Assessing classical swine fever control measures under uncertain viral constraints
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Classical Swine Fever (CSF) is a viral disease in wild boars (Sus scrofa) and domestic pigs causing huge economic impact on individual farmers and national economies. The management of the disease became even more complicated in the last decades due to endemicity in wild boar populations in several European countries. Huge effort is paid on CSF control in wild boar by oral mass vaccination, but few is known about the efficacy of the applied measures to control or eradicate the disease. Furthermore, virulence as a crucial parameter for disease dynamics varies widely between CSF virus strains and is highly uncertain. We implemented a spatially-explicit, individual-based wild boar population model, coupled with a CSF virus model on the level of individual traits. The model accounts for social behaviour of boar groups as well as individual variations in disease outcomes. Over a range of case mortality and duration of the infectious period (the virulence), we tested alternative spatial baiting strategies. We compared these scenarios regarding the performance of the management measured by final size of the infected area and long-term persistence. Our analysis showed that artificial immunisation can facilitate disease persistence under certain conditions. High success in virus eradication as well as prevention of disease spread was only possible with preventive vaccination in terms of baiting in front of the epidemic wave. Buffered vaccination was completely sufficient to exploit the effect of vaccination of the entire area, which translates strategic needs into a practical management plan. A buffer radius corresponding disease spread of one year revealed suitable to fully exploit the potential of oral mass vaccination. Although preventive baiting strategies are not yet implemented in the field due to EU legislation but with marker vaccines in sight, we recommend buffered baiting of the area with infected animals.

Epidemiology of subclinical salmonellosis in wild birds from NE Spain
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The epidemiology of subclinical salmonellosis in wild birds in a region of high Salmonella prevalence in pigs was studied. Three hundred and seventy nine fecal samples from 921 birds captured in 31 locations near pig premises and 431 (581 birds) from birds from 10 natural settings far from pig farms were analyzed for the presence of Salmonella spp. Positive samples were serotyped and antimicrobial resistance (AR) test performed. Phage typing and PFGE on isolates of S. Typhimurium were carried out. The prevalence of Salmonella positive samples was 1.85% (95%CI=0.93-2.77). A multivariable logistic regression, with observations clustered by site of capture, was used to determine major factors associated to prevalence of salmonellosis. Prevalence was positively associated with samples collected from birds in the proximity of a pig operation (OR=16.5; 95%CI=5.17, 52.65), and from non-migratory (or short distance migration) birds (OR=7.6; 95%CI=1.20, 48.04); and negatively related to mostly-granivorous birds (OR=0.4; 95%CI=0.15, 1.13). Typhimurium was the most prevalent serotype and 4 different XbaI PFGE patterns were detected that matched with the 4 phage types identified (U310, U311, DT164, DT56). The prevalence of multi-drug resistance was low (20%). In 3 farms a high degree of homogeneity among isolates from different birds was observed. These findings suggested that pig farms would facilitate the transmission of this infection among wild birds. The degree of bird congregation may have much to do on the infection transmission as phenotypic and genotypic relatedness among isolates from different birds were observed only in farms where abundant birds were seen.
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