

Development of a Formula for Calculating the Probability of the Spread of African Swine Fever

Anatolij Kovalenko¹, Jana Mojžišová², Vasil Koziy³, Nataliia Kozii⁴, Boris Vojtek⁵, Anna Ondrejková⁶, Marián Prokeš⁷ and Monika Drážovská⁸

Abstract

Robust epidemiological knowledge and predictive modelling tools are needed to address challenging objectives forecasting epidemics. Often, multiple modelling approaches can be used during an epidemic to support effective decision making in a timely manner. A formula has been developed for calculating the probability of spreading african swine fever from infected animals of a threatened pig farm to other farms. The formula allows you to calculate the probability of an outbreak of infection for pigs of each of the pig farms located in the analyzed area. This takes into account the possible ways of spreading the pathogen in the presence of mechanisms and factors of transmission of african swine fever in real time.

Keywords: Epizootiology, African Swine Fever, Control Epizootic Situation, Formula Spread of ASF

INTRODUCTION

African swine fever (ASF) is caused by a large and complex virus affecting only domestic pigs and wild boar. The virus can be transmitted either directly, i.e. from animal to animal, or indirectly through contaminated objects, pork and other products. Humans are the most important factors for disease spread over long distances. After a short incubation period, the acute infection initially progresses with severe but unspecific general signs, i.e. high fever, depression and inappetence. In the final phase, bleeding, disorientation and seizures may occur. The mortality rate is very high (often >90%) (Sánchez-Vizcaíno et al., 2012). In countries where ASF is endemic, milder and chronic infections can occur. In these cases, the animals can survive the disease and recover after a long period of virus persistence (Blome et al., 2012).

Since 2007, African swine fever, that has its roots in a so-called sylvatic cycle in Africa, was introduced into Georgia. Subsequently, the virus spread in the Transcaucasian region and reached the Russian Federation (Gogin et al., 2013). From Russia, the virus moved on and entered the European Union in 2014. Currently, Germany, Lithuania, Estonia, Latvia, Bulgaria, Moldova, Poland, Romania, Serbia, Slovakia, Ukraine and Hungary are affected in the European region (Nurmoja et al., 2020). Outbreaks of ASF in wild boar in the Czech Republic and Belgium were successfully controlled. In the Germany has also been affected by ASF in wild boar (Rzymiski, 2020). The outbreak areas located along the Polish border in Brandenburg and Saxony. In addition, the disease also reached the world's largest pig producer, China, in August 2018 and is now spreading

¹ University of Veterinary Medicine and Pharmacy in Košice, Department of Epizootiology, Parasitology and Protection of One Health, Komenského 73, 041 81 Košice, Slovak Republic

² University of Veterinary Medicine and Pharmacy in Košice, Department of Epizootiology, Parasitology and Protection of One Health, Komenského 73, 041 81 Košice, Slovak Republic

³ Bila Tserkva National Agrarian University, School of Veterinary Medicine, 09100, Bila Tserkva, Kyiv region, Ukraine

⁴ Bila Tserkva National Agrarian University, School of Veterinary Medicine, 09100, Bila Tserkva, Kyiv region, Ukraine

⁵ University of Veterinary Medicine and Pharmacy in Košice, Department of Epizootiology, Parasitology and Protection of One Health, Komenského 73, 041 81 Košice, Slovak Republic

⁶ University of Veterinary Medicine and Pharmacy in Košice, Department of Epizootiology, Parasitology and Protection of One Health, Komenského 73, 041 81 Košice, Slovak Republic

⁷ University of Veterinary Medicine and Pharmacy in Košice, Department of Epizootiology, Parasitology and Protection of One Health, Komenského 73, 041 81 Košice, Slovak Republic

⁸ University of Veterinary Medicine and Pharmacy in Košice, Department of Epizootiology, Parasitology and Protection of One Health, Komenského 73, 041 81 Košice, Slovak Republic E-mail: monika.drazovska@uvlf.sk (Corresponding Author)

to various Asian countries (Sun et al., 2021). Most recently, Papua New Guinea on the doorstep of Australia, and India were also affected in 2020.

Mathematical epidemiological models are key decision support systems for policy and decision making in public health, as recently illustrated by the SARS-CoV-2 pandemic (McCabe and Donnelly, 2021), but also in animal health, with key examples on regulated diseases such as African swine fever (Hayes et al., 2021; Lange and Thulke, 2017), as well as on endemic diseases (Picault et al., 2022). In the absence of deterrents for the spread of ASF, this infectious disease can lead to the loss of the pig population not only on individual pig farms where epizootic foci of ASF are formed, but also lead to the loss of the entire pig population in the region or in the country. Moreover, due to its high resistance, it is often difficult to pinpoint ASF primary route of transmission which, in most cases, might be mediated by human activities rather than by contact with wild animals (Scientific Opinion on animal health risk mitigation treatments as regards imports of animal casings, 2012; EFSA, 2018; Zani et al., 2019). The spread of African swine fever poses a grave threat to the global swine industry. Without an available vaccine, understanding transmission dynamics is essential for designing effective prevention, surveillance, and intervention strategies. These dynamics can often be unraveled through mechanistic modelling (Hayes et al., 2021).

Based on the current epizootic situation regarding the spread of ASF, it can be concluded that the existing veterinary instructions do not fully protect pig farms from this infectious disease. There are additional factors and mechanisms that are not taken into account when organizing the biological protection of pig farms from the spread of infection (Bezymennyi et al., 2023).

Calculating the probability of transmission of ASF can enable pig farms to use additional information and software-analytical tools to make an objective assessment of potential threats, taking into account additional factors and mechanisms for the spread of ASF. Some of them are not considered by veterinary regulations. For example, the time of export of liquid organic fertilizers to the fields, precipitation and the presence of water bodies, where biomaterial containing the pathogen can accumulate and migration of wild boars and wild animals can be present, contributing to the spread of the pathogen from the epizootic focus (Filatov et al. 2018). Previously, the developments of English epidemiologists Anderson and May (1991) were taken as the basis for calculating the probability of the spread of infections. Although their research was carried out to assess the risks of the transmission of infectious diseases in human medicine, in our opinion, the achievements of these scientists are also used in veterinary medicine to calculate the risks of spreading ASF. The formula proposed by Anderson and May (1991) and Anderson and Britton (2000) and Anderson et al. (2004) took into account the number of foci of an infectious disease among people at a certain point of time, the number of settlements in a certain territory, taking into account the duration of incubation period. Initially, this formula was developed to calculate the probability of the spread of infectious diseases, which can be transmitted from person to person by airborne droplets; through direct contact with a sick person; through household items, clothing, water and food that infected people have come into contact with.

In this article we make an attempt to develop a formula for calculating the probability of the spread of ASF using the value of the probability of occurrence of new outbreaks of infection among people described by Anderson and May (1991).

METHODOLOGY

To calculate the probability of spread of ASF, objective spatial data obtained on the basis of aerial photography made using unmanned aerial vehicles (in real time), a database being created and geospatial layers on objects participating in the epizootic distribution chain of ASF, software modules for data management and algorithms were used to calculate the risks of spreading ASF from the source of its occurrence. To construct a formula for calculating the probability of spreading ASF, the value of the calculated probability was used (P). It should range from 0 to 100, where 0 is no chance of ASF transmission and 100 is 100% chance of ASF transmission. However, in this case, the calculated value of P should not take on the values 0 or 100, since in practice there is no unconditional guarantee of the protection of pigs from ASF on farms ($P=0$), and the inevitable infection of the livestock with ASF under any external threats ($P=100$). A P value was used that takes on a value of 100

only when ASF occurs on the relevant pig farm or when an ASF outbreak is simulated on the selected pig farm for the purpose of visualization and alerting users. At the same time, the value of $P=100$ is not calculated, but is assigned “forcibly” at the site of the ASF outbreak (threatened pig farm) for the period of maximum threat (2 weeks from the moment ASF was registered on the farm). The calculations took into account the spatio-temporal dependence of ASF transmission. When the target farm is closer in distance and time to the threatened pig farm, the higher the P value should be for it. We used real data on the features of the presence of various mechanisms and factors of ASF transmission during the development of the epizootic process and the influence of anthropogenic impacts and the environment.

RESULTS AND DISCUSSION

The probability of new foci of infection among people according to Anderson and May (1991) was calculated using the following formula:

$$P_{t+t_0} = 1 - (1 - R_0/N)Y_t, \quad (1)$$

P – the probability of new unfavorable points (ASF) appearing at a certain time ($t+t_0$);

t_0 – duration of the incubation period of the ASF (days);

R_0 – the base rate of infection in settlements (that is, how many new foci of infection appear during the incubation period from the time the first outbreak was recorded);

N – number of settlements in a given area;

Y_t – number of ASF outbreaks at a point in time (t).

Further, using the value of the probability of occurrence of new outbreaks of infection among people, these scientists proposed a calculation formula (2) for predicting the occurrence of new outbreaks of infection:

$$Y_{t+t_0} = P_{t+t_0} \times (N-1), \quad (2)$$

Y_{t+t_0} – number of outbreaks of infection, taking into account the incubation period;

P – probability of occurrence of new outbreaks of infection at a given time ($t+t_0$);

N – number of settlements in the study area.

For the most dangerous human infections, the average value was calculated R_0 , which is actually a reference value and is automatically substituted by epidemiologists to calculate the probability of new outbreaks of a particular infection.

Belik et al. (2009) conducted research to adapt the previous described (Anderson and May, 1991; Andersson and Britton, 2000; Anderson et al., 2004) formula in the analysis of the spread of ASF in the Russian Federation. The main problem faced by the researchers was the calculation of the R_0 value, which is unknown for most infectious animal diseases. To calculate the value of R_0 , an analysis was made of the distribution of the pig population in the area of interest. Knowing the official number of outbreaks of ASF, Belik et al. (2009) an experiment to simulate the dynamics of the spread of ASF in the study region, supposed that at the initial moment the virus was introduced and the outbreak was detected only in the territory of one settlement or one farm. When carrying out calculations, the main task was to select such a value of R_0 (the basic rate of spread of infection in pigs of pig farms (settlements), which could satisfactorily express the dynamics of the onset and spread of infection. In this case, the base rate of infection spread among pig farms (communities) shows the average number of occurrences of secondary outbreaks of ASF (farms). This is within the acceptable average incubation period for a single primary outbreak (farm). For a certain time interval, this value was determined as $R_0 = 1.7$. This numerical value has become the first approximation of this epizootological parameter in relation to ASF for a specific area. The application of the calculated value of $R_0 = 1.7$ was confirmed when an ASF outbreak occurred. As a result of an outbreak of ASF on the territory of two farms, within 14 days, ASF was registered a second time on the territory of three settlements located in different parts of the region, at a distance of 20-100 km from the primary outbreak. To assess the likely scale of the spread of ASF, the formula

(1) and the numerical value of $R_0 = 1.7$ were applied; number of ASF outbreaks at time (t), $Y_t=1$; the number of settlements in the region $N = 2478$.

The ratio was obtained:

$$P_{t+t_0} = 1 - (1 - 1.7/2478)^1 \approx 0,001$$

Thus, the probable maximum number of new outbreaks among pigs on farms at time $t + t_0$ from X_t free points was determined from the ratio:

$$Y_{t+t_0} = P_{t+t_0} \times (N - 1) = 0.001 \times 2477 = 2.477$$

That is, the researches expected the appearance of two to three (2.477) new outbreaks (unfavorable points) of ASF after one incubation period.

We consider that this formula can be used to predict ASF outbreaks.

Our studies in the ASF infection formula below (3) use approaches that reflect in the original formula Anderson and May (1980, 1982a, 1982b) and Anderson (1982), as well as Belik et al. (2009).

$$P = AN+Y * Rasf * 100\%, \quad (3)$$

P – probability of spread of ASF from the outbreak site (threatened pig farm - the source of the infectious agent) to the target farm;

$Rasf$ – an integral risk factor, which includes possible factors and mechanisms for the spread of ASF during the development of an epizootic;

$AN+Y$ – a factor of potential and actual threats of active infection, taking into account the impact of the number of pig farms (settlements with backyards where pigs are kept) and animals threatened by farms within a radius of 5 km from the target farm.

Formula (3) contains two factors, each of which is responsible for the corresponding set of factors. The first multiplier - the factor of active threats of possible infection $AN+Y$ characterizes the impact on pigs (target farm) of the number of potential and real objects of infection (pig breeding enterprises, including threatened farms, as well as settlements where the population keeps pigs), which are within a 5 km radius.

The factor of active threats contributing to infection $AN+Y$ is calculated as follows:

$$AN+Y = [1 - 1 / (N_5 + 10 * L_5 * T_5 + 1)], \quad (4)$$

$AN+Y$ – a factor of potential and actual threats of active infection, taking into account the influence of the number of pig farms (farms where pigs are kept) and, in particular, threatened farms within a radius of 5 km from the target farm;

N_5 – number of pig farms (settlements whose population keeps pigs) within a radius of 5 km from the target farm;

L_5 – distance to the pigs of the endangered farm located within a radius of 5 km of the target farm area;

T_5 – the time elapsed since the outbreak of ASF in pigs (on a threatened farm) that is within a 5 km radius of the target farm area.

The second multiplier, the integral risk factor ($Rasf$), characterizes the impact on pigs of the target farm of the factors and mechanisms of ASF transmission, discussed earlier in the Scheme of the biological cycle of the development of the ASF pathogen in natural and anthropogenic environmental conditions.

The integral risk factor $Rasf$ is calculated as follows:

$$Rasf = L * T + PH + FB + SOK5 + WR5 \quad (5)$$

$Rasf$ – an integral risk factor that includes the factors and mechanisms of ASF transmission during the development of an epizootic chain;

L – distance from the ASF outbreak site (threatened pig farm) to the pigs of the target farm;

PH – belonging of the target pig farm to the agricultural holding, which includes (threatened farm) - characterizes the intensity of transport communication;

FB – the presence of a food base for wild boars (crops of crops), within a radius of 5 km from the target pig farm, the appearance of wild boars (the presence of haulouts of wild boars) within a radius of 20 km from the target pig farm;

SOK5 – removal of liquid organic fertilizers from the lagoons of the threatened farm to fields located within a radius of 5 km from the target pig farm;

WR5 – the presence of water bodies located within a radius of 5 km from the target pig farm.

Thus, the formula for calculating the probability of ASF transmission from an ASF outbreak site (threatened pig farm) to other pig farms (P) is:

$$P = (1 - 1 / (N5 + 10 * L5 * T5 + 1)) * (L * T + PH + FB + SOK5 + WR 5) * 100\% \quad (6)$$

The developed formula for calculating the probability of ASF transmission from the site of an ASF outbreak (threatened pig farm) to other farms makes it possible to calculate the probability of an ASF outbreak for each of the pig farms located in the analyzed area taking into account the mechanisms and factors of transmission of this infection.

The first task to create a formula for calculating the probability of spreading ASF was to create objective databases of aerial photography, according to real-time unmanned aerial vehicles, a database of geographical spatial layers on the territory of pig farms. Software modules have been developed to manage data and algorithms for calculating the risks of the probability of spreading ASF from the source of its occurrence.

To solve the second problem, when formulating the formula for calculating the probability of the spread of ASF, the value of the calculated probability (P) was used.

The goal was achieved to build a model of the spatio-temporal dependence of the transmission of ASF, indicating that the closer in distance and time to the threatened pig farm is the target farm, the greater the P value for it should be. The team successfully solved the problem of creating a formula for calculating the probability of spread ASF using real databases of the veterinary service in the presence of mechanisms and factors of ASF transmission during the development of the epizootic process, taking into account the influence of anthropogenic factors and environmental climatic conditions.

In the current challenge, there was need for immediate real-time analysis and comparison of team-results, since this was a real swine health crisis.

Open international challenges in epizootology (ASF) are time-consuming and require a significant involvement of organising and participating teams. Yet, they demonstrate a great potential, because they contribute to improving the preparation of the scientific community for future infectious disease emergence events. In particular, the study of infectious diseases emerging at the interface between wildlife and livestock seems necessary in view of the increasing frequency of their occurrence and the dramatic economic consequences they may have.

CONCLUSION

With outbreaks across 18 European and 12 Asian nations, ASF has become established as an urgent threat to the global swine industry. The development and use of the formula for calculating the probability of transmission of ASF in the conditions of an unfavorable region for ASF may be a useful tool declining the incidence of the disease. The formula contributes to timely informing the veterinary service of pig farms about the threat of ASF for their farms. Ultimately, these calculations and information obtained from the application of this formula allow additional preventive measures to be taken on pig farms to protect them in order to prevent the occurrence and spread of ASF.

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REFERENCES

- Anderson, P. K., Cunningham, A. A., Patel, N. G., Morales, F. J., Epstein, P. R., & Daszak, P. (2004). Emerging infectious diseases of plants: pathogen pollution, climate change and agrotechnology drivers. *Trends in ecology & evolution*, 19(10), 535–544. <https://doi.org/10.1016/j.tree.2004.07.021>
- Anderson, R. M. (1982). Population dynamics of infectious diseases: theory and applications. London, UK: Chapman and Hall.
- Anderson, R. M., & May, R. M. (1980). Infectious diseases and population cycles of forest insects. *Science*, 210(4470), 658–661. <https://doi.org/10.1126/science.210.4470.658>
- Anderson, R. M., & May, R. M. (1982a). Coevolution of hosts and parasites. *Parasitology*, 85(2), 411–426. <https://doi.org/10.1017/s0031182000055360>
- Anderson, R. M. & May, R. M. (1982b). Population biology of infectious diseases. Berlin, Germany: Springer.
- Anderson, R. M., & May, R. M. (1991). Infectious disease of humans: dynamics and control. Oxford: Oxford University Press.
- Andersson, H., & Britton, T. (2000). Stochastic epidemic models and their statistical analysis. Springer: New York.
- Belik, E. V., Dudnikov, S. A., Lyadsky, M. M. (2009). Analysis of the risk of introduction and spread of African swine fever in the Vladimir region //: information and analytical review - Vladimir, RU, 97 p.
- Bezymennyi, M., Tarasov, O., Kyivska, G. V., Mezhenska, N. A., Mandyhra, S., Kovalenko, G., Sushko, M., Hudz, N., Skorokhod, S. V., Datsenko, R., Muzykina, L., Milton, E., Sapachova, M. A., Nychyk, S., Halka, I., Frant, M., Huettmann, F., Drown, D. M., Gerilovych, A., Mezhenskyi, A. A., ... Lange, C. E. (2023). Epidemiological Characterization of African Swine Fever Dynamics in Ukraine, 2012-2023. *Vaccines*, 11(7), 1145. <https://doi.org/10.3390/vaccines11071145>
- Blome, S., Gabriel, C., Dietze, K., Breithaupt, A., & Beer, M. (2012). High virulence of African swine fever virus caucasus isolate in European wild boars of all ages. *Emerging infectious diseases*, 18(4), 708. <https://doi.org/10.3201/eid1804.111813>
- European Food Safety Authority (EFSA), Boklund, A., Cay, B., Depner, K., Földi, Z., Guberti, V., Masiulis, M., Miteva, A., More, S., Olsevskis, E., Šatráň, P., Spiridon, M., Stahl, K., Thulke, H. H., Viltrop, A., Wozniakowski, G., Broglia, A., Cortinas Abrahantes, J., Dhollander, S., Gogin, A., ... Gortázar, C. (2018). Epidemiological analyses of African swine fever in the European Union (November 2017 until November 2018). *EFSA journal*. European Food Safety Authority, 16(11), e05494. <https://doi.org/10.2903/j.efsa.2018.5494>
- Filatov, S., Gerilovych, A., Stegnyy, B., Pérez de León, A. (2018). African Swine Fever Research in Ukraine: Spatio-temporal Epidemiological Analysis & Outbreak Risk Mapping, presented at the The 4th Global African Swine Fever Research Alliance (GARA) Workshop, Cagliari-Sardinia, Italy 11–13 April 2018.
- Gogin, A., Gerasimov, V., Malogolovkin, A., & Kolbasov, D. (2013). African swine fever in the North Caucasus region and the Russian Federation in years 2007-2012. *Virus research*, 173(1), 198–203. <https://doi.org/10.1016/j.virusres.2012.12.007>
- Hayes, B. H., Andraud, M., Salazar, L. G., Rose, N., & Vergne, T. (2021). Mechanistic modelling of African swine fever: A systematic review. *Preventive veterinary medicine*, 191, 105358. Advance online publication. <https://doi.org/10.1016/j.prevetmed.2021.105358>
- Lange, M., & Thulke, H. (2017). Elucidating transmission parameters of African swine fever through wild boar carcasses by combining spatio-temporal notification data and agent-based modelling. *Stochastic Environmental Research and Risk Assessment*, 31(2), 379–391. <https://doi.org/10.1007/s00477-016-1358-8>
- McCabe, R., & Donnelly, C. A. (2021). Disease transmission and control modelling at the science-policy interface. *Interface focus*, 11(6), 20210013. <https://doi.org/10.1098/rsfs.2021.0013>
- Nurmoja, I., Mötus, K., Kristian, M., Niine, T., Schulz, K., Depner, K., & Viltrop, A. (2020). Epidemiological analysis of the 2015-2017 African swine fever outbreaks in Estonia. *Preventive veterinary medicine*, 181, 104556. <https://doi.org/10.1016/j.prevetmed.2018.10.001>
- Picault, S., Vergne, T., Mancini, M., Bareille, S., & Ezanno, P. (2022). The African swine fever modelling challenge: Objectives, model description and synthetic data generation. *Epidemics*, 40, 100616. <https://doi.org/10.1016/j.epidem.2022.100616>
- Rzymiski, P. (2020). Wszystko, co Warto Wiedzieć o ASF i Sposobach na Zwalczenie Wirusa (Everything Worth Knowing about ASF and Ways to Fight the Virus). Available online: <https://www.polityka.pl/tygodnikpolityka/nauka/1778644,1,wszystko-co-warto-wiedziec-o-asf-i-sposobach-na-zwalczenie-wirusa.read> (accessed on 1 February 2020).
- Sánchez-Vizcaíno, J. M., Mur, L., & Martínez-López, B. (2012). African swine fever: an epidemiological update. *Transboundary and emerging diseases*, 59 Suppl 1, 27–35. <https://doi.org/10.1111/j.1865-1682.2011.01293.x>
- Scientific Opinion on animal health risk mitigation treatments as regards imports of animal casings. (2012). *EFSA Journal*, 10(7). <https://doi.org/10.2903/j.efsa.2012.2820>
- Sun, E., Huang, L., Zhang, X., Zhang, J., Shen, D., Zhang, Z., Wang, Z., Huo, H., Wang, W., Huangfu, H., Wang, W., Li, F., Liu, R., Sun, J., Tian, Z., Xia, W., Guan, Y., He, X., Zhu, Y., Zhao, D., ... Bu, Z. (2021). Genotype I African swine fever viruses emerged in domestic pigs in China and caused chronic infection. *Emerging microbes & infections*, 10(1), 2183–2193. <https://doi.org/10.1080/22221751.2021.1999779>

Zani, L., Dietze, K., Dimova, Z., Forth, J. H., Denev, D., Depner, K., & Alexandrov, T. (2019). African Swine Fever in a Bulgarian Backyard Farm-A Case Report. *Veterinary sciences*, 6(4), 94. <https://doi.org/10.3390/vetsci6040094>