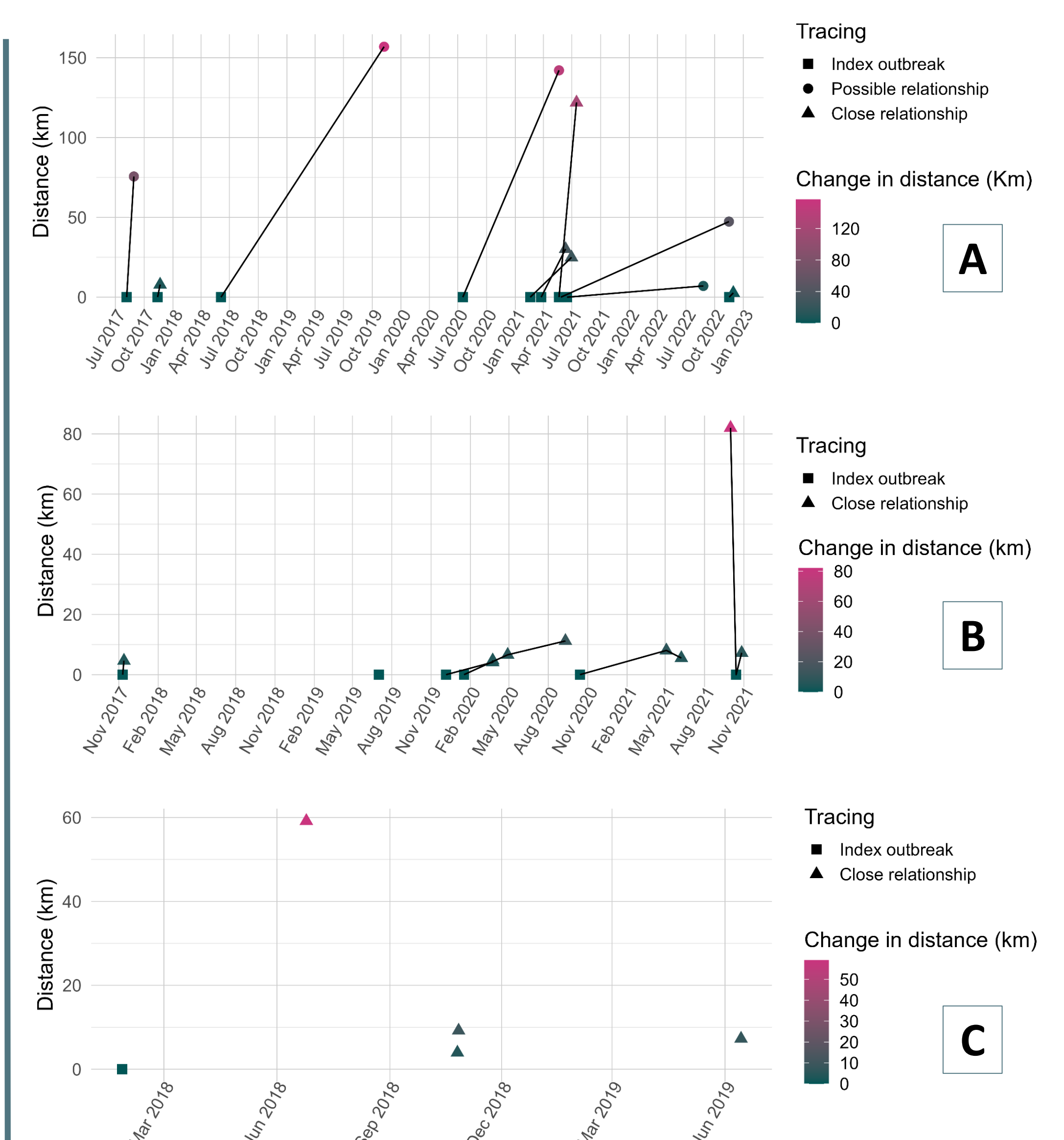
- **Cause:** Infectious salmon anemia virus (ISAV), an orthomyxovirus. Transitioning from the non-pathogenic HPR0 variant to the pathogenic HPR-deleted variant, which is associated with clinical outbreaks.
- **Geographical distribution:** ISA has occurred since the 1980s in Chile, North America, and Northern Europe, including Norway (Figure 1).
- **Impact:** Severe clinical signs (Figure 2), high mortality (20–90%) and costs related to control measures.
- **Transmission:** Horizontal through waterborne exposure to ISAV from infected fish. Vertical transmission has been considered less likely. ISAV present on the surface of broodstock could cross-contaminate egg and milt batches during stripping process, potentially contributing to transmission.
- **Norwegian surveillance program:** Involves passive surveillance throughout, with active surveillance specifically implemented within the containment zone (surveillance + protection zones; Figure 4).



**Figure 2:** Signs of ISA in salmon include pale gills, darkened liver, and bleeding in the internal organs and eyes (A and B). ISAV propagates in cells lining the luminal surface of blood vessels, as shown by head kidney endothelial cells colored red with IHC (C). When ISAV is secreted into the bloodstream, it attaches to the surface of salmon blood cells, indicated by ISAV colored green in IF staining (D). Photo: Frieda Betty Ploss, Adriana Magalhães Santos Andresen and Johanna Hol Fosse.



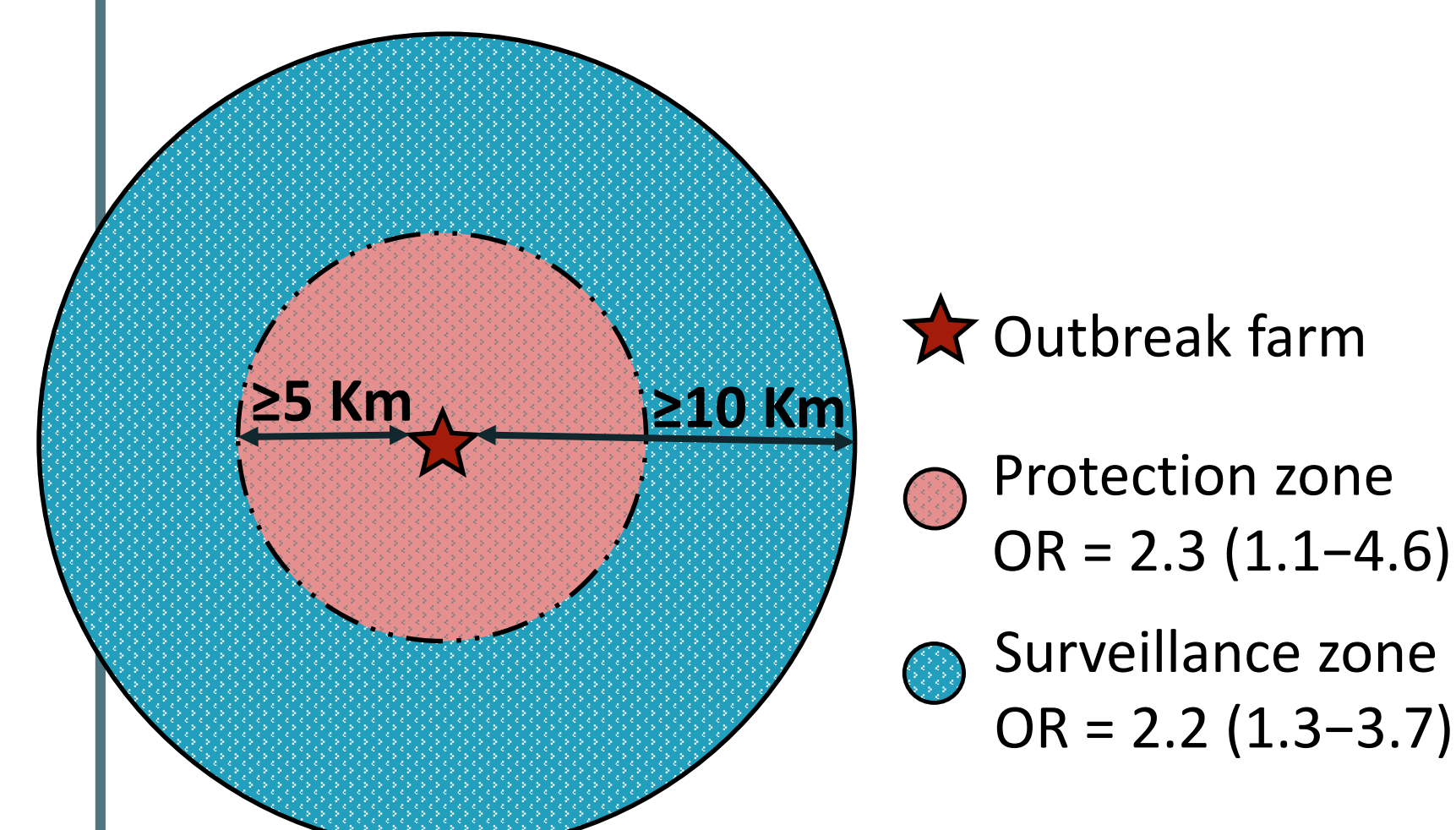
**Figure 1:** Yearly ISA prevalence has been between 1-3% across approximately 800-830 active salmon farms, affecting farms from the north to the south of the Norwegian coast.



**Figure 3:** Genetic similarity and tracing of ISAV samples from ISA outbreaks in salmon marine farms (2017-2022). A 'cluster' of samples is considered to be possibly or closely related if they share significant similarities in segments 5 and 6 of the ISAV genome and have a compatible deletion in the Highly Polymorphic Region (HPR) of the virus. 'Clusters' at marine salmon farms, involving two localities (A) or three farms (B), are interconnected by lines. Additionally, there was a cluster with five farms (C). The index farm does not always correspond to the earliest date in a cluster, as this designation depends on the analysis of genetic similarity. Farms with a suspected onset date before 2017 or with a sea distance greater than 200 kilometers are not included in the figure.

### Main findings

- Between 2017 and 2022, ISA outbreaks occurred at 93 sites: marine farms (n=86), hatcheries (n=1), and broodstock farms (n=6).
- 34 outbreaks were considered isolated, with no known relationship to other outbreaks.
- Some outbreaks were linked to smolt deliveries and to the ISAV HPR0 variant from nine different hatcheries.
- In assessing marine farm outbreaks with genetic connections, evidence for horizontal transmission via sea currents is inconsistent; while some cases suggest possible transmission, others show a lack of correlation in outbreak timing and spatial proximity (Figure 3).
- Considering marine farms, the odds of ISA outbreaks were higher within containment zones than outside these zones (Figure 4).



**Figure 4:** Illustration of the ISA containment zone, encompassing both protection and surveillance zones. Between 2019 and 2022, farms within these zones had higher odds of ISA outbreaks, as indicated by the odds ratio (OR) and its 95% confidence interval, presented in parentheses.

**Conclusion:** Analysis of genetic similarity, seaway distances, and surveillance data challenges the effectiveness of current zoning policies aimed at containing ISA outbreaks.