

Influence of Small Ruminant Lentivirus infection on the replacement rate in goat breeding.

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Small ruminant lentiviruses (SRLVs) represent a very heterogeneous group of viruses infecting goats and sheep. Based on a limited number of complete sequences, they were initially described as two distinct genetic groups evolving independently in sheep or goats, with the ovine strains being closely related to each other and distinct from the caprine ones. Over the past two decades, the description and phylogenetic analysis of many partial or complete sequences of caprine and ovine field isolated from various geographical regions have clearly highlighted the existence of a genetic continuum, with viruses that did not simply cluster according to the animal species they were isolated from. To date, SRLVs have been classified into five genotypes. With the exception of genotypes C, D and E, which seem to be geographically restricted to limited areas, genotypes A and B have been described worldwide with well-known associated diseases. They are characterized by the extreme slowness caused by the long incubation period. The symptoms are not immediately evident: they include arthritis, pneumonia, mastitis, and encephalitis or encephalomyelitis.

The pathology affects dairy breeds and leads to economic losses because of the decreasing in milk production of infected animals. No vaccine is available to prevent the insurgence of this pathology. In order to prevent the spread of the virus it is necessary to apply different control measures. One of the most used techniques, named “test-and-slaughter”, consists in selecting infected goats and directly slaughter them. This method represents a way to eradicate a virus but it can be used only if the infection prevalence is sufficiently low, allowing the survival of the flock. Among the five genotypes, the genotype B is the agent of the Caprine Arthritis Encephalitis in goats, also known as CAEV, firstly reported in 1974. Genotype B lentivirus, known to be pathogenic, could be transmitted in a vertical way from mother to offspring through the colostrum or the milk. Moreover, genotype B can be also transmitted horizontally, through the blood or the saliva of adult infected goats.

In this work we propose a basic demographic model together with several epidemiological models related to goat breeding, in order to study the fluctuations in goat populations of CAE infected breedings. We formulate our descriptions as compartmental models, with the population under study being divided into three compartments (susceptible, asymptomatic and symptomatic infected goats) and with assumptions on the nature and transfer rate from one compartment to another.

The independent variable in our compartment models is time (t). The transfer rates between compartments are expressed mathematically as derivatives of the compartments sizes with respect to time. As a results our models are formulated as a system of ordinary differential equations. A first model is derived to describe the dynamics of the breeding in absence of the infectious agent. This allows us to focus on the estimation of the replacement rate of the breeding, as a function of its different standard parameters: the reproduction rate and the mortality or goat removal rate. Then, we formulate a model where the goat breeding is infected by CAEV. Here, both vertical and horizontal transmission routes are considered, together with an eradication policy where newborns are separated from their mothers in order to avoid or at least reduce the vertical pathogen transmission. The study of this system leads to the formulation of the replacement rate as a function of both the demographic and epidemiological parameters. It is the replacement rate that the breeder should adopt to maintain the goat population size constant in his farm.

These systems are a first step in modeling breeding management in presence of a SRLV infection. Future work will try to model goat breedings with a coinfection caused by two different strains of lentivirus, as the B and E genotypes. This case study is particularly intriguing, as goats could be coinfecting without manifesting any symptom. Thus, we expect the model to draw a scenario where the symptomatic infected population vanishes through time, and the effect of the infectious agent on the replacement rate disappears. Such a behavior would support the thesis under investigation that genotype E, thanks to its biological properties, could represent a naturally attenuated vaccine for the SRLV genotype B infection.