The following supplement accompanies the article

Intensive oyster aquaculture can reduce disease impacts on sympatric wild oysters
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Endemic equilibrium of the wild oyster population $N_w$

Assuming the density of the wild oyster population at the endemic equilibrium of disease ($N_w^* = S_w^* + I_w^*$) is positive, from equations 1 & 2, $S_w^*$ and $I_w^*$ satisfy the following condition:

$$ b(S_w^* + \rho I_w^*) - (\delta + c N_w^*)S_w^* - (\delta + v_w + c N_w^*)I_w^* = 0. \quad \text{(S1)} $$

Using the equilibrium prevalence of infection in the wild oyster population ($i_w^*$), we substituted $S_w^* = (1 - i_w^*) N_w^*$ and $I_w^* = i_w^* N_w^*$, obtaining the condition:

$$ b(1 - i_w^*) N_w^* + b pi_w^* N_w^* - (\delta + c N_w^*) (1 - i_w^*) N_w^* - (\delta + v_w + c N_w^*) i_w^* N_w^* = 0. \quad \text{(S2)} $$

Rearranging equation S2, we obtained the density of the wild oyster population at the endemic equilibrium of disease as:

$$ N_w^* = \frac{b - \delta + i_w^* (b \rho - b - v_w)}{c}. \quad \text{(S3)} $$

To evaluate the effects of aquaculture activities on $i_w^*$ and hence $N_w^*$, it was convenient to express $i_w^*$ as a function of the density of the farmed oyster population at the endemic equilibrium of disease ($N_f^* = S_f^* + I_f^*$). Assuming $N_f^*$ is positive, from equations 3 & 4, $S_f^*$ and $I_f^*$ satisfy the following condition:

$$ \pi - (\delta + \sigma) S_f^* - (\delta + v_f + \sigma) I_f^* = 0. \quad \text{(S4)} $$

Using the equilibrium prevalence of infection in the farmed oyster population ($i_f^*$), we substituted $S_f^* = (1 - i_f^*) N_f^*$ and $I_f^* = i_f^* N_f^*$, obtaining the condition:

$$ \pi - (\delta + \sigma) (1 - i_f^*) N_f^* - (\delta + v_f + \sigma) i_f^* N_f^* = 0. \quad \text{(S5)} $$

Rearranging equation S5, and substituting $i_f^* = \Omega i_w^*$, where the ratio $\Omega$ describes the proportional change in the equilibrium prevalence of infection in the farmed population relative to the population in the wild, we obtained the equilibrium prevalence of infection in wild population as a function of activities on the farm:

$$ i_w^* = \frac{\pi N_f^* - \delta - \sigma}{v_f \Omega}. \quad \text{(S6)} $$

Estimate of $R_0$ at the disease-free equilibrium

We estimated the basic reproductive number for the farmed oyster population ($R_{0,f}$) using the next generation matrix approach of Diekmann et al. (2010). Assuming a completely
susceptible population \((S_f \approx N_f)\) and the absence of any oysters in the wild, we linearized equations 4 and 5 around the steady state \(\frac{dS_f}{dt} = 0\) and \(I_f << N_f\) and \(P << N_f\):

\[
\frac{dI_f}{dt} = \mu \rho_f N_f P - (\delta + \nu_f + \sigma) I_f \tag{S7}
\]

\[
\frac{dP}{dt} = \theta (\delta + \nu) I_f - s I_f - (i + f N_f) P \tag{S8}
\]

Equations S7 and S8 describe the infection subsystem, as they only describe the production of new infected hosts and changes in the states of already existing infected hosts and their shed parasite stages in the environment. We decomposed the Jacobian matrix describing this linear system of ordinary differential equations with the transmission matrix \(T\), describing the production of new infections, and the transition matrix \(\Sigma\), describing changes in the state of infected hosts, here through removal by death:

\[
T = \begin{bmatrix}
0 & \mu \rho_f N_f \\
\theta (\delta + \nu_f) + s & 0
\end{bmatrix} \tag{S9}
\]

\[
\Sigma = \begin{bmatrix}
-(\delta + \nu_f + \sigma) & 0 \\
0 & -(i + \rho_f N_f)
\end{bmatrix} \tag{S10}
\]

The large domain next generation matrix \(K_L\) describes new transmissions and transitions:

\[
K_L = -T \Sigma^{-1} = \begin{bmatrix}
0 & \frac{\mu \rho_f N_f}{\theta (\delta + \nu_f) + s} \\
\frac{\theta (\delta + \nu_f) + s}{\delta + \rho_f N_f} & 0
\end{bmatrix} \tag{S11}
\]

and the dominant eigenvalue of \(K_L\) \((\lambda)\) defines \(R_{0,f}\), where:

\[
\lambda = R_{0,f} = \frac{\mu \rho_f N_f (\theta (\delta + \nu_f) + s)}{(\delta + \rho_f N_f) (\delta + \rho_f N_f + \sigma)} \tag{S12}
\]

References