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Spatio-temporal kriging analysis to identify the role of wild boar in the spread of African swine fever in the Russian Federation

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ABSTRACT

The current situation of African Swine Fever (ASF) epidemic in continental Europe represents a serious economic risk for the European pig industry. It is well known that both domestic pigs and wild boar are involved in the ASF spread, but the exact mechanism of the domestic–wildlife interface remains under research. A spatio-temporal kriging analysis was carried out to estimate the most possible source of infection (domestic pigs or wild boar) for 1,323 notifications of ASF reported in the Russian Federation (RF) from 2013 to 2017. Results for the whole period of study showed that domestic pigs and wild boar were the potential source of infection for 55% and 45% of notifications, respectively. The analysis stratified by year showed fluctuation in this tendency through time. At the early stages of the ASF epidemic in the Southern regions of the RF in 2007–2008 wild boar appears to be the main source of infection, while the following stage of the epidemic in 2009–2012 may be more related to a domestic source of infection. At the latter stage of the epidemic (2013–2017) both, domestic and wild boar, play a similar role as a source of the disease in the newly infected areas but differences by geographical locations can be observed

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matching with the epidemiology of the disease. This paper provides useful information for better understanding of the ASF mechanism and domestic–wildlife interactions in the RF and describes a new spatio-temporal approach that can be easily applied to other similar animal diseases with a domestic–wildlife interface.

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1. Introduction

One of the world's current major health concerns is the recent increase in the number of important infectious human and animal diseases. Over the last six decades the rate of disease emergence has increased (Cunningham et al., 2017). Wild animals have played an important part in this phenomenon as spreaders or reservoirs or new hosts of diseases that interact with domestic animals (Jakob-Hoff et al., 2014). For this reason, specific knowledge of the role of wild animals in the dynamic of diseases shared with livestock is necessary as a means of improving their control or prevention; this is best achieved through integrated veterinary medicine, animal management and ecological approaches. One Health is the term used, when approaches to tackling disease consider all components that might lead to, or increase, the threat of disease, including environmental and ecological/wildlife components as well as livestock and human factors (Cunningham et al., 2017).

An example of this interaction is the current epidemiological situation of African Swine Fever (ASF) in Europe. ASF is an infectious and notifiable swine disease, although the virus does not cause disease in humans, it has devastating consequences for the swine production sector on the economy. In 2007, ASF was reported in Georgia and has since spread to the Caucasian region and the Russian Federation (RF), where it is currently regarded as an endemic disease (EFSA, 2014). Over the past three years, the disease has been notified in nine other European countries: the Ukraine, Belarus, Poland, Lithuania, Latvia, Estonia, Moldavia, the Czech Republic, in wild boar, and in August 2017 in Romania in backyard pigs (WAHID, 2017: World Animal Health Information System). This continued advance of ASF through eastern European countries represents a threat for the rest of Europe.

Although the role of wild boar in the first stages of the spread of ASF in southern areas of the RF has been well described (Gulenkin et al., 2011; Gogin et al., 2013), its contribution in the subsequent years in which this disease spreads into more northerly areas is less clear. It has been suggested that it was first introduced into the RF by infected wild boar from the Caucasus region. Subsequent interaction at local level between wild boar and domestic pigs led to infection in pigs, facilitated by the common practice in the region of free-range pig farming (Gogin et al., 2013; Oganesyanyan et al., 2013). The rapid, long-distance spread of the disease as an epidemic has been associated with human-related factors, probably caused by commercial movements and the illegal trade in domestic pigs (Gogin et al., 2013; Sánchez-Vizcaíno and Arias, 2012). Despite some evidence indicating that wild boar do not play an important role in maintaining ASF (Laddomada et al., 1994; Mur et al., 2012; Costard et al., 2013; Iglesias et al., 2016; Vergne et al., 2017), the current situation in the European Union (EU) represents a different scenario. ASF introduction in most EU countries, as well as local spread within them have been associated with wild boar movements (Gallardo et al., 2015a; Bosch et al., 2017). Indeed, just over 95% of ASF cases have been reported in wild boar (WAHID, 2017) in the EU. The role of this host as an effective mechanism for ASF spread and a probable mechanism for introducing this disease into unaffected regions has been well documented in current and previous epidemics (Gogin et al., 2013; Sánchez-Vizcaíno and Arias, 2012; de la Torre et al., 2015; Iglesias et al., 2016). Therefore, more knowledge about how the disease interacts between wild boar and domestic pigs is still required, especially in areas where both populations can interact such as regions where backyard and free-range pig farming are common, i.e. such as in the southern RF (Gogin et al., 2013).

The objective of this work was to characterise the spatio-temporal patterns of the epidemic in wild boar and domestic pigs and quantify the exact role of wild boar in the current RF epidemic as ASF propagation mechanisms during 2007–1st of June 2017. The kriging prediction of date of ASF occurrence was modelled throughout the study area for wild boar and for domestic pigs separately,

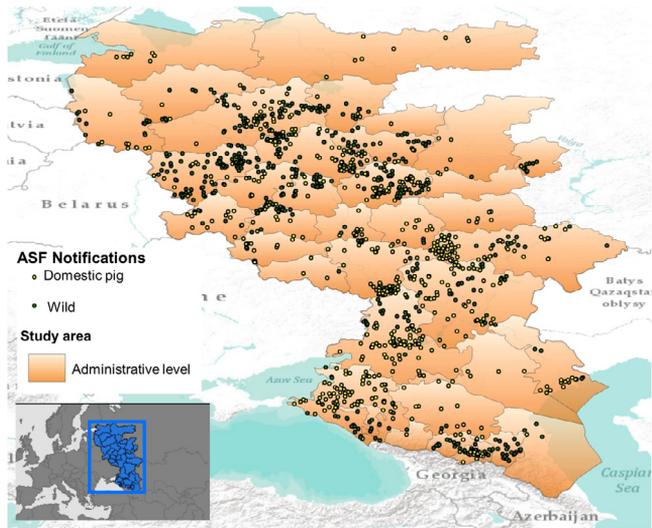


Fig. 1. ASF notifications in the Russian Federation in wild boar and domestic pigs in 2007–2017.

creating two prediction maps. Combination of both models assuming that the earlier date of notification in wild or domestic host could be interpreted as the potential source of infection allowed us to identify specie source of infection in areas over time. This will improve our understanding in quantifiable terms of the potential mechanisms of disease spread in Europe, and is a prerequisite for developing and focusing programmes for controlling or preventing the spread of ASF in this region, and for avoiding its economic consequences.

Previous analysis of this RF epidemic provided some insight into the pattern of ASF occurrence in space and time (Gulenkin et al., 2011; Gogin et al., 2013; Vergne et al., 2017). The spatio-temporal dependence of ASF between wild boar-to-domestic pig and farm-to-farm has been analysed in two of the most affected regions (Tver and Krasnodar) of the RF (Vergne et al., 2017) from 2008 to 2013. The paper here complements the previous one since: (1) It identifies not only the spatio-temporal dependence but also identifies which of either species represents the potential source of ASF infection; (2) Increases the study area to the whole ASF affected area of the RF; (3) Increases the study period from 2013 to 1st of June 2017.

2. Materials and methods

2.1. Study area and data source

The study area was the ASF-affected area of the RF (Fig. 1), in which 1323 notifications of ASF were reported between November 2007 and June 2017 (720 in domestic pig and 603 in wild boars). Data were obtained from the WAHID database (2017) and from the SRINRIVV-Russian Government information system. For each notification, the information related to the date, location (latitude, longitude) and affected species (domestic pig and wild boar) was included. ASF notifications were mapped using WGS84 projected coordinate system (ArcGIS 10.3 ESRI Inc. TM).

2.2. Geostatistical analysis of notifications in wild boar and domestic pigs: the kriging model

As is the case in many disease epidemics, detailed information from field investigations of the domestic-wildlife interface role of notifications outbreaks was unavailable. Thus, the potential source of infection (domestic pig or wild boar) for each ASF notification was indirectly estimated from the

dataset using geostatistical kriging analysis. Two spatio-temporal kriging analyses were carried out in both wild boar and domestic pig ASF notifications in the RF, creating two prediction maps. We assumed that the earlier date of notification in wild or domestic host could be interpreted as the potential source of infection in each cell.

The study area was rasterised into 10×10 km cells using WGS84 projected coordinate system and the date of the earliest ASF notification for either domestic pigs or wild boar was extracted for each cell. Universal kriging was used to interpolate the predicted date (day, referenced to 1/1/1900) of ASF notifications for both domestic pigs and wild boar throughout the study area. This geostatistical technique allows the interpolation of the spatial autocorrelation of the disease's progress, as well as the geographical trend of the predicted date, to be incorporated into the spatial prediction. The Universal Kriging model used was as follows:

$$Z(s_i) = \beta_0 f_0 + \beta_1 f_1(s_i) + \delta(s_i)$$

where $Z(s_i)$ is the predicted date at location s_i , β_0 and β_1 are the regression coefficients $f_0 \equiv 1, f_1(s_i)$ is the Y coordinate and $\delta(s_i)$ is a residual with spatial autocorrelation described through the variogram:

$$\gamma(h) = \frac{1}{2N(h)} \sum_{i=1}^{N(h)} (\delta(s_i) - \delta(s_i + h))^2$$

$\gamma(h)$ is the semivariance for the distance h and $N(h)$ are the number of pair of points located at a distance h ($s_i, s_i + h$). The sequential estimation of the generalised least-square residuals and the variance–covariance matrix proposed by Neuman and Jacobson (1984) were used for the variogram parameters and the simultaneous estimation of mean function coefficients (IRWLS method; Gotway and Stroup, 1997). Spatial autocorrelation was modelled using the spherical semi-variogram model for the predicted date of ASF notifications for both domestic pigs and wild boar. Cross-validation was used to check the fit of the models (Cressie, 2015). Universal kriging prediction at location s_0 was as follows:

$$p(Z, s_0) = \sum_{i=1}^n \lambda_i Z(s_i)$$

$$\sum_{i=1}^n \lambda_i f_j(s_i) = f_j(s_0) \quad j = 0, 1$$

The weights λ_i are estimated to minimise the prediction error providing unbiased predictions. $p(Z, s_0)$ is estimated for the pixels covering the study area to yield maps of the predicted date of ASF notifications for both domestic pigs and wild boar. Two kriging prediction maps of the date of ASF occurrence were modelled for wild boar and for domestic pigs separately. Then, the prediction dates from the wild boar map were subtracted from the prediction dates from the domestic pig map per cell, in order to identify the potential source of ASF in each cell (domestic pig or wild boar). Hence, negative cell values in the resulting map were considered to correspond to areas where the potential source of infection could be attributed to wild boar, while positive values were attributed to domestic pigs. The geostatistical analyses were conducted using MatLab[®] software developed by the authors, whilst ArcGIS 10.3 ESRI Inc. TM was used for the raster calculations and map drawings. Relationship between domestic pig and wild boar outbreaks and their potential sources of infection (domestic or wild) obtained from the model subtraction were described using a cross table, exploring if the frequency of the potential source of infection was similar for outbreaks occurring in wild boars and pigs.

The evolution of the disease was evaluated with the results obtained throughout the space and time describing the most relevant zones in each period. These most relevant zones (those that comprise 60% or represent a new area of spread of the disease) in 12-month period lags were represented as ellipses in the map. The epidemiological hypothesis of different authors related to the ASF wild boar–domestic pig interface and the disease evolution has been contrasted in each zone.

Table 1

Spherical variogram model parameters, trend function coefficients with their respective p-values and cross validation bias and root mean of the standardised squared errors (RMSEE) for the domestic pig and wild boar appearance date universal kriging models.

Model for appearance date (Day)	Nugget (Day ²)	Sill (Day ²)	Range (km)	b0	p-value b0	b1	p-value b1	Bias (Day)	RMSSE
Domestic	120 843	711 226	1390	37 725	0.27	0.5422	0.02	−2.47	0.88
Wild boar	24 844	604 872	1375	37 639	0.33	0.5904	0.02	−3.69	1.91

3. Results

The raster of the study area contains 82,731 grid cells, of which 638 and 525 have ASF notifications in domestic pigs and wild boar, respectively. The empirical semivariogram shows strong spatial autocorrelation for notification dates for both domestic pigs and wild boar, and increasing large-scale semi-variance representing the spatial trend. Fig. 2 shows the variogram model fitted (γ) to the residual variogram and the not detrended variograms and the linear combination $\gamma + (\sum(\beta_i * f_i))^2$. The difference between γ and the not detrended variogram indicates the variance linked to the geographical trend (Montes and Ledo, 2010).

The range of autocorrelation in the fitted spherical variogram was approximately 1400 km for the notification date in both models, whereas the nugget effect was greater for domestic pigs than for wild boar, which indicates greater spatial continuity in the spatial spread of the disease in the wild boar (Table 1). The kriging prediction bias was less than 3 days for domestic pig and less than 4 days for wild boar, while the root mean of the standardised squared errors was 0.88 in domestic pigs and 1.91 in wild boar (Table 1).

Subtractions of the two models were mapped (Fig. 3). The area in which the domestic pig was the likely source of ASF infection represents 1,177,445 km² (64%) of the total study area (1,841,230.6 km²) and the area in which the wild boar was identified as the potential source of infection represents 663,785 km² (36%).

The results of the model subtraction at each ASF notification allowed for the identification of the potential source of infection in each location. The description of the relationship of categories using a cross table showing that the probability of notification of an outbreak in domestic pig was 0.54 (720/1323) and in wild boar was 0.46 (603/1323). The probability that the potential source was domestic pig is very similar, 0.56 (735/1323), and the same occurs for wild boar as a potential source, 0.44 (588/1323). One could expect that a case in domestic pig would have domestic pig as its source of infection with a very high or at least higher probability (80%–100%) than if the source were wild boar. And the same would be expected in inverse proportions for wild boar. However, here, results show that the matches were $726/1323 = 56\%$, which is as close as one would expect to find by chance (~50%).

In the exploration of the ASF spatiotemporal evolution (Fig. 3) it is interesting to highlight that during 2008–2011 and 2016–2017 domestic pigs can be regarded as the main source of infection and wild boar during 2007 and 2015, however, from 2012 to 2014 both host played a similar role.

4. Discussion

Disease transmission mainly occurs over continuous time and space, especially in wild animals, and so the use of kriging techniques that exploit spatial autocorrelation can improve the accuracy of model predictions. The inclusion of the temporality of ASF notifications as a regionalised variable enables the spatio-temporal dynamics of the disease to be analysed. The approach used here to evaluate spatio-temporal information of notifications is justified given that: (1) notifications located close together in space and time are more likely to be interrelated than notifications located at distance in space and time and (2) local transmission of ASF has been identified as significant by different authors in Europe (Gallardo et al., 2015b; Bosch et al., 2017). Consequently, the kriging model could allow us to relate notifications and assume a high likely transmission between neighbouring notifications.

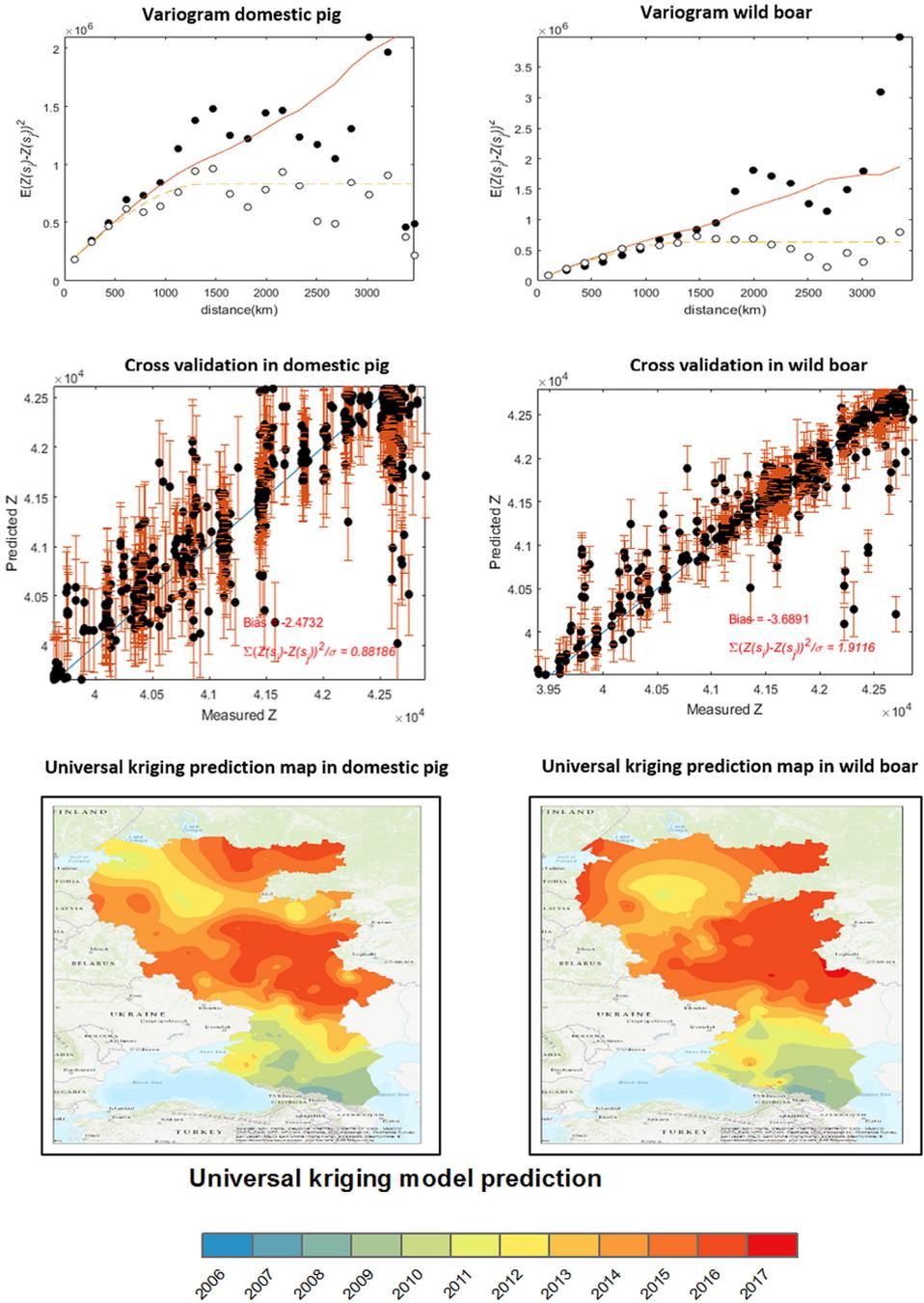


Fig. 2. Fitted theoretical variogram (orange line) vs. empirical semi variogram (black dots) combined to the variogram model γ (discontinuous line) fitted to the residual variogram (white dots) of the Universal kriging prediction maps for ASF notifications in domestic pig (top left) and wild boar (top right). Cross validation plots of kriging model in domestic pig (mid left) and wild boar (mid right). Universal kriging time prediction models in domestic pig (bottom left) and wild boar (bottom right). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

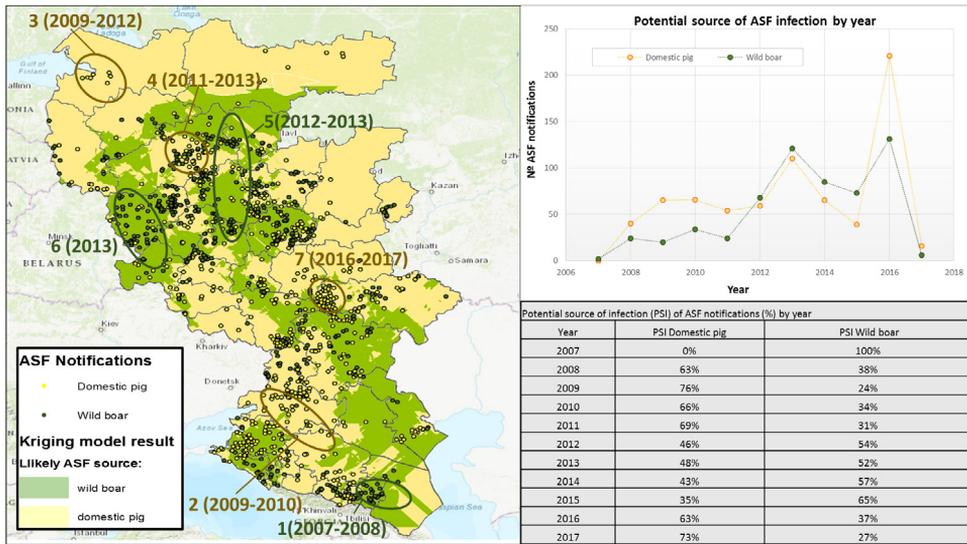


Fig. 3. The left panel shows the map of areas in which domestic pigs (yellow) or wild boar (green) were the potential source of ASF infection. Dots indicate ASF notifications in wild boar (green) and in domestic pig (yellow) from 2007 to 2017. Numbers and dates in brackets indicate zones of description of the evolution of the epidemic. The top right panel shows the graph comparing the results of the interpolation of the potential source of ASF infection in ASF notification by year (wild boar in green and domestic pigs in yellow). The bottom right table shows the percentages by year of the potential source of infection (domestic pig or wild boar) of ASF notifications as result of the interpolation of combining kriging models. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

The description analysis shows that most of the outbreaks were notified in domestic pig (54%) and that potential source of infection of most outbreaks was domestic pig (56%), indicating that domestic pig plays a higher role in the ASF spread in the RF than wild boar. However, a high interrelation between both hosts should be expected as wild boar was identified as the potential source of infection for 40% of domestic pig notifications and domestic pig was identified as the potential source of infection for 48% of wild boar notifications. Even if we evaluate coincidences between affected host (domestic or wild) and potential source of infection (domestic or wild), there is a large proportion of no coincidences (44%) which would be interpreted as a high connection between both populations and that the disease shows a behaviour as if it were a single population.

Accordingly, a positive feedback effect on virus circulation could be expected as has been previously suggested by other authors (Bosch et al., 2017). Additionally, results showed a greater spatial continuity in the spatial spread of the disease in wild boar than in domestic pigs, which could be explained due to the non-spatially structured variance of the disease related to long commercial movements in domestic pigs.

It means that wild boar should be considered a key factor in the ASF spread, specifically in areas with high density of free-range pigs overlapping with areas where wild boar are present (Gogin et al., 2013; Iglesias et al., 2016). This pattern has been specially observed on the southern border of the study area (Zone 1, Fig. 3), where the disease was introduced and started circulating in wildlife at the beginning of the epidemic (Oganesyanyan et al., 2013).

Stratification by year allowed to evaluate the differences between the role of domestic pig and wild boar in the ASF epidemic over time. Our results show that at the initial stage of the ASF epidemic in the RF (2007–2008) wild boar represented the potential source of infection for most of notifications (more than 70%, Fig. 3). This stage corresponds to the ASF introduction in the RF in November 2007 via contact with infected wild boar on the border with Georgia, and the subsequent spread through wild boar populations in the southern region of the RF around the Caucasus Mountains. Most of the

ASF notifications occurred in wild boar and were located in areas in which wild boar was identified as the potential source of infection (e.g. Zone 1, Fig. 3). The medium-to-high backyard pig density (Khomenko et al., 2013) in this area favoured the contact between the two species and subsequent disease transmission from wild boar to domestic pigs. From the end of 2008 to 2010, the ASF epidemic evolution was reversed. The disease remained limited to the southern study area where domestic pigs were the main potential source of infection (for more than 60% of notifications). It means that most of the ASF notifications occurred in domestic pigs and were located in areas where domestic pigs were identified as the potential source of infection (e.g. Zone 2, Fig. 3). During 2009 and 2011 ASF spread farther north by human movements (Gogin et al., 2013) creating two new zones in the northwest study area where domestic pigs were the main potential source of infection (Zone 3 and 4, Fig. 3). These results are consistent with the findings of Vergne et al. (2017) which suggest that the main driver of ASF infection in Krasnodar (southwest RF, including Zone 2) and Tver (Zone 4) was domestic pig. The main factors driving the spread of ASF by domestic pigs have been previously described (Gogin et al., 2013; Sánchez-Vizcaíno and Arias 2012), involving different sanitary, economic, environmental and sociological factors, among which the commercial movements or illegal trade of animals and infected meat are the most important. During 2012 and 2013, ASF spread in two new zones where wild boar was the main potential source of infection (Zones 5 and 6, Fig. 3). There, a low number of ASF notifications in domestic pig were reported, all of them in backyard farms (with the exception of an industrial farm in zone 5). In the latter stage of the epidemic (2013–2017) both species were equalised as potential sources of infection in new infected areas, with the exception of the spread of the disease in domestic pig in a new area (zone 7, Fig. 3), responsible for the spike in ASF notifications in 2016.

Differences in the timelines of reported notifications in domestic pigs and wild boars could represent a potential bias for the outcome of this study. It would be logical to expect to have timely reporting of notifications of ASF in domestic pigs because of the continuous monitoring based on clinical signs. In contrast, notifications in wild boars could go unnoticed in a system which does not apply active surveillance in all areas and relies on passive surveillance in some areas. Therefore, differences in the surveillance of hosts are likely to have partially influenced the results of this study, including a reporting bias derived from a variation in space and time of human behaviours reporting ASF (Vergne et al., 2014). However, the main objective here was to identify the potential source of infection in areas over time. Thus, the historical information on the temporal and spatial distribution of cases could be considered as a proxy that compensates this lack of information. However, further analysis should be considered including more information about differences in surveillance in wild boar to improve spatiotemporal analysis developed in wild boar populations.

The results show the role of wild boar as an effective mechanism for ASF spread and the probable mechanism for introducing ASF into new regions. Therefore, it seems important to emphasise that it is essential to control ASF in wild boar to prevent the spread of this infectious disease, especially in these areas of higher probability of effective contact in the domestic–wild interface. It is in this context that the concept of “One Health” and its new approaches are required to improve the prevention and control of animal diseases, especially in cases, such as ASF, which is emerging in new areas affecting both domestic and wildlife populations. ASF control strategies depend mainly on early disease detection followed by implementation of strict sanitary, because currently no vaccine or treatment exists (Gallardo et al., 2015a, b; Arias et al., 2017). Therefore, understanding the behaviour of the disease among both affected populations (wild boars and domestic pigs) is necessary to improve the only current means for the fight against the disease. The study here showed that the use of a kriging methodology applied to the temporality of notifications could provide a suitable new approach for evaluating and understanding the transmission of ASF between wildlife and livestock and could be easily applied in other similar infectious diseases in other areas.

5. Conclusions

This study shows, on one hand, the higher role of domestic pigs in ASF spread in the RF than wild boars, and, on the other hand, the high relation between both populations in the spread of ASF.

The differences in the role of both hosts during the evolution of the ASF epidemic showed that in the early stages wild boar was more likely a potential source of infection while in the later stages

of the epidemic in 2009–2012, ASF notifications were more related to a domestic source in several locations. However, in the latest stages of the epidemic (2013–2017) both populations seem to play a similar role as the source of the disease in new infected areas.

Kriging methodology has proved to be a useful tool in order to overcome the deficiencies in wildlife information allowing us to improve the understanding of the dynamics of diseases affecting the domestic–wild interface.

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