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LESSONS LEARNT FROM THE FIRST MODELLING CHALLENGE IN ANIMAL
HEALTH: IMPROVING PREPAREDNESS TO CONTROL AFRICAN SWINE FEVER
AT THE INTERFACE BETWEEN LIVESTOCK AND WILDLIFE

S. PICAULT*, P. EZANNO, S. BAREILLE, M. MANCINI AND T. VERGNE

SUMMARY

The 1st international modelling challenge in animal health aimed to improve the collective capacity to predict large-scale pathogen spread between livestock and wildlife and to support public decision during health crises. It provided an inspiring platform for exchanging knowledge and expertise. Comparing approaches allowed to assess the predictive capacity of models and identify areas for improving modellers' responsiveness facing a real crisis.

INTRODUCTION

Raising livestock in a sustainable and welfare perspective requires to manage animal health, especially infectious diseases which spread at large scale between animal populations (Ezanno et al., 2020). Health crises highlight the need for robust epidemiological knowledge and predictive tools to better cope with uncertainty, especially at the livestock-wildlife interface (Gortázar et al., 2007). Developing models that forecast disease spread is pivotal to better understand epidemics and to assess *ex ante* the efficacy of control measures (Grassly and Fraser, 2008), but doing so during an epidemic is extremely difficult. Modelling challenges, which are relatively short competitions, enhance cooperation between actors and modellers' ability to timely advise policy makers, improve the accuracy of model predictions and modellers' readiness when facing emerging threats, and promote international collaborations. After the first modelling challenge on seasonal influenza (Friedberg et al., 2015), annually renewed (Reich et al., 2019; Viboud and Vespignani, 2019), others were organized on Ebola (Viboud et al., 2018), Chikungunya (Del Valle et al., 2018) and Dengue (Johansson et al., 2019). However, none concerned an animal disease so far, while animal epidemiology has specific features which may induce different conclusions on the most suitable approaches and also require specific preparedness.

African swine fever (ASF) is an emerging disease currently spreading at the interface between wild boar and pig farms in Europe and Asia (Sánchez-Cordón et al., 2019). This viral disease is associated to a tremendous impact on swine production, livestock economy and international trade and neither a vaccine nor a treatment is available (Dixon et al., 2020). It is one of the most major livestock infectious disease threats for most countries as the virus can

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spread internationally via geographical proximity or due to movements of persons, swine and swine products (Vergne et al., 2017). To enhance the global preparedness to better face ASF epidemics, there is a need to consider explicitly the interface between livestock and wildlife, and to be able to assess various and combined control measures.

The objective of this paper is to present ASF Challenge, the first modelling challenge in animal health, the comparison of approaches mobilised by the five international teams involved, and to discuss lessons learnt throughout this process.

MATERIALS AND METHODS

Challenge organization

During the preparation step (July 2019-August 2020), a source model (called “M0”) was built to generate the synthetic data mimicking a ASF-like outbreak in a realistic west-European context. The challenge itself took place between August 27, 2020 and January 13, 2021. Three situation reports and synthetic epidemiological data corresponding to days 50, 80 and 110 after the detection of a first case, were released successively to the participants. These data were produced by the original model described below and represented detection events on pig farms or wild boar, with the location and cause of detection. Finally, the predictions of the participants’ models were compared and analysed.

Model M0 and simulated epidemics

The simulated outbreak was located on a hypothetical island built by aggregating the two French regions Auvergne-Rhône-Alpes and Occitanie, using three types of land use based on public GIS data[†] (agricultural, forest and urban) to define the location of individual wild boar and domestic pig farms. Assuming that the wild boar population was reduced by half during a hunting season, we used hunting bags per department provided by the *Office Français de la Biodiversité* (OFB) to determine the initial wild boar population (500,366) and distributed the centres of their home range randomly (80% in forest areas, 18% in agricultural areas, 2% in urban areas). The coordinates of the 4,775 pig farms registered in the two French regions were also randomly distributed as follows: 33% in Auvergne-Rhône-Alpes and 67% in Occitanie, and within each region 85% in agricultural areas, 10% in forests, 5% in urban areas. Besides, we endowed each farm with variable characteristics (size; commercial or backyard status; farrow, finisher, or farrow-to-finish; access to an outdoor area) which were used to generate a biosecurity score and simulate commercial movements between farms.

The synthetic epidemiological data were simulated using a stochastic, spatially-explicit agent-based model, with three kinds of agents: pig herds (compartmental sub-model), individual wild boar, and the whole island (as a metapopulation). A recent modelling software, EMULSION (Picault et al., 2019), was used for making model components explicit and more revisable.

In pig farms, we neglected natural mortality, thus driving the population only by pre-calculated commercial movements, sold animals being replaced with new ones. Wild boar were subject to hunting and natural mortality only. As the epidemic was taking place during the

[†] <https://www.diva-gis.org/>

hunting season (8 months), we indeed assumed no birth during the simulated period (Vetter et al., 2020).

Pigs and wild boar were categorised into mutually exclusive health states: susceptible (S), exposed i.e. asymptomatic but starting being infectious (E), fully infectious and symptomatic (I). All infected animals were assumed to die, resulting in an infectious carcass (C). Wild boar dying from natural causes produced either an infectious (C) or a healthy (D) carcass when E/I or S at death, respectively. In pig farms, carcasses were removed the next day, whereas wild boar carcasses could stay in the environment up to several months until fully decayed or removed by humans. The force of infection in pig farms was assumed density-dependent, with a higher transmission rate in backyard farms than in commercial farms.

We modelled several transmission pathways between epidemiological units. For pig farms, we considered: the movement of an infected pig from an infected farm, the contact with an infectious wild boar, and indirect contacts with infectious farms in the neighbourhood. For wild boar, we assumed contacts with infectious wild boar, with infectious carcasses, or with an infectious pig farm. Apart from pre-computed trade movements, all other transmission pathways were spatially explicit (based on transmission kernels) and, when farms were involved, depended on their biosecurity level and outdoor access.

Detection of ASF cases initially relied on passive surveillance: wild boar carcasses could be found and tested each day with a low probability, whereas each pig could be detected and tested each day and at death, with a probability that depended on the farm type (high in commercial farms, low in backyard farms). The detection of the primary outbreak resulted in increased detection probabilities. Current European regulatory measures were triggered immediately after the first detection, and applied to all confirmed pig farms: 1) the slaughter of all animals, 2) the installation of protection and surveillance zones subject to trade ban and increased vigilance, 3) the tracing of farms with recent trade contacts (same effect). Culled farms were repopulated after several weeks. Any infected wild boar carcass found was removed without delay and triggered an active search in the immediate neighbourhood, with a higher probability to find new carcasses. Also, a proportion of hunted wild boar were tested.

Several additional control measures were implemented successively in the simulation. First, assuming the forest near the primary case was a major threat, 300 km of fences were installed and became operational 60 days after the first detection. An increased hunting pressure started in the fenced area and in a buffer area around the fences, with systematic tests on hunted wild boar, the suspension of active search, and an increased probability of finding carcasses by passive surveillance. Then, 90 days after the first case, the detection of dead or alive infected wild boar led to the preventive culling (and testing) of all pigs from nearby farms.

Selection of synthetic data for the challenge

An exposed wild boar was introduced near a forest at the center of the island, a few weeks before the start of the hunting season. We ran 500 stochastic repetitions of the model to identify trajectories that were realistic enough and well suited for the challenge. After discarding those without any detection or detections later than 200 days after ASF introduction, we chose at random one of the trajectories that met five selection criteria: more than 250 infected wild boar before primary case detection to ensure disease installation in wildlife; primary case found in pig farm; less than 500 wild boar infected outside the fences at installation; more than 250 infected wild boar 110 days after primary case; and less than 30 infected wild boar 230 days after primary case (Fig. 1).

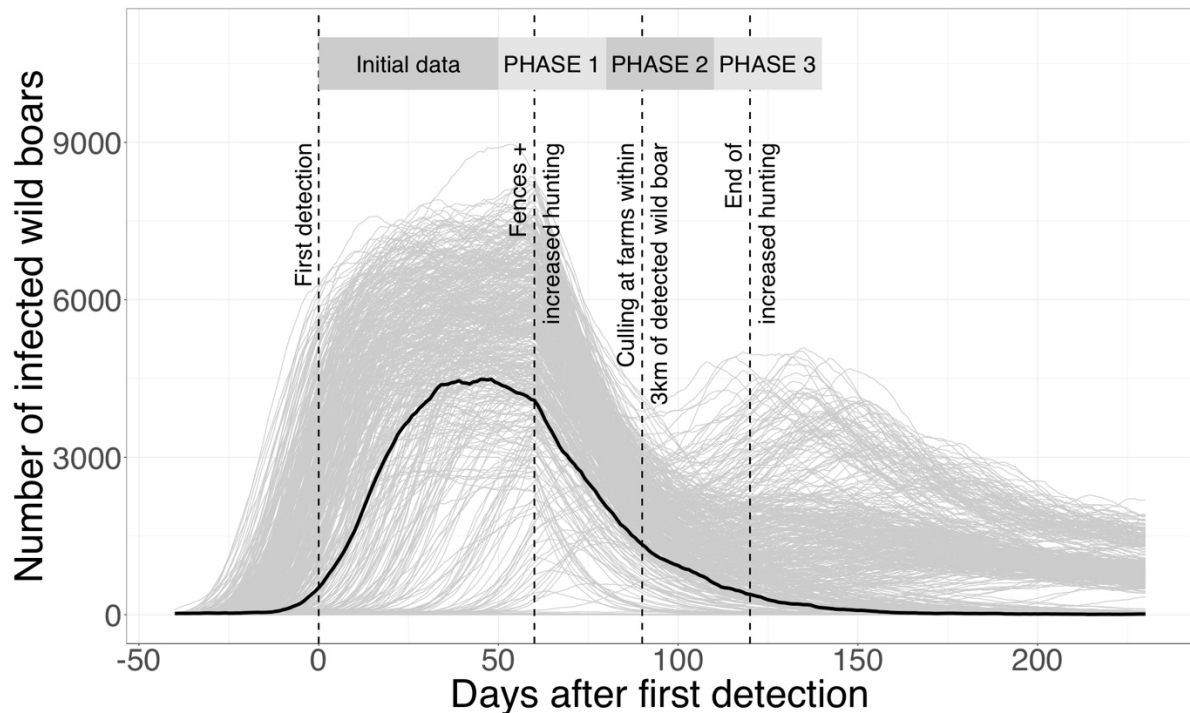


Figure 1. Temporal dynamics of the number of live infected wild boars (exposed + infectious) for the selected trajectory (black) and the stochastic repetitions where detection occurred before 200 days (gray), with the three prediction phases that followed the initial situation report. Vertical dashed lines: changes in control interventions.

Participants and their methods

Five modeller teams participated in the whole challenge (see Acknowledgements). In the narrative of the synthetic epidemics, phase 1 started 50 days after the detection of a first case in a pig farm near a forest. Participants were provided with a first situation reports and asked 1) to predict the number and location of wild boar and pig farm cases expected in the following 30 days, 2) to assess the effectiveness of surrounding the infected zone with fences, and 3) to advise on increasing hunting pressure in the fenced zone. At the end of phase 2 (110 days after first case), they were asked 1) to update their predictions on fences, now including a buffer zone and an increased hunting pressure, and 2) to advise on the effectiveness of five alternative control measures: culling all pigs from farms a) located within 3 km of a positive wild boar carcass, b) located in the protection zone, c) with a trade contact with an infected farm in the three preceding weeks; d) increasing the size of active search area around wild boar carcasses (from 1 km to 2 km); e) increasing the surveillance zone (from 10 to 15 km). At end of phase 3, teams were asked to update their predictions and estimate the fade-out probability for the next four months. Six weeks were left to the participants for answering each phase.

The participants were free to choose their own approach, hence developed either one single model or two separate models for wild boar/pig farm interactions, with a diversity of modelling paradigms and granularity regarding both the epidemiological and spatial units. Stochastic compartmental models were used almost for all epidemiological units (except “CIRAD” team which built a probabilistic model for pig farms). Wild boar were mostly modelled at individual scale (except “WUR” team which used a spatial area) and pigs at farm scale (except for “UK” team which used individual scale). Predictions were made at several spatial scales (discretized in squares, rectangles or hexagons) ranging from 1 to 195 km².

We compared their predictions regarding the temporal dynamics of ASF spread in pig farms and wild boar with the possible outcomes of model M0 in the same conditions, i.e. keeping the challenge trajectory up to the beginning of the prediction period, then simulating M0 from that point with the appropriate settings and new random seeds. For spatial predictions, we compared 1) the predicted probability for each pig farm to be infected with the locations of positive farms in model M0 with the same conditions, 2) the probability that each spatial unit contained an infected and detected wild boar with the locations of wild boar cases in M0.

RESULTS

Temporal model predictions

The temporal forecasts for pig farm cases were very good in most teams (Fig. 2A), whereas wild boar dynamics appeared much more difficult to capture (Fig. 2B). The installation of fences and increased hunting pressure was highlighted by most teams as difficult to integrate in their models.

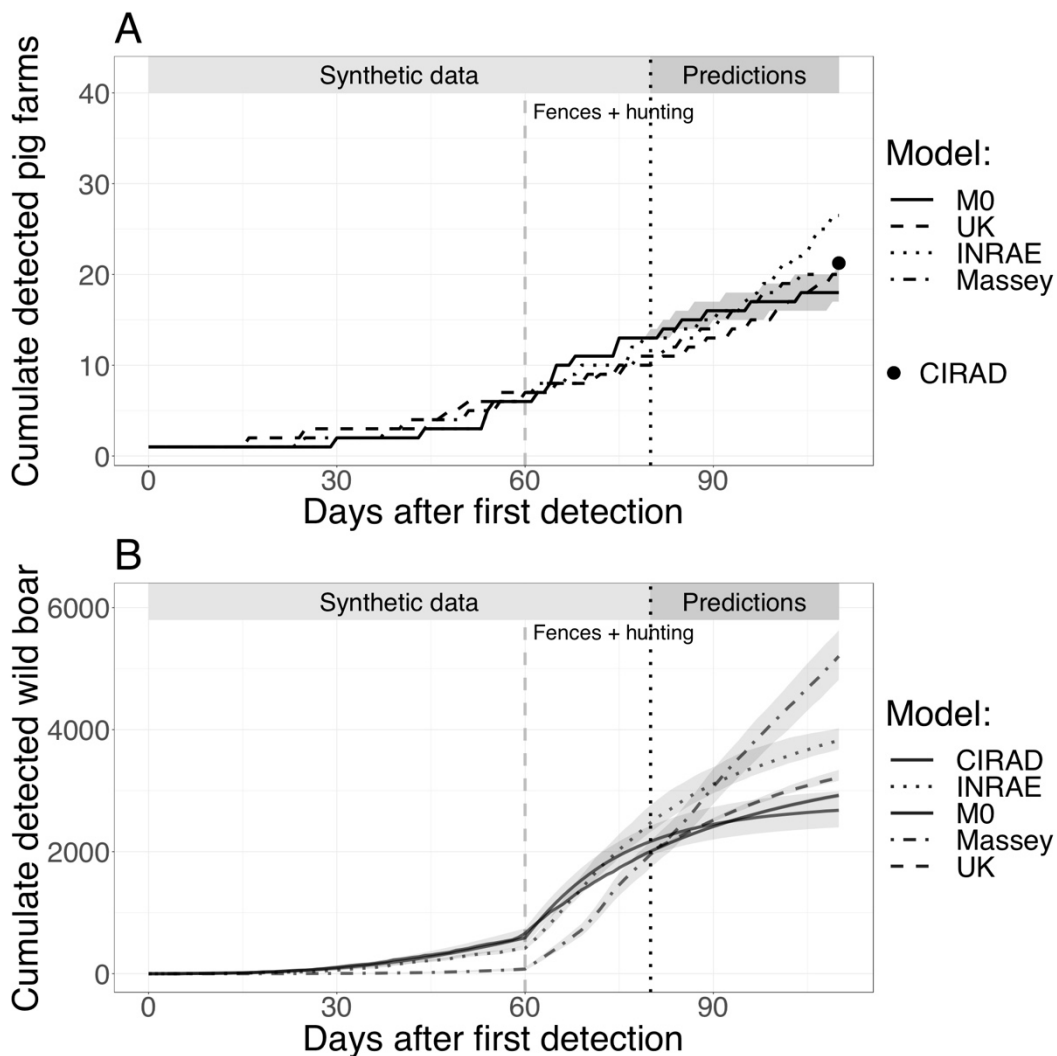


Figure 2. Median of the predicted numbers of detected pig farms (A) and detected wild boar (B) by each team during the second period of the challenge (days 80 to 110). Acceptable range of output variations is shown (10th to 90th percentiles obtained when running model M0 during the prediction period).

Spatial model predictions

Spatial predictions for pig farms (Fig. 3) were quite good (including one team, CIRAD, which successfully predicted the occurrence of a distant case due to trade contacts). Besides, the regulatory measures based on protection and surveillance zones do not require to predict the exact location of infected farms, since an increased vigilance may be sufficient to ensure reactivity on detection and culling.

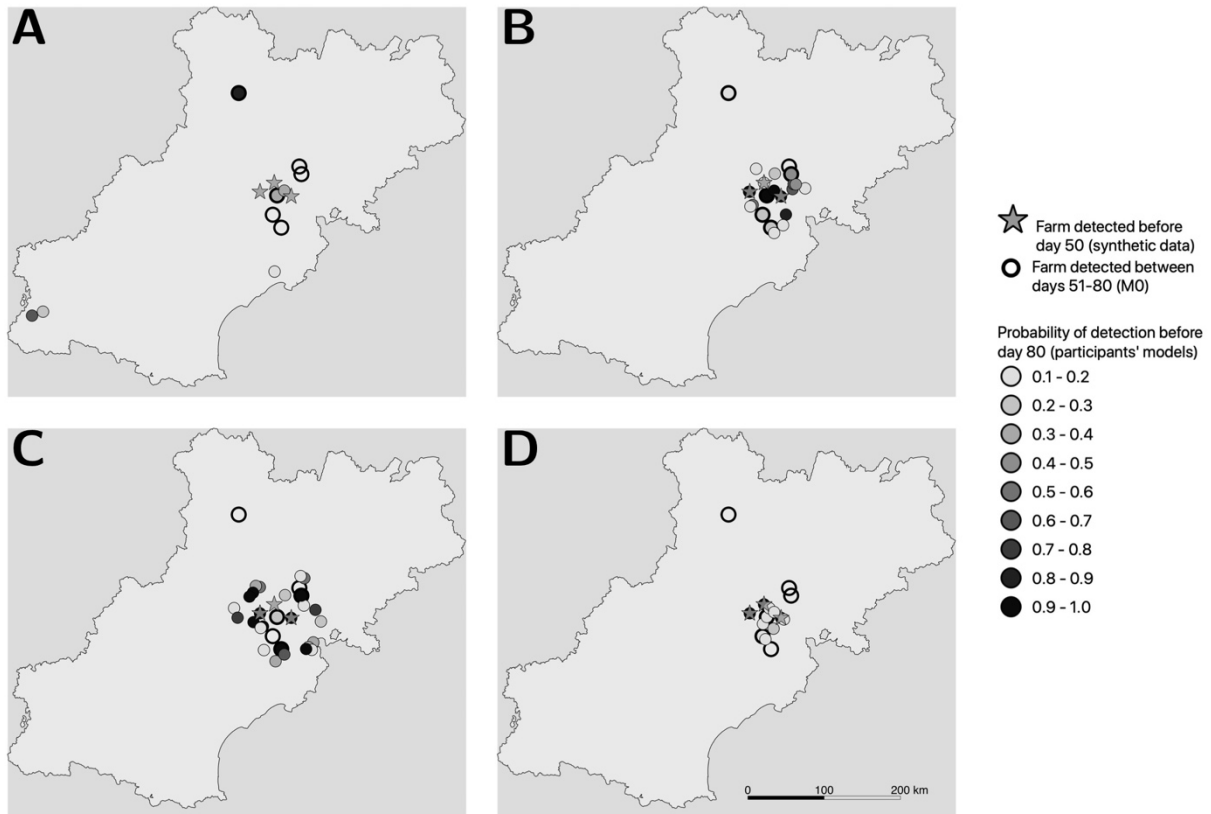


Figure 3. Detected pig farms between days 50 and 80 as predicted by each team (black circles: farms that would have been detected in model M0 with the selected trajectory in the absence of additional control measures). A: CIRAD; B: UK; C: Massey Univ.; D: WUR.

Spatial predictions regarding wild boar cases were much more heterogeneous, both in their granularity (e.g. from 1 km² to 195 km² tiles) and in the spread patterns (Fig. 4), reflecting the diversity of assumptions made by each team on wildlife and making the comparisons quite difficult.

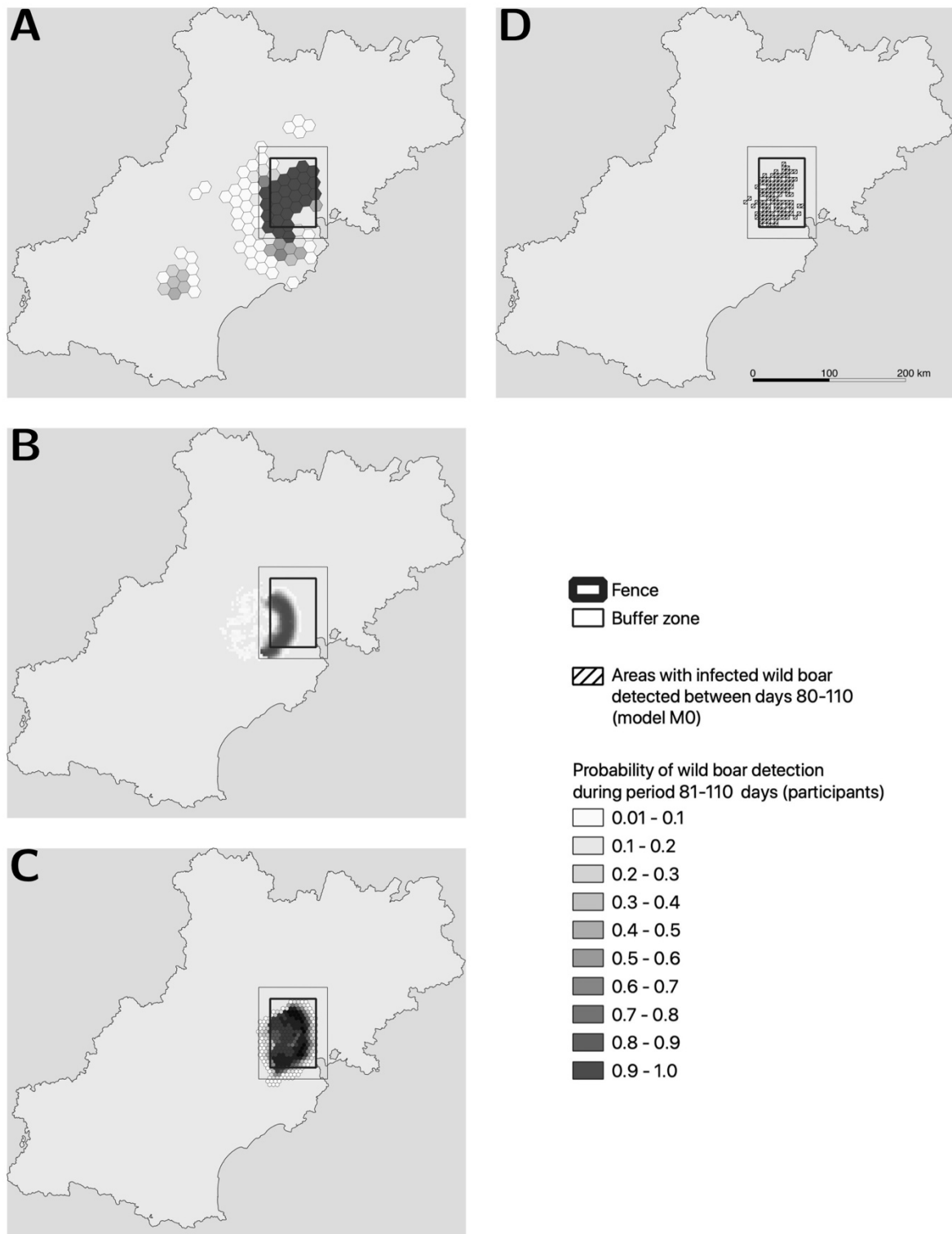


Figure 4. Predicted probability to detect infected wild boars between days 80 and 110, without additional control measures after day 80, as calculated by two teams: INRAE (A, 195 km² tiles), Massey Univ. (B, 1 km² tiles), and CIRAD (C, 86.8 km² tiles) compared to wild boar cases found in model M0 (D, 25 km² tiles).

DISCUSSION

Modelling challenges organized in human health over the last decade demonstrated their considerable value for the development and assessment of modelling and forecasting methods (Ajelli et al., 2018). The ASF Challenge, that ran between August 2020 and January 2021, was the first modelling challenge in animal health. Using a new mechanistic and stochastic metapopulation and multi-host model of ASF spread, we generated synthetic data mimicking an ASF-like epidemic detected at the interface between pig farms and wild boar in a typical European context. Land use, size and location of farms, as well as wild boar hunting bags per administrative units were derived from real data in the southern quarter of France. ASF incidence data (detected cases) were provided to the modelling teams while the epidemic developed. The objectives for the teams involved in the challenge were to reproduce the synthetic epidemic assuming a set of control strategies, predict its expansion and prioritize a finite number of alternative interventions. We compared 5 independent modelling approaches and their qualitative and quantitative spatio-temporal predictions over the three one-month periods of the challenge.

To make this challenge interesting and useful, the model that generated the synthetic epidemiological data needed to be more detailed than the different models that could be developed by participants to make their predictions. Hence, data generation were computationally intensive and calibrating the model to generate interesting and realistic “ASF-like” epidemic trajectories was extremely time-consuming, especially because of the lack of data on wild boar population dynamics and mobility patterns and their expected impact on fences’ efficacy.

The context of ASF provided an opportunity to address the specificities of infectious livestock diseases at the interface between wildlife and domestic farms. Still poorly observed (Vicente et al., 2021), this interface is key to increasing our effectiveness in controlling emerging animal diseases. All participants acknowledged the interest of explicitly modelling interactions at the interface between domestic and wild fauna to accurately predict the course and extent of the epidemics and account for the impact of control measures. The temporal and spatial predictions on domestic pigs were more accurate than for wild boar, which highlights the diversity on assumptions made on wild boar population dynamics and contact patterns due to the lack of knowledge on wildlife. Also, intensive hunting, a key control measure against ASF, was one of the most problematic feature to introduce in models (for participants and organisers), and their potential impact on wild boar ecology, possibly including increased contacts (Lange, 2015), was not modelled.

No specific modelling approach was better than all others on every prediction, and the added-value of their complementarity for policy makers will be addressed in further studies through ensemble models both for the temporal and spatial dynamics. This diversity, which was intentional in the challenge, also led to heterogeneous output formats, which made comparisons difficult and suggested stricter specifications for further challenges.

The choice of producing fictitious data as in the Ebola challenge (Viboud et al., 2018), rather than using historical records, required much work but provided the organisers with a total control and knowledge on the situation, on the noise level in the synthetic data (e.g. a proportion of small farms were not known from the beginning and discovered by participants as they became infected), and on the “representativity” of the selected trajectory compared to possible model outcomes. Such open international challenges are a privileged framework to anticipate emerging infectious diseases, including zoonotic threats at the interface between wildlife,

livestock and human activity, and to improve the readiness of modelling teams to face future epidemics.

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