

1 **SILENT ENEMIES: SUBLETHAL MACROPARASITES CAN DRIVE DISEASE-MEDIATED INVASIONS**

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35 **ABSTRACT**

36

37 Shared pathogens can alter the interaction between native and alien species resulting in disease-
38 mediated invasions (DMIs). Invasive species often harbour low-virulence macroparasites, but
39 empirical evidence for macroparasite-driven DMIs is still limited due to their sublethal impacts and
40 scarce prominence. Here we modelled the dynamics of native red squirrels, invasive grey squirrels
41 and their shared nematode *Strongyloides robustus* to assess whether macroparasites can drive
42 DMIs and lead to native species extinction. Our simulations showed that spillover of the alien
43 parasite can lead to red squirrel extinction, that grey squirrels amplify the infection in the native
44 host and that the infection accelerates the replacement of red squirrels compared to direct
45 competition alone, ultimately facilitating invasion by grey squirrels. These results demonstrate
46 that sublethal macroparasites can mediate invasions, suggesting that we are overlooking key
47 drivers of native species decline.

48 **INTRODUCTION**

49 Biological invasions are a major threat to biodiversity worldwide and their impact is predicted to
50 increase in the future (Seebens *et al.* 2021) and cause habitat alteration and native species
51 extinction at a global scale (Bellard *et al.* 2016; Pyšek *et al.* 2020). Once alien species are
52 introduced in a new range, they can interact with native species and the abiotic environment in
53 multiple ways, leading to diversity loss in the native ecosystem (Simberloff 2011).

54 Beyond direct interactions, such as predation or exploitation competition for resources, alien
55 species can impact native ones indirectly, for instance by acting as reservoirs for shared pathogens
56 (Bell *et al.* 2009; Bellard *et al.* 2016; Chinchio *et al.* 2020; Strauss *et al.* 2012). Invasive alien species
57 can carry alien pathogens that may spill over to native species, or they may acquire local
58 pathogens, possibly amplifying their circulation leading to spill-back (Kelly *et al.* 2009). Regardless
59 of its origin, when a shared pathogen has a more severe impact on the native species than the
60 alien one, parasite-mediated apparent competition (Bell *et al.* 2009; Holt & Bonsall 2017; Hudson
61 & Greenman 1998) will favour the latter, resulting in a disease-mediated invasion (DMI, Strauss *et al.*
62 *et al.* 2012). Although field evidence for DMIs in animals is still limited (Hatcher *et al.* 2006, 2012;
63 Prenter *et al.* 2004; Strauss *et al.* 2012), this phenomenon is likely to be common, as all organisms
64 harbour complex pathogen communities potentially able to mediate their ecological interactions
65 with competitors (Dobson *et al.* 2008).

66 In general, identifying and quantifying the impact of pathogens on wildlife population dynamics
67 can be challenging (Tompkins *et al.* 2011), and especially so for macroparasites (i.e., helminths and
68 parasitic arthropods). While viral and bacterial infections can be highly virulent, inducing overt
69 clinical symptoms and leading to mortality events that are easier to detect, macroparasitic
70 infections with more subtle pathogenic effects may often go unnoticed (McCallum & Dobson
71 1995). The quantification of such sublethal effects in natural conditions is difficult and field

72 experiments that manipulate pathogen transmission to demonstrate causal relationships are often
73 challenging (Shanebeck *et al.* 2022). However, theoretical studies show that pathogens do not
74 need to be highly prevalent or highly pathogenic to have regulatory effects on their host
75 populations (Anderson & May 1978). Moreover, in the context of DMIs, less virulent pathogens
76 are more likely to be introduced successfully in the new range compared to more virulent ones,
77 which can be lost at the initial stages of invasion due to high lethality in low-density populations
78 (Lymbery *et al.* 2014; MacLeod *et al.* 2010; Strauss *et al.* 2012). Therefore, the impact of a large
79 number of macroparasitic infections on native-invasive species interactions is likely overlooked,
80 leading to underestimates of the frequency of DMIs and to potentially miss the drivers of native
81 species extinctions.

82 Mathematical models can integrate field-derived data and system-specific biological processes and
83 thus provide a crucial tool for understanding population and epidemiological dynamics that may
84 be hidden in natural systems. In this way, rather than providing context-specific predictions,
85 mathematical models can be used to identify key processes and driving mechanisms by comparing
86 hypothetical scenarios with observed patterns (Restif *et al.* 2012). A mathematical approach was
87 pivotal in uncovering a well-known, case study example of disease-mediated invasion: the
88 replacement of native red squirrels (*Sciurus vulgaris*) by invasive grey squirrels (*S. carolinensis*)
89 driven by squirrel poxvirus (SQPV) in Great Britain and Ireland (Tompkins *et al.* 2003). Although red
90 squirrels can be replaced by the alien congener in the absence of disease through exploitation
91 competition for food (reviewed in Wauters *et al.* 2023), modelling studies disclosed how SQPV
92 carried by grey squirrels accelerates the process, ultimately facilitating invasion (Howell *et al.*
93 2024; Rushton *et al.* 2005; Tompkins *et al.* 2003). In Italy, where grey squirrels were introduced in
94 1948 (Bertolino and Genovesi, 2003), SQPV appears to be absent (Romeo *et al.* 2019). However
95 grey squirrels introduced a parasitic nematode, *Strongyloides robustus*, that can spill over to native

96 red squirrels, reducing their survival (Romeo *et al.* 2021). The impact of *S. robustus* on red
97 squirrels at population scale and whether it affects invasion by grey squirrels is not known.
98 In this study we will develop a general mathematical framework of a two host-one macroparasite
99 system that can represent the two squirrel species and *S. robustus* to assess the impact of this low-
100 virulence infection on the system dynamics. We will show that sublethal macroparasites can drive
101 DMIs and lead to native species extinction. Since sublethal diseases are likely to be carried by
102 invasive species (Lymbery *et al.* 2014; MacLeod *et al.* 2010; Strauss *et al.* 2012), our work will have
103 important consequences for understanding the potential threat posed by these infections to the
104 conservation of native species.

105

106 **MATERIALS AND METHODS**

107 **STUDY SYSTEM**

108 Grey squirrels are native to the Eastern part of North America and were introduced repeatedly
109 into Europe, first in Great Britain starting from the second half of the 19th century, and later in
110 Ireland and Italy. In most habitats grey squirrels outcompete the native red squirrel, ultimately
111 driving the species to local extinction (Wauters *et al.* 2023, but see also Slade *et al.* 2021).
112 Replacement of red by grey squirrels occurs mainly through competition for food leading to a
113 decrease in red squirrels population growth rate via reduced birth and recruitment rates
114 (reviewed in Wauters *et al.* 2023). In Great Britain and Ireland this process is also mediated by
115 SQPV, a shared viral pathogen that has a subclinical impact on grey squirrels (Chantrey *et al.* 2019;
116 Sainsbury *et al.* 2000; Tompkins *et al.* 2002), but is highly pathogenic to red squirrels, usually
117 resulting in death within a few weeks (Chantrey *et al.* 2014; Fiegna *et al.* 2016; Tompkins *et al.*
118 2002). The role played by grey squirrels as reservoirs of the disease that drives this DMI was
119 highlighted by modelling studies (e.g., Rushton *et al.* 2005; Tompkins *et al.* 2003). While SQPV is

120 absent in Italy (Romeo *et al.* 2019), grey squirrels introduced in the area do carry the gastro-
121 intestinal parasite *S. robustus* (Romeo *et al.* 2014b). *S. robustus* is a nematode native to North
122 America, where it commonly infects several squirrel species (Chandler 1942; Davidson 1976;
123 O'Brien *et al.* 2022). Adult female worms inhabit the small intestine of squirrels, where they
124 reproduce asexually shedding their eggs with host faeces (Bartlett 1995). Eggs hatch in the
125 environment and host exposure to infective larvae likely occurs in dreys and on ground
126 contaminated by faeces. The parasite appears to lack the adult free-living phase typical of other
127 *Strongyloides* species (Bartlett 1995). The prevalence of *S. robustus* in Italian populations of grey
128 squirrels varies between 57% and 81% (Romeo *et al.* 2014a, b, 2020; Santicchia *et al.* 2019), and is
129 similar to what is reported in their native range (e.g., Davidson 1976). *S. robustus* was found to
130 spill over to naïve red squirrels in areas coinhabited by grey squirrels, with prevalence in infected
131 populations of the native species ranging between 57% and 75% (Romeo *et al.* 2015, 2021;
132 Santicchia *et al.* 2020). Recently, two studies have demonstrated that infection by this alien
133 parasite is detrimental to red squirrels at the individual level, decreasing their investment in costly
134 behaviours (Santicchia *et al.* 2020) and significantly reducing their survival (Romeo *et al.* 2021).

135 MODEL STRUCTURE

136 We extend a general, continuous time, deterministic model of a single host-macroparasite system
137 (Ferrari *et al.* 2007; Greenman & Hudson 2000) to a two host, shared macroparasite system that
138 can represent the dynamics of red and grey squirrels and *S. robustus*. The model represents the
139 density of red, H_R , and grey, H_G , squirrels, the macroparasite abundance in red, P_R , and grey, P_G ,
140 squirrels and the density of a common pool of free-living infective larvae, L . We modelled parasite
141 abundance (i.e, the mean number of parasites per individual in the whole host population) instead
142 of the whole parasite population size because abundance better reflects field-collected data.

143 A schematic of the model is shown in Fig. 1 with the model consisting of the following five coupled
 144 differential equations:

$$145 \quad \frac{dH_R}{dt} = (d_R - b_R)H_R \left(1 - \frac{H_R}{K_R} - H_G \frac{c_G}{K_R} - \frac{\alpha_R}{d_R - b_R} P_R\right) \quad 1a$$

$$146 \quad \frac{dH_G}{dt} = (d_G - b_G)H_G \left(1 - \frac{H_G}{K_G} - H_R \frac{c_R}{K_G} - \frac{\alpha_G}{d_G - b_G} P_G\right) \quad 1b$$

$$147 \quad \frac{dP_R}{dt} = \beta_R \psi L - (\sigma + \alpha_R + b_R)P_R - \frac{\alpha_R}{k_R} P_R^2 \quad 1c$$

$$148 \quad \frac{dP_G}{dt} = \beta_G \psi L - (\sigma + \alpha_G + b_G)P_G - \frac{\alpha_G}{k_G} P_G^2 \quad 1d$$

$$149 \quad \frac{dL}{dt} = h(RH_R + H_G P_G) - \delta L - L(\beta_R H_R + \beta_G H_G) \quad 1e$$

150

151 For each species (represented by subscript R and G) the host has birth rate b and death rate d . The
 152 demographic growth is offset by intra-specific competition through the carrying capacity K , while
 153 inter-specific competitions is accounted for through coefficient c . The host population is also
 154 reduced by parasite-induced mortality α . We did not include a parasite effect on host fertility,
 155 since field investigations did not reveal any effect of *S. robustus* on squirrel reproduction (Romeo
 156 *et al.* 2021). Parasite abundance increases due to encounters of free-living stages with hosts with
 157 coefficient β , scaled by the proportion of infecting larvae that develop to adult stages ψ , and
 158 decreases with the adult parasite death rate σ . The parasite-induced mortality is scaled due to
 159 parasite aggregation k according to the negative binomial distribution (Anderson & May 1978;
 160 Ferrari *et al.* 2007; Greenman & Hudson 2000). Finally, the free-living larvae population increases
 161 with the instantaneous rate of production of infective stages by the two host species h , and
 162 decreases with their death rate δ and through encounters with hosts with coefficient β .

163 PARAMETER ESTIMATION

164 The host demographic parameters were taken from Tompkins *et al.* (2003) modelling SQPV
 165 dynamics in the same system (see Table 1). This allows a direct comparison of the effects of a low-

166 virulence macroparasite (our study) with that of a high-virulence microparasite (Tompkins *et al.*
167 2003) on the DMI impact on red squirrels. Parasitological parameters, when available, were taken
168 from long-term field studies carried out on this system in Italy or from studies on *S. robustus* in its
169 native range, otherwise they were estimated from studies on other *Strongyloides* species. *S.*
170 *robustus* adult parasite mortality (σ) was derived from *S. ratti* in rats, which has a lifespan of
171 approximately one month (Wilkes *et al.* 2004). The death rate of the free-living phase (δ) was
172 estimated from data on *S. robustus* eggs/larvae, whose survival in the environment varies
173 between 12 (Wetzel & Weigl 1994) and 30 days (Bartlett 1995). The fertility of a single adult
174 female (h) is set at 64 eggs/day, based on data from *S. robustus* in grey squirrels (Romeo *et al.*
175 2014a).

176 Infection by each *S. robustus* worm reduces the probability of red squirrel survival to the next year
177 by 0.1 in males and by 0.08 in females (Romeo *et al.* 2021). This corresponds to an average
178 parasite-induced death rate in red squirrels (α_R) of 0.095. In the absence of empirical data, we set
179 α_G as a quarter of α_R , based on the assumption of a better adaptation of grey squirrels to *S.*
180 *robustus* and on theoretical host-parasites dynamics (Anderson & May 1978) where lower α values
181 lead to higher parasite abundance, such as we observe in the alien species. Due again to lack of
182 empirical data, the proportion of larvae that successfully develop to the adult stage was arbitrarily
183 set at 0.7 and the encounter rate β was set *a posteriori*, in order to obtain the mean parasite
184 abundance of 11 worms/squirrel observed in Italian grey squirrels (Romeo *et al.* 2014b). Since *S.*
185 *robustus* is transmitted through environmental contamination and the two squirrels have similar
186 ecology, we considered the same transmission coefficient β for both host species. Finally, based
187 on previous data (Romeo *et al.* 2014a, b) the aggregation parameter (k) of the negative binomial
188 distribution was considered to be on average 0.05.

189 SIMULATED SCENARIOS

190 We simulated five different scenarios by changing the initial conditions of the model. In the one
191 host scenarios 1A) and 1B) we simulated host-parasite dynamics separately in the two squirrel
192 species (setting in turn H_R and H_G at zero). In the two host scenarios we simulated the population
193 dynamics of the two squirrel species together assuming in turn: 2A) infection by *S. robustus* but no
194 other forms of interaction between the two hosts (setting c_G and c_R at zero); 2B) infection by *S.*
195 *robustus* and direct interspecific competition; 2C) direct interspecific competition in the absence
196 of *S. robustus*, in order to quantify the relative contribution of parasite-mediated competition as
197 opposed to the impact of between species competition for resources only. We started all the
198 simulations assuming the introduction of two grey squirrels, while the red squirrel population was
199 always set at its disease-free steady state (except in 1B). In scenarios that included the parasite,
200 the *S. robustus* abundance in grey squirrels was initially set at 10 parasites/host, while for red
201 squirrels we assumed 2 parasites/host in scenario 1B.

202 We carried out a sensitivity analysis for all those parameters lacking empirical estimates, in order
203 to assess their impact on the population and epidemiological dynamics. We performed additional
204 simulations of scenario 2B, varying the values of these parameters within biologically plausible
205 ranges (Table S1). All simulations were performed using the package '*deSolve*' (Soetaert *et al.*
206 2010) in R software (version 4.3.2, R Core Team 2020).

207

208 **RESULTS**

209 ONE HOST SCENARIOS

210 The introduction of two grey squirrels infected by *S. robustus* in an area without other competing
211 squirrels (scenario 1A) leads to a sharp increase in the population size, almost reaching the

212 carrying capacity in 9 years. Then, the subsequent growth of the parasite population (that reaches
213 its maximum at 24 parasites/squirrel in 10 years), brings the host population down to 50
214 individuals, corresponding to 62.5% of the uninfected carrying capacity. The system reaches its
215 steady state in 15 years, with a parasite abundance of 12.6 parasites/host (Fig. 2a).

216 The introduction of *S. robustus* into a naïve red squirrel population at carrying capacity and
217 without competing grey squirrels (scenario 1B), leads to a rapid decrease in population size down
218 to 71.6% of the carrying capacity. The steady state of the system is reached in 6 years, with 43.4
219 red squirrels and a parasite abundance of 1.8 parasites/host (Fig. 2b).

220 TWO HOSTS SCENARIOS

221 In the hypothetical condition of two infected grey squirrels being introduced into a red squirrel
222 population and no direct competition for food occurring between the two species (scenario 2A),
223 the simulations show that red squirrels go extinct (i.e., population size < 2) in 15.2 years (Fig. 3a).

224 Just before extinction, parasite abundance in red squirrels increases to 8.5 parasites/host
225 (compared to 1.8 parasites/host in the sole red squirrel population). In this scenario, the grey
226 squirrel population reaches its steady state in 17.2 years, at 50 individuals (62.5% of the
227 uninfected carrying capacity as in the one host-one parasite scenario). When we account for both
228 the effect of parasite-mediated competition and of trophic competition between red and grey
229 squirrels (scenario 2B), the red squirrel population goes extinct more rapidly, in 10.3 years and
230 grey squirrels reach the steady state at 50 individuals in just 11.7 years (Fig. 3b). For comparison,
231 without parasites and accounting only for the effect of the trophic competition (scenario 2C) red
232 squirrels go extinct in 13.6 years and the grey squirrel population reaches the carrying capacity in
233 16.9 years (Fig. 3c).

234 PARAMETER SENSITIVITY

235 Within scenario 2B (i.e., simulating the combined effect of parasite-mediated competition and
236 trophic competition) all the tested parameter combinations drove the red squirrel population
237 towards extinction (Fig. S1) in a time frame between 7.5 and 16.5 years (Fig. 4).

238 The instantaneous death rate of grey squirrels due to *S. robustus* (α_G , Fig. 4a) is the parameter
239 with the greatest impact on the time to extinction for the red squirrel population, increasing it
240 from 9.1 years needed for a lower α_G of 0.01, to 16.5 years for an α_G of 0.1. An increase in
241 infection transmission between red squirrels and the parasite infective stages (β_R , Fig. 4c) also had
242 a strong effect, reducing the time to red squirrel extinction from 12.5 to 7.5 years. Notably, an
243 increase in infection transmission between grey squirrels and the parasite infective stages (β_G , Fig.
244 4b) had little effect on red squirrel replacement time, as did changes in h_R , ψ_G and σ_R (Fig. 4d, e and
245 f).

246

247 DISCUSSION

248

249 We modelled a two host-shared macroparasite system consisting of competing native red
250 squirrels, alien grey squirrels, and their gastro-intestinal nematode *S. robustus*. Our simulations
251 demonstrated that even sublethal macroparasites, such as helminths, can play a major role in
252 parasite-mediated competition and drive disease-mediated biological invasions.

253 The negative effect of alien *S. robustus* on individual red squirrels has been highlighted by
254 empirical studies (Romeo *et al.* 2021; Santicchia *et al.* 2020), however, it was unclear whether this
255 translated into impacts at the population scale. A key finding from our study is that grey squirrels
256 can amplify *S. robustus* load in red squirrels by a factor of 4.7. As a consequence, parasite spillover
257 facilitates invasion by grey squirrels reducing the time needed for red squirrel extinction by 24%
258 compared to in the absence of the parasite. Furthermore, our hypothetical model scenario that

259 excluded interspecific competition between red and grey squirrels showed that parasite
260 amplification from the invasive species alone may be sufficient to drive the native species to
261 extinction. Spillover and spillback DMIs have been shown to occur in a range of plant, invertebrate
262 and vertebrate systems (Strauss *et al.* 2012) and our study highlights how they can be driven by a
263 shared macroparasitic infection. Our findings further emphasise how subtle, sub-lethal infections
264 can play a key role in DMIs, but their lack of prominence in the native system means that they may
265 be overlooked as drivers of native species decline.

266 Our model findings demonstrate that grey squirrels are not mere carriers of the parasite but play a
267 pivotal role in the red squirrel-*S. robustus* epidemiological interaction. The model results are
268 supported by field data that indicate how grey squirrels are not essential for *S. robustus*
269 maintenance, as the infection was observed to persist in red squirrel populations several months
270 after grey squirrels' removal (Romeo *et al.*, unpublished data). Nevertheless, our results clearly
271 show the importance of grey squirrels as a source of infection, as their presence detrimentally
272 alters the outcome for red squirrels at the population scale. In the absence of the alien host, we
273 show that *S. robustus* would have a small impact on the native squirrel population, but when the
274 invasive species is present the native species is driven to extinction due to increased infection
275 transmission and heightened parasite load. In this context, our work opens some interesting
276 questions on what are the key properties that make a parasite able to mediate the interaction
277 between closely related species. For the red and grey squirrel system it has been shown that a
278 highly virulent pathogen (SQPV) can lead to DMI - but our work also indicates that a sub-lethal
279 parasite can play a key role in native species replacement.

280 We acknowledge limitations with our model study related to the lack of accurate empirical data
281 specific to this host-parasite system. For instance, with the exception of a few data gathered from
282 the opportunistic collection of roadkills (Romeo *et al.* 2013), no empirical estimates of adult

283 parasite abundance in red squirrels are available. To estimate the encounter rate with the
284 parasite, we had therefore to rely on the average adult *S. robustus* abundance observed in grey
285 squirrels, which is instead based on robust data collected from many individuals culled within
286 control programs (e.g., Romeo *et al.* 2014a, b). Furthermore, while an indirect measure of *S.*
287 *robustus*-induced mortality is available for red squirrels (Romeo *et al.* 2021), we lack an empirical
288 quantification of the parasite's impact in grey squirrels. However, analyses showed that the time
289 needed for red squirrels to go extinct was not sensitive to changes in most of the epidemiological
290 parameters. Key parameters were the level of disease-induced mortality in grey and red squirrels
291 and the transmission coefficient of the infection. The low pathogenicity of *S. robustus* in grey
292 squirrels leads to a high prevalence of infection, and, in turn, to an increase in the density of
293 parasite infective stages which can be transmitted to red squirrels. The time to replacement of red
294 squirrels is therefore sensitive to these parameters and can decrease if the pathogenicity in grey
295 squirrels is reduced or transmission of infection to red squirrels is increased. It is worth noting that
296 if the pathogenicity in grey squirrels is greater than in red squirrels, the time to red squirrel
297 replacement can increase and the invasion can potentially be prevented (see Hilker *et al.* 2005).
298 Our findings support a recent modelling study on red and grey squirrels and SQPV in Great Britain
299 (Howell *et al.* 2024), that found that infection transmission between red squirrels was a key factor
300 in their replacement by invasive grey squirrels. Howell *et al.* (2024) used recently-gathered
301 epidemiological and immunological evidence to highlight how partial immunity to SQPV in grey
302 squirrels will strongly influence the epidemiological dynamics. There is a lack of information about
303 the immune response against *S. robustus* in the red and grey squirrel system in Italy, but it is
304 known that the response against *Strongyloides* spp. is mainly directed at reducing parasitic
305 females' size and fecundity (Viney 2006). A differential immune response in the two host species
306 might therefore have relevant implications on the number of eggs shed with faeces and in turn on

307 encounter rates with infective stages. Interestingly though, our simulations suggest that the
308 number of eggs shed by red squirrels has a negligible effect on the dynamics of the system.
309 Although we are aware that the Italian red and grey squirrel system has different population
310 dynamics compared to populations in Great Britain (Gurnell *et al.* 2004; Wauters *et al.* 2023), we
311 took host demographic parameters from Tompkins *et al.* (2003) so we could compare our findings
312 to those that demonstrated SQPV-mediated competition. However, it would be important to test
313 habitat-specific model extensions, as host-parasite dynamics might be strongly affected by
314 environmental characteristics through their influence on target and reservoir host densities
315 (Altizer *et al.* 2006; Tompkins *et al.* 2011). Epidemiological theory states that the size of a reservoir
316 population should be above a specific critical threshold for the infection to be maintained and for
317 spillover to the target population to occur (Haydon *et al.* 2002; Viana *et al.* 2014). For instance,
318 modelling studies on SQPV showed that in conifer forests, where density of squirrels is low and
319 red squirrels seem to have a competitive advantage over the alien species (Slade *et al.* 2021), the
320 role of the disease in the interaction between the two hosts becomes negligible (Howell *et al.*
321 2024). Likewise, predators such as pine martens, who selectively prey grey over red squirrels
322 (Sheehy *et al.* 2018), are able to effectively suppress SQPV circulation by reducing the reservoir
323 host density (Slade *et al.* 2023). Indeed, grey squirrel control has been proven effective in
324 containing SQPV outbreaks in red squirrel populations (Schuchert *et al.* 2014) because without
325 continuous spillover from the reservoir host, high-virulence SQPV can fade out following outbreaks
326 in the red squirrel population (Macpherson *et al.* 2016; White *et al.* 2014). Our simulations and
327 field data suggest however that the epidemiology of *S. robustus* would be different as it may
328 persist indefinitely in red only populations even after grey squirrels have been removed. This latter
329 fact requires further investigation as it has potentially serious implications should *S. robustus* ever
330 be introduced to the UK system. Currently, red squirrels have a relative safe-haven in large,

331 conifer-dominated stronghold forests in the UK (Slade *et al.* 2021). An indefinitely persisting
332 macroparasite infection by *S. robustus* may alter the red-grey-SQPV-system in the UK in such a
333 way that no safe-haven remains for the native squirrel.

334 We currently lack long data-series that would allow us to test whether our model is able to
335 replicate the dynamics observed in the field. In this sense, our study serves as an example of the
336 model-guided fieldwork framework, in which feedback loops are established between empiricists
337 and modellers for the progression of research (Restif *et al.* 2012). Our work highlights critical
338 knowledge gaps that field studies should address to improve our understanding of these systems.
339 This study is nonetheless grounded on an extensive body of empirical and theoretical knowledge
340 gathered on this invasive-native vertebrate system, which is probably one of the most well-studied
341 biological invasions in animals (Wauters *et al.* 2023). Thanks to the research carried out over the
342 last 50 years, we now know that the interaction between these two squirrel species is much more
343 complex than previously thought, with several drivers concurring in mediating the invasion. It is
344 unlikely that this specific system is unique in its complexity, hence this highlights once again how
345 we are potentially missing several underpinning mechanisms of invasions.

346

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502 **TABLES**

503 **Table 1:** Parameter estimates for the two hosts-shared macroparasite system. R = red squirrel, G =
 504 grey squirrel.

Parameter	Value	Description	Reference
K_R, K_G	60, 80	Host population carrying capacity in a 5 Km ² area	Tompkins et al. 2003
d	0.4 (year ⁻¹)	Instantaneous death rate of host due to non-parasitic causes	Tompkins et al. 2003
b_R, b_G	1, 1.2 (year ⁻¹)	Instantaneous birth rate of host	Tompkins et al. 2003
c_R, c_G	0.61, 1.65	Competitive effect of one host species on the other	Tompkins et al. 2003
σ	12 (year ⁻¹)	Instantaneous death rate of adult parasites	Wilkes et al. 2004
h	17520 (year ⁻¹)	Instantaneous rate of production of infective stages	Romeo et al. 2014a
δ	17 (year ⁻¹)	Instantaneous death rate of infective free-living stages	Wetzel and Weigl 1994; Bartlett 1995
ψ	0.7	Proportion of infecting larvae that develop to adult stages	
k	0.05	Aggregation parameter of the Negative Binomial distribution	Romeo et al. 2014a, b
β	0.0004	Infection transmission coefficient	Romeo et al. 2014b
α_R, α_G	0.095, 0.0237 (year ⁻¹)	Instantaneous death rate of host due to parasite	Romeo et al. 2021

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506

507 **FIGURE CAPTIONS**

508 **Figure 1.** A schematic of the red and grey squirrel and *S. robustus* model system.

509 **Figure 2.** Population dynamics of red and grey squirrels in the one host scenarios 1A and 1B. Panel
510 (a) shows grey squirrel density (black solid line) and *S. robustus* abundance in grey squirrel (black
511 dashed line). Panel (b) shows red squirrel density (red solid line) and *S. robustus* abundance in red
512 squirrels (red dashed line).

513 **Figure 3.** Population density of red (red solid line) and grey squirrels (black solid line) and the
514 abundance of *S. robustus* in red (red dashed line) and grey squirrels (black dashed line). Panel (a)
515 shows the predicted dynamics for scenario 2A (only parasite-mediated competition), panel (b)
516 shows the predicted dynamics for scenario 2B (parasite-mediated competition and competition
517 for food), and panel (c) shows the predicted dynamics for scenario 2C (only competition for food).

518 **Figure 4.** Effect of a change in epidemiological parameters on the time to extinction of red
519 squirrels. Panel (a) shows variation in parasite-induced mortality in grey squirrels (α_G); panel (b)
520 the infection transmission between grey squirrels and parasite infective stages (β_G); panel (c) the
521 infection transmission between red squirrels and parasite infective stages (β_R); panel (d) the
522 instantaneous production of infective stages by red squirrels (h_R); panel (e) the proportion of
523 infective stages that develop into adult stages in grey squirrels (ψ_G); and panel (f) the death rate of
524 adult parasites in red squirrels (σ_R). The dashed line represents the time to extinction of red
525 squirrels in the absence of the parasite, when only direct competition occurs. Inner tick marks on
526 the x-axes indicate the value used in the simulated scenarios.

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