Modeling the Effect of Population Dynamics on the Impact of Rabbit Hemorrhagic Disease

CARLOS CALVETE

Centro de Investigación Agroalimentaria de Aragón (CITA), Apdo. 727, 50058 Zaragoza, Spain, email vetecal2003@jazzfree.com

Abstract: *The European wild rabbit* (Oryctolagus cuniculus) *is a staple prey species in Mediterranean ecosystems. The arrival and subsequent spread of rabbit hemorrhagic disease throughout southwestern Europe, however, has caused a decline in rabbit numbers, leading to considerable efforts to enhance wild rabbit populations, especially through habitat management. Because rabbit population dynamics depend on habitat suitability and changes in habitat structure and composition subsequent to habitat management, I evaluated the effects of population dynamics on the long-term impact of rabbit hemorrhagic disease on rabbit populations. I used an age-structured model with varying degrees of population productivity and turnover and different habitat carrying capacities, and I assumed the existence of a unique, highly pathogenic virus. My results suggest that disease impact may be highly dependent on habitat carrying capacity and rabbit population dynamics, and the model provided some insight into the current abundance of wild rabbits in different locations in southwestern Europe. The highest disease impact was estimated for populations located in habitats with low to medium carrying capacity. In contrast, disease impact was lower in high-density populations in habitats with high carrying capacity, corresponding to a lower mean age of rabbit infection and a resulting lower mortality from rabbit hemorrhagic disease. The outcomes of the model suggest that management strategies to help rabbit populations recover should be based on improving habitats to their maximum carrying capacity and increasing rabbit population productivity. In contrast, the use of strategies based on temporary increases in rabbit density, including vaccination campaigns, translocations, and temporal habitat improvements at medium carrying capacities, may increase disease impact, resulting in short-term decreases in rabbit population density.*

Key Words: epidemiology of RHD, habitat management, *Oryctolagus cuniculus*, wildlife disease control

Modelado del Efecto de la Dinámica Poblacional sobre el Impacto de Enfermedad Hemorrágica de Conejos

Resumen: *El conejo silvestre europeo* (Oryctolagus cuniculus) *es una especie presa en ecosistemas Mediterráneos. Sin embargo, el arribo y subsiguiente dispersión de la enfermedad hemorrágica de conejos en el suroeste de Europa ha provocado una declinación en el número de conejos, lo que ha generado esfuerzos considerables para incrementar las poblaciones de conejos, especialmente por medio de la gestión del hábitat. Debido a que la dinámica de las poblaciones de conejos depende de la adecuación del hábitat y de cambios en la estructura y composición del hábitat después de la gestión del hábitat, evalué los efectos de la dinámica poblacional sobre el impacto a largo plazo de la enfermedad hemorrágica de conejos sobre las poblaciones de conejos. Utilicé un modelo estructurado por edades con diferentes grados de productividad poblacional y recambio así como diferentes capacidades de carga del hábitat, y asumí la existencia de solo un virus altamente patogénico. Mis resultados sugieren que el impacto de la enfermedad puede ser altamente dependiente de la capacidad de carga del hábitat y de la dinámica poblacional de los conejos, y el modelo proporcionó una panorámica de la abundancia actual de conejos silvestres en diferentes localidades en el suroeste de Europa. Se estimó el mayor impacto de la enfermedad para poblaciones localizadas en hábitats con capacidad de carga baja y mediana. En contraste, el impacto de la enfermedad fue menor en poblaciones con alta densidad en hábitats con alta capacidad de carga, correspondiente a una menor edad promedio de infección y a la resultante menor mortalidad por enfermedad hemorrágica de conejos. Los resultados del modelo sugieren*

1232

que las estrategias de gestión para ayudar a que se recuperen las poblaciones de conejos deberán basarse en el mejoramiento del hábitat hasta su capacidad de carga máxima y en el incremento de la productividad de las poblaciones de conejos. En contraste, el uso de estrategias basadas en incrementos temporales de la densidad de conejos, incluyendo campañas de vacunación, translocaciones y mejoramiento temporal del hábitat a capacidades de carga medianas, puede incrementar el impacto de la enfermedad, lo que resultaría en disminuciones de la densidad poblacional de conejos en el corto plazo.

Palabras Clave: control de enfermedades de vida silvestre, epidemiología de EHC, gestión de hábitat, *Oryctolagus cuniculus*

Introduction

The European wild rabbit (*Oryctolagus cuniculus*) is among the most important vertebrate species in Spanish Mediterranean ecosystems. Usually, the biodiversity of these ecosystems is associated with large numbers of rabbits, and two of the most threatened predators in the world, the Iberian lynx (*Lynx pardina*) and the Imperial Eagle (*Aquila adalberti*), depend on rabbit abundance (Ferrer & Negro 2004). The arrival of rabbit hemorrhagic disease (RHD) in 1988 (Argüello et al. 1988), however, led to substantial initial reductions in rabbit population density (Villafuerte et al. 1994). This disease became enzootic, and currently mortality caused by annual outbreaks causes substantial reduction of wild rabbit populations (Calvete et al. 2002). Thus, many populations have continued to decrease (Villafuerte et al. 1995), some to the point of extinction. Consequently, considerable efforts have been made to enhance wild populations for conservation purposes.

Management strategies implemented to date to enhance rabbit populations include predator control, vaccination campaigns, restocking, and, especially, habitat management (Moreno & Villafuerte 1995; Angulo 2003; Calvete & Estrada 2004; Calvete et al. 2004b), but the success of these strategies has been generally negligible. For example, scrub and pasture have been managed over more than 1000 ha, and at least 18,000 wild rabbits have been translocated into Doñana National Park in southern Spain during the last 15 years, but the impact on rabbit abundance has been poor. Currently, therefore, the impact of RHD and the subsequent decline of rabbits are still a major problem for the conservation of the Iberian lynx and the Imperial Eagle (Angulo et al. 2004).

Rabbit hemorrhagic disease is an infectious viral disease, mainly transmitted by direct contact, that kills up to 90% of infected rabbits more than 2 months old (Xu and Chen 1989). The effect of this disease on rabbit abundance has a north-south gradient in Europe, with the greatest recorded declines in rabbit abundance in Spain and Portugal. In Great Britain and other countries of northern Europe, RHD has had a less severe impact on rabbit populations because of the occurrence in these areas of a putative, preexisting, protective, nonpathogenic RHD-like virus. To date, however, this virus has not been isolated from wild populations (Cooke & Fenner 2002; Marchandeau et al. 2005) and there is no evidence of its presence in southern European rabbit populations.

In Iberian wild rabbit populations, the pattern of RHD mortality is cyclical, with increased RHD mortality rates associated with the annual inflow of susceptible young rabbits during the breeding season. At present, more than 20% of adult rabbits in some Iberian populations die from RHD annually (Calvete et al. 2002). Nevertheless, some rabbit populations have made better recoveries than others, and in areas that were most favorable for rabbits before the spread of RHD there is a clear tendency for rabbit numbers to recover in geographically limited populations. Thus the current distribution of wild rabbits in Mediterranean areas is characterized by high variability (Fa et al. 1999; Virgós et al. 2003; Calvete et al. 2004a). Most rabbit populations are practically extinct or at low density and are located in a great diversity of habitats. Many sites with few or no rabbits, however, have habitats that appear as suitable as sites in which rabbits have maintained very high density, in spite of RHD.

The factors that enable the coexistence of high population densities of rabbits with enzootically circulating RHD virus are unknown, but their identification may signify a qualitative advance in the management of wild rabbit populations. Some modeling studies of RHD have explained the reduced impact of RHD in some populations. Authors of these models postulate the existence of a nonpathogenic, protective RHD-like virus (White et al. 2001) or a pathogenic RHD virus with both virulent and avirulent modes of transmission, as determined by rabbit demography (White et al. 2002). These models, however, have been used primarily to explain the differential impact of RHD along the north-south gradient in Europe, especially the low impact of this disease in Great Britain. Other approaches have modeled RHD epizootics and their spatial dynamics by means of models that are not age structured and are based on the existence of only one pathogenic RHD virus (Barlow & Kean 1998; Fa et al. 2001; Barlow et al. 2002). None of these models, however, has been extended to explain the effect of rabbit population dynamics on disease impact.

Calvete and Estrada (2000) suggest that the high variability of rabbit distribution in Spanish Mediterranean areas, especially the existence of high-density populations

in equilibrium with pathogenic RHD virus, may be explained on the basis of rabbit population dynamics. They propose that population dynamics could be modulated by habitat suitability, without the concurrence of genetic variations among rabbit populations or the presence of a protective, nonpathogenic RHD-like virus or a unique virus with several modes of transmission. They also suggest the possibility of reducing the impact of RHD by managing rabbit populations. Because of the unquestionable interest in the possibility of conserving wild rabbit populations and promoting threatened predator species in the Mediterranean areas of southwestern Europe (especially the Iberian Peninsula), I have evaluated the impact of RHD on rabbit populations with a simple, age-structured deterministic model that considered the existence of a unique pathogenic RHD virus with a unique mode of transmission. This model simulated the impact of RHD on rabbit populations with different dynamics (i.e., different population productivity and turnover) in habitats with different carrying capacities. Based on the outcomes of this model, I derived some management implications for the recovery of wild rabbit populations.

Methods

Modeling Rabbit Populations

Wild rabbits in the Iberian Peninsula are highly seasonal breeders with high fecundity and high juvenile mortality (Soriguer 1981). Reproduction is associated with the growth of vegetation, which is related to rainfall and temperature (Delibes & Calderón 1979; Villafuerte et al. 1997). Typically, there is a three- to fourfold increase in numbers from the minimum to the annual maximum. Gestation in rabbits lasts about 28–30 days, and female rabbits can be fertilized a few days after parturition. Newborn rabbits live in a breeding stop, a special burrow excavated by the mother in the soil, during their first 3–4 weeks of life and depend on their mother for survival. After this period they are weaned and emerge from the stop. Juvenile rabbits can reach sexual maturity at 3 months of age (Soriguer 1981), but most do not breed until the next breeding season, when they are older than 8 months (Myers et al. 1994; Calvete et al. 2002).

In the model I divided rabbit populations into 15 age classes (b), represented by $b\{w_1, w_2, w_3, w_4, w_5, w_6, w_7, w_8, m_3, m_4, m_5, m_6, m_7, m_8, \text{ad}\}$ (w, week; m, month). Age classes from w_1 to w_3 consisted of newborn rabbits living in breeding stops. Age classes from w_4 to m_8 were nonreproductive juvenile rabbits, and rabbits older than 8 months were considered adults (ad), the only reproductive class.

The yearly breeding period was simulated by a sine function $\Phi(t)$ with amplitude ranging from 0 to 1 in function of time t in days. Three breeding period lengths (4, 6, and 8 months) were simulated (Rogers et al. 1994), with the highest proportion of pregnant females ($\Phi[t] = 1$) occurring between the end of January and the beginning of February for all simulations. There was no reproduction during the remaining months.

The model ran at daily steps, and the daily total number (n) of newborn rabbits recruited into the w_1 age class, and therefore in the population, was defined by the equation

$$n = \Phi(t)\frac{\text{ad}}{2}l\frac{1}{g}, \tag{1}$$

where g is the duration of gestation (30 days), l is the mean litter size, and ad is adult. The model simulated the mean litter size at six values, ranging from 3 to 5.5 offspring/female in steps of 0.5, which constituted the overall range described for this species (Rogers et al. 1994). The sex ratio was 1:1 for all age classes.

The daily rate of rabbit loss due to non-RHD mortality was d_b. The annual mortality rate for adult rabbits in wild populations is highly variable, usually ranging from 20% to 80% (e.g., Wheeler & King 1985; Gibb 1993). Thus, I implemented the model to simulate this range of adult annual mortality rates. Fixed daily death rates (d_{ad}) were calculated from the corresponding simulated annual mortality rates.

Rabbits are territorial, and competition for refuge, feeding areas, and warrens increases juvenile mortality when carrying capacity is reached (Myers et al. 1994). I therefore assumed that juvenile daily mortality rate (d_b when $b \in [w_4, m_8]$) depends on adult density, based on the equation

$$d_b = d_{\text{max}}\frac{D_{\text{ad}}}{K_{\text{ad}}}, \tag{2}$$

where $d_{\text{max}} = 0.041$ is the maximum juvenile daily mortality rate (at this rate only 0.01% of rabbits recruited into age class w_4 reached adult [ad] age class), D_{ad} is the density of adult rabbits in the population (ad/hectare), and K_{ad} is the adult-density carrying capacity of the environment in the absence of RHD. Adult density was estimated by assuming that the simulated population was confined to a 1000-ha land surface without emigration or immigration processes. Given that newborn rabbits depend entirely on their mothers for survival, I set their daily mortality rate equal to that of their mothers, as the combination of RHD and non-RHD mortality.

Between successive age classes there was a daily maturation transition rate (a_b). Given that one simulated month had 30 days and 4 weeks equaled 1 month, simulated weeks were 7.5 days long. Thus, the daily maturation transition rate was set at $a_b = 1/7.5$ if $b \in [w_4, w_8]$, $a_b = 1/30$ if $b \in [m_3, m_8]$, and $a_b = 0$ if $b \in [\text{ad}]$.

Modeling RHD Epidemiology

Within each rabbit age class there were compartments for individuals according to their RHD status. These were defined as susceptible individuals or those without previous

contact with RHD virus (S_b), infected (I_b), chronically infected (C_b), and recovered (R_b) individuals.

All newborn rabbits were recruited into the Sw_1 age class because the virus is not transmitted vertically. Because newborn rabbits live in breeding stops and do not interact socially with other rabbits, they were not considered in the RHD dynamics. Maternal antibodies, however, influence the outcome of RHD virus infection (Robinson et al. 2002). Thus the model subdivided newborn rabbits into two maternal RHD-antibody levels based on the absence (rabbits born from S_{ad} and I_{ad} females) or presence (rabbits born from C_{ad} and R_{ad} females) of maternal antibodies, and newborn rabbits were tracked across the model until they were recruited into the w_4 juvenile age class, when they emerged from the stop.

For the remaining age classes (from w_4 to ad) the algebraic description of the model is described by the following equations:

$$\frac{dS_b}{dt} = S_{b-1}a_{b-1} - S_b\left(a_b + d_b + f\right), \qquad (3)$$

$$\frac{dI_b}{dt} = S_b f + I_{b-1}a_{b-1} - I_b\left[a_b + d_b + \sigma\alpha_b + \sigma\left(1 - \alpha_b\right)\right], \qquad (4)$$

$$\frac{dC_b}{dt} = I_b\sigma\left(1 - \alpha_b\right) + C_{b-1}a_{b-1} - C_b\left(a_b + d_b + u\right), \quad (5)$$

$$\frac{dR_b}{dt} = C_b u + R_{b-1}a_{b-1} - R_b\left(a_b + d_b\right). \qquad (6)$$

The daily rate of susceptible rabbits that were infected by RHD virus was determined by the force of infection f. The lethality of RHD (α_b) among rabbits older than 8 weeks usually reaches values of about 90%, but it is lower in younger rabbits (age resilience), even in the absence of maternal antibodies (Capucci et al. 1996; Mutze et al. 1998). In contrast, the presence of maternal antibodies does not protect young rabbits against infection but does preclude the development of severe forms of the disease, decreasing lethality even further. Thus, I set RHD lethality as a function of age class and the absence or presence of maternal antibodies (Table 1), following the estimates of Robinson et al. (2002).

Given that the mean survival time of RHD-infected rabbits is 2 days, the daily mortality rate due to RHD in infected rabbits was $\sigma\alpha_b$, where $\sigma = 0.5$, and infected individuals that survived acute infection developed a chronic, nonlethal form of RHD and were recruited into the chronic class (C_b) at a daily rate of $\sigma(1 - \alpha_b)$. Chronically diseased individuals shed infective virus for several weeks after infection (Shien et al. 2000). The model assumed that the chronic diseased state lasted for 20 days, after which the survivors became immune for life and rabbits were recruited into the recovered class (R_b) at a daily rate of $u = 1/20$.

Table 1. Lethality of rabbit hemorrhagic disease (RHD) virus infection simulated for each age class in the absence and presence of maternal RHD antibodies.[*]

Age class	Without maternal antibodies	With maternal antibodies
w_4	0.1	0
w_5	0.2	0
w_6	0.4	0.1
w_7	0.6	0.1
w_8	0.8	0.2
m_3	0.9	0.7
$h \in [m_4, ad]$	0.9	0.9

[*]*Key:* w, *weeks of age;* m, *months of age;* ad, *adults age class. The subindex is the number of weeks or months of age. There is an unique adult age class (ad > m_8).*

Force of Infection and Transmission Rates

Crucial for RHD dynamics was the expression of the force of infection (f), which is based on the assumption of true mass action (Jong et al. 1995), according to

$$f = \beta\varphi(H)\frac{\left(\sigma\sum_b I_b + \sum_b C_b + \omega\sum_b R_b\right)}{H}, \quad (7)$$

where population size (H) is composed only of rabbits in age classes w_4 to adult (i.e., rabbits living out of the breeding stops), and to

$$H = \sum_{b=w_4}^{b=ad}\left(S_b + I_b + C_b + R_b\right), \qquad (8)$$

where $\beta\varphi(H)$ is the transmission term (Heesterbeek & Roberts 1995). The numerator consisted of all rabbits that shed the RHD virus (i.e., infective rabbits on the second day of acute infection, chronically infected rabbits, and a proportion of recovered rabbits [ω]) and could act as reservoirs of the virus (I set $\omega = 0.1$ arbitrarily) (Moss et al. 2002).

Wild populations have a high variability in population density and a high intra- and interyear variability within populations. As home ranges become smaller, aggression rates between individuals increase, whereas the available feeding grounds remain communal as rabbit density increases (Myers & Poole 1959, 1961; Gibb 1993). In addition, intrayear increases in rabbit density are associated with reproduction, and juvenile rabbits disperse and exhibit increased exploratory behavior, especially at high densities (Myers et al. 1994; Kunkele & Von Holst 1996). I therefore assumed that the transmission term consisted of the transmission constant β and a contact rate function $\varphi(H)$ dependent on population size (in my model population size was directly related to population density).

Although several functional forms for the contact rate function have been proposed, for simplicity I assumed the simplest linear model forced through the origin $\varphi(H) = \delta H$, where δ is the slope of the regression model. The

Table 2. Annual mean parameters used to estimate the transmission term in the model of rabbit hemorrhagic disease (RHD).*

Parameter	Mean	95% confidence interval
Rabbit density/ha	7.86	6.67–9.06
Total mortality rate in adults (%)	57.54	42.75–68.51
RHD-mortality rate in adults (%)	23.62	11.28–34.24
RHD-antibody prevalence in adults (%)	73	66–81

Values were calculated from estimations carried out in a wild rabbit population by Calvete et al. (2002).

transmission term values were not known for the model, but because H was known, I estimated the constant $\beta\delta$ numerically by computation. To do this I rearranged the data for annual mortality rate due to RHD, total annual mortality rate, and annual mean prevalence of RHD antibodies estimated by Calvete et al. (2002) for adult rabbits in a wild rabbit population from 1993 to 1995, and calculated the overall annual mean for each parameter and its 95% confidence interval (Table 2). In addition, I transformed the rabbit abundance index, expressed as the number of pellets deposited per day, into annual mean rabbit population density, assuming the daily production of pellets per rabbit estimated by Taylor and Williams (1956). Then I ran the model for all combinations of 13 levels of annual adult non-RHD mortality rates (from 0.2 to 0.8 in steps of 0.05), 40 levels of carrying capacity for adult rabbits (from 1 to 40 adults/ha in steps of 1), and 1000 levels for $\beta\delta$ (from 10^{-3} to 10^{-6} in steps of 10^{-6}) until the model reached a steady state. The outcomes produced by the model fell into the 95% confidence intervals estimated from field data for all parameters simultaneously when $\beta\delta$ ranged from 115×10^{-6} to 140×10^{-6}. I set the mean value of this range ($\beta\delta = 127.5 \times 10^{-6}$) to parameterize the model, which reproduced intra-annual variations in rabbit abundance and yearly increases in RHD mortality of adult rabbits associated with breeding periods in accordance with those observed in wild populations (Calvete et al. 2002).

Modeling RHD in Scenarios of Varying Population Dynamics

To model RHD dynamics and their impact on rabbit populations with different population dynamics, populations were simulated for 30 adult-density carrying capacities; seven annual non-RHD mortality rates (from 20% to 80% in steps of 10%) for adult rabbits to simulate seven levels of population turnover; six mean litter sizes (from 3 to 5.5 kittens in steps of 0.5); and three breeding period lengths (4, 6, and 8 months). The combined simulations of these conditions yielded 3780 scenarios with populations of different rabbit density, productivity, and turnover.

To simulate each scenario I ran the model until population equilibrium was reached. I simulated each scenario twice, first in the absence of RHD and second by introducing the disease during the first year of simulation. I estimated the population growth rate $\lambda - 1$ by comparing the mean annual rabbit population density at equilibrium in the absence and presence of RHD. The population density in the presence of RHD was lower than before introduction of the disease when $\lambda - 1 < 0$, and the disease had no impact when $\lambda - 1 = 0$. I considered that the absolute value of the population growth rate was a direct measure of RHD impact in each population.

I implemented the model to calculate many outcomes at daily and annual rates. I presented the results, however, on the basis of parameters that can be measured easily in wild rabbit populations, such as adult annual mortality rates, annual prevalence of RHD-seropositive adult rabbits, and annual mean population density. In addition, I presented the mean age of rabbit infection by RHD calculated by the model. The age assigned to each infected rabbit was the median age in days of its age class; for adult rabbits I assumed an age of 360 days. I considered annual mean adult density reached at equilibrium in the absence of RHD the actual carrying capacity of the habitat for each population, instead of the K_{ad} values initially introduced to parameterize the model.

I performed a sensitivity analysis to assess the variation of RHD impact as a function of rabbit population dynamics by adjusting a multiple linear regression model. In this model, the log-transformed absolute value of the population growth rate was the dependent variable and mean litter size, breeding period length, annual adult mortality rate, and carrying capacity were the independent variables. Predictor variables were standardized to mean = 0 and variance = 1 to eliminate the effects of the different units of measure on the estimation of regression parameters.

Results

Outcomes of the model for RHD dynamics showed nonlinear patterns in relation to rabbit population density in the presence of RHD. This pattern was a consequence of the different rabbit population dynamics (Fig. 1). Increased mean annual population densities in the presence of RHD were associated with an increase in the force of infection and therefore with a decreased mean age of infection. This caused an initial increase in RHD mortality, followed by a subsequent decrease when the mean age of infection lessened and a greater proportion of rabbits was infected at ages at which RHD virus lethality was reduced by age resilience or the presence of maternal antibodies. This pattern was related to an increase in the prevalence of RHD antibodies in adult rabbits, reaching 100% prevalence at high population densities.

The RHD dynamics changed in a reduced interval of rabbit population density, where antibody prevalence,
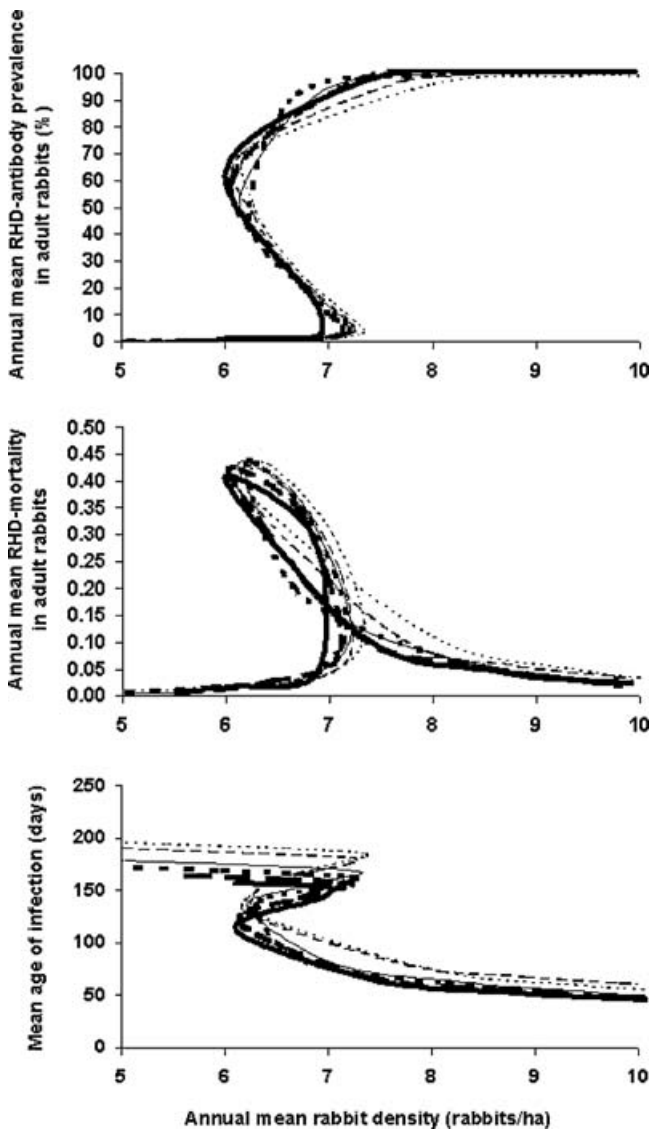
Figure 1. Three outcomes for rabbit hemorrhagic disease (RHD) dynamics as a function of annual mean rabbit density in the presence of the disease. Outcomes are estimated when rabbit population and RHD dynamics reach a steady state. The non-RHD mortality rate of adult rabbits and breeding period length are fixed at 0.5 and 6 months, respectively. There are six mean litter sizes: thin dotted line, 3; thin dashed line, 3.5; thin continuous line, 4; thick dotted line, 4.5; thick dashed line, 5; thick continuous line, 5.5.

RHD mortality, and mean age of infection were not directly related to population density. Within this reduced interval of rabbit population density, curves of Fig. 1 turned back on themselves or even created loops in the case of annual mean RHD mortality. Populations at low density were related to higher antibody prevalence and

RHD mortality than populations at high density and vice versa. This way, RHD dynamic exhibited alternate states in populations at the same low to medium rabbit density in presence of the disease, differences that were determined by the different rabbit population dynamics.

The impact of RHD, assessed as absolute population growth rate after the introduction of the disease, showed a high variation among populations, especially in relation to habitat carrying capacity (i.e., mean annual adult rabbit density in the absence of RHD) (Fig. 2). The lowest impact of RHD occurred in populations located in habitats with lowest carrying capacity, whereas the highest impact occurred in habitats with low to medium carrying capacity. Above that, RHD impact decreased as carrying capacity increased, and the impact of the disease was considerably lower in populations with high pre-RHD densities than in populations with medium to low pre-RHD densities.

To carry out the sensitivity analysis, simulated scenarios were divided into two sets as a function of increasing carrying capacity and the impact of RHD. Thus, for each fixed combination of mean litter size, breeding period length, and mean annual adult non-RHD mortality rate, simulated scenarios were assigned to (1) scenarios with increasing impact of RHD (i.e., scenarios that comprised the lowest carrying capacity to the carrying capacity at which the lowest growth rate was estimated) and (2) scenarios with decreasing impact of RHD (i.e., scenarios that comprised the next carrying capacity corresponding to the lowest growth rate to the highest simulated carrying capacity).

In scenarios with an increasing impact of RHD, the increase of the disease impact was positively related to the four predictor variables (Table 3). The RHD impact was
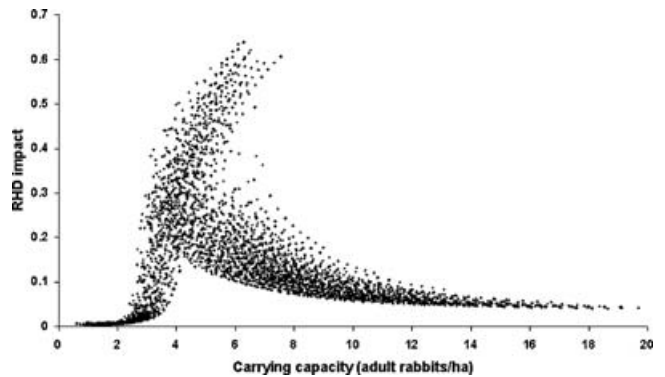

Figure 2. Simulated long-term impact of rabbit hemorrhagic disease (RHD) on wild rabbit populations. The RHD impact is the absolute value of population growth rate estimated by comparing the mean annual rabbit density of populations at equilibrium in the absence or presence of RHD. Carrying capacity is the annual mean density of adult rabbits in the absence of RHD.

**Table 3. Sensitivity analyses of variation in the impact of rabbit hemorrhagic disease (RHD) on rabbit populations, expressed as the log transformation of the absolute value of the population growth rate in relation to variation in factors determining population dynamics.*

Factor	Increasing RHD impact $R^2 = 0.85$; $F_{4,1418} = 2056$; $p<0.001$			Decreasing RHD impact $R^2 = 0.71$; $F_{4,2352} = 1423$; $p<0.001$		
	parameter	t	p	*parameter*	t	p
Litter size	0.0231	14.73	<0.001	−0.0182	−26.63	<0.001
Breeding period length	0.0170	10.92	<0.001	−0.0112	−15.94	<0.001
Non-RHD mortality	0.0044	2.89	0.004	0.0001	0.15	0.880
Carrying capacity	0.1419	90.64	<0.001	−0.0453	−60.42	<0.001

Simulations were divided into two sets following Fig. 2: simulations with increasing RHD impact and simulations with decreasing RHD impact as carrying capacity increased. Goodness of fit for every model is in the first row.

highly sensitive to variation in carrying capacity, somewhat sensitive to variation in mean litter size and breeding period length, and insensitive to variation in non-RHD adult mortality. In scenarios with decreasing impact of RHD, the magnitude of the impact was negatively associated with all predictor variables, except for non-RHD adult mortality. Similar to scenarios with increasing impact of RHD, the strength of association between RHD impact and carrying capacity was higher than that between RHD impact and mean litter size or breeding period length.

Discussion

The outcomes of this model showed that the impact of RHD was highly dependent on rabbit population dynamics and that the presence of a unique, highly pathogenic RHD virus was compatible with the existence of high-density populations at equilibrium with the disease. The simple RHD epidemiology simulated in this model made it unnecessary to postulate the concurrence of a non-pathogenic, protective RHD-like virus or genetic differences in rabbits to explain the current distribution and impact of the disease in Iberian populations. In addition, the outcomes of this model should be invariable if a non-pathogenic, but nonprotective, RHD-like virus is present, as has been suggested by Marchandeau et al. (2005).

The impact of RHD is thought to be related to climatic conditions (reviewed in Cooke & Fenner [2002]), and in Iberian populations, recovery after the initial spread of the disease seems to be better in populations located in the most suitable habitats (Villafuerte et al. 1995). Both observations are in agreement with the predictions of my model because the latter suggests that the long-term impact of RHD is conditioned by population dynamics, which are determined by habitat suitability and, therefore, partially by climatic conditions. Thus, the impact of this disease is lower in populations located in the most suitable habitats.

Currently, however, rabbit distribution and abundance show a high variability between and within habitats in the Iberian Peninsula (Virgós et al. 2003; Calvete et al. 2004*a*). A higher initial impact of RHD has been frequently associated with higher rabbit population densities before the arrival of the disease (Henzell et al. 2002; Parkes et al. 2002; Story et al. 2004) because high densities of susceptible rabbits favored the transmission of the virus. This fact, combined with long-term population trends predicted by the model and the long-term effects of factors not associated with habitat, such as hunting pressure (Calvete et al. 2005) or stochastic events such as flooding (Palomares 2003), may explain why, 15 years after the initial spread of RHD, many populations have not yet reached equilibrium with this disease, resulting in the high variability currently observed in rabbit populations. In addition, the marked intra- and interyear variations in rabbit population dynamics may increase this observed variability even more.

Regarding RHD outcomes, my model predicted that, at equilibrium, there will be a range of populations at medium rabbit density in which RHD will exhibit different disease dynamics with no correlation between observed rabbit density in the presence of the disease and RHD outcomes such as RHD mortality, antibody prevalence, and mean age at infection. Only in populations at low or high densities will the parameters of the disease be similar in populations with similar rabbit density. Given the simplistic nature of this modeling approach, however, the exact values obtained from the model cannot be used as management rules to determine the carrying capacity of a habitat or the population density at which the impact of RHD will decrease and cannot determine the exact correspondence between RHD parameters such as antibody prevalence, RHD mortality, and mean age at infection. The continuous nature of the model prevented us from calculating the effect of the RHD virus dying out at low rabbit density. In addition the model made several crucial assumptions in regard to RHD epidemiology, especially with respect to the virus transmission rate, and further research will be needed to estimate the true contact infection rate, its variations during the year, and its

relationships to population density, social structure, and habitat composition (White et al. 2003) because RHD dynamics seemed to be highly dependent on this parameter.

Despite the simplicity of the model, however, several key points can be derived. The first is that the impact of RHD may be substantially decreased by managing rabbit populations and RHD dynamics, primarily by increasing the carrying capacity of the habitat and the productivity of rabbit populations in those areas where climatic and soil conditions are favorable for the species. That is, the long-term stable recovery or promotion of rabbit populations should be mainly based on improving habitat suitability, not just on management tools with temporal effects, such as vaccination campaigns or translocations. Another key point is that when low density populations show an increase in density, the impact of RHD can increase substantially before populations reach a density at which the impact of the disease begins to decrease. During this transitional process, rabbit population density may again decline, so that interactions with events affecting non-RHD mortality, such as flooding, hunting pressure, predation impact or myxomatosis, may slow its recovery or even favor the practical extinction of rabbit populations.

Reddiex et al. (2002) found that predation, in combination with RHD, reduces rabbit populations to low levels; thus the predicted increased impact of RHD at low to medium densities may enhance the probability that rabbit populations fall into "predator pit" dynamics, with rabbit populations being maintained at low densities by predators (Trout & Tittensor 1989; Pech et al. 1995). This may be the reason many rabbit populations located in suitable habitats have died out or remain at low densities. Moreover, high-density populations are often located in small areas, and their geographical expansion is slow. Increased RHD impact on the periphery of populations, where rabbit density is lower, and its interaction with predation may decrease the spatial growth of populations.

Moreover, the use of management strategies such as vaccination campaigns or especially rabbit translocations, without an increase in habitat carrying capacity, may result in a temporary increase of rabbit density but may cause a temporal increase in RHD impact on native rabbit populations. Thus the repeated use of these strategies alone may be more harmful than beneficial. The results of my model suggest that habitat improvement alone should allow rabbit populations to reach a density at which the impact of RHD decreases. After the spread of RHD the highest rabbit densities are usually located in agricultural landscapes, mainly devoted to farming Gramineas (Chapuis & Gaudin 1995; Virgós et al. 2003; Calvete et al. 2004*a*). Conservation programs for rabbits and endangered predators, however, primarily consist of scrub management to create natural pasture areas or creation of crops that are cultivated only once (Angulo 2003; Angulo et al. 2004). These management practices may be insufficient for long-term increases in habitat carrying capacity and population productivity to reach a population density at which RHD impact decreases. Thus current habitat management practices in many conservation programs may have little effect on promoting rabbit populations or may even yield negative population growth rates.

In addition, changes in habitat structure may affect the spatial and social organization of rabbits and therefore the transmission process of the RHD virus (White et al. 2003). Thus, future research should be aimed at determining the association between habitat improvement and RHD impact and evaluating the effectiveness of the combined application of habitat management with other management strategies such as predator control, vaccination campaigns, and translocations.

Until these matters are assessed, my model results suggest that habitat management strategies in conservation programs should be aimed at increasing habitat carrying capacity and rabbit population productivity to the maximum possible levels, perhaps by replicating the landscape structure of traditional agricultural systems. These strategies necessitate the establishment of long-term programs and funding to sustain habitat quality for long periods of time. In addition, conservation programs should include strategies to conserve rabbit populations that have currently reached high densities in equilibrium with RHD because, following the outcomes of the model, the decrease in rabbit density caused by hunting pressure or overharvesting, leading to the translocation of rabbits to areas of low population density, may increase the impact of RHD and reduce rabbit population density even further.

Acknowledgments

Literature Cited

Angulo, E. 2003. Factores que afectan a la distribución y abundancia del conejo en Andalucía. Ph.D. thesis. Complutense University, Madrid (in Spanish).

Angulo, E., C. Calvete, S. Cabezas, and R. Villafuerte. 2004. Scrub management and rabbit translocations at Doñana National Park: long and short-term effectiveness. 2nd world lagomorph conference. Research Center in Biodiversity and Genetic Resources of the University of Porto (CIBIO/UP), Vairao, Portugal.

Argüello, J. L., A. Llanos, and L. I. Pérez. 1988. Enfermedad hemorrágica del conejo en España. Medicina Veterinaria **5:**645–50 (in Spanish).

Barlow, N. D., and J. M. Kean. 1998. Simple models for the impact of rabbit calicivirus disease (RCD) on Australasian rabbits. Ecological Modeling **109:**225–241.

Barlow, N. D., M. C. Barron, and J. Parkes. 2002. Rabbit haemorrhagic disease in New Zealand: field test of a disease-host model. Wildlife Research **29:**649–653.

Calvete, C., and R. Estrada. 2000. Epidemiología de enfermedad hemorrágica (VHD) y mixomatosis en el conejo silvestre en el valle medio del Ebro. Herramientas de gestión. Consejo de protección de la naturaleza en Aragón, Zaragoza, Spain (in Spanish).

Calvete, C., and R. Estrada. 2004. Short-term survival and dispersal of translocated European wild rabbits: improving the release protocol. Biological Conservation **120:**507–516.

Calvete, C., E. Angulo, and R. Estrada. 2005. Conservation of European wild rabbit populations when hunting is age and sex selective. Biological Conservation **121:**623–634.

Calvete, C., R. Estrada, E. Angulo, and S. Cabezas-Ruiz. 2004*a*. Habitat factors related to wild rabbit conservation in an agricultural landscape. Landscape Ecology **19:**533–544.

Calvete, C., R. Estrada, J. Lucientes, J. J. Osácar, and R. Villafuerte. 2004*b*. Effects of vaccination against viral haemorrhagic disease and myxomatosis on long-term mortality rates of European wild rabbits. Veterinary Record **155:**388–392.

Calvete, C., R. Estrada, R. Villafuerte, J. J. Osácar, and J. Lucientes. 2002. Epidemiology of viral haemorrhagic disease and myxomatosis in a free-living population of wild rabbits. Veterinary Record **150:**776–782.

Capucci, L., P. Fusi, A. Lavazza, M. L. Pacciarini, and C. Rossi. 1996. Detection and preliminary characterization of a new rabbit calicivirus related to rabbit hemorrhagic disease virus but nonpathogenic. Journal of Virology **70:**8614–8623.

Chapuis, J. L., and J. C. Gaudin. 1995. Utilisation des resources trophiques par le lapin de garenne (*Oryctolagus cuniculus*) en garrigue sèche aménagée. Gibier Faune Sauvage **12:**213–230 (in French).

Cooke, B. D., and F. Fenner. 2002. Rabbit haemorrhagic disease and the biological control of wild rabbits, *Oryctolagus cuniculus*, in Australia and New Zealand. Wildlife Research **29:**689–706.

Delibes, M., and J. Calderón. 1979. Datos sobre la reproducción del conejo, *Oryctolagus cuniculus* (L.), en Doñana, S.O. de España, durante un año seco. Doñana, Acta Vertebrata **6:**91–99 (in Spanish).

Fa, J. E., C. M. Sharples, and D. J. Bell. 1999. Habitat correlates of European rabbit (*Oryctolagus cuniculus*) distribution after the spread of RVHD in Cádiz Province, Spain. Journal of Zoology **249:**83–96.

Fa, J. E., C. M. Sharples, D. J. Bell, and D. DeAngelis. 2001. An individual-based model of rabbit viral haemorrhagic disease in European wild rabbits (*Oryctolagus cuniculus*). Ecological Modeling **144:**121–138.

Ferrer, M., and J. Negro. 2004. The near extinction of two large European predators: super specialists pay a price. Conservation Biology **18:**344–349.

Gibb, J. A. 1993. Sociality, time and space in a sparse population of rabbits (*Oryctolagus cuniculus*). Journal of Zoology **229:**581–607.

Henzell, R. P., R. B. Cunningham, and H. M. Neave. 2002. Factors affecting the survival of Australian wild rabbits exposed to rabbit haemorrhagic disease. Wildlife Research **29:**523–542.

Hesterbeek, J. A. P., and M. G. Roberts. 1995. Mathematical models for microparasites of wildlife. Pages 90–122 in B. T. Grenfell and A. P. Dobson, editors. Ecology of infectious diseases in natural populations. Cambridge University Press, Cambridge, United Kingdom.

Jong, M., O. Diekmann, and H. Heesterbeek. 1995. How does transmission of infection depend on population size? Pages 84–94 in D. Mollison, editor. Epidemic models: their structure and relation to data. Cambridge University Press, Cambridge, United Kingdom.

Kunkele, J., and D. Von Holst. 1996. Natal dispersal in the European wild rabbit. Animal Behaviour **51:**1047–1059.

Marchandeau, S., G. Le Gall-Reculé, S. Bertagnoli, J. Aubineau, G. Botti, and A. Lavazza. 2005. Serological evidence for a non-protective RHDV-like virus. Veterinary Research **36:**53–62.

Moreno, S., and R. Villafuerte. 1995. Traditional management of scrubland for the conservation of rabbits *Oryctolagus cuniculus* and their predators in Doñana National Park, Spain. Biological Conservation **73:**81–85.

Moss, S. R., S. L. Turner, R. C. Trout, P. J. White, P. J. Hudson, A. Desai, M. Armesto, N. L. Forrester, and E.A. Gould. 2002. Molecular epidemiology of rabbit haemorrhagic disease virus. Journal of General Virology **83:**2461–2467.

Mutze, G., B. Cooke, and P. Alexander. 1998. The initial impact of rabbit hemorrhagic disease on European rabbit populations in South Australia. Journal of Wildlife Diseases **34:**221–227.

Myers, K., and W. E. Poole. 1959. A study of the biology of the wild rabbit, *Oryctolagus cuniculus* (L.), in confined populations. I. The effects of density on home range and the formation of breeding groups. CSIRO Wildlife Research **4:**14–26.

Myers, K., and W. E. Poole. 1961. A study of the biology of the wild rabbit, *Oryctolagus cuniculus* (L.), in confined populations. II. The effects of season and populations increase on behaviour. CSIRO Wildlife Research **6:**1–41.

Myers, K., I. Parer, D. Wood, and B. D. Cooke. 1994. The rabbit in Australia. Pages 108–157 in H. V. Thompson and C. M. King, editors. The European rabbit. The history and biology of a successful colonizer. Oxford University Press, New York.

Palomares, F. 2003. The negative impact of heavy rains on the abundance of a Mediterranean population of European rabbits. Mammalian Biology **68:**224–234.

Parkes, J. P., G. L. Norbury, R. P. Heyward, and G. Sullivan. 2002. Epidemiology of rabbit haemorrhagic disease (RHD) in the South Island, New Zealand, 1997–2001. Wildlife Research **29:**543–555.

Pech, R. P., A. R. E. Sinclair, and A. E. Newsome. 1995. Predation models for primary and secondary prey species. Wildlife Research **22:**55–64.

Reddiex, B., G. J. Hickling, G. L. Norbury, and C. M. Frampton. 2002. Effects of predation and rabbit haemorrhagic disease on population dynamics of rabbits (*Oryctolagus cuniculus*) in North Canterbury, New Zealand. Wildlife Research **29:**627–633.

Robinson, A. J., P. T. M. So, W. J. Müller, B. D. Cooke, and L. Capucci. 2002. Statistical models for the effect of age and maternal antibodies on the development of rabbit haemorrhagic disease in Australian wild rabbits. Wildlife Research **29:**663–671.

Rogers, P. M., C. P. Arthur, and R. C. Soriguer. 1994. The rabbit in continental Europe. Pages 22–63 in H. V. Thompson and C. M. King, editors. The European rabbit. The history and biology of a successful colonizer. Oxford University Press, New York.

Shien, J. H., H. K. Shieh, and L. H. Lee. 2000. Experimental infections of rabbits with rabbit haemorrhagic disease virus monitored by polymerase chain reaction. Research in Veterinary Science **68:**255–259.

Soriguer, R. C. 1981. Biología y dinámica de una población de conejos (*Oryctolagus cuniculus*, L.) de Andalucía Occidental. Doñana, Acta Vertebrata **8:**1–378 (in Spanish).

Story, G., D. Berman, R. Palmer, and J. Scanlan. 2004. The impact of rabbit haemorrhagic disease on wild rabbit (*Oryctolagus cuniculus*) populations in Queensland. Wildlife Research **31:**183–193.

Taylor, R. H., and R. M. Williams. 1956. The use of pellet counts for estimating the density of populations of the wild rabbits, *Oryctolagus cuniculus* (L.). New Zealand Journal of Science and Technology **38:**236–256.

Trout, R. C., and A. M. Tittensor. 1989. Can predators regulate wild rabbit *Oryctolagus cuniculus* population densities in England and Wales? Mammal Review **19:**153–173.

Villafuerte, R., A. Lazo, and S. Moreno. 1997. Influence of food abundance and quality on rabbit fluctuations: conservation and management implications in Doñana National Park (SW Spain). Terre et la Vie-Revue d'Ecologie Apliquee **52:**345–355.

Villafuerte, R., C. Calvete, J. C. Blanco, and J. Lucientes. 1995. Incidence of viral hemorrhagic disease in wild rabbit populations in Spain. Mammalia **59:**651–659.

Villafuerte, R., C. Calvete, C. Gortazar, and S. Moreno. 1994. First epizootic of rabbit hemorrhagic disease in free living populations of *Oryctolagus cuniculus* at Doñana National Park, Spain. Journal of Wildlife Diseases **30:**176–179.

Virgós, E., S. Cabezas-Díaz, A. Malo, J. Lozano, and D. López-Huertas. 2003. Factors shaping European rabbit abundance in continuous and fragmented populations of central Spain. Acta Theriologica **48:**113–122.

Wheeler, S. H., and D. R. King. 1985. The European rabbit in Southwestern Australia. III. Survival. Australian Wildlife Research **12:**213–225.

White P. C. L., G. Newton-Cross, M. Gray, R. Ashford, C. White, and G. Saunders. 2003. Spatial interactions and habitat use of rabbits on pasture and implications for the spread of rabbit haemorrhagic disease in New South Wales. Wildlife Research **30:**49–58.

White, P. J., R. A. Norman, and P. J. Hudson. 2002. Epidemiological consequences of a pathogen having both virulent and avirulent modes of transmission: the case of rabbit haemorrhagic disease virus. Epidemiology and Infection **129:**665–677.

White, P. J., R. A. Norman, R. C. Trout, E. A. Gould, and P. J. Hudson. 2001. The emergence of rabbit haemorrhagic disease virus: will a non-pathogenic strain protect the UK? Philosophical Transactions of Royal Society of London Series B **356:**1087–1095.

Xu, Z. J., and W. X. Chen. 1989. Viral haemorrhagic disease in rabbits: a review. Veterinary Research Communications **13:**205–212.