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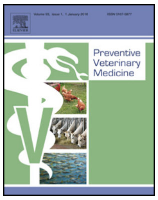

Analysis of spatio-temporal patterns of African swine fever cases in Russian wild boar does not reveal an endemic situation

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ABSTRACT

African swine fever (ASF) is a highly lethal viral disease of domestic pigs and wild boar. ASF was introduced into the southern Russian Federation in 2007 and is now reported to be spreading in populations of wild and domestic suids. An endemic situation in the local wild boar population would significantly complicate management of the disease in the livestock population. To date no sound method exists for identifying the characteristic pattern of an endemic situation, which describes infection persisting from generation to generation in the same population. To support urgent management decisions at the wildlife–livestock interface, a new algorithm was constructed to test the hypothesis of an endemic disease situation in wildlife on the basis of case reports. The approach described here uses spatial and temporal associations between observed diagnostic data to discriminate between endemic and non-endemic patterns of case occurrence. The algorithm was validated with data from an epidemiological simulation model and applied to ASF case data from southern Russia. Based on the algorithm and the diagnostic data available, the null hypothesis of an endemic situation of ASF in wild boar of the region was rejected.

1. Introduction

In recent reports on emerging livestock diseases wildlife were found to be involved in spreading the infection (Beltrán-Alcrudo et al., 2008; EFSA, 2012). The close link between domestic and wildlife populations, whether naturally or anthropogenically mediated, is well documented and gives rise to additional concerns (Bengis et al., 2002; Morgan et al., 2004). Such emergency situations demand a quick response and due to limited experience with the infection in the novel ecosystem, wild species are often considered a possible reservoir for the pathogen. Circulation of the infection in wildlife complicates disease control and requires extended disease management measures. Hence the earliest insight about the reservoir role of the involved wildlife populations can support better informed decision-making during contingency planning.

In the *epidemic* situation the resulting case pattern exhibits a wave of invasive infections travelling through the area of the naïve host population (e.g. Sayers et al., 1985; Craft et al., 2009; EFSA, 2009). An *endemic* situation is characterised by a qualitative change in the spatial pattern from epidemic waves to irregular local outbreaks with the infection persisting from year to year, between generations in

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the same population. In contrast to an epidemic situation and according to the proposed definition of endemicity, infections should be detected in sub-populations that were already previously infected.

Invasive spread through naïve wildlife host populations is usually well documented during the epidemic phase after pathogen introduction (e.g. EFSA, 2009). However, documentation efforts often weaken right when there is a high demand for forecasts to describe whether an introduced infection will die out or enter an endemic phase (e.g. EFSA, 2009). Despite the pressing need to improve our understanding of current disease situations, there is still no standardised approach for discriminating between endemic and epidemic situations. Consequently, the assessment of endemicity of an infection in a novel wildlife host population is primarily based on a longer duration of presence of the pathogen in the species, rather than on epidemiological reasoning.

A recent example was provided by the emergence of African swine fever (ASF) in Transcaucasia (Oganesyan et al., 2013). African swine fever virus (ASFV) originates from the African continent (Costard et al., 2009) and infects warthogs, bushpigs, wild boar and domestic pigs (Penrith et al., 2013). The disease causes up to 100% lethality in domestic pigs and wild boar (Gabriel et al., 2011; Blome et al., 2012), while warthogs do not develop clinical symptoms (Thomson et al., 1980). ASF is considered an endemic disease in most southern and eastern African countries, where the virus is maintained either in an ancient sylvatic cycle between warthogs and ticks of the *Ornithodoros moubata* complex or in a domestic cycle that involves pigs of local breeds, with or without tick involvement (Beltrán-Alcrudo et al., 2009; Penrith et al., 2009; Costard et al., 2013).

Recent emergence of the disease in the Caucasus region, Russia, Belarus, Ukraine and the EU (OIE, 2014) poses a threat to the European pig farming industry. The competence of arthropod vectors in the region is unknown (Beltrán-Alcrudo et al., 2008). Cases in wild boar were regularly reported and suitable control methods other than large-scale depopulation do not exist for ASF in wildlife populations (EFSA, 2010, 2014a). ASF turning into an endemic disease in wild boar population of southern Russia was recently discussed (EFSA, 2010, 2014b; Mur et al., 2012; Oganesyan et al., 2013).

Fig. 1 shows the progress of ASFV spread in southern Russia, highlighting observational reports in wild boar (OIE, 2014). The first case was detected in a wild boar in the Chechen Republic in November 2007 (blue in Fig. 1). From 2008 to 2010, ASF spread widely in the southern territories with cases reported in both wild boar and domestic pigs (Fig. 1). By June 2011, 189 cases had been reported from the southern territories, thereof 52 cases in free-ranging wild boars. Having case notifications for at least three consecutive years, the area would be considered ASF endemic (Khomenko et al., 2013).

Here we present a statistical approach for assessing the likelihood that endemic disease dynamics have led to the observed spatio-temporal structure in the diagnostic records. Our objective was to show that the data reported from South Russia was still compatible with epidemic spread, even though other sources stated that the situation had already become endemic.

2. Materials and methods

2.1. Concept

The idea behind the proposed test is based on a definition of disease endemicity which involves continued circulation and re-appearance in a previously affected area. These features contrast with an epidemic situation where a wave of infections sweeps through the naïve host population. According to the proposed endemicity definition, infections should be detected in previously infected sub-populations (spatially near to prior detection) and late enough after earlier detections to exclude relatedness (with a time-delay relative to prior detection).

If a case occurs in proximity to a previous case, but after a certain minimum time-span, it can be assumed to be unrelated to that previous case in the sense of epidemic spread. The case is then labelled as an ‘endemic case’ by the algorithm. The proportion of endemic cases can be compared between the original dataset and a number of simulated endemic datasets. The more the proportion of endemic cases deviates between the original data and the simulated data, the less likely it is that the null hypothesis is valid.

2.2. Test statistic

The test compares the proportion of ‘endemic cases’ between the original dataset and datasets simulated under the null hypothesis of an endemic situation. An endemic case is a case that occurs within a critical distance d_c around and at least a minimum critical time t_c after any previously detected case. The proportion of endemic cases is thus (Eq. (1)):

$$P_{end}(d_c, t_c) = \frac{1}{k}\sum_{i=n-k+1}^{n} A_i \quad \text{with}$$

$$A_i = \begin{cases} 1 \ \ if\ \ \exists\ \ j\in\{1,\ 2,\ \ldots,\ n\}:(d_{ij}<d_c\cap(t_i-t_j)>t_c) \\ 0 \ \ else \end{cases} \qquad (1)$$

Where n is the total number of cases, $k \le n$ specifies the number of data points included in the analysis, d_{ij} is the Euclidean distance between cases i and j, and t_i and t_j are the time points of cases i and j with $t_i \le t_{i+1}$.

The critical distance d_c represents a certain multiple of movement ranges of infected hosts while the critical time t_c represents the time required by the disease to cover that distance and within a circular area of radius d_c all infected hosts have finished their infectious period. This period is determined by individual disease courses. Within certain biological limits both parameters may comprise uncertainty and should be varied to calculate different values of P_{end}.

For every combination of t_c and d_c, the proportion of endemic cases P_{end} in the original data can be compared to the distribution of the proportion of endemic cases $\hat{P}_{end}$