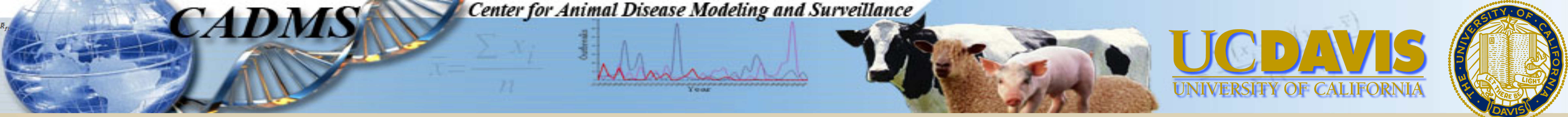

Evaluation of the magnitude and duration of potential African Swine Fever (ASF) epidemics in Bulgaria using a spatial and stochastic disease spread model (Be-FAST)

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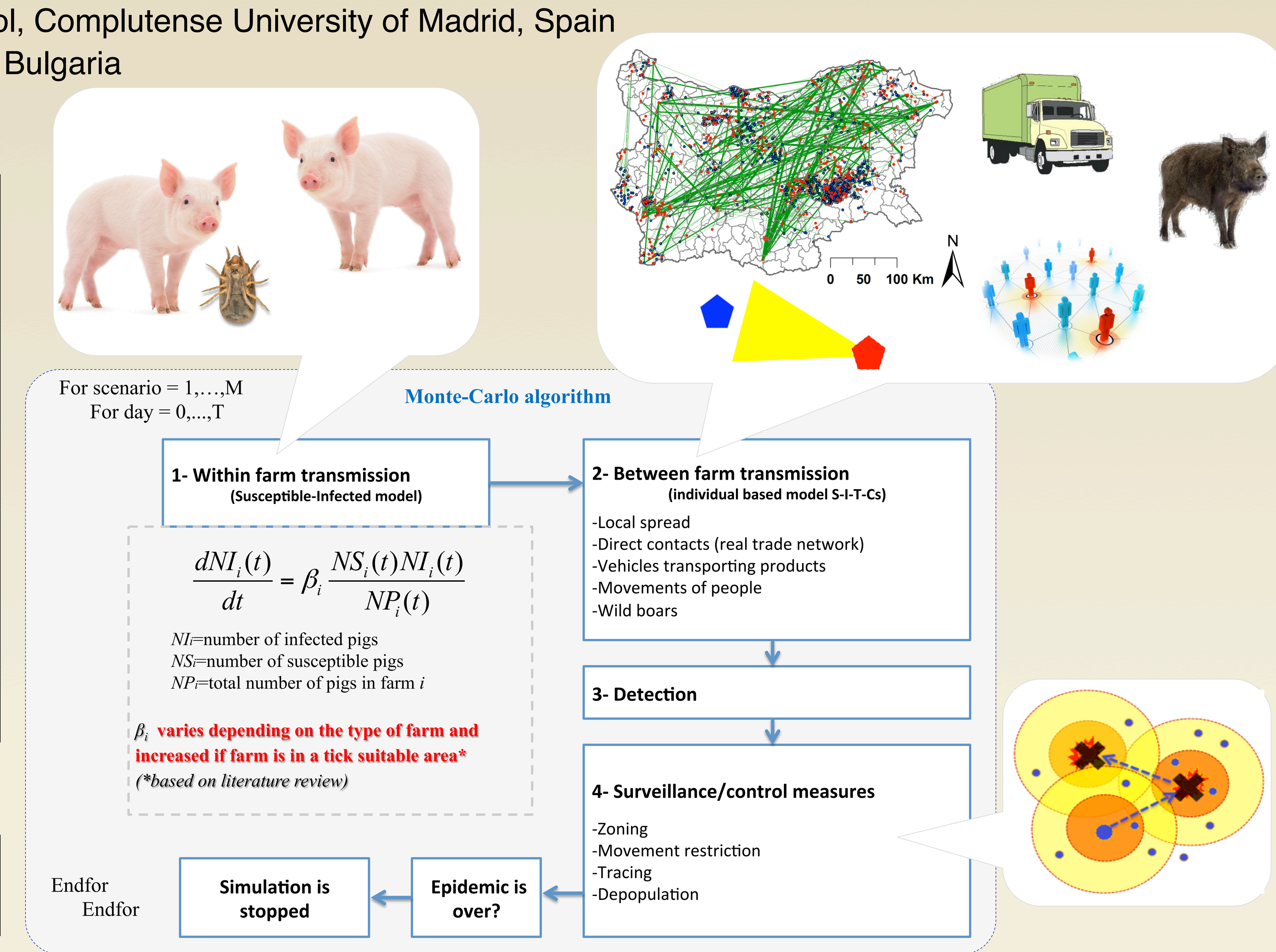
BACKGROUND

African swine fever (ASF) is one of the most important viral diseases affecting swine due to the severe sanitary and socioeconomic impact in the affected countries. ASF virus (ASFV) causes an acute hemorrhagic fever in domestic pigs and wild boar, with high mortalities and morbidities and for which no vaccine or treatment is currently available. Therefore options for preventing and rapidly controlling this OIE notifiable disease are limited to strict sanitary and biosecurity measures, early detection and stamping-out of infected animals[1]. The ASFV infection in the Caucasus region was primarily notified in 2007 in the Republic of Georgia, and rapid spread to Armenia, Russian Federation, Azerbaijan and even recently, infected cases has being reported in Ukraine (2012), Lithuania and Poland (2004)[2]. There are no published studies describing and quantifying aspects related to ASFV potential spread in Eastern European countries, where backyard pig production is predominant. Here, we focus on Bulgaria, which most (96%) of the farms are considered as backyard farms and for which detail information about pig farms and trade during 2011 and 2012 was available. Moreover, Bulgaria has been identified as a country with at risk of potential ASFV introduction by previous studies[3,4]. Model outcomes may be useful to inform decisions in the potential scenario that ASFV is introduced into the country.

OBJECTIVE

The ultimate goal of the present study was to evaluate the potential ASFV spread in a country where backyard pig farms are predominant using a stochastic and spatial disease spread model called Be-FAST[5,6,7].



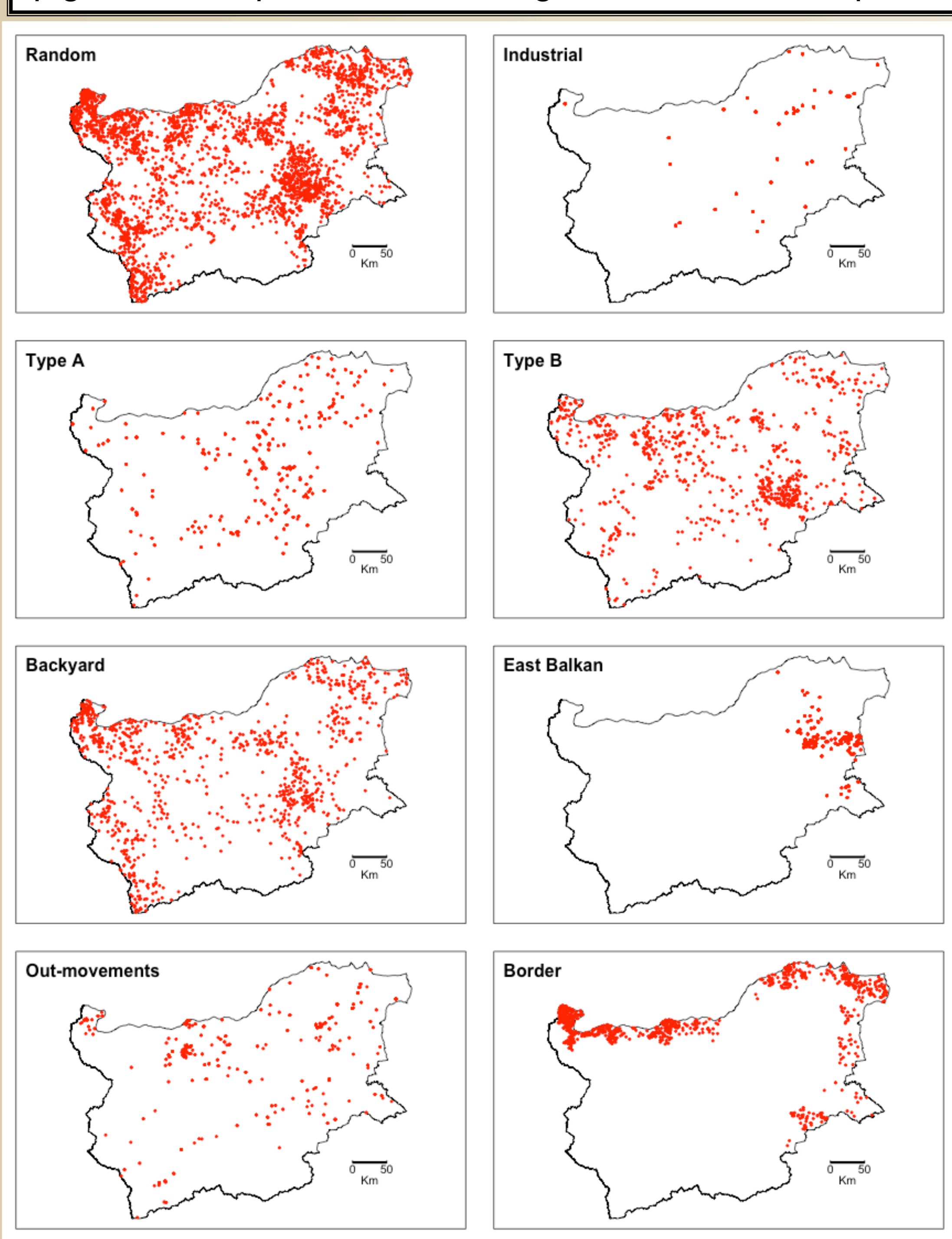


Figure.1. Geographical distribution of the index cases used to simulate the 10000 ASF epidemics per scenario in Bulgaria.

MATERIALS AND METHODS

- Data used in this study consisted of detailed pig demographics and trade patterns provided by the Bulgarian Food Safety Agency. Specifically, the number of farms per municipality and per type of farm, and the number of pigs per farm during 2011 and 2012 were available. Farms are categorized in five types including: Industrial, family type A, family type B, Backyard (BY), EAST Balkan, which is based on the level of biosecurity, the trade patterns, and the farm size[8].
- The spread of ASFV in Bulgaria both by direct contacts (i.e. pig movements and wild boar contacts) and by indirect contacts (i.e. vehicles, people, local spread and ticks) was modeled by expanding (to include wild boar and ticks) and re-parameterizing a previously described and validated spatial and stochastic model for Classical Swine Fever, referred to as Be-FAST[5,6,7]. [See diagram above].
- A Total of 10000 simulations and 8 scenarios were analyzed as follows: 1) random farms selected as index cases (10000 simulations) ; 2) random farms selected from industrial farms (3000 simulations) ; 3) random farms selected from farms type A (1000 simulations) ; 4) from farms type B (1000 simulations) ; 5) from BY farms (1000 simulations) ; 6) from East Balkan herds (1000 simulations); 7) random farms selected from those with outgoing shipments (outdegree > 0) (1000 simulations); 8) random farms selected from those located in municipalities bordering with Romania and Turkey (1000 simulations) [**Figure 1**].

RESULTS

Table.1. Mean, median, and 95% probability interval (PI) for the number of infected farms and animals per epidemic, and duration of the epidemic generated by 10000 simulated ASF epidemics using Be-FAST model for each farm type in Bulgaria.

Outputs: mean, median, (95%PI)	Overall	Industrial	Type A	Type B	Backyard	East Balkan	Outgoing movements	Border
Number of infected farms per outbreak	4, 3, (2, 16)	6, 5, (2, 17)	4, 3, (2, 10)	3, 2, (2, 6)	3, 2, (2, 8)	3, 2, (2, 6)	6, 5, (2, 19)	3, 2, (2, 5)
Number of infected animals per outbreak	1457, 7, (1, 16001)	3788, 18, (1, 30126)	102, 8, (2, 1696)	21, 4, (1, 120)	26, 4, (1, 88)	21, 5, (1, 151)	3776, 14, (1, 32002)	7, 3, (1, 29)
Duration of the outbreak	19, 14, (2, 59)	12, 9, (1, 25)	15, 12, (2, 44)	18, 15, (3, 52)	25, 19, (3, 71)	16, 12, (2, 54)	17, 11, (1, 49)	25, 19, (4, 80)

Magnitude and duration of an ASF simulated epidemics in Bulgaria were summarized in **Table 1** and **Figure 2**. Only 2777 simulations out of 10000 (27.7%) were spreading further than the index case and spread was mostly local. The mean, median and 95% PI number of infected farms per epidemic was, in general, low [4, 3 (2, 16)], being higher in Industrial and farms with outgoing movements while the longest duration of an epidemic was found when epidemics where initiating in Backyard and type B farms. High risk areas were mainly concentrated in East part of Bulgaria [**Figure 2**]. Most of the ASFV outbreaks were associated to local spread (39%). Wild boars were only contributing to 6% of the outbreaks and were source of infection mostly of BY, Type B and East Balkan farms.

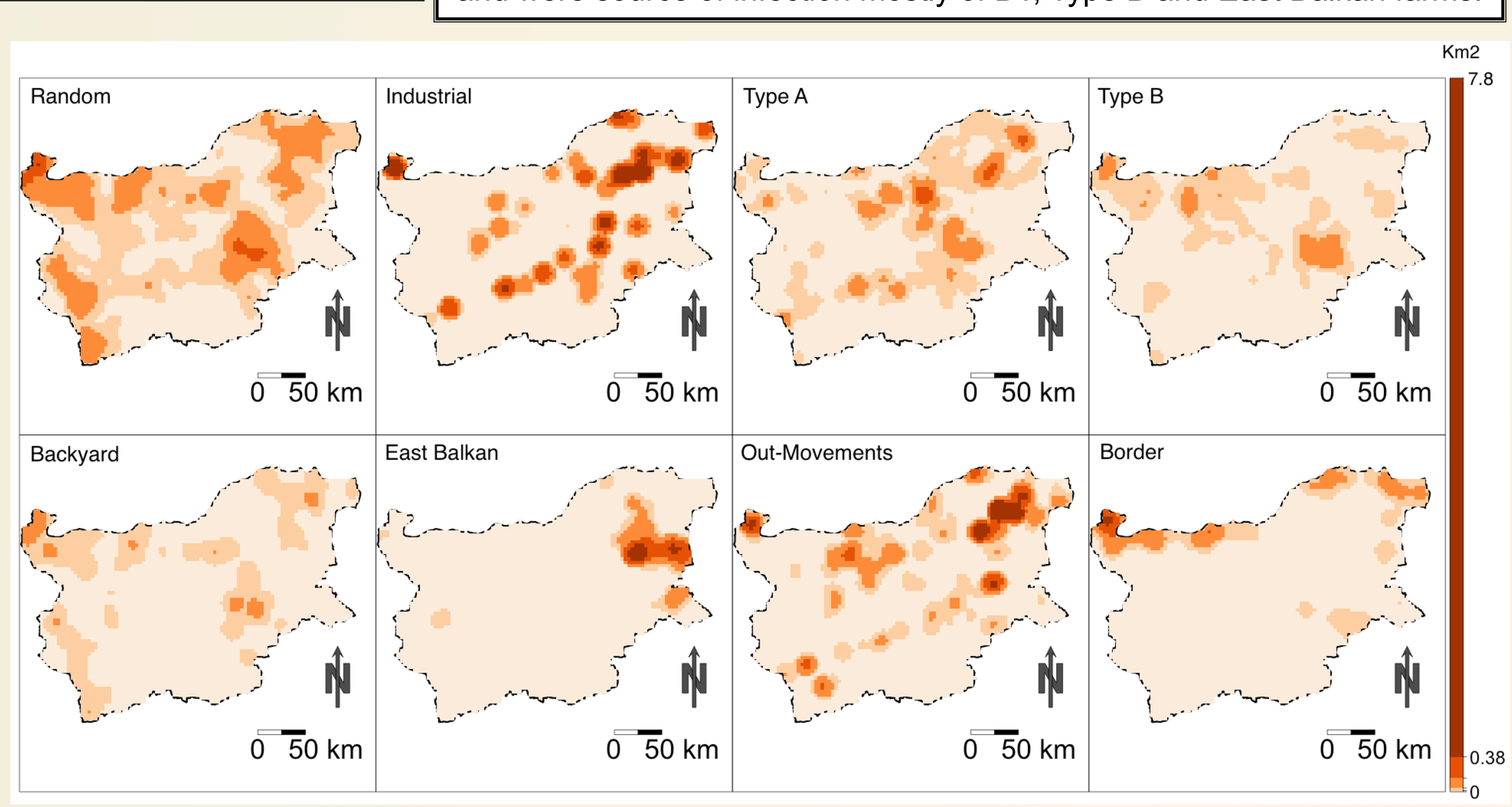


Figure.2. Spatial distribution of the Risk of ASF infection in Bulgaria after 10000 simulated epidemics per farm type. Maps have been produced using the Kernel density function.

CONCLUSIONS

The Be-FAST model presented here was intended to quantify the magnitude and duration of a ASFV epidemics and to identify areas at high risk for the introduction and spread of the disease. Model was adapted to simulate the within and between farm spread of ASFV in an environment with high number of backyard pig farms and considering the role that wild boar and tick presence may have in disease transmission. Results of the model reveal that, in general, magnitude of ASFV epidemics in Bulgaria were small, mainly when industrial or trade farms were not infected; however, infection of backyards and type B farms lead to small but longer epidemics with higher role of wild boar and tick in the ASFV transmission, which highlights the need to improve biosecurity measures in those holdings to prevent potential disease endemicity in the country. The established infection of ASFV in wild boars, swill feeding practices, lack of awareness amongst farmers, existence of areas of interaction between free-ranging pigs and wild boars, abundance of backyard pig production farms, and lack of traceability of some backyard and type B farms may lead to further ASFV spread and maintenance in Bulgaria. Therefore, further simulations of the disease spread considering endemic scenarios will be valuable. Methods and results presented here may support a more cost-effective prevention, surveillance and control of potential ASFV incursions into this and other countries with similar conditions in Easter Europe.

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