
Modelling brucellosis in a heterogeneous wild population of Alpine ibex (*Capra ibex*)

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Résumé

Ecological characteristics of the host are important drivers of pathogen spread and persistence in wild populations. If the complex interplay between host ecology and pathogen dynamics is not accounted for, naïve management strategies can have counter-intuitive effects. For instance, by interacting with density-dependent parameters such as survival and fertility rates [1] or with spatial heterogeneity [2], management may increase the number of susceptible hosts and thus promote pathogen transmission.

While France is officially free of brucellosis since 2005, one cattle herd infected with *Brucella melitensis* was detected in 2012 in the French Alps (Bargy massif). This outbreak probably originated from the local Alpine ibex population [3], in which high seroprevalences have been found since then (38 % in 2012-2013) [4]. This is the first case of *B. melitensis* persistence in European wildlife. In this context, a modelling approach is relevant to investigate the plausibility of different routes of transmission of *Brucella* within this population and to identify ecological factors influencing the persistence of *B. melitensis* in this population, in order to evaluate various management strategies.

A stochastic individual-based model was developed in 2014-2015 [5,6]. This model integrated several ecological characteristics of the Alpine ibex population of the Bargy massif, such as density-dependent demographic processes, seasonality of mating and births periods, characteristics of male behaviour during mating and changes in contact structure due to social segregation. The main hypothesis of the model was that, except for those factors,

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the contacts were homogeneous inside this closed population. However, new data are not in agreement with this hypothesis but suggest spatial as well as individual heterogeneity [7,8].

Here, we present and discuss the possible ways to incorporate these heterogeneities in the model. The first source of heterogeneity is in space use, especially among females, which is related to marked differences in seroprevalence [7] and could be accounted for using metapopulation, lattice or network models. The second source of heterogeneity is concerning both susceptibility and excretion, due to age and immunogenetic factors [8]. This model will then be numerically implemented and used to better understand transmission processes in the population and to evaluate management strategies.

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Mots-Clés: stochastic epidemiological modelling, Alpine ibex, *Brucella melitensis*, spatial model, wildlife disease