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Assessing the epidemiological risk at the human-wild boar interface through a one health approach using an agent-based model in Barcelona, Spain

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ABSTRACT

Wild boar (WB, *Sus scrofa*) populations are increasing in urban areas, posing an epidemiological risk for zoonotic pathogens such as hepatitis E virus (HEV) and antimicrobial-resistant *Campylobacter* (AMR-CAMP), as well as non-zoonotic pathogens such as African swine fever virus (ASFV). An epidemiological extension of a validated Agent-Based Model (ABM) was developed to assess the one-year epidemiological scenarios of HEV, AMR-CAMP, and ASFV in the synurbic WB-human interface in Barcelona, Spain. The predicted citizen exposure was similar for HEV and AMR-CAMP, at 0.79% and 0.80% of the human population in Barcelona, respectively, despite AMR-CAMP being more prevalent in the WB population than HEV. This suggests a major role of faeces in pathogen transmission to humans in urban areas, resulting in a non-negligible public health risk. The ASFV model predicted that the entire WB population would be exposed to the virus through carcasses (87.6%) or direct contact (12.6%) in 51–71 days after the first case, with an outbreak lasting 71–124 days and reducing the initial WB population by 95%. The ABM predictions are useful for animal and public health risk assessments and to support risk-based decision-making. The study underscores the need for interdisciplinary cooperation among animal, public, and environmental health managers, and the implementation of the One Health approach to address the epidemiological and public health risks posed by the synurbization of WB in urban areas. The spatially explicit epidemiological predictions of the ABM can be adapted to other diseases and scenarios at the wildlife-livestock-human interface.

1. Introduction

Zoonotic diseases account for 60.3% of human diseases and 71.8% of emerging infectious diseases originate from wildlife [1]. Outbreaks and epidemics of new human infectious diseases have demonstrated the risk posed by biological agents to public health and animal breeding [2], and recent highly pathogenic avian influenza and SARS-CoV-2 outbreaks have shown how rapidly emerging diseases can spread and become endemic, posing major public health concerns and severely impacting human health and economy. Integrated wildlife monitoring, which combines wildlife health and host community monitoring, is essential for early detection of emerging infections, tracking changes in disease dynamics, and evaluating the effectiveness of interventions in complex multi-host and multi-pathogen networks [3].

Eurasian wild boar (WB, *Sus scrofa*) has a major epidemiological role as host and reservoir for zoonotic and non-zoonotic pathogens shared

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Abbreviations: ABM, Agent-based model; AMR-CAMP, Antimicrobial-resistant *Campylobacter*; ASFV, African swine fever virus; BCN, Barcelona; CNP, Collserola Natural Park; HEV, Hepatitis E virus; MAB, Metropolitan area of Barcelona; Swb, Synurbic or habituated wild boar; WB, Wild boar; WIA, Wild boar interaction area; Wwb, Wild or non-habituated wild boar.

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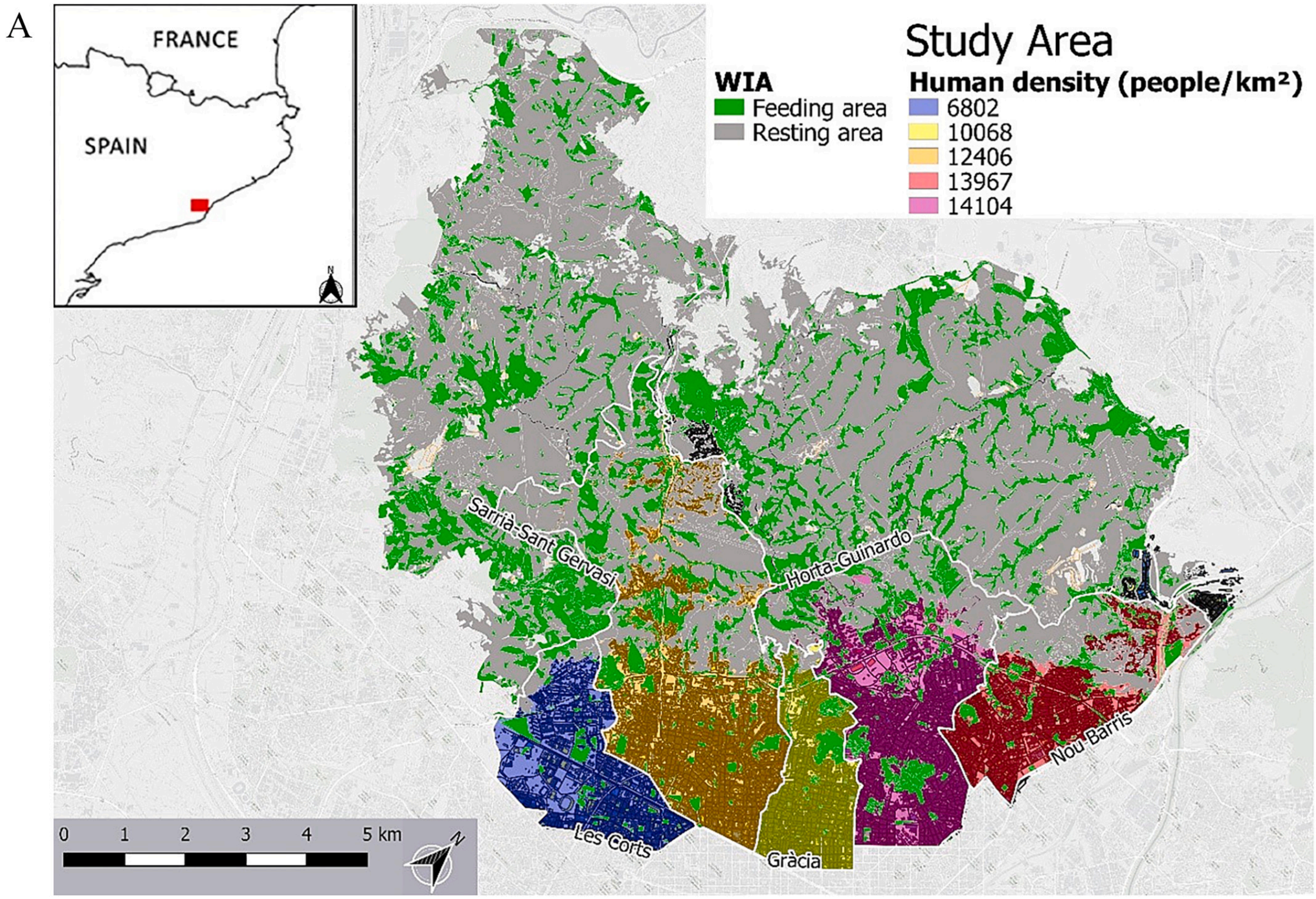


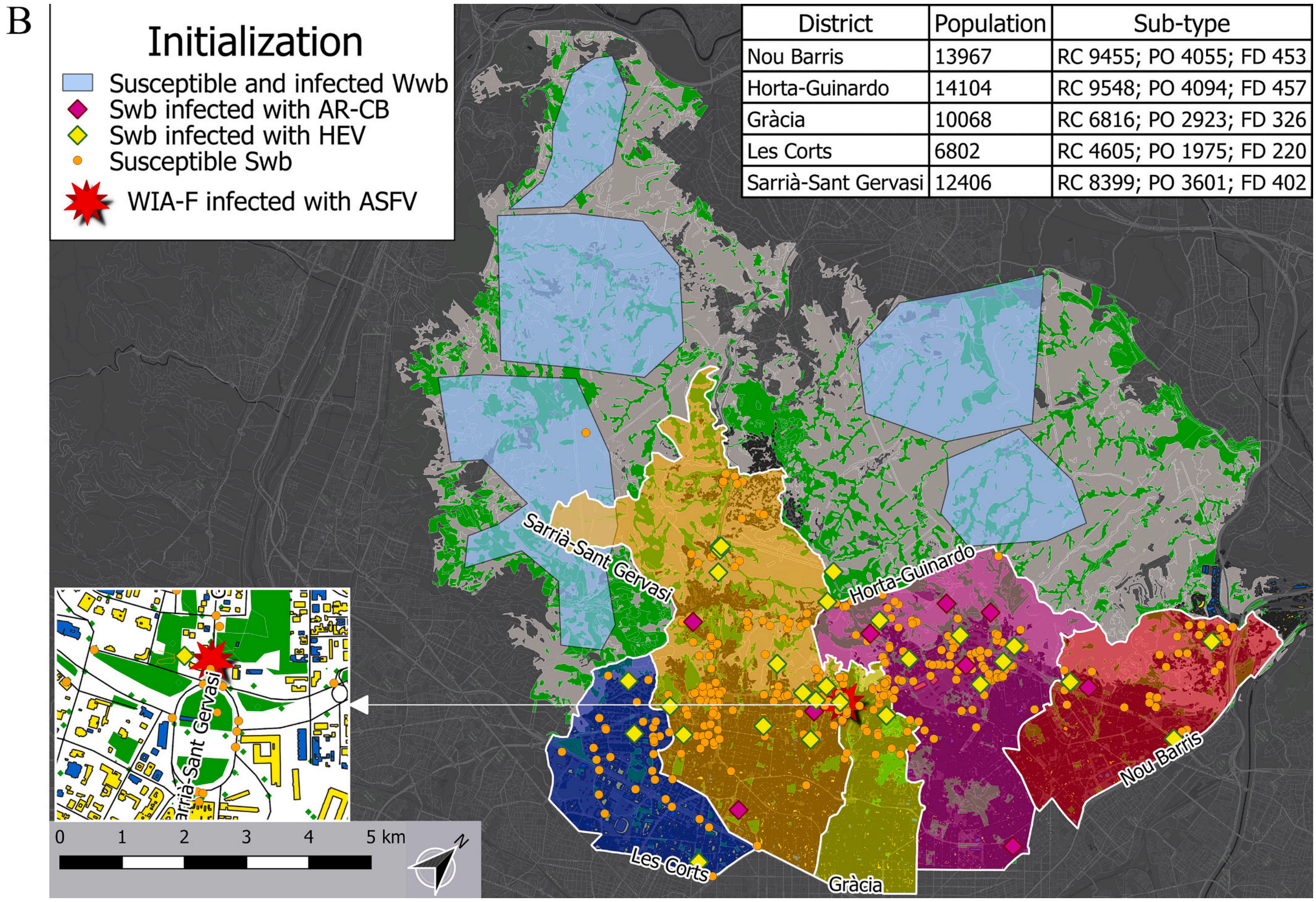
Fig. 1. A) Study area. Collserola Natural Park and the five districts of Barcelona included in the model (Les Corts, Sarrià-Sant Gervasi, Gràcia, Horta-Guinardó, and Nou Barris). Human population density and wild boar interaction areas (WIA, including feeding and resting areas) are shown; B) Initial location of the susceptible and infected synurbic-wild boar (Swb) and non-urban wild boar (Wwb) agents in the (a) AMR-CAMP, antimicrobial resistant *Campylobacter* scenario, (b) HEV, hepatitis E virus scenario, and initial location of the infected WIA-F agent in the AFSV, African swine fever virus scenario. The number of citizen agents by sub-type (RC, regular citizen; PO, pet owner; FD, feeder citizen) modelled in each district is also provided.

with livestock, companion animals and humans, participating in the maintenance of multi-host pathogens [4–8]. The increase in WB population abundance and distribution supposes a sanitary risk for game meat, swine production and public health [4,5,9]. Furthermore, WB is also colonizing urban areas [10–13], where they exploit anthropogenic food resources [10–12], in a process known as synurbization [14]. Host aggregation and tolerance promoted by anthropogenic resources may amplify pathogen spread in urban areas [15–21], enhancing the epidemiological role of WB.

According to the One Health framework, the dynamics of a zoonotic agent in a multi-host pathogen system involve transmission among host species (including humans), where contact, recovery, and mortality rates determine reservoir and disease emergence dynamics [7,15–21]. The risk of spillover to humans depends on infection prevalence in host population, contact rate between humans and other infected animal hosts, and infection probability upon contact [7,22]. Wild boar synurbization has modified the social-ecological system involved in human-wild boar direct and indirect interactions in densely populated areas [14,23], increasing contact rates between synurbic WB and citizens [10,13,15,16] and consequently the potential of WB as a source for pathogens and emerging human diseases [1,4,5,7].

The Metropolitan Area of Barcelona (MAB) harbours 3.2 million people in 636 km^2 (population density of 5000 people per km^2) [24]. The synurbic WB from the 80 km^2 Natura 2000 Collserola Natural Park (CNP), located within the MAB, are attracted by anthropogenic food resources to the (*peri*)urban area [10–12,17,23,25], where they contact with the urban environment and human citizens. Urban development and transport networks limit genetic exchange between the WB in CNP using the (*peri*)urban area of Barcelona and their rural counterparts [26], although WB move in and out of the CNP using riparian areas and dry riverbeds as corridors [10,26]. Previous studies on the WB population in the MAB have detected zoonotic hepatitis E virus (HEV) [8], *Streptococcus suis* [6], tick-borne pathogens such as *Rickettsia* spp. [27], and antimicrobial resistant bacteria such as *Campylobacter* spp. (AMR-CAMP), *Salmonella* sp., *Escherichia coli* and *Clostridioides difficile* [17–19].

Early warning systems to predict and detect emerging and re-emerging diseases are crucial for both economy and public health [2]. Accurate health risk assessments allowing effective mitigation strategies rely on better understanding of wildlife-pathogen dynamics at the human-wildlife-livestock interface. Since such understanding cannot be achieved through in vitro and field studies alone, theoretical epidemiology and simulated models allow testing hypotheses concerning environment, social structure, behaviour, and other factors [28]. Spatial models consider adaptive surveillance strategies for disease emergence [29], including the effects of anthropogenic resources on local dynamics and movement connectivity in order to understand the persistence and spatial spread of pathogens [15,16]. Although different epidemiological



District	Population	Sub-type
Nou Barris	13967	RC 9455; PO 4055; FD 453
Horta-Guinardo	14104	RC 9548; PO 4094; FD 457
Gràcia	10068	RC 6816; PO 2923; FD 326
Les Corts	6802	RC 4605; PO 1975; FD 220
Sarrià-Sant Gervasi	12406	RC 8399; PO 3601; FD 402

Fig. 1. (*continued*).

models have been proposed, spatially explicit Agent-Based Modeling (ABM) with a GIS approach can fully represent heterogeneous agents and their environment [28]. According to the previous reports of their presence in the study area [8,17,18], and/or to the relevance and implications to public health and national and regional economy, (1) hepatitis E virus (HEV), (2) antimicrobial-resistant *Campylobacter* (AMR-CAMP), and (3) African swine fever virus (ASFV) have been selected for this study.

HEV is a single-stranded RNA virus of the family Hepeviridae that can infect mammals [30]. Genotypes HEV3 and HEV4, which are shared with pigs worldwide, may be transmitted from wild boar to humans via the faecal-oral route [5,8]. HEV infections are generally self-limiting with low mortality, but immunocompromised individuals infected with HEV3 can develop chronic infections with rapid progression of liver disease and cirrhosis [30]. Prevalence of HEV infection in the MAB WB population is 20%, indicating that zoonotic transmission between wild boars and humans may be common [8].

WB is considered a reservoir of *Campylobacter* species [18], a common bacterial cause of human gastroenteritis worldwide [31]. Although *Campylobacter* commonly causes self-limiting disease, it also can produce severe symptoms and up to 10% of cases may require medical intervention [32]. Transmission can occur from animals or animal products to humans, particularly through faeces [31,32]. In the MAB, 60.8% of wild boars carried *Campylobacter* spp., with 35% of isolates having high virulence potential and 68.2% being multidrug resistant [17].

ASFV is a highly contagious virus affecting domestic pigs and wild boar, with up to 100% morbidity and mortality. ASFV is transmitted through direct contact, ingestion of contaminated feedstuffs, and by ticks [33], and has devastating economic impact for the pork industry [9]. ASFV has recently emerged and spread in Eastern and Central Europe associated to movement of WB and transport of anthropogenic food resources [34], which potentially could originate an ASFV outbreak in the growing human-wild boar interface at the MAB.

This study develops an epidemiological sub-model (BCNWB-EPI) for the previously developed the BCNWB prototype [35], an ABM of the WB synurbization process, the use of the urban ecosystem of the Barcelona city by synurbic WB, and the social-ecological system of human-WB interactions in the MAB. The prototype is a calibrated and validated ABM simulation that accurately predicts (multiple-resolution-goodness-of-fit = 0.75) the magnitude and location of wild boar movements compared to reported wild boar presences in Barcelona [35]. The BCNWB-EPI model aims to (1) identify high-risk areas for zoonotic pathogens (HEV and AMR-CAMP); (2) evaluate the potential risk of ASFV transmission through contaminated anthropogenic food resources, which could be a potential entry point of ASFV in the Spanish WB population; and (3) inform to support decision-making for prioritizing risk-mitigation strategies to reduce the exposure of BCN citizens to zoonotic pathogens.

2. Material and methods

2.1. Study area

As described in the BCNWB prototype model [35], the synurbic CNP WB forage essentially in the five districts of the city bordering the CNP [10], namely Les Corts (6.02 km^2 and 81,974 inhabitants); Sarrià-Sant Gervasi (19.91 km^2 and 149,260 inhabitants); Gràcia (4.19 km^2 and

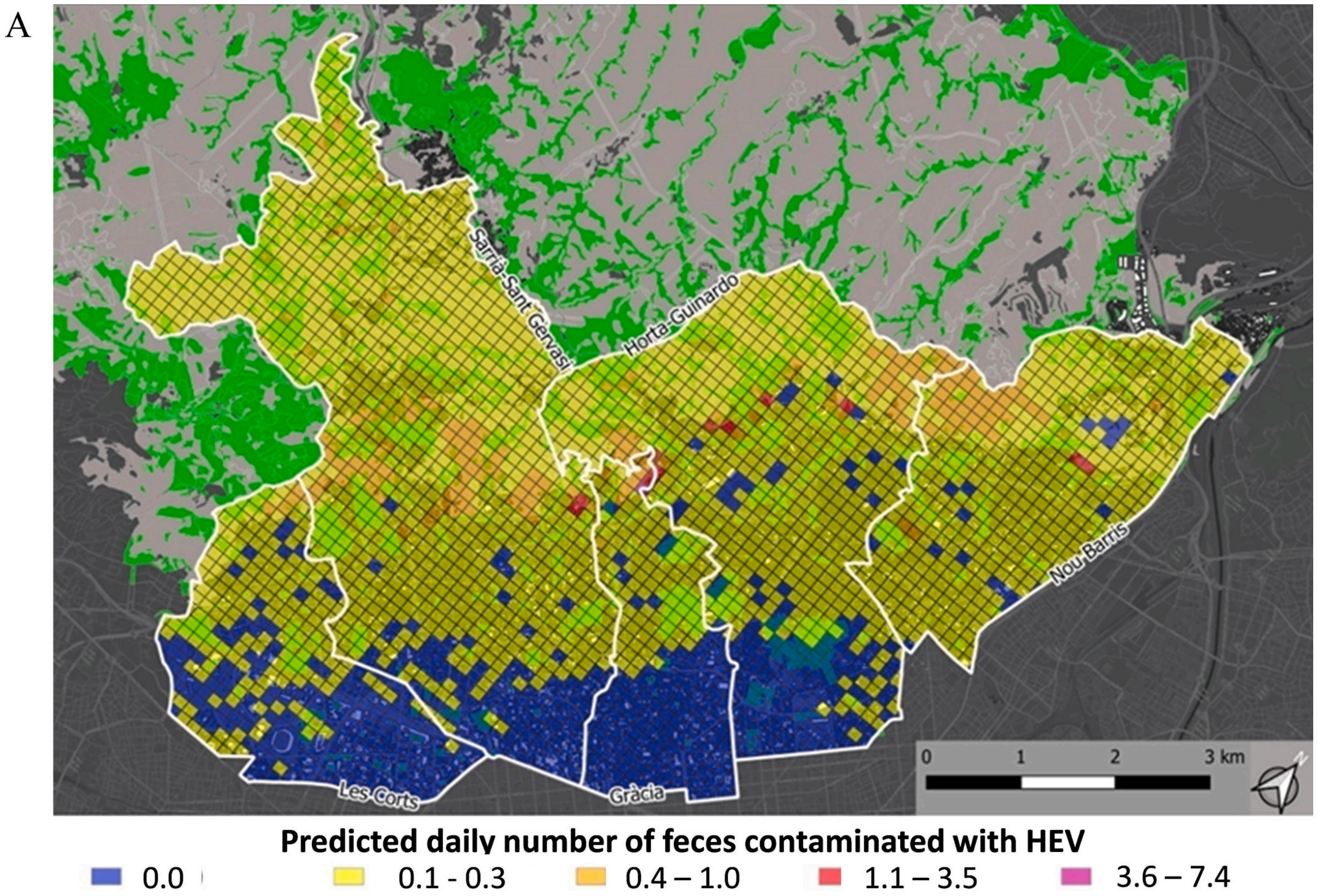


Fig. 2. A) Mean daily number of WB faeces contaminated with hepatitis E virus (HEV) in a modelled year; B) Number of citizens exposed to HEV-contaminated faeces over the study period, as predicted by the HEV scenario. Cells are 100 m side.

121,798 inhabitants); Horta-Guinardó (11.96 km^2 and 171,495 inhabitants); and Nou Barris (8.05 km^2 and 170,669 inhabitants) [36] (Fig. 1A). These districts include the main public hospital in Barcelona, and synurbic WB are actively fed by patients and visitors in the immediate surroundings of the hospital facilities, creating a chance for pathogen transmission in this new human-WB interface.

2.2. Model description

This study is an epidemiological expansion of the BCNWB prototype [35], an integrated ABM encompassing an Ecological sub-model and a Social sub-model. The Ecological sub-model comprises the Environmental and WB modules, which manage the environment of the simulation and the WB population from the CNP and BCN, respectively. The Social sub-model manages the human population of the city of BCN and includes three citizen subtypes (feeders, regular citizens, and pet owners). The ABM includes stochasticity due to environmental variation. In the Epidemiological sub-model presented in this study (Supplementary material 1 and 2), new agents were incorporated to account for pathogen transmission through environmental sources. These sources included WB faeces in the HEV and AMR-CAMP scenarios, and WB carcasses in the ASFV scenario, as they are key in the transmission of the respective pathogens [8,30,37–39].

The BCN-EPI model was implemented in GAML language using GAMA platform, an open-source and ABM multi-platform combined with GIS capabilities [40], and is completely described following the standard O.D.D. (Overview, Design concepts, Details) protocol [41] in Supplementary material 1. This Epidemiological sub-model simulated the spread of the three aforementioned pathogens among the WB populations in two ecosystems (natural and urban), assessing the risk of infection of the two zoonotic pathogens (HEV and AMR-CAMP) for the human population in Barcelona. Three independent epidemiological scenarios (one for each pathogen) were run following the SEIR (Susceptible, Exposed, Infected, and Recovered or Removed) model with WB-WB, human-WB, and environmental transmissions in the MAB over one year (Supplementary material 3).

The BCNWB-EPI model used actual data for synurbic WB (Swb) locations gathered by the BCN Local Police in 2019, simulating an initial population of 639 WB agents, classified as Swb ($n = 292$) and rural WB (Wwb, $n = 347$). The initial locations of the infected and susceptible WB agents were based on actual hunting or capture locations (Fig. 1B). Due to computational limitations, a 10% of the actual human population (i.e., 57,329 citizen agents) were randomly placed in residential buildings proportionally to the population in each district and initialized inside a resting building. Model dynamics were driven by input data representing the initial population distribution, movement patterns of wild boar, and environmental factors, as well as pathogen features such as transmission probability and incubation period. All the WB agents that were not exposed, infected or resistant were in a susceptible status, as well as the citizen agents, who were initially all susceptible.

The spatial resolution was defined by 100 × 100 m grid covering the MAB area modelled, and temporal resolution by one-hour time steps, running for 365 days. The model accounted for spatial data hourly, producing 8760 steps for each scenario. The most important processes of

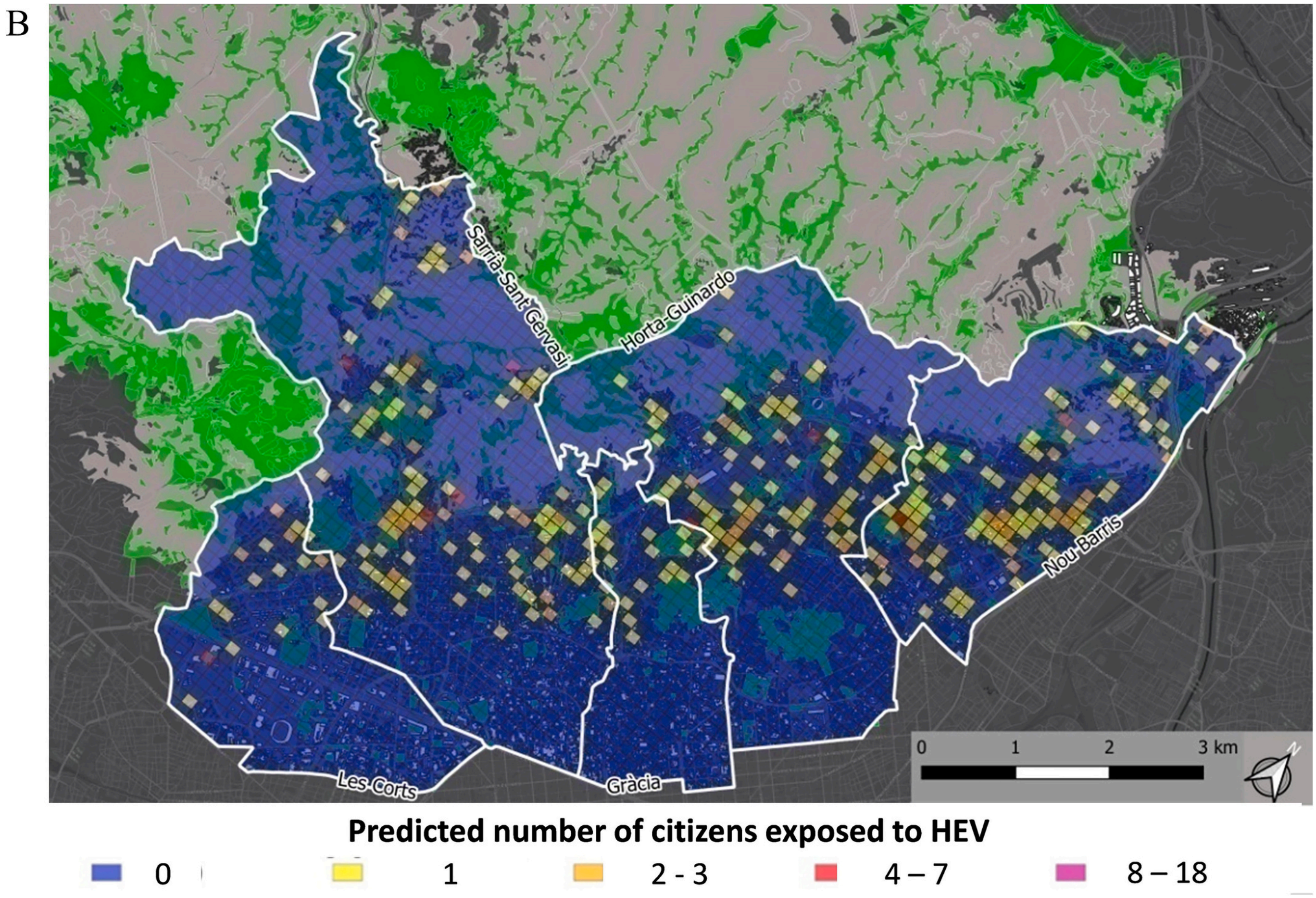


Fig. 2. (*continued*).

the model repeated every time step were i) movement of WB and citizen agents; ii) contact between susceptible and infected agents; iii) differential calculation of transmission probability for each pathogen; iv) incubation period for exposed agents; v) recovery or death for infected agents; and vi) periodic removal of environmental source agents.

Model input data for pathogen prevalence were obtained from previous studies in the MAB AMR-CAMP [17,19] and HEV [8], whereas the remaining epidemiological data were collected and calculated through literature review on WB epidemiology (section A.4 Model verification, calibration, and validation of O.D.D. protocol in Supplementary material 1, Supplementary material 4 and 5).

To temporally and spatially analyse the model outputs, the BCNWB-EPI model recorded the number of environmental sources (faeces or carcasses) and contact transmission events in each grid cell. The number of faeces was corrected by the simulated duration and area, thus calculating the annual probability of faeces occurring in each district. Additionally, the transmission event data were used to determine the probability of citizen exposure according to the day of the week and district. Spatial and temporal data statistical analyses were conducted through general linear models (Poisson distribution) and Tukey tests using the lme4 package [42] using the R 3.4.3 software [43].

3. Results

The BCNWB-EPI model captured the spatiotemporal dynamics of pathogen transmission within the study area, accounting for pathogen-specific variables, the potential influence of ASFV on WB population dynamics, and the impact of human-WB interactions on public health in Barcelona.

The BCNWB-EPI model predicted (Fig. 2) exposure to HEV of 452 citizen agents (0.79% of the modelled population) in the study area of Barcelona after 365 simulated days, 67 of them considered citizens at risk. The model's predictions matched World Health Organization (WHO)'s estimations of 0.8% of the human population exposed to HEV annually, equivalent to 480 humans in the modelled population [44].

As for AMR-CAMP scenario (Fig. 3), the model predicted 461 citizens (0.80% of the modelled population) exposed after 365 days, with 55 of them considered to be at risk. These findings fall within the estimated 0.44% to 0.93% annual human exposure range to AMR-CAMP (i.e., 264 to 558 individuals for the modelled population) [31].

The predicted citizen exposure to HEV and AMR-CAMP followed a temporal pattern both weekly (Table 1) and over the simulated period (Supplementary material 6), with greater exposure probability during and around the weekend and at the beginning of the spring season. This citizen exposure to HEV and AMR-CAMP also followed a spatial distribution pattern, with more overall contaminated faeces and consequently higher citizen exposure in Nou Barris, followed by Sarrià-Sant Gervasi and Horta-Guinardó as compared to Gràcia and Les Corts (Table 1).

In the ASFV scenario, the entire WB population in the CNP (including both the Swb and Wwb agents) was exposed to the virus between 51 and 71 days after the index case (Fig. 4). ASFV transmission (Fig. 5) occurred mainly through carcasses (87.6%) and to a lesser extent through direct contact (12.4%). The outbreak lasted between 71 and 124 days, resulting in a 95% reduction in the initial WB population. The model calculated an R0 value of 16.9 for the simulated ASFV pathogen, in the high part of the previously reported range from 1 to 17.3 for ASFV outbreaks [38,45–47].

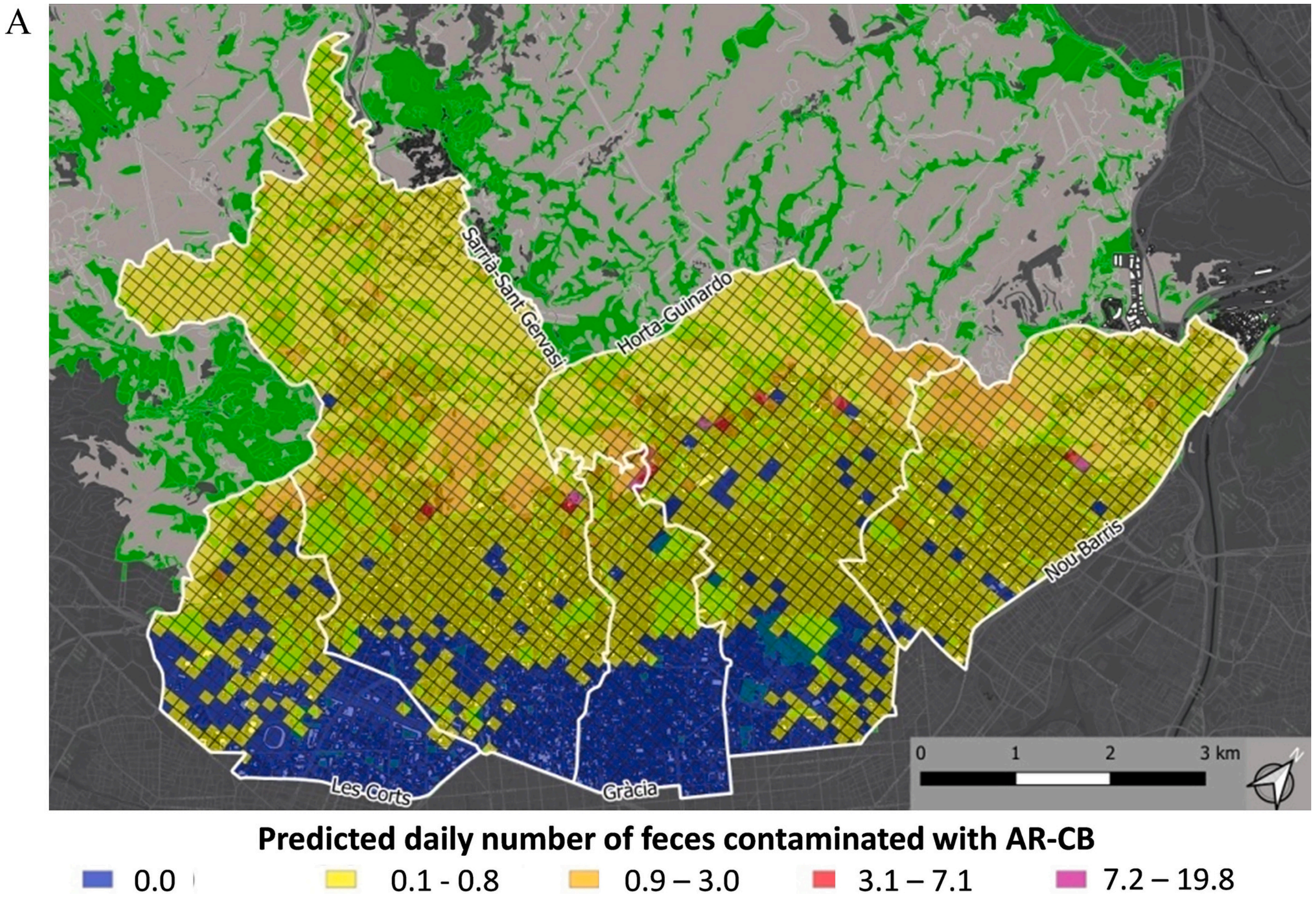


Fig. 3. A) Mean daily number of WB faeces contaminated with antimicrobial-resistant *Campylobacter* (AMR-CAMP) in a modelled year; B) Number of citizens exposed to AMR-CAMP-contaminated faeces over the same period, as predicted by the AMR-CAMP scenario. Cells are 100 m side.

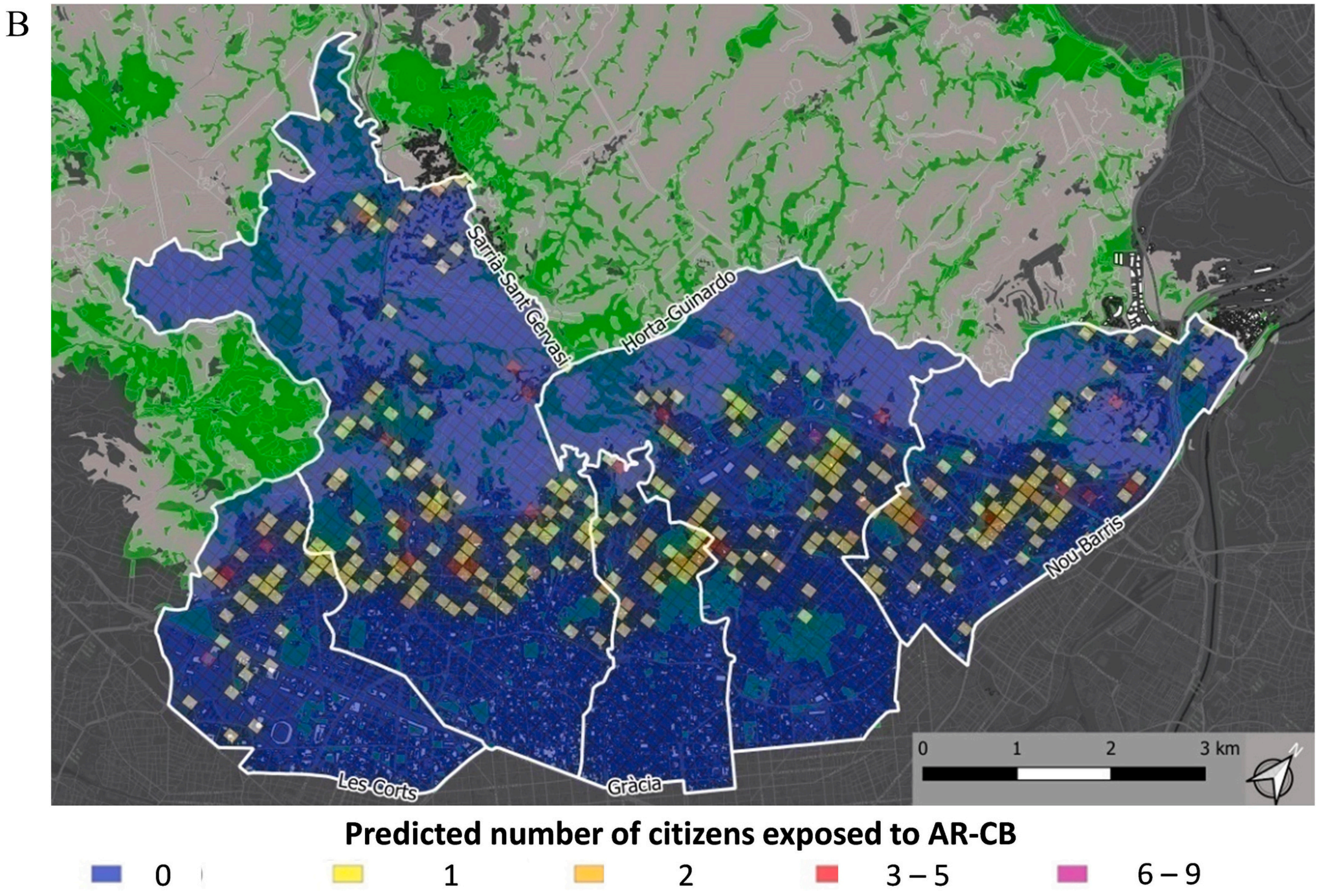


Fig. 3. (*continued*).

4. Discussion

The BCNWB-EPI model provided the first-ever modelled information on the zoonotic hazards of HEV and AMR-CAMP posed by urban WB, and assessed epidemiological and population dynamics consequences of an ASFV outbreak in the WB population of Barcelona and CNP. Furthermore, the model introduced the use of fine scale spatially explicit ABM to study urban wildlife epidemiology and disease and population management, including environmental, epidemiological, and biological variables, and successfully capturing the fine-scale epidemiological processes of the three pathogens in the human-urban wildlife interface. As a result, the model not only numerically identified the humans exposed to the zoonotic pathogens and the dynamics of potential WB ASFV epidemics, but also located the most relevant transmission hotspots within the WB population and from WB to humans through environmental sources (Figs. 2, 3, and 5).

The exposure of human citizens to HEV (0.79%) and AMR-CAMP (0.80%) after a year of simulation (Figs. 2 and 3) was similar, despite the three-fold higher prevalence of AMR-CAMP and the consequent higher probability of citizen exposure to AMR-CAMP than to HEV. This suggests that the higher infective viability of HEV in faeces may have contributed to the comparable levels of human exposure to both pathogens independently of the prevalence in WB. Thus, a key role of faeces in the indirect transmission of both pathogens from WB to humans in urban environments, even though shorter persistence of faeces in urban areas was considered in the model. To address epidemiology of zoonotic pathogens of wildlife in urban ecosystems in the human-WB interface, management measures should aim to prevent human-WB contact and the entry of WB in the urban area to avoid contamination with zoonotic pathogens [4–6,8,15,16].

The higher occurrence of HEV and AMR-CAMP transmission events on weekends can be attributed to increased human-WB interactions in wild boar interaction areas during these days, with a higher frequentation of urban green areas and trails in the CNP by humans and a higher likelihood of interacting with WB and/or encountering an infected environmental source. As for spatial heterogeneity of the predicted risk of exposure to HEV and AMR-CAMP across districts, the variability in 1) human population size (which was positively correlated with the interactions with pathogen-contaminated faeces) and density; and 2) edge border between the urban space and CNP determining WB infiltration in the district, could probably explain the highest exposure probability in Nou Barris, and the lowest predicted risk of exposure to HEV in Les Corts and Gràcia and to AMR-CAMP in Les Corts and Sarrià-Sant Gervasi. The identification of temporal and geographical hotspots for pathogen transmission risks achieved through the ABM should allow to target and focus management strategies to effectively reduce and mitigate zoonotic pathogen spread in the urban and (*peri*)urban environment.

ASFV-contaminated pork products pose a major risk for ASF transboundary emergence and spread [48], and have probably caused anthropogenic ASF outbreaks jumping hundreds of kilometres [49]. WB synurbization increased the probability of Swb feeding on ASF-contaminated anthropogenic food resources [12] (section C.1 Initialization of O.D.D. protocol in Supplementary material 1), and favoured rapid ASFV spread within the WB population with a high transmission rate due the high CNP WB population density [38,48], the low migration between CNP and other areas [26], and the increased contact rates due to aggregation induced by anthropogenic food resources [15,16,20]. As in other ASF outbreaks, WB carcasses were the main source of

Table 1

Above: Predicted temporal distribution of the probability of citizen exposure to hepatitis E virus and antimicrobial resistant *Campylobacter*. Below: Predicted spatial distribution of the annual probability of presence of faeces contaminated with *Campylobacter* or hepatitis E virus in the five urban districts of the study area, and citizen exposure to these faeces.

	Hepatitis E virus scenario	Antimicrobial resistant *Campylobacter* scenario
Citizen exposure		
Monday	0.8868^{a}	2.0189^{a}
Tuesday	0.1731^{b}	1.1346^{b}
Wednesday	0.2500^{b}	1.0192^{b}
Thursday	1.4423^{ac}	0.3269^{c}
Friday	1.2692^{a}	0.3846^{c}
Saturday	2.2115^{c}	1.0962^{b}
Sunday	2.4423^{c}	2.8462^{a}
	$p < 0.0001$	$p < 0.0001$

	Daily number of faeces	Citizen exposure	Daily number of faeces	Citizen exposure
Gràcia	0.0878^{ab}	0.0860^{ab}	0.2343^{a}	0.1505^{ab}
Horta-Guinardó	0.1332^{a}	0.1372^{a}	0.3809^{b}	0.1346^{ab}
Les Corts	0.0379^{b}	0.0707^{b}	0.1293^{c}	0.1195^{b}
Nou Barris	0.1371^{a}	0.2556^{c}	0.3445^{b}	0.1903^{a}
Sarrià-Sant Gervasi	0.1359^{a}	0.1441^{a}	0.3864^{b}	0.1300^{b}
	$p < 0.0001$	$p < 0.0001$	$p < 0.0001$	$P = 0.0156$

[a, b, c] Different superscripts within each column indicate statistically significant differences ($p < 0.05$) among days (above) and among districts (below).

transmission, enhancing ASFV survival, attracting WB, and increasing their exposure to the virus [9,33,37,50]. The higher probability of contact with ASFV-contaminated anthropic food sources and the dramatic epidemiological and demographic consequences in synurbic WB populations highlight the importance of effectively managing anthropogenic food waste and establish effective surveillance and control measures in urban environments, in order to prevent ASFV outbreaks.

Higher aggregation and interaction with humans of Swb increased contact probability between susceptible WB and human hosts, and ES spread pathogens in space and time, agreeing with previous reports of the effect of anthropogenic resources on wildlife host-pathogen dynamics [15,16]. Thus, synurbic WB in urban areas pose a potential epidemiological risk as disease reservoirs for both themselves and spillover events to humans. Food resources, faeces, and carcasses were key for pathogen maintenance and circulation [5,9,16,33,38,50,51]. Swb feeding on anthropogenic resources increase their probability of exposure to pathogens [10,12,15,16], and their movements between natural and urban ecosystems exposes other susceptible WB and humans. The temporal and spatial identification through ABM of hotspots for these transmission risks increased due to synurbization can inform management strategies aimed at reducing the risk of zoonotic spillover events and protecting both wildlife and human health.

To mitigate the risk of outbreak and spillover to humans, such strategies should aim at reducing the presence of WB in urban areas [4,5,7], using collective physical capture in (*peri*)urban areas where hunting is not allowed [52–54], and minimizing interactions between humans and WB. Due to their relevance, controlling ES by removing WB faeces from urban green areas and raising awareness should the public health risk posed by HEV and AMR-CAMP. As for ASF, the main measure to prevent an outbreak in urban WB populations would be reducing the accessibility of WB to anthropogenic food resources, since Swb preferably feed

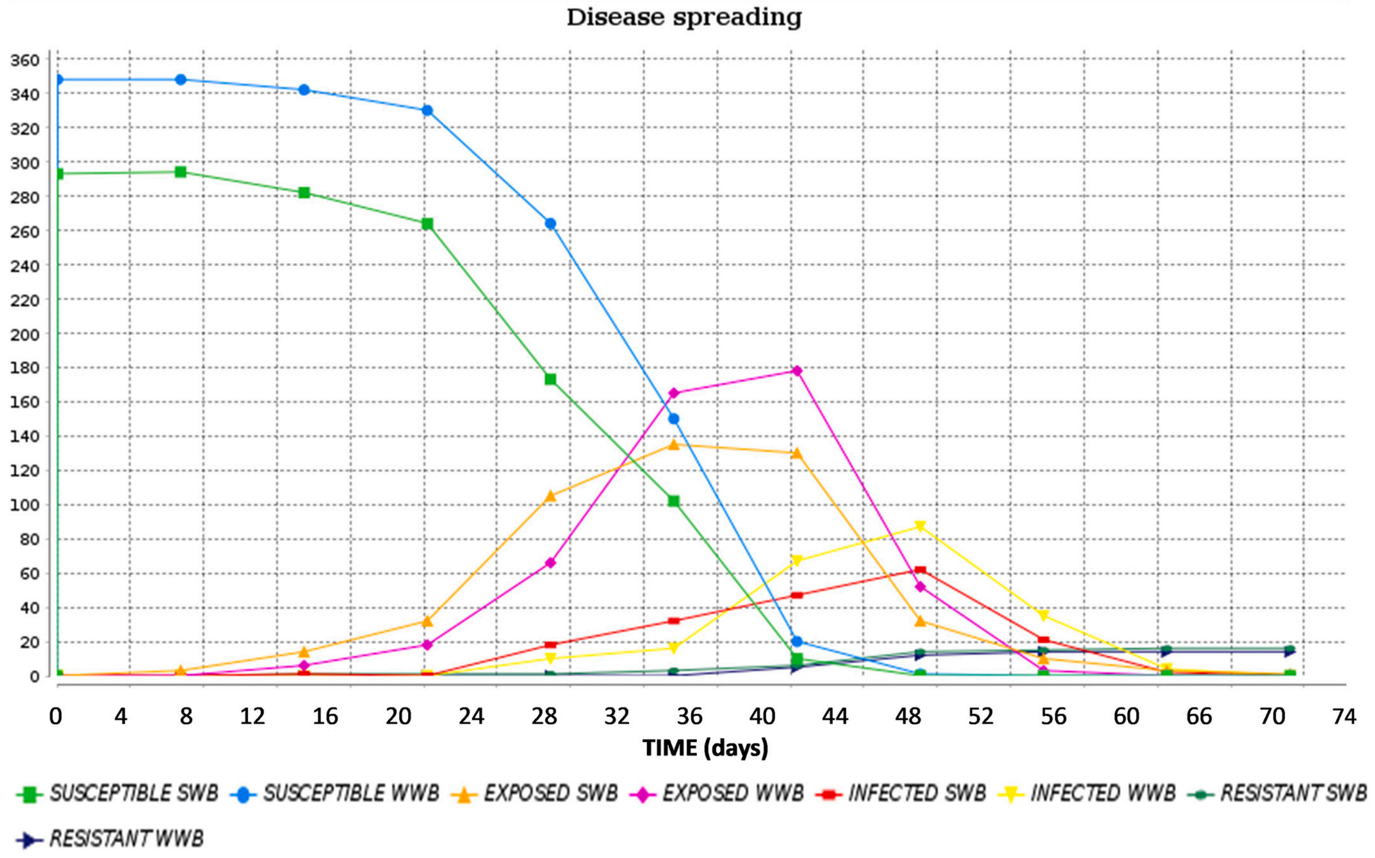


Fig. 4. Dynamics of the African swine fever virus outbreak in the wild boar (WB) population modelled. Each line shows the number of susceptible, exposed, infected and resistant non-urban (Wwb) and synurbic (Swb) WB agents.

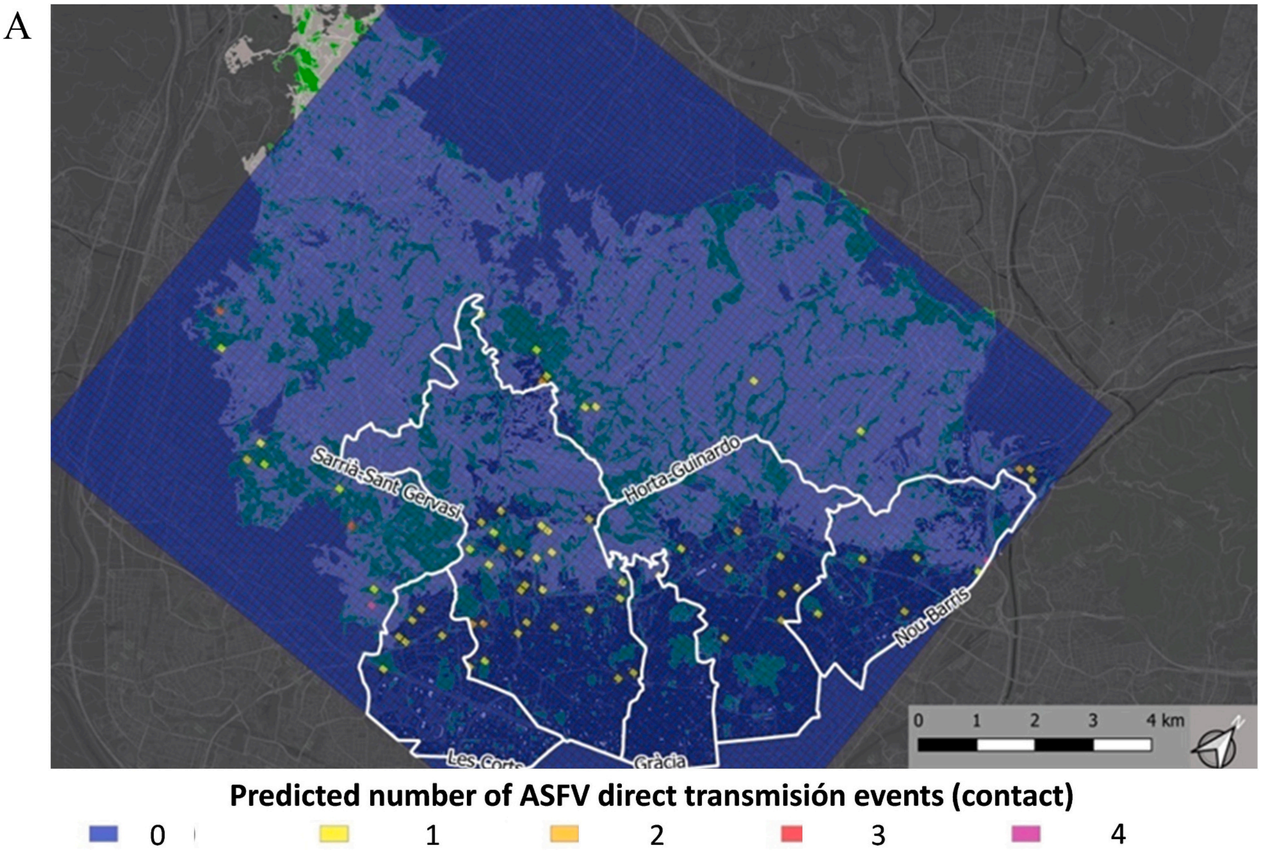


Fig. 5. Location and number of African swine fever virus (ASFV) transmission events over the study period predicted by the ASFV scenario. A) Direct transmission events between WB agents; B) Indirect transmission events from carcasses to WB agents. Cells are 100 m side.

on anthropogenic resources [12,13,16], which are a major concern and have provoked ASF outbreaks in WB populations in the past in urban areas [9,48,49,51].

ABM do not only provide realistic spatiotemporal framework, but also enable independent dynamic assessment of the environment. By programming WB and citizen agents accurately, the epidemiological extension also captured their spatial and temporal activity in the urban and natural ecosystems modelled, aligning with previous studies [55–57]. Overall, this ABM can be applied beyond the case study area of Barcelona as a powerful tool for local administrations to assess and manage the epidemiological risks posed by zoonotic pathogens in synurbic wildlife populations in urban areas. However, this model has calibration and validation limitations. A major challenge was the scarcity of published data on the epidemiological processes of zoonotic pathogens, which obliged to extrapolate transmission rates and population exposure [34,58–60]. As a result, the model may have overestimated transmission rates, leading to an overestimation of citizen exposure and worst-case risk assessment. However, the model's outputs were consistent with the estimated ranges provided by the WHO, suggesting good model performance despite these constraints. As more and more accurate epidemiological data become available, further model recalibration and refinement should improve its accuracy and predictive power.

As urbanization continues to expand, the risk of outbreaks of emerging diseases resulting from increased human-wildlife interactions in the new urban-wildlife-human interface is likely to continue increasing, requiring One Health approach and interdisciplinary cooperation among animal, public, and environmental health managers [2,3,16]. Improving knowledge on the evolving pathogen-host-environment relationships in each ecosystem and scenario is key to design effective surveillance systems and diagnose emerging pathogens [2,3]. This study demonstrates the usefulness and efficacy of ABM as an epidemiological decision-making support tool, adapted to the specific conditions and circumstances of the study area, as well as the specific conditions of human-wildlife interactions in the new urban-wildlife-human interface boosting the probability and consequences of disease outbreaks. Integration of urban biologists with human and animal health epidemiologists and healthcare professionals in urban planning and management is essential to reduce risks of emerging zoonosis transmission and anthropogenic disease outbreaks in wildlife, engaging in a One Health approach through interdisciplinary cooperation.

Data availability.

The data underlying this article are available in the article and in its online supplementary material.

Supplementary data to this article can be found online at https://doi.org/10.1016/j.onehlt.2023.100598.

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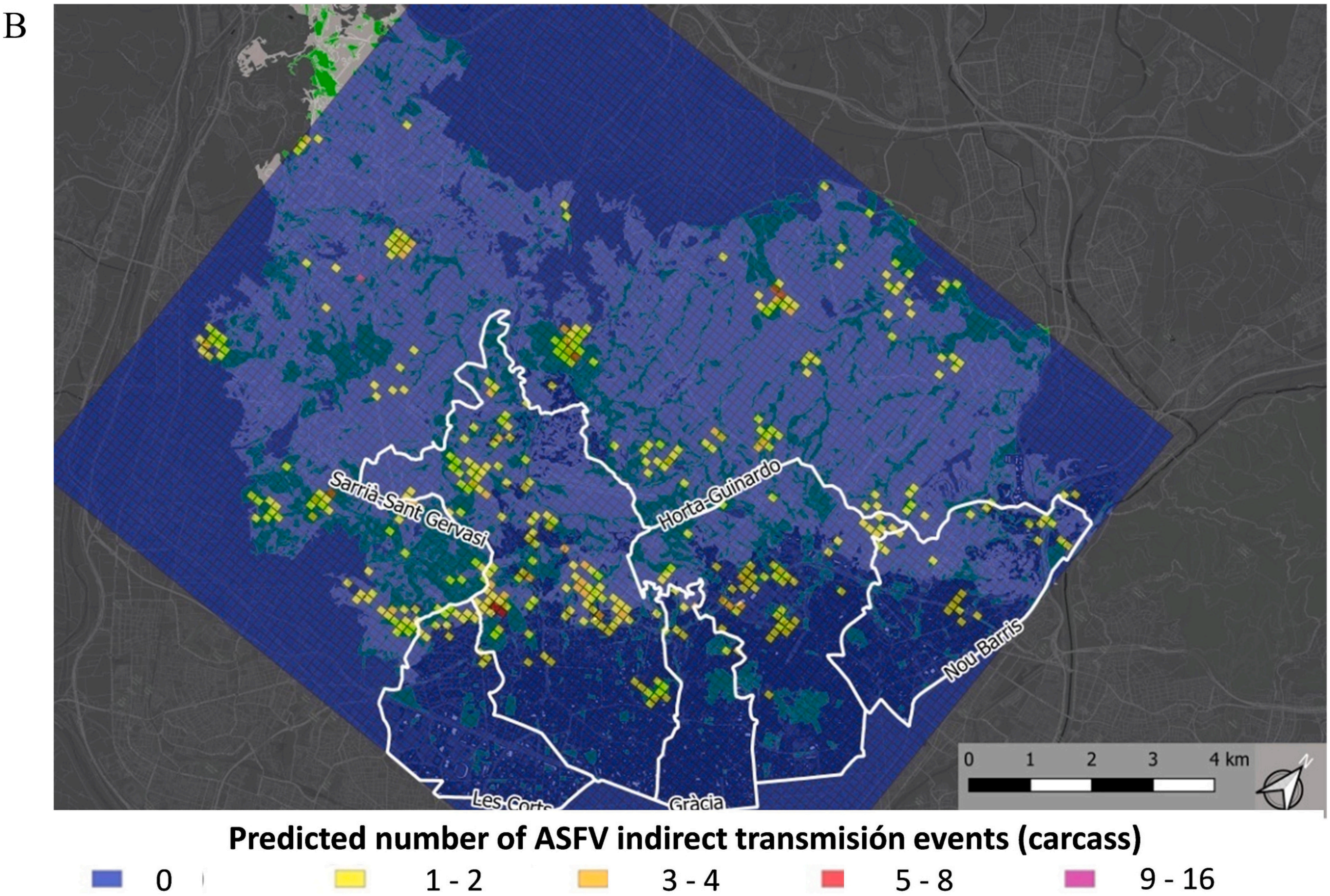

Fig. 5. (*continued*).

CRediT authorship contribution statement

González-Crespo Carlos: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Software, Writing – original draft. **Martínez-López Beatriz:** Conceptualization, Formal analysis, Investigation, Methodology, Software, Supervision, Writing – review & editing. **Conejero Carles:** Data curation, Investigation, Methodology, Writing – review & editing. **Castillo-Contreras Raquel:** Data curation, Investigation, Methodology, Writing – review & editing. **Serrano Emmanuel:** Conceptualization, Data curation, Investigation, Writing – review & editing. **López-Martín Josep Maria:** Data curation, Methodology, Writing – review & editing. **Serra-Cobo Jordi:** Funding acquisition, Resources, Supervision, Writing – review & editing. **Lavín Santiago:** Investigation, Methodology, Writing – review & editing. **López-Olvera Jorge Ramón:** Conceptualization, Data curation, Funding acquisition, Investigation, Project administration, Resources, Supervision, Writing – original draft, Writing – review & editing.

Declaration of Competing Interest

None declared.

Data availability

The data underlying this article are available in the article and in its online supplementary material

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