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Supporting Information

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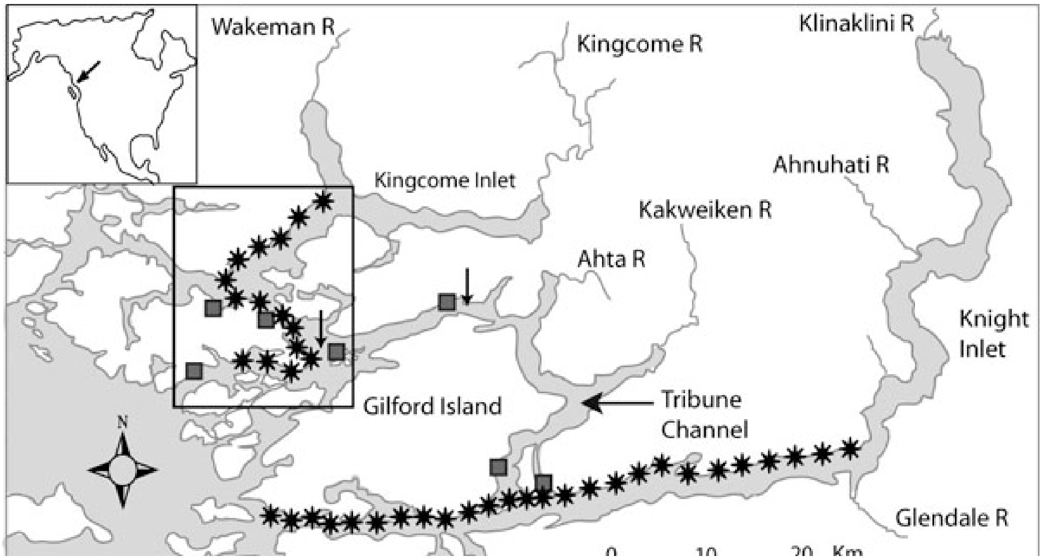
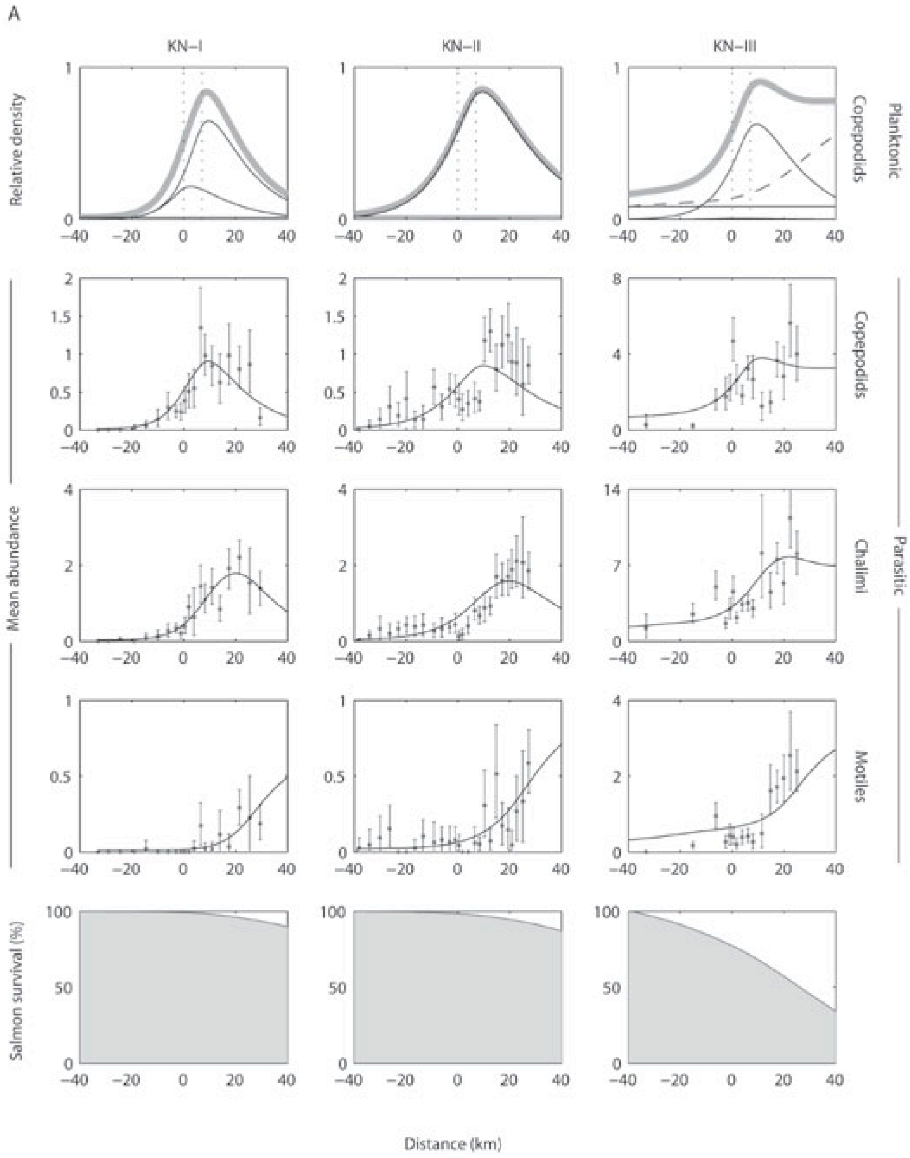


Fig. 4. Map of the study area showing sample sites (stars) and the studied farms (filled squares). The rectangle shows the 2005 Kingcome Inlet (KC) study sites and farm locations. The two white squares show farms excluded from the analysis, because the western farm was peripheral to the sample sites, and the eastern farm had nearly completed harvest. The remaining sites and farms outside the rectangle illustrate the 2004 Knight Inlet (KN) study sites and farm locations. The KN and TR datasets share the same data east of the second farm. The downward-pointing arrows indicate the locations where weekly lethal samples of juvenile salmon were collected to determine the species composition of lice. Fallow and smolt farms are not shown.



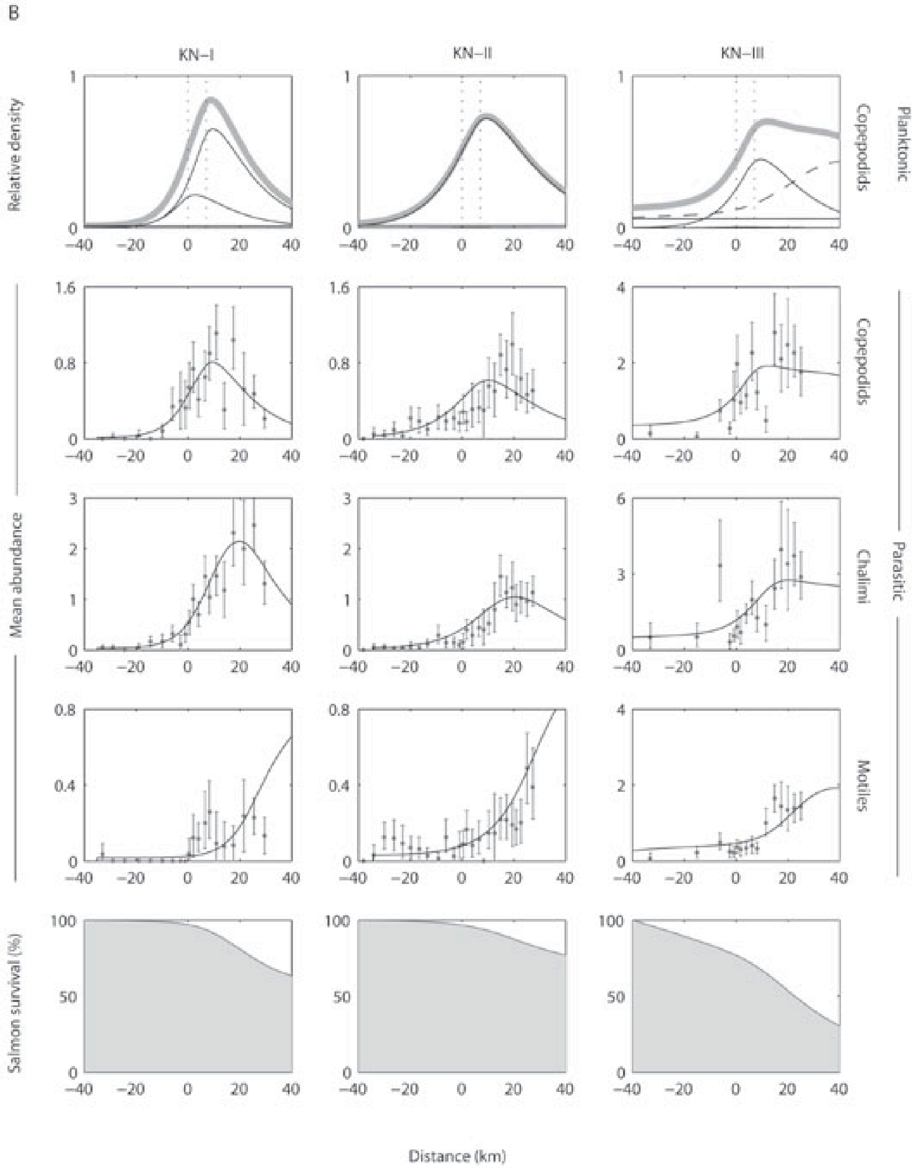


Fig. 5. Sea lice transmission dynamics and mortality impact on juvenile pink salmon (*a*) and chum salmon (*b*) migrating past two active salmon farms (vertical dotted lines in the first row) in the Knight Inlet migration corridor (Fig. 4). The seaward migration of salmon is from left to right. The three columns correspond to three replicate sets of samples taken 20-25 April (KN-I), 2-10 May (KN-II), and 21-31 May (KN-III), 2004 (note the change in scales). The first row shows the estimated spatial distributions of planktonic copepodids originating from all sources (thick gray line), from farm salmon (two thin curves), and from ambient sources (horizontal thin line) and the second generation of farm origin lice (dashed curve, KN-III only). Reproduction of lice parasitizing the juvenile salmon was not considered in KN-I and -II due to the absence of gravid female lice in those datasets. The middle three rows depict the mean abundances of lice (±95% bootstrap confidence interval) and maximum-likelihood model fits (black lines) along the migration route for parasitic copepodids, chalimi, and motiles. The bottom row depicts the estimated remaining juvenile salmon population that survived sea lice infestation. Temperature and salinity were measured at each site and averaged 8.8°C and 30.4‰ (KN-I), 9.9°C and 25.8‰ (KN-II), and 12.0°C and 21.1‰ (KN-III).

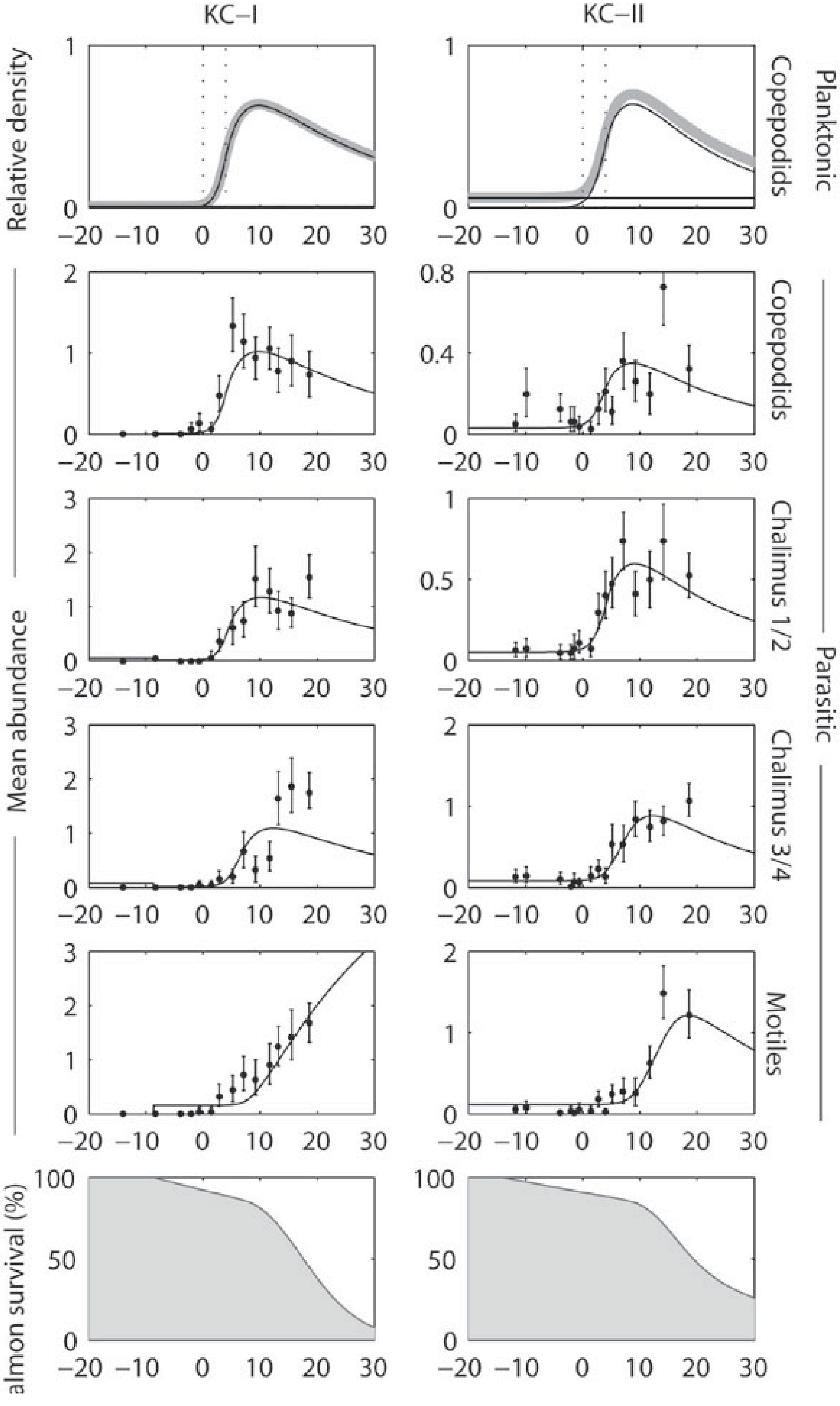
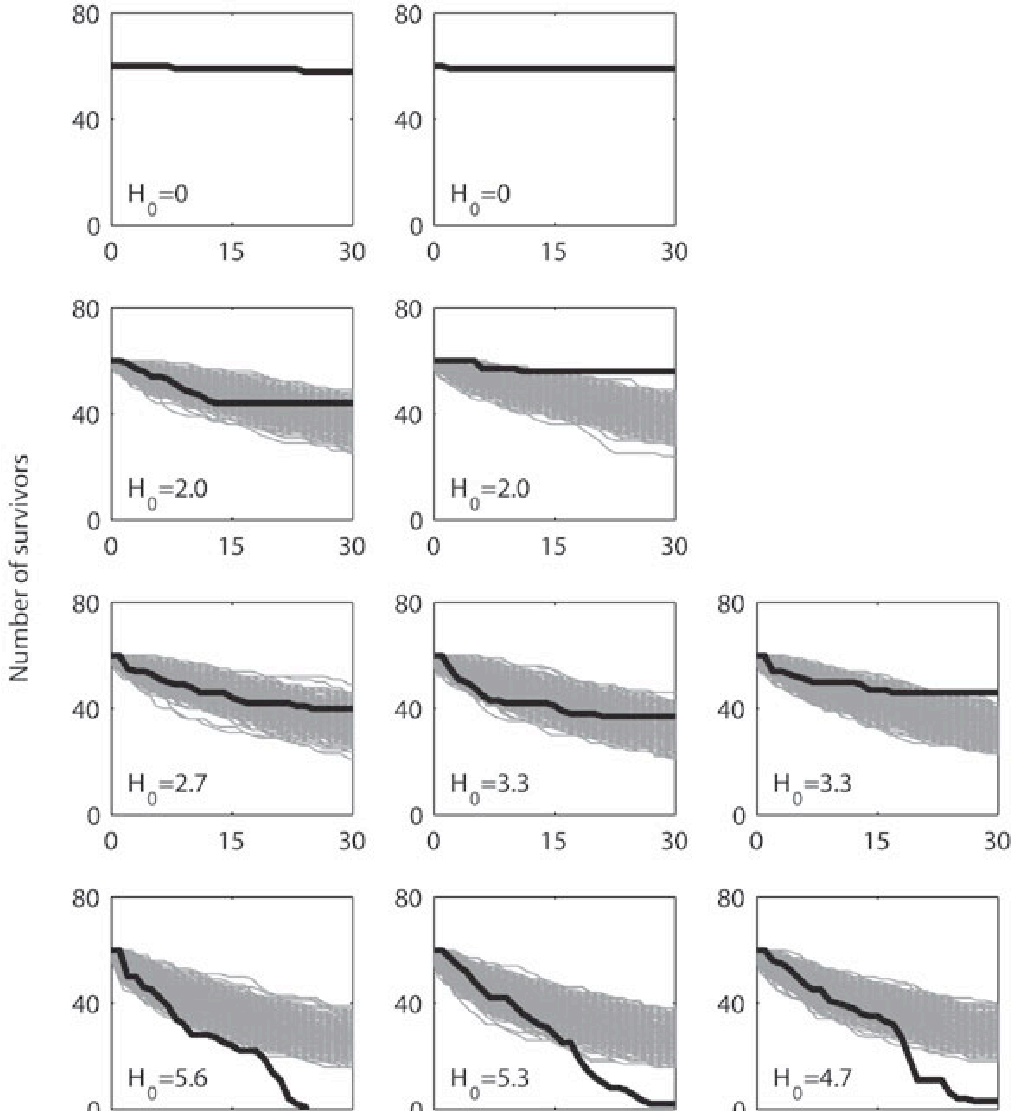

KC–I
KC–II
Relative density
Mean abundance
almon survival (%)
Planktonic
Copepodids
Parasitic
Copepodids
Chalimus 1/2
Chalimus 3/4
Motiles
0
1
0.4
0.8
0.5
2
3
50
100
−20
−10
10
20
30

Fig. 6. Sea lice transmission dynamics and mortality impact on juvenile pink salmon migrating past two active salmon farms (vertical dotted lines in the first row) in the Kingcome Inlet migration corridor (Fig. 4). The seaward migration of salmon is from left to right. The two columns correspond to replicate sets of samples taken 17-23 April (KC-I) and 22-25 April (KC-II), 2005. The first row shows the estimated spatial distributions of planktonic copepodids originating from all sources (thick gray line), from farm salmon (two thin curves), and from ambient sources (horizontal thin line). Reproduction of lice parasitizing the juvenile salmon was not considered due to the absence of gravid female lice. The middle three rows depict the mean abundances of lice (±95% bootstrap confidence interval) and maximum-likelihood model fits (black lines) along the migration route for parasitic copepodids, chalimi, and motiles. The bottom row depicts the estimated remaining juvenile salmon population that survived sea lice infestation. Temperature and salinity were measured at each site and averaged 7.8°C and 25.8‰ (KC-I) and 11.5°C and 22.5‰ (KC-II).



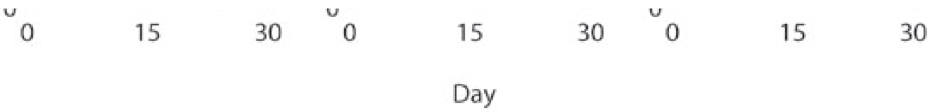


Fig. 7. Survival of juvenile pink salmon infested with sea lice in 2004. Sixty juvenile chum salmon infested with H_0 lice (all copepodids or chalimus I/II) were introduced into flowthrough ocean enclosures and provisioned with salmon feed. Each image corresponds to an individual enclosure. The black line shows the trajectory for the daily number of survivors. The light-gray lines are the trajectories of 1,000 simulations of the best-fit model. The model was simulated as a Markov chain tracking the number of survivors in time. Each day, the number of mortalities was drawn from the number of survivors on the previous day by using a binomial distribution with mortality probability calculated from the best-fit survival model. The model has the same parameter values for all treatment replicates, except for H_0, which is specific to each enclosure.

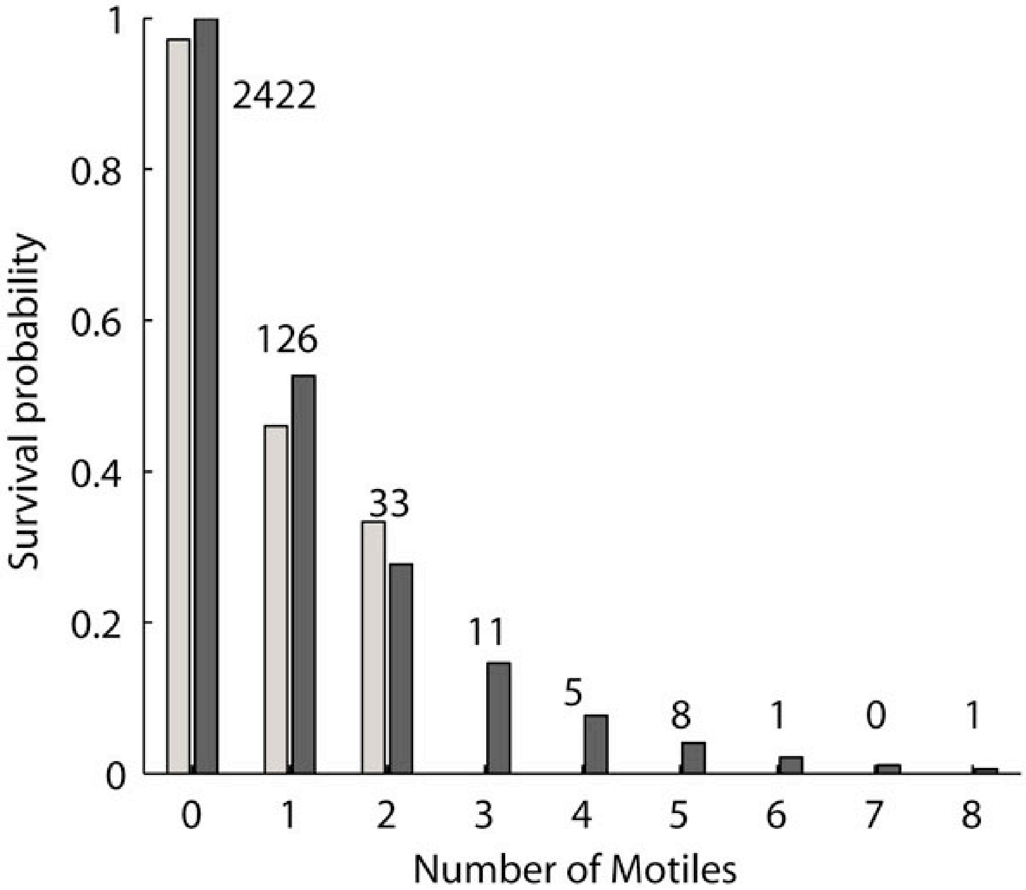


Fig. 8. Survival of juvenile pink salmon infested with sea lice in 2005. The plot shows the number of survivors in each infection category (light-gray bars) and the best-fit model for the survival probability of these fish after 28 days (the average duration of the observational trials; dark bars). The numbers above each light bar are the number of fish observed in each category.

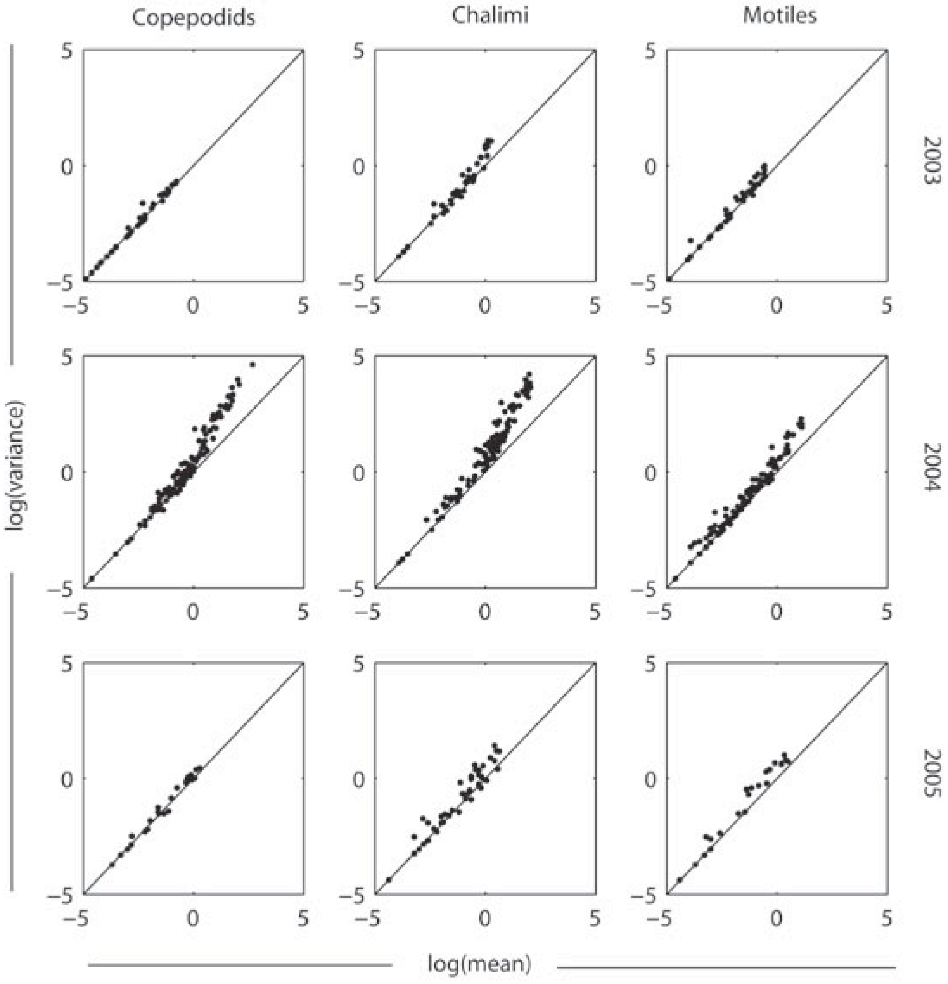


Fig. 9. Log variance vs. log mean for the three parasitic stages of sea lice infecting juvenile pink and chum salmon in the Broughton Archipelago in British Columbia from 2003-2005. Clustering of samples along the 1:1 variance to mean line is characteristic of a Poisson infection process. There are 41, 117, and 29 samples of »100 juvenile salmon from 2003, 2004, and 2005, respectively. Compare with figure 5 in ref 1.

1. Shaw DJ, Dobson AP (1995) *Parasitology* 111:S111-S133.

Table 1. Likelihood ratio tests of the null hypothesis that farm salmon do not infect wild salmon

Year	**Dataset**	***R***	**DF**	***P***
2004	TR-1	3,620	7	®0

	TR-2	3,350	7	®0
	TR-3	6,396	8	®0
	KN-1	2,068	6	®0
	KN-2	1,536	6	®0
	KN-3	1,666	7	®0
2005	KC-1	1,458	7	®0
	KC-2	1,107	7	®0

R is the likelihood ratio statistic, DF is the degree of freedom (difference in the number of parameters between nested models: ambient lice sources only and ambient plus farm sources), and P is the associated P value (P®0 means P<1 ´ 10^{-234}).

Table 2. Model selection statistics (DAIC and Akaike weights, w_j) for each model fit to each dataset

	Ambient		**Farm**		**Ambient plus farm**	
Dataset	DAIC	w_j	DAIC	w_j	DAIC	w_j
TR-1	3606	®0	48	4.6 ´ 10^{-11}	0	®1
TR-2	3336	®0	120	8.8 ´ 10^{-27}	0	®1
TR-3	6380	®0	214	3.4 ´ 10^{-47}	0	®1
KN-1	2088	®0	32	1.1 ´ 10^{-7}	0	®1
KN-2	1524	®0	121	6.5 ´ 10^{-27}	0	®1
KN-3	1652	®0	38	6.8 ´ 10^{-9}	0	®1
KC-1	1444	®0	26	2.3 ´ 10^{-6}	0	®1
KC-2	1093	®0	200	4.1 ´ 10^{-44}	0	®1

Models are defined by their lice-source components: ambient only, farm only, and ambient plus farm. (w_j ®0 means w_j<1 ´ 10^{-234}, and w_j ®1 means w_j>0.9999999).

Table 3. Parameter values estimated from the transmission dynamics model for each dataset in 2004

	Chums				**Pinks**				**Both species**			
	l_h, km	**v, , km×d^{-1})**	**s_c**	**s_h**	**l_h, km**	**v, km×d^{-1}**	**s_c**	**s_h**	**f_1/ k**	**f_2/ k**	**f_3/ k**	**D, km^{2}×d^{-1}**
TR-I	17.3	1.2	0.24	0.13	15.1	1.1	0.25	0.16	8,554	12,407	15,495	11
TR-II	10.4	0.7	0.18	0.17	8.6	0.6	0.17	0.23	5,987	12,425	21,308	25
TR-III	13.5	1.0	0.15	0.15	12.7	0.9	0.10	0.27	1,968	6,176.3	11,989	27
KN-I	18.7	1.3	0.15	0.19	18.0	1.3	0.21	0.20	5,877	17,754	-	16
KN-II	17.3	1.2	0.13	0.25	18.5	1.3	0.13	0.50	60	21,445	-	36
KN-III	16.1	1.1	0.20	0.22	12.2	0.9	0.14	0.41	28	2,611	-	21
KC-I	-	-	-	-	4.7	0.3	0.30	0.11	3,400	29,527	-	1.6
KC-II	-	-	-	-	6.4	0.5	0.19	0.26	240	2,595	-	2.2

Parameters: l_h, average distance salmon migrate during parasitic copepodid and chalimus stages; v, the average seaward migration velocity of juvenile salmon (calculated by dividing l_h by 14 days, approximately the mean duration of copepodid plus chalimus lice) (1); f_i, abundance of copepodids released from farm i; k, ambient density of copepodids; D, diffusion coefficient of planktonic larvae; s_c, survivorship of parasitic copepodids; s_h, survivorship of chalimi.

1. Stien A, Bjorn PA, Heuch PA, Elston DA (2005) *Mar Ecol Prog Ser* 290:263-275.

Table 4. Parameter estimates of the best-fit survival model to 2004 pink and chum data

Salmon	**a_1,**	**pa_2,**	**n**	**m_1^{-1}, days**

	days×lice^{-1}	**days×lice^{-1}**		
Pink	0.0078	0.0011	171	17
Chum	0.0011	0.0041	11	36

The mean time to the onset of increased pathogenicity is m_1^{-1}, and the variance in this onset is $(nm_1)^{-1}$

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