MOLECULAR ECOLOGY

Supplemental Information for:

Phoretic dispersal influences parasite population genetic structure

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Table S1. Microsatellite loci developed for this study. We developed 17 primer sets specific to wing lice (*Columbicola columbae*) and 13 primer sets specific to body lice (*Campanulotes compar*).

	#	Repeat	Forward Primer	Reverse Primer	Length
Body Lice *Campanulotes compar*	2B	(AG) * 19	M13_GACAAGTGACCGTCTCTATCGCG	AGTATGGCCGGTGACTTTCG	351
	5B	(ACT) * 23	M13_GACCGGCTCGAAGTCAAGAAACC	GCACTCTGACAGGCGTTC	423
	6B	(ACT) * 16	M13_GACAAGTCAGTTCGCTCCCTTTG	TCCACCTCCACAACTTTCCG	373
	9B	(AC) * 8	M13_GACTCTCGAAATTTCCACGTGCC	TTGTGTGGCCAAACTCTTCG	318
	10B	(AAG) * 7	M13_GACTTCCTCTCAGAACGCTCAGG	AAGCTTCCAGTTCCCTCTCG	167
	11B	(AG) * 18	M13_GACGAACCGGTTCGAGGAATGTC	AGGAGCGATTAATGCCAAGC	416
	12B	(AGC) * 6	M13_GACAAAGGGAGTGGAGGGTACGG	CGCGATCCAGGTCATTTCAC	277
	13B	(AT) * 7	M13_GACAGTAAGCAGTGGTCAGCAGG	CGTCTTTCCGCGTTAAGTTTG	414
Wing Lice *Columbicola columbae*	3W	(AG) * 14	M13_GACGGAGAGATAGGACGGGCTTG	AAACAAGGACCTCGGACCC	417
	6W	(AAG) * 7	M13_GACGGCGGTGGATGATTGAACAG	TCACGTATGGATCCGGACAG	376
	9W	(AG) * 9	M13_GACTCACACTGGAGGCAAGGAAG	GCACATTTGGACGAGTGGAG	327
	10W	(ATC) * 6	M13_GACTTGAAACTGAGAGGAGTGCC	TCAATTTGACGATCCTGCTGG	443
	12W	(AG) * 9	M13_GACAAAGTCTGGGAGAGGTCAGC	GTTGGTCGAGCAGGAATGAC	300
	13W	(AG) * 13	M13_GACGGTAACTTGTGCGTCCGTAAG	ATCTTCATTTCCGGTTGCGG	376
	15W	(ACAG) * 6	M13_GACGTCTTCTCTTGAGTGTTGCAAC	AATCGTGTGTAGCGTGCAAG	406
	16W	(AG) * 12	M13_GACTTATTCACAGCCTCCCTCCG	ACGGGTCATAAGTGGCAAAG	422

Table S2. Comparison of body and wing lice prevalence and abundance on pigeons at each site. Prevalence is the percent of pigeons sampled with at least one parasite. Abundance is the mean (± standard error) number of lice removed from each fumigated pigeon by ruffling (including parasite free birds).

Flock #	**Site #**	**# pigeons sampled**	**Parasite prevalence**		**Parasite abundance**	
			Body lice	Wing lice	Body lice	Wing lice
Flock 1	Site 1	83	71.1	100.0	6.0 ± 0.9	31.5 ± 3.4
Flock 2	Site 2	70	72.9	98.6	6.4 ± 1.3	33.8 ± 4.8
Flock 3	Site 3	72	70.8	83.3	8.7 ± 3.2	21.9 ± 3.5

Table S3. Indices of genetic diversity and subpopulation size for body and wing lice subpopulations on each host individual. The mean number of alleles observed (N_A), observed heterozygosity (H_O), expected heterozygosity (H_S), subpopulation size (N_C) and the inbreeding coefficient (F_{IS}) with lower and upper 95% CIs in brackets are reported.

			Body Lice *Camanulotes compar*					Wing Lice *Columbicola columbae*				
Sampling Site	Host Bird	Host Field ID	N_C	N_A	H_O	H_S	F_{IS}	N_C	N_A	H_O	H_S	F_{IS}
Flock 1	Bird1	1SLC4235	34	4.714	0.470	0.514	0.252 [0.142, 0.381]	50	4.500	0.707	0.685	-0.087 [-0.238, 0.039]
	Bird2	1SLC42	14	4.500	0.475	0.560	0.101 [-0.076, 0.253]	27	4.875	0.675	0.668	-0.063 [-0.202, 0.032]
	Bird3	1SLC67	29	4.500	0.549	0.616	0.056 [-0.112, 0.181]	84	3.875	0.556	0.608	0.029 [-0.166, 0.188]
	Bird4	1SLC72	43	2.750	0.500	0.459	-0.132 [-0.290, -0.000]	79	3.750	0.537	0.545	-0.039 [-0.248, 0.126]
	Bird5	1SLC50	17	3.750	0.475	0.489	-0.024 [-0.267, 0.239]	21	4.125	0.483	0.678	0.228 [0.019, 0.403]
	Bird6	1SLC78	13	4.625	0.562	0.565	-0.049 [-0.211, 0.050]	34	5.000	0.575	0.683	0.107 [-0.022, 0.194]
	Bird7	1SLC82	81	5.375	0.565	0.568	-0.049 [-0.214, 0.089]	145	4.250	0.556	0.604	0.021 [-0.112, 0.110]
	Bird8	1SLC56	10	4.375	0.415	0.546	0.189 [-0.142, 0.527]	66	4.000	0.532	0.569	0.006 [-0.165, 0.156]
	Bird9	1SLC77	42	4.000	0.615	0.550	-0.1704 [-0.338, -0.010]	43	4.000	0.584	0.678	0.085 [-0.098, 0.255]
	Bird10	1SLC4229	11	4.000	0.519	0.566	-0.008 [-0.245, 0.174]	71	4.250	0.507	0.620	0.130 [-0.020, 0.245]
Flock 2	Bird1	2SLC4290	20	5.000	0.581	0.570	0.151 [0.076, 0.210]	48	4.375	0.534	0.647	0.118 [-0.032, 0.244]
	Bird2	2SLC50	27	2.500	0.264	0.320	0.123 [-0.106, 0.315]	62	3.500	0.488	0.539	0.043 [-0.204, 0.288]
	Bird3	2SLC51	14	5.125	0.575	0.597	-0.013 [-0.154, 0.106]	43	4.625	0.583	0.641	0.037 [-0.101, 0.146]
	Bird4	2SLC56	65	4.250	0.519	0.522	-0.048 [-0.204, 0.078]	241	3.875	0.494	0.561	0.065 [-0.094, 0.189]
	Bird5	2SLC69	20	4.625	0.450	0.527	0.094 [-0.065, 0.250]	43	4.875	0.562	0.626	0.050 [-0.079, 0.145]
	Bird6	2SLC68	15	5.125	0.465	0.535	0.078 [-0.078, 0.194]	105	4.500	0.513	0.589	0.078 [-0.080, 0.207]
	Bird7	2SLC63	14	3.375	0.513	0.481	-0.119 [-0.426, 0.162]	28	3.750	0.460	0.532	0.084 [-0.083, 0.226]
	Bird8	2SLC53	16	2.125	0.339	0.271	-0.300 [-0.488, -0.081]	30	4.500	0.632	0.651	-0.025 [-0.167, 0.105]
	Bird9	2SLC57	45	2.375	0.263	0.318	0.123 [-0.277, 0.470]	35	3.750	0.625	0.569	-0.151 [-0.288, -0.025]
	Bird10	2SLC54	16	3.750	0.356	0.457	0.161 [-0.069, 0.312]	35	4.625	0.643	0.648	-0.047 [-0.207, 0.100]
Flock 3	Bird1	3SLC4316	203	5.143	0.481	0.574	0.295 [0.125, 0.450]	146	3.250	0.529	0.558	-0.002 [-0.218, 0.196]
	Bird2	3SLC46	91	3.250	0.444	0.516	0.085 [-0.122, 0.260]	82	4.250	0.625	0.611	-0.075 [-0.291, 0.104]
	Bird3	3SLC39	49	1.500	0.158	0.179	0.048 [-0.353, 0.470]	77	3.000	0.422	0.423	-0.051 [-0.283, 0.147]
	Bird4	3SLC45	23	5.000	0.562	0.587	-0.011 [-0.180, 0.141]	61	4.250	0.569	0.626	0.036 [-0.142, 0.173]
	Bird5	3SLC38	11	3.000	0.354	0.467	0.188 [-0.095, 0.408]	32	4.500	0.475	0.619	0.183 [0.029, 0.295]
	Bird6	3SLC54	24	5.000	0.519	0.537	-0.020 [-0.186, 0.114]	47	5.250	0.604	0.672	0.049 [-0.113, 0.182]
	Bird7	3SLC65	39	3.875	0.532	0.570	0.011 [-0.227, 0.250]	74	3.875	0.425	0.492	0.085 [-0.178, 0.332]
	Bird8	3SLC53	14	1.750	0.425	0.273	-0.593 [-0.810, -0.396]	38	4.375	0.713	0.653	-0.142 [-0.305, -0.003]
	Bird9	3SLC66	10	1.875	0.222	0.230	-0.023 [-0.249, 0.148]	94	3.750	0.550	0.538	-0.077 [-0.257, 0.063]
	Bird10	3SLC4315	12	4.375	0.390	0.493	0.154 [-0.022, 0.303]	32	4.000	0.550	0.576	-0.008 [-0.175, 0.170]

Table S4. Indices of genetic diversity for pigeon flocks. The mean number of alleles observed (N_A), observed heterozygosity (H_O), expected heterozygosity (H_S), and the inbreeding coefficient (F_{IS}) with lower and upper 95% CIs in brackets are reported.

Sampling Site	N_A	H_O	H_S	F_{IS}
Flock 1	9.94	0.550	0.540	-0.008 [-0.145, 0.101]
Flock 2	10	0.590	0.560	-0.059 [-0.152, 0.004]
Flock 3	9.59	0.550	0.540	-0.016 [-0.158, 0.083]

Table S5. Pairwise F_{ST} estimates for body lice (*Campanulotes compar*) populations estimated from 8 microsatellite markers. Population comparisons that are statistically significant after correcting for false discovery rates are shaded in gray.

		Flock 1										Flock 2										Flock 3									
	Body Lice	Bird1	Bird2	Bird3	Bird4	Bird5	Bird6	Bird7	Bird8	Bird9	Bird10	Bird1	Bird2	Bird3	Bird4	Bird5	Bird6	Bird7	Bird8	Bird9	Bird10	Bird1	Bird2	Bird3	Bird4	Bird5	Bird6	Bird7	Bird8	Bird9	Bird10
Flock 1	Bird1	0.00																													
	Bird2	0.07	0.00																												
	Bird3	0.04	0.07	0.00																											
	Bird4	0.23	0.18	0.19	0.00																										
	Bird5	0.14	0.10	0.09	0.22	0.00																									
	Bird6	0.08	0.11	0.08	0.20	0.12	0.00																								
	Bird7	0.05	0.10	0.07	0.24	0.15	0.05	0.00																							
	Bird8	0.14	0.11	0.04	0.24	0.10	0.12	0.16	0.00																						
	Bird9	0.08	0.08	0.07	0.20	0.10	0.09	0.14	0.10	0.00																					
	Bird10	0.12	0.09	0.03	0.16	0.09	0.05	0.07	0.11	0.08	0.00																				
Flock 2	Bird1	0.11	0.00	0.04	0.10	0.07	0.02	0.01	0.12	0.02	0.03	0.00																			
	Bird2	0.34	0.27	0.28	0.44	0.34	0.31	0.30	0.28	0.36	0.37	0.36	0.00																		
	Bird3	0.00	0.05	0.05	0.19	0.08	0.05	0.04	0.10	0.06	0.02	-0.02	0.29	0.00																	
	Bird4	0.06	0.11	0.10	0.24	0.16	0.15	0.12	0.18	0.12	0.12	0.05	0.35	0.09	0.00																
	Bird5	0.04	0.10	0.04	0.24	0.13	0.10	0.08	0.12	0.10	0.09	0.05	0.31	0.04	0.09	0.00															
	Bird6	0.04	0.07	0.03	0.18	0.07	0.05	0.07	0.09	0.07	0.04	0.00	0.28	0.04	0.08	0.04	0.00														
	Bird7	0.11	0.13	0.11	0.21	0.13	0.10	0.12	0.15	0.11	0.05	0.05	0.32	0.08	0.18	0.13	0.09	0.00													
	Bird8	0.35	0.26	0.30	0.46	0.32	0.30	0.28	0.37	0.33	0.38	0.32	0.42	0.26	0.38	0.30	0.29	0.31	0.00												
	Bird9	0.26	0.20	0.25	0.41	0.26	0.25	0.23	0.33	0.28	0.32	0.25	0.39	0.21	0.32	0.25	0.22	0.25	0.00	0.00											
	Bird10	0.09	0.11	0.10	0.28	0.12	0.10	0.09	0.18	0.13	0.14	0.07	0.32	0.07	0.09	0.08	0.07	0.11	0.23	0.14	0.00										
Flock 3	Bird1	0.09	-0.01	-0.02	0.15	0.05	0.04	0.00	0.07	0.04	0.02	0.04	0.30	-0.03	0.06	0.00	0.00	0.08	0.31	0.26	0.09	0.00									
	Bird2	0.11	0.14	0.11	0.22	0.15	0.08	0.13	0.15	0.14	0.10	0.06	0.36	0.09	0.19	0.14	0.09	0.12	0.38	0.32	0.15	0.07	0.00								
	Bird3	0.46	0.55	0.47	0.61	0.56	0.52	0.50	0.52	0.51	0.58	0.50	0.66	0.49	0.53	0.51	0.52	0.55	0.71	0.68	0.59	0.51	0.56	0.00							
	Bird4	0.02	0.03	0.04	0.15	0.07	0.08	0.07	0.10	0.05	0.03	-0.05	0.32	0.03	0.09	0.05	0.05	0.09	0.28	0.22	0.07	-0.08	0.10	0.52	0.00						
	Bird5	0.09	0.24	0.21	0.35	0.25	0.21	0.27	0.25	0.22	0.19	0.11	0.45	0.17	0.23	0.21	0.21	0.24	0.48	0.42	0.28	0.14	0.22	0.54	0.19	0.00					
	Bird6	0.04	0.08	0.06	0.21	0.11	0.07	0.09	0.14	0.07	0.09	0.00	0.33	0.04	0.10	0.05	0.07	0.07	0.29	0.22	0.03	0.02	0.06	0.53	0.01	0.18	0.00				
	Bird7	0.12	0.11	0.12	0.23	0.13	0.12	0.18	0.12	0.15	0.11	0.07	0.31	0.09	0.21	0.17	0.12	0.16	0.33	0.30	0.23	0.06	0.14	0.51	0.11	0.16	0.15	0.00			
	Bird8	0.32	0.38	0.34	0.42	0.44	0.39	0.35	0.40	0.42	0.39	0.38	0.53	0.35	0.39	0.34	0.39	0.41	0.55	0.52	0.42	0.32	0.45	0.71	0.33	0.46	0.38	0.41	0.00		
	Bird9	0.36	0.35	0.32	0.48	0.40	0.34	0.31	0.41	0.36	0.41	0.33	0.51	0.31	0.36	0.34	0.33	0.34	0.50	0.43	0.27	0.34	0.34	0.73	0.30	0.47	0.22	0.44	0.62	0.00	
	Bird10	0.11	0.10	0.08	0.23	0.10	0.06	0.10	0.12	0.09	0.10	0.03	0.34	0.07	0.14	0.10	0.06	0.07	0.31	0.25	0.08	0.05	0.05	0.59	0.05	0.22	0.02	0.15	0.43	0.28	0.00

Table S6. Pairwise F_{ST} estimates for wing lice (*Columbicola columbae*) populations estimated from 8 microsatellite markers. Population comparisons that are statistically significant after correcting for false discovery rates are shaded in gray.

		Flock 1										Flock 2										Flock 3									
	Wing Lice	Bird1	Bird2	Bird3	Bird4	Bird5	Bird6	Bird7	Bird8	Bird9	Bird10	Bird1	Bird2	Bird3	Bird4	Bird5	Bird6	Bird7	Bird8	Bird9	Bird10	Bird1	Bird2	Bird3	Bird4	Bird5	Bird6	Bird7	Bird8	Bird9	Bird10
Flock 1	Bird1	0.00																													
	Bird2	0.07	0.00																												
	Bird3	0.02	0.03	0.00																											
	Bird4	0.16	0.07	0.13	0.00																										
	Bird5	-0.02	0.01	0.04	0.12	0.00																									
	Bird6	0.04	0.01	0.01	0.09	0.00	0.00																								
	Bird7	0.05	0.06	0.02	0.16	0.02	-0.02	0.00																							
	Bird8	0.05	0.02	0.00	0.08	0.07	0.00	0.05	0.00																						
	Bird9	0.01	0.03	0.02	0.11	0.03	0.03	0.07	0.03	0.00																					
	Bird10	0.05	-0.01	0.04	0.07	0.02	0.01	0.05	0.00	0.03	0.00																				
Flock 2	Bird1	0.09	-0.01	0.02	0.05	0.06	0.01	0.07	0.03	0.04	0.00	0.00																			
	Bird2	0.11	0.02	0.06	0.13	0.07	0.10	0.13	0.07	0.06	0.04	0.04	0.00																		
	Bird3	0.06	0.00	0.01	0.11	0.01	0.01	0.04	0.03	0.03	0.01	0.00	0.04	0.00																	
	Bird4	0.11	0.04	0.10	0.10	0.11	0.07	0.14	0.05	0.05	0.02	0.05	0.10	0.05	0.00																
	Bird5	0.03	0.04	-0.01	0.09	0.01	0.03	0.05	0.00	0.02	0.03	0.02	0.07	0.03	0.06	0.00															
	Bird6	0.11	0.03	0.08	0.04	0.06	0.05	0.10	0.02	0.06	0.02	0.02	0.08	0.07	0.02	0.06	0.00														
	Bird7	0.13	0.09	0.10	0.09	0.10	0.08	0.13	0.03	0.11	0.08	0.09	0.14	0.14	0.11	0.09	0.01	0.00													
	Bird8	0.06	0.03	0.03	0.05	0.04	0.05	0.10	0.01	0.03	0.02	0.01	0.06	0.05	0.04	0.04	0.01	0.03	0.00												
	Bird9	0.09	0.06	0.04	0.13	0.06	0.05	0.06	0.02	0.11	0.06	0.08	0.12	0.09	0.15	0.06	0.09	0.05	0.08	0.00											
	Bird10	0.04	0.03	0.05	0.06	-0.01	0.07	0.10	0.07	0.02	0.03	0.04	0.06	0.04	0.08	0.02	0.06	0.13	0.06	0.10	0.00										
Flock 3	Bird1	0.09	0.10	0.09	0.16	0.05	0.11	0.15	0.12	0.11	0.11	0.10	0.11	0.14	0.14	0.09	0.07	0.10	0.09	0.12	0.10	0.00									
	Bird2	0.06	0.02	0.01	0.08	0.01	0.01	0.00	0.00	0.05	0.00	0.03	0.07	0.03	0.07	0.02	0.05	0.07	0.04	0.04	0.06	0.11	0.00								
	Bird3	0.21	0.16	0.19	0.15	0.17	0.22	0.26	0.21	0.16	0.19	0.15	0.11	0.20	0.24	0.13	0.13	0.19	0.14	0.23	0.10	0.17	0.20	0.00							
	Bird4	0.06	0.01	0.01	0.09	0.03	0.03	0.04	0.02	0.03	0.01	0.00	0.02	0.02	0.07	0.03	0.04	0.09	0.02	0.07	0.06	0.08	0.01	0.12	0.00						
	Bird5	0.08	-0.01	0.02	0.03	0.03	0.02	0.05	0.00	0.05	0.00	-0.01	0.04	0.03	0.06	0.02	0.00	0.05	0.02	0.05	0.04	0.07	0.00	0.12	0.00	0.00					
	Bird6	0.04	0.03	0.02	0.07	0.02	0.00	0.02	0.01	0.02	0.01	0.02	0.09	0.04	0.05	0.02	0.02	0.06	0.02	0.08	0.06	0.09	0.00	0.19	0.02	0.00	0.00				
	Bird7	0.15	0.12	0.14	0.11	0.15	0.18	0.24	0.14	0.12	0.14	0.11	0.09	0.16	0.18	0.10	0.13	0.16	0.09	0.18	0.10	0.15	0.16	0.04	0.10	0.11	0.17	0.00			
	Bird8	0.06	0.01	0.02	0.05	0.02	0.03	0.06	0.02	0.02	0.02	0.00	0.05	0.03	0.06	0.02	0.02	0.07	0.03	0.09	0.03	0.09	0.01	0.12	0.02	-0.01	0.00	0.11	0.00		
	Bird9	0.09	0.10	0.04	0.20	0.09	0.06	0.09	0.09	0.10	0.09	0.07	0.17	0.08	0.12	0.06	0.12	0.18	0.11	0.15	0.13	0.10	0.07	0.28	0.08	0.06	0.05	0.24	0.07	0.00	
	Bird10	0.08	0.09	0.09	0.15	0.04	0.12	0.17	0.10	0.09	0.08	0.09	0.10	0.11	0.09	0.03	0.09	0.12	0.09	0.12	0.05	0.03	0.11	0.16	0.11	0.09	0.10	0.13	0.09	0.14	0.00

Table S7. (a) Global estimates of F_{ST} values with lower and upper 95% CIs in brackets for body and wing lice. (b) Global estimates of G''_{ST} values with lower and upper 95% CIs in brackets for body and wing lice.

a

F_{ST}	Body Lice	Wing Lice
All sites	0.226 [0.210, 0.244]	0.069 [0.053, 0.087]
Site 1	0.130 [0.103, 0.162]	0.043 [0.017, 0.075]
Site 2	0.204 [0.173, 0.237]	0.061 [0.036, 0.091]
Site 3	0.316 [0.289, 0.345]	0.090 [0.062, 0.123]

b

G''_{ST}	Body Lice	Wing Lice
All sites	0.444 [0.421, 0.468]	0.181 [0.150, 0.214]
Site 1	0.295 [0.248, 0.347]	0.130 [0.071, 0.198]
Site 2	0.376 [0.331, 0.423]	0.161 [0.110, 0.216]
Site 3	0.576 [0.546, 0.607]	0.220 [0.169, 0.274]

Table S8. The optimal number of genetic clusters chosen from body lice genotypes. Cluster membership and host identity of individual lice are indicated in the table.

			Cluster #													
Sampling Site	Host Bird	Host Field ID	1	2	3	4	5	6	7	8	9	10	11	12	13	14
Flock 1	Bird1	1SLC4235							4			1		3		2
	Bird2	1SLC42	1			2	3	2						2		
	Bird3	1SLC67				2		2			1			3		2
	Bird4	1SLC72								10						
	Bird5	1SLC50				5								5		
	Bird6	1SLC78							3	2	4			1		
	Bird7	1SLC82				1					7			1		1
	Bird8	1SLC56				3		1						3		3
	Bird9	1SLC77				1	2	6	1							
	Bird10	1SLC4229				1		2			2			1		1
Flock 2	Bird1	2SLC4290				5		2	1	1	1					
	Bird2	2SLC50											10			
	Bird3	2SLC51	1			3		1			3	1				1
	Bird4	2SLC56					4									6
	Bird5	2SLC69						1	2		1		1			5
	Bird6	2SLC68							1		2			5		2
	Bird7	2SLC63				6		1	1		1					1
	Bird8	2SLC53	10													
	Bird9	2SLC57	9						1							
	Bird10	2SLC54	3				1		4							2
Flock 3	Bird1	3SLC4316				3		2		1	2			1		1
	Bird2	3SLC46				1		1	2		4			2		
	Bird3	3SLC39		10												
	Bird4	3SLC45				1	3	2		1	1					2
	Bird5	3SLC38										9		1		
	Bird6	3SLC54				1	3	1	3						1	1
	Bird7	3SLC65				1		2				4				
	Bird8	3SLC53			10									3		
	Bird9	3SLC66							1						9	
	Bird10	3SLC4315				3		1	3		2					1
		Total # of lice	24	10	10	39	16	27	27	15	31	15	11	31	10	31
		Total # of hosts in cluster	5	1	1	16	6	15	13	5	13	4	2	13	2	15

Table S9. The optimal number of genetic clusters chosen from wing lice genotypes. Cluster membership and host identity of individual lice are indicated in the table.

			Cluster #									
Sampling Site	Host Bird	Host Field ID	1	2	3	4	5	6	7	8	9	10
Flock 1	Bird1	1SLC4235			1	1		4		2	2	
	Bird2	1SLC42	3					1	1		2	3
	Bird3	1SLC67		1	1	4		1		3		
	Bird4	1SLC72				1	2	1				6
	Bird5	1SLC50	1	1	2	1	1	2	1	1		1
	Bird6	1SLC78		1			2	3		1	3	
	Bird7	1SLC82	2			2		3		1	2	
	Bird8	1SLC56	1	3		2			1	2	2	
	Bird9	1SLC77				4	1	1	1		1	2
	Bird10	1SLC4229	2			1			1	1	3	2
Flock 2	Bird1	2SLC4290	2						3	1	1	3
	Bird2	2SLC50	5				1		1	2		
	Bird3	2SLC51	2			2	1	1			3	1
	Bird4	2SLC56							6	1	2	
	Bird5	2SLC69			2	5		1	1	1		
	Bird6	2SLC68	1	3		1			2			3
	Bird7	2SLC63	1	7		1						1
	Bird8	2SLC53		3			2		2	1	1	1
	Bird9	2SLC57	3	3		2		1			1	
	Bird10	2SLC54			5	2		1				2
Flock 3	Bird1	3SLC4316		2	5			2	1			
	Bird2	3SLC46	2			1		1	1	4	1	1
	Bird3	3SLC39			2		7					
	Bird4	3SLC45	2	1		1	1		2	1	1	1
	Bird5	3SLC38	1		1	1			2	1		4
	Bird6	3SLC54	1			1		1	4	2		1
	Bird7	3SLC65		1	1		6		1	1		
	Bird8	3SLC53				2	1		1	4		2
	Bird9	3SLC66				1		2		6		1
	Bird10	3SLC4315		1	7	1			1			
		Total # of lice	29	27	27	37	25	26	33	36	25	35
		Total # of hosts in cluster	15	12	11	20	11	16	19	17	14	16

Figures

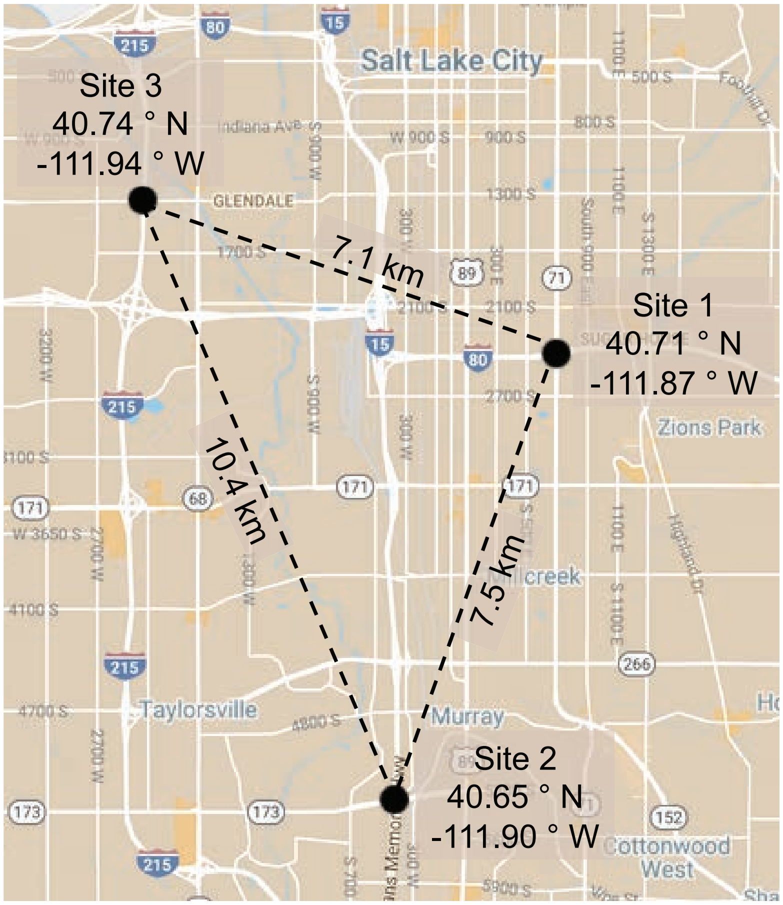

Figure S1. Map of sampling sites in Salt Lake City, Utah. Pigeon flocks were sampled at each of the three sites (Flock 1 = Site 1, Flock 2 = Site 2, Flock 3 = Flock 3).

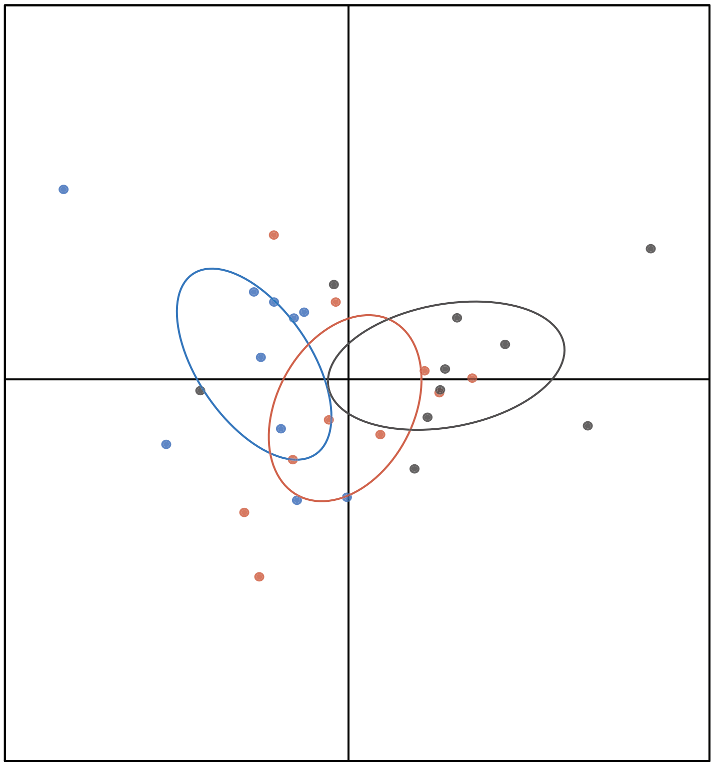

Figure S2. Ordination plot showing the first two principal components of the DAPC for pigeons. Colors show the sites/flock from which birds were collected (Site 1: blue; Site 2: red; Site 3: gray). Dots represent individual pigeon genotypes. Circles represent confidence intervals of the DAPC.

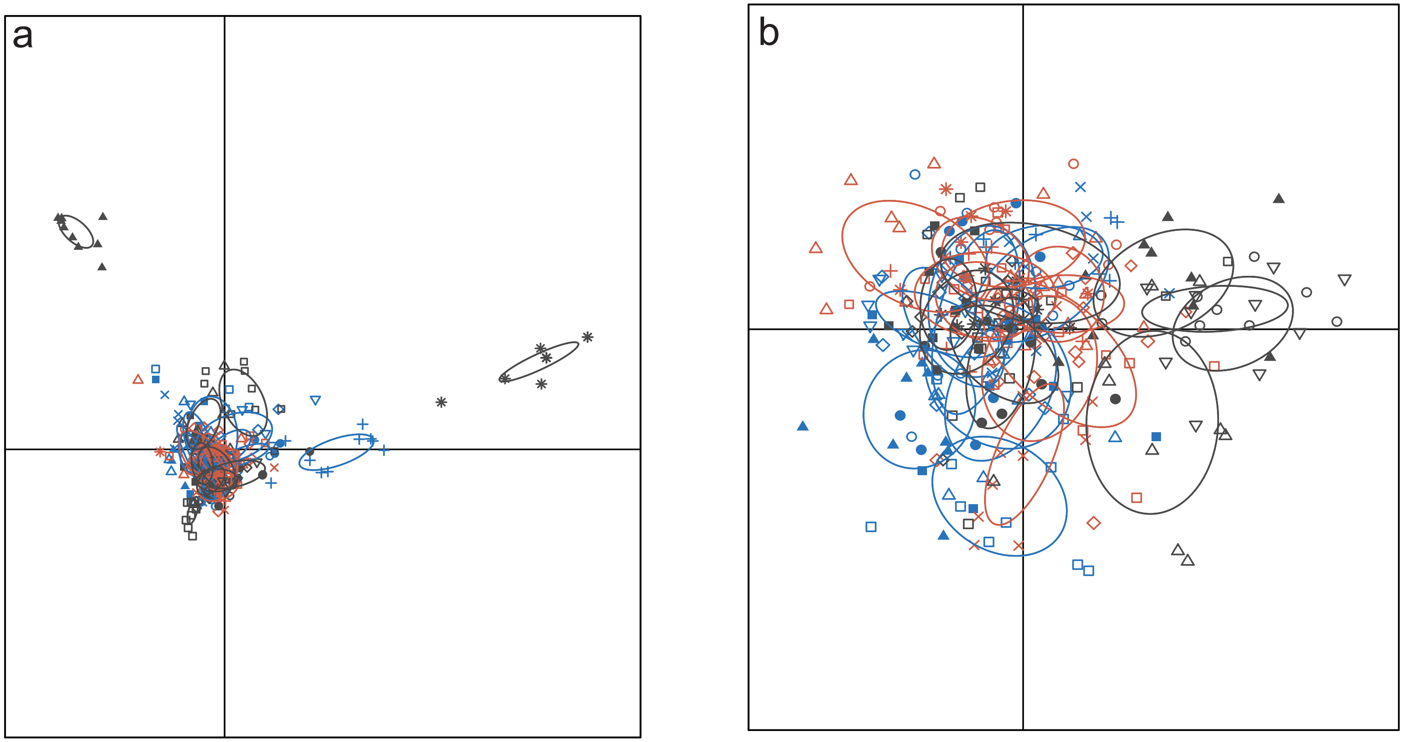

Figure S3. Ordination plots showing the first two principal components of the DAPC for (a) body lice and (b) wing lice, grouped by bird. Colors show the sites from which lice were collected (Site 1: blue; Site 2: red; Site 3: gray). Different symbols represent different subpopulations of lice. Circles represent confidence intervals of the DAPC.

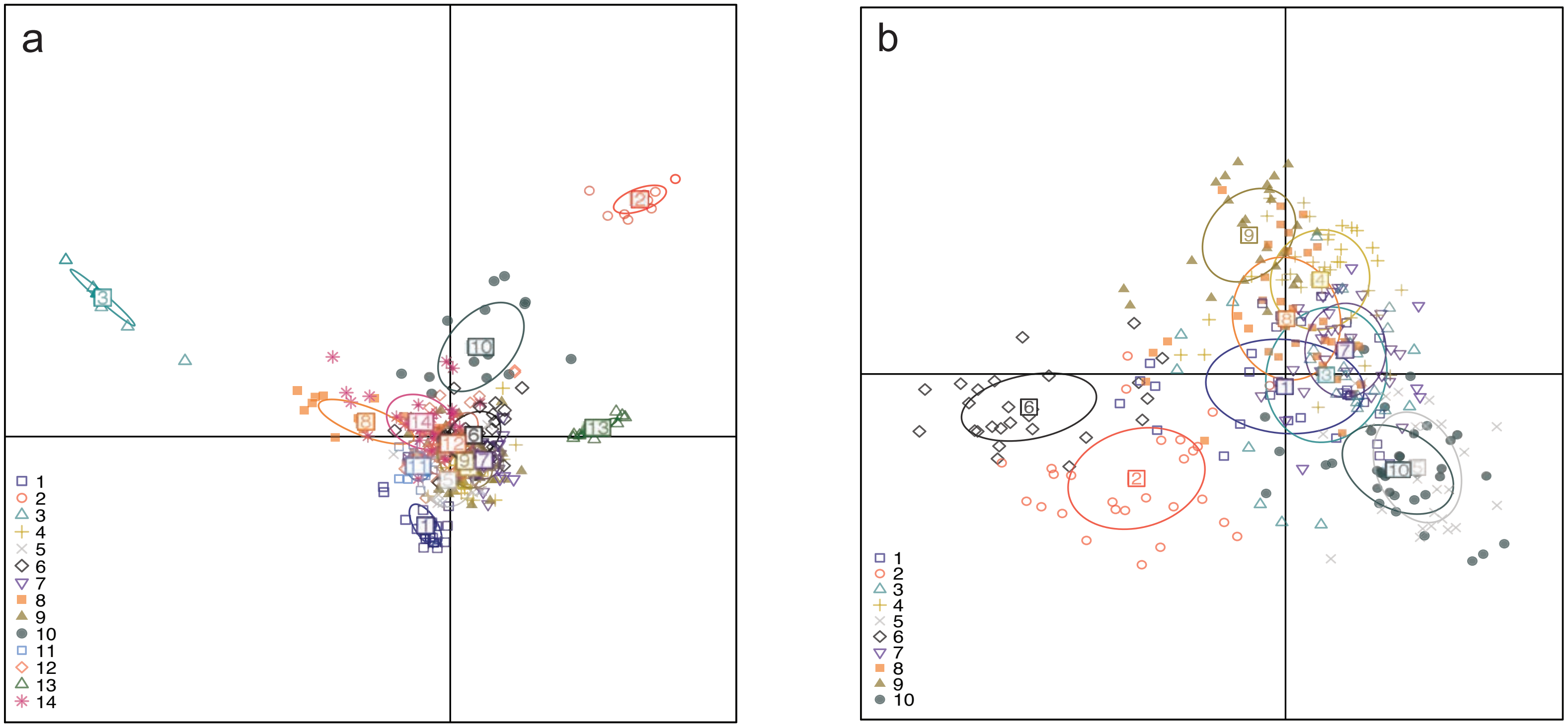

Figure S4. Ordination plots showing the first two principal components of the DAPC for (a) body lice and (b) wing lice grouped by k means clustering assignments. Different colors indicate different genetic clusters and different symbols represent different louse subpopulations. Circles represent confidence intervals of the DAPC. See Table S7 for individual body lice cluster assignments and Table S8 for individual wing lice cluster assignments.

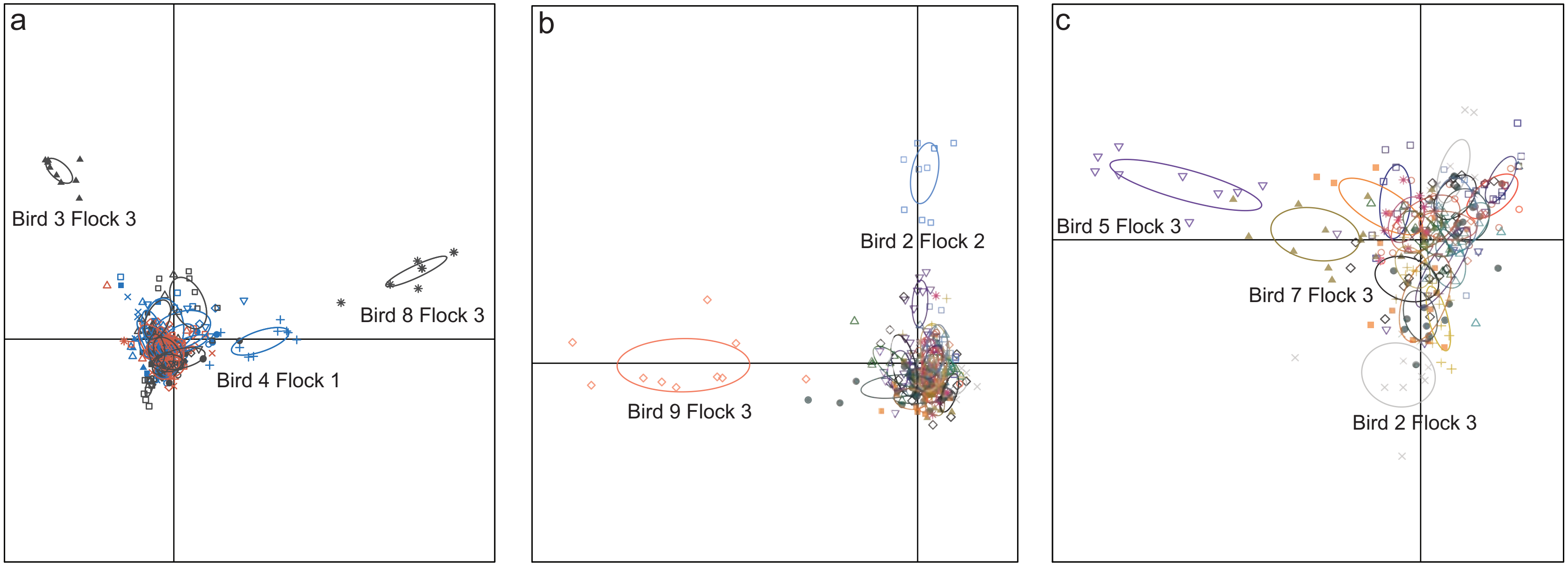

Figure S5. Ordination plots showing the first two principal components of the DAPC for body lice. Figure S4a is shown here (a) for easy reference. Colors indicate the sites from which lice were collected (Site 1: blue; Site 2: red; Site 3: gray). Different symbols represent genotypes of individuals belonging to one subpopulations of lice. Circles represent confidence intervals of the DAPC. This plot shows a clear separation of three body louse supopulations (bird 4 - flock 1, bird 3 - flock 3, bird 8 - flock 3). (b) Ordination plot showing the same data as S5a but with the three most genetically distinct body louse subpopulations (those labeled in S5a) removed. In this plot, colors indicate different hosts from which lice were collected. Two body louse subpopulations have non-overlapping clusters indicating a high degree of genetic differentiation (bird 2 - flock 2, bird 9 - flock 3). (c) Ordination plot showing the same data as S4a but with the five most genetically distinct body louse subpopulations (those labeled in S5a and S5b) removed. In this plot, colors indicate the different hosts from which lice were collected. Although this plot shows a separation of three additional body louse subpopulations (bird 5 - flock 3, bird 7 - flock 3, bird 2 - flock 3), the clusters are fairly close together. Thus, even when the most unique body louse subpopulations are excluded from the analysis, body lice are more differentiated than wing lice (Fig. S3b).

R code

Data Files birdglm.csv and locglm.csv will be uploaded to Dryad

By Bird Host

```
birdglm <- read.csv("birdglm.csv", header=T)

(NovelAllele.modbird <- glmer(cbind(novel,shared) ~ (louse)+(1|bird),data=birdglm, family="binomial"))

summary(NovelAllele.modbird)
```

By Location

```
locglm <- read.csv("locglm.csv", header=T)

(NovelAllele.mod1 <- glmer(cbind(novel,shared) ~ (louse) +(1|location),data=locglm, family="binomial"))

summary(NovelAllele.mod1)
```