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Supporting Online Material for

Species Interactions in a Parasite Community Drive Infection Risk in a Wildlife Population

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Materials and Methods

Data collection

Between May 2001 and March 2007, field vole populations were trapped every 28 days (March-November) or every 56 days (November-March), using a 0.3ha grid at four grassy sites within a man-made spruce forest, Kielder Forest, UK, ($55^{o}13$'N, $2^{o}33$'W). Individuals were identified using subcutaneous microchip transponders. Each time an animal was trapped, data were collected on mass, reproductive condition, and numbers of ticks and fleas, and a 20-30µl blood sample taken from the tail tip. Antibody to cowpox virus was detected in sera by immunofluorescence assay (*S1*). DNA extracts were prepared from red blood cell pellets by alkaline digestion (*S2*). Polymerase chain reaction assays were used to detect infection by *Anaplasma phagocytophilum* (*S3*), *Babesia microti* (*S4*) and *Bartonella* spp. (*S5*). Trappability in this system is high (*S6*). "Resident" animals (animals trapped in more than one month, n=3141), had high capture probabilities, with only 728 animals missing captures (i.e. not sampled during one month, even though they were caught before and after this month), and most of these (64%) only missing a single trapping session. Consequently, the full dataset contains detailed information on infection histories.

Data analyses

We investigated whether concomitant and/or recently cleared infections influence an animal's susceptibility to becoming infected with each of the parasites. A capture in a specific month (t_0) was included in the dataset if the animal had been caught the previous month (t_{-1}) and tested negative for the parasite in question. Animals positive at t_0 were assumed to have become infected during the previous month and animals negative assumed to have remained uninfected. For cowpox virus, animals seroconverting between t_{-1} and t_0 may have become infected between 2 and 6 weeks before t_0 (*S1*). However, here, this only increases the likelihood that infections present at t_{-1} will influence susceptibility. If an animal had been infected previously with the microparasite in question (before t_{-1}), the capture at t_0 was not included in the dataset. Four closely-related *Bartonella* spp. are known to infect these field vole populations (*S7*). Here, all were grouped together, as the different species are likely to exhibit similar interactions with the other microparasites. Generalised linear mixed models (GLMM) were used (logit link, binomial errors) fitted using a Laplace approximation to maximum likelihood estimation in R (v.2.9.1).

Analysis was conducted in two stages: first accounting for extrinsic and intrinsic factors that may have influenced infection risk, then investigating the impact of infection with each of the other microparasites at t_{-1} and/or t_0. In both stages, to account for spatial and temporal non-independence, we included site as a fixed effect, trap session as a random effect and allowed the effect of site to vary with trap session. Individuals could contribute more than one observation to the dataset. However, models with individual identity included as a random effect often failed to converge and most individuals contributed only 1 observation (e.g. *B. microti,* range =1-13, mean=1.87). To ensure that pseudo-replication at the level of individual did not affect conclusions, we randomly selected one observation per individual and re-fitted the final stage 2 model. This was repeated 1000 times. All results for the effects of other parasites remained similar, with the average from the distribution of the resulting coefficients close to the coefficients estimated from the full dataset.

Factors considered in stage 1 included: site; two sinusoidal variables to describe seasonal cycles (seassin: $\sin(2\pi d/365)$ and seascos: $\cos(2\pi d/365)$, where d=number of days between 28/5/01 and t_0); sex; weight (a proxy for age); √weight, (to allow for nonlinearity in relationships); presence of attached ticks (for *B. microti* and *A. phagocytophilum*) or of fleas

(for *Bartonella* spp.) at t_{-1} or t_0. Weight and √weight were standardised by subtracting the relevant mean for the dataset. All two way interactions between covariates were considered. Following initial model selection, we checked whether the effects of remaining individual level covariates varied with season.

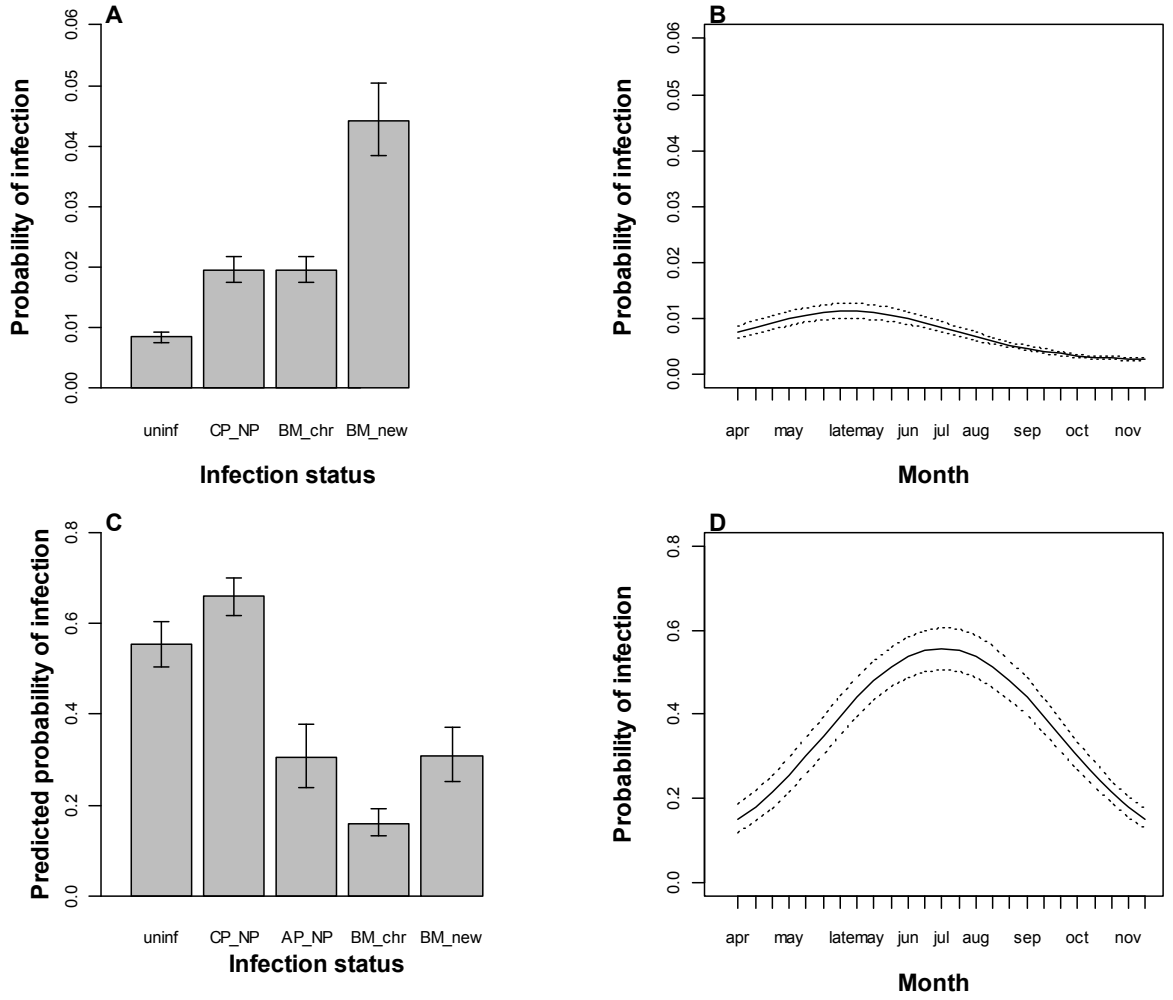
Stage 2 started with the best final model from stage 1 (model selection details below; best model shown in table S1) and included additional effects of other parasites. For the self-limiting infections *A. phagocytophilum* and *Bartonella* spp., we assessed whether any effect was best described by infection at t_0, infection at t_{-1}, an additive effect of infection at both, or an interaction between infection at each (t_{-1}*t_0). Caution is necessary as infection status at t_{-1} and t_0 are likely to be correlated; we therefore examined the impact of infection at t_{-1} with and without including infection status at t_0, and vice versa. As *B. microti* is a chronic infection, we used a 3 level categorical variable that distinguished uninfected (NN, negative at both time points), previously infected (PP) and newly infected individuals (NP). For cowpox, we used the probability of infection based on the serological history of the animal (*S8*), conservatively excluding captures where infection probabilities utilized assumptions based on age or population-level prevalence. Consequently, for cowpox, stage 2 used a smaller dataset than stage 1. We considered whether any cowpox effect was best described by the probability of infection at t_{-1}, the probability at t_0 or the additive effect of both.

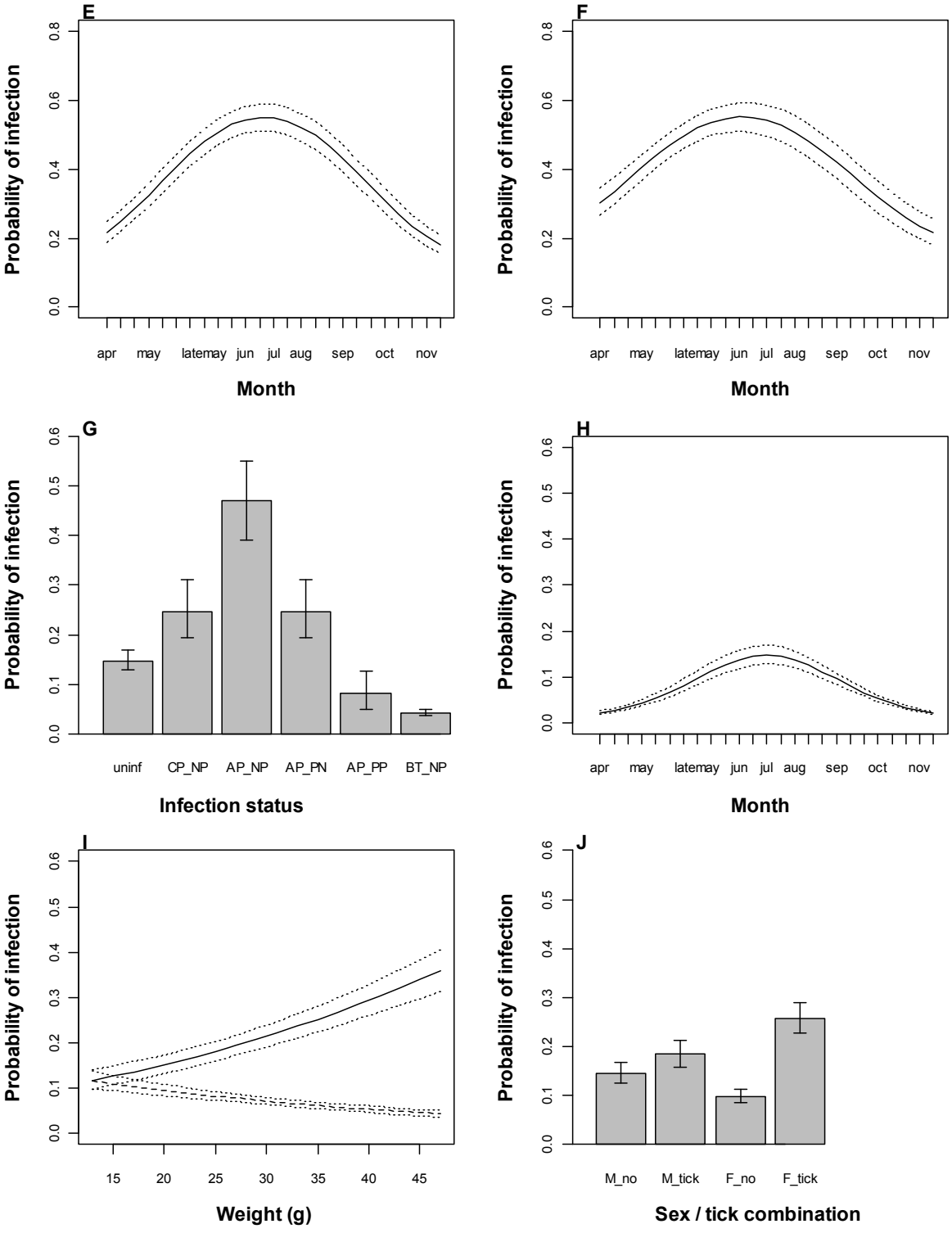
In stage 1 we used the Akaike Criterion Information index (AIC (*S9*)) for model selection. Models with an AIC within 2 of the model with the lowest AIC are equally likely to be the best model (*S10*), and therefore, following the principle of parsimony, we selected the simplest model within 2 of the lowest AIC. Model selection in GLMM remains a debated issue. However, for large datasets such as ours, the issues are less important (*S11*). Furthermore, in stage 2, to ensure robust conclusions, we used Akaike weights to assess the strength of evidence for infection variables (*S10*), We considered all parasite combinations, calculated Akaike weights, and report (table S2) all models within 7 of the lowest AIC value (since these may be considered to have some support (*S10*)). We did not use model-averaged parameter coefficients due to problems of interpretation when some models include interactions. However, we limit our discussion to effects included in the most parsimonious model (chosen as above), and in all cases these effects had overwhelming support (accumulative AIC weights all > 0.91; table S3). Odds ratios (OR=exp β; see table S3) are used in Fig. 1 to demonstrate magnitude of effects and are relative to uninfected individuals.

Positive associations between parasites could be caused by individuals in low condition having increased susceptibility to a range of parasites. To test for this, we used data for a 2 year period at 3 sites, where having additional information (*S12*), we could check whether including body condition (3 level categorical variable based on the fat cover over the vertebral column and dorsal pelvic bones (*S13*)) and haematological condition (number of red blood cells, number of lymphocytes, standardised by subtracting the mean) at t_{-1} weakened the case for effects of infection or significantly changed coefficients. Effects of infection remained similar (table S4).

There may be temporal variation in exposure risk not related to season (e.g. due to temporal correlations in host density). We therefore also checked the consequence of explicitly accounting for year as a fixed effect. This resulted in a decrease in AIC for some parasites (*A. phagocytophilum* (ΔAIC=16); cowpox virus (ΔAIC=21.3); *Bartonella* spp. (ΔAIC=7.7)), indicating annual variation in risk, but in all cases the effects of co-infection remained with similar coefficients (data not shown).

Figure S1: The effects of various covariates on the probability of infection for **A-B**, *A. phagocytophilum*, **C-F**, *Bartonella* spp., **G-J**, *B. microti* and **K-N**, cowpox virus. To ease comparisons between the effects of infection status and the effects of non-infection covariates, for each microparasite the appropriate part of Fig. 2 is repeated and the y-axis scale is held constant. Predictions are based on the models in table S3. For each microparasite, we show the strength of effects for all covariates that result in drops of AIC>2 in the final model (table S3). Covariates not being examined are held constant as follows: an 18g male with no ticks and uninfected by other microparasites, caught in July at one specific site. Where necessary, several graphs are used to demonstrate the effects of an interaction between continuous variables (e.g. season*weight). Dotted lines and error bars represent 95% confidence intervals, averaged over random effects. The graphs show the following effects: **A**, effect of other infections on *A. phagocytophilum* infection risk; **B**, effect of season on *A. phagocytophilum* infection risk; **C**, effect of other infections on *Bartonella spp.* infection risk; **D-F**, effect of season on *Bartonella* spp. infection risk for 18g, 27g and 36g animals respectively; **G**, effect of other infections on *B. microti* infection risk; **H**, effect of season on *B. microti* infection risk; **I**, effects of sex and weight on *B. microti* infection risk (solid line =males, dashed line =females); **J**, effects of sex and ticks on *B. microti* infection risk; **K**, effect of other infections on cowpox infection risk; **L-N**, effects of season and sex on cowpox infection risk for 18g, 27g and 36g animals respectively (solid line =males, dashed line =females).




E
Probability of infection
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Month
F
Probability of infection
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0.2
0.4
0.6
0.8
apr
may
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G
Probability of infection
0.0
0.1
0.2
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0.5
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uninf
CP_NP
AP_NP
AP_PN
AP_PP
BT_NP
Infection status
H
Probability of infection
0.0
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Probability of infection
0.0
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0.6
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35
40
45
Weight (g)
J
Probability of infection
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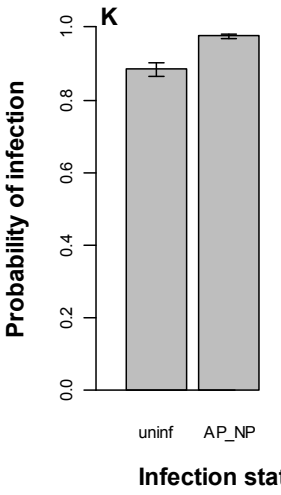
0.4
0.5
0.6
M_no
M_tick
F_no
F_tick
Sex / tick combination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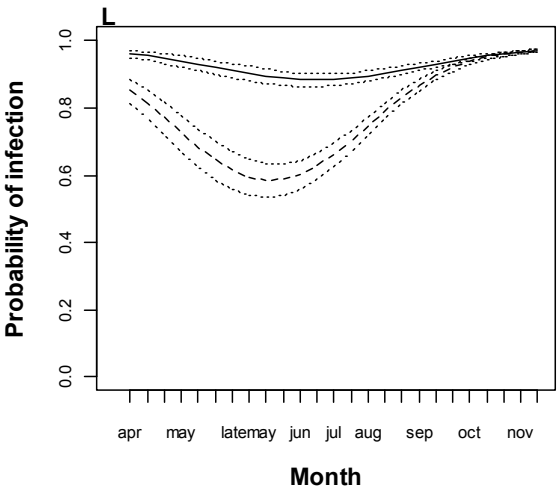
Infection status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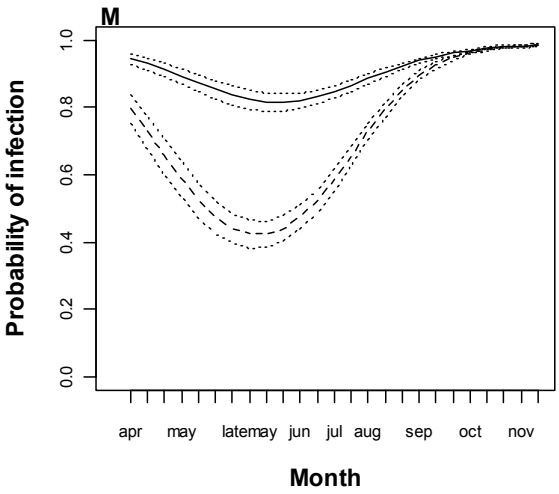
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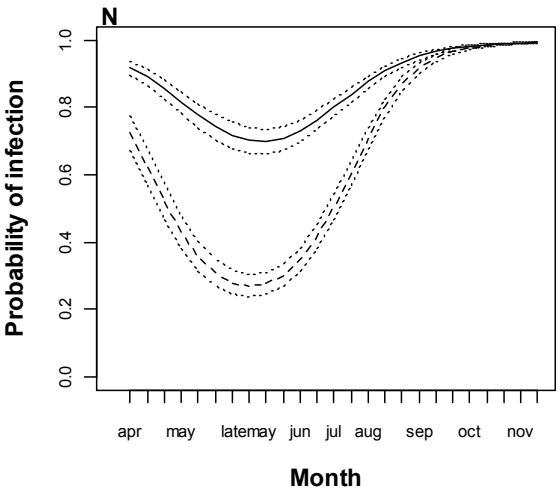
N
Probability of infection
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Table S1: Best model of infection risk from stage 1 for each of the microparasites (excludes infection explanatory variables). n= sample size; i=number of infections; β=parameter coefficient; SE = standard error of coefficient; ΔAIC = change in AIC when parameter is excluded. ΔAIC not shown for main effect if the covariate is included in an interaction. Both season covariates are included to accurately describe the seasonal pattern. Only fixed effects are shown. Random effects allowing the effect of site to vary with trap session were also included. As site was included in all models, ΔAIC is not shown.

Covariate	β	SE	ΔAIC
A. phagocytophilum (n=4993, i=130)			
Intercept	-4.778	0.337	-
Site 2	0.623	0.253	-
Site 3	0.325	0.321	-
Site 4	-0.371	0.294	-
Seassin	1.114	0.347	-
Seascos	0.801	0.220	11
Sex Male	0.809	0.347	-
Tick	0.655	0.252	-
Weight	-0.025	0.014	2
Sex (Male) *Tick	-0.923	0.384	5
Seassin*Sex (Male)	-0.910	0.398	4
B. microti (n=3572, i=488)			
Intercept	-3.155	0.187	-
Site 2	0.251	0.170	-
Site 3	0.134	0.161	-
Site 4	-0.625	0.157	-
Seassin	1.079	0.192	27
Seascos	0.523	0.154	16
Sex Male	0.835	0.148	-
Tick	0.961	0.152	-
Weight	-0.022	0.011	-
Sex (Male)*Tick	-0.684	0.211	9
Sex (Male)*Weight	0.058	0.013	18
***Bartonella* spp.** (n=2181, i=677)			
Intercept	-1.336	0.151	-
Site 2	-0.106	0.151	-
Site 3	-0.229	0.179	-
Site 4	-0.122	0.155	-
Seassin	0.907	0.156	-
Seascos	0.803	0.128	27
Weight	-0.006	0.010	-
Seassin*Weight	-0.075	0.014	26
Cowpox virus (n=955, i=647)			
Intercept	2.389	0.723	-
Site KCS	-1.464	0.647	-
Site PLJ	-0.560	0.445	-
Site ROB	-0.419	0.457	-
Seassin	-0.525	0.508	-
Seascos	-2.062	0.384	-
Sex Male	0.925	0.225	-
Weight	0.0004	0.018	-
Seascos*Sex (Male)	0.996	0.356	5.9
Seascos*Weight	-0.077	0.030	4.4

Table S2: All models within 7 of the model with the lowest AIC in stage 2. All the variables identified as important in stage 1 (table S1; the base model) were included in all models. n= sample size; i=number of infections; np= number of parameters; ΔAIC = change in AIC from the lowest AIC; weight=AIC model weight. AP= A*. phagocytohilum*, BM= *B. microti*, BT= *Bartonella* spp., CP= cowpox virus. Numbers signify the trap session considered (e.g. AP_0 = infection status for AP at t_0). The most parsimonious model (model with fewest parameters within 2 of lowest AIC) is shown in bold.

Covariates included	np	AIC	ΔAIC	weight
A. phagocytophilum (n=3421, i=81)				
$BM+BT_{-1}+CP_0$	25	715.98	0.00	0.23
$BM+CP_0$	**24**	**716.75**	**0.77**	**0.16**
$BM+BT_{-1}*BT_0+CP_0$	27	716.85	0.86	0.15
$BM+BT_{-1}+BT_0+CP_0$	26	717.01	1.03	0.14
$BM+BT_0+CP_0$	25	717.18	1.20	0.13
$BM+BT_{-1}+CP_{-1}+CP_0$	26	718.01	2.03	0.08
$BM+CP_{-1}+CP_0$	25	718.68	2.70	0.06
$BM+BT_0+CP_{-1}+CP_0$	26	719.21	3.23	0.05
B. microti (n=2250, i=277)				
$AP_{-1}*AP_0+BT_0+CP_{-1}+CP_0$	27	1384.68	0.00	0.36
$AP_{-1}*AP_0+BT_{-1}*BT_0+CP_{-1}+CP_0$	29	1385.78	1.10	0.21
$AP_{-1}*AP_0+BT_0+CP_0$	**26**	**1386.63**	**1.95**	**0.14**
$AP_{-1}*AP_0+BT_{-1}+BT_0+CP_{-1}+CP_0$	28	1386.73	2.05	0.13
$AP_{-1}*AP_0+BT_{-1}*BT_0+CP_0$	28	1387.73	3.05	0.08
$AP_{-1}*AP_0+BT_{-1}+BT_0+CP_0$	27	1388.68	4.00	0.05
$AP_0+BT_0+CP_{-1}+CP_0$	25	1391.58	6.90	0.01
***Bartonella* spp.** (n=1162, i=311)				
$AP_0+BM+CP_0$	**24**	**1149.06**	**0.00**	**0.37**
$AP_0+BM+CP_{-1}+CP_0$	25	1149.14	0.09	0.36
$AP_{-1}+AP_0+BM+CP_0$	25	1151.14	2.09	0.13
$AP_{-1}*AP_0+BM+CP_0$	26	1152.24	3.18	0.08
AP_0+BM	23	1152.97	3.91	0.05
$BM+CP_0$	23	1153.97	4.91	0.03
$BM+CP_{-1}+CP_0$	24	1154.06	5.00	0.03
$AP_{-1}+AP_0+BM$	24	1155.06	6.00	0.02
$AP_0+BM+CP_{-1}$	24	1155.06	6.00	0.02
$AP_{-1}+BM+CP_0$	24	1156.06	7.00	0.01
Cowpox virus (n=937, i=630)				
AP_0	**21**	**754.51**	**0.00**	**0.23**
AP_0+BT_{-1}	22	756.01	1.50	0.11
AP_0+AP_{-1}	22	756.31	1.80	0.10
AP_0*AP_{-1}	23	756.51	2.00	0.09
AP_0+BT_0	22	756.61	2.10	0.08
$AP_0+BT_{-1}*BT_0$	24	757.42	2.91	0.05
$AP_0+BT_{-1}+AP_{-1}$	23	757.71	3.20	0.05
$BT_{-1}+AP_{-1}*AP_0$	24	758.02	3.51	0.04
$AP_0+BT_0+BT_{-1}$	23	758.11	3.60	0.04
$AP_0+BT_0+AP_{-1}$	23	758.21	3.70	0.04
$BT_0+AP_{-1}*AP_0$	24	758.52	4.01	0.03
AP_0+BM	23	758.71	4.20	0.03
$AP_0+BT_{-1}*BT_0+AP_{-1}$	25	759.03	4.52	0.02
$AP_{-1}*AP_0+BT_{-1}*BT_0$	26	759.74	5.23	0.02
$AP_0+BM+BT_{-1}$	24	760.02	5.51	0.01
$BT_0+AP_{-1}*AP_0+BT_{-1}$	25	760.13	5.62	0.01
$AP_0+BM+AP_{-1}$	24	760.42	5.91	0.01
$BM+AP_{-1}*AP_0$	25	760.63	6.12	0.01
$AP_0+BM+BT_0$	24	760.72	6.21	0.01
$AP_0+BT_{-1}*BT_0+BM$	27	761.26	6.75	0.01

Table S3: Most parsimonious model of infection risk for each of the microparasites (see table S2). β =parameter coefficient; SE = standard error of coefficient; ΔAIC = change in AIC when the parameter is excluded; weight = accumulated weight for co-infection parameters based on the model set shown in table S2. If the covariate is included in an interaction, the ΔAIC shown next to the main effect demonstrates the effect of total exclusion of this covariate (i.e. dropping of both interactions and main effect). Exclusion of some covariates included in the original base model (table S1) no longer results in substantial increases in AIC (ΔAIC >2), primarily due to a drop in power caused by decrease in sample size in some analyses (negative ΔAIC means that the AIC decreased when the parameter is excluded). Such covariates were still included in the model to ensure effects of infection by other parasites were not acting as surrogates for these covariates. Only fixed effects are shown. Random effects allowing the effect of site to vary with trap session were also included. As site was included in all models, ΔAIC is not shown.

Covariate	β	SE	ΔAIC	weight
A. phagocytophilum				
Intercept	-5.368	0.445	-	
Site 2	0.298	0.330	-	
Site 3	0.322	0.541	-	
Site 4	-0.500	0.400	-	
Seassin	0.929	0.430	1.6	
Seascos	0.713	0.280	4.7	
Sex Male	0.367	0.463	-0.9	
Tick	0.412	0.329	-1.9	
Weight	-0.031	0.021	0.4	
Sex*Tick	-0.666	0.526	-0.3	
Seassin*Sex	-0.831	0.524	0.8	
CP_0	1.707	0.548	8.0	1.0
BM chronic	0.851	0.311	22.3	1.0
BM new	1.692	0.342	-	-
B. microti				
Intercept	-3.030	0.252	-	
Site 2	0.012	0.197	-	
Site 3	-0.316	0.225	-	
Site 4	-0.829	0.212	-	
Seassin	1.224	0.262	15.4	
Seascos	0.663	0.214	6.4	
Sex Male	1.080	0.217	38.4	
Tick	1.145	0.208	24.0	
Weight	-0.032	0.017	12.4	
Sex (Male)*Tick	-0.862	0.301	5.4	
Sex (Male)*Weight	0.074	0.018	14.4	
AP_{-1}	0.635	0.369	6.4	
AP_0	1.637	0.346	18.4	
AP_{-1}*AP_0	-2.944	0.974	8.4	0.99
BT_0	-1.377	0.162	76.4	1.0
CP_0	1.274	0.337	11.4	1.0
***Bartonella* spp.**				
Intercept	-0.547	0.218	-	
Site 2	-0.066	0.240	-	
Site 3	-0.255	0.299	-	
Site 4	-0.342	0.235	-	
Seassin	0.903	0.182	17	
Seascos	0.621	0.150	13	
Weight	0.025	0.014	0	
Seassin*Weight	-0.031	0.019	4	
AP_0	-1.052	0.417	5	0.93
BM chronic	-1.885	0.179	117	1.0
BM new	-1.035	0.283	-	
CP_0	0.894	0.348	4	0.91

Cowpox virus				
Intercept	2.449	0.759	-	
Site 2	-1.517	0.679	-	
Site 3	-0.618	0.458	-	
Site 4	-0.442	0.463	-	
Seassin	-0.714	0.540	-0.4	
Seascos	-2.193	0.409	21.7	
Sex Male	0.934	0.233	16	
Weight	0.0004	0.019	2.5	
Seascos*Sex (Male)	0.947	0.368	4.6	
Seascos*Weight	-0.079	0.031	4.3	
AP_0	1.677	0.518	9.3	1.0

Table S4: Models of infection risk when covariates related to host condition were considered. Due to the reduced sample size it was not possible to estimate random effects, and results from Generalised Linear Models are presented. Covariates related to host condition (see methods) were added to the most parsimonious model of infection risk for each of the microparasites (see table S2) and are presented in italics. n= sample size; i=number of infections β =parameter coefficient; SE = standard error of coefficient, ΔAIC = change in AIC when the parameter is excluded (negative ΔAIC means that the AIC decreased when the parameter is excluded). ΔAIC > 2 are presented in bold. * indicates infection parameters that no longer have ΔAIC > 2 but, importantly, have similar coefficients as before (compare with table S3).

Covariate	β	SE	ΔAIC
A. phagocytophilum (n=600, i=19)			
Intercept	-7.117	1.548	
Site 2	1.025	1.020	
Site 3	0.310	0.788	
Site 4	-0.127	0.715	
Seassin	3.444	1.714	**3.88**
Seascos	1.677	0.610	**6.22**
Sex Male	2.765	1.687	0.41
Tick	0.542	0.802	-3.53
Weight	-0.055	0.055	-0.94
Sex (Male)*Tick	-0.468	1.164	-1.84
Seassin*Sex (Male)	-3.878	1.914	**3.82**
CP_0	3.919	1.323	**7.87**
BM chronic	1.311	0.738	**3.24**
BM new	2.122	0.832	
Body cat2	*-1.918*	*0.663*	***5.75***
Body cat3	*-0.649*	*0.831*	
Red Blood cell	3.58×10^{-8}	6.69×10^{-8}	*-1.72*
Lymphocyte	9.16×10^{-5}	7.66×10^{-5}	*-0.65*
B. microti (n=316, i=40)			
Intercept	-2.35	0.622	
Site 2	0.644	0.943	
Site 3	-0.445	0.566	
Site 4	-1.088	0.544	
Seassin	-0.446	0.482	-1.15
Seascos	0.198	0.392	-1.75
Sex Male	0.558	0.908	1.36
Tick	1.421	0.528	**5.55**
Weight	-0.008	0.043	**5.43**
Sex (Male)*Tick	-0.392	1.048	-1.87
Sex (Male)*Weight	0.137	0.053	**5.21**
AP_{-1}	1.516	0.838	**5.5**
AP_0	3.383	1.079	**9.75**
AP_{-1}*AP_0	-5.819	1.989	**7.48**
BT_0	-1.333	0.476	**6.86**
CP_0	1.294	1.086	-0.6*
Body cat2	0.135	0.510	-1.74
Body cat3	-0.836	0.800	
Red Blood cell	-1.08×10^{-7}	6.09×10^{-8}	1.57
Lymphocyte	1.05×10^{-4}	5.62×10^{-5}	1.39
***Bartonella* spp.** (n=267, i=57)			
Intercept	-0.776	0.572	
Site 2	0.394	0.999	
Site 3	0.042	0.544	
Site 4	-0.072	0.439	
Seassin	0.871	0.454	0.89
Seascos	0.479	0.341	-0.01
Weight	0.031	0.035	-2.89

Seassin*Weight	0.003	0.045	-1.99
AP_0	-1.615	1.162	0.56*
BM chronic	-1.959	0.408	**23.73**
BM new	-1.958	0.894	
CP_0	0.770	0.923	-1.3*
Body cat2	-0.179	0.457	-1.82
Body cat3	0.689	0.543	
Red Blood cell	1.86×10^{-8}	5.61×10^{-8}	-1.89
Lymphocyte	-6.58×10^{-5}	6.79×10^{-5}	-1.02
Cowpox virus (n=208, i=109)			
Intercept	0.582	0.813	
Site 2	0.304	0.993	
Site 3	0.083	0.700	
Site 4	0.292	0.645	
Seassin	-1.136	0.818	0.02
Seascos	-1.438	0.537	**8.35**
Sex Male	1.447	0.683	1.03
Weight	-0.022	0.053	**34.25**
Seascos*Sex (Male)	0.684	0.975	-1.52
Seascos*Wght	-0.126	0.080	0.6
AP_0	1.749	1.020	1.03*
Body cat2	*0.899*	*0.616*	*-1.37*
Body cat3	*0.032*	*0.928*	
Red Blood cell	3.32×10^{-8}	7.35×10^{-8}	*-1.79*
Lymphocyte	-5.17×10^{-5}	-8.46×10^{-5}	*-1.63*

Table S5: Description of the abbreviations used for the different variables.

Variable	**Description**
Site	Four level categorical variable for site
Seassin and Seascos	Two sinusoidal variables to describe seasonal cycles
Sex	Categorical variable for sex
Weight	Used as a proxy for age and standardized by subtracting the mean weight for the dataset
Tick	Categorical variable. Tick=1 if the individual had a tick attached at the current (t_0) or previous trap session (t_{-1})
BM	Three level categorical variable describing infection status for *Babesia microti*: not infected, chronic infection and new infection
AP_{-1} and AP_0	Categorical variable describing infection status for *Anaplasma phagocytophilum* at t_{-1} and t_0 respectively.
BT_{-1} and BT_0	Categorical variable describing infection status for *Bartonella* spp. at t_{-1} and t_0 respectively.
CP_{-1} and CP_0	Categorical variable describing infection status for cowpox virus at t_{-1} and t_0 respectively.
Bodycat	Three level categorical variable describing body condition: 1 = poor, 2 = average, 3 = good
Red Blood cell	Used as an index of condition. Number of red blood cells per microlitre of blood, standardised by subtracting the mean for the dataset.
Lymphocyte	Used as an index of condition. Number of lymphocytes per microlitre of blood, standardised by subtracting the mean for the dataset.

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