

**PREPUBLICACIONES DEL DEPARTAMENTO  
DE MATEMÁTICA APLICADA  
UNIVERSIDAD COMPLUTENSE DE MADRID  
MA-UCM 2012-14**

**Evaluation of the risk of Classical Swine Fever spread  
in Bulgaria by using the epidemiological model Be-FAST**

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Octubre-2012

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# Evaluation of the risk of Classical Swine Fever spread in Bulgaria by using the epidemiological model Be-FAST.

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October 24, 2012

**Abstract:** *The objective of this article is to find the optimal trajectory of a pumping ship, used to clean oil spots in the open sea, in order to pump the maximum quantity of pollutant on a fixed time period. We use a model previously developed to simulate the evolution of the oil spots concentration due to the coupling of diffusion, transport from the wind, sea currents and pumping process and reaction due to the extraction of oil. The trajectory of the ship is directly modeled by considering a finite number of interpolation points for cubic splines. The optimization problem is solved by using a global optimization algorithm based on the hybridization of a Genetic Algorithm with a Semi-Deterministic Secant Method, to improve the population. Finally, we check the efficiency of our approach by solving several numerical examples considering various shapes of oil spots based on real situations.*

**Keywords:** Epidemiological modeling; Simulation; Classical Swine Fever; Bulgaria.

# 1 Introduction

Classical Swine Fever (CSF) is a highly contagious viral disease of pigs and wild boars that causes severe economic impact due to the trade restrictions imposed to the affected countries. Considering that the pig sector in the European Union (EU) maintains a high level of production and exports, contributing with more than €32 billion per year to the EU's economy [2], the eradication of CSFV has become a chief priority in the EU.

Yearly, the EU is investing a huge amount of money in the co-financing of the CSF monitoring and eradication programs in several Member States (MS). As an example, the EU funding for the eradication of CSF from 2005 to 2009 has amounted to €17 million [2]. This financial effort has resulted in a significant reduction of the CSF outbreaks in most of the countries, with the practical eradication of the disease in domestic pig populations. Nevertheless, sporadic CSF outbreaks still occur in, approximately, 20% of the MS. For example, from January 2005 to July 2012 a total of 351 outbreaks were notified in Europe, affecting countries such as Hungary (142 outbreaks), Croatia (130), Russia (49), Bulgaria (11), Germany (8), Lithuania (6), Slovakia (3) and Serbia (2) [11]. Most of these CSF outbreaks have been associated either with low biosecurity premises (mainly backyard pigs) and/or with wild boar.

Certainly, backyard pigs have been recognized as key players for disease (not only CSF) occurrence [2, 7, 10]; however, there are no studies addressing and quantifying their epidemiological role in the CSFV endemicity and/or in the potential CSFV transmission to other domestic pigs. This lack of studies is, most likely, associated to the scarceness of complete and reliable information about backyard pig demographics and contact patterns, which are key factors to estimate disease transmission in countries/regions where backyard pig production is predominant. Certainly, a better understanding of the role that backyard pigs have in the CSFV transmission will enhance the CSF eradication program, helping to better allocate the surveillance and control strategies not only to more cost-effectively prevent and control CSF but, ultimately, to achieve CSF eradication into the EU and other territories.

In this study, we used detailed information of backyard pig population and contact patterns from Bulgaria, which is one of the EU countries in which backyard pig production is predominant (96% of backyard farms), to evaluate the potential evolution of CSFV epidemics in Bulgaria. Our aim was, particularly, to assess the CSFV-spread from backyard pigs to other domestic pigs by using a stochastic and spatial disease spread model called Be-FAST [3, 8, 9]. Methods and results presented here may be useful to guide risk-based interventions not only in Bulgaria, but also in other similar countries where backyard pig production is predominant.

## 2 Materials and methods

### 2.1 Definitions and data

Bulgarian pig farms are categorized in five types based on [1]:

- i) the level of biosecurity,
- ii) the trade patterns allowance,
- iii) the farm size.

The first type of farm is referred to as "Industrial", which is characterized by high levels of biosecurity, no restrictions for pig trade and large number of pigs on farm. "Family farm type A" is the second type of farm, which is similar to industrial farms in trade allowances but, usually, with a smaller farm size and lower level of biosecurity (i.e. medium instead of high). "Family farm type B" is the third type of farm characterized by none or poor biosecurity, smaller farm size and pig trade only allowed to other non-industrial pig farms. The fourth type is the "Backyard" pig farm, which has none or poor biosecurity, a very small farm size (up to 5 pigs and no sows) and in which pig trade is not allowed (pigs are only for self-consumption). Finally, the last type of farm is the "East-Balkan" pig herd, which is managed traditionally (i.e. free-range pigs feed in open grass areas), has none or poor biosecurity level, has usually medium to small farm size and in which trade is only allowed to other East-Balkan pig herds.

Data used in this study consisted on detailed pig demographics and trade for each pig farm, which was provided by the Bulgarian Food Safety Agency (<http://babh.government.bg/en/>). Specifically, the number of farms per municipality, the type of each farm (i.e. industrial, family type A, family type B, backyard and East Balkan) and the number of pigs per farm during 2010 were available. Because the specific location of farms was not detailed, we used ArcGIS9.3 (ESRI®) to assign latitude and longitude coordinates for each farm within each municipality (Figure 1). Pig movement records were also obtained and used to simulate CSFV spread by direct contacts. Specifically, the farm of origin, the farm of destination, the day of shipment and the number of pigs shipped from January to October 2010 were used (Figure 2).

### 2.2 The model

The spread of CSFV in Bulgaria both by direct contacts (i.e. pig movements) and by indirect contacts (i.e. vehicles, people and local spread) was modeled by adjusting a previously described and validated spatial and stochastic model for CSF, referred to as Be-FAST [3, 8, 9]. Briefly, the Be-FAST model combines a discrete time stochastic 'Susceptible'-'Infected'

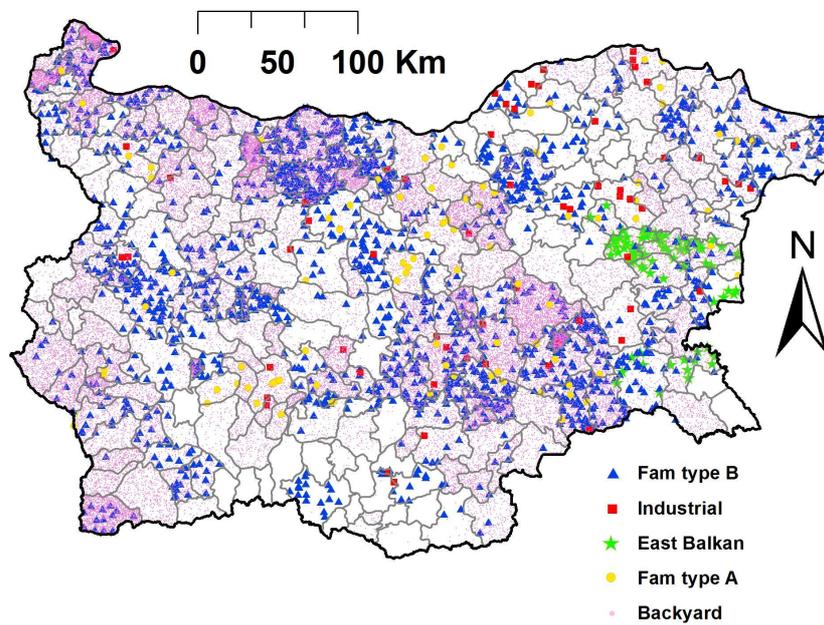


Figure 1: Spatial distribution of the different types of pig farms in Bulgaria during 2010.

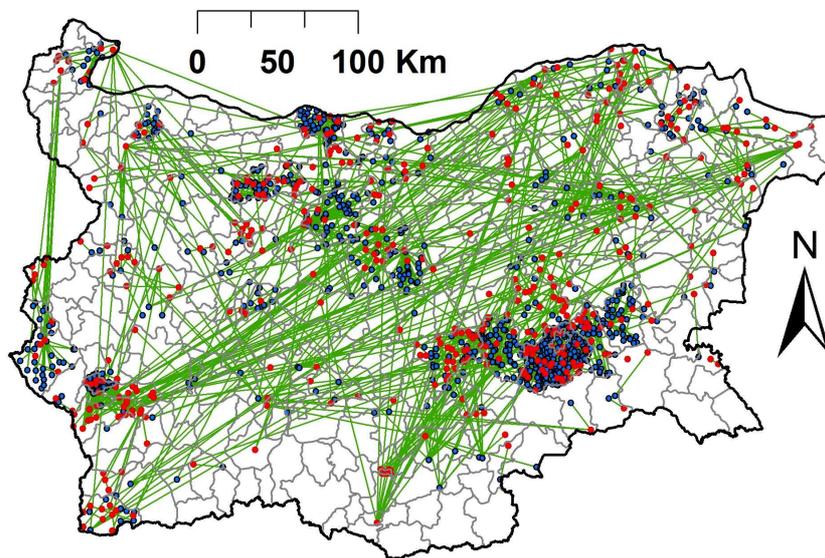


Figure 2: Pig contact network from January to October 2010 in Bulgaria. Red and blue points represent farms of origin and destination, respectively. Shipments of pigs are represented by using green lines.

model (SI) to simulate the daily CSFV spread within a particular farm with an Individual Based model (in which farms are considered as individuals and are assumed to be in either 'Susceptible', 'Infected', 'Infectious' or 'Clinical signs' state) to simulate the CSFV spread between farms. At the beginning of a simulation all farms are in the 'Susceptible' state except one randomly selected farm, which is assumed to have one infected pig and which is classified as an 'Infectious' farm. After this initial infection, the within- and between-farm transmission processes occur throughout the study region considering the parameterization of the model, the spatial location and demographics of farms and the contact patterns among them. Moreover, when the first farm is detected as CSFV-infected, a daily process for simulating the control measures (such as zoning, movement restriction, tracing and stamping-out) is also implemented. Each simulation finishes when, at the end of a simulated day, the CSFV epidemic has disappeared.

In this study, model parameters were adapted to the Bulgarian conditions by using information from an expert opinion elicitation conducted on the 31 May 2012 in Hannover and from the expert knowledge of Bulgarian Vet Authorities. Values of parameters that have changed from those described for the original model are detailed in Table 1.

A total of 5000 different epidemics were run assuming different randomly selected index cases. Specifically, for the first 1000 epidemics the index case was assumed to be a randomly selected backyard pig farm; for the next 1000 epidemics the index case was assumed to be a family type B farm; for the next 1000 epidemics, a family type A farm; for the next 1000 epidemics, an industrial farm and; for the last 1000 epidemics an East Balkan pig herd. As a result, 5000 different epidemics, originated from 5000 random and different farms, were run during, approximately, 92 hours. Magnitude, duration and transmission patterns of the simulated CSF epidemics in Bulgaria were summarized using the median value, the mean value and the 95% probability intervals (PI). Values for the effective reproduction ratio of a farm  $i$  ( $R(i)$ ), which was defined as the number of times that farm  $i$  infects another farm in a 'Susceptible' state considering all the simulations; and the risk of CSFV introduction into a farm  $i$  ( $Risk(i)$ ), which was defined as the number of times that farm  $i$  becomes infected considering all the simulations were also calculated (Anderson and May, 1979, 1991). Raster maps for the  $R$  and  $Risk$  values were generated with the Kernel density function implemented in ArcGIS 9.3 (ESRI®) and using the Jenks optimization method (i.e. Natural Breaks) for mapping the risk categories [5]. Epidemic curves were also produced using Microsoft Office Excel 2010.

Table 1: Parameters different to the default ones implemented in the Be-FAST model (see [3, 8, 9]) used to simulate the CSFV spread in Bulgaria.

<b>Parameter</b>	<b>Distribution or Value</b>
Within-farm transmission parameter ( $B_h$ )	$\beta_{hI} = 0.656; \beta_{hA} = 0.600, \beta_{hB} = 0.500, \beta_{hBY} = 0.050, \beta_{hEB} = 0.050$
Probability of infection by contacts with vehicles transporting products	I=Bernoulli [0.0065] A= Bernoulli [0.0075] B= Bernoulli [0.01] BY= Bernoulli [0.02] EB= Bernoulli [0.02]
Probability of infection by contact with people	I=Bernoulli [0.0068] A= Bernoulli [0.008] B= Bernoulli [0.01] BY= Bernoulli [0.034] EB= Bernoulli [0.034]
Probability of restriction of movements outside the control and surveillance zones	I=Bernoulli [0.40] A= Bernoulli [0.35] B= Bernoulli [0.30] BY= Bernoulli [0.10] EB= Bernoulli [0.10]
Probability of tracing an animal movement	I=Bernoulli [0.99] A= Bernoulli [0.95] B= Bernoulli [0.90] BY= Bernoulli [0.30] EB= Bernoulli [0.30]
Probability of tracing a people movement	I=Bernoulli [0.67] A= Bernoulli [0.60] B= Bernoulli [0.50] BY= Bernoulli [0.10] EB= Bernoulli [0.10]
Probability of tracing a vehicle transporting products	I=Bernoulli [0.95] A= Bernoulli [0.9] B= Bernoulli [0.80] BY= Bernoulli [0.20] EB= Bernoulli [0.20]

I=Industrial; A= Family type A; B= Family type B; BY= Backyard; EB= East Balkan

### 3 Results

A total of 85% of the 5000 simulations resulted in a non spread of the CSFV (i.e. 85% of the intentionally infected index farms did not further spread the disease). Specifically, from those 1000 simulations whose index farm was a backyard type, only 73 resulted in further spread of the disease. This number, when index cases were industrial, family type A, family type B and East Balkan pig herds were 387, 116, 86 and 105, respectively.

From those simulations that did result in CSFV spread, the median and mean [95% PI] numbers of infected farms per epidemic were 1 and 2 [1, 4], respectively. The median and mean [95% PI] numbers of infected pigs were 2 and 371 [1, 4477], respectively. The median and mean [95% PI] durations of the epidemic were 44 and 52 [17, 101] days, respectively. The median and mean [95% PI] numbers of infected Municipalities per epidemic were 1 and 1 [1, 3] respectively.

Simulations in which the index cases were industrial farms resulted in the largest epidemics (Figure 3-a). Conversely, the magnitude and duration of the epidemics when index cases were backyards, family type A, family type B or East-Balkan pig herds were much smaller (Figure 3-b).

The routes of infection in simulations in which the index cases were backyards were, primarily, vehicles (50.6%) and people (43.7%) and, in a very small proportion, the local spread (5.7%). Contrarily, routes of infection in simulations in which the index cases were industrial farms were, mainly, local spread (61.8%) followed by animal movements (17.3%), vehicles (12.8%) and people (8.1%). Routes of infection for simulations in which the index cases were family type A farms were local spread (28.9%), vehicles (28.8%), people (23.7%) and movement of animals (18.6%) and for simulations in which the index case were family type B farms were vehicles (49.5%), people (42.1%) and local spread (8.4%). Finally, routes of infection for simulations in which the index case were East-Balkan pig herds were vehicles (45.5%), people (41.3%) and local spread (13.2%).

Detection of CSF outbreaks occurred, primarily (69%), by observation of clinical signs whereas zoning and tracing accounted for 21% and 10% of the detections, respectively.

A detailed description of the transmission patterns after 5000 simulations is presented in Table 2. Most (95%) of the infected premises were backyards whereas most (56%) of the infectious premises were industrial farms. Industrial farms became infected very rarely (2.3%) and, always, the source of infection was another industrial farm. Family type B farms were also rarely infected (2.6%), but the source of infection was more diverse, including industrial, family type A and backyard farms. In the case of backyard farms, industrial farms were the main source of infection (52%) but all other types of farms were also contributing to the CSFV infection in backyards.

In general, the median [95% PI] of the R and Risk values for a pig farm

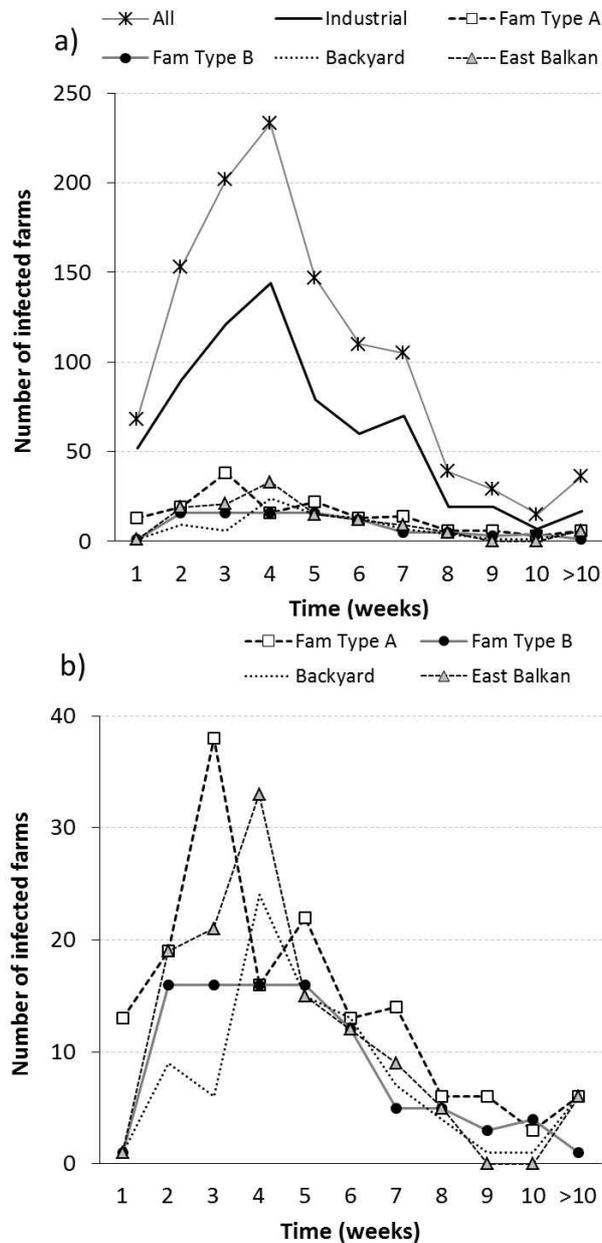


Figure 3: Epidemic curves of the 5000 CSFV epidemics in Bulgaria simulated with Be-FAST model. **a)** Lines represent the number of infected farms per week when the index case is an "industrial" farm (first 1000 simulations) or "family type A" (other 1000 simulations) or "family type B" (other 1000 simulations) or "Backyard" (other 1000 simulations) or "East Balkan" (other 1000 simulations) or for "All" the 5000 simulations. **b)** Zoomed view for the epidemic curves of family type A, family type B, backyard and East Balkan.

Table 2: Transmission patterns indicated by using the percentage of infections regarding the 5000 simulations of Be-FAST from (i.e. infectious) and to (i.e. infected) the different types of farms.

Infectious farm type	Infected farm type					Total
	Industrial	Family type A	Family type B	Backyard	East Balkan	
<b>Industrial</b>	2.3%		2.1%	51.7%		<b>56.1%</b>
<b>Family type A</b>			0.3%	12.1%		<b>12.4%</b>
<b>Family type B</b>				7.9%		<b>7.9%</b>
<b>Backyard</b>			0.2%	13.0%		<b>13.2%</b>
<b>East Balkan</b>				10.4%		<b>10.4%</b>
<b>Total</b>	<b>2.3%</b>		<b>2.6%</b>	<b>94.1%</b>		<b>100%</b>

Table 3: Median [95% probability intervals] for the R and Risk values obtained after 5000 runs of the Be-FAST model in Bulgaria.

	R	Risk
<b>Industrial</b>	7.5 [1, 43]	2 [1, 17]
<b>Family type A</b>	1 [1, 21]	
<b>Family type B</b>	1 [1, 2]	1 [1, 10]
<b>Backyard</b>	1 [1, 2]	1 [1, 5]
<b>East Balkan</b>	1 [1, 5]	

in Bulgaria after 5000 simulated CSFV epidemics were 1 [1, 18] and 1 [1, 5.4]. Detailed values of R and Risk per type of farm are presented in Table 3. As expected, industrial farms had the highest potential to infect other farms (R=7.5) although they were concentrating a much lower risk of becoming infected (Risk=2). The spatial distribution of the risk of CSF infection, which was very similar to the spatial distribution of R (not shown), is presented in Figure 4.

## 4 Discussion and Conclusions

The study presented here is one of the very firsts to quantitatively describe the potential spread of CSFV from backyard pig premises to other

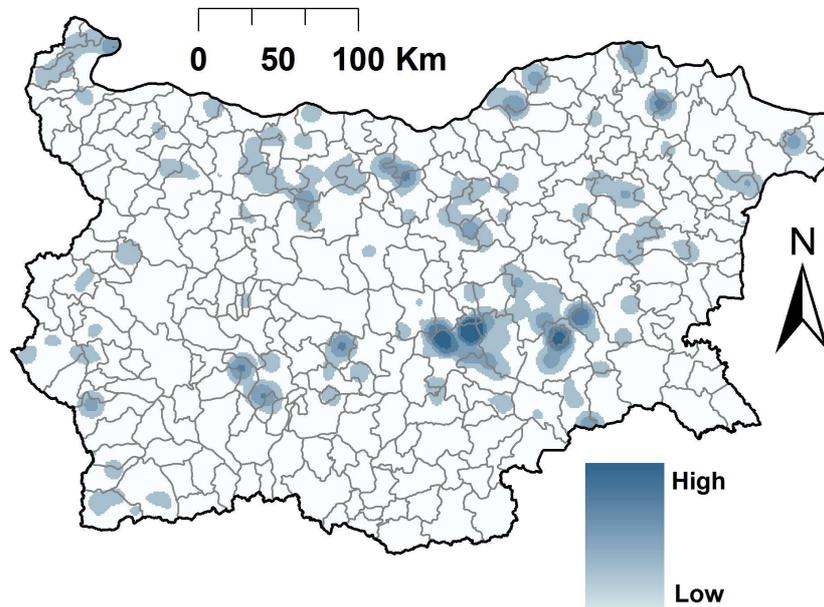


Figure 4: Spatial distribution of the risk of CSFV infection in Bulgaria after 5000 simulated epidemics. Map has been produced using the Kernel density function implemented in ArcGIS 9.3 (ESRI®).

domestic pig farms. Specifically, we used an already verified and validated [3, 8, 9] spatial and stochastic simulation model, called Be-FAST, to simulate the within and between farm CSFV-transmission in Bulgaria, in which backyard pig production is predominant. It is important to note that the presence of both very large (i.e. industrial) and very small (i.e. backyard and family type B) pig farms in Bulgaria required the incorporation of both the within- and between- farm transmission processes in order to realistically estimate a CSFV epidemic in this country. Among other reasons, this was an important motivation to select the Be-FAST model to be used and adapted for the simulation of CSFV-spread in Bulgaria. Unfortunately, most of the published models (see for example [4, 6]) do not incorporate the within-farm transmission component and, as a result, they will be importantly overestimating the magnitude and duration of a potential CSF epidemic in Bulgaria. Furthermore, Be-FAST allows the possibility to easily incorporate the network of contacts among farms, which allows to more realistically simulating the real trade patterns in the study region.

In general, the CSFV simulations produced small and short epidemics, which agreed with the historical magnitude and duration of the CSFV epidemics in Bulgaria in the last ten years [11]. Results also revealed that CSFV-infection from backyard pigs to other domestic pigs was generally

rare, despite that backyard pigs were at high risk of becoming infected (95% of the infected farms were backyards) (Table 2). In fact, backyard farms were only able to infect other backyards (13% of infections) or, in very few occasions (0.2% of infections) family type B farms. This low potential of CSF transmission from backyards to other domestic pigs may be explained, at least in part, by the combination of:

- i) the pig trade restrictions imposed to backyard farms in Bulgaria,
- ii) the use of backyard pigs and pork primarily for self-consumption,
- iii) the low number of pigs in backyard farms, which also limits the potential CSFV-airborne or local spread to nearby farms.

These socio-cultural practices and characteristics of backyard pig production in Bulgaria, seems to guarantee that, even if a backyard farm becomes infected with CSFV, it will unlikely further spread the disease to other domestic pig premises. However, it is important to highlight that the definition of backyard pigs and backyard farms importantly differs among countries within the European Union and, therefore, the epidemiological role of backyard pigs in other territories may be not the same than in Bulgaria. As a consequence, results presented here are valid just for Bulgaria and should not be extrapolated to other countries without previous adjustments of the model to incorporate the specific characteristics and trade patterns between backyard farms and other type of domestic pig farms in the country of interest.

Interestingly, the model suggested that indirect contacts were crucial to spread CSFV in Bulgaria. In this regard, fomites, particularly vehicles and people, were the most important routes of CSFV transmission in low biosecurity premises (i.e. backyard, family type B and East-Balkan herds). In family type A farms, local spread, vehicles and people were equally important as source of infection whereas local spread and animal movements were the most important routes of transmission in industrial farms. Risk and R values and raster maps also revealed that there are certain areas presenting higher risk for CSFV-introduction (Figure 4) and/or spread (not shown). These results suggest, firstly, that measures and interventions aimed to increase biosecurity on farm or to reduce the presence of contaminated fomites (such as disinfection of vehicles, the use of showers on farms, etc.) should significantly reduce the risk of CSFV-spread in Bulgaria and, secondly, that those interventions may be particularly focalized in those areas/farms at higher risk of introducing/spreading the disease. Nevertheless, we suggest conducting further investigations to evaluate more deeply the role that indirect contacts, particularly in family type B farms, and the incidence of practices such as swill feeding, may have in the CSFV transmission between backyard farms and industrial/family type A farms. These investigations

will certainly help to reduce the uncertainty of the parameters related with CSFV transmission through indirect contacts, improving the reliability of model results.

To sum up, simulation studies conducted here were useful for:

- i) identifying high risk areas for CSFV spread (Figure 4),
- ii) evaluating the specific transmission patterns between different types of farms, including backyards, in Bulgaria (Table 2),
- iii) assessing the main routes of transmission for the different types of farms,
- iv) estimating the potential risk of introduction or spread of CSFV into specific types of premises by the use of R and Risk values, respectively (Table 3).

Further simulations may be run to compare different CSFV-surveillance and control strategies which may guide the implementation of future risk-based surveillance methods.

## Acknowledgments

Authors would like to acknowledge the provision of data and support of the Bulgarian Food Safety Agency. This work has been funded by the European Project CSFV\_goDIVA (KBBE-227003), the Spanish Ministry of Science and Innovation under projects MTM2008-04621, MTM2011-22658; the "Comunidad de Madrid" and "European Social Fund" through project S2009/PPQ-1551. Beatriz Martínez-López currently holds a Juan de la Cierva contract (JCI-2011-10724).

## References

- [1] Alexandrov, T., Kamenovi, P., Depner, K. 2011. Surveillance and control of classical swine fever in Bulgaria, a country with a high proportion of non-professional pig holdings. *Epidemiol. et santé anim.* 59/60, 140-142.
- [2] Food Chain Evaluation Consortium, 2011. Report on the outcome of the EU co-financed animal disease eradication and monitoring programmes in the MS and the EU as a whole: *Report - DG SANCO*. Available at: [http://ec.europa.eu/food/animal/diseases/eradication/docs/fcec\\_report\\_ah\\_eradication\\_and\\_monitoring\\_programmes.pdf](http://ec.europa.eu/food/animal/diseases/eradication/docs/fcec_report_ah_eradication_and_monitoring_programmes.pdf)

- [3] Ivorra, B., Martínez-López, B., Sánchez-Vizcaíno, J.M., Ramos, A.M., in press. Mathematical formulation and validation of the Be-FAST model for Classical Swine Fever Virus spread between and within farms. *Annals of Operations Research*.
- [4] Jalvingh, A.W., Nielen, M., Maurice, H., Stegeman, A.J., Elbers, A.R.W., Dijkhuizen, A.A., 1999. Spatial and stochastic simulation to evaluate the impact of events and control measures on the 1997-1998 classical swine fever epidemic in The Netherlands. I. Description of simulation model. *Vet. Microbiol.*, 42, 271-295
- [5] Jenks, G. F., 1967. The data model concept in statistical mapping. In: Frenzel, K. (Ed.), *International Yearbook of Cartography*. Vol. 7. ICA, Rand McNally & Co, USA, pp. 186-190.
- [6] Kartsen, S., Rave, G., Krieter J., 2005. Monte Carlo simulation of classical swine fever epidemics and control. I. General concepts and description of the model. *Vet. Microbiol.*, 108, 187-198.
- [7] Lupulovic, D., Lazic, S., Prodanov-Radulovic, J., Jiménez de Oya, N., Escribano-Romero, E., Saiz, J-C, Petrovic, T., 2010. First Serological Study of Hepatitis E Virus Infection in Backyard Pigs from Serbia. *Food Environ. Virol.*, 2, 110-113
- [8] Martínez-López, B., Ivorra, B., Ngom, D., Ramos, A.M., Sánchez-Vizcaíno, J.M. 2012. A novel spatial and stochastic model to evaluate the within and between farm transmission of classical swine fever virus: II Validation of the model. *Vet Microbiol.*, 155, 21-32.
- [9] Martínez-López, B., Ivorra, B., Ramos, A.M., Sánchez-Vizcaíno, J.M., 2010. A novel spatial and stochastic model to evaluate the within and between farm transmission of classical swine fever virus: I. General concepts and description of the model. *Vet Microbiol.*, 147, 300-309.
- [10] Pozio, E, Alban, L., Boes, J., et al. 2010. Development of harmonised schemes for the monitoring and reporting of Trichinella in animals and foodstuffs in the European Union. *SCIENTIFIC REPORT - EFSA*. Available at: <http://www.efsa.europa.eu/en/supporting/doc/35e.pdf>
- [11] WAHID, 2012. Available at: [http://www.oie.int/wahis\\_2/public/wahid.php/Wahidhome/Home](http://www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home). Last Accessed: 3 September 2012

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