Hantavirus infections in fluctuating host populations: the role of maternal antibodies

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Infected females may transfer maternal antibodies (MatAbs) to their offspring, which may then be transiently protected against infections the mother has encountered. However, the role of maternal protection in infectious disease dynamics in wildlife has largely been neglected. Here, we investigate the effects of Puumala hantavirus (PUUV)-specific MatAbs on PUUV dynamics, using 7 years' data from a cyclic bank vole population in Finland. For the first time to our knowledge, we partition seropositivity data from a natural population into separate dynamic patterns for MatAbs and infection. The likelihood of young of the year carrying PUUV-specific MatAbs during the breeding season correlated positively with infection prevalence in the overwintered parent population in the preceding spring. The probability of PUUV infection varied between seasons (highest in spring, lowest in late summer) and depended on population structure, but was also, in late autumn, negatively related to summer MatAb prevalence, as well as to infection prevalence earlier in the breeding season. Hence, our results suggest that high infection prevalence in the early breeding season leads to a high proportion of transiently immune young individuals, which causes delays in transmission. This suggests, in turn, that MatAb protection has the potential to affect infection dynamics in natural populations.

Keywords: bank vole; infection transmission; maternal antibody; Puumala hantavirus; transient immunity

1. INTRODUCTION

A common expectation for infectious diseases transmitted directly (without a vector) and horizontally (but not sexually or congenitally) is that infection prevalence will increase with host abundance, and there will be a threshold host density below which the pathogen will not persist (e.g. Mills et al. 1999; McCallum et al. 2001; Begon et al. 2002; Hudson et al. 2002; Lloyd-Smith et al. 2005), but this expectation is not always borne out. Davis et al. (2005) and Adler et al. (2008) have recently reviewed studies on the relationship between the prevalence of rodent-borne diseases and host abundance. For example, studies on hantaviruses (genus Hantavirus, family Bunyaviridae), carried by specific rodent or insectivore hosts and causing several human diseases in Eurasia and the Americas (Vaheri et al. 2008), have shown great variation in this relationship. Seroprevalence for Sin Nombre hantavirus has shown either a positive, a negative or no significant relationship with the abundance of its main host, the deer mouse, Peromyscus maniculatus (Davis et al. 2005; Adler et al. 2008), while the relationship between Puumala hantavirus (PUUV) seroprevalence and the density of its host, the bank vole (Myodes glareolus), has sometimes been positive (Brummer-Korvenkontio et al. 1982; Niklasson et al. 1995; Linard et al. 2007), but in other cases has shown no clear correlation (Escutenaire et al. 2000; Sauvage et al. 2002; Olsson et al. 2005; Linard et al. 2007; Tersago et al. 2008).

Often, the absence of a positive correlation has been associated with the relationship being followed over different seasons (Mills et al. 1999; Davis et al. 2005). Relatively few studies have followed PUUV in bank vole populations over the course of a breeding season, but in those cases, the seroprevalence has peaked in spring, at the beginning of breeding season, and decreased, together with increasing host population density, during the breeding season (e.g. Verhagen et al. 1986; Niklasson et al. 1995; Escutenaire et al. 2000; Sauvage et al. 2002). Similar results have also been reported from other hantavirus–host systems (Calisher et al. 1999, 2005; Douglass et al. 2001). A high influx of newborns during the breeding season may decrease hantavirus prevalence, and this ‘juvenile dilution effect’ has been proposed to be the mechanism through which the expected positive relationship between prevalence and abundance is lacking or delayed (Mills et al. 1999; Davis et al. 2005; Adler et al. 2008).

Newborn individuals may, however, induce an additional effect in the relationship between infection...
prevalence and host abundance. Infected females commonly transfer maternal antibodies (MatAbs) to their offspring, providing temporary protection against the infection(s) the mother has encountered (Grindstaff et al. 2003; Boulinier & Staszewski 2008; Hasselquist & Nilsson 2009). Hantavirus-infected female rodents transfer MatAbs to their offspring in utero and during lactation (Dohmae et al. 1993), and the temporary immunity against PUUV lasts for up to 80 days in bank voles (Gavrilovskaya et al. 1990; Kallio et al. 2006a), a relatively long period when compared with their average lifespan, three to five months (Innes & Millar 1994). The presence of MatAbs among young individuals has been acknowledged in several hantavirus studies (e.g. Mills et al. 1997, 1999; Borucki et al. 2000; Escutenaire et al. 2000; Calisher et al. 2007; Dearing et al. 2009). However, their role in infection dynamics has largely been neglected in studies on hantaviruses and on natural populations generally, despite recent acknowledgement of the potential of MatAbs to influence disease dynamics in wildlife populations through altering the amount of susceptible individuals (Gasparini et al. 2001; Staszewski et al. 2007; Boulinier & Staszewski 2008), and their recent inclusion in theoretical studies (Fouchet et al. 2006, 2007, 2008).

Here, we test whether the transmission dynamics of infectious pathogens in our wildlife host populations are influenced by the presence of MatAb-protected individuals in the population. We hypothesize that the proportion of MatAb-protected young individuals in the population should itself be determined by earlier infection prevalences (the proportion of the population, and specifically females that are infected) in the host population. Therefore, high infection prevalence at the beginning of a breeding season may lead to high numbers of maternally protected young individuals during the breeding season, delaying the influx of susceptible individuals until the maternal protection disappears. Consequently, the expected positive relationship between host abundance and infection prevalence by the end of the breeding season may be lacking despite an earlier increase in host abundance. Here, we test these ideas using a 7 year dataset on PUUV and bank vole dynamics in Central Finland. For the first time to our knowledge, we partition data on seropositivity from a natural population into separate dynamic patterns for MatAbs and infection. Our aim is to elaborate seasonal and host density-dependent patterns in PUUV infection dynamics, and in particular to evaluate the evidence on effects of MatAbs on the transmission of PUUV.

2. MATERIAL AND METHODS

(a) Study species

PUUV is carried by the bank vole (Brummer-Korvenkontio et al. 1980), in which the infection does not cause clinical illness (Gavrilovskaya et al. 1990; Bernshtein et al. 1999) but may have deleterious fitness consequences (Kallio et al. 2006a, 2007). The infection is chronic (Meyer & Schmaljohn 2000), transmission is horizontal (e.g. Niklasson et al. 1995; Kallio et al. 2006b) and the virus is excreted during the first two months after becoming infected (Hardestam et al. 2008). Also, the transmission may take place indirectly via a contaminated environment, where the shed virus remains infectious for prolonged time periods depending on the temperature (Kallio et al. 2006b).

The bank vole is a common species in most of Europe. Seasonal fluctuations with occasional mast-driven outbreaks characterize the populations of continental temperate Europe (e.g. Tersago et al. 2009), but in northern Fennoscandia, bank vole populations show multi-annual cyclic fluctuations (Henttonen et al. 1985). The length of the vole cycle varies from 3 to 5 years, being synchronous over large areas and determined predominantly by specialist mammalian predators and the voles’ winter food resources (Hansson & Henttonen 1988; Hanski et al. 1991; Korpimäki et al. 2005; Huitu et al. 2007).

(b) Data collection

Voles were trapped in the Konevesi area in Central Finland (62°38′N, 26°82′E) four times per year from May 2002 to October 2008. The first trapping (‘spring’) was carried out early in the breeding season in May. The second (‘summer’) was conducted typically during the first week of July, in the middle of the breeding season. The third (‘late summer’) was typically in late breeding season in late August, and the fourth (‘late autumn’) was carried out in late October to early November, after the breeding season. Based on these annual trappings, monthly bank vole incidences were computed using linear interpolation (for details and justification, see Kallio et al. 2009). The bank vole populations in the study area fluctuate cyclically, and this study period covered three ‘peak’ years (2002, 2005 and 2008), two ‘crash/low’ years (2003 and 2006) and two ‘increase’ years (2004 and 2007) (figure 1) (Kallio et al. 2009). The trappings were carried out in 20 permanent trapping sites and in each site four Ugglan Special multiple-capture live traps (Grahneb, Hillerstorp, Sweden) were set over two nights (altogether 160 trapping nights in each trapping session).

Captured voles were taken to a laboratory where their sex, breeding status and body mass were recorded and blood or tissue samples taken (Kallio et al. 2009) for antibody detection using immunofluorescence assay (IFA) (Vapalahti et al. 1995). Pregnant females gave birth in the laboratory and their postpartum weight was measured. To diminish the influence of pregnancy on body mass, the postpartum
weight (when it was lower than the trapping weight) was used in the analyses. As the exact age of the trapped individuals could not be determined, we used body mass as a proxy for age (see, e.g. Telfer et al. 2008).

Seasonally reproducing rodents may mature at different ages and weights at different cyclic phases. Maturity and related hormonal and immunological changes may, therefore, sometimes explain, better than weight does, the probabilities of being infected. Unfortunately, reproductive status could not be recorded for all animals. Therefore, to test for the effects of maturity, we used subsets of the data where maturity status had been determined, distinguishing two categories, immature versus mature, where 'mature' describes an animal that is or has previously been reproductively active.

(c) Data analyses

(i) Separation between maternal antibodies and genuine infection
Because we used a serological diagnostic method and all individuals were sampled only once, it was not feasible to distinguish individuals that carried MatAbs directly from those that were infected (both detected as seropositive by IFA). However, we analysed the probability of being seropositive in relation to individuals' weight, using a generalized additive mixed model approach (gamm4 function in gamm4 library in R software, available under GNU licence at http://www.r-project.org) with binomial distributions and with the models fitted using the Laplace approximation method. Splines were fitted using thin plate regression, and the model with the lowest k-value (least complex) within 2 of the model with the lowest Akaike information criterion (AIC) value was selected. To control for the correlation among individuals that were captured at the same trapping site in the same trapping session, trapping year * trapping site was included as a random effect in the models. These models were fitted separately for each trapping season. This allowed us to detect any tendency for seroprevalence first to decline with increasing weight (declining prevalence of MatAbs) and then to increase (increasing prevalence of infection). When this relationship indicated a U-shaped curve, the weight at the lowest probability was used as a cut-off value (§3, figure 2): when a seropositive individual's weight was below the cut-off, the individual was recorded as carrying MatAbs, whereas with weight above the cut-off, the individual was recorded as genuinely infected. However, the effects of this should be negligible, because the period in an individual's life of possible misclassification is short—from the age of ca 45 days (first appearance of antibody following weaning and infection) to ca 60 days (by which time 95% have lost MatAb; Kallio et al. 2006a)—and so the numbers will themselves be small. Consequently, infection prevalence has been calculated as the number infected (PUUV seropositive) divided by the total number of animals tested. MatAb prevalence has been calculated as the number of MatAb positives also divided by the total number of

Figure 2. Predicted probability, at the individual level, of being PUUV antibody positive in relation to body mass (g) in (a) spring, (b) summer, (c) late summer and (d) late autumn. Cut-off weight values below which the seropositive result is considered as maternal antibody positivity are indicated with vertical lines. In summer (b), the cut-off value was 16.4 g and in late summer (c), the cut-off was 15.9 g. Observed data are shown with dots (PUUV seropositive = 1, PUUV seronegative = 0).
animals tested, since it is used as a possible explanatory variable for infection prevalence in the whole population.

(ii) Probability of carrying MatAbs
The likelihood of carrying MatAbs was investigated among the individuals with body mass below or equal to the detected cut-off value (above). The presence of MatAb (binomial response variable) was studied in relation to gender, weight, the trapping season (summer or late summer), i.e. when MatAb-positive individuals were detected, see §3 and the infection prevalence in the bank vole population during the spring and summer trapings. Instead of using infection prevalence among breeding females only, we used infection prevalence in the whole population because the numbers of captured females were lower than males, and because there was no significant difference in the mean infection prevalence of males and females in spring and summer. In addition, current bank vole abundance \( N_t \) and bank vole abundances two \( (N_{t-2}) \), four \( (N_{t-4}) \) and six \( (N_{t-6}) \) months earlier (natural log-transformed data) were used as predictors. The analyses were carried out using a generalized linear mixed model (GLMM) with a logit link function and binomial errors, and the models were fitted using the Laplace approximation method (lmer function in lme4 library in the R software package). To control for the correlation among individuals that were captured at the same trapping site in the same trapping session, trapping year \( * \) trapping site was included as a random effect in the models. Starting from a full model, terms were omitted if they did not reduce the AIC by more than two units when included (see electronic supplementary material, table S1, for the model selection) (Burnham & Anderson 2002).

(iii) Probability of being PUUV-infected
To study the probability of an individual being genuinely infected, we first analysed whether there was any seasonal pattern in the dependent variable using the entire dataset with a GLMM (as described above) with trapping session \( * \) trapping site as a random effect in the models. Because the trapping season had a significant influence on the probability of being infected (§3), and because our unequal trapping interval meant that explanatory variables referring to preceding trapping sessions were not comparable between seasons (electronic supplementary material, table S2), we analysed the four trapping seasons separately.

For each of the four trapping seasons, the probability of being genuinely infected was analysed in a similar way. First we fitted a full model using a generalized linear model (see above) that included population-level predictors—phase of the population cycle, current bank vole abundance \( (N_t) \), bank vole abundance during preceding 12 months \( (N_{t-1}, \ldots, N_{t-12}) \) (natural log-transformed data) and PUUV infection prevalence during the three preceding trapping sessions (electronic supplementary material, table S2)—and the individual-level predictors weight and sex. Preceding MatAb prevalences were not included at this stage (but see below) because of the functional linkage between these and the infection prevalences that precede them. Second, we restricted the full model, including two-way interactions, using the stepAIC procedure (see above). The selected model was then applied to a GLMM (see above) where the best model (the simplest model within two units of the lowest AIC value; electronic supplementary material, table S1) was selected manually. Then, the effect of maturity status was tested using the subset of data where maturity status had been determined, where it was applied as a predictor to the best model and additional model selection carried out (results provided only if this improved the final model).

Finally, we carried out separate analyses to clarify the effect of MatAb prevalence in the population (see above) during the breeding season on the probability of being infected in late autumn using GLMM as explained above. As the effects of MatAbs on infection prevalence are likely to be observable only after a delay (since their effect is an absence of infection seropositives that would otherwise have appeared), this effect is likely to be seen only in autumn. Hence, the MatAb prevalence in summer and late summer was used as covariates to predict the probability of being infected in late autumn. Also, individual-level variables (sex and weight) were included in the model selection procedure (electronic supplementary material, table S1).

3. RESULTS
Bank vole abundance varied both seasonally and multi-annually (figure 1). Of 2576 animals captured, 2476 were examined for the presence of anti-PUUV antibodies, and of these, 818 (33.3%; 95% CI: 31.2–34.5) were PUUV seropositive. Seroprevalence varied between trapping sessions from 10 to 80 per cent, being highest in spring (mean prevalence \( \pm \) s.e.: 48.8 \( \pm \) 6.1%), decreasing through the breeding season (summer: 40.9 \( \pm \) 4.0%; late summer: 26.3 \( \pm \) 2.0%) and being lowest in late autumn (22.9 \( \pm \) 3.8%) (figure 1).

(a) Maternal antibodies versus genuine infection
PUUV seropositivity was studied in relation to weight to distinguish individuals that were carrying MatAbs from those that were genuinely infected (§2). In spring, most individuals were over-wintered and therefore too old to carry MatAbs. In support of this, all seropositive individuals weighed 18.4 g or more and the model describing the probability of being PUUV seropositive in relation to weight did not show any indication of the presence of MatAb-positive individuals (figure 2a). Hence, in spring, all seropositive individuals were classified as infected. In summer, the model was markedly nonlinear and indicated that the lowest likelihood of being seropositive was at a weight of 16.4 g (figure 2b). Hence, only seropositive individuals that weighed more than this cutoff were considered to be infected: 40 out of 262 seropositive individuals in summer were considered to be carrying MatAbs. In late summer, the model again indicated the presence of MatAb-positive individuals, and the lowest probability of being seropositive was at a weight of 15.9 g (figure 2c), and consequently, 70 out of 218 seropositives were considered to be carrying MatAbs. In late autumn (ca eight weeks after the end of the breeding season), there were no indications of the presence of MatAb-positive individuals (figure 2d) and therefore all positive records were considered to be a result of genuine infection.

(b) Probability of carrying maternal antibodies
During the breeding season, the probability that an individual was carrying MatAbs was positively related to the infection prevalence in spring (figure 3a) and was higher in summer (July) than in late summer (August) (table 1).
Also, current bank vole abundance was positively related, and bank vole abundance six months before negatively related, to the probability of carrying MatAbs (table 1).

(c) Probability of being PUUV-infected
Overall, the probability of PUUV infection was highest in spring and lowest in late summer (table 2), depending on different variables in different trapping seasons (best selected models and parameter estimates in table 3). Of the individual characteristics, weight was included in all models, and individuals’ probability of being infected increased with weight. Sex was selected in the summer and late summer models, and there were interactions with weight, indicating that prevalence tended to be higher in males, especially heavier males (table 3). Breeding status was selected only in the late summer model, where the probability of being infected was higher in the sexually mature voles (table 3).

Of the population-level variables, few were included in the best models (table 3). In late autumn, the infection probability was negatively related to the PUUV infection prevalence in the populations in the previous spring, approximately five and a half months earlier (table 3 and figure 3b).

The effect of earlier MatAb prevalence on the infection status in late autumn was studied separately. The probability of being infected was negatively related to the MatAb prevalence in summer, approximately three and a half months earlier (predictors in the selected GLMM were MatAb prevalence in summer and weight; parameter estimate for MatAb prevalence in summer (logit scale) $\beta = -0.086, \text{s.e.} 0.034, z = -2.571, p = 0.010$; figure 3c).

4. DISCUSSION
Previously, we have shown the protective effect of MatAbs against PUUV in bank voles at the individual level (Kallio et al. 2006a). Here, we hypothesised that young host individuals may have a significant effect on infection dynamics in wildlife host populations through MatAb protection, and this has been supported.

PUUV infection prevalence was highest in spring and decreased during the breeding season. In spring, the population consisted mostly of individuals born during the previous breeding season (which ended eight to nine months earlier) that are most likely to be infected with PUUV (Bernshtein et al. 1999; Olsson et al. 2002). During the breeding season, there was naturally an influx of young uninfected individuals. The decrease in hantavirus prevalence over a breeding season has generally been attributed to this influx (Mills et al. 1999; Davis et al. 2005; Adler et al. 2008), and the seasonal variation in PUUV prevalence observed here and previously (Verhagen et al. 1986; Escutenaire et al. 2000; Sauvage et al. 2002) may in part be caused by such a juvenile dilution effect (Mills et al. 1999). But it may often not be the whole story. Ultimately, increasing the host (especially susceptible host) density should facilitate transmission and increase infection prevalence (Mills et al. 1999; Adler et al. 2008). However, this increase may be substantially delayed if maternally protected individuals are prevalent in the host population, since this will delay the influx of susceptible individuals into
Table 1. Best selected GLMM model and parameter estimates (logit scale) for the probability of carrying maternal antibodies during the breeding season (summer and late summer). (Bank vole abundances indicate natural log-transformed data. $\sigma^2$, the variance attributable to random effect; s.d., standard deviation of $\sigma^2$.)

<table>
<thead>
<tr>
<th>source of variation</th>
<th>coefficient (s.e.)</th>
<th>$z$-value</th>
<th>$p$-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>intercept</td>
<td>$-2.101 (3.648)$</td>
<td>$-0.794$</td>
<td>0.427</td>
</tr>
<tr>
<td>weight</td>
<td>$-0.276 (0.078)$</td>
<td>$-3.556$</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>infection prevalence in preceding May</td>
<td>$0.025 (0.013)$</td>
<td>1.954</td>
<td>0.051</td>
</tr>
<tr>
<td>breeding season (late summer)</td>
<td>$-1.439 (0.464)$</td>
<td>$-3.099$</td>
<td>0.002</td>
</tr>
<tr>
<td>current bank vole abundance</td>
<td>$1.536 (0.803)$</td>
<td>1.912</td>
<td>0.056</td>
</tr>
<tr>
<td>bank vole abundance six months before</td>
<td>$-0.849 (0.456)$</td>
<td>$-1.869$</td>
<td>0.062</td>
</tr>
<tr>
<td>random effect: site * year</td>
<td>$\sigma^2 = 1.212$; s.d. = 1.101</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Table 2. Parameter estimates (logit scale) on the influence of trapping seasons on the probability of an individual bank vole being PUUV-infected. (Intercept represents season spring (May). $\sigma^2$, the variance attributable to random effect; s.d., standard deviation of $\sigma^2$.)

<table>
<thead>
<tr>
<th>source of variation</th>
<th>estimate (s.e.)</th>
<th>$z$-value</th>
<th>$p$-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>intercept</td>
<td>$0.086 (0.132)$</td>
<td>0.651</td>
<td>0.515</td>
</tr>
<tr>
<td>season</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>summer (July)</td>
<td>$-0.572 (0.159)$</td>
<td>$-3.847$</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>late summer (August)</td>
<td>$-1.757 (0.152)$</td>
<td>$-11.549$</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>late autumn (October)</td>
<td>$-1.342 (0.151)$</td>
<td>$-8.903$</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>random effect: site * session</td>
<td>$\sigma^2 = 0.323$; s.d. = 0.569</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Table 3. Parameter estimates (logit scale) for the best selected GLMMs on bank vole PUUV infection probability separately for spring, summer, late summer and late autumn using the full datasets. ($\sigma^2$, the variance attributable to random effect; s.d., standard deviation of $\sigma^2$.)

<table>
<thead>
<tr>
<th>source of variation</th>
<th>coefficient (s.e.)</th>
<th>$z$-value</th>
<th>$p$-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>spring (May)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>intercept</td>
<td>$-2.584 (0.986)$</td>
<td>$-2.621$</td>
<td>0.009</td>
</tr>
<tr>
<td>weight</td>
<td>$0.103 (0.041)$</td>
<td>2.527</td>
<td>0.012</td>
</tr>
<tr>
<td>random effect: site * year</td>
<td>$\sigma^2 = 0.202$; s.d. = 0.449</td>
<td></td>
<td></td>
</tr>
<tr>
<td>summer (July)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>intercept</td>
<td>$-5.830 (1.181)$</td>
<td>$-4.938$</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>cycle</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>increase phase</td>
<td>$0.008 (0.430)$</td>
<td>0.019</td>
<td>0.985</td>
</tr>
<tr>
<td>peak phase</td>
<td>$2.156 (0.868)$</td>
<td>2.485</td>
<td>0.013</td>
</tr>
<tr>
<td>infection prevalence in preceding October</td>
<td>$-0.068 (0.037)$</td>
<td>$-1.862$</td>
<td>0.063</td>
</tr>
<tr>
<td>sex</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>male</td>
<td>$-2.475 (1.476)$</td>
<td>$-1.676$</td>
<td>0.094</td>
</tr>
<tr>
<td>weight</td>
<td>$0.248 (0.042)$</td>
<td>5.923</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>sex * weight</td>
<td>$0.140 (0.063)$</td>
<td>2.232</td>
<td>0.026</td>
</tr>
<tr>
<td>random effect: site * year</td>
<td>$\sigma^2 = 0.483$; s.d. = 0.697</td>
<td></td>
<td></td>
</tr>
<tr>
<td>late summer (August)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>intercept</td>
<td>$-7.611 (1.002)$</td>
<td>$-7.596$</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>sex</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>male</td>
<td>$-5.980 (1.735)$</td>
<td>$-3.446$</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>weight</td>
<td>$0.270 (0.052)$</td>
<td>5.272</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>maturity</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>mature</td>
<td>$1.016 (0.367)$</td>
<td>2.768</td>
<td>0.005</td>
</tr>
<tr>
<td>sex * weight</td>
<td>$0.351 (0.090)$</td>
<td>3.981</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>random effect: site * year</td>
<td>$\sigma^2 = 1.129$; s.d. = 1.062</td>
<td></td>
<td></td>
</tr>
<tr>
<td>late autumn (October)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>intercept</td>
<td>$-3.616 (1.011)$</td>
<td>$-3.578$</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>weight</td>
<td>$0.200 (0.044)$</td>
<td>4.605</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>infection prevalence in preceding May</td>
<td>$-0.030 (0.012)$</td>
<td>$-2.514$</td>
<td>0.012</td>
</tr>
<tr>
<td>random effect: site * preceding May</td>
<td>$\sigma^2 = 1.788$; s.d. = 1.337</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
the population until the MatAb effect has disappeared (Gavrilovskaya et al. 1990; Kallio et al. 2006a).

The proportion of MatAb-protected individuals during the breeding season was positively correlated with the infection prevalence at the beginning of the breeding season. Further, in late autumn, the probability of being infected was negatively related to the MatAb prevalence in summer. In addition, infection prevalence earlier in the breeding season, the key element in MatAb effect, showed a negative relationship with infection probability in late autumn. All these results support the proposition that MatAbs may reduce PUUV transmission: a high PUUV infection prevalence in the early breeding season can lead to a high proportion of maternally protected young individuals during the summer, which, in turn, decreases later infection likelihoods.

In spring, infection prevalence varied substantially (between 32% and 80%). Our analyses support the idea that high spring infection prevalence may cause delays in the spread of PUUV via a MatAb effect. When the spring prevalence was very high in our study (peak phases 2002, 2005 and 2008), the prevalence of infection declined substantially over the year (and numbers of infected individuals did not increase) despite the increasing bank vole density (figure 1). By contrast, low infection prevalence in spring should result in only a small proportion of summer-born individuals being maternally protected, allowing transmission to proceed without any substantial time lags. This was indeed observed in the increase phase years 2004 and 2007, where the numbers of infected individuals increased together with host abundance over the breeding season (though prevalence remained stable; figure 1).

Factors influencing the likelihood of being infected varied with season. Individual-level characteristics were the most important predictors in spring and late summer, whereas population-level predictors were also selected in the best models for summer and late autumn. Interestingly, none of the host population abundances was selected in any of the best models, and of the cycle phases, only the peak phase had a significant positive effect on the infection likelihood and only in summer. The individual-level characteristics sex and weight (and their interaction) were often important: increasing body mass increased the probability of infection and males were more often infected than females. These observations are in line with other studies (e.g. Gavrilovskaya et al. 1990; Bernshtein et al. 1999; Escutenaire et al. 2000; Olsson et al. 2002).

Hence, we have, for the first time, evaluated data on seropositivity from a natural population and partitioned those data into separate dynamic patterns for MatAb and infection. Our main aim was to test whether MatAbs have a detectable influence on pathogen transmission dynamics in wildlife populations. This study supports that idea. Such effects have been neglected in the past. We suggest that more detailed investigations on the role of MatAb-protected individuals in transmission dynamics in a range of systems are highly desirable.

This research adhered to the Association for the Study of Animal Behaviour/Animal Behaviour Society Guidelines for the Use of Animals in Research, the legal requirements in Finland and all institutional guidelines.

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MatAbs role in disease transmission


