



Multi-event capture–recapture modeling of host–pathogen dynamics among European rabbit populations exposed to myxoma and Rabbit Hemorrhagic Disease Viruses: common and heterogeneous patterns

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Multi-event capture–recapture modeling of host–pathogen dynamics among European rabbit populations exposed to myxoma and Rabbit Hemorrhagic Disease Viruses: common and heterogeneous patterns

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Abstract

Host–pathogen epidemiological processes are often unclear due both to their complexity and over-simplistic approaches used to quantify them. We applied a multi-event capture–recapture procedure on two years of data from three rabbit populations to test hypotheses about the effects on survival of, and the dynamics of host immunity to, both myxoma virus and Rabbit Hemorrhagic Disease Virus (MV and RHDV). Although the populations shared the same climatic and management conditions, MV and RHDV dynamics varied greatly among them; MV and RHDV seroprevalences were positively related to density in one population, but RHDV seroprevalence was negatively related to density in another. In addition, (i) juvenile survival was most often negatively related to seropositivity, (ii) RHDV seropositives never had considerably higher survival, and (iii) seroconversion to seropositivity was more likely than the reverse. We suggest seropositivity affects survival depending on trade-offs among antibody protection, immunosuppression and virus lethality. Negative effects of seropositivity might be greater on juveniles due to their immature immune system. Also, while RHDV directly affects survival through the hemorrhagic syndrome, MV lack of direct lethal effects means that interactions influencing survival are likely to be more complex. Multi-event modeling allowed us to quantify patterns of host–pathogen dynamics otherwise difficult to discern. Such an approach offers a promising tool to shed light on causative mechanisms.

Introduction

Emerging and re-emerging infectious diseases present one of the most pressing issues facing wild vertebrate populations in the 21st century [1]. However, relatively little is yet known about the exposure dynamics of infectious agents in their individual hosts, and what determines their impact on life-history traits such as survival [2]. A comprehensive understanding of the ecological processes influencing pathogen dynamics in natural host populations is of crucial importance to predicting both

the dynamics of infectious diseases and the risks that they may entail for animal populations [3,4].

The European wild rabbit (*Oryctolagus cuniculus*) and the two main viral diseases that affect them (myxomatosis, and Rabbit Hemorrhagic Disease) represent an important system for addressing wildlife eco-epidemiological issues. European rabbits are a multifunctional keystone species; not only do they alter plant species composition and vegetation structure, but they also represent the bulk of the diet of a wide variety of Iberian predators [5]. These include the Iberian lynx (*Lynx pardinus*) and the Spanish imperial eagle (*Aquila adalberti*), both seriously threatened [5-7]. The arrival of myxoma virus (MV) and Rabbit Hemorrhagic Disease Virus (RHDV) on the Iberian Peninsula has caused a marked decline in rabbit populations over the last 50 years [8-11], threatening further

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