

The following supplement accompanies the article

Population genetic structure of the parasitic copepod *Lepeophtheirus salmonis* throughout the Atlantic

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Supplement 1. Summary statistics for the full Atlantic, reduced Atlantic, and Norway data sets

Table S1. Genetic variation in all 27 samples throughout the Atlantic (full Atlantic data set). N = number of individuals per sample, A_T = total number of alleles, A_M = mean number of alleles, H_o = observed heterozygosity, H_e = expected heterozygosity, F_{is} = inbreeding coefficient, F_{st} = fixation index. *Significant deviation from Hardy-Weinberg equilibrium (HWE) ($\alpha = 0.05$), **significant deviation from HWE following correction ($\alpha = 0.001$)

Sample	N	Locus	Summary																		
			<i>LsNUIG14</i>	<i>LsdistA1</i>	<i>LsdistA4</i>	<i>LsdistA5</i>	<i>LsdistA2</i>	<i>LsNUIG09</i>	<i>Lsdl110EUVc</i>	<i>Lsdl111EUVc</i>	<i>Lsdl103EUVc</i>	<i>Lsdl109EUVc</i>	<i>LsdistA3</i>	<i>Lsdl105EUVc</i>	<i>Lsdl106EUVc</i>	<i>Lsdl108EUVc</i>	A_T	A_M	H_o	H_e	F_{is}
N771	84	10	16	6	25	14	8	5	4	3	6	24	4	4	4	10	139	9.9	0.467574	0.480829	0.0276
N722	92	7	14	7	17*	15	11	5	4**	2	6	24	5	4	9	130	9.3	0.443346	0.475793	0.0682	
N793	94	7	16	4	26*	19	8	4	4	5	7	22	4	4	9	139	9.9	0.442541	0.471206	0.0608	
N798	93	8	18	5	22	16	8	5*	3	7	8	22	7	5*	9	143	10.2	0.442188	0.462278	0.0435	
N800	93	7	16	7	25	20	9*	4	1**	5	7	24	4	3	11	143	10.2	0.450867	0.481233	0.0631	
N802	93	7	16	6	23	17	11	4	4	5	7	22	5	4*	11	142	10.1	0.455147	0.469254	0.0301	
N813	93	9	17	4	19	16	7**	2	2	5	6	21*	4	4	9	125	8.9	0.448018	0.473512	0.0538	
N814	89	8	15	5	22	16	10	5	5	8*	8	22**	7	3	9	143	10.2	0.468679	0.479142	0.0218	
N820	94	5	15	5	21	19	10*	4	4	4	8	22	5	4	9	135	9.6	0.453824	0.476696	0.0480	
N823	93	5	19	5	24*	16	8	5	4	3	6	19*	5	4	9	132	9.4	0.452450	0.473751	0.0450	
N824	94	7*	15	6	23	17	8	4	4	6	7	22	5	5	11	140	10.0	0.468862	0.477084	0.0172	
N825	93	7*	17	6	23	18*	11	4	4	6	6	21*	4	5	11	143	10.2	0.463306	0.494238	0.0626	
N832	93	6*	15	7	19*	17	7	5	5	7	8	23	5*	5	11	140	10.0	0.469565	0.493945	0.0494	
N833	93	6	17	6	22	13	8*	4	4	4	6	21	5	5	10*	131	9.4	0.456538	0.488536	0.0655	
N837	94	8	20	6	21	16	11	4	5	6	9	22	3	4	8	143	10.2	0.457348	0.490268	0.0671	
N838	94	6	18	7	21	19	9*	5	5	5	7*	22	4	4	10	142	10.1	0.454349	0.491779	0.0761	
N849	93	6	19*	7	30*	15	9	4	3	4	7	24	6	4	11	149	10.6	0.455338	0.482921	0.0571	
F850	94	7	19	6	23	16	11	5	2	5	8	22	4	6	8	142	10.1	0.475000	0.495422	0.0412	
F851	79	6	16	6	23	16	9	5	3	6	7	24	3	4	8	136	9.7	0.479382	0.480261	0.0018	
I852	93	7	15	6	25	16	8	5	3	5	8	21*	6	4	9	138	9.9	0.474026	0.482857	0.0183	
I853	94	7	17	8	23	17	11	4	4	4	7	18	5	5	7	137	9.8	0.435093	0.455017	0.0438	
N854	94	5	15	7	23	16	11	4	3	3	8	22	4	5	9	135	9.6	0.454223	0.478374	0.0505	
S855	94	8	17	4	26*	13	11	4	3	6	7	18	4	5	9	135	9.6	0.456268	0.473585	0.0366	

Table S2: Genetic variation observed in 11 samples chosen to represent the Atlantic distribution (reduced Atlantic data set). See Table S1 for abbreviations

Sample	N	Locus	Locus											Summary						
			<i>LsNUG14</i>	<i>LsST1</i>	<i>LsST14</i>	<i>LsST15</i>	<i>LsST12</i>	<i>LsNUG09</i>	<i>LsI110EUTC</i>	<i>LsI111EUTC</i>	<i>LsI103EUTC</i>	<i>LsI109EUTC</i>	<i>LsST13</i>	<i>LsI105EUTC</i>	<i>LsI106EUTC</i>	<i>LsI108EUTC</i>	<i>A_T</i>	<i>A_G</i>	<i>H₀</i>	<i>H_e</i>
<i>H_e</i> (gene diversity)	0.705764	0.860234	0.526913	0.935815	0.819853	0.513087	0.207984	0.045028	0.074151	0.676301	0.908438	0.083153	0.077850	0.550362						
	0.000577	0.001283	0.002221	0.002235	-0.000168	-0.001126	-0.000381	-0.001826	0.000326	-0.000825	0.014967	0.000027	-0.001015	0.004950						
	0.260200	0.021400	0.045200	0.000100	0.580600	0.810100	0.588500	0.977600	0.336500	0.832900	0.000100	0.458700	0.829300	0.000100						
	94	5	18	5	22	18	7	4	4	4	7	19	4	3	8	128	9.1	0.443165	0.459458	0.0355
	94	6	16	5	22	17	10	4	3	5	8	19	4	3	8	130	9.3	0.458424	0.473481	0.0318
	94	7	19	6	23	16	12	4	4	4	7	22	3	4	8	139	9.9	0.456569	0.463495	0.0149
	93	7	18	5	23	16	8	3	6	4	9	23*	5	5	11	143	10.2	0.445522	0.468098	0.0482
	2495	17	30	15	35	37	16	6	9	12	11	30	12	10	17	257	18.4			
	Global <i>F_{ST}</i>	0.000577	0.001283	0.002221	0.002235	-0.000168	-0.001126	-0.000381	-0.001826	0.000326	-0.000825	0.014967	0.000027	-0.001015	0.004950					
	<i>p</i>	0.260200	0.021400	0.045200	0.000100	0.580600	0.810100	0.588500	0.977600	0.336500	0.832900	0.000100	0.458700	0.829300	0.000100					
	<i>H_e</i> (gene diversity)	0.705764	0.860234	0.526913	0.935815	0.819853	0.513087	0.207984	0.045028	0.074151	0.676301	0.908438	0.083153	0.077850	0.550362					
Global <i>F_{ST}</i>	0.000526	0.001570	-0.001710	0.004352	0.001153	0.000977	0.000834	-0.001974	0.000418	0.000191	0.029706	0.001465	-0.000847	0.012608						
<i>p</i>	0.321800	0.059100	0.808400	0.000100	0.147300	0.263000	0.287200	0.883500	0.344600	0.402600	0.000100	0.166700	0.668100	0.000100						
<i>H_e</i> (gene diversity)	0.704015	0.867224	0.524116	0.937211	0.817439	0.520046	0.211927	0.040963	0.072492	0.678563	0.893226	0.092172	0.080916	0.516651						

Table S3. Genetic variation observed in 19 samples from Norway (Norway data set). See Table S1 for abbreviations

Sample	N	Locus	Summary																		
			<i>LsNUG14</i>	<i>LsdST1</i>	<i>LsdST4</i>	<i>LsdST5</i>	<i>LsdST2</i>	<i>LsNUG09</i>	<i>Lsd110EUC</i>	<i>Lsd111EUC</i>	<i>Lsd103EUC</i>	<i>Lsd109EUC</i>	<i>LsdST3</i>	<i>Lsd105EUC</i>	<i>Lsd106EUC</i>	<i>Lsd108EUC</i>	<i>A_T</i>	<i>A_C</i>	<i>H₀</i>	<i>H_e</i>	<i>F_{is}</i>
N771	84	10	16	6	25	14	8	5	4	3	6	24	4	4	4	10	139	9.9	0.467574	0.480829	0.0276
N722	92	7	14	7	17*	15	11	5	4**	2	6	24	5	4	4	9	130	9.3	0.443346	0.475793	0.0682
N793	94	7	16	4	26*	19	8	4	4	5	7	22	4	4	9	139	9.9	0.442541	0.471206	0.0608	
N798	93	8	18	5	22	16	8	5*	3	7	8	22	7	5*	9	143	10.2	0.442188	0.462278	0.0435	
N800	93	7	16	7	25	20	9*	4	1**	5	7	24	4	3	11	143	10.2	0.450867	0.481233	0.0631	
N802	93	7	16	6	23	17	11	4	4	5	7	22	5	4*	11	142	10.1	0.455147	0.469254	0.0301	
N813	93	9	17	4	19	16	7**	2	2	5	6	21*	4	4	9	125	8.9	0.448018	0.473512	0.0538	
N814	89	8	15	5	22	16	10	5	5	8*	8	22**	7	3	9	143	10.2	0.468679	0.479142	0.0218	
N820	94	5	15	5	21	19	10*	4	4	4	8	22	5	4	9	135	9.6	0.453824	0.476696	0.0480	
N823	93	5	19	5	24*	16	8	5	4	3	6	19*	5	4	9	132	9.4	0.452450	0.473751	0.0450	
N824	94	7*	15	6	23	17	8	4	4	6	7	22	5	5	11	140	10.0	0.468862	0.477084	0.0172	
N825	93	7*	17	6	23	18*	11	4	4	6	6	21*	4	5	11	143	10.2	0.463306	0.494238	0.0626	
N832	93	6*	15	7	19*	17	7	5	5	7	8	23	5*	5	11	140	10.0	0.469565	0.493945	0.0494	
N833	93	6	17	6	22	13	8*	4	4	4	6	21	5	5	10*	131	9.4	0.456538	0.488536	0.0655	
N837	94	8	20	6	21	16	11	4	5	6	9	22	3	4	8	143	10.2	0.457348	0.490268	0.0671	
N838	94	6	18	7	21	19	9*	5	5	5	7*	22	4	4	10	142	10.1	0.454349	0.491779	0.0761	
N849	93	6	19*	7	30*	15	9	4	3	4	7	24	6	4	11	149	10.6	0.455338	0.482921	0.0571	
N854	94	5	15	7	23	16	11	4	3	3	8	22	4	5	9	135	9.6	0.454223	0.478374	0.0505	
N891	93	7	18	5	23	16	8	3	6	4	9	23*	5	5	11	143	10.2	0.445522	0.468098	0.0482	
Total	1759	17	28	14	33	35	16	6	9	11	11	30	12	7	17	246	17.6				
Global <i>F_{ST}</i>	-0.000099	0.000748	0.003712	0.000626	-0.000864	-0.002059	-0.001467	-0.001800	0.000380	-0.001068	0.000603	-0.000817	-0.001102	-0.001184							
p	0.505600	0.152200	0.016600	0.113100	0.848300	0.928700	0.846600	0.947800	0.333300	0.845700	0.142900	0.749500	0.800400	0.898400							
<i>H_e</i> (Gene diversity)	0.704377	0.857622	0.528573	0.935362	0.819283	0.505660	0.203967	0.047523	0.071704	0.673690	0.913912	0.081204	0.074260	0.578983							