Table S1. Sentinel cage data sets from the Institute of Marine Research (IMR). The data are available at **www.nmdc.no**.

Data set	Reference
IMR sentinel cages 2012	(Asplin et al. 2017a)
IMR sentinel cages 2013	(Asplin et al. 2017b)
IMR sentinel cages 2014	(Asplin et al. 2017c)
IMR sentinel cages 2015	(Asplin et al. 2017d)
IMR sentinel cages 2016	(Asplin et al. 2017e)
IMR sentinel cages 2017	(Asplin et al. 2017f)
IMR sentinel cages 2018 Boknafjorden	(Asplin et al. 2018a)
IMR sentinel cages 2018 Hardangerfjorden	(Asplin et al. 2018b)
IMR sentinel cages 2018 Sognefjorden	(Asplin et al. 2018e)
IMR sentinel cages 2018 Romsdal	(Asplin et al. 2018d)
IMR sentinel cages 2018 Trondheimsfjorden	(Asplin et al. 2018f)
IMR sentinel cages 2018 Namsen	(Asplin et al. 2018c)
IMR sentinel cages 2019 Boknafjorden	(Asplin et al. 2020a)
IMR sentinel cages 2019 Hardangerfjorden	(Asplin et al. 2020b)
IMR sentinel cages 2019 Sognefjorden	(Asplin et al. 2020d)
IMR sentinel cages 2019 Namsen	(Asplin et al. 2020c)
IMR sentinel cages 2020 Hardangerfjorden	(Asplin et al. 2020e)
IMR sentinel cages 2021 Boknafjorden	(Nilsen et al. 2021a)
IMR sentinel cages 2021 Hardangerfjorden	(Nilsen et al. 2021b)

Text S1. Calculating spatiotemporal variation in infestation pressure

Here follows a detailed description of the calculation of infestation pressure.

The daily number of eggs produced ($N^E_{j,t}$ in Eq. 1) was calculated by multiplying the total number of adult female salmon lice ($N^{AF}_{j,t}$) with the number of eggs per egg batch ($B_{j,t}$) divided by the number of days between egg batches, which was approximated by the egg development time to hatching ($D^E_{j,t}$):

$$N^E_{j,t} = N^{AF}_{j,t} \cdot B_{j,t} / D^E_{j,t} \text{ (S1)}$$

The total number of reproductive female salmon lice, $N^{AF}_{j,t}$, was calculated by multiplying the reported mean number of adult female lice per fish with the number of fish at the farm.

We assumed that each egg batch consisted of two egg strings with temperature-dependent egg batch size following experimental results by Samsing et al. (2016):

$$B_{j,t} = 2 \cdot \exp\left(5.6 - 0.43 \cdot \ln\left[\frac{Temp_{j,t}}{10}\right] - 0.78 \cdot \left[\ln\left(\frac{Temp_{j,t}}{10}\right)\right]^2\right) \text{ (S2)}$$

The time (days) between egg batches depended on sea temperature reported at the farm ($Temp_{j,t}$), following experimentally derived minimum egg development times to hatching (Stien et al. 2005, Kristoffersen et al. 2018):

$$D^E_{j,t} = \left(41.98 \,/\, \left[Temp_{j,t} - 10 + 41.98 \cdot 0.338\right]\right)^2 \text{ days (S3)}$$

The fraction of eggs produced at time t that reached the infective larval stage and survived to time T ($s_{j,t,T}$ in Eq. 1) was a function of egg development time to hatching ($D^E_{j,t'}$), larval development time from hatching to infective stage ($D^L_{j,t''}$), duration of the infective stage ($D^I_{j,t'''}$), daily mortality rate of eggs and larvae (M) and egg viability ($v^E_{j,t}$):

$$s_{j,t,T} = \begin{cases} (1-M)^{T-t} \cdot v^E_{j,t}, \ if \ (D^E_{j,t'} + D^L_{j,t''}) \leq (T-t) \leq (D^E_{j,t'} + D^L_{j,t''} + D^I_{j,t'''}) \\ 0 \ , \ if \ (D^E_{j,t'} + D^L_{j,t''}) > (T-t) \ or \ (T-t) > (D^E_{j,t'} + D^L_{j,t''} + D^I_{j,t'''}) \end{cases}$$

(S4)

The “if”-statement in the equation ensured that the fraction was only non-zero if eggs produced at time *t* were in the infective larval stage at time *T*. The fraction of eggs surviving to time *t* was the product of the daily survival values (1 minus mortality) from time *t* to *T*. We assumed that the mortality rates of eggs and larvae were identical, $M = 0.17$ (Kristoffersen et al. 2018). The notations *t'*, *t''* and *t'''* referred, respectively to the successive time intervals for the egg stage, the non-infective larval stage and infective larval stage, for eggs starting to develop at time *t*.

Temperature-dependent larval development followed experimental results (Stien et al. 2005, Samsing et al. 2016) as calculated by Stige et al. (2021):

$$D^L_{j,t} = (26.2 \ / \ \left[Temp_{j,t} - 10 + 26.2 \cdot 0.509\right])^2 \ \text{(S5)}$$

The duration of the infective stage ($D^I_{j,t}$ in Eq. S4) was assumed to be temperature-dependent, following experimental results by Samsing et al. (2016):

$$D^I_{j,t} = \exp\,(2.6 - 0.26 \cdot \ln[\frac{Temp_{j,t}}{10}] - 1.03 \cdot [\ln(\frac{Temp_{j,t}}{10})]^2\,) \ \text{(S6)}$$

The development times depended on the temperatures reported at the farm from time *t* onwards ($Temp_{j,t}$, $Temp_{j,t+1}$, $Temp_{j,t+2}$,...). To calculate the egg development time based on the temperatures reported at a farm, we assumed that the daily values of $1/D^E_{j,t}$ described the fractional egg development and considered the eggs to be fully developed and hatch when the sum of development fractions exceeded 1. Correspondingly, the daily values of $1/D^L_{j,t}$ described the fractional larval development based on the temperatures reported from the egg-hatching time onwards. The duration of the infective stage was calculated based on the temperatures reported at the farm, by finding when the sum of developmental fractions ($1/D^I_{j,t}$) exceeded 1.

Egg viability was temperature-dependent following experimental results by Samsing et al. (2016):

$$v^E_{j,t} = \text{logit}^{-1}\left(-1.765 + 0.494\,Temp_{j,t}\right) \ \text{(S7)}$$

Here, logit^{-1} is the inverse logit function, $\text{logit}^{-1}(X) = \exp(X)\,/(1 + \exp(X))$.

The probability of dispersal of larvae from farm *j* to geographic position *i* ($r_{i,j}$ in Eq. 1) was a function of the seaway distance, $d_{i,j}$ (km), from farm *j* to geographic position *i* (Aldrin et al. 2019):

$$r_{i,j} = 0.582 \cdot \exp(-0.374[d_{i,j}^{0.692} - 1]/0.692) \ \text{(S8)}$$

The dispersal probability was scaled to be 1 at distance 0 and set to zero for distances larger than 200 km. This function shows how the concentration of infective salmon lice larvae decreases as a function of distance from each farm of origin.

The factor controlling for temperature-dependent infectivity ($I_{i,j}$, in Eq. 1) was as a function of farm temperature at time *T* ($Temp_{i,T}$, °C) (Stige et al. 2021) and combined data from several experiments (Tucker et al. 2000, Samsing et al. 2016, Dalvin et al. 2020, Skern-Mauritzen et al. 2020):

$$I_{i,j} = \text{logit}^{-1}\left(-3.89 + 4.33\,\frac{Temp_{i,T}}{10} - 1.18\,\frac{Temp_{i,T}^{2}}{10}\right) \text{(S9)}$$

Weekly mean infestation pressure for each location was calculated from the daily values of infestation pressure (Eq. 1) and saved as 100×100 m raster maps.

Text S2. Comparison with expert group conclusions

The expert group for the traffic light management system has assessed the most likely category of salmon lice-induced mortality (< 10%, 10–30% or >30%) for each management area and year from 2016 to 2021 (Vollset et al. 2021). The assessment is an expert judgement based on results of three observation data sets, including data from post-smolt trawling, sentinel cage experiments and observations of sea lice on sea trout in the area, and four model products, including three virtual post-smolt models and an area-based infestation pressure model. The conclusions by the expert group are compared with our model results in Table S2.

Table S2. Categorisation of salmon lice-induced mortality for seaward-migrating salmon post-smolts for each management area and years 2016–2021 based on the main model calibrated to trawl data. Low: <10%, moderate (mod.): 10–30%, high: >30% salmon lice-induced mortality. Categories shown in normal font are based on the expected mortality. Categories that include the random effect of management area and year on infestation rate are shown in bold font when data exist. Arrows show categorisations that differ from the assessment by the expert group for the traffic light system (Vollset et al. 2021), with upward-pointing arrows indicating that the expert group concluded with a higher category and downward-pointing arrows a lower category. No differences were larger than one category.

Management area	2016	2017	2018	2019	2020	2021
1	Low	Low	Low	Low	Low	Low
2	Mod	**Low**	**Mod**	**Mod↓**	**High**	**Low**
3	**High**	**High**	**High**	**Mod**	**High**	**High**
4	Mod	**High**	**High↓**	**High**	**Low↑**	**High**
5	**Low↑**	**Low↑**	**Low↑**	**High**	**Low**	**Mod**
6	**Low↑**	**Mod↓**	**Mod↓**	Mod↓	Mod↓	Mod↓
7	**Mod**	**Mod↓**	**Mod**	**Mod↓**	Mod	Mod
8	Mod↓	Mod↓	Mod↓	Low	Low	Mod↓
9	Low	Low	Low	Low	Low	Mod↓
10	Low	Low	Low	Low↑	Low	Low
11	Low	Low	Low	Low	Low	Low
12	Low	**Low**	Low	Low	Low	Low
13	Low	Low	Low	Low	Low	Low

We would expect the best correspondence between the expert group’s conclusions and model predictions that include the random area-year effects (shown in bold font in Table S1), as these predictions integrate post-smolt data from the particular management area and year. For management areas 2 to 4, the model-predicted mortality with random effects coincided with the expert group’s categorisation for 13 of 16 area-year combinations. For management area 5, the model-predicted mortality was in a lower category than the expert group’s conclusions from 2016 to 2018, but has matched since 2019. The expert group reports for 2016 to 2018 show that the sentinel cage and trawl data were mostly from northern parts of the management area, which had lower infestation pressure than southern parts (which were only covered by lice observations on sea trout) (Nilsen et al. 2017, Nilsen et al. 2018). The random-effect adjustment of model-predicted mortality based on cage and trawl data then did not represent the areas with highest infestation pressure, making the representativeness of the adjustment uncertain. For management areas 6 to 8, the model-predicted mortality has often been higher than the expert group's conclusions. We see no obvious reason for this difference and cannot determine whether it reflects over-estimation of modelled mortality, under-estimation by the expert group or if the apparent difference is due to chance. For these management areas, we lack trawl data with genetically determined river of origin, which increases the uncertainty of the predictions.

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